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2016

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THE GENETIC BASIS OF SINGING ABILITY: A TWIN STUDY

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Submitted in total fulfilment of the requirement of the degree of
Doctor of Philosophy

September, 2016

Melbourne Conservatorium of Music

THE UNIVERSITY OF MELBOURNE

Produced on Archival Quality Paper

Abstract

Music is a human universal, an integral part of all known human culture. While most people possess the capacity for music perception and production, individual differences in various forms of music abilities are evident in the general population. The diversity in abilities has sparked intense debates regarding the relative importance of nature and nurture in shaping music ability. While in recent years, researchers have begun to explore the genetic basis of music perception abilities, the interrogation of the genetic basis of music production abilities has been relatively scarce. Singing is an ideal paradigm for investigating the genetic basis of music ability; it is a universal, multifaceted music ability that is spontaneously emergent and shaped by formal and informal music learning environments. The present study therefore employed a twin study design to investigate the genetic basis of singing ability and estimate the relative contribution of genetic and environmental factors influencing singing ability using a comprehensive set of singing tasks and measures. The study also aimed to identify environmental factors associated with singing ability and examine whether these factors have a genetic component, and whether shared genetic influences might explain the association between singing ability and these factors. The twin study was conducted online using a purpose-built online program *Let's Hear Twins Sing*, which enabled twins to participate regardless of their geographical location. The 30 minutes online twin study comprised three singing tasks (vocal pitch-matching, singing a familiar song, and melody imitation), two music perception tasks and a questionnaire on music and singing background. The study took approximately 30 minutes to complete and the study data were captured online in real-time and saved on a server for subsequent analyses. The final sample consisted of 70 monozygotic (55 female; 15 male) and 38 dizygotic (24 female; 7 male; 7 male-female) twin pairs (mean age = 32.4 years), the majority were recruited through the Australian Twin Registry. Univariate genetic modelling revealed that both the objectively-assessed singing ability across all tasks and self-rated singing ability had similarly significant and substantial genetic components ($A = 69-72\%$). Additive genetic influences also contributed significantly to the variation observed in various singing task measures, with moderate to large heritabilities ($A = 44-71\%$), negligible to moderate common environmental ($C = 0-37\%$) and moderate unique environmental ($E = 19-40\%$) influences. Significant moderate to large genetic components were also estimated for environmental variables associated with singing ability: instrumental expertise ($A = 68\%$), years of music training ($A = 46\%$), and public singing engagement ($A = 66\%$). Bivariate genetic analyses revealed that the associations between singing ability and both instrumental expertise and years of music training were mediated significantly by shared additive genetic influences. The novel findings therefore provided preliminary evidence for the role of genes in influencing singing ability and formal music training, as well as a partially shared genetic basis for singing ability and music training. The promising results establish a valuable background that encourages further behavioural and molecular genetic interrogations into the genetic bases of various types of music abilities.

Declaration

This is to certify that

1. The thesis comprises only my original work toward the PhD, except where indicated in the Preface.
2. Due acknowledgement has been made in the text to all other material used.
3. The thesis is less than 100,000 words in length, exclusive of tables, maps, bibliographies and appendices.

Yi Ting Tan, September 2016

Preface

The content of Chapter 2 (The Genetic Basis of Music Ability) in this thesis was adapted from the following multi-authored publication in which the candidate was the first author.

Tan, Y. T., McPherson, G. E., Peretz, I., Berkovic, S. F., & Wilson, S. J. (2014). The genetic basis of music ability. *Frontiers in Psychology*, 5.

The layout and the tasks of the online program, Let's Hear Twins Sing, as outlined in Chapter 5, were designed by the candidate, with advice from her supervisors and Professor Isabelle Peretz. The program itself was entirely developed and implemented in Adobe Flash by Mr. Mark Solly.

The study was primarily funded by an internal grant from the Melbourne Neuroscience Institute. This PhD was also supported by the International Postgraduate Research Scholarship (IPRS) and Australian Postgraduate Award (APA) funded by the Australian Government, as well as John Hodgson Scholarship and Faculty Small Grant awarded by the Melbourne Conservatorium of Music.

Acknowledgements

First and foremost, I would like to thank all the twins who volunteered their time to take part in the online twin study, especially those who helped to remind or persuade their twin to participate, as well as those who helpfully introduced the study to other potential participants — this study would not have been possible without their interest and willingness to participate. I am also very thankful to the staff at the Australian Twin Registry, especially Ms Jenny Boadle, Ms Janine Lam and Ms Shaie O' Brien, for their help and support throughout the entire recruitment phase.

I would also like to thank my supervisors, Professor Gary McPherson and Professor Sarah Wilson for generously sharing their wealth of knowledge and research experience with me throughout my candidature. The work in this thesis could not have been achieved without their guidance, support and encouragement. A special thanks also goes to Associate Professor Neil McLachlan, Professor Isabelle Peretz and Professor Sam Berkovic, who had provided helpful insight and feedback on methodological development and interpretation of the behavioural and genetic findings, and Mr. Mark Solly for his help with implementing the online program.

I am also extremely grateful for the expert advice offered by Professor Yi Xu, Dr. Robert Kirkpatrick, Professor Nick Martin, Associate Professor Hermine Maes, and many other helpful researchers on the OpenMx Behavioral Genetics Forum. I really appreciate them taking the time to respond to my questions on sound analysis or behavioural genetic analysis via email or the forum. Their patience and willingness to help a newbie researcher whom they have never met before really inspire me to do the same when the opportunity arises. I would also like to thank Dr. Sandy Clarke from the statistical department, not only for her professional advice in statistics, but also for her friendship and prayers these past few years.

A big thank-you also goes out to my dear friends and fellow colleagues, Solange Glasser and Valerie Yap. I feel very blessed to have such faithful friends during this long PhD journey, whose presence remind me that I am not alone in this battle, and often lend a listening ear to me and encourage me to keep going. I would also like to thank my dear parents, my family and friends who have constantly supported me with their love, words of encouragement and prayers. An exceptionally big thank-you to my dear sister Evelyn, for being one of the greatest blessings in my life — taking such good care of me and offering her unconditional love and support while I was swamped with my research. Finally, I would like to thank God, who has truly been with me through all the ups and downs that I have encountered, sustaining me physically, emotionally and spiritually. This PhD journey has led me into a deeper experience of His faithfulness and grace. Without Him, I am nothing.

But He said to me, "My grace is sufficient for you, for my power is made perfect in weakness." Therefore I will boast all the more gladly about my weaknesses, so that Christ's power may rest on me. (2 Corinthians 12:9)

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List of Abbreviations

<i>A</i>	Proportion of trait variance due to additive genetic effects
ACC	Anterior cingulate cortex
AIC.....	Akaike's Information Criterion
aINS	Anterior insula
AP	Absolute pitch
ATR	Australian Twin Registry
AVP	Arginine vasopressin
Bpm.....	Beats per minute
<i>C</i>	Proportion of trait variance due to common environmental effects
CNV	Copy number variation
CNVR	Copy number variable regions
dPFC	Dorsal prefrontal cortex
dPMC	Dorsal premotor cortex
DZ	Dizygotic
DZF.....	Dizygotic female twins
DZM.....	Dizygotic male twins
DZO	Dizygotic opposite-sex twins
<i>E</i>	Proportion of trait variance due to unique environmental effects
f_0	Fundamental frequency
FTP.....	File Transfer Protocol
GWAS.....	Genome-Wide Association Study
HDAC	Histone-Deacetylase
ICC.....	Intraclass correlations
ID	Mean absolute interval deviation
IFG	Inferior frontal gyrus
IPS.....	Intraparietal sulcus
KD.....	Key deviation
KMT.....	Karma Music Test
LOD	Logarithm of odds score
LTD.....	Long-Term Depression

M1	Primary motor cortex
MBEA	Montreal Battery of Evaluation of Amusia
<i>Mdn</i>	Median
MIDI	Musical Instrument Digital Interface
MZ	Monozygotic
MZF	Monozygotic female twins
MZM	Monozygotic male twins
NGS	Next-Generation Sequencing
PAG	Periaqueductal grey
PCM	Pulse-code modulation
PD	Mean absolute pitch deviation
PPL	Posterior probability of linkage
PPLD	Posterior probability of linkage disequilibrium
PT	Planum temporale
R^2	Multiple correlation squared; measure of strength of association
r_{MZ}	Intraclass correlation of monozygotic twins
r_{DZ}	Intraclass correlation of dizygotic twins
<i>SD</i>	Standard deviation
SEM	Structural equation modelling
Sib RR	Sibling relative risk
SINGCOMB	Combined singing score (averaged from all singing task measures)
SMDT	Swedish Musical Discrimination Test
SMA	Supplementary motor area
SNP	Single-nucleotide polymorphism
SP	Seashore Pitch Test
SPT	Cortex of the dorsal Sylvian fissure at the parieto-temporal junction
ST	Seashore Time Test
STG	Superior temporal gyrus
STS	Superior temporal sulcus
VBA	Visual Basic for Applications
VSL	Vocal sensorimotor loop
WAV	Waveform Audio File Format

Gene nomenclature

<i>ADCY8</i>	Adenylate Cyclase 8
<i>ATP5J</i>	ATP Synthase, H ⁺ Transporting, Mitochondrial Fo Complex Subunit F6
<i>ATP5L</i>	ATP Synthase, H ⁺ Transporting, Mitochondrial Fo Complex Subunit G
<i>AVPR1A</i>	Arginine Vasopressin Receptor 1A
<i>CASP8</i>	Caspase 8
<i>CCR4</i>	C-C Motif Chemokine Receptor 4
<i>CDH7</i>	Cadherin 7, Type 2
<i>CDH19</i>	Cadherin 19, Type 2
<i>CHRNA9</i>	Cholinergic Receptor, Nicotinic, Alpha Polypeptide 9
<i>CLN8</i>	Ceroid-lipofuscinosis, neuronal 8
<i>COMT</i>	Catechol-O-methyltransferase
<i>DOPEY2</i>	Dopey Family Member 2
<i>DUSP1</i>	Dual Specificity Protein Phosphatase 1
<i>EPHA7</i>	Ephrin Type-A Receptor 7
<i>FAM49B</i>	Family with Sequence Similarity 49, Member B
<i>FKBP8</i>	FK506 Binding Protein 8
<i>FOS</i>	FBJ Murine Osteosarcoma Viral Oncogene Homolog
<i>FOXP1</i>	Forkhead Box P1
<i>FOXP2</i>	Forkhead Box P1
<i>GALM</i>	Galactose Mutarotase (Aldose 1-Epimerase)
<i>GATA2</i>	GATA Binding Protein 2
<i>GPR98</i>	G Protein-Coupled Receptor 98
<i>GRIN2B</i>	Glutamate Receptor, Ionotropic, N-Methyl D-Aspartate 2B
<i>GSG1L</i>	Germ Cell-Specific Gene 1-Like
<i>GZMA</i>	Granzyme A
<i>HDAC4</i>	Histone Deacetylase 4
<i>HDC</i>	Histone Deacetylase Complex
<i>IL1A</i>	Interleukin 1, Alpha
<i>IL1B</i>	Interleukin 1, Beta;
<i>KCTD8</i>	Potassium Channel Tetramerization Domain Containing 8
<i>KLF4</i>	Kruppel-Like Factor 4

LOXHD1 Lipoxygenase Homology Domains 1
NDFIP1.....Nedd4 Family Interacting Protein 1
NPTN Neuroplastin
NRGN.....Neurogranin
PCDH7.....Protocadherin 7
Pcdha 1-9.....Protocadherin Alpha 1 to 9
PDGFRA.....Platelet-Derived Growth Factor Receptor, Alpha Polypeptide
PHOX2B Paired-Like Homeobox 2b
RAPGEF5 Rap Guanine Nucleotide Exchange Factor (GEF) 5
RGS9.....Regulator of G-Protein Signaling 9
ROBO1 Roundabout Guidance Receptor 1
SLC6A4.....Solute Carrier Family 6 (Neurotransmitter Transporter, Serotonin),
Member 4
SNCA.....Synuclein, Alpha
TPH1 Tryptophan Hydroxylase 1
TRPA1 Transient Receptor Potential Cation Channel, Subfamily A,
Member 1
UGT8 Uridine Diphosphate Glycosyltransferase 8
UNC5C.....UNC-5 Homolog C (C. elegans)
USH2A Usher Syndrome 2A
VLDLR Very Low Density Lipoprotein Receptor
ZDHHC11 Zinc Finger, DHHC-Type Containing 11

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1

THESIS OVERVIEW

Music is widely regarded as a human universal (Blacking, 1995; Brown, 1991) and a fundamental component of the human design (Welch & Adams, 2003). Music's ubiquity across all cultures, its importance in social and religious practices, its evocative power in eliciting and communicating a myriad of emotions, the sheer pleasure one experiences from music-making and music listening... all of these properties suggest that music is a realm worthy of careful exploration, so as to understand this special attribute which makes us uniquely human.

While not everyone is able to play a musical instrument, all humans possess an endogenous musical instrument: our vocal apparatus. Humans are therefore equipped with the necessary physical capacity to make music vocally. In addition, the ability to sing appears to emerge spontaneously without requiring formal musical training. From approximately two months onwards, infant babbling already contains definite musical features such as pitch and rhythmic patterns (Tafuri & Villa, 2002), and by age two, a clear distinction between speaking and singing behaviour emerges as infants begin to sing short phrases of melodies (Dowling, 1984; Gembris, 2006). Some researchers have also observed that in the majority of the general population, good pitch-matching skill appears to develop naturally with age without the need for formal instruction (Bentley, 1969).

Despite its early emergence, singing ability, whether self-reported or objectively measured, seems to vary across the general population (Amir, Amir, & Kishon-Rabin, 2003; Pfordresher & Brown, 2007). A sizeable portion of the population believe that they are not able to sing in tune. In a sample of 1,105 university students, 59% reported that they could not accurately imitate melodies (Pfordresher & Brown, 2007). In another sample of 2,000 university students, approximately 17% of the students believed that they were "tone deaf" (Cuddy, Balkwill, Peretz, & Holden, 2005). While tone deafness (scientifically known as congenital amusia) in reality refers to a pitch perception deficit

(Peretz, Champod, & Hyde, 2003), the general public tend to associate tone deafness with a low level of singing ability, as revealed by a factor analysis in the same study.

Even though difficulty in pitch discrimination would understandably affect singing accuracy, the actual prevalence of congenital amusia is low, and estimated to be less than 4% (Henry & McAuley, 2010; Kalmus & Fry, 1980; Pfeifer & Hamann, 2015). The stark difference in the proportions of people who self-report as inaccurate singers and people who are classified as congenital amusics suggest two possibilities. One possibility is that the general population may be unduly harsh on their singing ability. A study conducted by Dalla Bella, Giguère, and Peretz (2007) supported this, as the majority of the participants ($N = 62$) drawn from the general population were able to sing a familiar melody with reasonable accuracy, making few pitch interval errors that exceeded one semitone. Their pitch accuracy further improved when they sang at a slower tempo. The findings were replicated in a follow-up study comprising 39 participants with no formal music training (Dalla Bella & Berkowska, 2009). In another study, 87% of the participants were able to imitate novel 4-note melodies accurately, within one semitone from the pitch targets (Pfordresher & Brown, 2007). Another possibility is that out-of-tune singing may occur independently from a pitch perception deficit. Several studies have confirmed this. Pfordresher and Brown (2007) reported that 10 to 15% of the participants made pitch errors exceeding one semitone from the targets when imitating novel melodies, despite possessing comparable pitch discrimination ability as that of accurate singers. Dalla Bella et al. (2007) also described two participants who were markedly out-of-tune when singing a familiar melody, and yet performed above average for the pitch perception task. Hutchins and Peretz (2012) demonstrated that both musically trained and musically untrained groups of participants were more accurate pitch-matching manually using a slider than matching the same target pitches vocally. Their overall findings also suggested there are possibly multiple causes underlying inaccurate singing, an opinion already espoused by Dalla Bella and Berkowska (2009), whose study findings showed a diversity of poor singing “phenotypes”.

The variability in singing ability in the general population as well as the diverse patterns of inaccurate singing lead us to ask: What could have caused such variability in

singing? Are some people naturally good singers, or do environmental factors have an overriding influence on singing ability?

There is evidence that gives credence to both positions. Anecdotally, singing ability appears to cluster in families (e.g., the Jackson 5, the Bee Gees and the Osmonds). Findings from a behavioural study also suggested there may be an inborn aspect to singing accuracy. Watts, Murphy, and Barnes-Burroughs (2003) identified individuals who had no formal vocal training and yet consistently performed better on pitch-matching tasks, even when compared with trained singers who had at least three years of professional vocal training. A large study involving 1,008 participants from 73 extended Mongolian families also yields evidence that pitch accuracy in singing may be heritable in this population (estimated heritability of 40%) and possibly associated with a linkage region on chromosome 4q (Park et al., 2012).

On the other hand, the influence of cultural environment on singing abilities is particularly evident in some non-Western cultures. Compared with children from Western culture, Zimbabwean children display precocious singing ability (Koops, 2011; Kreutzer, 2001). Likewise, Gambian and Venda children are also “expected to be musical” because in their musically-rich cultural environment, there are frequent opportunities for music participation (Koops, 2011; Radocy & Boyle, 2012). While the ability to harmonise is considered a specialised singing skill in Western societies, part-singing is an indispensable element in the Fijian singing culture, whereas singing in unison and solo singing are not commonly practised (Russell, 1997). In Western culture, however, various social and cultural influences may have created an environment where singing participation is no longer commonplace (Whidden, 2010). This may be why a considerable portion of the Western population possess such low self-perceptions of their own singing proficiency (Cuddy et al., 2005; Pfordresher & Brown, 2007). These findings suggest that the development of singing expertise can be influenced by one's exposure to culture-specific musical expectations, activities and forms.

The nature-nurture question is not foreign to the domain of music. In fact, it has been the subject of much debate for over a century. Initially people might have believed more readily in the existence of inborn predisposition to the development of music expertise, based on anecdotal accounts as well as case studies of musical child prodigies and

families (Galton, 1876). Advances in the field of behavioural science, however, with its increased emphasis on carefully designed scientific studies, have brought about significant change which sees the importance of environmental factors being increasingly lauded by educationists and psychologists in the development of musical expertise. Propositions of the existence of natural endowment have been relegated by some to the realms of “folk psychology” (Sloboda, 2005), as if such a standpoint is unlikely to be substantiated by rigorous scientific research. Some have even gone as far as suggesting that innate talent is a “myth” (Howe, Davidson, & Sloboda, 1998), and expert performance in music can be chiefly explained by deliberate practice over an extended period (Ericsson, Krampe, & Tesch-Römer, 1993). Despite this, there remain staunch proponents of the existence of predisposed inter-individual variability in music abilities (Gagné, 2004; Lykken, 1998; Simonton, 2005; Winner, 2000), as well as many others who at least deem it premature to discredit the nature account totally without judicious scientific inquiry. Examples include the commentaries by numerous noted researchers (Plomin, 1998; Rowe, 1998; Rutter, 1998; Sternberg, 1998; Vitouch, 1998), in response to the contentious review by Howe et al. (1998).

Indeed, in the most comprehensive meta-analysis on the heritability of human traits to date, based on twin studies over the past 50 years, there was compelling evidence that all human traits are heritable, with an estimated average heritability of 49% across all traits (Polderman et al., 2015). Therefore, instead of imposing a false dichotomy between nature and nurture, a more pertinent question to ask is: What are the relative contributions of nature and nurture to singing ability, or music ability in general?

Although numerous environmental factors influencing music and singing ability have been identified (Aherne, 2011; Atterbury & Silcox, 1993; Brand, 1986; Persellin, 2006), most of these studies have only examined these environmental components in and of themselves, without considering how genes may influence or interact with them (Sternberg, 1998; Vinkhuyzen, Van Der Sluis, De Geus, Boomsma, & Posthuma, 2010). A few studies published recently have spearheaded a paradigm shift to reconcile the roles of genes and environment in the development of music ability, and in particular, examining environmental factors in light of potential genetic influences. A meta-analysis revealed that although deliberate practice is positively correlated with expert performance in various domains, it could only account for 21% of the variance in music

performance, which implies that a large percentage of individual differences in music ability remain unexplained (Macnamara, Hambrick, & Oswald, 2014). Moreover, a genetic basis for music practice has been reported by two different twin studies, with estimated heritabilities ranging from 38% to 69% (Hambrick & Tucker-Drob, 2014; Mosing, Madison, Pedersen, Kuja-Halkola, & Ullén, 2014). Both studies also revealed that the correlation between music practice and music ability is partially mediated by shared genetic influences. In addition, Hambrick and Tucker-Drob (2014) observed gene-environment interactions whereby a genetic contribution to music accomplishment was larger for participants who engaged in music practice (heritability = 43%) as compared to those who reported no music practice (heritability = 1%). It is therefore warranted that more studies should continue in this direction and explore the relationship between environmental factors and music ability using genetically sensitive experimental designs.

A survey of the handful of genetic studies on music ability reveals that a majority have placed undue emphasis on tests of music perception such as pitch and rhythm discrimination to operationalise music ability (Tan, McPherson, Peretz, Berkovic, & Wilson, 2014). Music production abilities however, are equally important in defining musicality (McPherson & Hallam, 2008). Singing ability, in particular, is worthy of greater attention. Of all the music production abilities, the ability to sing is distinct from the others because it appears to be a natural human disposition. Its early and spontaneous emergence, ubiquitous existence in human societies and functional importance in the social context allow the investigation of singing ability to provide fruitful insights into the origins of music behaviour (Peretz, 2009). So far, there has only been one familial molecular genetics study on singing ability as measured by a vocal pitch-matching task (Park et al., 2012). Given the multi-faceted nature of singing ability, a simple pitch-matching task is unlikely to fully capture singing ability in all its complexity, nor enable the identification of aspects of singing ability that are more heritable compared to those that are more influenced by environmental factors such as music training. Furthermore, there have not been any behavioural genetics studies that formally assess singing ability through objective measures. In previous twin studies, singing ability only featured as a subcomponent of musical ability and the competence levels were based on self-report questionnaires. The reliability of these findings may thus be disputable (Coon & Carey, 1989; Vinkhuyzen, Van Der Sluis, Posthuma, &

Boomsma, 2009). Consequently, there is an apparent gap in the literature for studies that examine singing ability objectively while taking both genetic and environmental influences into account.

Given that singing entails manifold nested subskills, as well as its status as the most universal means of music making, it provides a valuable model for investigating the genetic basis of music abilities. Such genetic interrogation can help advance knowledge about the level at which genetic factors and gene-environment interplay shape complex human behaviours. From a music education perspective, understanding the extent to which individual differences in singing and music abilities are explained by genetic influences will provide compelling grounds for the development of more individually tailored educational and community-based music learning programs, which are better suited to a person's background, skills and abilities. This can potentially help foster positive experiences with singing and music, thereby motivating individuals to maintain active engagement in these activities across the lifespan and enjoy the numerous physical, cognitive, emotional and social benefits music and singing afford.

In view of the research gaps identified above, as well as the appropriateness of singing ability as a model to interrogate the genetic basis of music ability, this thesis aimed to investigate the relative contributions of genetic and environmental components underpinning singing ability using a classical twin design. It was the first twin study to examine the heritability of singing ability in depth, using both objectively-assessed tasks and measures of singing ability, as well as subjectively-assessed singing ability based on self-report. Furthermore, following the examples of recent behavioural genetic studies on music ability, this study aimed to identify environmental factors associated with singing ability in order to explore whether these factors are also underpinned by genetic influences, and whether some of these genetic influences were also implicated in singing ability.

Besides interrogating the genetic basis of singing ability, the use of assorted singing tasks also enabled the current thesis to inspect how singing proficiency varied across tasks or measures. Collectively, the behavioural and genetic findings presented in this thesis served to advance our understanding of the nature of singing ability and provide insights into the individual differences in singing proficiency across the population.

This thesis is organised into three main parts. The first part (Chapters 2 to 4) reviews the literature pertaining to the nature of music ability and singing ability. Chapter 2 covers the genetic basis of music ability and provides an introduction to the behavioural and molecular genetic approaches commonly employed in music genetic studies, followed by the accumulated genetic evidence for music ability and music-related phenotypes to date. In Chapter 3, an overview of the environmental determinants of music ability is presented, grouped according to cultural, home and formal music learning environments. This chapter concludes with a consolidation of the genetic and environmental determinants of music ability in a schematic representation. The nature of singing ability is detailed in Chapter 4, beginning with an outline of the typical developmental trajectory for singing ability, followed by a description of a neurocognitive model of singing and the neural correlates underlying the sensory-motor control of singing. The chapter then built a case for singing as an ideal model for investigating the genetic basis of music ability. This chapter concludes with a statement of study aims and hypotheses which are then addressed in the subsequent chapters.

In the second part of the thesis, methods developed to conduct the study are first described in Chapter 5, including the design and development of an online singing and music program, as well as the technical development of this online software. The study methods are then described in Chapter 6, including the details about the participants, task measures, how the acoustical data were processed, the study procedure, and the proposed statistical analyses for the behavioural and genetic analyses.

Chapters 7 to 11 form the third part of the thesis. To contextualise the subsequent genetic findings, Chapter 7 reports the descriptive statistics of the singing and music task performances, self-reported interests and abilities in singing and music, and the singing and music background components that were extracted from the questionnaire. The rest of the chapter examines potential variables that might have confounded task performance and questionnaire responses. A discussion of these behavioural findings is provided in Chapter 8. The genetic findings are then detailed in Chapter 9, organised according to the study aims and hypotheses. The intraclass correlations of monozygotic and dizygotic twins and the estimated genetic and environmental contribution on the various singing task measures and self-rated abilities and interests are reported first,

followed by the genetic analyses on the singing and music background components associated with singing ability. The possibility of partially shared genetic basis between the background components and singing ability is then interrogated by bivariate genetic analyses. The genetic findings are discussed in Chapter 10. Finally, Chapter 11 provides a summary of the key findings and discusses their broader implications on research and education. The limitations of the current study and recommendations for future work are then presented, followed by some concluding comments.

2

GENETIC BASIS OF MUSIC ABILITY

2.1 The Nature of Music Ability

The term “music ability”, owing to the heterogeneous nature with which the phenotype presents itself, can be considered as a generic, umbrella term which encompasses assorted musical subskills. The multifaceted nature of music ability means that it could refer to one or more subskills that can be so diverse that they are mutually exclusive (Levitin, 2012). For example, music ability could mean being able to label or produce a pitch without external reference (i.e., absolute pitch), or technical prowess in playing an instrument, or creative power in composing an opus.

While different researchers may have different concepts about what music ability should entail (Law & Zentner, 2012), to adequately account for the various ways music ability presents itself, it can be delineated into a number of component skills that are broadly categorised as perceptual or productive music skills for the purpose of this literature review. The fractionation of music ability into different musical sub-phenotypes is also beneficial for uncovering the genetic basis of music ability (Levitin, 2012; Tan et al., 2014). Given the heterogeneity of the phenotype for music ability, it is unlikely that there exists one single “music” gene that influences all assorted musical skills. Instead, as with other complex human traits, music ability and its sub-phenotypes are likely influenced by multiple genes with different effect sizes (Plomin, Owen, & McGuffin, 1994). Delineating music ability into more precisely defined sub-phenotypes will thus enable molecular genetic studies to detect genes implicated in each subskill with greater sensitivity and also direct more research efforts toward those subskills that have been scantily researched (Tan et al., 2014).

The subskills considered in the two broad categories of music perception and production abilities are adapted from two studies that have covered a wide scope of music perception and production skills, respectively, in their development of assessment measures of these skills (Law & Zentner, 2012; McPherson, 1995). **Figure 2.1** shows a tree diagram of music ability and its constituent music perception and production subskills. Music perception comprises six main subskills in evaluating pitch, melody, tuning (chord intonation), rhythm, tempo and timbre (Law & Zentner, 2012), whereas music production consists of seven main types of music performance skills, namely the abilities to sight-read, to perform rehearsed music from a score, to perform from memory, to play by ear, to improvise, to compose and to arrange music. The first five of these music production skills overlap with the types of music performance skills identified by McPherson (1995). Composing and arranging music are added to the figure because these abilities can also be considered important forms of music production ability. As these seven types of music production abilities assess music production at a macroscopic level, six additional subskills (in the dashed oval) analogous to the music perception subskills are appended to the music production skills to clarify the musical subskills needed for the execution of a music performance. In addition, the arrow pointing from music production to music perception indicates how music production abilities are essentially contingent on music perception abilities.

Although the musical subskills listed in **Figure 2.1** are by no means exhaustive, they serve to provide a useful heuristic for the ensuing literature review on the genetic and environmental determinants of music ability presented in Chapters 2 and 3. It will be apparent from the literature reviews that some of the musical subskills, such as those pertaining to music perception, have featured more frequently and prominently in current research, while others have received comparatively less attention. There are also other forms of music ability that have not been investigated in the nature-nurture debate and this lies beyond the scope of the current literature review. Examples include musical expressivity to convey emotions through music performance, and when listening, musical sensitivity to discern the emotional content of a piece of music.

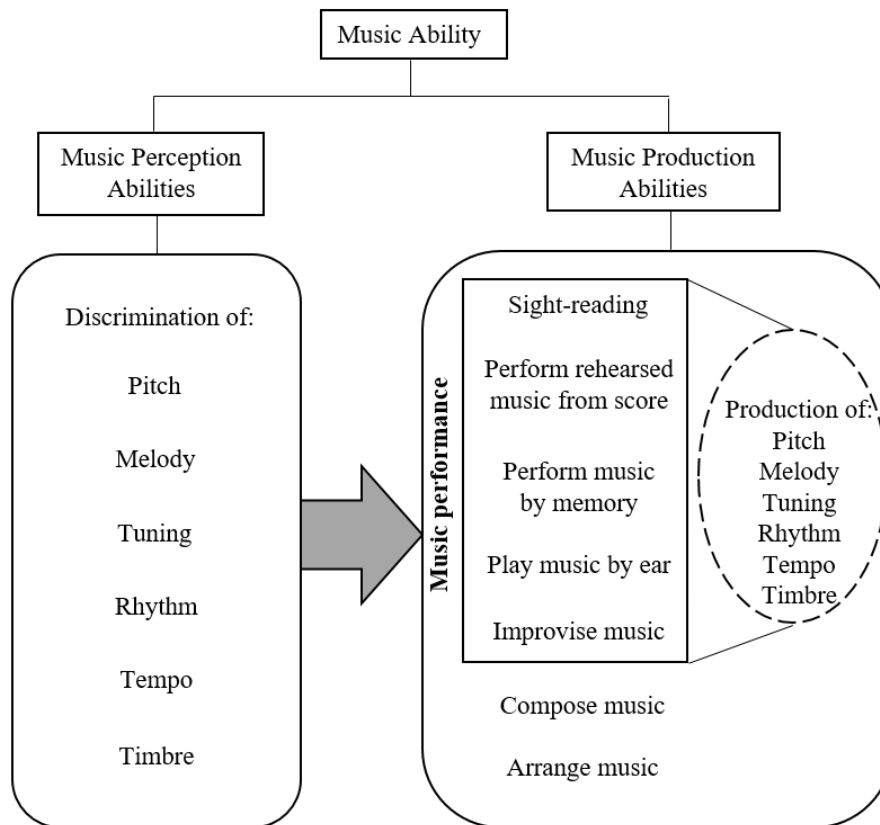


Figure 2.1. Music ability and its constituent perception and production subskills.

In the remainder of this chapter, **Sections 2.2** and **2.3** describe the behavioural and molecular genetic approaches commonly used in human genetic analyses and **Section 2.4** then provides an overview of what is currently known about the genetic basis of music ability, by consolidating the behavioural and molecular genetic findings on music-related traits that have been investigated to-date.

2.2 Behavioural Genetic Approaches

2.2.1 Familial aggregation

One of the first questions asked in human genetic analysis is whether a trait clusters in families above chance level. Familial aggregation can address this question by comparing whether the prevalence of a trait is higher within the family of a proband¹ than what is expected in the general population (Naj, Park, & Beaty, 2012). This

¹ A proband is the first person within a family who is ascertained to exhibit the trait of interest.

approach is non-invasive because only phenotypic information is gathered from the families and controls. One common measure arising from familial aggregation is the sibling recurrence-risk ratio (λ_s), which determines the proportion of proband siblings also exhibiting the studied trait, relative to the population prevalence. The magnitude and patterns of familial correlations observed in familial aggregation studies can yield useful clues to the roles played by genes and the environment (Naj et al., 2012). While a λ_s close to 1 suggests genetic influences are unimportant, higher values (>5) indicate that a genetic hypothesis is worth pursuing (Mitry et al., 2011). A related measure is the sibling relative risk (sib RR), which is the ratio of the proband λ_s to the control λ_s .

It is important to note, however, that familial aggregation measures such as λ_s may be inflated by ascertainment bias (Guo, 1998). Moreover, familial aggregation only serves to determine the existence of familial clustering. It does not seek to explain how much of the familial clustering is due to genetic or environmental factors. Such questions can be addressed through follow-up studies, such as twin and adoption studies.

2.2.2 Twin studies

Twin studies take a step further to investigating genetic influences by disentangling the relative contributions of genetic and environmental factors on trait variation (Verweij, Mosing, Zietsch, & Medland, 2012). Using twin studies, the effects of additive genetic influences, common environment (shared environment), and unique (unshared) environment on the variation of a trait within a sample or population can be estimated. Common environmental influences include family environment, which are experienced similarly by each pair of twins raised in the same household. Unique environmental influences, on the other hand, refer to divergent experiences that are only experienced by one twin and not the other, such as different social groups or education. Monozygotic (MZ) twins share nearly 100% of their genes whereas dizygotic (DZ) twins share on average 50% of their genes.

As the degree of within-twin-pair similarity for a trait is essentially the sum of effects due to shared genes and common environmental influences, it can be inferred that any excess of MZ similarity relative to DZ similarity is due to a greater degree of shared genes between the MZ twin pairs, hence suggesting a genetic basis for the trait.

In univariate twin analyses, the most basic model is the ACE model, which decomposes the total trait variance into the proportion of variance due to additive genetic (A), shared environmental (C) and unique environmental (E) effects (Eaves, Last, Young, & Martin, 1978; Neale & Cardon, 1992). A graphical representation of the model is shown in **Figure 2.2**.

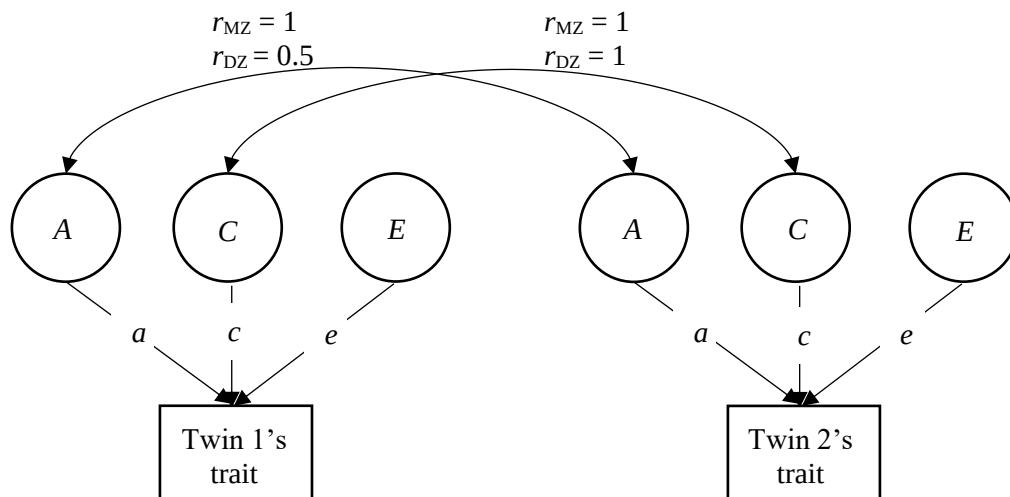


Figure 2.2. Classic ACE model. The single-headed arrows (a , c , e) are the path coefficients that reflect the effects of latent variables, ie. additive genetic (A), common environmental (C), and unique environmental (E) influences, on the observed trait of the twins. The curved double-headed arrows across the top represent the correlations between a pair of twins for a particular latent variable; r_{MZ} is the correlation between an MZ twin pair, whereas r_{DZ} is the correlation between a DZ twin pair.

As can be observed from **Figure 2.2**, MZ twin pairs correlate perfectly for the additive genetic component A as they share almost 100% of their genes. DZ twin pairs, however, only correlate 0.5 for A since they share on average 50% of their genes. As for the common environmental component C, the correlation is 1 for both MZ twin pairs and DZ twin pairs, assuming both twins were raised in the same household. Unique environmental influences, E is uncorrelated between the twins. In addition to A, C and E, non-additive genetic effects such as dominance (D) can potentially be a source of trait variance.

A rudimentary way to estimate the variance components would be to compute the intraclass correlations (ICC) for MZ and DZ twins separately and algebraically solve for

the variance components using Falconer's formula (Rijsdijk & Sham, 2002). The total trait variance in an ACE model can be expressed as

$$V = A + C + E$$

If the total variance is standardised (i.e., scaled to 1), the equation is expressed as

$$a^2 + c^2 + e^2 = 1$$

where a^2 , c^2 and e^2 are the standardised squared path coefficients representing the covariances between a twin pair due to additive genetic (A), common environmental (C) and unique environmental (E) effects, respectively.

As the similarity or correlation between a pair of twins is the sum of the genetic and common environmental effects, the intraclass correlation coefficients, r , of MZ twins and DZ twins are therefore

$$\begin{aligned} r_{MZ} &= a^2 + c^2 \\ r_{DZ} &= 0.5a^2 + c^2 \end{aligned}$$

Solving algebraically the above equations will therefore yield the following solutions:

$$\begin{aligned} a^2 &= 2(r_{MZ} - r_{DZ}) \\ c^2 &= 2r_{DZ} - r_{MZ} \\ e^2 &= 1 - r_{MZ} \end{aligned}$$

By examining the ICCs, we can therefore assess the relative importance of A , C and E on the trait variance. For instance, if r_{MZ} is approximately twice the size of r_{DZ} , based on Falconer's formula, c^2 is negligible whereas a^2 explains a large proportion of the trait variance. In contrast, if r_{MZ} and r_{DZ} are of comparable magnitude, c^2 is likely to be large while a^2 is negligible.

The Falconer approach, however, while adequate as a preliminary gauge of expected contributions of the different variance components, has some serious limitations. For

example, negative estimates of variance components may arise, preventing meaningful interpretation of the results. Moreover, confidence intervals cannot be estimated for the parameters. In addition, it is not possible to estimate the parameters in more complex models, such as testing for sex differences or simultaneously analysing more than one trait, nor is it possible to compare the relative goodness-of-fit of one model to another (Rijsdijk & Sham, 2002). Therefore, twin analyses now typically use structural equation modelling (SEM) to estimate the variance components by means of maximum likelihood model-fitting techniques. The relative merits of SEM include providing useful information about parameter estimates, confidence intervals and model-fitting (Rijsdijk & Sham, 2002). OpenMx is a specialised software which can perform SEM in R, an open-source software environment for statistical computing (Neale et al., 2016). The following section describes in greater detail how univariate and bivariate genetic analyses are typically conducted using SEM.

2.2.2.1 Structural equation modelling (SEM)

In SEM, model parameters are estimated by iteratively adjusting the values of the unknown parameters until the discrepancies between actual data and the predicted model are minimised. The optimal parameter estimates for a particular model can be estimated using the maximum-likelihood criterion, where maximum log-likelihood will yield parameter estimates that result in the least discrepancy between actual data and the fitted model (Rijsdijk & Sham, 2002).

a) Univariate analysis

Testing equality of means, variances and covariances

Prior to fitting univariate ACE models to estimate the variance components for the task and questionnaire measures, basic assumptions concerning the equality of means and variances within twin pairs and across zygosity were tested. In an ACE model, the means and variances within twin pairs and across zygosity are set to be equal, as it is assumed that all twins in the sample come from the same base population, regardless of zygosity. To test the validity of this assumption, a saturated model in which the means, variances and covariance were free to vary within twin-pairs and across zygosity was first built. Subsequent nested models with increasing constraints imposed on means and variances were then fitted and the goodness-of-fit of the nested models relative to the

saturated model were evaluated by likelihood ratio chi-square difference tests. A non-significant chi-square difference ($p > .05$) between a model and the saturated model means that the model is not significantly different from the saturated model, and therefore the imposed constraints on the means and variances remain compatible with the data. Conversely, a significant p value indicates that the current model is a poor fit to the data and suggests that the current imposed constraint of equal means or variances across co-twin or zygosity may not be valid. In such cases, univariate analysis for the particular measure would not proceed further.

Similarly, covariances of the various zygosity groups can be constrained to test for potential sex limitation effects in the variation of a trait. There are two types of sex-limitation effects; quantitative sex limitation is said to occur if magnitudes of the genetic or environmental variances differ between sexes, whereas qualitative sex limitation refers to instances where variation of a trait is caused by different types of genes for males and females. A lower DZO covariance compared to those of DZM and DZF is often indicative of a qualitative sex limitation. Therefore, to assess whether a quantitative sex limitation was present, models that constrained the covariances between male and female twins of the same zygosity to be equal were built (i.e., $Cov_{MZF} = Cov_{MZM}$; $Cov_{DZF} = Cov_{DZM}$) and compared with the saturated model. If the covariances could be equated without significant worsening of model fit, this would suggest an absence of quantitative sex differences and thus both the female and male groups of the same zygosity could be combined. Correspondingly, if the covariance of the DZF, DZM and DZO groups could all be equated without significant deterioration of model fit from the saturated model, this would suggest a lack of evidence for qualitative sex differences, thus allowing all three DZ groups to be pooled.

Model-fitting

For each performance measure derived from the tasks and questionnaire, in addition to fitting the full ACE model, where all three model parameters (A , C and E) were estimated, nested submodels such as AE, CE and E were fitted to the data. The AE model was built from the full ACE model by dropping the C parameter. Likewise, the CE and E submodels were built by dropping A and both A and C , respectively. The goodness-of-fit of the submodels was compared to the full ACE model by likelihood ratio tests. If the chi-square difference between a nested submodel and the full ACE

model was significantly different, this meant that the dropped parameter was significantly greater than zero, thus suggesting its importance in explaining the trait variance. Besides goodness-of-fit, the principle of parsimony was also taken into account when choosing the best-fitting model. According to the principle of parsimony, the simpler, nested submodel with fewer parameters is preferred over the full ACE model, provided that there is no significant worsening of fit, as indicated by the chi-square difference statistic. To this end, Akaike's Information Criterion (AIC) is used to determine the best-fit model (Akaike, 1987). AIC adjusts the chi-square statistic for the number of estimated parameters, and it can be used to compare models that are fitted to the same data, even if they are not nested (Schermelleh-Engel, Moosbrugger, & Müller, 2003). Among all the competing models fitted to the same data, the model with the lowest or most negative AIC offers the best balance between goodness-of-fit and parsimony. However, one study has cautioned against using AIC to determine the best-fitting model in the case of discrete (e.g., ordinal) data, as it was shown that the AIC-guided model tended to choose the incorrect model and resulted in upward-biased parameter estimates, especially when the sample size was small (Sullivan & Eaves, 2002). Although the same study showed that AIC model selection was robust for continuous data and hence the caution above was unlikely to be applicable in this case, both the parameter estimates from the full ACE model and the submodel with the lowest AIC were examined for completeness.

b) Bivariate analyses

While univariate genetic modelling allows the estimation of the proportion of variances due to *A*, *C*, and *E* for a single variable, bivariate analysis can be employed to examine the extent to which genetic and environmental influences explain the association between two traits.

One common bivariate model is the Cholesky decomposition model, where the first trait's latent *A*, *C*, *E* factors are loaded on both traits, while the second trait's latent *A*, *C* and *E* factors are only loaded on the second trait. **Figure 2.3** shows an illustration of the bivariate Cholesky model.

After fitting the full bivariate ACE model, additional submodels can be fitted to the data to test the significance of correlations due to *A*, *C* and *E*, respectively. This is achieved

by removing the additive genetic, shared, or unique environmental influences common to both traits (i.e., constraining a_{21} , c_{21} or e_{21} to zero) in turn in each submodel, and examine whether the removal of a_{21} , c_{21} or e_{21} would deteriorate the fit to the data significantly relative to the full bivariate ACE model. Significant fit deterioration will be reflected by a significant chi-square difference test ($p < .05$) from the full bivariate ACE model, and it indicates that the dropped component a_{21} , c_{21} or e_{21} is significant in explaining the association between both traits. For instance, if a submodel which constrained a_{21} to zero significantly differs from the full bivariate model, it suggests that shared additive genetic influences significantly mediate the association between the two traits, which means the two traits have a partially shared genetic basis.

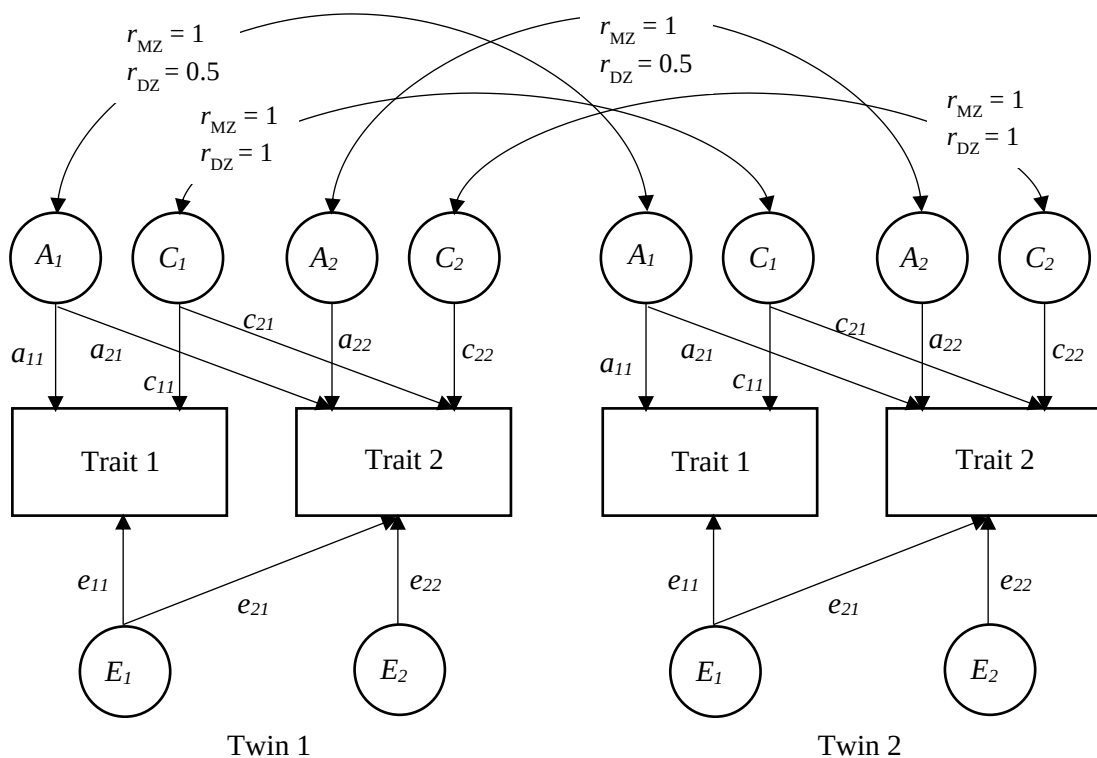


Figure 2.3. The bivariate Cholesky model. The measured/observed traits for Twin 1 and for Twin 2 are shown in the boxes. Latent factors are shown as circles. a_{11} , c_{11} , e_{11} and a_{22} , c_{22} , e_{22} are the additive genetic, common environmental and unique environmental effects acting on Trait 1 and Trait 2, respectively, whereas a_{21} , c_{21} , e_{21} are the additive genetic, common environmental and unique environmental influences common to both Trait 1 and Trait 2.

There are some criticisms surrounding the validity of twin studies given that the twin design is built on a number of assumptions (Richardson & Norgate, 2005). For instance, the “equal environment” assumption presupposes that regardless of zygosity, all twins

raised together experience equally similar common environments. Some research, however, suggests that MZ twins may be treated more similarly than DZ twins (Plomin et al., 1976, but see Borkenau et al., 2002).

Besides twin studies, heritability can also be estimated from family pedigrees. Heritability in the narrow sense (h^2) is the ratio of the additive genetic variance to the total phenotypic variance of a trait, which is equivalent to the standardised additive genetic component, a^2 . Since the magnitude of h^2 can indicate the statistical power for discovering the causal genes of a trait, heritability estimation serves as a good precursor to molecular genetic studies (Bochud, 2012). If the h^2 estimates of multiple related traits are available, the trait with the best h^2 estimate can be chosen for subsequent gene mapping. In human research, the general consensus is that h^2 estimates below 0.2 are considered low, those between 0.2 and 0.5 are moderate, and estimates above 0.5 indicate high heritability. High h^2 estimates suggest that the genotype is closely correlated with the trait phenotype, but it should be noted that this does not necessarily imply that every gene associated with the trait has a large effect on the phenotype (Visscher, Gordon, & Neale, 2008). Some limitations of heritability estimation include a lack of information on the mode of inheritance of the trait, and the possibility that h^2 estimates may vary across populations or with time. In large pedigrees, there may also be cohort effects across different generations living under different socioeconomic circumstances, which may confound the “equal environment” within the sample population (Bochud, 2012).

2.2.3 Segregation analysis

After estimating the heritability of a trait of interest, the mode of inheritance of the trait can be elucidated through segregation analysis. Different segregation models representing various inheritance patterns of the trait are fitted to the family data. Using maximum likelihood procedures, the genetic model of best fit (i.e., the inheritance pattern which best explains how the trait is transmitted down the family line) can be identified. An important measure from segregation analysis is the segregation ratio, which is the proportion of offspring who inherit the trait of interest from a parent (Strachan & Read, 1999). The expected segregation ratios for autosomal dominant

inheritance² and autosomal recessive inheritance³ are 0.5 and 0.25, respectively. As these expected segregation ratios are for Mendelian traits, deviation from these values indicate that the trait of interest may have incomplete penetrance, be predisposed by several genes in different loci, or that it is determined by both genetic and environmental factors. For instance in a study by Theusch and Gitschier (2011), absolute pitch was reported to have a segregation ratio of .089, which suggests that the trait is not inherited in a simple Mendelian fashion. Similar to familial aggregation, a potential problem with segregation analysis is ascertainment bias, which may inflate the segregation ratio (Nandram, Jai-Won, & Hongyan, 2011; Strachan & Read, 1999). It is possible, however, to statistically correct for this type of inflation (Li, Chakravarti, & Halloran, 1987; Li & Mantel, 1968; Nandram et al., 2011; Yao & Tai, 2000).

Segregation analysis often serves as a precursor to parametric linkage analysis, as the latter requires the inheritance pattern of the studied trait to be specified (Schnell & Sun, 2012).

2.3 Molecular Genetic Approaches

2.3.1 Linkage analysis

Once the genetic basis of a trait has been established using some of the above-mentioned methods, the next step is to conduct linkage analysis to map the potential genetic loci predisposing the trait. Linkage analysis requires each family member of a large family, or of several family pedigrees to be genotyped, typically using single-nucleotide polymorphism (SNP) arrays. If a genetic locus is thought to predispose a trait, family members who share the same markers near this locus should exhibit greater trait resemblance compared to those who do not share the markers. Therefore, linkage analysis aims to identify the markers on the SNP array that are commonly present in participants within or across pedigrees who exhibit the trait of interest. It should be noted that the identified markers are not the actual genes predisposing a trait; they are

² A pattern of inheritance in which a phenotype can be expressed in individuals who have received just one copy of a particular gene on an autosome (non-sex chromosome). An example of a trait with autosomal dominant inheritance is brown eyes.

³ A pattern of inheritance in which a phenotype is expressed only in individuals who have received two copies of a particular gene on an autosome (non-sex chromosome). An example of a trait with autosomal recessive inheritance is blue eyes.

merely known locations on the genome that are near the gene of interest (Carey, 2003a). “Linkage” is said to occur when two gene loci that are in close proximity on the same chromosome are inherited together. In other words, if a marker is commonly shared among family members with the trait of interest, this marker is likely to be in linkage with the actual locus of the trait.

There are two common approaches to estimate linkage. The non-parametric or model-free linkage analysis basically tests whether relatives exhibiting the trait of interest share more alleles than would be expected by chance (Xu, Bull, Mirea, & Greenwood, 2012). In contrast, parametric or model-based linkage analysis requires the specification of the mode of inheritance, as ascertained by segregation analysis. Linkage is then tested by comparing the probability of obtaining the current test data if a marker locus and the trait locus are linked, to the probability of obtaining the test data if the two loci are not linked (Schnell & Sun, 2012). The ratio of the two probabilities expressed on a logarithmic scale is known as the LOD score. LOD scores are computed across all markers for each pedigree and then summed across different pedigrees. A LOD score ≥ 3 is typically considered significant evidence for linkage, as it indicates that the odds that the two loci are linked and inherited together are greater than 1000 to 1. Alternatively, a LOD score ≤ -2 is considered significant evidence to reject linkage. In general, scores within the range of $-2 < x < 3$ are regarded as inconclusive evidence for linkage, with those between $2 \leq x < 3$ warranting additional study.

Linkage analysis is often successful in identifying Mendelian traits with a simple mode of inheritance, such as Huntington’s disease. It has been less effective for complex traits predisposed by multiple genes as each gene individually exerts only a small effect on the trait (Nsengimana & Bishop, 2012). Large sample sizes are therefore needed to obtain adequate statistical power to detect linkage. Statistical power can also be increased by performing multipoint analysis (i.e., using multiple markers simultaneously), allowing more precise identification of the trait locus (Lathrop, Lalouel, Julier, & Ott, 1984).

As parametric linkage analysis requires the pattern of inheritance to be specified, misspecification of the genetic model may lead to loss of power (Schnell & Sun, 2012). While this potential problem can be alleviated by testing more than one genetic model,

multiple-testing issues increase the likelihood of false positives (Weeks, Lehner, Squires-Wheeler, Kaufmann, & Ott, 1990). A further shortcoming of linkage analysis is that the identified linkage region typically contains numerous genes. Fine-mapping of the linkage region is therefore necessary to narrow down the locus and determine the possible causative gene (Carey, 2003b). With the development of exome sequencing technologies (see Section 2.3.3, p. 23), fine-mapping is now less essential as all genes in the linkage region can be quickly analysed.

2.3.2 Association analysis

Association analysis is a statistical method used to investigate the association between a genetic variant and a trait (Carey, 2003b). Association analysis can be used to test potential genetic variants that lie in significant linkage regions. It can also be employed when there are well-founded reasons to suspect a gene's involvement in predisposing a trait. An association analysis can either adopt a population-based design involving unrelated cases and controls, or a family-based design in which relatives of cases serve as controls for the study.

In the candidate gene approach, statistical tests are performed to determine whether the cases have a higher frequency of a particular allelic variant⁴ of the candidate gene, as compared with the controls. The possible association between an allelic variant and the trait of interest may yield valuable information about the variant's role in the biological pathway of the trait. One major limitation of candidate gene studies is that only specific allelic variants are investigated; the success of an association study thus hinges on the accuracy of a researcher's "educated guess" of the potential candidate genes. Moreover, if the trait of interest is complex and multiple genes are involved, the candidate gene approach is not able to detect the influence of the predisposing genes in other loci.

By contrast, a genome-wide association study (GWAS) can be conducted without prior knowledge of potential candidate genes. It involves an "agnostic" or non-candidate driven search of the entire human genome, typically using SNP arrays with a large number of common SNP markers found throughout the genome (Sun &

⁴ Allelic variant is a particular alternate form of an allele.

Dimitromanolakis, 2012). If certain SNPs have a higher incidence in the cases relative to the controls, this will indicate a possible association of these SNPs with the trait of interest.

GWAS is a useful approach to find novel candidate genes predisposing a trait of interest, especially if the biological pathway of the trait is not well-understood. It is also possible to identify multiple genetic contributors to a complex trait, even if each of these may be conferring only a small effect (Reich & Lander, 2001). The downside is that to identify such SNPs of low effect size, large sample sizes are needed to achieve adequate power (typically thousands or even tens of thousands of cases and controls) (Spencer, Su, Donnelly, & Marchini, 2009). However, large sample sizes may give rise to confounding factors such as population stratification and cryptic relatedness that result in false positives (Nsengimana & Bishop, 2012). Moreover, GWAS does not identify complete genes; it only identifies the genomic regions possibly associated with the trait, which in some cases may not even have a protein-coding gene in the vicinity.

A common problem faced by both the candidate gene approach and GWAS is the minimal replication of significant results across association studies (Lewis & Knight, 2012). Researchers must therefore exercise caution and critically examine the validity of published association studies, and make prudent design decisions for their own association studies (Attia et al., 2009).

2.3.3 Exome sequencing

With the advancement of high-throughput next-generation sequencing (NGS) technologies, exome sequencing has emerged as a rapid and cost-effective method for human genetic analysis (Singleton, 2011). The exome is the portion of the genome containing protein-coding information and represents about 1.5% of the whole genome. Exome sequencing is based on the assumption that changes in exons may modify the function of proteins coded by exons, thereby leading to changes in the phenotype. By targeting the exome instead of the entire genome, exome sequencing presents a cost- and time-effective means to find possible genetic variants predisposing a trait. Exome sequencing uses sequence capture methods to selectively capture exons from a DNA

sample and enrich the available information from each sample, before using high-throughput sequencing to identify coding variants in the exome (Ku et al., 2012).

Since the publication of the first proof-of-concept study which used exome sequencing to identify causal variants for a rare Mendelian disorder (Ng et al., 2009), exome sequencing has shown much promise in discovering coding variants for both Mendelian and non-Mendelian traits (Singleton, 2011). Like GWAS, exome sequencing can be performed without the foreknowledge of potential candidate genes or genetic variants. Its usefulness has also been shown in the diagnosis of disorders characterised by genetic heterogeneity (Singleton, 2011). Another advantage of exome sequencing is that it can identify uncommon causal variants predisposing rare Mendelian traits, which cannot be identified through linkage studies due to inadequate study power (Singleton, 2011).

Ultimately, exome sequencing may become a valuable genetic screening and diagnostic tool, allowing robust diagnoses to be reached rapidly and cost-effectively (Ku et al., 2012). However, it has some limitations. For instance, some regions of interest in the exome are difficult to sequence with the current technology, and the large amount of sequencing data generated poses computational challenge for analysis. Moreover, exome sequencing is unable to detect large deletions or rearrangements in the genome, and there is a major risk of false positives due to difficulties determining the biological relevance of coding variants to the trait of interest.

2.3.4 Copy number variation (CNV) analysis

Copy number variants are structural variants (>1,000 base pairs) whose copy numbers deviate from those found in the human reference genome. Such variation in the genome (known as copy number variation) includes insertions, deletions, duplications, inversions and translocations (Wain, Armour, & Tobin, 2009). More than 300 known causal genes for diseases are found to overlap with CNVs (Sebat et al., 2004), highlighting the impact CNVs may exert on genetic mechanisms and phenotypic variation. Understanding the functional impact of CNVs, therefore, offers a fruitful means of elucidating the genetic basis of complex phenotypes.

There are several approaches to CNV detection. Microarray-based CNV analysis techniques typically use SNP arrays or aCGH (array comparative genomic hybridisation) platforms to detect copy number gains or losses in the test sample compared with a reference sample (Alkan, Coe, & Eichler, 2011). CNV detection can also be achieved through a sequencing-based approach.

CNV analysis has shown its utility in the diagnosis of syndromes with heterogeneous phenotypes (Coughlin II, Scharer, & Shaikh, 2012). However, understanding the significance and effect of detected CNVs on a trait of interest remains challenging. In addition, microarray-based CNV analysis has a number of drawbacks. Copy neutral alterations (such as inversions and translocations) that do not cause a change in the total amount of genetic material cannot be identified by the microarray-based approach, even though such alterations are potentially deleterious. The microarray-based approach is also less sensitive in detecting duplications than deletions.

Given the continued advancement in sequencing technologies, sequencing-based approaches are likely to supersede microarray-based CNV analysis. In time, the ability of NGS to detect various forms of genetic variants (including small insertions/deletions and copy neutral variants) will improve and the cost of massive parallel sequencing will become less expensive. Nevertheless, this approach has not yet reached maturity and standard protocols and measures for sequencing-based CNV analysis have not been established. Moreover, the bioinformatics infrastructure, support and cost required for managing, analysing and storing large amounts of sequencing data need to be carefully considered (Teo, Pawitan, Ku, Chia, & Salim, 2012). In addition, the relatively short read lengths of NGS pose mapping issues in aligning the sequenced reads with the reference genome, especially in the duplicated regions of the genome. Thus, as with a microarray-based approach, copy number duplications remain less detectable than deletions with the sequencing-based method. Longer read lengths afforded by improvements in sequencing technology will potentially mitigate this issue.

2.4 Genetic Evidence for Music Ability and Music-Related Phenotypes

Studies on the genetic basis of music ability are relatively scarce compared with more extensive investigation conducted on the nature of language ability (for recent reviews of the genetic findings on speech and language, see Newbury and Monaco, 2010; Carrion-Castillo et al., 2013; Graham and Fisher, 2013; Raskind et al., 2013; Szalontai and Csiszar, 2013). Fortunately, the advent of molecular genetics in the post-genomic era holds much promise for improving understanding in this relatively underexplored field. This section consolidates the various music-related phenotypes investigated in behavioural and molecular genetic studies in the last three decades (**Table 2.1**). The behavioural genetic studies prior to that are not included in this review as the few genetic investigations on music ability lacked scientific rigour or suffered from small sample sizes (see Rowley, 1988 for a review of the early behavioural genetic studies on music ability) .

2.4.1 Music perception

From **Table 2.1**, it can be observed that the majority of studies (61%) have focused on music perception abilities. These include basic musical perception abilities such as the perception of pitches and note durations, higher level music perception abilities such as the perception of melody, rhythm and musical patterns, music listening behaviour, and uncommon music perception ability (absolute pitch ability), and deficit (congenital amusia). Recent genetic findings on each of these traits will be outlined in this section. The main findings from the behavioural and molecular genetic findings are summarised in **Table 2.2** and **Table 2.3**, respectively.

Table 2.1. The Number of Genetic Studies Investigating Various Music Traits

Music Ability Category	Music subskill	No. of studies	Authors
Music perception	Basic music perception abilities	3	Pulli et al. (2008); Oikkonen et al. (2014); Ullén et al. (2014)
	Higher level music perception abilities	7	Alcock et al. (2000); Drayna et al. (2001); Pulli et al. (2008); Ukkola et al. (2009); Ukkola-Vuoti et al. (2013); Oikkonen et al. (2014); Ullén et al. (2014); Seesjärvi et al. (2015); Liu et al. (2016)
	Music memory	2	Granot et al. (2007); Granot et al. (2013)
	Music listening	2	Ukkola-Vuoti et al. (2011); Kanduri, Raijas, et al. (2015)
	Congenital amusia	1	Peretz, Cummings, and Dubé (2007)
	Absolute pitch	10	Profita & Bidder (1988); Gregersen & Kumar (1996); Baharloo et al. (1998); Gregersen et al. (1999); Baharloo et al. (2000); Gregersen et al. (2001); Theusch, Basu, & Gitscher (2009); Theusch & Gitschier (2011); Gregersen et al. (2013); Gervain et al. (2013)
Music production	Music performance	1	Kanduri, Kuusi, et al. (2015)
	Music practice*	2	Mosing et al. (2014); Hambrick & Tucker-Drob (2014)
	Music flow*	1	Butkovic et al. (2015)
	Music creativity*	3	Ukkola et al. (2009); Ukkola-Vuoti et al. (2013); Oikkonen et al. (2016)
	Singing participation*	2	Coon & Carey (1989); Morley et al. (2012)
	Singing accuracy	1	Park et al. (2012)
	Rhythm production	1	Alcock et al. (2000)
Music accomplishments*		3	Coon & Carey (1989); Vinkhuyzen et al. (2009); Hambrick & Tucker-Drob (2014)
Music culture		2	Pamjav et al. (2012); Brown et al. (2013)

*based on subjective, self-report measures

Table 2.2. Summary of Behavioural Genetic Studies Investigating Various Music Traits

Trait	Type of study	Findings
Basic music perception abilities	Pedigree study (Pulli et al., 2008); 15 Finnish musical families (N=234)	Heritability estimates for SP: 57%; ST: 21%
	Pedigree study (Ukkola et al., 2009); 19 Finnish musical families (N=343)	Heritability estimates for SP: 52%; ST: 10%
	Pedigree study (Oikkonen et al., 2014); 76 Finnish families (N=767)	Heritability estimates for SP: 68%; ST: 21%
	Twin study (Ullén et al., 2014); 2,569 twin pairs	Heritability estimates for pitch discrimination: M: A = 12% [0-35%]; F: A = 30% [9-52%]
Higher level music perception abilities	Twin study (Drayna et al., 2001); 284 female twin pairs	Melodic perception ability: A = 71% [61-78%] (continuous measure) or A = 80% [65-90%] (dichotomous categories)
	Twin study (Ullén et al., 2014; Mosing et al.; 2014); 2,569 twin pairs	Melody discrimination: M: A = 31% [5-53%]; F: A = 61% [50-66%]; Combined: A = 59% [43-64%] Rhythm discrimination: M: A = 41% [7-59%]; F: A = 52% [23-59%]; Combined: A = 50% [33-57%]
	Twin study (Seesjärvi et al., 2015); 113 twin pairs	MBEA scale test: A: 58% [42-70%] OTA out-of-key test: C: 61% [49-70%] OTA off-beat test: E: 82% [61-100%]
	Pedigree study (Pulli et al., 2008); 15 Finnish musical families (N=234)	Heritability estimates for KMT: 42%; COMB: 48%
	Pedigree study (Ukkola et al., 2009); 19 Finnish musical families (N=343)	Heritability estimates for KMT: 39%; COMB: 44%
	Pedigree study (Oikkonen et al., 2014); 76 Finnish families (N=767)	Heritability estimates for KMT: 46%; COMB: 60%
Congenital amusia	Familial aggregation (Peretz et al, 2007); 9 proband families & 10 control families	λ_s : 10.8 [CI: 8-13.5] λ_o : 2.3 [CI: 0-5]

Trait	Type of study	Findings
Absolute pitch (AP)	Family segregation analysis (Profita & Bidder, 1988); 35 AP probands from 19 families	SR: .24 to .37
	Familial aggregation (Gregersen & Kumar, 1996); 101 AP probands	λ_s : ~20
	Familial aggregation (Baharloo et al., 1998); 92 self-reported AP probands 520 non-AP probands	λ_s : ~7.5 [CI: 2.2-21.2] (controlled for early music training)
	Familial aggregation (Gregersen et al., 1999); 2,707 tertiary music students	Sib RR: ~8.3
	Familial aggregation (Baharloo et al., 2000); 74 AP-1 probands with 113 siblings 625 controls	λ_s : 7.8-15.1 (controlled for early music training)
	Familial aggregation (Gregersen et al., 2001); 1,067 music theory students	Sib RR: ~12.2
	Family segregation analysis (Theusch & Gitschier, 2011); 1,463 families with AP-1 probands	SR: .089 [SE: .006]
	Twin study (Theusch & Gitschier, 2011); 14 MZ and 31 DZ female twin pairs	CCR _{MZ} : 78.6%; CCR _{DZ} : 45.2%
Music practice	Twin study (Mosing, Madison, Pedersen, Kuja-Halkola & Ullén; 2014); 2,569 twin pairs	Hours of music practice: M: A = 69% [56-75%]; F: A = 41% [26-56%]
	Twin study (Hambrick & Tucker-Drob, 2014); 850 twin pairs	A = 38%; C = 44%; E = 19%
Music flow	Twin study (Butkovic, Ullén, Mosing, 2015); 2,570 twin pairs	Heritability: 40%
Music creativity	Pedigree study (Ukkola et al., 2009); 19 Finnish musical families (N=343)	Heritability for Music creativity: 84%; Composing: 40%; Arranging: 46%; Improvising: 62%
	Pedigree study (Oikkonen et al., 2016); 79 Finnish families (N=474)	Heritability for Composing: 33.3%; Arranging: 33.4%; Improvising: 11.6%; Non-musically creative: 28.9%

Trait	Type of study	Findings
Participation in singing activities	Twin study (Coon & Carey, 1989); 850 twin pairs	M: A = 71%; F: A = 20%
Singing (pitch accuracy)	Pedigree study (Park et al., 2012); 73 extended families (N=1,008)	Heritability: 40% [CI: 20.4-59.6%]
Music accomplishments	Twin study (Coon & Carey, 1989); 850 twin pairs	Heritability estimates for Vocational interest in music: M: A = 21%; F: A = 17% Instrumental music engagement: M: A = 30%; F: A = 14% Professional music engagement: M: A = 38%; F: A = 10% Receiving music prizes: M: A = 38%; F: A = 20%
	Twin study (Vinkhuyzen et al., 2009); 1,685 Netherlands twin pairs (12-24 years)	Musical aptitude: M: A: 66% [52-77%]; F: A: 30% [16-36%] Exceptional musical talent: A: 86% [22-98%]
	Twin study (Hambrick & Tucker-Drob, 2014); 850 twin pairs	A = 26% (Practice: A = 43%; No practice: A = 1%)

Note. λ_s : Sibling recurrence risk; λ_o : Offspring recurrence risk; CCR_{MZ}: Casewise Concordance rate for MZ twins; CCR_{DZ}: Casewise concordance rate for DZ twins; CI: 95% confidence interval; COMB: Combined test scores of KMT, SP and ST; A: Additive genetic variance (heritability); C: common/shared environmental variance; E: Unique environmental variance; F: females; KMT: Karma Music Test; M: males; MBEA: Montreal Battery of Evaluation of Amusia; OTA: Online Test of Amusia; SE: Standard error; SP: Seashore's Pitch Discrimination Test; ST: Seashore's Time Discrimination Test; Sib RR: Sibling relative risk; SR: Segregation ratio
95% confidence intervals or standard errors are provided in square brackets where available

Table 2.3. Summary of Molecular Genetic Studies Investigating Various Music Traits

Trait	Study type/ Participants	Locus implicated	Gene implicated
Perception of pitch and rhythm	Genome-wide linkage study (Pulli et al., 2008); 15 musical families (N=234)	4q22	<i>UNC5C</i>
		8q13-21	<i>TRPA1</i>
	Candidate-gene association study (Ukkola et al., 2009); 19 musical families (N=343)	12q14-q15	<i>AVPR1A</i> RS1+RS3 haplotype
	Genome-wide CNV analysis (Ukkola-Vuoti et al., 2013); 5 extended families, 172 unrelated individuals	5q31.1	<i>Pcdha 1-9</i>
		8q24.22	<i>ADCY8</i>
	Genome-wide linkage and association study (Oikkonen et al., 2014); 76 families (N=767)	3q21.3	<i>GATA2</i>
		4p15-q24	<i>PCDH7</i> , <i>PDGFRA</i> , <i>KCTD8</i> , <i>CHRNA9</i> , <i>PHOX2B</i>
	Genome-wide positive selection analysis (Liu et al., 2016)** 148 participants	Best positive selection regions: 12q15-q21.2; 2p13	
		12p13.1	<i>GRIN2B</i>
		2q13	<i>IL1A</i> , <i>IL1B</i>
		1q32.3-41	<i>USH2A</i>
		3p13	<i>FOXP1</i>
		5q11-q12	<i>GZMA</i>
		5q14.3	<i>GPR98</i>
		7p15.3	<i>RAPGEF5</i>
		9p24.2	<i>VLDLR</i>
		17q24	<i>RGS9</i>
Music memory	Candidate-gene association study (Granot et al., 2007); 82 university students	12q14-q15	<i>AVPR1A</i> RS1+RS3 haplotype
		17q11.2	<i>SLC6A4</i> <i>HTTLPR</i>
	Pharmacological study (Granot et al., 2013); 50 male participants		<i>AVP</i>
Music listening	Candidate-gene association study (Ukkola-Vuoti et al., 2011); 31 families (N=437)	12q14-q15	<i>AVPR1A</i> active current music listening: RS1+AVR haplotype; lifelong active music listening: RS1+RS3 haplotype

Trait	Study type/ Participants	Locus implicated	Gene implicated
Music listening	Genome-wide transcriptome study (Kanduri et al., 2015a)**; 48 adult participants	4q22.1	<i>SNCA</i>
		2q37.3	<i>HDAC4</i>
		8q24.21	<i>FAM49B</i>
Absolute pitch (AP)	Genome-wide linkage study (Theusch, Basu & Gitschier, 2009); 73 AP families*	8q24	<i>ADCY8</i>
		8q24.21	<i>FAM49B</i>
		7q22.3, 8q21.11, 9p21.3	-
	53 AP multiplex families, 36 synaesthesia multiplex families	6q14.1-16.1	<i>EPHA7</i>
		2q24.1; 2q22.1	
	Pharmacological study (Gervain et al., 2013); 24 adult male participants		<i>HDAC enzyme</i>
Music performance	Genome-wide transcriptome study (Kanduri et al, 2015b)**; 20 professional musicians	4q22.1	<i>SNCA</i>
		8p23	<i>CLN8</i>
		14q24.3	<i>FOS</i>
		21q22.2	<i>DOPEY2</i>
Music creativity	Genome-wide CNV analysis (Ukkola-Vuoti et al., 2013); 5 extended families, 172 unrelated individuals	5p15	<i>ZDHHC11</i>
		2p22.1	<i>GALM</i>
		2p12, 3p14.1, 3q28	-
	Genome-wide linkage analysis (Oikkonen et al., 2016)**; 79 families (n=474) & 103 unrelated participants	16p12.1 (arranging)	<i>GSG1L</i>
		4q22.1 (composing)	<i>SNCA</i>
		18q21 (non-musically creative)	<i>CDH7, CDH19</i>
Choir participation	Candidate gene association study (Morley et al., 2012); 262 amateur choir singers, 261 controls	17q11.2	<i>SLC6A4</i> (17q11.2)
Singing (pitch accuracy)	Genome-wide linkage and association study; exome sequencing; CNV analysis (Park et al., 2012); 73 families (N=1008)	4q23	
		4q26	<i>UGT8</i>
Rhythm perception and production	Candidate gene study (Lai et al., 2001); A three-generation family pedigree	7q31	<i>FOXP2</i>

Note. CNV: copy number variation. For full names of the gene symbols, please refer to the List of Abbreviations.

* Families with at least two AP possessors who were not simply a parent-child relative pair

* **Due to the large number of differentially expressed genes in these studies, only more notable genes such as those implicated in other music studies are listed. For comprehensive information on all the differentially expressed genes, please refer to the respective articles.

2.4.1.1 Basic music perception abilities

The genetic basis of basic musical auditory capacities was investigated by Järvelä and her collaborators in several large molecular genetic studies (Oikkonen et al., 2014; Pulli et al., 2008). These abilities were measured with the pitch and time tests from the Seashore Measures of Musical Talents, in which participants were asked to detect differences in the pitch and duration of 50 paired tones (Seashore, Lewis, & Saetveit, 1960). Three separate studies from the same laboratory reported high heritability estimates (52-68%) for pitch discrimination ability and low to moderate heritability (10-21%) for note duration perception (Oikkonen et al., 2014; Pulli et al., 2008; Ukkola, Onkamo, Raijas, Karma, & Järvelä, 2009).

In contrast, a large Swedish twin study which used a similar paired pitch discrimination paradigm only found modest heritability estimates ($A = 12-30\%$) for pitch perception ability, with significant sex differences (Ullén, Mosing, Holm, Eriksson, & Madison, 2014). While significant and moderate genetic influences ($A = 30\%$) were estimated for female twins, significant common environmental influences ($C = 38\%$) were estimated for male twins, which led the researchers to surmise possible etiological difference in the pitch perception ability of males and females. Taken together, the majority of the evidence suggests that genetic influences play a significant role in the variation of basic musical auditory abilities in the general population.

As shown in **Table 2.3**, number of possible genetic substrates underlying basic music perception have been reported by Järvelä and colleagues. Genome-wide linkage analysis revealed some evidence of linkage on chromosome 10 ($LOD = 1.67$) for pitch discrimination, and on chromosome 4q ($LOD = 1.18$) for note duration discrimination (Pulli et al., 2008). A subsequent larger-scaled genome-wide linkage and association study (Oikkonen et al., 2014) also found evidence that chromosome 4 was implicated in music perception. For pitch discrimination, the best linkage (posterior probability of linkage [PPL] = 0.86) was obtained at 4p14, with some evidence of linkage (PPL = 0.68) also observed at 22q11.21. In addition, the chromosomal region 3q21.3 was found to be associated with pitch and note duration discrimination.

Interestingly, some of these implicated chromosomal loci contain genes that are expressed in the auditory pathway. For instance, the *PCDH7* gene is located next to 4p14, and is known to be expressed in the developing cochlea of chicken and the amygdala of mice (Hertel, Redies, & Medina, 2012; Lin et al., 2012), providing suggestive evidence for the gene's role in music perception and music-evoked emotions. On the other hand, located close to 3q21.3 is the *GATA2* transcription factor, which likely plays an important role in the development of cochlear hair cells and the inferior colliculus (Haugas, Lilleväli, Hakanen, & Salminen, 2010; Lahti, Achim, & Partanen, 2013). The inferior colliculus is a core structure in the peripheral auditory pathways for music perception, supporting the initial integration of pitch, direction and loudness information (McLachlan & Wilson, 2010). Moreover, *GATA2* is expressed in dopaminergic neurons (Scherzer et al., 2008), which release dopamine during pleasure-evoking activities such as music listening and performance (Salimpoor, Benovoy, Larcher, Dagher, & Zatorre, 2011). Finally, the region 22q11.21 is linked to DiGeorge syndrome (also known as 22q11.2 deletion syndrome), which typically includes symptoms of conductive and sensorineural hearing losses (Digilio, Marino, Capolino, & Dallapiccola, 2005).

2.4.1.2 Higher level music perception abilities

The abilities to perceive tonal and rhythmic structure in music are understandably more cognitively advanced forms of music perception abilities as compared to pairwise discrimination of pitches or note durations. Since the dawn of the new millennium, there has been increasing evidence supporting the presence of genetic influences underlying higher level musical perception abilities.

A twin study conducted in 2001 investigated melodic perception ability by asking twins to judge whether snippets of familiar melodies contained incorrect pitches that rendered them "out-of-tune" (Drayna, Manichaikul, De Lange, Snieder, & Spector, 2001). A substantial genetic component ($A = 71\text{-}80\%$) was found, with no effect of common environmental influences. High heritability estimates ($A = 58\text{-}59\%$) for melodic perception were also reported by two other recent twin studies using paired melody discrimination tasks in which the second melody may have a different pitch from the first (Seesjärvi et al., 2015; Ullén et al., 2014). Intriguingly, in the latter study, the

abilities to detect violation of tonal and rhythmic structure of a melody by an errant tone were found to be explained mostly by common environmental influences ($C = 61\%$) and unique environmental influences ($E = 82\%$), respectively (Seesjärvi et al., 2015). The researchers proposed that the discrepant heritability estimates for melodic perception and tonal structure perception could be due to differences in task demands, as violation of melodic or rhythmic structure may rely more on implicit or prior musical knowledge, whereas pairwise comparison of melodies may impose a greater cognitive load on working memory, which may conceivably be influenced by a larger genetic component. The high heritability estimate for paired discrimination of rhythmic sequences ($A = 50\%$) as reported by (Ullén et al., 2014) is also in line with the working memory explanation.

Järvelä's research team investigated the ability to discern melodic and rhythmic patterns (referred to as auditory structuring ability) using the Karma Music Test (KMT) in two family pedigree studies and reported sizeable genetic influences (39-46%) for this ability (Oikkonen et al., 2014; Pulli et al., 2008; Ukkola et al., 2009). In addition, these studies also obtained moderate to high heritability estimates of 44-60% for the combined score of the KMT and Seashore's pitch and time tasks. In the earlier study, genome-wide linkage analysis revealed promising evidence of linkage at 4q22 for KMT ($LOD = 2.91$) and significant evidence of linkage ($LOD = 3.33$) for the combined score (Pulli et al., 2008). The subsequent genome-wide linkage and association study also found some evidence of linkage for 4q21.23–22.1, and 4q24 being linked to the KMT (Oikkonen et al., 2014). A possible candidate gene at 4q22 is the netrin receptor *UNC5C*. Netrins are responsible for directing axon extension and cell migration during neural development, and studies have shown interactions between netrins and robo family receptors (Stein & Tessier-Lavigne, 2001). One such receptor, *ROBO1*, is a candidate gene for dyslexia (Carrion-Castillo et al., 2013). The results indicate possible shared molecular substrates between music and language, which is further strengthened by previous behavioural findings that KMT significantly predicts dyslexia (Karma, 2002).

The genome-wide linkage and association study also found potential linkage evidence ($PPL = 0.57$) for KMT at 16q21-22.1 (Oikkonen et al., 2014), which overlaps with a previously proposed hearing impairment locus (Basit et al., 2011). Furthermore,

association analysis conducted in the study revealed that KMT was associated with 5q31.3 (posterior probability of linkage disequilibrium [PPLD] = 0.61), 1p31.1 (PPLD = 0.70) and 11q21 (PPLD = 0.58). While the associations at 1p31.1 and 11q21 could not be linked to any known gene near these loci, the gene *NDFIP1* is located at 5q31.3 and has a function in immune signalling regulation (Wang, Tong, & Ye, 2012). In addition, this study also revealed that some of the chromosomal regions showing evidence of linkage for the combined score (KMT and Seashore's pitch and time tasks) contain genes implicated in the auditory pathway. For instance, the linked region 18q12.3-21.1 contains the gene *LOXHD1* which is expressed in the inner ear hair cells and would result in auditory defects in the case of mutation (Grillet et al., 2009). In another linked region, 4p12-q12, the gene *PDGFRA* is expressed in the cochlea of mice (Ballana et al., 2008) and the gene *KCTD8* is expressed in the spiral ganglion, a group of nerve cells in the cochlea.

In a genome-wide CNV analysis, Järvelä and her collaborators detected several copy number variable regions (CNVRs) containing genes that influence neurodevelopment, learning and memory (Ukkola-Vuoti et al., 2013). Notably, a deletion on 5q31.1 was present in some participants with a low combined score on the Karma Music Test and the Seashore's pitch and time tasks. This particular region covers the protocadherin- α gene cluster (*Pcdha 1-9*), which is involved in the synaptogenesis and maturation of serotonergic projection neurons, as well as learning and memory (Fukuda et al., 2008; Katori et al., 2009). The authors proposed *Pcdha* as a plausible candidate for music perception since learning and memory are important for music perception and the development of musical expertise (McLachlan, Marco, Light, & Wilson, 2013). Also noteworthy was the identification of a large duplicated region on 8q24.22 in an individual with a low combined score, which happens to overlap with a major linkage region for absolute pitch (Theusch, Basu, & Gitschier, 2009). Duplication in the putative AP linkage region may have a negative impact on pitch perception, since large duplications are potentially detrimental to neurodevelopment (Almal & Padh, 2012; Grayton, Fernandes, Rujescu, & Collier, 2012).

In addition, a candidate gene study by Järvelä and her team demonstrated significant associations between the haplotype RS1 and RS3 of the *AVPR1A* gene on chromosome 12q and the combined score for Karma Music Test and the Seashore's pitch and time

tasks (Ukkola et al., 2009). Arginine vasopressin has been implicated in social cognition and behaviour (Bielsky, Hu, Szegda, Westphal, & Young, 2004; Depue & Morrone-Strupinsky, 2005; Ferguson, Young, & Insel, 2002; Hammock & Young, 2005) and in social and spatial memory (Aarde & Jentsch, 2006; Ferguson et al., 2002). Its association with auditory structuring ability in this study suggests a potential link between music perception and human social functioning. Interestingly, an association between an *AVPR1A* polymorphism (in conjunction with a *SLC6A4* polymorphism) and music memory have also been previously reported by another research group (Granot et al., 2007; see also Granot, Uzefovsky, Bogopolsky, & Ebstein, 2013 for findings from the follow-up study) .

More recently, Järvelä and her collaborators conducted genome-wide selection analysis on the music perception ability of 148 Finnish participants, as measured by the combined score for Karma's music test as well as Seashore's pitch and note duration perception tasks (Liu et al., 2016). Using a case-control design (74 cases with high combined scores and 74 controls with low combined scores), the researchers identified 12 chromosomal regions showing differential positive selection signals between cases and controls using several haplotype-based and frequency-based selection methods. The three best case-specific positive selection regions were namely 12q15-q21.2, 12q21.2, and 2p13, which contain many brain-related genes.

Several genes found within the positive selection regions are involved in inner-ear development and auditory perception, two of which are *GPR98* and *USH2A*. *GPR98* at 5q14.3 is necessary for proper development of auditory hair bundles (McGee et al., 2006) and has a possible function in birdsong (Pfenning et al., 2014). *USH2A* at 1q32.3-41 is also required in the development of cochlear hair cells, which influence hearing sensitivity (Liu et al., 2007). Both *GRP98* and *USH2A* have also been associated with Usher syndrome, which includes symptoms of deafness. Some genes found within the positive selection regions were also implicated in cognition and memory (e.g., *GRIN2B*, *IL1B* and *RAPGEF5*). *GRIN2B* at 12p13.1 is involved in learning and neural plasticity in the temporal lobe (Kauppi, Nilsson, Adolfsson, Eriksson, & Nyberg, 2011; Milnik et al., 2012). It is also one of the expressed genes in the singing control network of the zebra finch (Pfenning et al., 2014; Whitney et al., 2014). *IL1B* at 2q14 is linked to cognition and working memory (Benke et al., 2011; McClay et al., 2011) and

RAPGEF5 at 7p15.3 may also have implications in learning and memory (Kawasaki et al., 1998; Ostroveanu, Van Der Zee, Eisel, Schmidt, & Nijholt, 2010). It is noteworthy that an earlier genome-wide linkage and association study on music perception ability identified genes associated with inner-ear development and cognition (Oikkonen et al., 2014). On the other hand, *GZMA* at 5q11-q12 is known to be involved in neurodegeneration and has been observed to be downregulated after music listening (Ilžeka, 2011).

Located within the positive selection region on chromosome 17, *RGS9* gene (17q24) is putatively associated with reward mechanisms, as the longer splice variant of the gene (*RGS9-2*) has been reported to interact with dopamine receptors in the striatum (Taymans, Leysen, & Langlois, 2003). As already noted, dopamine release has been linked to music-induced reward (Salimpoor et al., 2011) and recent studies have shown that other genes associated with the dopaminergic pathways are upregulated after performing and listening to music (Kanduri, Kuusi, et al., 2015; Kanduri, Raijas, et al., 2015). Notably, *RGS2*, another gene from the *RGS* family, was upregulated after music listening and has been implicated in vocal learning in songbirds (Clayton, 2000). The researchers therefore conjecture that RGS proteins may be potential candidate genes for the evolution of music, but their associations with music aptitude need to be further elucidated.

Interestingly, approximately 5% of the identified candidate genes (e.g., *FOXP1*, *RGS9*, *GRIN2B*, *GPR98*, *VLDLR*) are related to song perception and production in songbirds (Pfenning et al., 2014; Whitney et al., 2014), which suggest a possible cross-species evolutionary conservation of genes associated with auditory perception. Among these candidate genes, *FOXP1* at 3p13 and *VLDLR* at 9p24.2 are known to be involved in language development (Chen, Heston, Burkett, & White, 2013; Vernes et al., 2007), which may possibly indicate a common genetic and evolutionary background for music and language.

One major limitation of the study by Liu et al. (2016) is that the large positive selection regions spanned numerous genes, making it difficult to interpret the functional importance of these regions, especially since the functions of many of the identified genes remain unknown. As such, the authors only described in detail the genes

important in brain function, hearing, and the singing network of songbirds, and more functional studies on the other candidate genes are warranted.

As for a possible genetic substrate underlying rhythm perception, one study has reported that in a three-generation family pedigree (KE family) with multiple probands of severe speech and language disorder, the affected individuals also showed impairment in rhythm perception and production, while their pitch perception and production abilities remained intact (Alcock, Passingham, Watkins, & Vargha-Khadem, 2000). Subsequent gene sequencing showed that the affected KE family members has a point mutation in the *FOXP2* gene (Lai, Fisher, Hurst, Vargha-Khadem, & Monaco, 2001). These findings suggest a possible shared genetic basis for speech and rhythm, while pitch-based music abilities are likely to be influenced by other genetic factors (Peretz, 2009).

2.4.1.3 Music memory

There is evidence that six to eight-month old infants have already developed long-term memories for music and are able to distinguish between familiar and novel music (Plantinga & Trainor, 2003; Saffran, Loman, & Robertson, 2000). In addition, exposure to melodies presented prenatally for three weeks elicits significant heart rate change in one-month old infants compared to unexposed controls, suggesting that newborn infants are capable of retaining music representations up to six weeks following prenatal exposure (Granier-Deferre, Bassereau, Ribeiro, Jacquet, & DeCasper, 2011). Genetic determinants of memory have been reported in the broader literature, with some studies indicating that memory ability can be predicted by a particular SNP Val66Met variant of the *BDNF* gene (Egan et al., 2003; Hariri et al., 2003). *BDNF* is evident in the hippocampus (a structure fundamental to new learning and memory) and has been implicated in neuronal growth, survival and maturation, including arborisation and synaptic plasticity in the adult brain (Park & Poo, 2012).

Granot and colleagues (2007) investigated the possible association of phonological and music memory with the genes *AVPR1A* and *SLC6A4*. The rationale for targeting these two genes included a previously reported relationship between arginine vasopressin (AVP) and spatial and social memory (Aarde & Jentsch, 2006; Ferguson et al., 2002). There is also evidence that serotonin interacts with AVP in the hypothalamus (Albers,

Karom, & Smith, 2002) and that serotonin increases the secretion of AVP (Gálfi et al., 2005). This points to a possible epistatic relationship⁵ between the gene *AVPR1A*, which contains the blueprint to synthesise the AVP receptor, and the gene *SLC6A4*, which is the serotonin transporter protein crucial for regulating serotonin supply to serotonin receptors. In view of this, Granot and colleagues genotyped 82 university students with minimal music training for the *AVPR1A* (RS1 and RS3 haplotypes) and the *SLC6A4* (HTTLPR) polymorphisms using population-based and family-based association analyses. Specifically, the music memory performance of the participants was assessed using four melodic memory tests and two rhythmic memory tests. Results revealed significant gene by gene epistatic interactions between the *AVPR1A* and *SLC6A4* polymorphisms for two melodic memory tasks (as measured by the Gordon melodic imagery subtest from the Musical Aptitude Profile, and the interval subtest from the Montreal Battery of Evaluation of Amusia), one rhythmic memory task (Seashore's rhythm perception task), and one phonological memory task, even after applying conservative Bonferroni corrections for multiple testing. This provides initial evidence for an epistatic relationship between *AVPR1A* and *SLC6A4* polymorphisms that may be linked to short-term memory for music, or more generally, to phonological memory.

In a follow-up study, AVP was administered intranasally to 50 male adults with little or no music training in a double-blind, placebo-controlled, crossover study (Granot, Uzefovsky, Bogopolsky, & Ebstein, 2013). At the end of each session (AVP/placebo), the participants' music working memory was assessed using the melodic imagery subtest from Gordon's Musical Aptitude Profile and the interval subtest from the MBEA, whereas their verbal working memory was assessed with the forward and backward digit span tasks. While AVP administration was not found to significantly affect the performance in the digit span task, a complex pattern emerged for the music memory tasks. For the MBEA test, in both sessions, the group that received AVP first performed worse than the group that received placebo first. For Gordon's music test, both groups performed significantly better in the second session, while a marginal session effect and a Group $\times$ Session interaction effect were observed. It was also found that in the group that received AVP first, their music memory scores were significantly positively correlated with affective state scores. The researchers posited that the

⁵ The interaction between genes at two different loci.

complex findings suggest that the intriguing detrimental effects of AVP on music memory may be mediated by mood, attention and arousal, such that only those who scored low on happiness and attentiveness were negatively affected by AVP in terms of their music working memory. In light of music's propensity for modulating arousal and AVP's influence on mood and arousal, it is conceivable that the documented associations between AVP and music perception, creativity and memory could reflect individual differences in arousal and attention modulation rather than individual differences in cognitive or social abilities *per se*.

2.4.1.4 Music listening

Listening to music is a ubiquitous behaviour evident in all known human cultures. Järvelä and her team investigated the role of *AVPR1A* gene polymorphisms in active and passive music listening behaviour in 31 Finnish families using family-based association analysis (Ukkola-Vuoti et al., 2011). They found that current active music listening was significantly associated with the RS1 and AVR haplotype, whereas lifelong active music listening was significantly associated with the RS1 and RS3 haplotype. A shared genetic basis for the frequency of lifelong active music listening and music perception ability was suggested by the authors, as the same haplotype (RS1 and RS3) was previously demonstrated to be associated with music perception (Ukkola et al., 2009). Given the well-established role of arginine vasopressin in mediating social behaviour (Bielsky et al., 2004; Depue & Morrone-Strupinsky, 2005; Ferguson et al., 2002; Hammock & Young, 2005), the current finding suggests that music listening may share common neurobiological substrates with social attachment and communication.

Recently, the same Finnish research group investigated the effect of listening to classical music on the human transcriptome (i.e., all the RNA transcripts in a cell that are read from the DNA code) using genome-wide transcriptional profiling (Kanduri, Raijas, et al., 2015). It was found that in participants with high musical experience (based on years of music training or music perception ability), several genes implicated in dopamine secretion, transport and signaling were upregulated (i.e., increasingly expressed), which converged with previous evidence of music listening inducing dopaminergic release and transmission (Salimpoor et al., 2011; Sutoo & Akiyama,

2004). Most notably, one of the most upregulated genes was *SNCA*, a known risk gene for Parkinson's disease (Oczkowska, Kozubski, Lianeri, & Dorszewska, 2013; Scherzer et al., 2008). Interestingly, *SNCA* is located on the most significant linkage region for music perception ability, 4q22.1 (Oikkonen et al., 2014; Pulli et al., 2008). In addition, *SNCA* is regulated by *GATA2*, a transcription factor which has a possible association with music perception ability (Oikkonen et al., 2014). Other upregulated genes in participants with high musical experience included those that are associated with learning, memory and cognition (e.g., *SNCA*, *NRGN*, *NPTN*), synaptic function and neurotransmission (e.g., *SNCA*, *HDAC4*, *FKBP8*), neuroprotection and neurogenesis (e.g., *SNCA*, *KLF4*), and auditory cortical activation and absolute pitch (e.g., *FAM49B*, *HDAC4*). It is worth noting that some of the upregulated genes (e.g., *SNCA*, *NRGN*, *RGS2*) are also known to be associated with song perception and production in songbirds (Wada et al., 2006), which suggests a potential cross-species shared evolutionary background for sound perception. On the other hand, several of the downregulated genes (e.g., *ATP5J*, *ATP5L*, *GZMA*, *CASP8*) are involved in neurodegenerative processes. Taken together, the downregulation of genes implicated in neurodegeneration and the upregulation of genes involved in neurogenesis and neuroprotection indicate that music listening may have a neuroprotective role and supports the utility of music therapy as a potential means for managing neurodegenerative diseases.

2.4.1.5 Congenital amusia

While most people in the general population commonly engage in music listening behaviour, there are some individuals who cannot enjoy listening to music due to a fine-grained pitch perception deficit, known as congenital amusia. Commonly known as “tone deafness”, congenital amusia is a fine-grained pitch perception deficit characterised by the inability to detect “wrong” notes in melodies, despite normal intellect, language and hearing abilities (Peretz & Hyde, 2003). It is uncommon in the general population, with an estimated population prevalence of 4% or less (Henry & McAuley, 2010; Kalmus & Fry, 1980; Pfeifer & Hamann, 2015). While the neurological basis of congenital amusia has been well-investigated (Hyde et al., 2007; Loui, Alsop, & Schlaug, 2009; Mandell, Schulze, & Schlaug, 2007; Mignault Goulet,

Moreau, Robitaille, & Peretz, 2012; Peretz & Hyde, 2003), few studies have explored its genetic basis.

In the first familial aggregation study on congenital amusia, Peretz et al. (2007) administered an online amusic diagnostic test to 13 amusic probands and 17 controls, as well as 58 family members of the probands (from 9 large families) and 58 family members of the controls (from 10 families). The results showed that 39% of first-degree relatives have congenital amusia, whereas only 3% of controls were similarly diagnosed. Notably, the λ_s for congenital amusia was 10.8, whereas the offspring recurrence risk was much lower at 2.3. While the high λ_s suggests a probable genetic basis for congenital amusia, Peretz and colleagues speculated that exposure to an enriched musical environment may mitigate the risk for offspring of amusic probands. However, Mignault Goulet and colleagues (2012) reported that after four weeks of daily music listening, the music perception scores and electrophysiological measures of seven amusic children (aged 10-12 years) did not vary essentially. This suggests that daily music listening is insufficient to improve pitch perception performance or stimulate neuroplasticity in amusic children.

2.4.1.6 Absolute pitch

Absolute pitch (AP) or “perfect pitch” is the rare music ability of being able to identify or produce pitches without relying on an external reference. It has an estimated prevalence of less than 1 in 10,000 (Bachem, 1955), although some recent studies have suggested the prevalence could be closer to 1 in 1,500 (Profita & Bidder, 1988). While AP is neither a prerequisite nor a predictor for outstanding musicianship, its rarity and the musical advantages it confers have generated much research interest into its etiology. Altogether, 24% of the genetic studies on music ability have investigated AP.

It has been observed that AP appears to cluster within families. A segregation study by Profita and Bidder (1988) reported significant familial incidence for AP in 19 families, with a segregation ratio estimated to lie between 0.24 to 0.37. Based on the segregation ratio, the researchers surmised that the etiology of AP is possibly an autosomal dominant gene with incomplete penetrance. A more recent segregation analysis on a larger sample, however, yielded a low segregation ratio of .089, which suggests that AP

was unlikely to be inherited in a simple Mendelian fashion (Theusch & Gitschier, 2011). Within this larger sample, however, the casewise concordance rate for AP among identical twin pairs (78.6%) was significantly different from that of non-identical twin pairs (45.2%), which suggests a genetic basis for AP.

Several familial aggregation studies also demonstrated evidence of familial clustering of AP. In their familial aggregation study, Gregersen and Kumar (1996) reported a sibling recurrence risk-ratio (λ_s) estimate of 20, meaning that siblings of AP possessors are approximately 20 times more likely to develop AP compared to the general population. Gregersen and colleagues subsequently conducted two more familial aggregation studies and reported sibling relative risk (sib RR) estimates of 8.3 and 12.2, respectively (Gregersen, Kowalsky, Kohn, & Marvin, 1999, 2001). In other words, the siblings of the AP possessors in these studies have 8.3 and 12.2 times greater likelihood of developing AP compared to the siblings of the controls. It is worth noting that high familial aggregation estimates do not necessarily point to a strong genetic basis for AP, since familial aggregation does not distinguish between genetic and environmental influences.

Evidence from several studies have indicated that environmental factors such as early music training may also contribute to the development of AP (Gregersen, Kowalsky, & Li, 2007; Miyazaki, 1988; Profita & Bidder, 1988; Sergeant, 1969; Wilson, Lusher, Martin, Rayner, & McLachlan, 2012). Baharloo and colleagues (Baharloo, Johnston, Service, Gitschier, & Freimer, 1998) therefore controlled for early music training by recruiting only families where participants and one or more of their siblings had received music training before 6 years of age, and the sibling recurrence risk-ratio (λ_s) for this study was estimated to be 7.5 (Gregersen, 1998). In a subsequent study (ref), Baharloo and colleagues estimated the sibling recurrence risk-ratio for the highest level of AP ability (termed AP-1) and reported that after controlling for early music training, the estimated λ_s ranged from 7.8 to 15.1, with a greater likelihood of the true value being near the upper end of the range. The consistent sizeable estimates of λ_s from various familial aggregation studies with or without controlling for early music training suggests that genetic influences likely play a key role in the development of AP.

More recently, evidence suggests that multiple genetic factors may be involved in the etiology of AP (Theusch & Gitschier, 2011). A segregation analysis performed on 1,463 AP-1 probands yielded a segregation ratio of .089, which is considerably lower than the estimate from the small AP sample in Profita and Bidder (1988) and the segregation ratios of 0.25 and 0.5 for autosomal recessive and autosomal dominant inheritance, respectively. This suggests that AP was not inherited in a simple Mendelian fashion. However, genetic factors likely play a role since within this larger sample, 11 out of 14 MZ twin pairs were concordant for AP-1 in comparison to only 14 out of 31 DZ twin pairs. These results yielded a significantly different casewise concordance rate of 78.6% and 45.2%, respectively.

Other supporting evidence for a possible genetic basis for AP comes from ethnicity effects observed in music students. While Gregersen et al. (1999) reported an overall sib RR of 8.3 for AP in 2,707 tertiary music students, a higher sib RR of 11.1 was observed for an Asian subsample. Gregersen et al. (2001) also reported that in a sample of 1,067 music theory students, Chinese, Korean and Japanese students had a substantially higher incidence of AP (47.5%) compared to Caucasian students (9%). A possible genetic explanation could be that the frequencies of susceptibility alleles may vary in different ethnic groups (Gregersen et al., 1999). Although some other researchers have attributed this “Asian advantage” to early tone-language exposure (Henthorn & Deutsch, 2007), this is unlikely to fully account for the higher incidence of AP among all Asian ethnic subgroups since essentially, Korean and Japanese are not tone languages (Kubozono, 2012; Sohn, 1999; Zatorre, 2003). Further analysis of Gregersen’s 2001 study data revealed that the age of onset of music training and exposure to a “fixed do” training method before the age of 7 were the only strong predictors of AP acquisition in this sample (Gregersen et al., 2007).

Possible ethnicity effects for AP can also be observed from a genome-wide linkage study of 73 families of European, East Asian, Ashkenazi Jewish and Indian descent (Theusch et al., 2009) in the United States and Canada. In each family there were at least two AP possessors, not limited to a parent-child relative pair. Non-parametric multipoint linkage analyses were suggestive of linkage on chromosomes 8q24.21 (LOD = 2.330) and 8q21.11 (LOD = 2.069) for the European/Ashkenazi Jewish/Indian combined dataset. Notably, one of the four genes found near the linkage peak on

8q24.21 was *ADCY8*, which is expressed almost exclusively in the brain and is implicated in learning and memory processes (De Quervain & Papassotiropoulos, 2006; Ludwig & Seuwen, 2002; Wong et al., 1999). When only the subset of 45 AP families of European descent was examined, there was strong evidence of linkage on chromosome 8q24.21 (LOD = 3.464 at SNP rs3057), suggesting that at least one gene within this linkage region could predispose AP in individuals of European descent. Two such genes are *FAM49B*, a protein coding gene, and *ADCY8*, which is implicated in learning and memory. A number of other linkage peaks were found in the European families, namely on loci 8q21.11 (LOD = 2.236), 7q22.3 (LOD = 2.074) and 9p21.3 (LOD = 2.048). These peaks suggest that different genetic factors may underpin the etiology of AP, even within the same population. The linkage region on 7q22.3 was also observed in a subset of 19 AP families of East Asian ancestry, albeit with a smaller linkage peak (LOD approximately 1 to 1.5). These findings support a strong genetic contribution to AP, which is likely to be heterogeneous. In other words, AP may be predisposed by different genetic variants at different chromosomal regions, both within and across populations of different ancestries.

A recently published study investigated the genetic relationship between AP and synaesthesia through a combined genome-wide linkage analysis of 53 multiplex families with AP (i.e., families in which multiple family members have AP) and 36 multiplex families with synaesthesia (Gregersen et al., 2013). Interestingly, 28 of the 126 AP possessors from the AP families reported synaesthesia, while eight synaesthesia families had a member with AP. Separate non-parametric linkage analysis of the AP and synaesthesia datasets revealed overlaps in several linkage regions (LOD > 2), especially on chromosomes 2 and 6. Given this overlap and the hypothesis that the two phenotypes may be jointly influenced by genes underpinning brain structural and functional connectivity, the researchers combined the AP and synaesthesia datasets for analysis. This revealed significant linkage on chromosome 6q14.1-6q16.1 (LOD = 4.68), where notably, a small linkage peak (LOD = 1.72) had been reported for the subset of 45 AP families of European ancestry studied by Theusch and colleagues (2009). Upon sequencing several potential candidate genes in this region, Gregersen and colleagues found that AP possessors from four of the AP multiplex families shared one or more of three non-synonymous variants of the gene *EPHA7*. *EPHA7* has been implicated in brain development, particularly establishing neural connectivity between

auditory cortex and other cortical regions with the thalamus (North, Clifford, & Donoghue, 2013; Torii, Hackett, Rakic, Levitt, & Polley, 2013). Since neuroimaging studies have reported that both AP and synaesthesia are marked by atypical structural and functional connectivity (Dovern et al., 2012; Loui, Li, Hohmann, & Schlaug, 2011; Rouw & Scholte, 2007), it is conceivable that *EPHA7* variants may influence these two phenotypes. More research involving extensive resequencing on the *EPHA7* gene is needed in order to confirm its involvement. Using parametric linkage analysis, a more complex pattern of linkage was also observed on chromosome 2 in the combined AP and synaesthesia dataset, with a heterogeneity LOD score of 4.7 at SNP rs1482308 on 2q24.1. When only the AP families were considered, a maximum heterogeneity LOD score of 3.93 was observed at SNP rs6759330 on 2q22.1.

Inherent neuroanatomical differences between AP and non-AP possessors may also be genetically influenced. AP possessors show increased leftward asymmetry of the planum temporale (PT) due to a significantly smaller right mean PT volume compared with non-AP possessors (Keenan, Thangaraj, Halpern, & Schlaug, 2001; Wilson, Lusher, Wan, Dudgeon, & Reutens, 2009). Keenan et al. (2001) suggested that the “pruning” of the right PT may be prenatally determined rather than due to early music training, since non-AP musicians with early music training do not manifest similar asymmetry. Wilson et al. (2009) subsequently demonstrated a striking difference in the right mean PT volumes of musicians with AP and quasi-absolute pitch (participants who scored between 20-90% on a note-naming test), even though the age of onset of music training did not differ significantly between these groups. Other supporting evidence comes from the discovery of an adult AP possessor, R.M., who had minimal music training but was able to perform a pitch memory task at a level indistinguishable from AP musicians. This case suggests that an early onset of music training (or any music training) may not be necessary for AP to emerge (Ross, Olson, & Gore, 2003), and that AP and non-AP possessors may be using different pitch processing mechanisms (McLachlan, Marco, & Wilson, 2013) that in part, reflect genetically influenced neuroanatomical differences.

Apart from this one documented case of a musically-naïve AP possessor (Ross et al., 2003), most AP possessors report early onset of music training (Levitin & Zatorre, 2003; Miyazaki & Ogawa, 2006; Russo, Windell, & Cuddy, 2003), which indicates a

possible critical time window for the development of AP. Previous studies have found that the inhibition of *HDAC* (histone-deacetylase), an enzyme which serves as a “brake” to critical-period neuroplasticity, could reopen the critical window and alter music preference or enable recovery from amblyopia in adult mice (Putignano et al., 2007; Silingardi, Scali, Belluomini, & Pizzorusso, 2010; Yang, Lin, & Hensch, 2012). In view of this, Gervain et al. (2013) investigated whether the administration of valproate, a *HDAC* inhibitor may potentially reopen the critical period for AP development and facilitate pitch naming ability in 24 musically naïve adult males. Using a randomised, double-blind, placebo-controlled crossover study, during each treatment arm, the participants took either valproate or placebo capsules over the course of 15 days and underwent daily 10-minute pitch association online training from days 8 to 14 before taking the AP assessment task on day 15. Results showed that in the first treatment arm, the valproate group performed significantly above chance level but the placebo group performed at chance level. Intriguingly, in the second treatment arm, no significant difference in performance was observed between the two groups as both performed at chance level. It was suggested that the worse performance in both groups during the second treatment arm could be due to a memory conflict whereby the set of pitches learned in the first treatment interfered with those learned in the second treatment. From these results, the researchers concluded that the significant findings from the first treatment arm offered a preliminary, proof-of-concept demonstration that valproate has an effect on AP perception, potentially by reactivating critical period learning through *HDAC* inhibition. It is noteworthy, however, that no significant correlation between AP performance and valproate levels in the blood was observed.

2.4.2 Music production

This section will describe the genetic findings of various music production abilities such as singing accuracy and music creativity (music improvising, arranging and composing), as well as other traits related to music production such as music flow, music practice, and singing participation.

2.4.2.1 Music performance

The Finnish research group behind numerous molecular genetics studies on music (Kanduri, Raijas, et al., 2015; Oikkonen et al., 2014; Pulli et al., 2008; Ukkola-Vuoti et al., 2013; Ukkola-Vuoti et al., 2011; Ukkola et al., 2009) recently investigated the effect of performing music on the human transcriptome in 10 musicians by conducting genome-wide transcriptional profiling (Kanduri, Kuusi, et al., 2015). Peripheral blood samples from 10 professional musicians before and after a 2-hour concert performance and 10 musician controls before and after a 2-hour session without music exposure were analysed and compared. Similar to their transcriptome study on music listening (Kanduri, Raijas, et al., 2015), music performance was observed to upregulate several genes involved in dopaminergic neurotransmission, one of which was *SNCA* (*alpha-synuclein*), a gene on chromosome 4q22.1 previously identified as a strong candidate for music perception ability (Oikkonen & Järvelä, 2014; Pulli et al., 2008), listening to classical music (Kanduri, Raijas, et al., 2015), and a possible early biomarker for Parkinson's disease (Scherzer et al., 2008). In addition, other motor behavior-related genes including *CCR4* and *FOS* were also upregulated, which may potentially shed light on the molecular mechanisms for executing music-related fine motor skills. Other upregulated genes included those implicated in learning and memory (e.g., *FOS*, *HDC*, *CLN8*, *DOPEY2*), and biological processes crucial for neuronal survival and neuroprotection such as calcium ion and iron ion homeostases (e.g., *SNCA*, *FOS*, *CLN8*).

It is noteworthy that this study also found some genes known to be involved in song perception and production in songbirds (e.g., *SNCA*, *FOS*, *DUSP1*) upregulated in music performance, suggesting possible evolutionary conservation in sound perception or production molecular mechanisms. In addition, several of the upregulated genes such as *SNCA*, *FOS*, *CLN8* and *DOPEY2* have been implicated in neuropsychiatric or neurodegenerative disorders (Byun et al., 2013; Scherzer et al., 2008; Smith et al., 1997; Vantaggiato et al., 2009). The researchers therefore conjectured that modulation of these genes by music performance may serve to explain music's therapeutic effects (Conrad, 2010).

2.4.2.2 Music practice

While music practice is often construed as an environmental variable (see **Section 3.4.2**, p. 72), two recent studies have demonstrated that music practice itself not only has a genetic basis, but its association with music ability is also mediated by shared genetic influences. The aforementioned Swedish twin study by Ullén et al. (2014) which investigated music perception using the Swedish Musical Discrimination Test (SMDT) also collected data on hours of music practice, yielding a sum-score estimate of total hours of music practice accumulated by each participant (Mosing, Madison, et al., 2014). Participants who did not have music training were thus given a score of 0. There was a significant sex difference on hours of music practice, with males accumulating more hours of practice than females. Univariate genetic analyses were thus performed separately for male and female twins, yielding considerable heritability estimates of 69% and 21% for males and females, respectively. Bivariate genetic modelling was conducted between music practice and each of the measures of music ability to determine the relative genetic and environmental contributions to the correlation between music practice and music ability. Model-fitting results revealed significant genetic correlations between music practice and all measures of music ability in both males and females (i.e., pitch, melody and rhythm discrimination), except for pitch discrimination ability in female twins. On the other hand, common environmental influences were significant in explaining the associations between music practice and melody discrimination in males, as well as pitch discrimination in both males and females. Unique environmental influences were not essential in explaining the correlation between music practice and any of the music ability measures. Taken together, the findings suggest that the relationship between music practice and musical auditory discrimination was mainly explained by shared genetic influences and (for pitch and melody discrimination) some shared common environmental influences.

Hambrick and Tucker-Drob (2014) also found evidence for gene-environment correlation and interaction between music practice and music accomplishment. Using data from over 800 twins from the National Merit Twin Study in 1962, music practice was constructed as a trichotomous variable: frequently, occasionally or none at all. Univariate genetic analysis revealed a moderate heritability estimate of 38%. Bivariate model-fitting results indicated that the percentages of shared genetic, common

environmental and unique environmental influences between music practice and music accomplishment were 23%, 69% and 25%, respectively, which suggests that music practice and music accomplishment shared a high proportion of common environmental influences and modest amounts of genetic and unique environmental influences. In addition, a gene-environment interaction between music practice and music accomplishment was observed, which suggests the importance of music practice in the expression of genetic influences on music accomplishment (see **Section 2.4.3**, p. 58).

Collectively, these two studies challenge many of the beliefs held by proponents of deliberate practice. First, there is a genetic basis for music practice, with heritability estimates ranging from 21% to 69%. This indicates that regarding music practice as a pure environmental variable is untenable. Second, gene-environment correlations were observed between music practice and music ability or accomplishment. While Mosing, Madison, et al.'s findings (2014) indicate that the association between music practice and music perception was largely genetically mediated, music practice and music accomplishment only shared a small proportion of genetic influences in Hambrick & Tucker-Drob's study (2014). This is likely due to the different ways in which music ability and accomplishment were defined in the two studies. Music accomplishment appeared to be more closely related to music production ability as it included items such as receiving music prizes or engaging in public music performance. The large proportion of unique genetic influences on music accomplishment not shared with music practice could potentially be explained by other genetically influenced factors such as music aptitude and motor abilities (Hambrick & Tucker-Drob, 2014). Finally, the findings regarding gene-environment interaction on music practice and music accomplishment challenge the prevailing conception that genetic influences on music expertise will become attenuated with practice (Ericsson, 2006). The research evidence from Hambrick & Tucker-Drob (2014) suggests a contrasting view, whereby genetic effects on music accomplishment become magnified and more fully expressed when fostered by music practice.

2.4.2.3 Music flow

While technically not a music production ability, music-specific flow, defined as a pleasurable state of complete and effortless absorption in musical activity, is without

doubt closely associated with music-making. Music-specific flow and openness-to-experience are two important predictors of music practice (Butkovic, Ullén, & Mosing, 2015), and in the large Swedish twin study on music aptitude conducted by Ullén and his team, the researchers reported that genetic influences explained 40% and 55% of the variation in music flow and openness, respectively, with negligible common environmental influences (Butkovic et al., 2015). Moreover, multivariate genetic modelling reveal significant genetic (*A*) and unique environmental (*E*) correlations between music practice and music flow, as well as between music practice and openness. Specifically, approximately 76% of the correlation between music practice and music flow and 75% of the correlation between music practice and openness were explained by shared genetic influences. The association between openness and music flow was also mediated by shared genetic influences to a large extent (61%). The shared genetic influences observed among these variables suggest that genetic influences predisposing an individual to be more open also play a part in influencing one to experience more music flow and engage in more music practice. While association does not necessary imply causation, it is plausible that higher openness encourages one to seek out new musical experiences, and the pleasurable state of flow one experiences during music-making may serve as an intrinsic motivation for more music practice (Butkovic et al., 2015).

2.4.2.4 Music creativity

Although a study has previously shown that music-accompanied creative dance performance was associated with *SLC6A4* and *AVPR1A* (Bachner-Melman et al., 2005), the genetic basis of music creativity was first investigated in 19 Finnish musical families using a web-based questionnaire by Järvelä's team (Ukkola et al., 2009). Participants were asked about their music background and participation in creative music activities, such as music composition, improvisation or arrangement. The findings indicated that creative functions in music may have a strong genetic component in this sample population, with a heritability estimate of .84. A significant positive association between music creativity and high music perception test scores was also observed. However, no significant associations between music creativity and the polymorphisms of candidate genes such as *TPH1*, *COMT* and *AVPR1A* were found.

Ukkola-Vuoti et al. (2013) performed a subsequent CNV analysis on five multigenerational Finnish families and 172 unrelated individuals using the same music creativity questionnaire. A “creative phenotype” was characterised by engagement in one or more creative music activities (composing, improvising or music arranging). Results showed that a deletion on 5p15.33 was present in 48% of family members and 28% of unrelated participants who exhibited the creative phenotype, while a duplication on 2p22.1 was present in 27% of creative family members in two families. The region 2p22.1 contains the gene *GALM*, which is associated with serotonin transporter binding potential in the human thalamus (Liu et al., 2011). The medial geniculate nucleus of the thalamus forms part of the auditory pathways, and more generally has been implicated in music-related functions such as beat perception (McAuley, Henry, & Tkach, 2012), sensorimotor synchronisation (Krause, Schnitzler, & Pollok, 2010) and musical imagery (Goycoolea et al., 2007). Other studies have found a link between the serotonin transporter gene (*SLC6A4*) and music-related functions such as choir participation (Morley et al., 2012) and creative dance (Bachner-Melman et al., 2005).

On the other hand, deletions in three CNV regions (2p12, 3p14.1 and 3q28) occurred quite commonly in individuals from two or more families without the creative phenotype, with frequencies ranging from 19% to 31%. The authors acknowledged the preliminary nature of their findings, highlighting their use of uncorrected multiple comparisons. Replication of the findings is clearly warranted, including the potential use of objective measures of music creativity in future research.

The same Finnish research group recently performed genome-wide linkage analysis on a large Finnish sample consisting of 474 participants from 79 families and 103 unrelated individuals to investigate the engagement in three forms of music creativity (composing, arranging and improvising) using a more detailed questionnaire (Oikkonen et al., 2016). The heritabilities for the various phenotypes estimated from the family data are moderate in general (composing: 33.3%; arranging: 33.4%; non-musically creative: 28.9%), with the exception of improvising which has a low heritability estimate of 11.6%. The researchers suggested that the much lower heritability estimates for music creativity as compared to that from Ukkola et al. (2009) were likely to be more robust estimates, as these were estimated using a much larger sample with more carefully delineated musically creative phenotypes. The phenotypes with moderate

heritabilities were then selected for genome-wide linkage analysis. For arranging, suggestive linkage evidence was observed at 16p12.1-q12.1 (LOD = 2.75), which is near the previously identified chromosomal region for music perception (Oikkonen et al., 2014). The best linkage evidence in the region was obtained at 16p12.1 (LOD = 4.22), in the intron⁶ of the *GSG1L* gene, which is implicated in fast synaptic transmission in the central nervous system (Shanks et al., 2012). Suggestive linkage evidence at 4q22.1 was found for composing (LOD = 2.15), which overlaps with the previously identified loci (4q22-23) for music perception ability (Oikkonen et al., 2014; Pulli et al., 2008) and is in the vicinity of the implicated locus (4q26) for vocal pitch-matching accuracy (Park et al., 2012). Furthermore, two recent human transcriptome studies have reported that the *SNCA* gene at 4q22 was observed to be one of the most up-regulated genes after music listening and music performance (Kanduri, Kuusi, et al., 2015; Kanduri, Raijas, et al., 2015). These findings therefore add credence to the chromosome 4 region being a candidate region for various music-related traits and suggests a common genetic background for these traits. Functional analysis of putative genes in the implicated chromosomal region for composing indicated an overrepresentation of the cerebellar long-term depression (LTD) pathway: 17 out of the 141 known genes involved in the LTD pathway were found in the analysis for genes suggestively associated with composing. Notably, the LTD pathway is purportedly a cellular model for synaptic plasticity and memory (Collingridge, Peineau, Howland, & Wang, 2010), which may be favourable cognitive attributes for music composing. Interestingly, the LTD pathway also comprises AMPA receptors (*AMPA*), including the aforementioned *GSG1L* gene suggestively associated with arranging. The results therefore imply that individual differences in genes affecting the LTD pathway may potentially influence music creativity.

Interestingly, there was significant linkage evidence for a non-musically creative phenotype (musically trained individuals who do not engage in music composing or arranging activities) at 18q21 (LOD 3.09). The best linkage evidence in the region is in the vicinity of the *CDH7* (Cadherin 7, Type 2) and *CDH19* (Cadherin 19, Type 2) genes from the cadherin family, which has been linked to neuropsychiatric conditions such as schizophrenia (Redies, Hertel, & Hübner, 2012). *CDH7* is also implicated in the vocal

⁶ A segment of the DNA that does not code for proteins.

development of songbirds (Matsunaga & Okanoya, 2008). The significant linkage region at 18q21 has also been associated with the 18q deletion syndrome which may cause hearing loss and intellectual disability and is adjacent to a previously identified loci (18q23-21.1) for music perception ability (Oikkonen et al., 2014).

One limitation of the study by Oikkonen et al. (2016) is that the creative phenotypes used in this study were not defined quantitatively by objective testing nor were they indicative of actual creative ability. Therefore, there is a possibility that these phenotypes may reflect a willingness or motivation to engage in music creativity rather than the actual ability itself.

2.4.2.5 Singing participation

Coon and Carey (1989) analysed the music ability of 11th grade twins by extracting music-related questionnaire data from an earlier study (Loehlin & Nichols, 1976). For participation in singing activities, the heritability estimates were reported as 71% for males and 20% for females, while the corresponding shared environment estimates were 8% and 59% respectively. The significant gender difference in the estimates indicates that a shared environment exerted a stronger effect on females than males, while heritability was much higher in males than females. The researchers suggested this may be due to a stereotypical perception that singing is a feminine activity and therefore, males might require greater interest and intrinsic ability to take part in such activities. As this study relied on self-reported data and did not objectively assess the singing ability of the twin pairs, more investigation is warranted to ascertain the genetic contribution to singing ability.

Similar to the association study on music memory by Granot et al. (2007), a candidate gene association study by Morley et al. (2012) tested the relationship between choir membership and allelic variants of the genes *AVPR1A* and *SLC6A4*. An overall association with choral singer status was observed at the STin2 (intron 2) polymorphism in the *SLC6A4* gene, with the STin2 9-repeat and 12-repeat alleles⁷ being more common in choral singers, and the 10-repeat alleles more common in non-musically active

⁷ Allelic variants that differ by the number of repeat units, resulting in alleles of different lengths.

controls. No significant differences in allele frequencies were observed between the two groups for other *SLC6A4* and *AVPR1A* polymorphisms. Previous studies have reported possible involvement of *STIN2* in personality traits and reward behaviour (Kazantseva et al., 2008; Saiz et al., 2010; Zhong et al., 2009). *SLC6A4* polymorphisms (together with *AVPR1A*) have also been linked to participation in creative dance (Bachner-Melman et al., 2005). As several studies have observed associations between *AVPR1A* polymorphisms and certain music traits (Granot et al., 2007; Ukkola-Vuoti et al., 2011; Ukkola et al., 2009), the non-significant *AVPR1A* association in this study led the authors to speculate that the observed *STIN2* effect may predispose social behavioural characteristics (i.e.. a “predisposed to group activity” phenotype) rather than music ability *per se*.

2.4.2.6 Singing accuracy

Across all cultures humans have a propensity to sing. From two months onwards, infants begin to produce “musical babbling” containing definite music features such as pitch and rhythmic patterns (Welch, 2006). Most children begin imitating songs at approximately age two, by age four they can sing complete songs, and by age 5 most of them can accurately reproduce entire songs (McPherson & Williamon, 2006; Parncutt, 2006).

Although it is likely that variability in children’s singing competency is, in part, attributable to environmental factors, such as early music exposure and training, a behavioural study has suggested there may also be an inborn aspect to singing accuracy. Watts et al. (2003) identified individuals who received no professional vocal training yet were described by professional voice teachers as “exhibiting expressed singing talent”. These individuals showed consistently superior performance on pitch-matching tasks, especially in the absence of external auditory feedback, even when compared with trained singers who had at least three years of professional vocal training.

Park et al. (2012) investigated the genetic factors underpinning singing ability by conducting family-based linkage and association analyses on 1,008 participants from 73 extended Mongolian families. They administered a pitch production accuracy test and found that 357 of the participants (35.4%) were accurate pitch-matchers, reliably

singing the target pitches with deviations of less than one semitone. Using pedigree data, the heritability of singing accuracy was reported as 40%. A genome-wide linkage analysis was then conducted, with the most significant linkage peak observed on 4q23 (LOD = 3.1 at marker D4S2986). The findings overlap with regions on chromosome 4q, where there is linkage evidence for music perception ability (Oikkonen et al., 2014; Pulli et al., 2008). A family-based association analysis performed at the 4q23 linkage peak using 53 of the families revealed that SNP rs12510781 was most significantly associated with singing accuracy. This is an intergenic SNP near the gene *UGT8*, whose encoded protein is highly expressed in the brain, especially the substantia nigra (see online supplementary Figure S2 of Park et al., 2012). *UDP* glycosyltransferase 8 catalyses the transfer of galactose to ceramide, an essential step in the biosynthesis of galactocerebrosides, which are implicated in myelin sheath formation. The researchers also utilised exome sequencing to find other potential candidate SNPs and discovered a non-synonymous SNP (rs4148254) in *UGT8* on 4q26 that was significantly associated with singing accuracy. In addition, CNV analysis using an array comparative genomic hybridisation (aCGH) platform showed that a copy number loss at 5.6kb (5,600 base pairs) upstream of *UGT8* may be negatively associated with singing accuracy. Although environmental factors such as education and music training were not considered in this study, the researchers argued that because the participants resided in an isolated region with homogeneous culture and most were educated in the same school without additional music training, environmental factors were unlikely to impact greatly on the results. In other words, this study yields evidence that singing accuracy may be heritable in this population and possibly associated with the gene *UGT8* on chromosome 4q.

2.4.2.7 Rhythm production

So far, no genetic studies have focused specifically on rhythm production ability. A study investigating speech and language disorder in a family pedigree showed that the affected family members were impaired in rhythm perception and production (Alcock et al., 2000), and all of them had a mutated copy of the *FOXP2* gene (Lai et al., 2001)

2.4.3 Music accomplishments

In addition to examining participation in singing activities in 11th grade twins, Coon and Carey (1989) used the music-related questionnaire data from Loehlin and Nichols (1976) to investigate other aspects of self-reported music ability, including vocational interest in music, instrumental music experience, professional music engagement, and receiving music prizes. Their results showed that while there were significant genetic influences across all the variables excluding music vocational interest, the effects of a shared environment were almost always larger across all the variables, with the exception of singing participation (see **Section 2.4.2.5**, p. 55) and professional music engagement in male twins. Apart from the extremely high heritability ($A = 71\%$) of singing participation for male twins, the other heritability estimates typically ranged from 10% to 38%, whereas shared environmental estimates were between 18% to 76% (see **Table 2.2**, p. 28 for details).

Genetic analyses performed separately on twins concordant for private music lessons and concordant for no music lessons revealed interesting gene-environment interaction effects. Excluding music vocational interest for male twins, relatively higher heritability estimates were observed for the other four variables for both male and female twins without formal music training ($A = 29-116\%$)⁸ compared to twins with music training ($A = -21-57\%$). In particular, significant group differences in genetic and common environmental influences were observed for out-of-school music performance experience, whereby twins without music training had large heritability estimates and low estimates for common environmental influences while twins with music training showed the opposite trend. Based on the results, the researchers proposed a strong shared environmental component in music ability which is augmented by formal music training.

A recent twin study also used the same twin data to investigate the genetic and environmental contributions of music accomplishment. Hambrick & Tucker-Drob (2014) constructed a dichotomous music accomplishment variable from the National Merit Twin Study data (Loehlin & Nichols, 1976), based on the endorsement of one or

⁸ The differences between MZ and DZ correlations of twin pairs concordant for music lessons or no music lessons for some variables were too great, which resulted in A estimates that exceeded 100% and C estimates that were less than 0%.

more questionnaire items pertaining to music prizes received or out-of-school music performance experience. Similar to the findings from Coon and Carey (1989), although the heritability estimate was significant, the common environmental component was considerably larger ($A = 26\%$; $C = 61\%$, $E = 12\%$). Intriguingly, a gene-environment interaction effect was observed, where the heritability estimate for music accomplishment was substantially higher for twins who practised occasionally or frequently ($A = 43\%$) than for twins who did not engage in music practice at all ($A = 1\%$), whereas the common environmental component was much lower for twins who practised ($C = 43\%$) than for twins who did not practice ($C = 86\%$). This led the researchers to infer that music practice helps to express the genetic potential for music accomplishment. Although the findings contradict the somewhat related gene-environment interaction effect found between music ability and music training from Coon and Carey (1989), it is worth noting that Hambrick and Tucker-Drob (2014) still obtained similar results when they performed genetic modelling solely on twins with formal music training, which indicated that the interaction effect is indeed between music accomplishment and music practice, not music training *per se*.

Interestingly, higher heritability estimates for music ability were obtained in a more recent Netherlands twin study involving 1,685 twin pairs aged 12 to 24 years (Vinkhuyzen et al., 2009). Using a self-report questionnaire, this study examined the heritability of domain-specific aptitude (defined as ability within the normal range) and exceptional talent. In particular, the participants were asked to rate their level of competence in various domains such as music, arts, language and sports. For self-reported music aptitude, the heritability estimates for males and females were 66% and 30% and the estimates for common environmental influences were 8% and 54%, respectively. As for self-reported exceptional music talent, the heritability estimate was 92% with no shared environment effect. The researchers concluded that genetic influences possibly account for a large extent of the variation in aptitude and exceptional talent across domains, including intellect, creativity, and sporting ability. As the above twin studies were based on self-reports of music ability, it is uncertain whether self-reported music ability truly reflected actual music ability, thus raising concerns about the reliability of the findings.

2.4.4 Music culture

Similar to music practice, music culture is usually conceived as an environmental factor influencing music ability (see **Section 3.2**, p. 65). Intriguingly, a relationship between music culture and genes has been demonstrated in several recent studies. In one study, traditional songs from 39 African cultures were classified by their music characteristics such as yodeling and tempo. When the music styles of the various African cultures were compared with a database of African genotypes, a correlation between genes and music culture was found, which suggests that cultures that are musically similar also exhibit greater genetic similarity. Notably, the researchers also discovered that the correlation between music culture and geographical distance was weaker than the correlation between music culture and genes (Callaway, 2007).

Similarly, in the first comparative phylogenetic study of genetics and folk music, Pamjav, Juhász, Zalán, Németh, and Damdin (2012) established a relationship between folk music styles in 31 Eurasian cultures and genetic distance, with maternal lineages more strongly linked with folk music traditions than paternal lineages. Specifically, it was found that significantly similar folk music cultures could predict significant genetic connections in 82% of the cases examined. Interestingly, the reverse was not true; close genetic connections were only able to predict similar folk music styles in 28% of the cases. The researchers speculated that a close genetic relation between two populations is indicative of prior physical and biological contact between ancestors of both populations, which may have in turn brought about an interaction and transmission of musical cultures between the two groups, resulting in the similar folk music styles. The study also identified a common musical style that was prevalent in a large subset of the cultures studied, most of which were closely related genetically. This led the researchers to posit the potential existence of a common musical “parent language” from which various folk music traditions branched out and evolved.

Brown et al. (2014) also demonstrated a statistically significant correlation between folk song structure and mitochondrial DNA variation in nine indigenous Taiwanese populations, even after controlling for geographical proximity. Notably, although a significant correlation between language and genes in the populations studied was also found, the correlation became insignificant after controlling for geographical proximity.

In addition, the correlation between music and language was insignificant, which indicates that the genetic components of music and language may be partially distinct. In particular, an examination of the population structure for genes, music and language for the nine indigenous populations revealed greater similarities in the population structures between music and genes as compared to language and genes. Taken together, the findings suggest the possibility of the coevolution of music and genes and promote the use of music as a novel cultural marker for the study of population migration history, which can serve to complement more extensively researched markers such as language.

Collectively, convergent findings from diverse cultural samples give credence to a link between music culture and genes. This is particularly noteworthy since music cultural environment is a well-established environmental factor influencing music ability. The observed relationship between genes and music culture therefore highlights the importance of underlying genetic influences in shaping the music environment of a human culture.

2.5 Summary

In this chapter, the genetic correlates of different aspects of music ability and music-related phenotypes were examined. A schematic representation of the genetic determinants of music ability reviewed is presented in **Figure 2.4**.

Several twin studies and family pedigree studies have estimated the heritabilities for various music-related phenotypes, and demonstrated sizeable heritabilities particularly for pitch and melodic perception, music creativity, singing accuracy and self-reported music accomplishments (see **Table 2.2**, p. 28).

In addition, a few recent twin studies have demonstrated that the association between music ability and certain correlates are mediated by significant shared genetic influences, such as between music ability and intelligence (Mosing, Pedersen, Madison, & Ullén, 2014), music ability and music practice (Hambrick & Tucker-Drob, 2014; Mosing, Madison, et al., 2014), music practice and openness, and music practice and

music flow proneness (Butkovic et al., 2015). This suggests the possibility that the same set or sets of genes are exerting influence on music ability and factors that contribute to music ability.

To date, some promising and converging findings have begun to emerge. Several loci on chromosome 8q have been implicated in more than one music-related phenotype. For instance, loci 8q21 and 8q24 have been implicated in absolute pitch ability and music perception (Pulli et al., 2008; Theusch et al., 2009; Ukkola-Vuoti et al., 2013).

Similarly, loci on chromosome 4 have been implicated in music perception and music composing (Oikkonen et al., 2014; Oikkonen et al., 2016; Pulli et al., 2008), while the neighbouring locus 4q23 has been implicated in pitch accuracy of singing (Park et al., 2012).

A number of genes have featured quite prominently in music genetics research thus far. In recent transcriptome studies, *SNCA* on chromosome 4q22.1 has emerged as a potential candidate gene for music listening and music performance in musically experienced individuals (Kanduri, Kuusi, et al., 2015; Kanduri, Raijas, et al., 2015). These findings are particularly noteworthy given that the locus 4q22 and nearby 4q23 are also implicated in music perception, music composing and vocal pitch-matching ability (Oikkonen et al., 2014; Oikkonen et al., 2016; Park et al., 2012; Pulli et al., 2008). Given the role of *SNCA* in dopamine-related functions and music's association with dopamine release, as well as *SNCA*'s implication in song perception, learning and production in songbirds, it appears that *SNCA* is a strong contender for influencing music behaviour. Moreover, the putative links between *SNCA* and other songbird-related genes (e.g., *GRIN2B*, *FOXP1*, *VLDLR*, *RGS9*, *FOS*) and various music traits indicate the possibility of cross-species evolutionary conservation for auditory perception and vocal production (Kanduri, Kuusi, et al., 2015; Kanduri, Raijas, et al., 2015; Liu et al., 2016; Oikkonen et al., 2016).

Apart from *SNCA*, the gene *AVPR1A* on chromosome 12q has been implicated in music listening (Ukkola-Vuoti et al., 2011), music perception (Ukkola et al., 2009), and music memory (Granot et al., 2007; Granot, Israel-Kolatt, et al., 2013). On the other hand, the gene *SLC6A4* has been associated with music memory (Granot et al., 2007) and choir

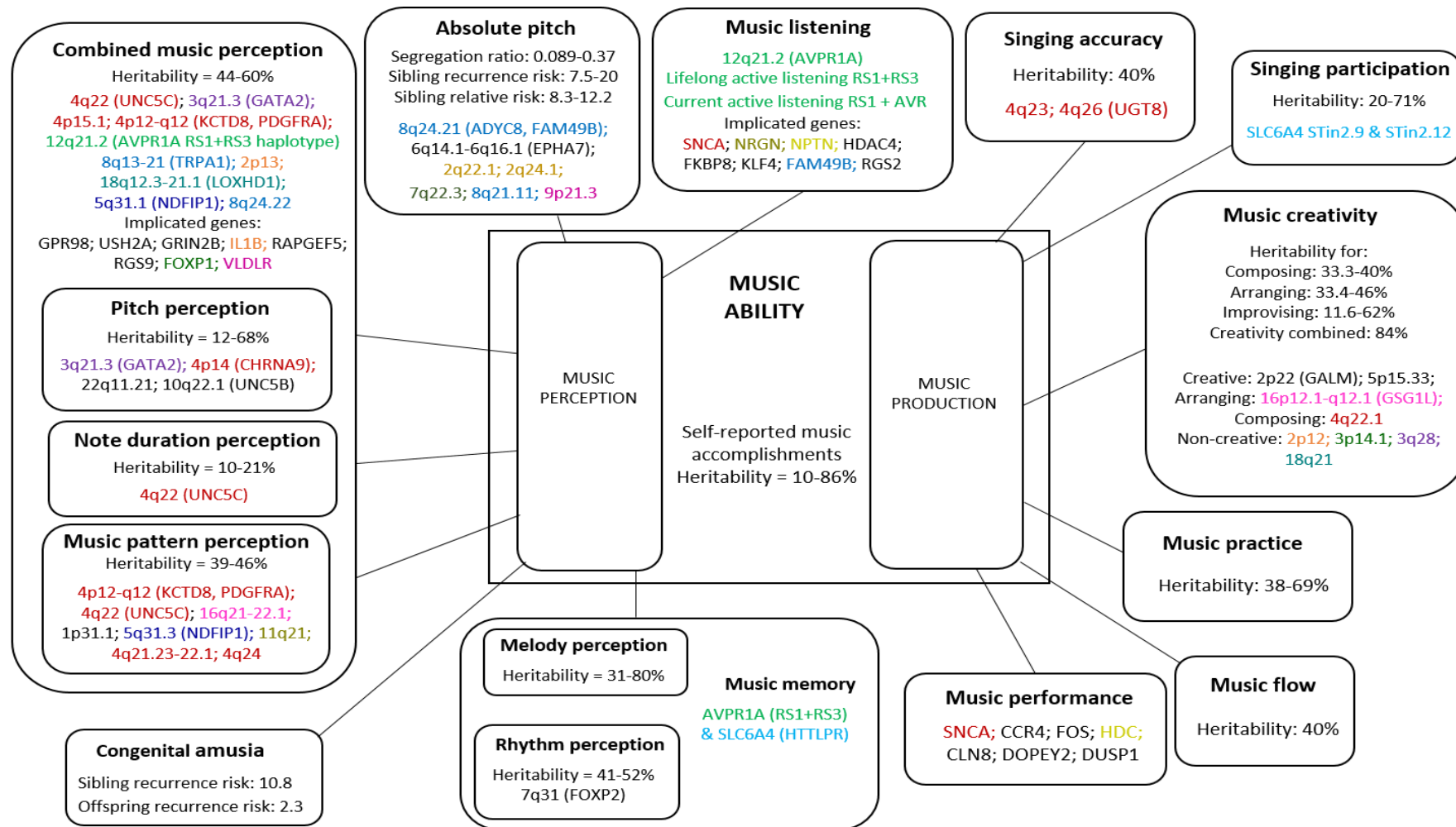


Figure 2.4. A schematic representation of the genetic determinants influencing music ability and music-related traits. Genes or loci that are in the vicinity of one another are represented in the same font colours.

participation (Morley et al., 2012). The role of *AVPR1A* in social cognition and behaviour has been well-investigated, as has the possible interaction between *AVPR1A* and *SLC6A4* in communicative behaviour. The associations of these two genes with various music functions raises the intriguing possibility of an overlap in the neurobiological basis of music functions and social behaviour.

Finally, it is interesting to note that recent studies have found evidence of genetic influences for variables such as music practice and music culture, which have until now been commonly regarded as environmental factors. Given the pervasive influence of genetic factors on a vast array of human traits (Polderman et al., 2015), however, it is not surprising to observe a growing body of genetic evidence for music ability and music-related traits.

The exciting developments and emerging evidence in music genetics research thus make the stance of radical environmentalism increasingly implausible. It is understandable that some may be uncomfortable with the notion of music ability being influenced by genes, as they are concerned with ethical implications that may potentially arise if genetic makeup is used as a basis to reserve music learning resources for a select few and exclude the less endowed from having the opportunity to learn music. It should be recognised, however, that both biological determinism and radical environmentalism are problematic, and that a complete account of music ability and the development of expertise requires both genetic and environmental factors and their interaction to be considered.

3

ENVIRONMENTAL DETERMINANTS OF MUSIC ABILITY

3.1 Definition

According to Gembris and Davidson (2002), environmental factors that influence the development of music ability can be broadly understood as “the sum of all external conditions that bear on musical experiences and activities”. They can also be more narrowly defined as “the regularly recurring situations that impact on musical experience and activities” (p. 18).

In this chapter, the environmental factors that have been documented to affect the development of music ability are organised and discussed in terms of three main environmental contexts: the cultural environment, the home environment, and the formal music learning environment. Finally, the genetic and environmental determinants discussed in both Chapter 2 and the current chapter will be summarised and schematically represented in **Section 3.5** (p. 81).

3.2 The Cultural Environment

Our cultural environment plays a crucial role in influencing the ways we interact with music and how our soundscape is shaped (Bond, 2011; Hannon & Trainor, 2007). Such cultural influences commence spontaneously and subconsciously: infants begin to perceive pitch and meter in a culture-specific manner from approximately one year of age onwards (Trehub, 2006), and the basic music competency necessary for music engagement in one’s culture is typically developed within the first 10 years of life

(Gembris, 2006). Interestingly, while musical enculturation enhances culture-specific melodic perception ability with age, it also brings about a relative decrease in sensitivity for non-culture-specific tonal music structure (Lynch & Eilers, 1991; Morrongiello, 1992).

Depending on the sociocultural norms, the definition of music ability, the methods of music learning, and the forms of musical participation all vary from one culture to another. In the next few paragraphs, some examples highlighting the importance of musical enculturation are described. For a more comprehensive survey of how music learning and development vary across countries due to differences in culture and education system, please refer to Hargreaves and North (2002).

Both cultural environment and home environment are important breeding grounds for music ability to develop through informal learning contexts. A musically rich sociocultural environment may result in earlier development of music abilities as compared to another culture where music assumes a lesser social function (Kelley & Sutton-Smith, 1987). This is particularly evident in some non-Western cultures such as the African culture, where music is part and parcel of everyday life, seamlessly incorporated into various work, social, religious and familial settings (Primos, 2002).

The notion of learning music formally in a classroom situation is foreign to many Africans. The inseparability of music and dance in the African culture means that musical activities are informally learned through exposure and active participation, through oral transmission and memorisation. Notably, memorisation in this case does not suggest rote learning, but rather the framework for past musical materials is memorised in order to provide fodder for future improvisation, recreation and variation. Musical creativity is therefore an important element in the African music culture, where children are encouraged and expected to develop musical creativity from a young age for their personal and social development, such as by making up songs during singing games. As a result of this pervasive music enculturation, widespread musical achievements can be readily observed in various African cultures. For instance, while many people from the Western general population provide low ratings of their singing ability (Cuddy et al., 2005; Pfordresher & Brown, 2007), Zimbabwean children and Anang children from Nigeria display precocious singing ability (Koops, 2011; Kreutzer,

2001; Messinger, 1958). Likewise, Gambian and Venda children from Africa are also "expected to be musical" because in their musically-enriched cultural environment, there are frequent opportunities for music participation (Blacking, 1995; Koops, 2011; Radocy & Boyle, 2012). Interestingly, while African children are expected to learn to sing and dance without exception, it was noted that they acquire these skills at different rates (Primos, 2002, p. 438).

South America is also blessed with a rich multicultural musical heritage (Oliveira, 2002). It is the cradle of various distinct South American musical forms such as *bossa nova* and *tropicália*. These popular and folk musical traditions are indispensable in the daily lives of the majority of the South Americans, who acquire and promulgate these musical traditions through informal social contexts, such as in games, bars and nightclubs, or families, rather than through formal music instruction.

In Portugal, members of local communities can learn how to read and perform music through participation in *Bandas filarmónicas*, which are local amateur bands (Brucher, 2013). Regardless of one's age or skill level, *Bandas* provide the locals with opportunities to play music together and perform publicly at local sacred and secular events, thereby playing an important role in fostering community music-making and transmitting Portuguese musical traditions across generations (Brucher, 2013; Mota, 2002).

Given the extensive evidence that the development of musical expertise can be influenced by one's exposure to culture-specific musical activities and forms, music education researchers therefore recommend the provision of culturally-relevant music listening and music making experiences to young children as a strategy to cultivate and shape their understanding of music (Bartel & Cameron, 2007).

On a different note, several studies have observed that cultures in which tonal languages are spoken may have a singing advantage over their Western counterparts. Chinese first-graders were reported to have better singing abilities than age-matched American children. Likewise, American preschool children who speak both Cantonese and English were observed to have superior vocal pitch-matching ability than children who speak only English (Trollinger, 2004). It may be possible that the better singing

accuracy of the tonal language speakers in these studies was facilitated by increased pitch experiences (Tsang, Friendly, & Trainor, 2011). Other researchers have also observed a higher incidence of absolute pitch among tonal language speakers (Deutsch, Dooley, Henthorn, & Head, 2009; Deutsch, Henthorn, Marvin, & Xu, 2006). It is also possible, however, that the enhanced vocal pitch-matching and pitch perception abilities were due to ethnicity effects, thereby indicating genetic influences (Gregersen et al., 2001; Hove, Sutherland, & Krumhansl, 2010; Theusch et al., 2009).

3.3 The Home Environment

As the level of musical ability ultimately attained is associated with the quality and extent of musical exposure (Trehub, 2006), it is not surprising that both anecdotal experiences and empirical evidence have supported the important role played by family environment in musical development, especially from infancy to childhood (Gembris & Davidson, 2002).

A considerable body of evidence from infant research has suggested that humans demonstrate musical predispositions and propensities from a young age, even at the prenatal stage (Trainor, Tsang, & Cheung, 2002; Trehub, 2001; Trehub, 2006; Winkler, Háden, Ladinig, Sziller, & Honing, 2009; Zentner & Kagan, 1996). From approximately seventh month in utero, the inner ear of a human foetus begins to function, marking the onset of auditory learning and memory (Gembris, 2006). The capacity for music perception at the prenatal stage is apparent from studies showing that the foetus can feel rhythms and hear melodic inflections in speech and music (Moon & Fifer, 2000). There is also evidence that neonates can remember melodies heard prenatally (Hepper, 1991; Satt, 1984) and develop long-term neural representations of these melodies (Partanen, Kujala, Tervaniemi, & Huotilainen, 2013).

Informal music learning in a home setting is especially important for infants at the preverbal stage. By using nonverbal interaction in a quasi-musical manner (e.g., *motherese* at elevated pitch levels), parents are their infants' first music mentors through intuitive musical parenting (Noy, 1968; Papoušek & Papoušek, 1995; M. Papoušek, 1996). In such infant-directed communication, musical content such as pitch, melody,

rhythm and dynamics are introduced incidentally to infants, and serve to nurture their basic musical competency. Tafuri and Villa (2002) observed a positive correlation between the frequency of maternal singing and the frequency and quality of infant musical babbling. The parent-child emotional connection in such intuitive musical parenting is also likely to have a positive influence on an infant's music learning process (Gembris & Davidson, 2002), given that the emotional aspect of a learning experience can help strengthen memory for knowledge acquired (Levitin, 2006).

Children often exhibit their inherently musical nature through spontaneous musical behaviours such as vocalisations and dance movements (Bond, 2012; Marsh & Young, 2006). Parents and caregivers need to be cognizant of these musical behaviours in the home environment and encourage their occurrence (Trehub, 2006). For instance, vocalisations usually emerge at 6 to 8 weeks of infancy (Papoušek & Papoušek, 1995). Parents can vocally imitate these vocalisations to positively reinforce such behaviour. By encouraging vocal play and allowing infants frequent opportunities for vocal exploration and imitation, singing ability can be nurtured in the home environment (Mang, 2003; Welch, 2005; Young, 2002). Singing practice or experience has been found to increase the number of distinct tones children can sing by 30%, as well as accelerate the age onset for vocal pitch-matching (Jersild & Bienstock, 1931; Levinowitz, 1989a; Phillips, 1992).

Parents can also actively create a musically rich family environment to foster music development in children. One way of achieving this is through participation in musical activities as a family, such as singing and playing instruments together, attending concerts and discussing music (Gembris & Davidson, 2002). Parent-initiated musical behaviours were observed to be significantly correlated with the early onset of singing in children (Howe, Davidson, Moore, & Sloboda, 1995). Custodero (2006) also observed that children who were regularly involved in music-making with their parents developed a huge song repertoire which they would use when engaging in singing activities by themselves. Several other behavioural studies have also reported moderately low to strong correlations between a musical family environment and the vocal achievement of young children (Aherne, 2011; Atterbury & Silcox, 1993; Kirkpatrick, 1962; McPherson & Williamon, 2006; Persellin, 2006; Shelton, 1965).

Being brought up in a ‘musical family’ has also been demonstrated to have a positive effect on the music aptitude of preschool children. Mallett (2000) found that home musical environment positively correlated with preschool children’s music aptitude as measured by Audie (1989), a preschool appropriate music aptitude game devised by Edwin E. Gordon. Interestingly, no relationship was found between home musical environment and the music aptitude scores of school-aged children (Aherne, 2011; Atterbury & Silcox, 1993; Brand, 1985, 1986). It is possible that these findings suggest that home musical environment has a more significant impact on children’s early musical development before school begins, but its importance diminishes when other environments (e.g., classroom music environment, formal music learning environment) become more influential settings for music exposure and engagement. Despite this, parents can still exert positive influence on their children’s musical development by actively supporting formal music learning.

Several empirical studies found that parental involvement and interest in their child’s music learning is positively correlated with the latter’s musical achievement (Brand, 1986; Creech, 2010; but see Gagné, 1999; Sloboda & Howe, 1991). Such involvement includes monitoring music practices and touching base regularly with the music teacher. A biographical study of successful Polish classical musicians found that parental support of their music learning (e.g., in selecting the right music teachers and monitoring progress) strongly influenced these musicians’ decision to pursue classical music as a career (Gembris & Davidson, 2002). A series of studies conducted by Davidson, Sloboda, Howe and Moore in the 1990s also consistently found the parent-teacher relationship to be crucial for a child’s musical development (Davidson, Howe, Moore, & Sloboda, 1996, 1998; Davidson, Howe, & Sloboda, 1997; Davidson, Sloboda, & Howe, 1995/1996). The importance of parental support and involvement in positively influencing music learning outcomes appears to diminish as children get older, however. Davidson et al. (1995/1996) found that the high music achievers in their sample experienced consistent and strong parental support in their music learning until age 11, after which they became more self-motivated to practise music regularly. In contrast, the low music achievers and those who eventually quit reported weak parental support during their initial music learning and increasingly forceful parental pressure during adolescence. This finding therefore demonstrates the value of early and consistent parental support in encouraging formal music learning.

Interestingly, while parental support is important for musical development, parental music expertise is not essential for a child's music ability to flourish. Sloboda and Howe (1991) found that surprisingly, parents of students with average musical abilities have significantly greater music expertise and interest than the parents of exceptionally talented students. Similarly, in a study analysing the family environment of 20 of the most talented American concert pianists, Sosniak (1985) found that the parents of these pianists were no more musically active than a representative sample of the American general population. Sloboda and Davidson (1996) also identified support and encouragement from non-musician parents as one of the key determinants of music expertise.

3.4 The Formal Music Learning Environment

Some researchers have suggested that while basic musical competence can be developed naturally through informal learning in one's cultural and family environments up until puberty, formal or explicit music training is essential in order to attain amateur to professional levels of music ability (Lehmann, 1997).

The formal music learning environment supports the acquisition of procedural and declarative knowledge pertaining to music. The procedural knowledge includes the motor skills to play a musical instrument, the aural skills to process and analyse musical stimuli, and the visual skills to comprehend music notation, whereas declarative knowledge includes facts about music, such as the theory and history of music.

As the impartment of musical skills and knowledge is a key feature of the formal music learning environment, the instructional figure (i.e., the teacher), understandably plays a central role in this environment.

3.4.1 The role of music teacher

Music teachers not only help their students develop music abilities, but also serve as musical role models and shape their musical tastes as well as values and motivation

towards music (Gembris & Davidson, 2002). Music teachers who are friendly and skilled have been identified as one of the factors influencing musical expertise (Sloboda & Davidson, 1996). In particular, the first music teacher appears to be of special import in influencing subsequent musical achievement (Davidson et al., 1998). It was observed that children who are high-achieving musically have positive perceptions about their first teachers' musical skills and personality, whereas music learners with low achievements viewed their first teachers in the opposite manner (Davidson et al., 1995/1996). With increasing age and self-motivation, however, the high music achievers were observed to value the professional qualities of the teacher over personality. From these findings, one can infer that personable qualities of teachers may set a positive emotional climate that helps motivate younger children to learn music, especially in the initial learning stages (Gembris & Davidson, 2002). In addition, music teachers may help support music development by teaching students good music practising strategies, which is an important music-related skill (Lehmann, 1997).

While music teachers undoubtedly play an important role in the development of musical expertise, especially in the first stages of music learning, much of the research findings are in fact limited to the domain of classical music, and thus may not be generalisable to other musical domains. For example, it is observed that formal music instruction is not as important in jazz music, where much of a teacher's role is replaced by self-learning through listening and analysing the recordings of famous jazz musicians (Gruber, Degner, & Lehmann, 2004).

The next section will describe empirical findings relating to musical skills and abilities that are facilitated by formal music training, and demonstrate how such musical development is supported by physiological and neurological evidence.

3.4.2 Music training and music practice

In the pitch domain, several behavioural studies that compared musically-trained participants (referred to as musicians) and non-musically trained participants (referred to as non-musicians) report that musicians exhibit enhanced pitch discrimination ability for both pure and complex tone stimuli, as demonstrated by significantly smaller pitch discrimination thresholds or more accurate detection of fine pitch changes than non-

musicians (Bianchi, Santurette, Wendt, & Dau, 2016; Kishon-Rabin, Amir, Vexler, & Zaltz, 2001; Micheyl, Delhommeau, Perrot, & Oxenham, 2006; Spiegel & Watson, 1984; Tervaniemi, Just, Koelsch, Widmann, & Schröger, 2005). In particular, Kishon-Rabin et al. (2001) showed that pitch discrimination thresholds decrease (i.e., better pitch discrimination abilities) as a function of years of music training, and musicians with more than 15 years of music training exhibit less variance in their discrimination thresholds compared to musicians with fewer years of training. Schellenberg and Moreno (2010) also showed that musicians showed superior pitch processing ability in terms of pitch processing speed and pitch discrimination ability than non-musicians, although both groups were comparable in general intelligence (*g*). Interestingly, the enhanced pitch processing ability of musicians was only limited to tone stimuli that were within the typical pitch range for music, and not for extremely high pitches. This indicates that the superior pitch processing was a result of music training.

Given that instrumental music typically involves performing melodies and not isolated pitches, it is not surprising that other behavioural studies show that musicians demonstrated better interval and melodic contour processing. For example, Zarate, Ritson and Poeppel showed that musicians performed better than non-musicians in interval discrimination, even when discriminating between melodic intervals with altered timbres (Zarate, Ritson, & Poeppel, 2013) or starting pitches (Zarate, Ritson, & Poeppel, 2012). Musicians were also able to detect alterations in melodic contours (Morrongiello & Roes, 1990; Morrongiello, Roes, & Donnelly, 1989; Schön, Magne, & Besson, 2004), distinguish between different melodies (Orsmond & Miller, 1999), recognise melodic transposition (Cuddy & Cohen, 1976), key changes (Halpern, 1984) and imitate a novel tonal melody (Oura & Hatano, 1988) better than non-musicians. Moreover, music training was shown to positively impact on higher-order melodic processing ability, such as the understanding of tonal hierarchy (Cuddy & Cohen, 1976; Koelsch, Jentschke, Sammler, & Mietchen, 2007; Krumhansl & Shepard, 1979; Pechstedt, Kershner, & Kinsbourne, 1989).

Besides enhanced music processing ability, several studies have shown that instrumental music training plays a positive role in improving pitch accuracy in singing (Amir, Amir, & Kishon-Rabin, 2003; Dalla-Bella, Giguère, & Peretz, 2007; Moreti, 2006; Murry, 1990; Nikjeh et al., 2009; Watts, Murphy, & Barnes-Burroughs, 2003, but

see also Zarate, Delhommeau, Wood, & Zatorre, 2010). In particular, Nikjeh et al. (2009) reported that not only do musicians display superior pitch discrimination and pitch production abilities compared to non-musicians, the two abilities are significantly correlated only in instrumental musicians, suggesting the possibility that music training strengthens the association between pitch perception and vocal pitch production.

In the rhythm domain, a body of behavioural evidence indicates superior timing abilities of musicians compared to non-musicians across a broad range of tasks. In terms of perceptual timing abilities, musicians are more accurate than non-musicians in discriminating time interval durations (Rammsayer & Altenmüller, 2006), and detecting timing or tempo changes in music sequences (Jones et al., 1995; Jones & Yee, 1997; Lim et al., 2003; Rammsayer & Altenmüller, 2006; Yee et al., 1994; Drake & Botte, 1993; but see Manning, 2016). Musicians also perform better than non-musicians in motor timing tasks, demonstrating greater accuracy and lower variability in performance than non-musicians in isochronous tapping tasks (Aschersleben, 2002; Aschersleben & Prinz, 1995; Chen, Penhune, & Zatorre, 2008; Krause, Pollok, & Schnitzler, 2010; Repp, 2000, 2010; Repp & Doggett, 2007; Repp, London, & Keller, 2013), whereby tapping accuracy appears to improve with increased music training (Repp, 1999).

While music training is demonstrated to bring about a general enhancement in music processing and production skills, differential training-specific enhancements can be observed amongst musicians. For instance, professional conductors exhibit superior auditory spatial processing in peripheral auditory spaces than pianists, possibly because as a conductor, they often need to direct their attention to a particular musician or orchestral section while monitoring the entire orchestra at the same time (Nager, Kohlmetz, Altenmüller, Rodriguez-Fornells, & Münte, 2003). In addition, musicians who play by ear display superior melodic encoding ability over musicians who rely less on aural practising strategies (Seppänen, Brattico, & Tervaniemi, 2007; Tervaniemi, Rytkönen, Schröger, Ilmoniemi, & Näätänen, 2001). Furthermore, percussionists demonstrate superior timing perception and motor synchronisation abilities than other musicians (Cameron & Grahn, 2014; Ehrlé & Samson, 2005; Krause, Pollok, et al., 2010).

Music development due to formal music training is not only evident at a behavioural level. The development of musical skills are in fact accompanied by adaptive physiological, anatomical and neurological changes in musicians. For instance, brass musicians and singers were found to have increased lung capacity as a result of their music training (Sundberg, 1987; Tucker, Horvath, & Faulkner, 1971). Similarly, due to differences in the way they play their instruments, pianists and violinists were observed to exhibit significantly different forearm motions as characterised by supination and pronation, respectively (Wagner, 1988).

As the musicians' brain has been regarded as a useful model to study neuroplasticity (Habib & Besson, 2009; Zatorre, 2005), a considerable body of evidence has accrued documenting widespread experience-dependent structural and functional changes in the brain due to music training (please refer to Herholz & Zatorre, 2012; Merrett & Wilson, 2013 for recent comprehensive reviews on this subject). In addition, Merrett and Wilson (2013) examined at times discrepant neural evidence in light of possible mediating factors, such as age of onset of music training, type and instrument of training). Among other things, these reviews indicate that musicians exhibit enhanced encoding of pitch patterns at the brainstem level (Hannon & Trainor, 2007; Wong, Skoe, Russo, Dees, & Kraus, 2007), greater auditory evoked responses and grey matter concentration in the auditory cortex (Bermudez, Lerch, Evans, & Zatorre, 2009; Bermudez & Zatorre, 2005; Schneider et al., 2002; Shahin, Bosnyak, Trainor, & Roberts, 2003), increased grey matter density in Broca's area and the planum temporale (Keenan et al., 2001; Sluming et al., 2002), and larger fibre density in the anterior corpus callosum (Schlaug, Jancke, Huang, & Steinmetz, 1995).

Many of the neural changes that have been documented are specific to the instrument of training or the type of training undertaken (Merrett, Peretz, & Wilson, 2013), providing compelling proof that the observed neuroplasticity results from the music training. For example, Pantev, Roberts, Schulz, Engelien, and Ross (2001) demonstrated that violinists and trumpeters exhibited enhanced neuronal representations in the auditory cortex for their instrument tones, as compared to sine tones. Similar findings were reported for pianists (Pantev et al., 1998), as well as violinists and flautists (Margulis, Misna, Uppunda, Parrish, & Wong, 2009). In the motor cortex, differential cortical representations were also observed for different types of musicians. While singers have

an enlarged cortical representation of the vocal tract in the motor cortex (Kleber, Birbaumer, Veit, Trevorrow, & Lotze, 2007), pianists and violinists exhibited enlarged hand representation that differs in shape, size and laterality due to their respective instruments (Bangert & Schlaug, 2006; Elbert, Pantev, Wienbruch, Rockstroh, & Taub, 1995). Instrument-specific neural responses were also reported in the sensorimotor cortex, cerebellum and brainstem (Gebel, Braun, Kaza, Altenmüller, & Lotze, 2013; Strait, Chan, Ashley, & Kraus, 2012). Moreover, musicians whose training emphasises playing by ear and improvisation showed an advantage over classically trained musicians in detecting deviant pitch contours in complex melodies, which corresponds with differential auditory evoked responses in the two groups (Tervaniemi et al., 2001).

The evidence discussed thus far clearly establishes that formal music instruction facilitates the development of numerous music-related skills in the pitch and rhythmic domains. There is, however, research evidence showing that music training is not crucial for the development of certain music abilities. For example, one study found that good auditory structuring ability (i.e., the ability to detect pitch or rhythmic patterns in music sequences) is not dependent on music training (Karma, 2007). Bigand and Poulin-Charronnat (2006) also reviewed a set of studies illustrating that formal music training is not necessary for the acquisition of certain music abilities, such as abstracting the underlying musical structure of a piece of music (e.g., comprehending the structural similarity underlying a musical theme and its variations) (Bigand, 1990), learning a new musical idiom (e.g., serialism) (Bigand, D'Adamo, & Poulin, 2003; Bigand, Perruchet, & Boyer, 1998), forming appropriate musical expectancies (Bharucha & Stoeckig, 1986, 1987; Bigand & Pineau, 1997; Bigand, Poulin, Tillmann, Madurell, & D'Adamo, 2003; Tillmann, Bigand, & Pineau, 1998), perceiving tension and release in music (Bigand & Parncutt, 1999; Bigand, Parncutt, & Lerdahl, 1996; Bigand & Pineau, 1996), and understanding the emotional content of a piece of music (Bigand, Tillmann, Poulin-Charronnat, & Manderlier, 2005; Bigand, Vieillard, Madurell, Marozeau, & Dacquet, 2005).

On the other hand, there is evidence that the development of some musical abilities are not only predicated on music training *per se*, but are also strongly associated with the age of onset of music training. Specifically, numerous studies have reported a relationship between AP ability and early onset of music training (Costa-Giomi,

Gilmour, Siddell, & Lefebvre, 2001; Levitin & Zatorre, 2003; Miyazaki, 1988; Miyazaki & Rakowski, 2002; Russo et al., 2003). For example, Sergeant (1969) found a substantial negative correlation of -0.983 between the age of onset of music training and the incidence of AP in musicians. Baharloo et al. (Baharloo et al., 1998) also indicated that 78% of the AP possessors in their musician sample began music training before 6 years of age. Early onset of music training appears to facilitate the development of motor-related musical skills in particular (but see Furuya et al., 2015). Expert pianists and world-famous violinists were observed to commence music training earlier than amateur or lesser experts (Ericsson et al., 1993; Howe et al., 1995; Krampe & Ericsson, 1995; Manturzewska, 1979, 1990). In laboratory-based studies, musicians with early music training also showed superior visual-motor and auditory-motor skills compared to those who began training later (Pantev et al., 1998; Penhune, 2011; Schlaug et al., 1995), and such early training facilitation remains evident even after accounting for total years of training (Bailey & Penhune, 2010; Watanabe, Savion-Lemieux, & Penhune, 2007). Furthermore, although musicians understandably have less hand-skill asymmetry than non-musicians due to their use of both hands in playing an instrument, musicians with early training exhibited further reduced hand-skill asymmetry compared to late-trained musicians (Jäncke, Schlaug, & Steinmetz, 1997).

The effects of early training are evident from neural studies, where compared to late-trained musicians, early-trained musicians had a relatively larger anterior corpus callosum (Schlaug et al., 1995), early-trained violinists had relatively larger cortical left-hand representation (Elbert et al., 1995), and early-trained pianists exhibited stronger auditory neural responses to piano tones (Pantev et al., 1998).

Besides onset and duration, another important parameter of music training is the amount of practice. "If at first you don't succeed, try, try again." As this old adage has prescribed, music practice in the formal music learning environment exerts important influence on the development of music expertise. In particular, deliberate practice, which is characterised by goal-directed, efficient practice and rectification of weaknesses, has been propounded as a key mediator in the acquisition of musical expertise (Lehmann, 1997).

For instance, an investigation into the level of engagement in music-related activities of three groups of expert violinists with different levels of accomplishment revealed that while all three groups of violinists spent 50-60 hours per week on music-related activities, the three groups could be discriminated by the amount of solitary weekly practice: the two most accomplished groups of violinists spent about 25 hours in solitary practice whereas the least accomplished group of experts spent about 10 hours (Ericsson et al., 1993). In addition, Ericsson et al. (1993) observed that by the age of 20, professional and highly accomplished expert violinists had already accumulated over 10,000 hours of solitary practice, which is 2,500 and 5,000 hours more than what was reported by less accomplished expert violinists at the same age. Several other studies by Ericsson and collaborators also indicate that the total amount of music practice accrued over the lifetime by expert musicians corresponds with their respective levels of behavioural performances in music-related tasks (Krampe & Ericsson, 1995; Krampe & Ericsson, 1996).

Besides evidence of the influence of deliberate practice on musical achievement at the highest expert level, other researchers have demonstrated an association between practice and music performance at other proficiency levels (for more details see the meta-analysis by Platz et al., 2014). For example, correlations of .57 to .67 between accumulated music practice and music performance were reported for music beginners with up to three years of music training (Hallam, 1998; McPherson, 2005). Moderate correlations ($r = .30$ to $.46$) were reported for school-aged children (Jabusch, Young, & Altenmüller, 2007; Sloboda, Davidson, Howe, & Moore, 1996; Sloboda, Davidson, Moore, & Howe, 1994). Notably, Sloboda et al. (1994) observed that at all age groups investigated, the more proficient students consistently reported significantly higher amountsof accumulated practice. Data from Sloboda et al. (1996) also indicated that regardless of one's perceived "talent", attaining the highest level (Grade 8) of the Associated Board (ABRSM) graded music examinations required similar amounts of practice. Moreover, music students who won prizes in a national level music competition in Germany reported a greater amount of regular and pre-competition music practice per week, compared to the unplaced competitors (Lehmann, 1997). Moderate to high correlations (.44 to .86) between accumulated practice and instrumental performance accuracy were also demonstrated at the tertiary level among university music majors (Ericsson et al., 1993; Jabusch et al., 2007).

Other measures of instrumental performance expertise, such as music accompaniment skills and sight-reading skills, also showed an influence of deliberate practice. Studies reveal moderate correlations of .36 to .57 between sight-reading performance and practice-related predictors such as the number of pieces sight-read, the number of piano accompaniment performances and the number of hours practising sight-reading (Kopiez, 2012; Kornicke, 1992; Meinz, 2000; Meinz & Hambrick, 2010). Moderate to large correlations (.42 to .72) were also reported between piano accompaniment experience and the accuracy of piano accompaniment performance (Lehmann & Ericsson, 1996; Tufflash, 2002).

Although it has been amply demonstrated that deliberate practice positively correlates with musical expertise, several recent studies have challenged the dominating influence of deliberate practice on music ability. Ruthsatz, Detterman, Griscom, and Cirullo (2008) found that although practice is a mediating factor for expert musical performance, other factors such as intelligence and domain-specific skills are necessary to explain outstanding musical achievement. Moreover, in a study investigating potential predictors influencing motor virtuosity in 24 musically active pianists, Furuya et al. (2015) discovered that neither age of music training onset nor accumulated hours of music practice before the age of 20 were significant predictors for motor virtuosity, as measured by the maximal rate of alternately striking two piano keys repeatedly with the right thumb and little finger. Instead, two significant predictors that emerged from the regression analysis were single finger tapping rate and the strength of the elbow extensor muscle. The authors therefore inferred that genetic predisposition may influence finger movement agility, as other evidence has indicated the role of genes in influencing muscle fibre composition (Park, Brown, Park, Cohn, & Chance, 1988). The authors, however, acknowledged that specific strength training of the elbow extensor could potentially enhance the rate of keystrokes, and may be construed as a form of deliberate practice.

In addition, a large Swedish twin study by Mosing, Madison, et al. (2014) found that in identical twin pairs, the difference in hours of practice was not a significant predictor of differences in music ability for pitch, melody and rhythm perception. The findings indicated that when genes were controlled for, the supposed causal influence of music

practice on music ability disappeared. Furthermore, a meta-analysis of 88 studies revealed that deliberate practice accounted for 26% or less of the individual differences in performance in each major domain studied. Specifically, deliberate practice only explained 21% of the variance in music performance (Macnamara et al., 2014). Those findings were challenged by another meta-analysis conducted by Platz et al. (2014) which only focused on 13 music performance studies purportedly with more robust measures of deliberate practice, and yielded a large aggregated effect size (r_c) of .61 ; 95% CI: [.54, .67] (but see the response from Hambrick et al, 2014).

Taken together, while research evidence suggests an undeniable association between music practice and music ability, findings from other studies indicate that the amount of music practice or music training *per se* are unlikely to fully account for the variation in music ability. It is possible that the variation in ability could be explained by individual differences in the ease and speed of skill acquisition, which has been regarded by some as the "hallmark of natural abilities" (Gagné, 1999; Heller & Ziegler, 1998). In a study conducted by Sloboda and Howe (1991) which investigated the biographical precursors of musical excellence through interview, it was found that the rate with which one progressed through graded music examinations before admission to a music specialist school was "the most clear predictor of later exceptionality" (Sloboda & Howe, 1991). Similarly, in a study investigating the amount of practice needed for chess players to attain expert level, Gobet and Campitelli (2007) estimated that although on average about 11,000 hours were needed, the hours of practice required to attain expertise varied substantially from 3,016 hours to 23,608 hours. Some players were also reported to accumulate more than 25,000 hours of practice without achieving expert level (Chassy & Gobet, 2010).

The differences in the rate of learning can be observed at a neurological level. In one study, participants were classified as slow or fast learners in an auditory discrimination training task. Differences in behavioral performance were reflected in differential patterns of training-induced functional activation on fMRI (functional magnetic resonance imaging) between the two groups (Gaab, Gaser, & Schlaug, 2006). Compared with the slow learners, fast learners recruited the left supramarginal gyrus and left Heschl's gyrus to a greater extent during the post-training phase. (Jäncke, Gaab, Wüstenberg, Scheich, & Heinze, 2001) obtained similar findings for participants who

improved at a frequency discrimination task, and exhibited a different short-term functional activation pattern than those who showed no improvement. Likewise, (Zatorre, Delhommeau, & Zarate, 2012) found that participants who learned a micromelody task more quickly had relatively steeper fMRI BOLD (blood-oxygen-level dependent) responses to pitch changes in their auditory cortex, even before they trained on the task. These findings may indicate the presence of genetic influences in music learning capacity.

Some variables associated with music training, such as intelligence and openness-to-experience, have been shown to be genetically influenced (Butkovic et al., 2015; Corrigall & Schellenberg, 2015; Corrigall, Schellenberg, & Misura, 2013; Hille & Schupp, 2015). The effect of genetic influences therefore should not be discounted in music ability research, even when considering ostensible environmental factors like music training and practice (see also **Section 2.4.2.2** for evidence of the heritability of music practice and the genetic correlation between music practice and music ability, p. 50).

3.5 The Genetic and Environmental Determinants of Music Ability: A Summary

To summarise the research reviewed thus far, **Figure 2.4** (p. 63) and **Figure 3.1** below present schematic representations of the genetic and environmental determinants of music ability, respectively. It is apparent from **Figure 2.4** that extensive regions in chromosomes 4 (in red font) contain promising genetic evidence for various music skills, particularly those pertaining to music perception, but also music production skills such as singing, music performing and composing. In addition, genetic loci on chromosomes 8 (in blue font) and 12 (in green font) also appear to exert an influence on various types of music perception skills.

Although the investigation of the genetic basis of music ability is still in its infancy, it is interesting to observe from **Figure 3.1** that numerous music skills and even certain environmental variables, such as cultural environment and music practice (highlighted in yellow) have a genetic component. The three main environmental contexts reviewed

in this chapter have been shown to influence various music perception and music production skills, although the extent and the types of skills influenced may vary. For instance, in terms of music production skills, while instrumental performance abilities are primarily developed in the formal music learning environment, singing ability is observed to be shaped by all three environments, whether informally through the cultural and home environments, or through formal music learning.

The unanimous contribution of the three main environmental contexts to singing development makes singing ability a particularly suitable model to study the genetic basis of music ability as it provides a sufficient and balanced consideration of environmental factors. The next chapter therefore examines singing ability in greater detail, including its developmental trajectory, a neurocognitive model of singing, the tasks and measures commonly used to evaluate singing ability in research studies, and a discussion of why singing ability provides an ideal paradigm for genetic analysis. The chapter concludes with the rationale, aims and hypotheses of the empirical study reported in this thesis.

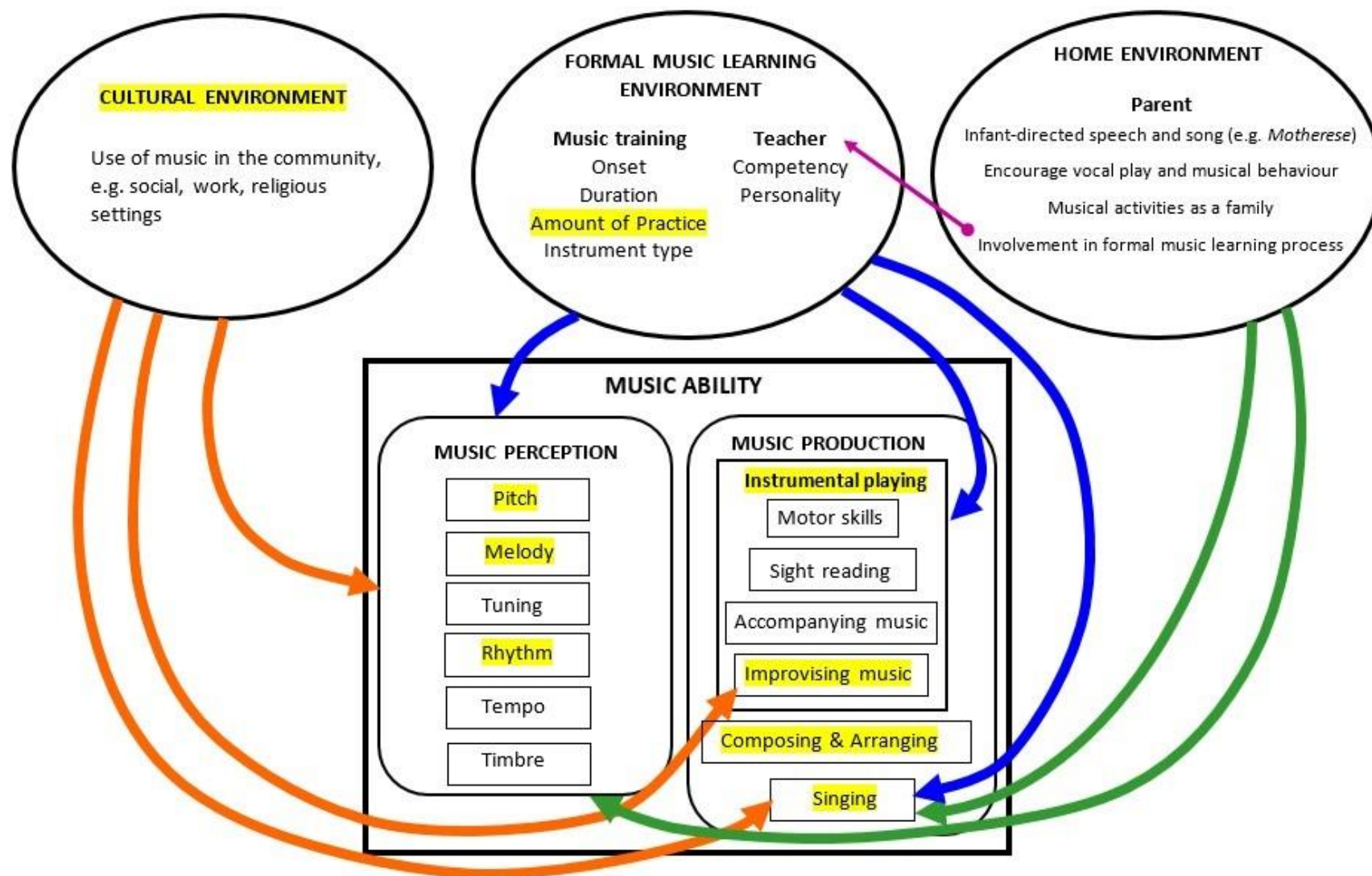


Figure 3.1. A schematic representation of the environmental determinants of music ability. The variables highlighted in yellow are also genetically influenced.

4

THE NATURE OF SINGING ABILITY

This chapter focuses specifically on singing ability. In the following section, the typical age-related developmental trajectory of singing ability is described.

4.1 The Typical Developmental Trajectory for Singing

Although singing ability emerges spontaneously in the human population, there is general consensus that the subsequent development of singing ability is also dependent on maturational as well as experiential factors (Davidson, McKernon, & Garnder, 1981; Hedden, 2012; Stadler Elmer, 2006; Welch, 1985). Therefore, it should be noted that while the developmental trajectory of singing ability below documents the typical age-related developmental milestones for singing, considerable individual differences may exist with regards to the age at which one attains each milestone (Gembris, 2006).

0-2 months

The earliest vocal behaviour manifested by newborn babies such as crying and babbling may already exhibit certain musical features such as pitch and rhythmic patterning and phrasing, as well as variation of intensity (Vihman, 1996).

3-6 months

Infants begin to develop vocal control and start exploring the voice through vocal play around this time (M. Papoušek, 1996). The pitch content of an infant's vocalisations is influenced by the prosodic features of the mother tongue (Meltzoff, 2002; Welch, 2006), but descending melodic contours are prevalent in the first few months of infancy (Fox, 1990). Some infants are able to match single pitches vocally (Kessen, Levine, & Wendrich, 1979), and the vocal exchange between parent and infant is marked by a high

incidence of reciprocal imitation of vocal patterns (Masataka, 1999; M. Papoušek, 1996). As noted in **Section 3.3** (p. 68), such nonverbal quasi-musical communication (e.g., Motherese) between parent and child as well as maternal singing have positive impact on the quality and frequency of infant musical babbling (H. Papoušek, 1996; Tafuri & Villa, 2002).

12-18 months

More experimentation with the voice ensues, as the child tries to explore the vocal range and what can be done with one's voice through vocal play (Gembris, 2006). An increasing distinction between singing and speech also emerges by the end of the first year (Gembris, 2006). First actual singing is observed between 6 to 18 months, which is characterised by monosyllabic glissando vocal improvisations that are narrow in range (Dowling, 1999).

2 years

At two years of age, children can sing short one-line phrases and reproduce music intervals with some degree of accuracy (Gembris, 2006). They are also able to sing brief phrases with recognisable melodic contours and rhythmic patterns (Dowling, 1999). By this age, singing is reliably distinct from speech (Tsang et al., 2011).

3-4 years

One-phrase singing is rarer at this age, as children can typically sing three different phrases by now (Dowling, 1988, 1999). Children at this age also like to improvise and create “pot-pourri” songs by combining phrases or fragments from different songs (Moog, 1976). By the age of 4, children are able to reproduce the majority of the lyrical and rhythmic content as well as the formal structure of a song (Shuter-Dyson & Gabriel, 1981).

6-7 years

Children are able to comfortably sing with a full octave range or even one and a half octaves (from G3 to C5) around this age (Davidson, 1994; Tsang et al., 2011). It was observed from a study that about 67% of first-grade children had a singing range exceeding one octave (Wassum, 1979).

8 years

The average child can sing a song accurately by the age of 8, and according to some researchers, the level of singing ability will plateau off at this point unless the child undertakes formal music instruction and practice (Gembris, 2006).

10-11 years

At 10 years of age, children typically have a nearly two-octave singing range, spanning F3 to D#5 (Moore, 1991; Tsang et al., 2011), and by 11 years old, out-of-tune singing is a rare phenomenon (Howard, Angus, & Welch, 1994; Welch, 1979; Welch, 2000). Another study reported that approximately 98% of sixth-grade children in a large sample had a singing range exceeding one octave (Wassum, 1979).

4.2 A Neurocognitive Model of Singing

Even though singing ability typically develops with age, individual differences in singing ability are commonly observed in the general population (Amir et al., 2003; Dalla Bella et al., 2007; Pfordresher & Brown, 2007). Diverse patterns of inaccurate singing have been reported, which indicates that there are possibly different underlying causes to poor singing phenotypes (Dalla Bella & Berkowska, 2009). For instance, some possible causes for inaccurate singing may be poor motor control of the vocal organs, a pitch perception or memory deficit, or problems with sensorimotor translation that hamper the mapping of perceptual information to the correct vocal response (Hutchins & Peretz, 2012). In order to better contextualise the various possible causes of singing accuracy, the following section will outline a recent neurocognitive account which has gained traction in the current state of singing research.

4.2.1 The vocal sensorimotor loop

Dalla Bella and his team proposed a neurocognitive model of singing that focused on the core role of the vocal sensorimotor loop (VSL) of singing as a model for the singing network (**Figure 4.1**) (Berkowska & Dalla Bella, 2009a; Dalla Bella, Berkowska, & Sowinski, 2011). Partly inspired by Levelt's Perceptual loop theory (1989) for speech, in this model, pitch and temporal information are retrieved from memory and then

translated into vocal-motor responses during auditory-motor mapping. The translated motor representations guide subsequent motor planning to generate singing output. The sung output then becomes an auditory input which forms a feedback loop, enabling the singer to constantly self-monitor and compare the actual vocal output with the planned output as dictated by the internal pitch and temporal information accessed from memory. The singer is thus able to make use of the auditory feedback to make online corrections to adjust the motor output accordingly.

The VSL model takes into consideration two different scenarios for singing: with or without an external auditory stimulus. Singing a familiar song without an external auditory cue requires the retrieval of the song's pitch and temporal information from the long-term memory, followed by fine motor planning and production. On the other hand, vocally matching an external auditory stimulus involves the perceptual analysis of the auditory input and retaining the information in working (short-term) memory. This information is then utilised during auditory-motor mapping of appropriate motor representations to guide motor planning and generate vocal output. In both scenarios, the vocal output will serve as auditory feedback to enable self-monitoring and correction of vocal response.

The VSL model describes two distinct perceptual pathways. The overt perceptual pathway is necessary for an individual to discriminate pitch differences, such as judging pitch direction. In the case of individuals with pitch perception deficits, such as those with congenital amusia, it is possible that the overt perceptual pathway is malfunctioning or underdeveloped (Berkowska & Dalla Bella, 2009a). Several studies have reported however, that despite impaired pitch discrimination ability, some congenital amusics are able to vocally produce intervals in the right direction (Dalla Bella, Gigùre, & Peretz, 2009; Griffiths, 2008; Loui, Guenther, Mathys, & Schlaug, 2008). These findings suggest that auditory perception and action are dissociable and may belong to two separate processing streams (Griffiths, 2008). Moreover, the observation that pitch production ability is preserved to some degree despite impaired pitch perception may be taken as an evidence that another pitch perception pathway exists, guiding vocal production covertly in a less fine-tuned manner (Berkowska & Dalla Bella, 2009a). The existence of a second covert perceptual pathway may explain the observations that singers unconsciously adjust their voice in the opposite direction

when counteracting pitch-shifted auditory feedback, even when the pitch change is imperceptible to them (Hafke, 2008).

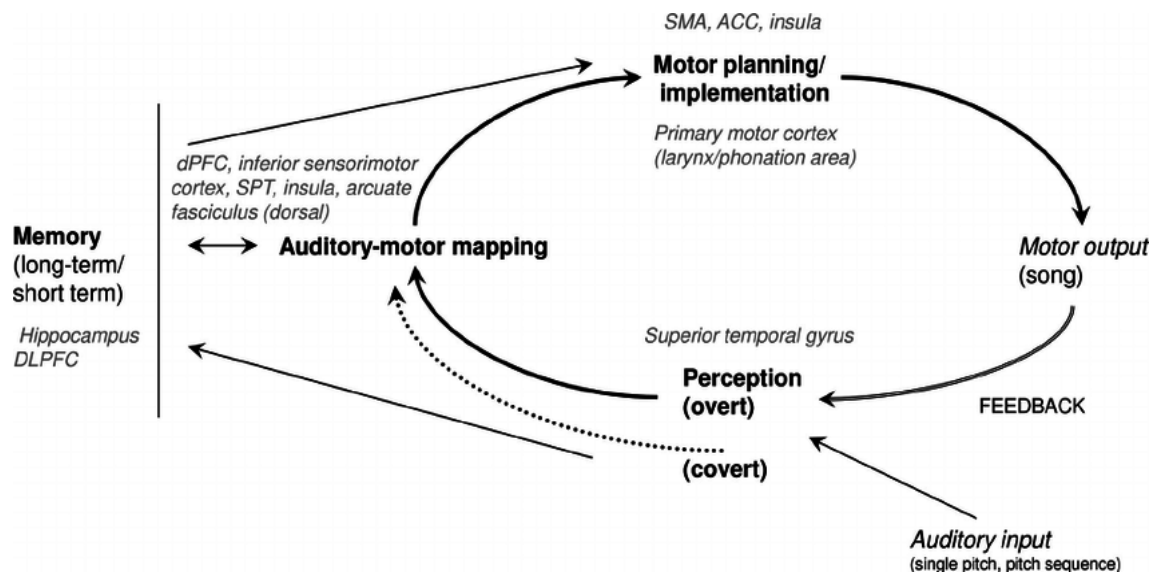


Figure 4.1. The schema of the vocal sensorimotor loop (VSL). The putative brain regions associated with the functional components of the VSL are indicated in grey. SMA: supplementary motor area; ACC: anterior cingulate cortex; dPFC: dorsal prefrontal cortex; SPT: cortex of the dorsal Sylvian fissure at the parieto-temporal junction. Adapted from “Disorders of pitch production in tone deafness,” by Dalla Bella et al. (2011), *Frontiers in Psychology*, 2(164), p.5.

4.3 Neural Correlates of Singing

The following section provides an outline of the putative neural correlates of singing, with reference to the above model where appropriate. For a detailed review of the neural substrates of singing, please refer to Zarate (2013).

4.3.1 Pitch and melody perception and auditory feedback processing

As a pitch or melody is perceived, it is transmitted and processed along the ascending auditory pathway (cochlear nucleus, superior olive, inferior colliculus, lateral lemniscus, and the medial geniculate nucleus of the thalamus) before being further processed in the primary auditory cortex within Heschl’s gyrus (Griffiths, Uppenkamp, Johnsrude, Josephs, & Patterson, 2001). A pitch-sensitive area in right lateral Heschl’s gyrus is thought to be responsible for conscious pitch perception (Bendor & Wang, 2006;

Griffiths, 2003), whereas additional auditory cortical areas beyond Heschl's gyrus, such as the right superior temporal gyrus (STG), planum polare and planum temporale, are enlisted to process pitch changes and melodic phrases (Hyde, Peretz, & Zatorre, 2008; Patterson, Uppenkamp, Johnsrude, & Griffiths, 2002; Zatorre, Evans, & Meyer, 1994). In particular, for pitch comparison within a melody, right auditory and frontal cortical areas are observed to manifest increased activity. For comparing melodies of the same key, bilateral STG and auditory cortical areas along the STG are extensively activated whereas for the comparison of melodies in different keys, additional recruitment of the intraparietal sulcus (IPS) has been observed (Foster & Zatorre, 2010).

Sound stimuli of different timbres are also reported to be processed by different areas of the auditory cortex. Specifically, functional imaging studies have revealed that an area within the anterior STG shows stronger activation to music than the human voice (Angulo-Perkins et al., 2014; Fedorenko, McDermott, Norman-Haignere, & Kanwisher, 2012; Leaver & Rauschecker, 2010; Rogalsky, Rong, Saberi, & Hickok, 2011), whereas there are apparently functionally distinct regions within the superior temporal sulcus (STS) that are involved in vocal timbre processing. Specifically, anterior STS and posterior STS have been implicated in familiar and unfamiliar voice recognition, respectively (Kriegstein & Giraud, 2004; Warren, Scott, Price, & Griffiths, 2006). Posterior STS may also be involved more generally in processing spectral changes in sound over time (Warren et al., 2006).

4.3.2 Auditory-motor mapping

The anterior insula is implicated in the sensory-motor control of vocalisation as it is a multimodal association area that integrates different modalities and serves as a gateway for sending both auditory information and somatosensory information to the anterior cingulate cortex (ACC).

4.3.2.1 An experience-dependent network for the auditory-motor control of singing

Some studies have demonstrated that the neural substrates for auditory-motor mapping are different for novice and experienced singers (Zarate, Wood, & Zatorre, 2010; Zarate

& Zatorre, 2008). In singing tasks with pitch-shifted auditory feedback, information from the auditory feedback is thought to be processed and extracted by the STG and STS of the auditory cortex as well as the IPS. The IPS has been implicated in the translation of sensory input for motor planning (Astafiev et al., 2003; Grefkes, Ritzl, Zilles, & Fink, 2004; Tanabe, Kato, Miyauchi, Hayashi, & Yanagida, 2005). In the case of pitch-shifted auditory feedback, Zatorre and colleagues speculated that auditory information is translated in the IPS into spatial frequency information (Foster & Zatorre, 2010; Zatorre, Halpern, & Bouffard, 2010). They also argued that when participants have to adjust their vocal output to compensate for pitch-shifted auditory feedback, individuals with minimal vocal training recruit the dorsal premotor cortex (dPMC) more than the experienced singers, whereby the dPMC is thought to utilise the spatial frequency information received from the IPS via the insula to prepare an appropriate vocal motor response. On the other hand, for experienced singers, instead of recruiting the dPMC, the spatial frequency information from the IPS is sent to the ACC via the anterior insula to generate suitable motor plans (Zarate, Wood, et al., 2010; Zarate & Zatorre, 2008). Moreover, experienced singers appear to be able to disengage the right anterior insula to ignore somatosensory feedback where necessary (Kleber, Zeitouni, Friberg, & Zatorre, 2013).

Interestingly, other research has shown that pitch discrimination training alone does not improve singing accuracy nor enable the enlistment of training-sensitive neural correlates for auditory-motor mapping (Zarate, Delhommeau, et al., 2010).

4.3.3 Vocal motor control

Several brain regions are implicated in vocal motor control and it has been proposed that vocal motor control in humans follows a hierarchical pattern (Zarate, 2013). At the first level, the reticular formation of the pons and medulla is directly connected to motor neurons of the phonatory muscles. These connections enable the phonatory muscles to receive input from the brain and generate complete vocal patterns. The second level consists of the periaqueductal gray (PAG) and the anterior cingulate cortex (ACC), which are implicated in voluntary initiation and emotional or motivational intonation in vocalisations (Jürgens, 2002, 2009). The highest level comprises the primary motor cortex (M1) and its modulatory brain regions (e.g., cerebellum, putamen and globus

pallidus), which are involved in the production of learned vocalisations in speech and song. As M1 also has direct connections with the motor neurons of the phonatory muscles which bypasses the first and second levels, lesions to brain regions at either the second or third level of the vocal motor control hierarchy will lead to selective impairment in certain types of vocalisations and not destroy all vocalisations.

4.3.4 Somatosensory feedback processing

Somatosensory information, such as the awareness of articulator placement and respiration are transmitted along the ascending somatosensory pathway to the primary and secondary somatosensory areas (S1 and S2). Notably, S1 is posteriorly adjacent to the portion of M1 which is in charge of phonation (e.g., vocalisation and articulator movement) (Penfield & Rasmussen, 1950). In addition, S1 is observed to be incrementally activated as a function of vocal training and practice (Kleber, Veit, Birbaumer, Gruzelić, & Lotze, 2010).

4.3.5 Dual-stream model for singing

Converging neural findings have supported a dual-stream model of singing with two dissociable pathways for auditory perception and vocal production, respectively (Zarate, 2013). With reference to the VSL, Zarate (2013) proposed that the covert perception route or ventral stream, likely consists of a pathway linking the auditory cortex (STG/STS) to the inferior frontal gyrus (IFG) which processes identity information of a sound object. On the other hand, the overt vocal production route or dorsal stream, comprises the auditory cortex (STG/STS), IPS, anterior insula, dPMC and ACC. The dorsal stream is potentially involved in the spectrotemporal processing of auditory information and executing appropriate motor commands based on the processed information (**Figure 4.2**).

UPDATED VOCAL SENSORIMOTOR LOOP MODEL

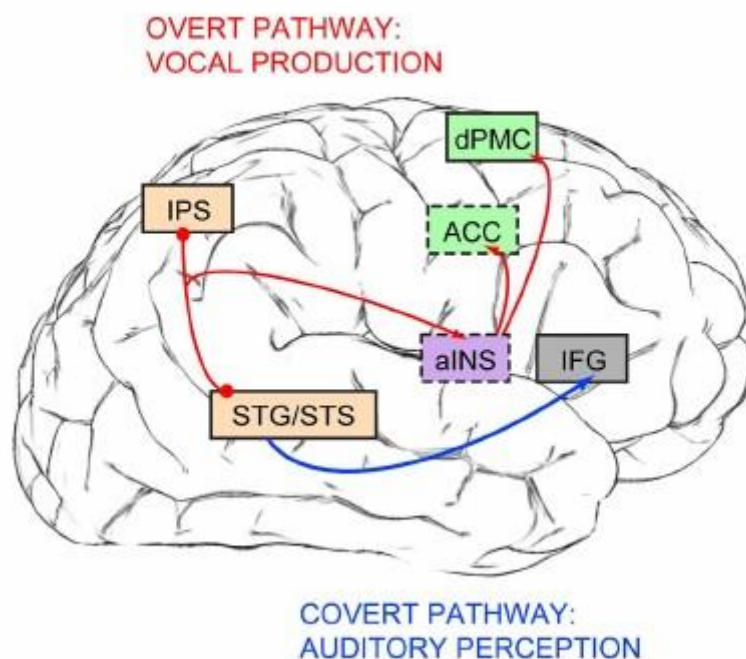


Figure 4.2. The vocal sensorimotor loop (Berkowska & Dalla Bella, 2009a; Dalla Bella et al., 2011) updated with findings from Zarate and Zatorre (2008); Zarate, Wood, et al. (2010). Brain regions linked by the red arrows represent the overt pitch production route (dorsal stream), whereas brain regions linked by the blue arrow represent the covert pitch perception route (ventral stream). Orange boxes indicate brain regions implicated in auditory processing, green boxes for vocal motor control, and purple for multimodal processing. ACC: anterior cingulate cortex; aINS: anterior insula; dPMC: dorsal premotor cortex; IFG: inferior frontal gyrus; IPS: intraparietal sulcus; STG: superior temporal gyrus; STS: superior temporal sulcus. Adapted from “The neural control of singing,” by Zarate (2013), *Frontiers in Human Neuroscience* 7(Jun), p.8.

4.4 The Evaluation of Singing Ability

To assess singing ability in a study setting, researchers in the past few decades have used several types of tasks as well as a variety of metrics for accuracy. In the following section, the typical tasks and measures used to assess singing ability will be surveyed. As pitch accuracy is fundamental to in-tune singing, there is a common consensus among researchers and professional singing pedagogues alike that pitch accuracy is a key yardstick of singing ability (Hutchins & Peretz, 2012; Watts et al., 2003). In addition, pitch accuracy in singing relies in part on the ability to accurately perceive pitches, which has been demonstrated to have a genetic component (see **Section 2.4.1.1**, p. 33). In the current thesis, singing ability was therefore assessed in terms of pitch

accuracy. In view of this, only tasks and measures pertaining to pitch accuracy will be discussed in this section.

4.4.1 Tasks

Singing ability can be evaluated with a variety of tasks such as song-singing or pitch-matching tasks. It is often advisable to use different types of tasks to evaluate singing ability as individuals may exhibit varying success for each task, due in part to the fact that different tasks may recruit partially different components of the singing network (Dalla Bella, 2015). Therefore, establishing a comprehensive understanding of singing proficiency requires a good range of tasks.

There are two main types of singing tasks – imitative and recollective. Imitative tasks require participants to listen to external auditory stimuli and vocally match the target pitches, whereas recollective tasks typically require participants to sing a song from memory, with or without lyrics. While a few other singing tasks have also been used in singing research, such as sight-singing or improvised singing (Brown, Martinez, & Parsons, 2006; Mishra, 2014), these tasks are less common because formal music training and singing experience are most likely required to perform these tasks. Moreover, improvised singing tasks are difficult to assess using objective measures. In contrast, imitative and recollective tasks do not pose these constraints, thus enabling all people to participate. The two types of tasks and the components of these tasks are described below.

4.4.1.1 Imitative singing tasks

Imitative singing tasks are generally deconstructed singing tasks, in which the ability to vocally match a single pitch, interval or short melodic sequences are assessed. As these tasks involve matching the exact pitches of the auditory stimuli, it is important to ensure the stimuli presented are of an appropriate range and register for the participants according to their sex and age, so that any pitch inaccuracy that arises is not due to register limitations (Demorest et al., 2015). In these tasks, a set of range-appropriate pitches, intervals or novel melodies are typically presented over a number of trials, in a randomised or pseudo-random order.

The three commonly used imitative singing tasks are as follows:

a) *Single pitch*

Single pitch-matching tasks have been used in numerous research studies to assess singing ability, possibly due to the ease of constructing and administering such task (Goetze, Cooper, & Brown, 1990; Hutchins, Zarate, Zatorre, & Peretz, 2010; Pfordresher & Brown, 2007; Watts et al., 2003). A variant of this task can be used to investigate the dissociation between the proposed pitch perception and production pathways in the brain. Such task typically involves altering the auditory feedback of the participant's vocal output and asking the participant to either ignore the altered feedback and maintain the produced pitch, or compensate for the altered feedback by adjusting one's vocal output to suit the perceived pitch height (Hafke, 2008; Zarate & Zatorre, 2008). One concern for the single pitch-matching task, however, is that the task is so deconstructed that success in this task may not generalise to good singing ability in real-world settings.

b) *Melodic intervals or short melodic sequences*

Sometimes interval or melody-matching tasks are also used in conjunction with the single pitch-matching task, as some researchers have noted that there is a difference in task performance between the two (Pfordresher & Brown, 2007; Wise & Sloboda, 2008). This difference may be due to the greater memory demands of interval and melody-matching tasks as well as the richer tonal context that they afford. This richer tonal context ensures greater ecological validity for these tasks.

c) *Novel songs*

Some researchers have also used unfamiliar songs to assess singing ability, although this is not widely practised. For instance, in the AIRS Test Battery of Singing Skills (ATBSS), an unfamiliar tonal song "We Are One" is presented to the participants twice before they have to sing it back. The song comprises five phrases of varying melodic contours and is of moderate musical and linguistic difficulty, thus allowing for improvement in memory and performance over a number of test sessions (Cohen, 2015).

When choosing auditory stimuli for imitative tasks, researchers need to take into consideration how timbre may influence pitch-matching accuracy. Research has shown that inexperienced or inaccurate singers generally perform better if the timbre of the auditory stimuli is similar to their own voice (Green, 1990; Hutchins & Peretz, 2012; Yarbrough, Green, Benson, & Bowers, 1991), and vocal stimuli are generally more accurately matched than non-vocal stimuli such as sine-wave models (Price, Yarbrough, Jones, & Moore, 1994). Therefore, using different timbres for the same imitative task may be useful for the identification of individuals whose pitch-matching abilities are differentially affected by timbre (Demorest et al., 2015; Hutchins & Peretz, 2012; Price et al., 1994).

4.4.1.2 Recollective singing tasks

In these tasks, participants are usually asked to sing a familiar song from memory. Such tasks have also been commonly used for assessing singing (Berkowska & Dalla Bella, 2013; Pfordresher & Brown, 2007; Rutkowski, 1990; Rutkowski & Miller, 2003a) and it has been reported that people generally perform better for recollective singing tasks than imitative singing tasks (Berkowska & Dalla Bella, 2013). Researchers typically choose songs that are extremely familiar and widely sung in their culture, e.g., *Happy Birthday* or *Brother John*. It is also necessary to consider the participant's age when choosing a familiar song to ensure the difficulty and vocal range of the familiar song is appropriate for the age group (Erman, 1981).

The singing of familiar songs from memory can be assessed using different conditions to investigate whether singing accuracy varies with each condition. For instance, research has shown that adults in the general population are typically more accurate when singing familiar songs on neutral syllables such as 'la' compared to singing with lyrics (Berkowska & Dalla Bella, 2009b, 2013), although congenital amusics exhibited the opposite pattern (Dalla Bella & Berkowska, 2009), and studies involving children also reported mixed findings (Goetze et al., 1990; Lange, 2000; Levinowitz, 1989b; Smale, 1988). According to Dalla Bella et al. (2007), singing familiar songs at a prescribed slower tempo also appears to have a positive effect on pitch-matching accuracy than singing at a self-determined tempo.

Besides singing tasks, in order to determine whether poor-pitch singing is accompanied by a concurrent pitch perception deficit, some researchers have included a pitch discrimination task as a subcomponent for singing ability assessment (Bradshaw & McHenry, 2005; Demorest et al., 2015; Hutchins & Peretz, 2012).

4.4.2 Measures

Pitch accuracy in singing can be evaluated by subjective or objective measures. Subjective assessment of singing ability is typically conducted by music experts, such as musicians, singers and music educators (Dalla Bella, 2015; Hébert, Racette, Gagnon, & Peretz, 2003; Racette, Bard, & Peretz, 2006; Schön, Lorber, Spacal, & Semenza, 2004; Wise & Sloboda, 2008), and allows quick and easy assessment of singing ability with generally high interrater reliability (Guerrini, 2006; Rutkowski & Miller, 2003b). Some researchers have considered subjective rating to be the easiest way to reliably assess song-singing ability (Demorest & Pfordresher, 2015; Wise & Sloboda, 2008), as objective acoustic analyses for songs are time-consuming and challenging at present, especially for songs with lyrics (Dalla Bella, 2015). However, a major shortcoming of subjective assessment is that the subjective rating is rather general and does not provide enough detail about the properties of the inaccuracies present in the singing performance (Dalla Bella, 2015; Demorest et al., 2015). Furthermore, though the interrater agreement is usually high, some studies have documented inconsistencies among expert raters (Kinsella, Prior, & Murray, 1988; Prior, Kinsella, & Giese, 1990).

In view of these limitations, objective measures have been employed in recent studies as they afford more precise and reliable estimations of pitch accuracy (Dalla Bella & Berkowska, 2009; Dalla Bella et al., 2007; Murayama, Kashiwagi, Kashiwagi, & Mimura, 2004; Pfordresher, Brown, Meier, Belyk, & Liotti, 2010) and provide rich quantitative information to profile singing ability and differentiate among various poor singing phenotypes. In addition, findings based on quantitative objective measures are more easily compared across tasks and studies (Dalla Bella, 2015).

Before examining some common objective measures for pitch accuracy in singing, the methods to segment and extract pitches from raw singing data in acoustic analyses are first described.

4.4.2.1 Pitch segmentation and extraction methods

Prior to the advancement of computer technology in the past two decades, singing researchers lacked the technical resources to assess singing accuracy objectively. A more objective assessment of singing accuracy in those times would require the use of a quartz tuner to quantify each sung pitch, which is a very labour-intensive process (Green, 1990; Price, 2000). Fortunately, the progress in acoustic speech analysis has brought about the development of useful software such as CSpeech (Milenkovic & Read, 1992), Computerized Speech Lab (Kay Elemetrics, 2001), and Praat (Boersma & Weenink, 2013). These software programs or applications allow the user to visualise the recorded sound and facilitate the measurement of its acoustic properties such as pitch, intensity and duration. In addition to these standalone programs, researchers have developed pitch extraction methods that can be run in the Matlab environment, with a popular example the YIN algorithm (De Cheveigné, 2002). Singing research has greatly benefited from the development of these software applications and methods, and numerous studies investigating singing have reported their use for objective assessment of singing accuracy (Pfordresher et al., 2010; Trollinger, 2003; Zarate, Delhommeau, et al., 2010). Among these, Praat and YIN are the most commonly used as they are freely available for download online (although YIN would need to be run in Matlab, which needs to be purchased).

While it is no longer difficult to generate a fundamental frequency curve from a sound file for visualisation and analysis purposes, there is, however, still a lack of consensus on determining the portion of a pitch to be segmented such that it is representative of the actual sung note

One of the most prevalent methods has been to select the middle section of a sustained note manually by visual inspection. The rationale behind this is that the middle portion of a note tends to be more stable than the onset and transition or offset sections, where perturbations in fundamental frequency tend to occur. Researchers, however, vary in their choice of the duration of the middle portion. The length of the middle portion has ranged from 0.5 second (Bradshaw & McHenry, 2005), 1 second (Watts & Hall, 2008), 2 seconds (Estis, Coblentz, & Moore, 2009) to 4 seconds (Moore, Keaton, & Watts,

2007). Other studies do not prescribe a fixed duration for the selected segment, but may either choose the middle 50% of each sound sample (Amir et al., 2003), or exclude the boundary segments of each pitch (Demorest & Clements, 2007; Hutchins et al., 2010; Larrouy-Maestri, Lévêque, Schön, Giovanni, & Morsomme, 2013; Larrouy-Maestri, Magis, & Morsomme, 2014; Nikjeh et al., 2009; Pfordresher et al., 2010) .

Although it is understandable why researchers would select a steady-state portion of a sung pitch for subsequent acoustic analysis, some researchers have also suggested that selecting the most stable portion may overlook inaccuracies (e.g., glides) that occurred near the boundaries of each note, which could yield important information about one's singing ability (Salvador, 2010). However, Pfordresher (2007) noted that using different pitch segmentation strategies on the voice samples of the four least and most accurate participants in his study produced minimal differences in the determination of the mean fundamental frequency of each pitch segment, as the strategies still yielded .99 reliability.

Another commonly used segmentation strategy is to identify vowel onset of a sung pitch and mark it as the onset of a pitch. There are two reasons for this: it has been observed that vowel onsets are usually synchronised with the pulses in a song (Sundberg & Bauer-Huppmann, 2007). Moreover, vowel onsets are often easy to identify visually as vowels are always voiced (Dalla Bella et al., 2009; Murayama et al., 2004). While many studies use visual inspection to manually mark the vowel onsets and perform pitch segmentation (Berkowska & Dalla Bella, 2013; Dalla Bella & Berkowska, 2009; Larrouy-Maestri & Morsomme, 2014), Tremblay-Champoux, Dalla Bella, Phillips-Silver, Lebrun, and Peretz (2010) ran a script called EasyAlign (Goldman, 2011) within Praat to identify the vowel onsets and segment the pitches in a semi-automatic manner. Similarly, Demorest and Pfordresher (2015) also ran an automated Matlab algorithm to identify note onsets. While the method of using vowel onsets to segment pitches has its merits, the efficacy of such semi-automatic or automatic segmentation strategies is largely dependent on the syllables uttered by the singer. Demorest et al. (2015) have noted that in certain singing tasks, if participants are asked to sing using a neutral syllable with a stop consonant such as “doo” instead of one with a liquid consonant like “la”, it will presumably be easier to perform the segmentation. On the other hand, in

song-singing tasks that involve lyrics, such strategies may not be as effective in parsing the individual pitches.

In sum, the current pitch segmentation strategies have several challenges. First, the strategies often involve manual selection of pitch segments by visual inspection, which is time consuming and labour intensive. Moreover, the selection of a stable portion of the pitch is usually based on an arbitrary decision of the researcher, which may vary from study to study or even within a study among different experimenters (Granot, Israel-Kolatt, et al., 2013). The labour intensive and subjective nature of the prevalent pitch segmentation methods may potentially affect inter- and even intra-rater reliability, especially when large samples of singing performance are involved. While pitch segmentation methods relying on semi-automatic or automatic detection of vowel onsets hold some promise, the efficacy of such method in song-singing tasks with lyrics is uncertain due to the variability of attacks and cutoffs of the sung lyrics (Demorest et al., 2015). It is hoped that future technological advancement will improve current procedures and enable acoustic analyses to be conducted in a more automatic fashion (Dalla Bella, 2015). In the current study, some of the aforementioned challenges in pitch segmentation were mitigated through the development of a novel semi-automatic pitch segmentation method (see **Section 6.2.2**, p. 156).

4.4.2.2 Objective measures of pitch accuracy

There are two main types of objective metrics that are used to evaluate pitch accuracy: absolute pitch and relative pitch measures. Both types of measures are described below.

a) Absolute pitch metrics

Absolute pitch metrics generally compute the pitch difference (in cents or semitones) between each produced note and the target pitch and compute the mean across the entire task.

The direction of pitch error (i.e., the produced pitch is higher or lower than the target) can be taken into account by noting whether the sign of the deviation is positive or negative. *Mean signed pitch deviation* is computed by averaging all the signed pitch errors for the entire task. However, if a participant makes pitch errors in both directions

throughout the task, this measure could cause the positive and negative deviations to cancel each other out and overestimate the participant's singing accuracy. *Mean absolute pitch deviation* which averages the absolute values of all the pitch errors can thus avoid this potential pitfall (Dalla Bella, 2015).

b) *Relative pitch metrics*

While absolute pitch metrics can be computed for all singing tasks, whether it is matching single- pitch, interval, melodic sequences or songs, relative pitch metrics are only applicable to singing tasks that consist of two or more pitches per trial. This metric is computed by measuring the size of every two consecutive pitches (i.e., an interval) produced, and calculating the difference between each sung interval with the corresponding target interval. Similar to the absolute pitch metrics, the sign of the interval error will indicate whether the produced interval is smaller (negative) or larger (positive) than the target interval. Taking the averages across all the signed interval errors and absolute interval errors will yield the *mean signed interval deviation* and *mean absolute interval deviation*, respectively (Berkowska & Dalla Bella, 2013; Hutchins et al., 2010; Pfordresher & Brown, 2007; Pfordresher et al., 2010). It has been reported in one study that the mean absolute interval deviation is significantly and highly correlated with subjective ratings of pitch accuracy for *Happy Birthday* ($r = .87$, $p < .01$) (Larrouy-Maestri et al., 2013). However, it should be noted that mean absolute interval deviation will be less sensitive than mean absolute pitch deviation in detecting and duly penalising unintentional key changes during singing.

For both absolute and relative pitch measures, it is possible to compute percentage accuracy scores by calculating the number of correct pitches or intervals sung based on a benchmark for accuracy (Dalla Bella, 2015). Some studies have adopted an accuracy criterion that considers all pitch or interval deviations less than one semitone (in absolute terms) from the target pitch or interval as accurate, although some researchers have argued that this criterion may not be stringent enough (Dalla Bella, 2015). Other studies have therefore used deviations of less than a quartertone (half a semitone) in absolute terms as the accuracy criterion.

In interval or melody singing tasks, some studies have also used the number of contour errors made as an accuracy measure (e.g., Dalla Bella et al., 2007), which is a less

stringent criterion than the above measures, as it only penalises melodic intervals that are sung in the wrong direction compared to the corresponding target intervals.

c) Other singing ability measures

Several studies have also utilised other measures to assess singing ability.

Pitch stability measures the ability to sustain each pitch stably and is obtained by computing the standard deviation within each extracted pitch segment and taking the mean across the task (Dalla Bella & Berkowska, 2009; Dalla Bella et al., 2007).

Pitch precision examines the consistency in producing a pitch over all the trials of the same target pitch or interval. It is obtained by computing the standard deviation separately for all the trials with the same target pitch or interval, and then taking the mean across all the standard deviations computed (Pfordresher et al., 2010).

For singing research studies that focus on identifying inaccurate singers, certain criteria can be used to dichotomise the absolute and relative pitch metrics described above to distinguish poor-pitch singers from accurate singers. For instance, some studies have used a mean absolute pitch or interval deviation which exceeds a fixed cut-off value such as 0.5 or 1 semitone to indicate poor-pitch singing ability (Berkowska & Dalla Bella, 2013; Demorest & Clements, 2007; Hutchins & Peretz, 2012; Hutchins, Roquet, & Peretz, 2012; Pfordresher & Brown, 2007; Pfordresher et al., 2010). However, other studies have shown that using a fixed cut-off of a quartertone may be overly stringent as it classified 64-84% of participants in a study as poor-pitch singers (Berkowska & Dalla Bella, 2013). In addition, the norms for singing accuracy or precision may differ for different tasks or different sample populations. Some researchers therefore expound the use of variable criterion to differentiate accurate and inaccurate singers, such as classifying pitch or interval deviations beyond 2 standard deviations from the mean of the sample population for the task (Dalla Bella, 2015). This variable cut-off was demonstrated to yield a more reasonable percentage (28%) of poor-pitch singers (Berkowska & Dalla Bella, 2013), although the variability may also make it difficult to define poor-pitch singing consistently across tasks or studies (Dalla Bella, 2015).

Each measure examined above has its own merits and may be helpful to tease apart diverse patterns of pitch inaccuracies (Dalla Bella, 2015). For example, if an individual has low accuracy for absolute pitch metrics but high accuracy for relative pitch metrics, this would indicate that the individual has possibly made pitch transposition errors in the task. However, the assortment of tasks and singing ability measures may make it potentially difficult to compare results across studies if each study uses a different set of tasks and measures.

More recently, there has been a push for singing ability researchers to adopt a standardised approach to assessing singing accuracy, using a common set of tasks and measures. A recent initiative is the Seattle Singing Ability Protocol (SSAP) developed by several leading researchers in the field, which aims to devise a minimum set of singing tasks that can be easily administered and evaluated through objective or subjective means (Demorest et al., 2015). If the protocol becomes the ‘golden standard’ in singing ability assessment, it may help to expand the state of knowledge about the prevalence, patterns and causes of inaccurate singing across different populations, how various types of singing inaccuracies vary as a function of age or training, and the neural correlates of poor-pitch singing. This standard protocol could also be used to evaluate the efficacy of singing interventions (Demorest et al., 2015).

4.5 Singing: An Ideal Model for Genetic Analysis

The above sections provided an overview of singing ability, outlining its typical developmental stages and neural correlates, and describing how singing ability is usually evaluated in research settings. Utilising the information reviewed in this chapter and the two previous chapters, this section presents several arguments to demonstrate why singing is an ideal paradigm for investigating the genetic basis of music ability.

4.5.1 Singing is a multifaceted music ability

Singing is a complex, multifaceted music ability which enlists an extensive range of music perception and production subskills. Although singing is essentially a form of music production ability, music perception ability is also crucial in singing due to the

complex auditory-motor interactions that occur between music perception and music production during singing or other music performances (Zatorre, Chen, & Penhune, 2007). As the neurocognitive model presented in **Section 4.2** has elucidated, music perception ability is necessary in singing not only to perceive external auditory input, but also to monitor auditory feedback of one's voice for effective control of the pitch produced. **Figure 4.3** shows the music perception and production subskills involved in singing, as adapted from the figure on music ability and its constituent music subskills in **Figure 2.1** (p. 11).

As evident from **Figure 4.3**, singing encompasses most of the constituent subskills of music ability listed in **Figure 2.1** (except for music composing and music arranging). This indicates that singing is representative of music ability. Moreover, singing ability is commonly regarded as an indicator of music ability in many different cultures (Sloboda, Wise, & Peretz, 2005), which affirms its suitability to be used to investigate the genetic basis of music ability.

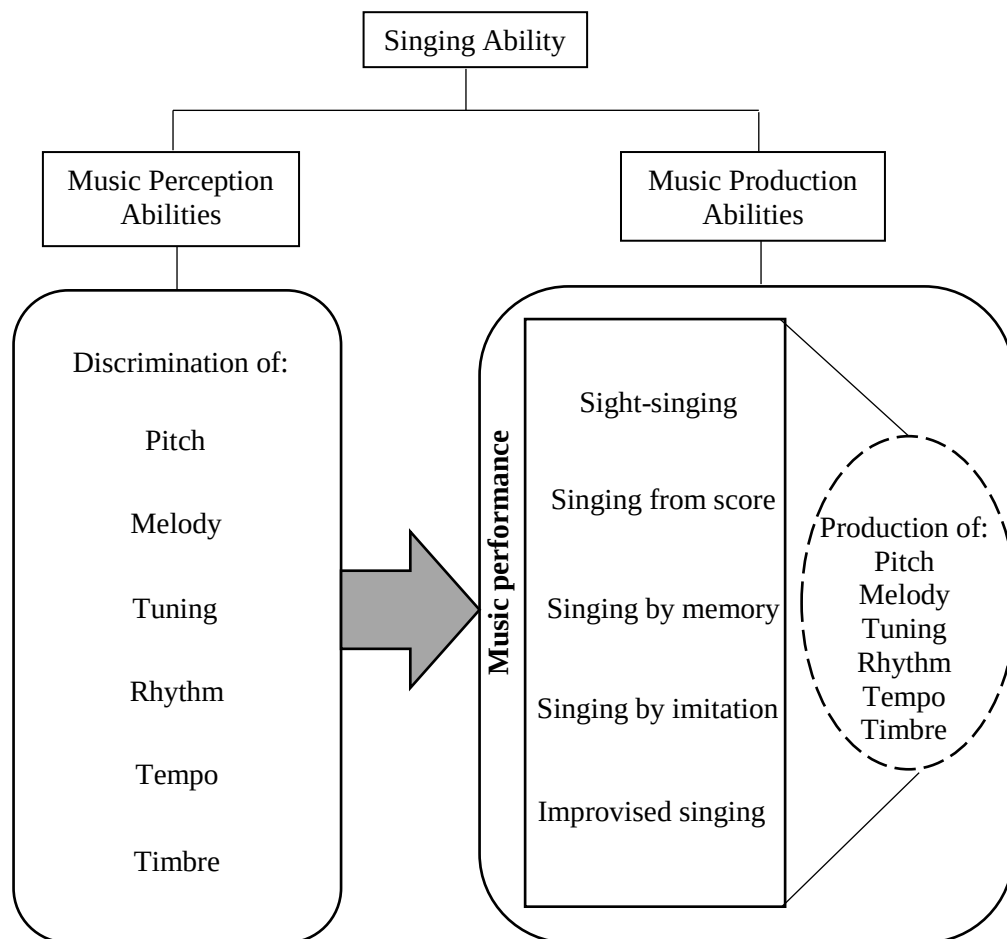


Figure 4.3. Singing ability and its constituent perception and production subskills.

4.5.2 Singing is a universal musical behaviour

Besides being a multifaceted music ability, singing is also a universal musical behaviour present across all known human cultures (Lomax, 1968). The human voice is possibly the first musical instrument, and as noted in **Section 4.1** (p. 84), singing ability emerges early and spontaneously at around 6 to 18 months of age. Singing's ubiquity in various cultures and its spontaneous development set it apart from other music performance abilities, which typically require formal instrumental learning. Despite its spontaneous emergence, diversity in singing abilities is still evident across the general population (Dalla Bella et al., 2007). Even in cultures where singing behaviour is commonly practised in everyday life, different rates of singing ability development across individuals can be observed (see **Section 3.2**, p. 65). The inter-individual variability in singing ability and the rate of singing skill acquisition even in musically-rich cultures make it reasonable to expect that singing ability has a heritable component, and allows assessment of both novice and trained experts.

It has been shown in **Section 4.3** (p. 88) that there is now an emergent understanding of the neurobiological basis of singing ability, and how the neural substrates may vary depending on one's singing experience and expertise. The presence of training-induced neuroplasticity, however, does not preclude the possibility of pre-existing neurological differences that are present even prior to vocal training (Merrett et al., 2013).

Anecdotally, some individuals appear to possess a natural ability to sing in tune (Watts et al., 2003), and singing ability has been observed to cluster in families (e.g., the Jackson 5). It is therefore conceivable that such pre-training interindividual behavioural and neurological variability is genetically influenced. Compared to other music production abilities that require formal learning, greater pre-training interindividual variability can be expected from singing, making it highly suitable for genetic analysis. This is further bolstered by the fact that evidence of genetic influences have already been reported for some of the subskills of singing ability (e.g., pitch, melody and rhythm discrimination), as described in **Sections 2.4.1.1** (p. 33) and **2.4.1.2** (p. 34).

4.5.3 Singing is shaped by both formal and informal music learning environments

As discussed earlier in **Section 3.5** (p. 81), singing is arguably the only music production ability which is jointly influenced by a formal music learning environment, as well as informal music learning environments such as cultural and family environments (as shown in **Figure 3.1**, p. 83). Other music production abilities such as instrumental performance abilities and even composing and arrangement, are principally developed in the formal music learning environment, especially in Western culture. This makes it difficult for instrumental production abilities to fully account for environmental influences from other contexts such as culture and home environments. Moreover, studying the performance abilities of expert musicians appears to treat music as an elite skill instead of fully capturing the essence of music as a universal human behaviour. Singing ability, however, is not only able to reflect a greater range of environmental contexts, its ubiquity also makes it representative of music ability in the general population. Singing ability, therefore, is arguably a more appropriate music production skill to investigate the genetic basis of music ability than other music production abilities.

4.5.4 Singing ability has received minimal research attention

Table 2.1 (p. 26) shows that the majority (61%) of the genetic investigations on music abilities and music-related traits have focused on music perception skills. In many of these studies, music perception abilities are referred to as “music aptitude”, which implies that music perception ability in and of itself can encapsulate what it means to be “musical”. Music production abilities, however, are equally important, and are probably more salient and demonstrable forms of music ability than music perception *per se*. While there has been increasingly more genetic studies in recent years that focus on music production abilities (see **Section 2.4.2**, p. 48), the only studies that have investigated singing ability have only assessed singing with (i) self-report measures of participation in singing activities (**Section 2.4.2.5**, p. 55), and (ii) simple single-pitch vocal imitation tasks (**Section 2.4.2.6**, p. 56).

Although vocal pitch-matching is an important subskill of singing, it is not sufficiently complex to exemplify singing ability in everyday life. As singing proficiency may vary considerably depending on the complexity and nature of the singing task, it is therefore preferable to use different types of singing tasks to evaluate singing ability in order to establish a comprehensive profile of singing proficiency (Berkowska & Dalla Bella, 2013). In view of the promising heritability estimate (40%) reported by Park et al. (2012) for vocal pitch-matching, more research attention is clearly warranted to investigate the genetic basis of singing ability with a comprehensive range of singing tasks, which would offer greater ecological validity to the findings.

Moreover, although it has been demonstrated in several recent studies that music perception ability and formal music training (measured in terms of the total amount of music practice) have a partially overlapping genetic basis (see **Section 2.4.2.2**, p. 50), the possibility of a shared genetic basis between singing ability and formal music training has not been similarly investigated to date. As music perception ability is a subskill of singing ability (**Figure 4.3**), it is conceivable that singing ability and formal music training may also have shared genetic influences.

To summarise, singing ability, being a universal, multifaceted music ability that is spontaneously emergent and shaped by formal and informal music learning environments, is an ideal model to investigate the genetic basis of music ability and deserves more careful examination using a variety of singing tasks. The next step to consider is: What is a suitable genetic approach to study singing ability?

As noted earlier in **Section 4.5.3**, the development of singing ability is not contingent on formal music learning, and cultural and family environments also play an important role. It follows then that any pre-training behavioural and neurological differences in singing ability can be a result of genetic influences or environmental influences from cultural and family musical environments. It will therefore be expedient to use a genetic approach that can disentangle genetic influences from environmental influences due to formal training as well as pre-training environmental influences such as family and culture.

A twin study (**Section 2.2.2**, p. 12) is particularly suited for this purpose. The twin study design estimates the relative contributions of genetic and environmental factors on trait variation, and distinguishes between the effects of common (or shared) and unique environmental factors. In the context of music ability, common environmental influences include the family musical environment, which is experienced in like manner by each twin pair raised in the same household. Unique environmental influences, on the other hand, can account for divergent musical experiences within the twin pair, such as differences in duration and type of formal music training. It is therefore clear that the twin study design may be extremely effective in disentangling genetic and environmental influences on singing ability, and thus estimating the extent to which singing ability is genetically influenced in a population.

4.6 Aims and Hypotheses

Having established the rationale for conducting a twin study to investigate the genetic basis of singing ability in the previous section, this section will describe the aims and hypotheses of the thesis.

The primary aim of the current twin study was to address a fundamental question:

- A. Is there a sizeable genetic component for singing ability?

To this end, singing ability was determined in the two following ways:

- i. Objectively, using a comprehensive range of singing tasks and objective pitch accuracy measures.
- ii. Subjectively, based on self-report of singing ability by participants

With reference to the primary aim, it was hypothesised that:

- 1) Objectively-assessed singing ability across all tasks would be significantly influenced by genetic factors, as demonstrated by significantly higher intraclass correlations for MZ compared to DZ twins, and a significant heritability estimate in univariate genetic modelling.

Specifically:

- a. The ability to vocally match single pitches would have a significant genetic component, as demonstrated by higher intraclass correlations for MZ compared to DZ twins, and a significant heritability estimate in univariate genetic modelling.
- b. The ability to sing a familiar song in tune would have a significant genetic component, as demonstrated by higher intraclass correlations for MZ compared to DZ twins, and a significant heritability estimate in univariate genetic modelling.
- c. The ability to sing new melodies in tune would have a significant genetic component, as demonstrated by higher intraclass correlations for MZ compared to DZ twins, and a significant heritability estimate in univariate genetic modelling.

- 2) Subjectively-assessed singing ability (based on self-report) would have a significant genetic component, as demonstrated by higher intraclass correlations for MZ compared to DZ twins, and a significant heritability estimate in univariate genetic modelling.

In addition to the main aim above, the current study also aimed to address the following question:

- B. Is there evidence of genetic influences on the environmental components associated with singing ability?

To investigate this, a singing and music background questionnaire was used to identify environmental factors associated with singing ability.

It was hypothesised that:

- 1) Environmental factors related to formal music training would have a significant genetic component, as demonstrated by significantly higher intraclass correlations for MZ compared to DZ twins, and a significant heritability estimate in univariate genetic modelling.
- 2) Singing ability and environmental factors related to formal music training would have a partially shared genetic basis, as demonstrated by a significant additive genetic correlation between singing ability and these environmental factors.

To address the aims and hypotheses, it was necessary to consider how to develop the methodology for the study. The next chapter details the methodological development process for an online program, Let's Hear Twins Sing!, which was purpose-designed for this study.

5

METHODOLOGICAL DEVELOPMENT

This chapter describes the methodological development of the online twin study.

Section 5.1 explains the rationale for conducting an online study and **Sections 5.2** and **5.3** recount the development process of the online program and detail the tasks and questionnaire that comprise the program. Finally, **Section 5.4** gives an account of the piloting of the online program, and discusses some of the technical issues that arose and the troubleshooting measures undertaken.

5.1 Rationale for an Online Twin Study

In order to conduct a twin study, the first and foremost question was to consider the source of recruitment. The most effective means of recruitment for the purpose of the current study was through the Australian Twin Registry (ATR), one of the largest volunteer twin registries in the world, that has enrolled over 33,000 pairs of Australian twins since its formation. As the ATR twins could live anywhere in Australia, it was vital that participation was broadly available to interested twins regardless of their geographical location, so as to maximise the response rate and the sample size of the study. Although it would be ideal to arrange for interested participants to commute to Melbourne and take part in the study in a carefully controlled laboratory-based setting, this was not logistically nor financially feasible. A viable and more cost-effective alternative was therefore to design and develop an online program which could be accessed by participants via the internet, and also have the functionality to reliably capture and record singing data from the participants in real-time, so that the data could be retrieved and analysed subsequently.

To the researcher's knowledge, none of the existing studies in the field of singing research have collected singing data in an online setting using a program with real-time sound recording capability. In view of this, the online program Let's Hear Twins Sing! (<http://twinsing.sollysweb.com>) was jointly designed by the author and her two supervisors, with the advice of Professor Isabelle Peretz, a professor of psychology from the University of Montreal and the co-director of the international laboratory for Brain, Music, and Sound research (BRAMS). The program was created on the Adobe Flash platform by an experienced programmer who has worked on the development of other music-based projects within the Clinical, Auditory, and Affective Neuroscience (CAAN) Lab in the Melbourne School of Psychological Sciences in The University of Melbourne. As the online program Let's Hear Twins Sing! pioneered online real-time recording and collection of singing data, the current study was probably the world's first singing study to be conducted online.

5.2 Program Development

The order of tasks and estimated duration for completing each task are summarised in **Table 5.1**. In total, the online program comprised six main tasks (three singing tasks, two music perception tasks and one tongue twister task) and a singing and music background questionnaire. The estimated time of completion of the study was approximately 30 minutes. Before describing each task in detail, the following section will discuss the methodological and technical issues that need to be taken into consideration in developing the online program.

5.2.1 Program design

Musch and Reips (2000) and Nosek, Banaji and Greenwald (2002) have highlighted concerns regarding web-based research that researchers need to take into consideration when conducting studies online. Most of the issues pertain to the researcher not being present to monitor the study participant, as opposed to a laboratory setting. Examples include the lack of control over participant behaviour during the study, the lack of control over dropout or participant motivation in taking part, the possibility of participating multiple times or fraud, and potential ethical issues such as ensuring

adequate informed consent and debriefing. These concerns were recognised and addressed during the program design phase, and preemptive measures that were undertaken are described below.

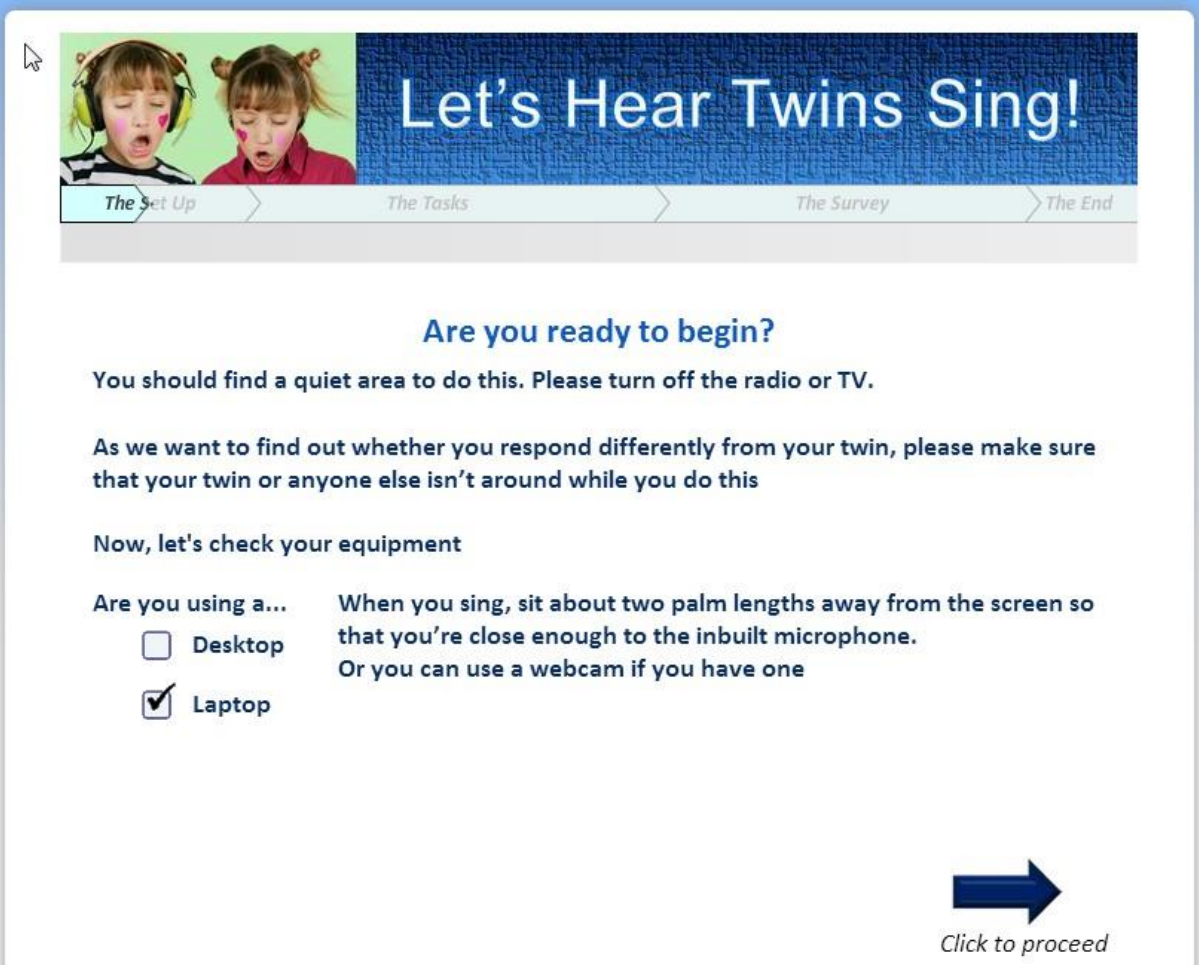
Table 5.1. Breakdown of the Components in Let's Hear Twins Sing!

Component	Duration (min)	Description
Welcome and instructions	1.5	Brief description of the assessment and instructions for participants before commencing the tasks
Sound and mic check		Test the functionality of speakers and microphone
Demographic information		Enter details of demographical information
Task 1: Happy Birthday Singing Task	3.5	Sing <i>Happy Birthday</i> in several different conditions (e.g., paced/unpaced, with/without lyrics), in a key of choice.
Task 2: Match The Note Task	5	Fine-grained perceptual pitch-matching. Using a pitch slider, participants match a random sequence of five different sine tones as closely as possible by moving a pitch slider on the screen (15 trials; tone range for females = 246.94-397 Hz, tone range for males=123.47-196 Hz)
Task 3: Sing The Note Task	5	Listen to five different sine tones and sing these back (15 trials; tone range for females = 246.94-397 Hz, tone range for males=123.47-196 Hz)
Task 4: Sing The Tune Task	5	Participants listened to five different short novel melodies and were asked to sing these back (15 trials; tone range for females = 220-440 Hz, tone range for males=110-220 Hz)
Task 5: Tongue Twister	3	Say a one-phrase tongue twister 4 times in a row in unpaced and paced conditions.
Task 6: Happy Birthday Melody Perception Task	2	Identify the correct version of <i>Happy Birthday</i> from two other mistuned versions.
Questionnaire	5	Singing and Music Background Questionnaire (35 items for non-musicians or 44 items for musicians)
Concluding remarks		Option to leave expression of interest for future study Feedback on Match The Note Task provided Thank You page
Total duration	30	

5.2.1.1 Lack of control over participant behaviour

An online research study setting presents difficulties in monitoring participant behaviour. In the context of the current twin study, one of the main challenges was ensuring that the singing data were of sufficiently good quality to undergo subsequent acoustic analyses. Although it was impossible to control for poor recording quality that

stemmed from inferior technical equipment used by the participants, clear instructions were provided to prompt the participants to do the online study in a favourable setting. At the beginning of the program, the participants were asked to complete the study alone in a quiet location, independent of their co-twin. They were also advised on the hardware required for the study and how far they should position themselves from their recording device to ensure an optimal recording volume (**Figure 5.1**).



Let's Hear Twins Sing!

The Set Up *The Tasks* *The Survey* *The End*

Are you ready to begin?

You should find a quiet area to do this. Please turn off the radio or TV.

As we want to find out whether you respond differently from your twin, please make sure that your twin or anyone else isn't around while you do this

Now, let's check your equipment

Are you using a...

☐ Desktop

☒ Laptop

When you sing, sit about two palm lengths away from the screen so that you're close enough to the inbuilt microphone. Or you can use a webcam if you have one

Click to proceed

Figure 5.1. Set-up page of Let's Hear Twins Sing!

To ensure that the sound stimuli could be heard clearly and at a comfortable volume, the program set-up then proceeded with the sound volume calibration process, during which a test sound was played and the participant could move the onscreen slider to adjust the volume (**Figure 5.2**). This was followed by a microphone check that the microphone was functioning and sound output from the microphone could be reliably detected by the program (**Figure 5.3**).

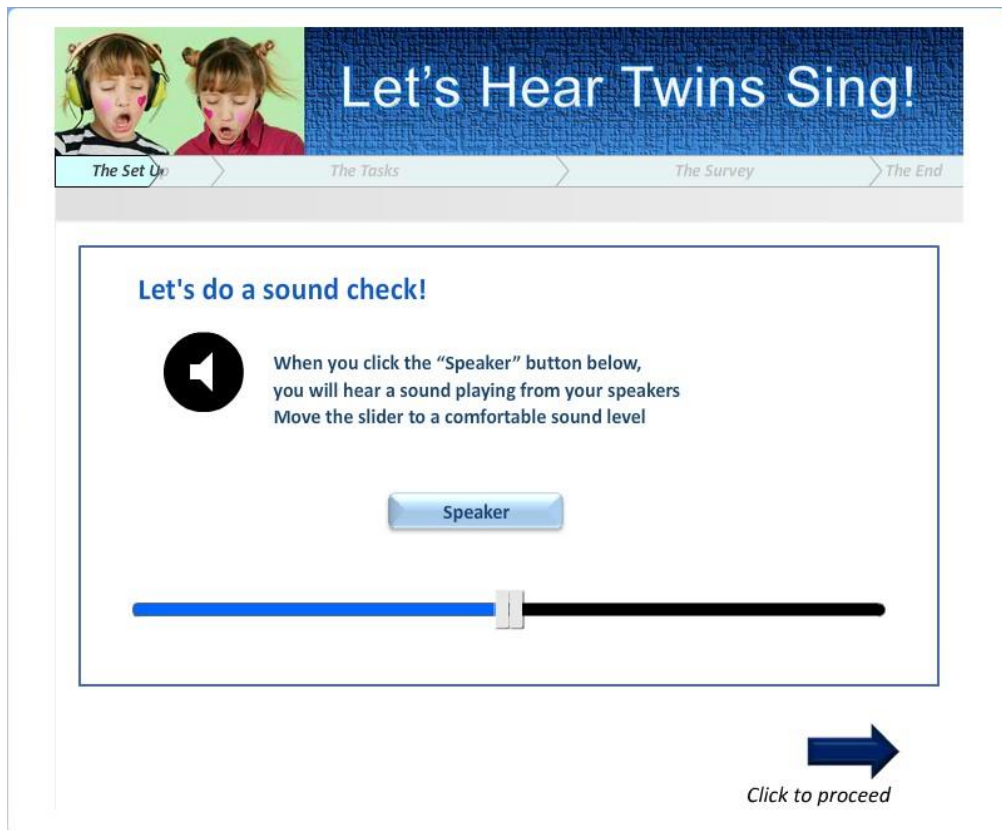


Figure 5.2. Sound volume calibration page of Let's Hear Twins Sing!

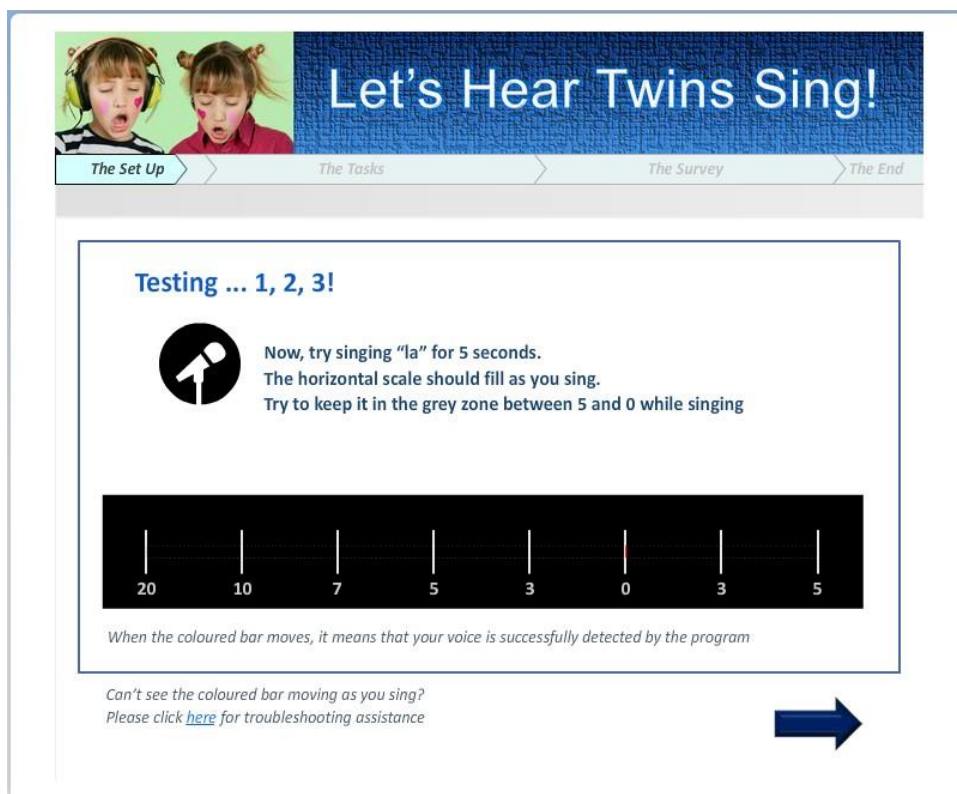


Figure 5.3. Microphone detection page of Let's Hear Twins Sing!

As the researcher was unable to explain the tasks to the participants in person, care was taken to ensure that task instructions were worded as clearly and simply as possible (see figures from **Section 5.3**, p. 125). In addition, for the singing and pitch perception tasks that involved listening to sound stimuli, at the beginning of each new trial, the green musical note icon would blink once to prompt the participant to click on it in order to listen to the sound stimulus of this trial. To prevent participants from clicking the record button before listening to the stimulus, the record button remained disabled (as shown by its greyed out state) until the sound stimulus has ceased playing (**Figure 5.4**).

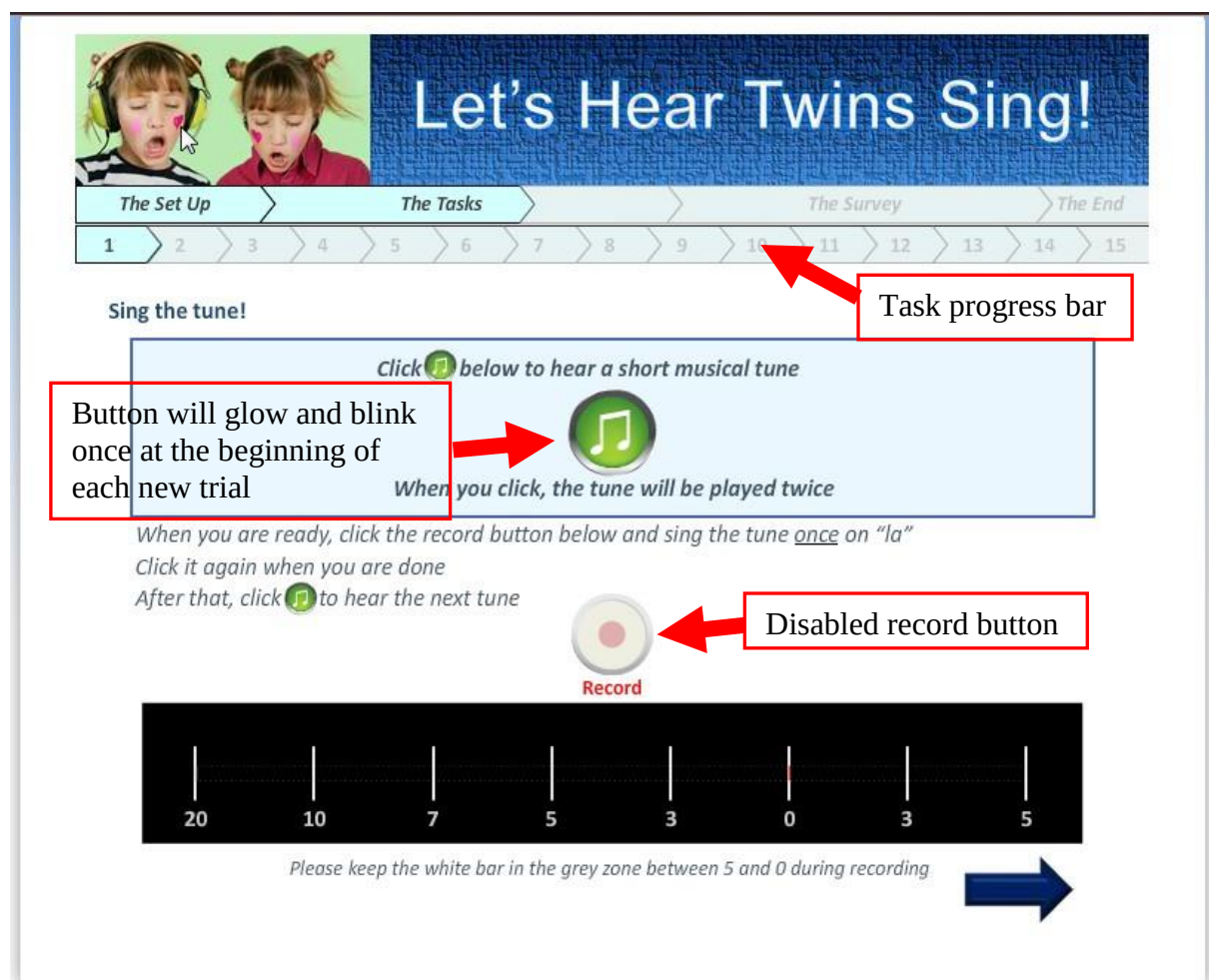


Figure 5.4. Basic layout of the online tasks in Let's Hear Twins Sing! A task progress bar at near the top of the screen indicates the participant's progress in the current task. The green button with musical icon will glow and blink at the beginning of every trial to prompt the participant to click on it to hear the music stimulus. The record button will remain disabled until the music stimulus of the current trial has been played.

Another challenge of a web-based study is the possibility that participants may inadvertently miss responding to some trials or questionnaire items. To prevent such

occurrences, the blue “Click to proceed” arrow in the lower right hand corner of the screen would only be activated (indicated by the appearance of the ‘Click to proceed’ text under the blue arrow) when the participant had successfully completed the entire singing or music task, or when each questionnaire item on the screen received a response (**Figure 5.5**).

Let's Hear Twins Sing!

The Set Up > The Tasks > The Survey > The End

In your everyday life right now, how often do you currently sing?
Make sure you respond to every statement.

	Never	Rarely	Sometimes	Often	Always
By yourself	☐	☐	☐	☐	☐
With your family	☐	☐	☐	☐	☐
With your friends	☐	☐	☐	☐	☐
In a choir/group	☐	☐	☐	☐	☐
As a solo performer	☐	☐	☐	☐	☐

➔

Figure 5.5. Screenshot from the questionnaire. As no responses have been made, the blue arrow in the lower right hand corner is inactive, making it impossible to proceed to the next screen. Once responses have been made to all the questionnaire items, the text “Click to proceed” appears under the arrow, indicating that the arrow is active.

In sum, the lack of control over participant behaviour was minimised by providing clear instructions in the program and by implementing a forced selection design to ensure that the participants would navigate through the tasks and questionnaire correctly.

5.2.1.2 Lack of control over participant dropout

Besides being unable to monitor participant behaviour during the study, it is also not possible to exercise control over participant dropout in an online research setting, given the setting is voluntary in nature. As a result, if participants found the online study too lengthy, too challenging or too boring, they may not be interested or motivated enough to complete the study. This is an important issue to deal with, because participant dropout results in incomplete data and reduces the amount of useable data for analysis. Some deliberations were therefore made towards the program design.

First, while the current study aimed to assess singing ability with a comprehensive range of tasks, it was necessary to balance comprehensiveness with a consideration of the length of the study. For instance, an online study which takes one hour or more than one sitting to complete would be untenable, as many people would not be motivated to complete such a lengthy study. The current online study therefore endeavoured to be as short as possible, with an estimated duration of 30 minutes while still collecting an adequate amount of data for analysis. In view of this, for the perceptual and vocal imitation tasks (i.e., Match The Note Task, Sing The Note Task and Sing The Tune Task), five different stimuli were used. Each stimulus was presented in three trials, resulting in a total of 15 trials per task. Having five different stimuli in 15 trials per task was deemed sufficient to allow for a reasonable estimation of a participant's singing proficiency on a particular task, while also maintaining enough variety and challenge to keep the participant motivated and engaged. Moreover, to minimise missing data, the study was designed to be completed in one sitting without the option to save progress for later completion.

Apart from task duration, the order with which the tasks were presented could also encourage or deter participants from completing the entire study. After completing the equipment setup procedure and filling in the demographic information, the participants commenced the study tasks with Happy Birthday Singing Task, as it was considered the most familiar, and therefore, the least intimidating. It was then followed by Match The Note Task, to offer some variety and provide an activity other than singing. Sing The Note Task, which was the vocal analogue of Match The Note Task came next, before progressing to Sing The Tune Task, which was relatively harder. After completing all

the singing tasks, the tongue twister task then infused a light-hearted fun element to the study. This was followed by Happy Birthday Melody Perception Task, before concluding with the music and singing background questionnaire.

Clipart with encouraging text such as “Well done!”, “Awesome!” and “Keep it up!” accompanied by sound effects appeared after each task was completed, so as to provide the participants with some form of positive reinforcement to persevere. Within each task, the participants were able to keep track of their progress from the task progress bar situated near the top of the screen (**Figure 5.4**), which also served to motivate the participants to keep going.

Finally, financial incentives were offered to encourage participants and their co-twins to complete the study. Each twin pair where both individuals completed the online study was eligible to enter an iPad Mini lucky draw to win two iPad mini 2 (16gb with Wi-Fi) with retina displays. Moreover, in conjunction with the Twins Plus Festival 2015 in Melbourne, an exclusive promotion was conducted in which WISH eGift cards valued at \$40 each were given to the first 40 pairs of twins who completed the online study during the promotional period (10AM AEST Sunday 22 March 2015 to 11:59PM AEST Sunday 5 April 2015).

5.2.1.3 Multiple participation or fraud

A challenge commonly faced by internet-based research studies is the likelihood of having the same participant respond to the study multiple times, or having unverified individuals accessing and attempting the online study. To minimise such possibilities, invited access to the study was carefully implemented. In the case of twins recruited from the ATR, they received an invitation email from the ATR containing information and a web-link to the study. When the ATR participants accessed the online program, on the demographic information page they were asked to enter a unique ATR ID, as well as supply identifying information such as their name and birthdate (**Figure 5.6**). This information enabled the researcher to verify the ATR participants’ identities with the Twin Registry.

Let's Hear Twins Sing!

The Set Up > The Tasks > The Survey > The End

Please enter your full name

Please enter your Twin Registry (ATR) ID - (You can find your ID in the email from the ATR)

I'm not an ATR member, but both my twin and I are interested in participating in this study ☐

Gender ☐ Male ☐ Female

Date of birth

Years of education completed

What is your first language

What is your second language

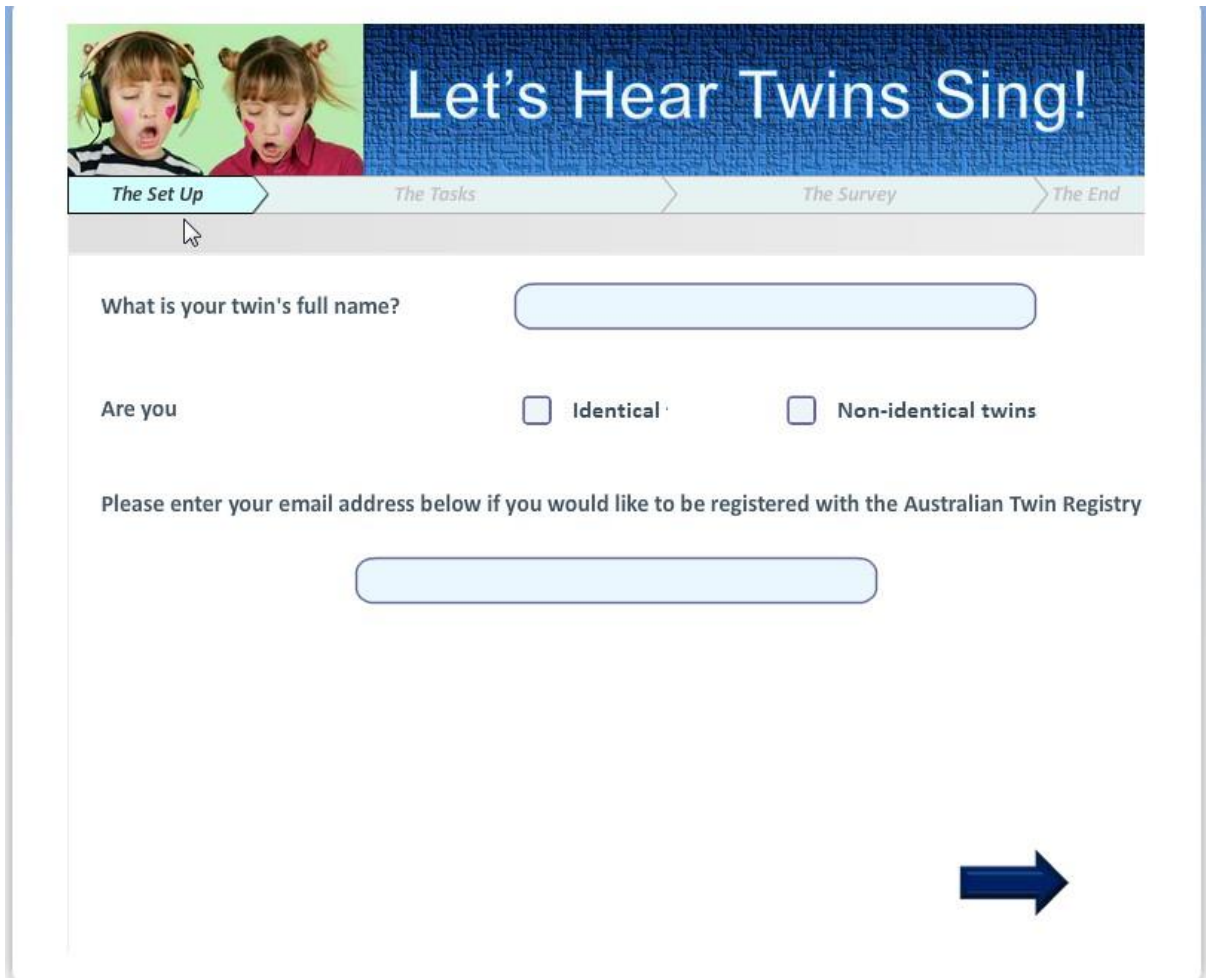
(Write 'None' if you don't have one)



Figure 5.6. Demographic information page of the online program.

As for potential participants not registered with the Australian Twin Registry (ATR) who lodged expressions of interest to participate with the researcher through phone or email (see **Section 6.1.1.2**, p. 149), they were contacted via email and asked to fill in a pre-screening zygosity questionnaire which included supplying personally identifiable information about themselves and their twin (see **Appendix A-3**, p. 297). The pre-screening questionnaire not only helped to determine the zygosity of these participants, but also served as a hurdle to prevent fraud participation. Only after the researcher received the pre-screening questionnaire responses from the interested non-ATR participants and was convinced of the veracity of the responses, was an email with the study information and the web-link for the online program sent to the interested participants.

On the demographical information page in the program (**Figure 5.6**), non-ATR participants were required to select a checkbox indicating their non-ATR status, which would then take them to another page where they were again asked to state their zygoty as well as supply their co-twin's name (**Figure 5.7**). Such identifying information was utilised subsequently to cross-check with responses from their co-twins as a further check of its veracity.



The screenshot displays the 'Let's Hear Twins Sing!' program interface. At the top, there is a header with a blue background and the title 'Let's Hear Twins Sing!' in white. To the left of the title is a small image of two young girls wearing headphones and singing. Below the header is a navigation bar with four tabs: 'The Set Up' (highlighted in light blue), 'The Tasks', 'The Survey', and 'The End'. The main content area is white and contains the following form elements:

- A text input field labeled 'What is your twin's full name?'.
- A section labeled 'Are you' followed by two checkboxes: 'Identical' and 'Non-identical twins'.
- A text input field labeled 'Please enter your email address below if you would like to be registered with the Australian Twin Registry'.
- A large blue arrow pointing to the right at the bottom right of the form.

Figure 5.7. Additional identifiable information required from non-ATR participants.

To summarise, the prerequisite for all participants (whether or not registered with the ATR) to take part in the online study through rigorous invited access, and the need for participants to supply verifiable, identifiable information in the online program not only helped to prevent fraud participation, but also made it unlikely that individuals would participate multiple times.

5.2.1.4 Potential ethical issues

There are also concerns in the online research setting that the absence of the researcher may result in participants not receiving adequate informed consent. To ensure that all the participants had sufficient information to make an informed decision about participation, a web-link to the information sheet (see **Appendix A-4**, p. 299) was provided in the recruitment email. Moreover, the welcome page of the online program included a link to the information sheet, to ensure that the participants were given adequate opportunity to understand what the study entailed before deciding to proceed (**Figure 5.8**). It was also worded clearly on the welcome page that the decision to proceed through the program was considered implied consent to participate.

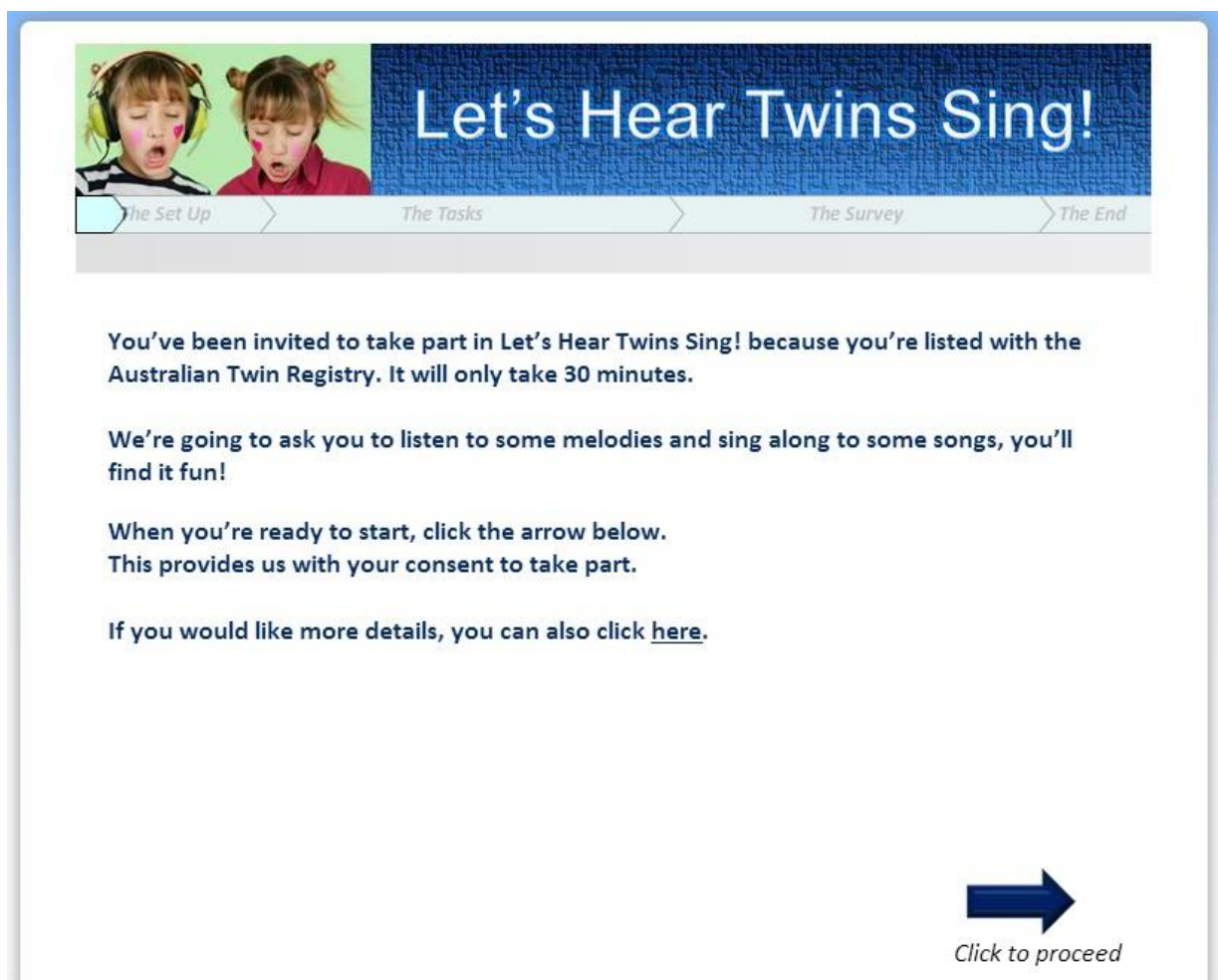


Figure 5.8. Welcome page of the online program.

In adherence with the University of Melbourne Human Research Ethics guidelines, the information sheet provided details of the purpose of the study, as well as what

participation involved and the expected time commitment. The information sheet also clearly stated that involvement in the project was voluntary and that participants were free to withdraw consent at any time. In addition, participants were assured of the confidentiality of the data they supplied and their right to withdraw any unprocessed data previously supplied if they chose to withdraw from the study. Contact details of the principal and student researchers as well as those of the Executive Officer of the Human Research Ethics Committee at the University of Melbourne were also available on the information sheet in case participants had any concerns about the study.

As the targeted age range for the participants was 15 years and above, for minors between the age range of 15-17 years, parental consent were first sought by the ATR, by sending the parents the invitation email with the study information attached. The parents could then consent to or decline participation on their children's behalf by replying to the invitation email. If consent were given by the parents, the ATR then contacted the minors about the online study using the children's email addresses provided by the parents.

The study was independently reviewed and received ethics clearance from the Australian Twin Registry and the University of Melbourne's Behavioural and Social Sciences Human Ethics Sub-Committee (Ethics ID: 1238728) as having significant scientific value and meeting all necessary ethical requirements.

5.2.2 Technical considerations

Being the first online research study that involved recording singing data in real-time, the current study had to address a number of technical challenges in order for the online program to be properly accessed and run smoothly for the majority of participants. The considerations and measures undertaken are described below.

5.2.2.1 Software requirements

The online program was created on the Adobe Flash platform, a multimedia software platform that is frequently used to produce animations, browser games, and internet applications. To run the program, participants needed to have Adobe Flash Player

installed on their personal computer, a free software that could be downloaded from the Adobe Flash Player website (<https://get.adobe.com/flashplayer/>). Once the Adobe Flash Player was installed, the online program could be run from any web browser. To increase the likelihood of the program being able to run smoothly during the study, using the most up-to-date versions of the web browser and Adobe Flash Player to access the program was recommended. To facilitate this, upon accessing the web link to the online study, the program would check and inform whether the participant's web browser and Adobe Flash player plugin were up-to-date. If the browser or the Flash player was not the latest version available, participants were prompted to click on a link on the screen to update the browser or Flash player accordingly (**Figure 5.9**).

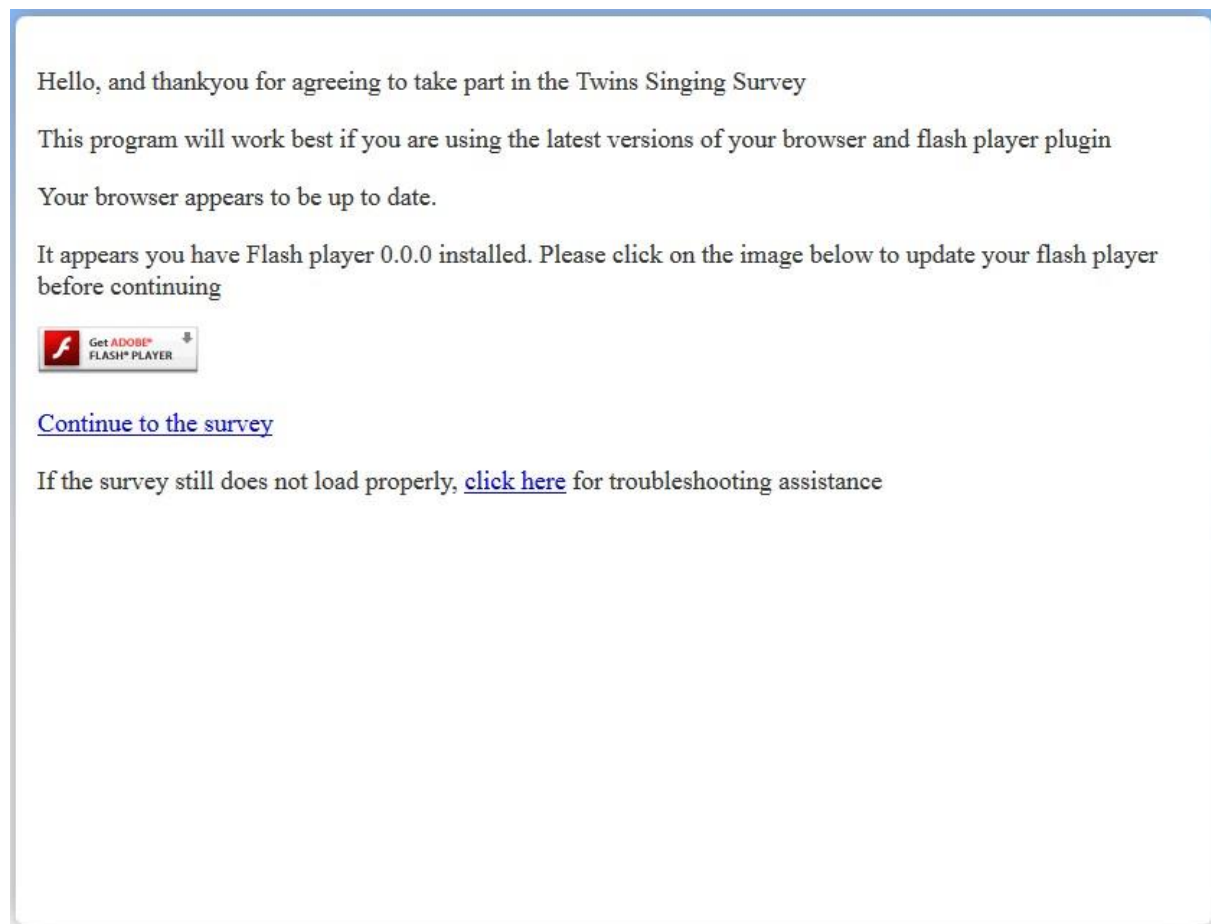


Figure 5.9. Browser and Adobe Flash Player version detection implemented at the beginning of the program.

In addition, if a participant noticed that the program failed to load and thus was unable to proceed with the study, troubleshooting instructions were available from a web-link on the same screen to navigate participants through possible explanations and solutions

(see **Appendix B-1**, p. 302). Participants still having problems following this were requested to contact the researcher directly, using the contact details supplied in the instructions.

5.2.2.2 Hardware requirement

a) *Desktop or laptop computers*

To run the online program successfully, desktop or laptop computers were essential. This is because the Adobe Flash Player could only be run on Windows, Macintosh and Linux web platforms, and not mobile devices such as Android or Apple smartphones or tablets. To ensure that interested participants were aware of the hardware requirements, the invitation email sent to the participants clearly stipulated the need to use a desktop or laptop computer to run the program. In addition, the link to the troubleshooting instructions on the start screen of the program (**Appendix B-1**, p. 302) included this information.

b) *Recording capabilities*

As the online study's main aim was to capture and assess singing ability, it was necessary for the participant's computer to be able to detect singing input. While most laptop computers and newer models of desktop computers have inbuilt microphones, some computers need to use an external microphone (such as a computer microphone, headset or web camera) to run the program and perform the tasks. To ensure that the participants had functional recording hardware to do the online study, prior to commencing the singing and music tasks, they were guided through a microphone check (**Figure 5.3**, p. 114). Participants whose voice could not be detected by the program could not continue with the study since the "Click to proceed" arrow in the lower right corner of the screen could only be activated if sound was detected. To assist participants who were unable to proceed, a troubleshooting link was provided at the bottom of the screen which helped participants identify and rectify any microphone detection problems (**Appendix B-2**, p. 304). Phone and email details of the researcher were also available in the troubleshooting guide if participants required direct assistance.

5.2.2.3 Online data collection and storage

To ensure maximal online data security, the data of the participants collected by the online program was stored on a highly secure, password-protected FTP (file transfer protocol) server hosted by the developer of the online program. Each participant's data was saved in a separate folder on the server. For participants from the Australian Twin Registry (ATR), their folders were named according to their respective ATR IDs. As for non-ATR participants, their folder names consisted of randomly-generated characters and they were only identifiable by accessing the text file in the data folder that contained their sociodemographic information.

Each participant's folder contained: 1) sound recordings from the three singing tasks; 2) sound recordings from the tongue twister task; 3) a text file detailing the participant's pitch-matching responses (in Hz) for all 15 trials of Match The Note Task; 4) a text file containing the participant's sociodemographic information, and responses from Happy Birthday Melody Perception Task and the music and singing background questionnaire.

To ensure high fidelity of the sound recordings, each trial of the singing and tongue twister tasks was saved separately in WAV (waveform audio) format, which is an uncompressed audio file format. The quality of the recording devices and presence of any background noises in the recordings, however, were user-end factors beyond the researcher's control.

Finally, to maximise the amount of data collected from the participants in the event of intentional or unintentional dropout (e.g., due to an internet connection problem or program freeze), the sound data from the participants were perpetually saved to the server after each trial, as opposed to only saving all the data at the end of the program, as the latter would result in no data being saved to the server in the case of dropout early or in the middle of the study.

5.3 Online Task Development

The following subsections describe the online tasks and questionnaire items that constituted the study.

5.3.1 Singing tasks

The main focus of study was to assess singing ability using a comprehensive range of singing tasks. Based on the two main types (imitative and recollective) of singing tasks reviewed in **Section 4.4.1** (p. 93), the three following singing tasks were selected for the study.

5.3.1.1 Sing The Note Task

In view of the fact that a vocal pitch-matching task is probably the most prevalent task used in singing research (Demorest & Pfordresher, 2015), a pitch-matching task was selected to facilitate comparison of the current study findings with other research studies that have used similar tasks.

This task also served as the vocal counterpart of a perceptual pitch-matching task (Match The Note Task) which will be described in **Section 5.3.2** (p. 133). Comparison of the performance of these two tasks would help distinguish participants with both perceptual and vocal imitation deficits, from those whose inaccuracy was only restricted to one domain, with other variables being held constant.

Two gender-specific sets of sine tones were constructed in Audacity (version 1.3.13 Beta), using its build-in sine tone generator from the “Generate” menu. Each sine tone had a duration of one second, and was set to an amplitude value of one, the maximum possible volume attainable without clipping. The sine tones were exported from Audacity and saved as WAV 16-bit PCM (pulse code modulation) format, which is an uncompressed audio format to ensure ideal audio quality.

The set for female participants consisted of sine tone pitches B3 (246.94 Hz), C#4 (277.18 Hz), D#4 (311.13 Hz), F4 (349.23 Hz) and G4 (392 Hz), whereas the set for male participants was an octave lower, comprising the pitches B2 (123.47 Hz), C#3 (138.59 Hz), D#3 (155.56 Hz), F3 (174.61 Hz) and G3 (196 Hz). The sine tone stimuli were of the same fundamental frequencies as the ones used in a pitch-matching task by Hutchins and Peretz (2012). These six pitches were chosen as stimuli to ensure they fell within a comfortable singing range (which spanned a minor sixth from the lowest to highest pitch) for the participants.

Each of the five pitch stimuli was presented three times in a randomised order, constituting 15 trials altogether. In each trial, participants were asked to vocally imitate the sine tone presented and maintain this steady pitch for 5 s. Figure 5.10 shows an image of the screen presented to participants while performing this task.

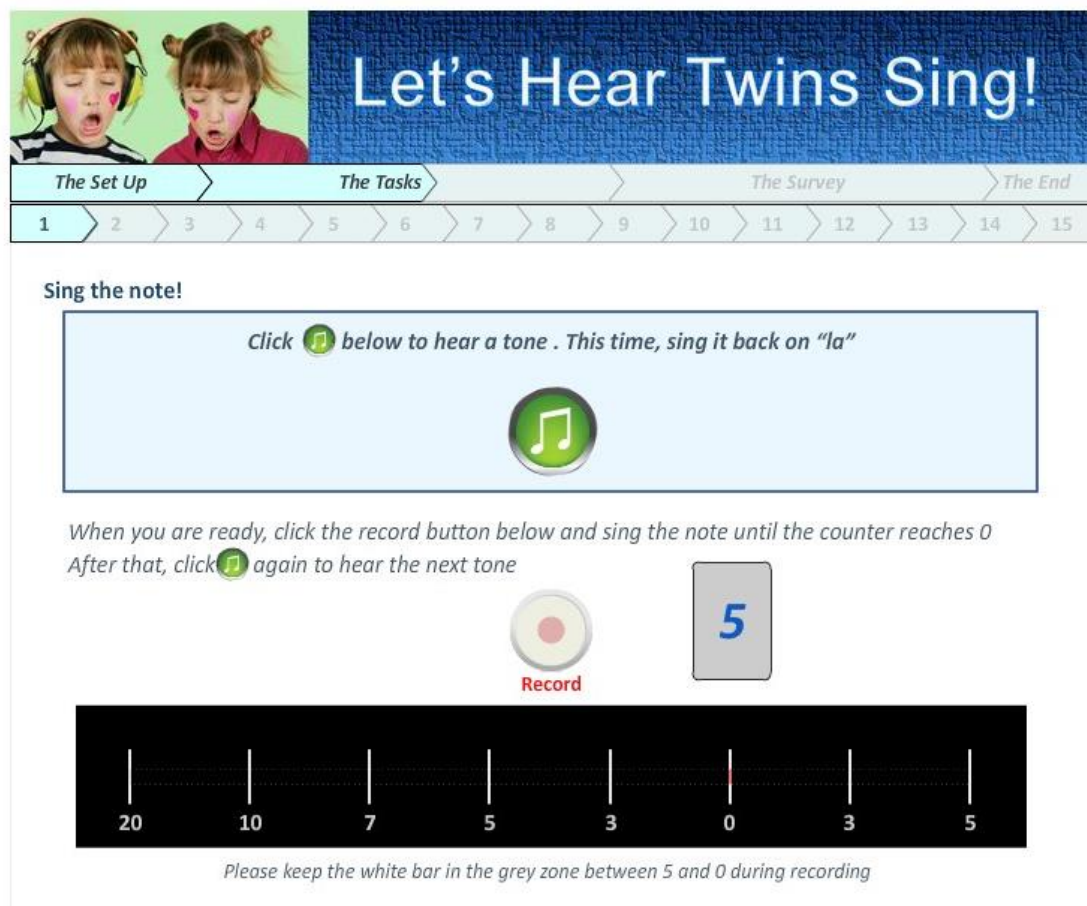


Figure 5.10. Screenshot from Sing The Note Task.

5.3.1.2 Sing The Tune Task

A second, more complex imitative singing task was also used to assess the singing ability of the participants. Imitating melodic sequences is understandably more challenging than imitating single pitches, as a greater cognitive load is incurred in order to perceive, recall and reproduce a string of successive melodic intervals correctly. As noted in **Section 4.4.1.1** (p. 93), the richer tonal context of melody imitation also lends greater ecological validity to the singing assessment.

In this singing task, five seven-note novel melodies of varying difficulty were constructed with reference to the 48 four-note tonal patterns used by Sinor (1984) in her research investigating the relative difficulty of each pattern for preschool-aged children (**Figure 5.11**). Specifically, each seven-note melody was created by selecting two four-note tonal patterns of similar difficulty that could be meaningfully combined to form a musically sensible short melody. The five melodic stimuli in this task were constructed with the intention of incorporating a good range of ascending and descending musical intervals from the diatonic scale. As evident from **Table 5.2**, with the exception of diminished fifth (i.e., tritone), major sixth, and minor and major sevenths, other intervals were all present in the five stimuli. The melodic stimuli were constructed using Sibelius 7 with a MIDI piano timbre at a tempo of 100 bpm (beats per min).

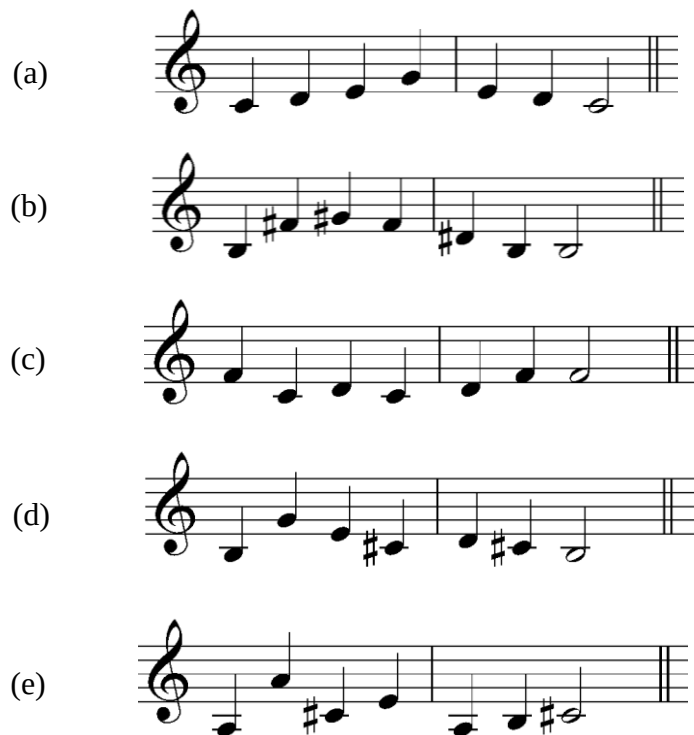


Figure 5.11. The five tonal patterns that were used in the melody imitation task for female participants. The tonal patterns for male participants were an octave lower.

Table 5.2. A Breakdown of the Incidence of the Different Types of Intervals in Sing The Tune Task

Interval	Name	U	m2	M2	m3	M3	P4	d5	P5	m6	M6	m7	M7	8ve
	Semitones	0	1	2	3	4	5	6	7	8	9	10	11	12
Ascending (n)		N/A	1	7	3	0	0	0	1	1	0	0	0	1
Descending (n)		N/A	1	5	4	1	1	0	1	1	0	0	0	0
Total		2	2	12	7	1	1	0	2	2	0	0	0	1

Note. U: unison; m: minor; M: major; P: perfect; d: diminished; 8ve: octave

The rationale for using seven-note tonal patterns in this task was to make the two melody singing tasks used in this study (i.e., the current task and a familiar song production task) as closely matched as possible, in terms of the length of each phrase and the variety of intervals used. This would facilitate the comparison of the performances in these two tasks solely along the familiar versus novel dimension with other variables potentially affecting voice accuracy largely held constant. In addition, human working memory capacity was reported to be approximately seven (plus minus) two items (Baddeley, 1994; Miller, 1994), a seven-note novel melody will therefore be of a suitable length for participants to imitate vocally.

The span of the melodic stimuli was constrained to A3-A4 (220-440 Hz) for females and A2-A3 (110-220 Hz) for males, which falls within the typical female and male singing ranges. Just like in Sing The Note Task, the five novel melodies were presented three times each in a randomised order, totalling 15 trials. In each trial, by clicking the green musical note icon (**Figure 5.12**), the melody would be played twice, separated by a short interposing silence of 0.5s. The repetition of the melodic stimuli was achieved by converting the original MIDI files to WAV files, and using Audacity to manipulate the stimuli by inserting a 0.5 second silence in between two instances of each melody.

Participants could click on the icon to listen to the melody as many times as they wished, because the task was meant to test singing ability more than memory. Once they were ready, they could click on the record button and imitate the melody.

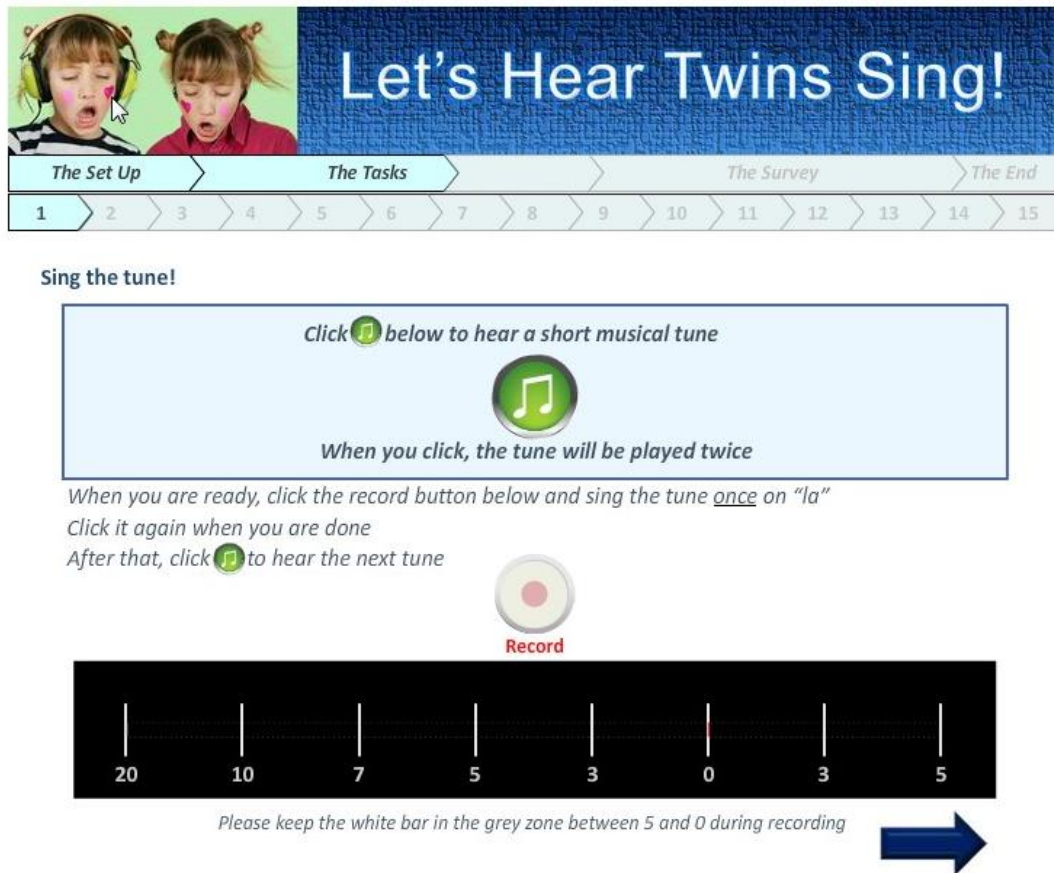


Figure 5.12. Screenshot from Sing The Tune Task.

5.3.1.3 Happy Birthday Singing Task

Finally, a recollective singing task was included in the study. Using a familiar song production task in the assessment enabled singing ability to be evaluated in a condition that was as close as possible to a real world context, thereby ensuring good ecological validity (Welch, 1994).

Happy Birthday was chosen as the familiar song for a number of reasons. First, being a celebratory song commonly sung during birthdays in many different cultures, *Happy Birthday* is a song most people are familiar with. The participants therefore could be expected to easily recall the song and sing it without needing external reference, and any pitch errors made by the participants were unlikely to be due to memory problems (Demorest & Pfordresher, 2015). Furthermore, even though *Happy Birthday* is widely known and sung, it presents a number of challenges, including the octave leap in the third phrase, as well as the presence of other wide intervals (4th, 5th and 6th) in the song.

Therefore, *Happy Birthday* was deemed an adequately challenging song to assess one's singing ability in terms of pitch accuracy.

In this task, participants were asked to sing *Happy Birthday* from memory in a key of their choice under several different conditions: (i) with lyrics at a self-determined tempo, (ii) without lyrics (on the syllable “la”) at a self-determined tempo, and (iii) without lyrics (on the syllable “la”) at a prescribed tempo of 120 beats per minute (bpm). These conditions were imposed on the task because singing accuracy may vary with each condition, with better pitch accuracy expected when the song is sung on a neutral syllable and at a prescribed moderate tempo (see **Section 4.4.1.2**, p. 95). Specifically, the tempo 120 bpm was chosen as the prescribed tempo, based on previous findings which suggest that people generally prefer listening to music at a tempo of approximately 120 bpm (Moelants, 2002).

For the first condition, the participants sang *Happy Birthday* at a self-determined tempo with lyrics. A fictional context for singing *Happy Birthday* was provided (“it is Ashley's birthday today”), and the participants were asked to click the “Record” button before commencing to sing *Happy Birthday* for Ashley (**Figure 5.13**). Once the song was finished, the same button was clicked to terminate the recording process. As with the other singing tasks, the program was designed such that participants would not be able to repeat a trial and they could only proceed forward to the next trial.

In the second condition, the participants were asked to sing *Happy Birthday* again, at a self-determined tempo and key, but this time using the syllable “la”. In the final condition, the participants sang *Happy Birthday* as per the second condition, but at a prescribed tempo of 120 bpm (**Figure 5.14**). The participants clicked on a drum icon on the screen to listen to the song rhythm delivered with a MIDI snare drum timbre, constructed using Sibelius 7. The snare drum was used to produce the rhythm of *Happy Birthday* at the prescribed pace instead of a pitched instrument, due to the consideration that the latter might unduly influence the participants' subsequent starting pitch for the song, which could have a negative impact on their singing accuracy if the starting pitch was not suitable for their singing range.

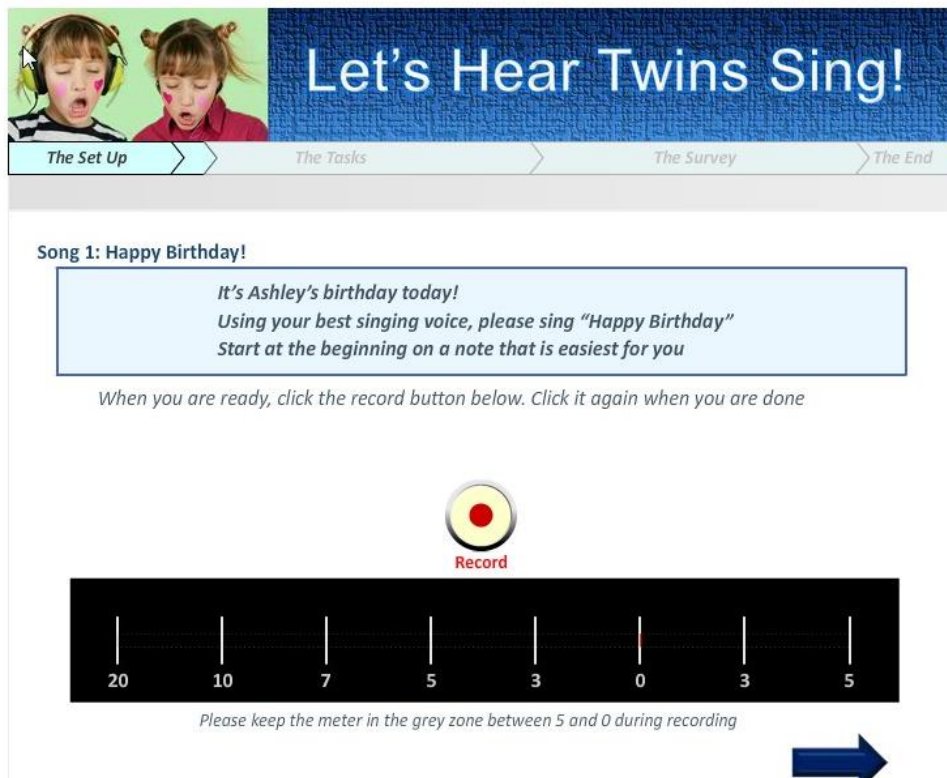


Figure 5.13. Screenshot from Happy Birthday Singing Task (first condition).

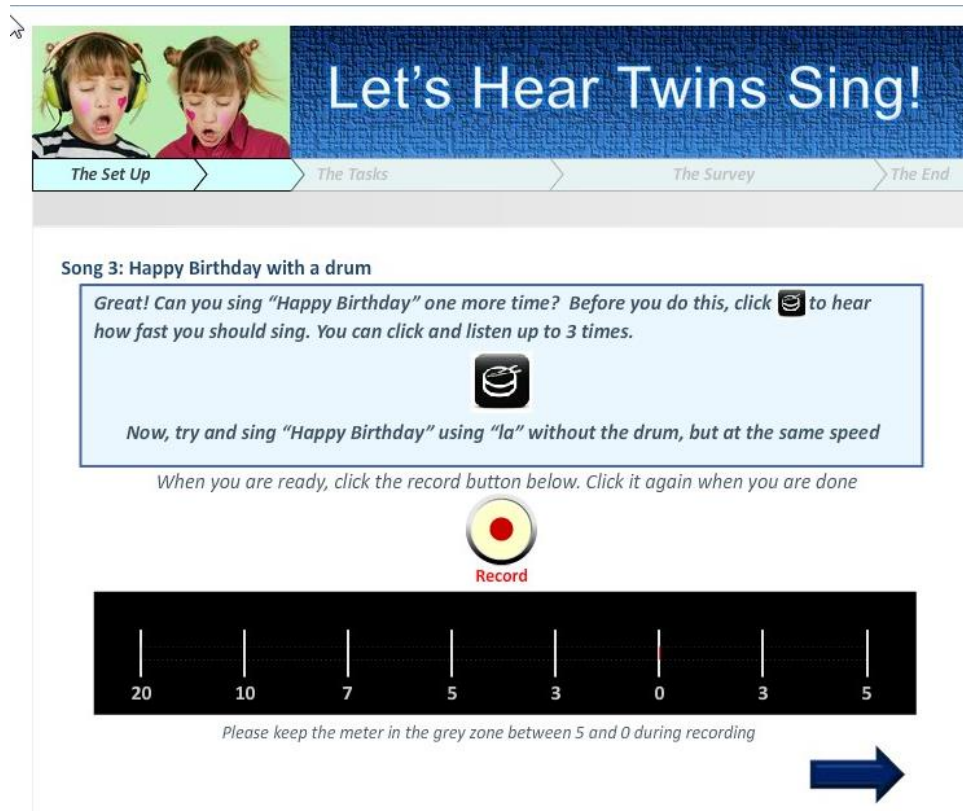


Figure 5.14. Screenshot from Happy Birthday Singing Task (third condition).

After listening once to the rhythm, participants had the option to replay the rhythm for two more times. The participants were then asked to sing the song at the prescribed tempo on their own in two separate trials.

The final condition was expected to elicit the best singing accuracy out of the three conditions due to singing on a neutral syllable at a prescribed tempo. In addition, the first two conditions essentially served as practice runs which gave participants the chance to warm up their voices, familiarise themselves with the general task procedures, and also experiment with the ideal key for them to sing the song comfortably. As such, the two trials sung in the final condition should give the most optimal estimate of a participant's singing proficiency in this task. In view of this, during analysis, only these two trials in the final condition were used to assess the participants' performance of this task, whereby the mean pitch accuracy from the two final trials were averaged. In instances where one of the recordings from the paced condition was not available (e.g., corrupted or was not uploaded onto the server successfully), singing data from the second condition (self-determined tempo on syllable "la") was used as the replacement. In cases where both recordings from the prescribed tempo condition were unavailable, recordings from the first two conditions were used for analysis instead. The rationale for using the average of two trials to determine singing proficiency was to ensure consistency of singing performance can be taken into account. Exceptions were made when only one trial was available from the entire task, whereby the pitch accuracy would only be computed from the single trial.

5.3.2 Music perception tasks

As inaccurate pitch production in singing can occur with or without a deficit in pitch perception (see **Section 4.2.1**, p. 86), two perceptual tasks were included in the study to investigate the fine-grained pitch discrimination ability and melody perception ability of the participants, and to examine the relationship between music perception and singing ability in this sample.

5.3.2.1 Match The Note Task

The two sets of gender-specific pitch stimuli used in Sing The Note Task were used in this task. The set for female participants consisted of sine tone pitches B3 (246.94 Hz), C#4 (277.18 Hz), D#4 (311.13 Hz), F4 (349.23 Hz) and G4 (392 Hz), whereas the set for male participants was an octave lower, comprising the pitches B2 (123.47 Hz), C#3 (138.59 Hz), D#3 (155.56 Hz), F3 (174.61 Hz) and G3 (196 Hz). The rationale for selecting the exact same stimuli as Sing The Note Task was to make the two pitch-matching tasks analogous and facilitate the comparison between perceptual and vocal pitch-matching abilities when timbre and pitch range were held constant.

The method for assessing fine-grained pitch discrimination ability in this task was adapted from the perceptual pitch-matching task of Hutchins and Peretz (2012). In particular, participants were asked to listen to a sine tone by clicking on a musical note icon, and then asked to locate a match for the tone by moving a knob along a pitch slider displayed on the screen with the computer mouse. The slider spanned an octave and along its length contained a continuous spectrum of sine tones (A2 to A3 for males; A3 to A4 for females) that played in real-time when the participant moved the knob along the slider. Each of the five sine tones was presented three times in a randomised order, resulting in a total of 15 trials. In each trial, the participants could listen to the tone and move the knob along the slider as many times as they required, although it was not possible to do both simultaneously (**Figure 5.15**). Once the participants were satisfied that they had located a match for the tone on the pitch slider, they clicked the “Found a match!” button to proceed to the next trial.

5.3.2.2 Happy Birthday Melody Perception Task

In order to ascertain that the participants had a robust internal representation of *Happy Birthday* in their long term memory, participants were asked to listen to three renditions of *Happy Birthday* and identify the correct version from two other modified versions that had one note altered, as shown in **Figure 5.16** and **Figure 5.17**. The three versions were constructed with a MIDI piano timbre in Sibelius 7 and each version was in a different key. Success in this task helped eliminate the possibility that any pitch inaccuracy in Happy Birthday Singing Task was due to low familiarity with the song.

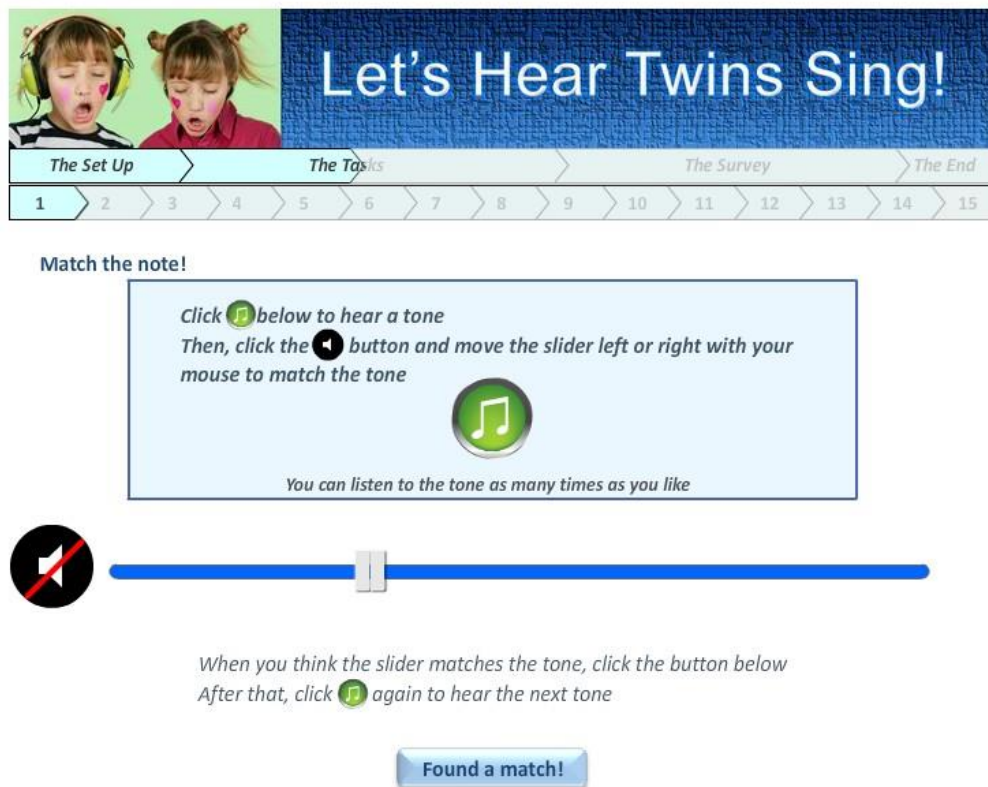


Figure 5.15. Screenshot from Match The Note Task.



Figure 5.16. *Happy Birthday* in C major, with one note altered.



Figure 5.17. *Happy Birthday* in A major, with one note altered.

5.3.3 “Twist your tongue!” Tongue Twister Task

The relationship between music and language processing in the brain has long been contended. Thus far, the evidence related to shared pitch processing mechanisms in music and language has been mixed (Patel, Wong, Foxton, Lochy, & Peretz, 2008; Peretz, 2009). While many previous studies focused on the relationship between speech

and music perception, the current study hoped to explore possible relationships between the pitch production aspects of participants' singing and speech by comparing the task performances of the participants on the singing tasks with their median fundamental frequency and pitch range for a tongue-twister task.

In this task, the one-phrase tongue-twister “She sells sea shells by the sea shore” was presented to the participants on-screen and they were asked to recite the tongue-twister four times consecutively at a self-determined tempo (**Figure 5.18**).

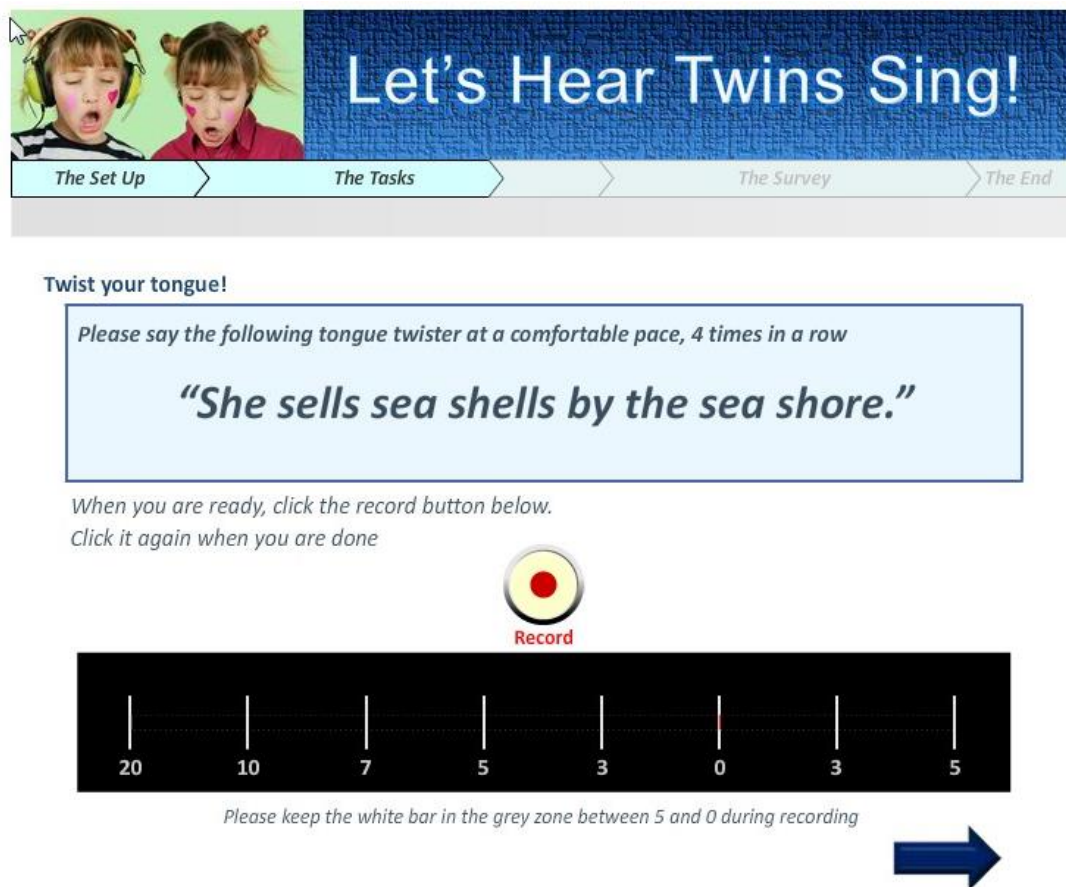


Figure 5.18. Screenshot from the tongue-twister task.

In a similar manner to the final condition of Happy Birthday Singing Task, the second part of this task asked the participants to listen to the rhythm of the tongue-twister delivered at a prescribed tempo (150 beats per minute with a MIDI snare drum timbre, constructed using Sibelius 7) before reciting the tongue-twister four times consecutively at that tempo over two attempts. As per Happy Birthday Singing Task, the two trials in

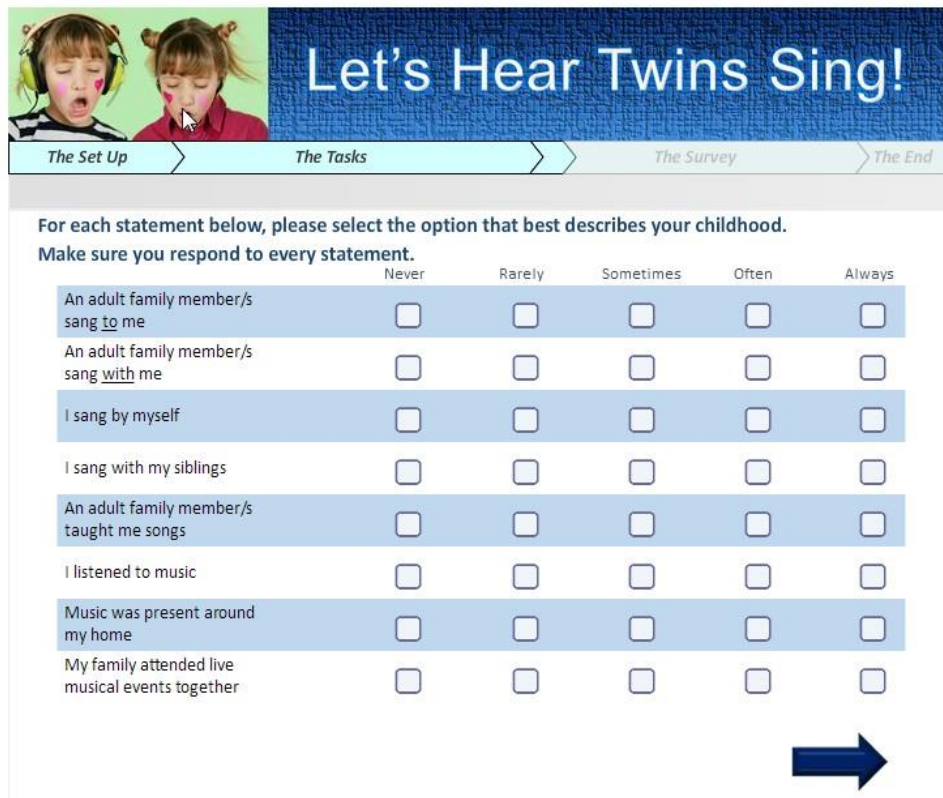
the prescribed tempo condition were intended to be used to assess performance in this task (but see **Section 7.1.2**, p. 195).

The syllabic length of the chosen tongue-twister and its four repetitions ensured that this task matched the length and structure of Happy Birthday Singing Task as closely as possible.

5.3.4 Questionnaire

Besides the singing and music tasks, the online program included a comprehensive questionnaire to identify possible factors that might influence a participant's performance of the singing and music tasks. Taking into account the strong influence that family musical environment exerts on singing and music ability during childhood, the first part of the questionnaire asked the participants about their level of engagement in singing and musical activities at home during their childhood, indicating the frequency of these activities on a 5-point Likert scale (**Figure 5.19**). As current level of singing engagement might also have an impact on singing ability, the participants were then asked to indicate their current frequency of singing across a range of settings (e.g., by themselves, with family and friends, in a group) on a 5-point Likert scale (**Figure 5.20**).

In order to make a comparison between self-perception of singing and music abilities with objective assessments from the singing and music tasks, participants were asked to assess their singing and music abilities on a 7-point Likert scale, as well as their level of interest in music and singing. Moreover, each twin was asked to estimate the level of interest and ability of their co-twin and their parents in singing and music (**Figure 5.21**).



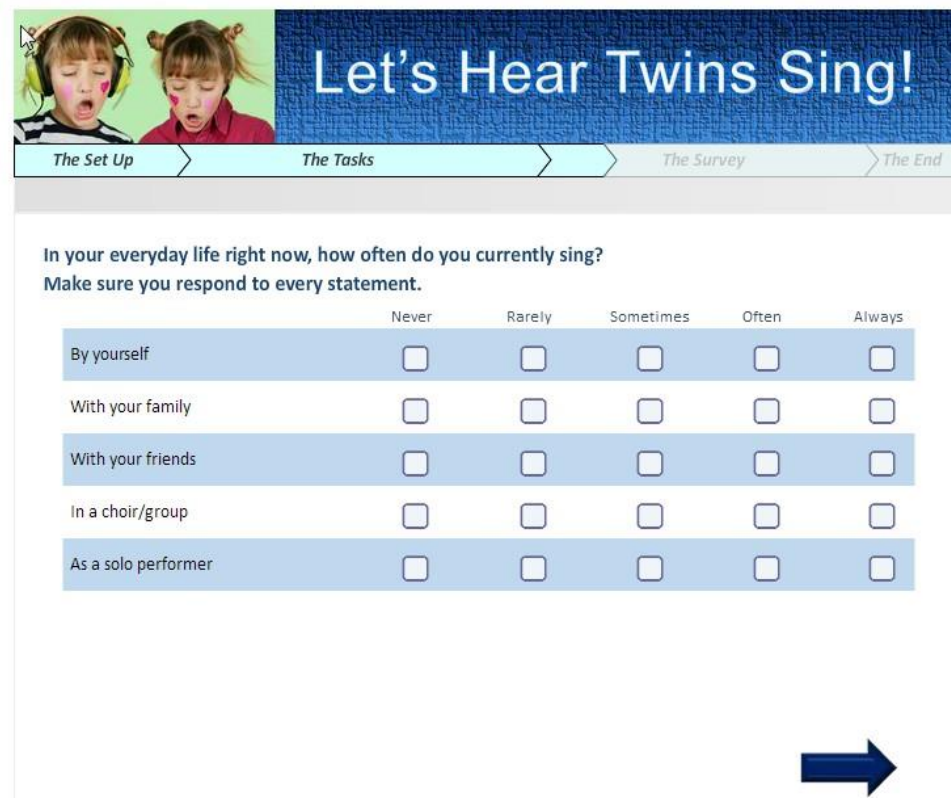
Let's Hear Twins Sing!

The Set Up *The Tasks* *The Survey* *The End*

For each statement below, please select the option that best describes your childhood.
Make sure you respond to every statement.

	Never	Rarely	Sometimes	Often	Always
An adult family member/s sang <u>to</u> me	☐	☐	☐	☐	☐
An adult family member/s sang <u>with</u> me	☐	☐	☐	☐	☐
I sang by myself	☐	☐	☐	☐	☐
I sang with my siblings	☐	☐	☐	☐	☐
An adult family member/s taught me songs	☐	☐	☐	☐	☐
I listened to music	☐	☐	☐	☐	☐
Music was present around my home	☐	☐	☐	☐	☐
My family attended live musical events together	☐	☐	☐	☐	☐

Figure 5.19. Questions about childhood engagement in singing and musical activities.



Let's Hear Twins Sing!

The Set Up *The Tasks* *The Survey* *The End*

In your everyday life right now, how often do you currently sing?
Make sure you respond to every statement.

	Never	Rarely	Sometimes	Often	Always
By yourself	☐	☐	☐	☐	☐
With your family	☐	☐	☐	☐	☐
With your friends	☐	☐	☐	☐	☐
In a choir/group	☐	☐	☐	☐	☐
As a solo performer	☐	☐	☐	☐	☐

Figure 5.20. Questions about the frequency of singing across a range of settings.



Let's Hear Twins Sing!

The Set Up

The Tasks

The Survey

The End

How much musical ability do you have? Click on the number to estimate this for:

	Not interested							Highly interested
Yourself	1	2	3	4	5	6	7	
Tour Twin	1	2	3	4	5	6	7	
Tour Mum	1	2	3	4	5	6	7	☐ Don't Know
Tour Dad	1	2	3	4	5	6	7	☐ Don't Know

Figure 5.21. Assessment of music ability of self, twin and parents on a 7-point Likert type scale.

To examine whether having AP ability has a positive effect on the performance of the singing tasks, participants were asked to report whether they possess AP. Taking into account the possibility that some participants might not fully understand what AP ability entails, a simple definition of AP ability as well as its colloquial term (i.e., perfect pitch) were provided. Furthermore, as several genetic studies have demonstrated the genetic basis and familial nature of AP ability, participants were asked about the presence of AP in family members.

Finally, to investigate the effect of any formal music training on singing and music ability, participants were asked about the type and duration of any formal music training undertaken, self-assessed level of instrumental ability, peak and current music practice intensity, as well as time since last regular practice. In addition, given that self-motivation plays a key role in successful instrumental learning, participants were asked to assess their level of motivation when learning the instrument on a 7-point Likert scale.

At the conclusion of the study, participants were encouraged to remind their co-twins to participate in the study. Those who were keen to participate in future follow-up studies

were also asked to leave their email addresses. The online program then provided feedback to the participants on their performance in the perceptual pitch-matching task (Match The Note Task), before concluding with a Thank You page. All sound recordings and questionnaire data from the participants were stored on a highly secure, password-protected FTP server.

5.4 Piloting of Program

After the programmer finished building the program in early April 2013, and prior to the commencement of recruitment in early May 2013, the program was piloted for four weeks, by the researcher, the researcher's supervisors, the ATR personnel, as well as the colleagues and personal contacts of the researcher ($N = 13$). The pilot testers assessed the program's capability to be run on their own computers and navigated through the program, noting the presence of any program bugs and providing suggestions for improvement. Several pilot testers ($N = 3$) were initially unable to load the program successfully on their computer, the loading issues were reported to the programmer, who rectified the problem and the pilot testers did not report further technical issues. All the tasks and sound stimuli were also tested to ensure they could be loaded successfully. Task instructions were checked to correct any spelling errors and to improve clarity of expression. The data of the pilot testers that were saved on the FTP server were also examined to ensure they were intact and could be accessed and opened to process the data.

The timeline of the entire program development phase is outlined in **Table 5.3**.

Table 5.3. Timeline of Methodological and Program Development

Year	Month	Description
2012	May to September	Commenced the methodological development process: Researched possible tasks to use in the study Researched possible items to include in the questionnaire Considered possible methodological and technical issues that need to be addressed in an online study setting Formulated the tasks and questionnaire items Revised the methodology and tasks based on feedback from supervisors and advisor (Professor Isabelle Peretz)
	September	Commenced working on the program design and layout Revised the program design and layout based on feedback from supervisors and advisor Made initial contact with the Australian Twin Registry (ATR) to discuss the feasibility of recruiting twin participants from the registry
	November to January	Developed detailed storyboard for the design and layout of the online program using Microsoft Powerpoint Revised the storyboard based on feedback from supervisors and advisor Discussed the technical aspects of program development with the programmer (i.e., how to implement the program design, layout and functionality) Developed study information sheet and recruitment email for the study Submitted formal application to the ATR (December) to recruit participants from the registry Submitted application to the Human Research Ethics Sub-Committee (HESC) of Behavioural and Social Sciences at the University of Melbourne
2013	February to April	Final revisions of the program design and layout as well as wording of study instructions prior to coding Constructed the task stimuli using Audacity and Sibelius 7 Programmer commenced coding the online program Received application approval from the ATR and ethics approval from the HESC
	April to May	Programmer completed coding the online program. Commenced piloting and debugging of online program ($N = 13$) Made final revisions to the wording of task description and graphics of the program
	May	Commenced recruitment

5.5 Troubleshooting of Program

Despite the numerous pre-emptive measures undertaken to counteract some of the common issues encountered in an online research setting (as detailed in **Section 5.2**, p. 111), some user-end technical problems still arose during the recruitment phase. The most prevalent issues included a program loading problem, a microphone detection problem, and program freezes and saving problem. In view of these problems, after approximately two months of recruitment (May to July 2013), the ATR advised recruitment to be put on hold until the technical issues were addressed satisfactorily. The recruitment eventually recommenced in late November 2013 after four months of intensive troubleshooting.

Table 5.4 detailed the timeline of the program troubleshooting and the action undertaken to address the problems.

As described in **Sections 5.2.2.1** and **5.2.2.2** (pp. 122-125), the program loading and microphone detection problems were addressed by providing troubleshooting instructions to guide the participants to solve the problems themselves, and also providing the contact details of the researcher to offer direct technical assistance if needed. It is likely that some potential participants were unable to meet the hardware and software requirements and therefore were prevented from taking part, despite their interest in the study. To help such participants to take part, those residing in Melbourne were given the option in their recruitment email to complete the online study at the University of Melbourne, using technical equipment supplied by the researchers.

The problem with program freezes was harder to rectify, as both the researcher and the program developer could not replicate such problems when testing the online program themselves across multiple computers and browsers. It was possible that the program freezes occurred as a result of sudden dropout of the internet connection, thereby disrupting the online data saving process, or due to participants using less-than-ideal technical equipment to access the program. Some participants were therefore unable to complete the entire study due to these technical issues, resulting in incomplete data.

Table 5.4. Timeline of Program Troubleshooting

Month/Yr	Description of problem	Action taken
May to July 2013	Missing data from a sizeable number of initial participants (10 out of 35): mostly questionnaire data. Possible problem with the final saving process Program could not load at the beginning (blank screen)	Created another website specifically for participants to redo the questionnaire
		Modified recruitment email and study information to make it clearer that the program would not run on mobile devices
		Implemented additional functionality at the beginning of the program to check if the internet browser and Adobe Flash plugin were up-to-date and advising participants to download the latest versions
		Created a link at the beginning of the program with troubleshooting instructions to enable participants to identify and rectify possible causes for the problem
		Ran program on various internet browsers and operating systems (OS) to determine whether the problem was browser or OS-specific.
	Microphone not detected by the program	Created a link at the soundcheck page with troubleshooting instructions to enable participants to identify and rectify possible causes for the problem
	Some of the fonts were not displaying properly on Apple Macintosh OS	Rectified the font problem on Macintosh OS
	Program froze in the middle of a task or during data saving. As the participant data was only saved at two points of the program, making it especially vulnerable to missing data when internet dropped out.	Identified possible issue with intermittent internet connection. Modified the program such that participants' data were saved after every screen to minimise missing data
Aug to Nov 2013	Intermittent internet connections still causing program freezes and data saving problem	Modified the program to show internet connection error message when it occurred and lead the participant back to redo the previous trial which failed to save. Program would attempt data saving for 5 times before proceeding with the next trial
	The duration of the data saving process after each screen was too long	Modified the program to speed up the saving process by saving the recording data asynchronously and simultaneously
Nov 2013 to 2014	Some participants still encountered program freezes in the middle of the program (right before Sing The Tune Task)	Unable to further identify or rectify problem with the program. A pared down version of the program (from Sing The Tune onwards) was created to enable the participants to complete the study

Since the participants were identifiable from their ATR ID and also demographic details, the ATR were able to contact them on the research team's behalf to give them the opportunity to complete the study if they had previously encountered technical difficulties. Depending on the point in the program they encountered the program freeze, the participants could choose to redo the study from the beginning, commence from the final singing task, or just complete the questionnaire, using specific web-links supplied by the present author.

In addition, to minimise the effect of incomplete data due to technical issues, perpetual saving of participant's data throughout the program was implemented to maximise data collection. To speed up the data saving process after each screen, the programmer also modified the program such that each audio file was saved in asynchronous chunks simultaneously.

Although much effort was made to address these technical difficulties, potential participants might still have been deterred from attempting or completing the study. The lack of control over the technical equipment used by participants, however, was a necessary trade-off in order to allow twins the chance to participate in the study regardless of their geographical location. As the current study was the first study in the field to involve large scale online recording and collection of singing data across locations, in retrospect, the pilot testing conducted prior to recruitment might not have been sufficiently extensive to anticipate the technical issues that arose during the recruitment phase. As a result, many of the technical issues were only identified and addressed after recruitment had commenced. While such arrangement was not ideal and might have detrimentally affected the study response rate, the experience of troubleshooting the technical issues was nonetheless valuable and served as helpful pointers for future researchers to consider when they design similar online studies.

6

METHODS

This chapter comprises six main sections describing the participants recruited, the materials used, the study procedure, data processing procedure, study measures and proposed statistical analyses.

6.1 Participants

Altogether, 293 individuals participated in the study, 245 of which were registered with the ATR, which was the study's main source of recruitment. Among all the participants, there were 111 pairs of twins who completed the study: 73 pairs of MZ twins (58 female pairs; 15 male pairs) and 38 pairs of DZ twins (24 female pairs, 7 male pairs and 7 opposite-sex pairs). When the singing data were processed (see **Section 6.2.2**, p. 156), two pairs of non-ATR MZ female twins were aurally assessed to have done the study in a half-hearted manner while all the recorded data from an ATR MZ female twin (ATR ID: 57336-1) were corrupted. As such, data from these three pairs of twins were deemed unusable and were excluded from the subsequent analysis.

The final sample included for data analysis therefore consisted of 108 complete twin pairs: 55 MZ female (MZF), 15 MZ male (MZM), 24 DZ female (DZF), 7 DZ male (DZM) and 7 DZ opposite-sex (DZO) pairs. The basic demographic characteristics of the final sample are summarised in **Table 6.1**. The participants were aged between 15 and 80 ($M = 32.36$, $SD = 12.15$), and 76.4% of the participants were female. Most of the participants from the study were highly educated: More than 70% reporting an education level of at least Tertiary Year 3, and approximately 20% reporting an education level of Tertiary Year 6 and above.

Table 6.1. Demographic Characteristics of the Final Sample

	Males	Females	All
<i>N</i>	51 (23.6%)	165 (76.4%)	216
Monozygotic twins	30	110	140 (70 pairs)
Dizygotic twins	21	55	76 (38 pairs)
Mean age (SD)	35.10 (13.89)	31.51 (11.47)	32.36 (12.15)
Age range	18-66	15-80	15-80
Education			
Secondary	5 (9.8%)	38 (23.5%)	43 (20.2%)
Year 9	-	6 (3.7%)	6 (2.8%)
Year 10	1 (2.0%)	7 (4.3%)	8 (3.8%)
Year 11	2 (3.9%)	12 (7.4%)	14 (6.6%)
Year 12	2 (3.9%)	13 (8.0%)	15 (7.0%)
Tertiary undergraduate	25 (49.0%)	67 (41.4%)	92 (43.2%)
Year 1	2 (3.9%)	5 (3.1%)	7 (3.3%)
Year 2	2 (3.9%)	7 (4.3%)	9 (4.2%)
Year 3	10 (19.6%)	28 (17.3%)	38 (17.8%)
Year 4	11 (21.6%)	27 (16.7%)	38 (17.8%)
Tertiary graduate	21 (41.2%)	57 (35.2%)	78 (36.6%)
Year 5	7 (13.7%)	28 (17.3%)	35 (16.4%)
≥ Year 6	14 (27.5%)	29 (17.9%)	43 (20.2%)
Missing	-	3	3

The following subsection reports the methods of recruitment employed in the study.

6.1.1 Recruitment

Recruitment officially commenced on 9 May 2013 and concluded on 5 April 2015.

While the ATR was the main source of recruitment, due to lower-than-expected response rate (possible reasons discussed in **Section 6.1.1.1**, p. 148), participants were also recruited through other avenues (**Section 6.1.1.2**, p. 149).

6.1.1.1 Recruitment via the Australian Twin Registry (ATR)

The ATR is a non-profit national twin registry established in 1981, whose goal is to facilitate and support medical and scientific studies involving twins. One of the largest volunteer twin registries in the world, the ATR has enrolled over 33,000 pairs of Australian twins since its formation. The investigators of the current study therefore engaged the ATR's services to invite ATR-registered twins to participate in the study.

Participant recruitment officially commenced following a media launch organised by the ATR at the Melbourne Conservatorium of Music (9 May 2013), which helped to publicise the twin study through the media and encouraged twins across Australia to participate in the study.

Following the media launch, on behalf of the investigators of the study, the ATR sent invitation emails and study information sheets to a subset of twins on the registry (see **Appendix A-1**, p. 295 and **Appendix A-4**, p. 299). The invitation email specified that monozygotic (MZ) and dizygotic (DZ) twin pairs aged 15 and above, with no diagnosed hearing deficits or vocal cord lesions (e.g., nodules, polyps and cysts), no current mental illness (excluding anxiety and/or depression), and no history of brain injury, stroke, genetic or neurological disorders could participate in the study. In addition, the ATR sent the invitation email and study information to individuals who expressed interest about the study after learning about it from the media.

In total, 1,692 pairs of ATR twins were approached in nine rounds of mail-outs. The total number of participants recruited from the ATR was $n = 245$, including 89 complete twin pairs and 67 single twins whose co-twins did not participate. The recruitment summary of each zygosity group from the ATR is detailed in **Table 6.2**.

Table 6.2. Recruitment Summary of Twins Approached by the Australian Twin Registry (ATR)

Zygosity Group	No. of pairs approached	No. of complete pairs participated	No. of single twins participated	No. of pairs who explicitly declined participation	No. of pairs who did not respond
MZF	447	49 (11.0%)	19 (2.1%)	20 (4.5%)	359 (80.3%)
MZM	256	10 (3.9%)	7 (1.4%)	12 (4.7%)	227 (88.7%)
DZF	655	19 (2.9%)	34 (2.6%)	22 (3.4%)	580 (88.5%)
DZM	234	6 (2.6%)	5 (1.1%)	21 (9.0%)	202 (86.3%)
DZO	100	5 (5%)	2 (1.0%)	9 (9%)	84 (84%)
Total	1692	89 (5.3%)	67 (2.0%)	84 (5.0%)	1452 (85.8%)

Note. MZ: Monozygotic (identical); DZ: dizygotic (non-identical); F: female; M: male; O: opposite-sex. Percentages are in brackets.

The participant recruitment rate was 7.3% (i.e., sum of percentage of complete pairs who participated and percentage of single twins who participated), which was

substantially lower than what would normally be expected of an online survey (approximately 20% to 40%, see Nulty, 2008) . Factors that may have accounted for the low response rate are discussed below.

a) Duration of online study

Although the balance between study duration and comprehensiveness of assessment was already carefully weighed during the program development phase (see **Section 5.2.1.2**, p. 117), its relatively long duration (~30 minutes) might have still deterred some from participating. The quality assurance calls conducted by the ATR to some of the non-participating twins confirmed that while some twins were interested in participating, they tended to put off doing the online study until they could find a more ideal time and setting to complete the study in one sitting. Despite the two rounds of reminder emails that were sent out subsequent to the invitation email, it was possible that many twins eventually just forgot to complete the online study.

b) The nature of the study

The online study's focus on assessing singing ability using actual singing tasks might have deterred some twins. Although the participants could do the singing tasks in the privacy and comfort of their own home, some twins still might have felt daunted by the nature of the singing tasks. The considerably lower participation rates (and higher percentages of participant expressly declining to participate) of the ATR male twins might also reflect a commonly held stereotype by many males from the Western population that singing is a feminine activity (Adler & Harrison, 2004; Ashley, 2009; Gates, 1989; Green, 1997).

c) Requirement of multimedia software and hardware

The hardware and software requirements of the study (see **Section 5.2.2**, p. 122) might have prevented some twins from participating, despite being interested. This was supported by a number of twins who contacted the ATR or the researcher requiring technical assistance to run the online study. As detailed in **Sections 5.4 and 5.5** (pp. 140-145), while the online program was piloted to ensure that it could run smoothly on most operating systems and up-to-date internet browsers, it was not possible to guarantee the successful running of the program in all possible scenarios due to the variability of the equipment owned by the participants. The lack of adequate or up-to-

date technical equipment thus might have discouraged potential participants from taking part.

6.1.1.2 Other recruitment approaches

Due to the lower-than-expected response rate from the ATR twins, four recruitment approaches were added to enhance the response rate to the study.

a) iPad Mini Lucky Draw

At the recommendation of the project coordinators at the ATR, an iPad Mini lucky draw was introduced as an incentive for both members of a twin pair to participate. In particular, when both twins completed the online study (ATR or non-ATR recruited), the twin pair was entered into the lucky draw to win two iPad mini 2 (16gb with Wi-Fi) with retina display, one for each twin.

The lucky draw was conducted on 13 April 2015 at 3pm at the Melbourne Conservatorium of Music, using a computer randomised process in Microsoft Excel. The winning pair of twins were a pair of ATR-recruited female MZ twins (ATR ID: 55759), who were notified of the outcome by the ATR. Orders for two iPad Minis were placed via the online Apple Store and delivered to their home address on 15 April 2015.

b) Campus-wide recruitment and the option of doing the assessment on-campus

Recruitment was extended to University of Melbourne staff and students as well as the broader community. Online advertisements about the study were posted through the community events listing of websites, such as the Australian Broadcasting Corporation's Big Diary. The researcher was also invited to talk about the study and invite listeners to participate during a radio interview on 3RRR, as part of the show "Hullabaloo". Online advertisements were also posted on the University of Melbourne's Online Notices system of the student portal and the Graduate Student Association E-Newsletter. In addition, recruitment posters were put up around the Parkville and Southbank campuses of the University (**Appendix A-2**, p. 296). Affiliated residential colleges were also contacted and consent was given to disseminate information about the study to the college residents via email through the college

administration. In total, seven complete twin pairs were recruited from the University of Melbourne.

To assist participants who might have been prevented from doing the study due to inadequate technical equipment, those in Melbourne (including twins approached by the ATR) were provided with the option to do the online study at the University of Melbourne Parkville campus. In total, two Melbourne participants opted to do the study on campus.

c) Personal contacts

The researcher utilised social media to disseminate the study information to personal contacts and their friends who might be interested in participating. In total, 15 complete twin pairs were recruited through this method.

d) Participation at the Twins Plus Festival

The researcher was invited by the ATR to set up a booth to promote the study at the Twins Plus Festival held on 22 March 2015. The Twins Plus Festival is a triennial event organised by the ATR and the biggest twins festival in the southern hemisphere. More than 2000 families with twins attended the Festival, thereby providing access to a large pool of potential recruits. In order to increase the attractiveness of the study among other research studies that had booths during the Festival, an exclusive promotion was conducted in conjunction with the Festival. WISH eGift cards valued at \$40 were given to the first 40 pairs of twins who completed the online study during the promotional period (10AM AEST Sunday 22 March 2015 to 11:59PM AEST Sunday 5 April 2015). This promotion was also extended to interested participants at the University of Melbourne and publicised via the University of Melbourne's Online Notices system of the student portal and the Graduate Student Association E-Newsletter. During the Festival, interested participants were given the option to complete the study onsite in a quiet, secluded area on the Festival premises using laptops provided by the researcher. One pair of twins completed the assessment this way and 32 individuals left expressions of interest with the researchers at the Festival, and they were subsequently contacted by the ATR and provided with the study information. Altogether, nine pairs of twins completed the online assessment during the promotional period and received the \$40 WISH eGift cards as reimbursement.

6.1.2 Demographics

6.1.2.1 Zygosity information

The breakdown of the final sample of twin pairs from ATR and non-ATR sources according to zygosity type is outlined in **Table 6.3**. The two largest zygosity groups in the final sample were monozygotic female (MZF) and dizygotic female (DZF) twins, who made up 50.9% and 22.2% of the sample, respectively. The third largest group was the monozygotic male twin pairs (13.9%), while the dizygotic males and dizygotic opposite sex twin pairs each constituted 6.5% of the final sample.

Table 6.3. Breakdown of Final Sample According to Zygosity Type

Zygosity	ATR twin pairs	Non-ATR twin pairs		Total
		From University of Melbourne	Personal contacts	
MZF	46 (83.6%)	4 (7.3%)	5 (9.1%)	55 (50.9%)
MZM	10 (66.7%)	-	5 (33.3%)	15 (13.9%)
DZF	19 (79.2%)	2 (8.3%)	3 (12.5%)	24 (22.2%)
DZM	6 (85.7%)	-	1 (14.3%)	7 (6.5%)
DZO	5 (71.4%)	1 (14.3%)	1 (14.3%)	7 (6.5%)
Total	86 (79.6%)	7 (6.5%)	15 (13.9%)	108

Note. MZ: Monozygotic (identical); DZ: dizygotic (non-identical); F: female; M: male; O: opposite-sex. Percentages are in brackets.

For the twins recruited from the ATR, zygosity information was obtained from the ATR database. The zygosity of 26.1% of all ATR-registered twin participants was determined by genotyping, 28.4% by zygosity-determination questions in a twin lifestyle questionnaire, 3.4% by doctor's report, 5.7% were opposite-sex pairs (and were therefore DZ twins), 19.3% by parents' report, 5.7% by self-report and for the remaining 11.4%, the means of determining zygosity was unknown.

As for the non-ATR recruited participants, where possible, zygosity information of the participants was obtained using a questionnaire prepared by the researcher in collaboration with the ATR (see **Appendix A-3**, p. 297). Information about the zygosity determination of the final sample is outlined in **Table 6.4**.

Table 6.4. Breakdown of Zygosity Determination of the Final Sample

Zygosity determination method	ATR twins	Non-ATR twins	Total
DNA genotyping	46 (26.1%)	0	46 (21.3%)
Zygosity questionnaire	50 (28.4%)	0	50 (23.1%)
DZO twins	10 (5.7%)	4 (10.0%)	14 (6.5%)
Doctor report	6 (3.4%)	4 (10.0%)	10 (4.6%)
Parent report	34 (19.3%)	10 (25.0%)	44 (20.4%)
Self-report	10 (5.7%)	22 (55.0%)	32 (14.8%)
Unknown	20 (11.4%)	0	20 (9.3%)
Total	176	40	216

While the zygosity of only 21.3% of our final sample was determined through DNA genotyping, it is worth noting that numerous studies have affirmed that questionnaire-based zygosity determination, which typically comprises questions about physical resemblance and confusion by others (Cederlöf, Friberg, Jonsson, & Kaij, 1961; Pedersen & Lichtenstein, 2000), has a high level of validity upon ascertainment by genotyping, with reported accuracy of 91% to 98% (Bonnelykke, Hauge, Holm, Kristoffersen, & Gurtler, 1989; Charlemaïne et al., 1997; Chen et al., 1999; Christiansen et al., 2003; Jackson, Snieder, Davis, & Treiber, 2001; Ooki, Yamada, Asaka, & Hayakawa, 1990; Peeters, Van Gestel, Vlietinck, Derom, & Derom, 1998; Song et al., 2010; Spitz et al., 1996; Torgersen, 1979).

6.1.2.2 Language and music background profile

The language and music background profile of the final sample are shown in **Table 6.5**.

The vast majority (96.7%) of the participants reported a non-tonal language as their first language, with 91.5% of the participants listing English as their first language. Approximately 28% of the participants also spoke a second language. Among these participants, 32.2% reported speaking a tonal second language (Chinese or a Chinese dialect e.g., Hokkien or Cantonese), whereas English, French and Italian were the three most common non-tonal second languages reported.

Table 6.5. Language and Music Background Profile of the Final Sample

	Males	Females	All
<i>N</i>	51 (23.6%)	165 (76.4%)	216
First language			
Non-tonal	46 (90.2%)	160 (98.8%)	206 (96.7%)
English	44 (86.3%)	151 (93.2%)	195 (91.5%)
Spanish	-	4 (2.5%)	4 (1.9%)
Dutch	-	4 (2.5%)	4 (1.9%)
German	-	1 (0.6%)	1 (0.5%)
Afrikaans	2 (3.9%)	-	2 (0.9%)
Tonal	5 (9.8%)	2 (1.2%)	7 (3.3%)
Chinese	4 (7.8%)	2 (1.2%)	6 (2.8%)
Teochew	1 (2%)	-	1 (0.5%)
Missing	-	3	3
Second language	18 (35.3%)	41 (25.3%)	59 (27.7%)
Non-tonal	13 (72.2%)	27 (65.9%)	40 (67.8%)
English	6 (33.3%)	10 (24.4%)	16 (27.1%)
French	3 (16.7%)	6 (14.6%)	9 (15.3%)
Italian	1 (5.6%)	5 (12.2%)	6 (10.2%)
Swahili	-	2 (4.9%)	2 (3.4%)
Dutch	-	1 (2.4%)	1 (1.7%)
Greek	-	1 (2.4%)	1 (1.7%)
German	1 (5.6%)	1 (2.4%)	2 (3.4%)
Tamil	1 (5.6%)	1 (2.4%)	2 (3.4%)
Japanese	1 (5.6%)	-	1 (1.7%)
Tonal	5 (27.8%)	14 (34.1%)	19 (32.2%)
Cantonese	-	4 (9.8%)	4 (6.8%)
Hokkien	1 (5.6%)	-	1 (1.7%)
Chinese	4 (22.2%)	10 (24.4%)	14 (23.7%)
Absolute pitch possessor	1 (2%)	7 (4.5%)	8 (3.9%)
Missing	1	8	9
Received music training	42 (85.7%)	135 (86%)	177 (85.9%)
Missing	2	8	10
Years of music training			
≤ 5	28 (70%)	76 (58.4%)	104 (61.2%)
6-10 years	6 (15%)	40 (30.8%)	46 (27.1%)
11-15 years	5 (12.5%)	13 (10%)	18 (10.6%)
> 16 years	1 (2.5%)	1 (0.8%)	2 (1.2%)
Missing	2	5	7
Mean years of music training (SD)	4.65 (3.78)	4.67 (4.63)	4.66 (3.98)

	Males	Females	All
Main instrument			
String	15 (35.7%)	16 (11.8%)	31 (17.5%)
Guitar	14 (33.3%)	8 (5.9%)	22 (12.4%)
Violin	1 (2.4%)	6 (4.4%)	7 (4.0%)
Viola		2 (1.5%)	2 (1.1%)
Woodwind	2 (4.8%)	29 (21.4%)	31 (17.5%)
Flute	1 (2.4%)	15 (11.1%)	16 (9.0%)
Clarinet		11 (8.1%)	11 (6.2%)
Recorder	1 (2.4%)	3 (2.2%)	4 (2.3%)
Brass	7 (16.6%)	4 (3.0%)	11 (6.2%)
Saxophone	3 (7.1%)	2 (1.5%)	5 (2.8%)
Trumpet	3 (7.1%)	2 (1.5%)	5 (2.8%)
Tuba	1 (2.4%)		1 (0.6%)
Keyboard	14 (33.4%)	54 (40.0%)	68 (38.5%)
Piano	13 (31.0%)	51 (37.8%)	64 (36.2%)
Keyboard	1 (2.4%)	3 (2.2%)	4 (2.3%)
Voice	4 (9.5%)	23 (17.0%)	27 (15.3%)
Others*		9 (6.7%)	9 (5.1%)
Missing	2	8	10

*Include euphonium, harp, oboe, organ, piano accordion and tin whistle

Despite the definition and description provided in the program, some participants, especially those without music training, still might not have comprehended what possessing absolute pitch meant and therefore misjudged themselves or their co-twins as possessing absolute pitch (AP). Hence, as a precaution, only instances where self-reports of AP were confirmed by the co-twin's report were considered for analysis. In other words, if a participant claimed to possess AP and yet his/her co-twin's report did not reflect this, it was determined that this participant did not possess AP.

Based on this criterion, eight participants (3.9%; 7 females and 1 male) reported possessing AP. Out of the self-reported AP possessors, two were non-related DZ participants, and the remaining 6 were 3 pairs of MZ female twins. The prevalence of AP in the current sample (3.9%) is higher than the estimates for the general population in previous studies (1 in 10,000 and 1 in 1,500; see **Section 2.4.1.6**, p. 43), but lower than the values reported for music majors in tertiary institutions (4.7 to 24.6%; Gregersen et al., 1999).

As for information on music background, the majority (85.9%) of the final sample was musically-trained (mean years of training = 4.66, *SD* = 3.98), approximately 61% of which had 5 years or less of music training. Among the musically-trained participants, the most prevalent musical instruments learned were the piano (36.2%), followed by voice (15.3%) and the guitar (12.4%). There was a slight difference in popular instrument choice between male and female participants. While the piano was the predominant musical instrument of choice for females (37.8%), the two most prevalent musical instruments learned by males were the guitar (33.3%) and the piano (31.0%). In instances where participants listed more than one musical instrument, only the first one listed was regarded as their main instrument.

6.2 Data Processing Procedure

Before commencing data processing, the following steps were undertaken to access, download and de-identify the participants' data that were saved on the online server.

6.2.1 De-identification of participants

At the conclusion of the recruitment phase, FileZilla (Version 3.10.1.1), an FTP (File Transfer Protocol) client, was used to access and download the data from the secure online FTP server for subsequent data processing.

To prevent confirmation bias that might arise during the data processing phase from knowledge of the zygosity of the twin pairs, de-identification of the participants was undertaken to ensure the researcher was blind. Specifically, each participant was assigned a Twin ID as well as a Participant ID. First, all 108 complete twin pairs (both ATR and non-ATR) in the final sample were assigned a new Twin ID spanning from 001 to 108. Each twin in a twin pair was assigned the suffix "A" or "B" according to his or her birth order. Second, each participant was assigned a random Participant ID from 1 to 216, using the RAND() function in Microsoft Excel.

The rationale for having two IDs for each participant was as such: Twin IDs were needed so that a unified identification system could be used for both ATR and non-ATR

twin pairs. The random assignment of Participant IDs was also necessary to allow the twin pairs to be sufficiently randomised in order to achieve an ideal blind analysis, where the researcher had no knowledge of a participant's identity nor the identity of his/her co-twin (MacCoun & Perlmutter, 2015).

The participant folders downloaded from the server were thus assembled in a new folder and each was relabelled according to the Participant ID. In the data processing phase, participant data was processed one by one in the order of the randomly assigned Participant IDs. As the main data text file contained the name and other identifying details of a participant, the questionnaire data was processed only after all the acoustical data from every participant had been processed.

6.2.2 Data processing for the singing tasks

A particular challenge in assessing singing tasks objectively is the segmentation of individual pitches in a melody (Demorest & Pfordresher, 2015). Accurate segmentation of pitches is crucial in order to determine the fundamental frequency that is representative of each stable pitch region, so that a participant's pitch accuracy can be reliably assessed. The pitch segmentation process is often done manually, and decisions such as where a pitch ends and where the next pitch begins are subjectively based on visual and auditory inspection. As a result, the procedure is very time-consuming and subject to individual rater bias (Dalla Bella, 2015; Demorest & Pfordresher, 2015).

In this study, a novel, semi-automatic approach was developed to facilitate the processing of singing data from the melodic singing tasks, i.e., Happy Birthday Singing Task and Sing The Tune Task. This method only required a preliminary "coarse" labelling of the pitch segments, and subsequently the onset and offset of the stable portion of each individual pitch were more precisely determined automatically by running an algorithm which utilised the rate of change of the fundamental frequency f_0 (henceforth referred to as f_0 velocity) for fine-grained pitch segmentation.

The entire data processing procedure consisted of four main steps; the first two steps were performed in the Praat environment (version 5.4.01; Boersma & Weenink, 2014),

while the third and fourth steps were carried out in Microsoft Excel 2013. The procedure is described in detail as follows.

6.2.2.1 Coarse demarcation of pitch segments

As the first step, preliminary coarse segmentation of the pitches was achieved by running ProsodyPro version 6.0 beta, a Praat script (Xu, 2013) in the Praat environment. Although ProsodyPro has multiple functionalities aimed at facilitating the batch processing of large amounts of sound data, the current study mainly utilised its batch processing as well as sound segmentation and labelling features. The following is a brief sketch of the five-step workflow for the initial coarse pitch segmentation:

1. Run ProsodyPro script in Praat. When the startup window appears (**Figure 6.1**), select the “Label sentences” radio button and set the folder destination to the appropriate folder which contains the data of a de-identified participant.

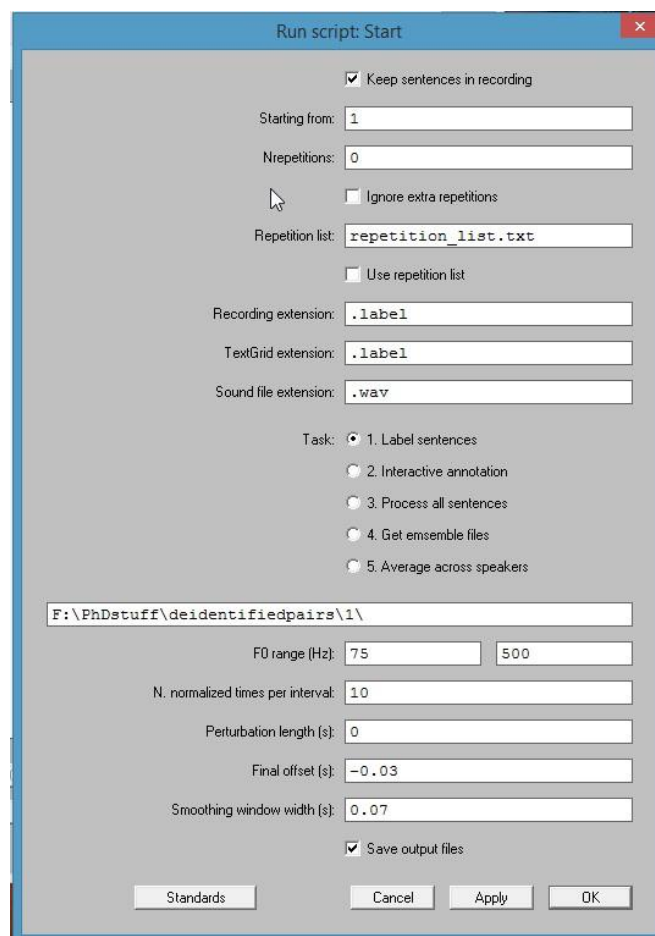


Figure 6.1. Startup window of ProsodyPro (version 6.0 beta).

2. Click OK and three windows are generated as a result. The window of interest is the TextGrid window, which displays the sound waveform, spectrogram and annotation panels (**Figure 6.2**). By clicking along the first annotation tier, starting from the onset of the first note and ending on the offset of the last note, demarcate boundaries for each pitch, using the fundamental frequency (f_0) curve displayed on the spectrogram as a guide. To demarcate two adjacent pitches, click approximately in the middle portion of the transitional region between the pitches, although precision is not essential. Use auditory judgment to also guide the decision of demarcating pitch boundaries.

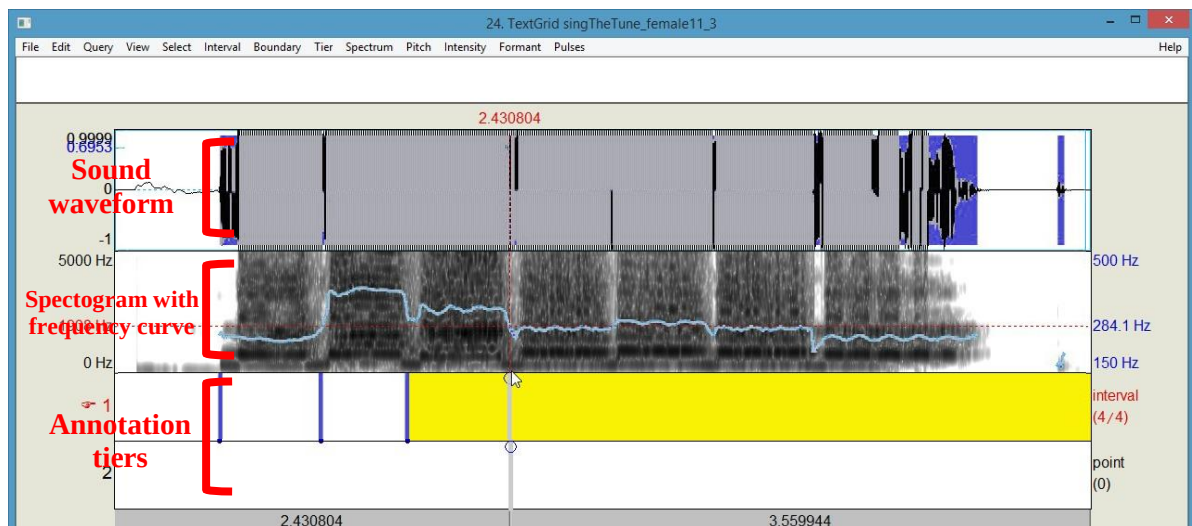


Figure 6.2. TextGrid window in the Praat environment. The sound waveform is displayed in the top panel, followed by the spectrogram with the frequency curve in the middle panel, and the annotation tiers are displayed in the bottom panel.

3. Click on each of the demarcated boundaries to label the pitch segments in order. As illustrated in **Figure 6.3**, if there are 7 pitches in the sound file, label the pitch segments from 1 to 7.

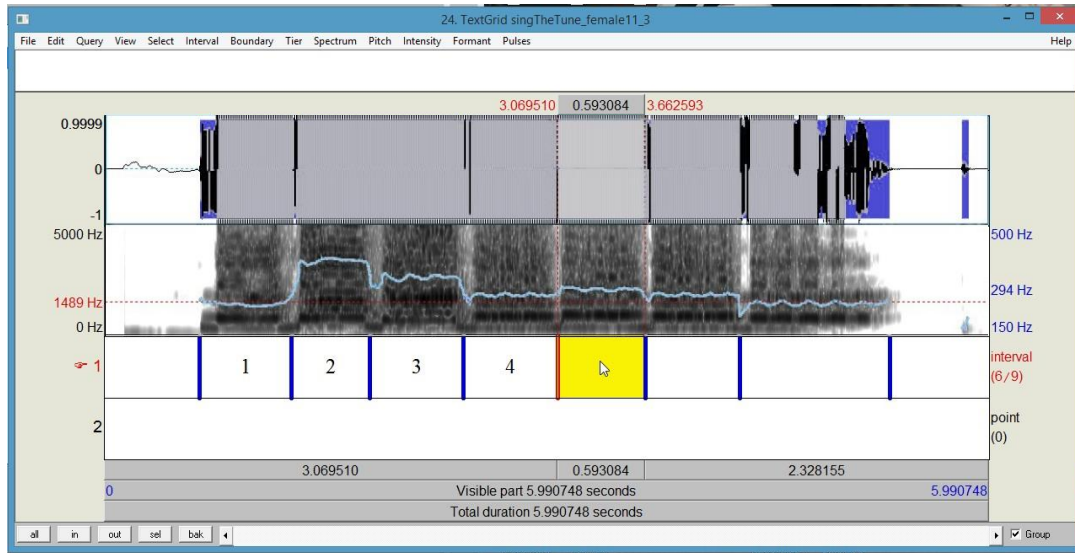


Figure 6.3. Labelling the coarse pitch segments in the first tier of the annotation panel of the TextGrid window.

4. If there are gaps or spaces along the f_0 curve that need to be excluded from the fundamental frequency estimation, label such segments as ‘g’. As for regions within a pitch that need to be excluded due to noise, label such segments as ‘n’. If the sound file contains more than one phrase (such as in the case of Happy Birthday Singing Task), label the segment in between the phrases as ‘p’ and in each new phrase, label the pitch segments anew from 1 (**Figure 6.4**). This labelling facilitated the subsequent export of fundamental frequency data onto the Excel spreadsheet.

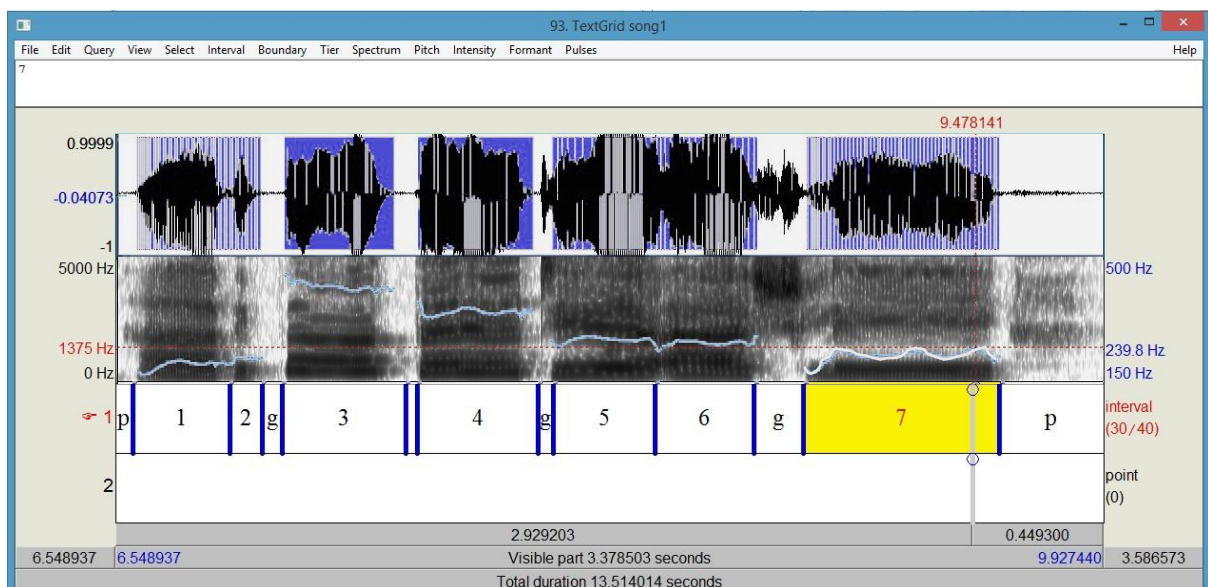


Figure 6.4. Labelling of pitch segments from song files containing more than one phrase.

5. After the labelling of pitch segments in the current sound file is completed, go to the Pause Window (**Figure 6.5**) and click 'Next' to proceed to the next sound file in the participant's folder to label its segments. One can click 'Back' to revisit previously labelled files, or click 'jump' to skip to other files according to their file order in the folder. Click 'Done' when all the sound files have been labelled.

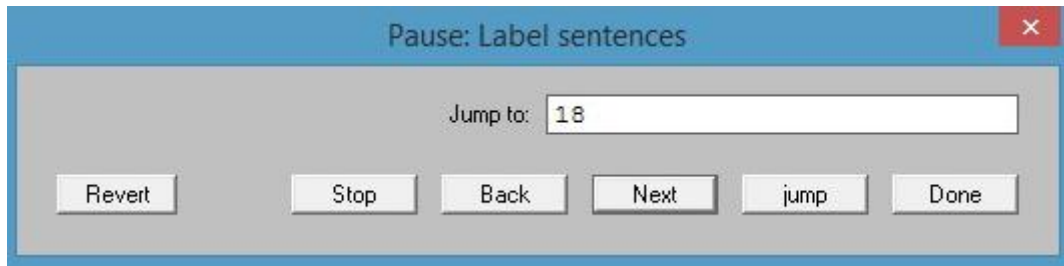


Figure 6.5. Use of the Pause Window of ProsodyPro (version 6.0 beta) to proceed to the next sound file in the destination folder.

During the labelling step, the appropriate range (in Hz) for the maximum and minimum pitches as well as other parameters were determined by visual inspection of the f_0 curve and listening to the sound file. It is especially crucial to recognise that the appropriate pitch ranges for female and male participants were different as the pitch stimuli for female participants in Sing The Note Task and Sing The Tune Task were one octave higher than those of the male participants. If the f_0 curve's contour displayed according to the default settings in Praat was not consistent with the expected f_0 contour, this could be rectified by readjusting the maximum or minimum pitch values (Choose "Pitch settings..." from the Pitch Menu in Praat).

As an illustration of the importance of selecting the appropriate pitch range, **Figure 6.6** shows the pitch contour of the fifth novel melody of Sing The Tune Task sung by a female participant (see **Figure 5.11e**, p. 128), with the maximum and minimum pitches of the range specified as 500 Hz and 150 Hz respectively. Visual inspection reveals that the contour corresponded well with the expected contour of the stimulus.

In contrast, when the maximum pitch was set too low (to 300 Hz), the pitch contour became distorted as octave errors occurred for the second and fourth notes (**Figure 6.7**).

Other parameters can also be adjusted from the Advanced pitch settings in the Pitch menu to lessen the impact of noise (by raising the silence threshold), enhance the pitch detection of softer sound files (by lowering the voicing threshold), or to rectify octave errors (by adjusting octave cost or octave jump cost), based on visual inspection.

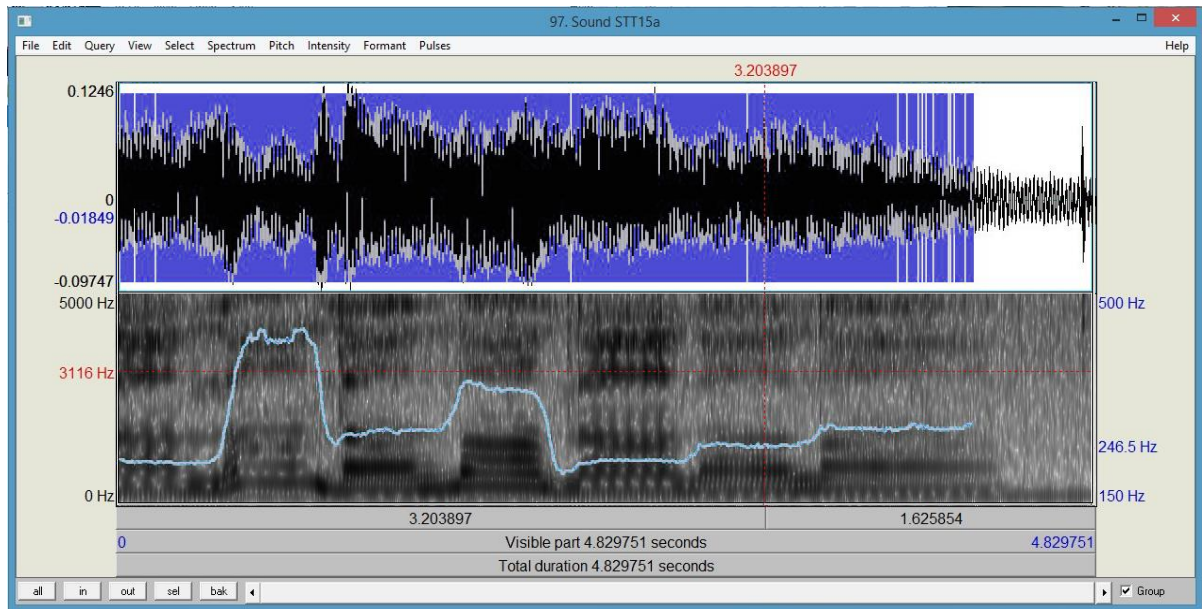


Figure 6.6. Fundamental frequency (f_0) contour of a participant's trial from Sing The Tune Task (5th novel melody).

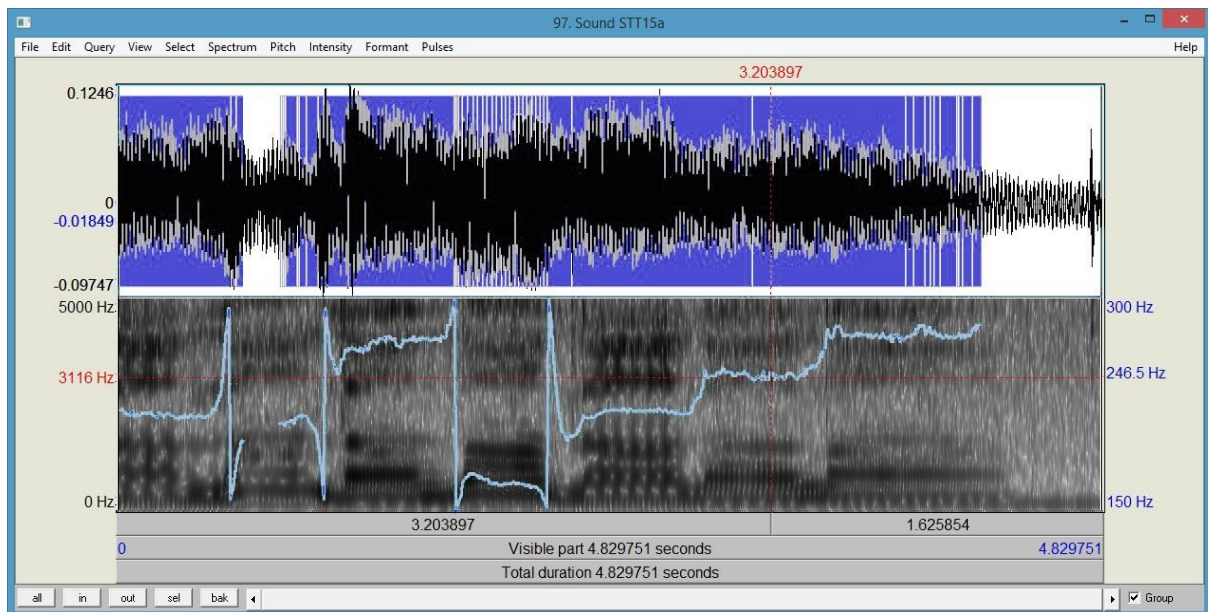


Figure 6.7. Fundamental frequency (f_0) contour of a participant's trial from Sing The Tune Task when an inappropriate pitch range was selected, causing octave errors in the display.

The appropriate parameter values often varied from one participant to another (and in some cases, from one task to another), depending on factors such as participant sex, voice quality, and vocal range, as well as the recording quality. Therefore, suitable parameter values were recorded in an excel file during the labelling step, as this information was needed for the subsequent step.

6.2.2.2 Obtaining sampled f_0 for the labelled pitch segments

For each sound file segmented, ProsodyPro automatically generates a text file with a ‘.label’ extension that contains information about the start time and end time of each labelled segment. The label file has the exact same name as the corresponding sound file. A second Praat script written by the researcher (**Appendix C-1**, p. 307) was then run to estimate the f_0 values (in Hz) in each labelled segment, sampled at 0.01s intervals.

Upon running the script, a startup window appeared (**Figure 6.8**). For this, after assigning the appropriate folder destinations, enter the pitch analysis parameters in the fields according to the suitable parameter values that have been determined during the pitch segment labelling step. Click “OK” and the script automatically generates the estimated f_0 values for all the labelled segments in each sound file of the folder. The f_0 values were saved in text files sharing the same name as the corresponding sound and label files, but with a .samplef0 extension (e.g., “song1.samplef0”). Each samplef0 file contained three columns: The first column contained the segment labels (e.g., ‘1’, ‘g’, ‘p’), the second column contained the sampling time series, and the third column contained the corresponding f_0 values (Hz).

Run script: Get F0

Directory of sound files
F:\PhDstuff\deidentifiedpairs\230\
Sound file extension: .wav

Directory of TextGrid files
F:\PhDstuff\deidentifiedpairs\230\
TextGrid file extension: .label

Pitch analysis parameters

time step: 0.01
minimum pitch: 200
maximum pitch: 600
voicing threshold: 0.45
silence threshold: 0.03
octave jump cost: 0.35
octave cost: 0.01

Standards Cancel Apply OK

Figure 6.8. Startup window of the Praat script to estimate the fundamental frequency at the sampled time intervals.

The fundamental frequency (f_0) data were exported into Microsoft Excel 2013 by running an Excel VBA macro specially written for the purpose (**Appendix C-2**, p. 309). The exported f_0 data were saved in individual Excel files according to tasks. In the case of Sing The Note Task and Sing The Tune Task, the f_0 data were organised into five separate spreadsheets in the Excel file, one for each stimulus. The f_0 data from the three trials of each stimulus were distributed into three separate columns in each spreadsheet.

As for Happy Birthday Singing Task, the f_0 data from each trial was exported to a separate spreadsheet. In each spreadsheet, the f_0 data were distributed into four separate columns, according to the four phrases of *Happy Birthday*.

After all the f_0 data were exported to the spreadsheets, the following fine-grained segmentation algorithm was run to automatically determine boundaries of each pitch segment with greater precision.

6.2.2.3 Fine-grained pitch segmentation

a) *Generating the f_0 velocity profile*

An Excel VBA macro was written to run a fine-grained segmentation process. First, undefined f_0 values and regions marked ‘n’ (i.e., noise that needed to be excluded) were removed from the numbered segments. Undefined f_0 values might occur occasionally where Praat was unable to detect or estimate the f_0 at a particular sampled time point. The ‘g’ segments were padded with zeros for f_0 values to facilitate subsequent f_0 velocity calculations. All the f_0 values in the numbered segments were then converted from Hz to cents. Using central differentiation, the rate of change of f_0 (in cents) at time t_i in a phrase was computed with the following formula, where the instantaneous rate of change of f_0 at a time point i equals the change in f_0 over the change in time between the next time point $i + 1$ and the previous time point $i - 1$:

$$v_i = \frac{f0_{i+1} - f0_{i-1}}{t_{i+1} - t_{i-1}}$$

The two-point central differentiation is commonly used to calculate derivatives due to its speed, simplicity, and accuracy (Bahill et al., 1982). For time points preceding or succeeding ‘g’ segments, calculation of f_0 velocities were omitted to prevent generating spuriously large f_0 velocities due to the zero f_0 values of the ‘g’ segments.

For the purpose of the subsequent fine-grained pitch segmentation, absolute f_0 velocity was computed. The absolute f_0 velocities were scaled to a tenth of the original values so that displaying both the f_0 and the absolute f_0 velocity profiles on the same graph would be possible.

Figure 6.9 shows a participant’s f_0 and absolute f_0 velocity profiles from a trial in Sing The Tune Task (first novel melody; see **Figure 5.11a**, p. 128). The peaks of the absolute f_0 velocity coincided with where the participant transitioned from one pitch to another,

and that the regions of low absolute f_0 velocities corresponded with the regions where individual pitches were held with relative steadiness. Thus, a suitable onset and offset could be estimated with good precision for each pitch segment by determining a threshold that separates the regions of low f_0 velocities from the regions of high f_0 velocities. The fine-grained demarcation of pitch segment boundaries could in turn aid the robust estimation of the mean or median f_0 for each pitch segment for subsequent data analyses. The use of f_0 velocity information to determine stable pitch segments is a novel approach in the field.

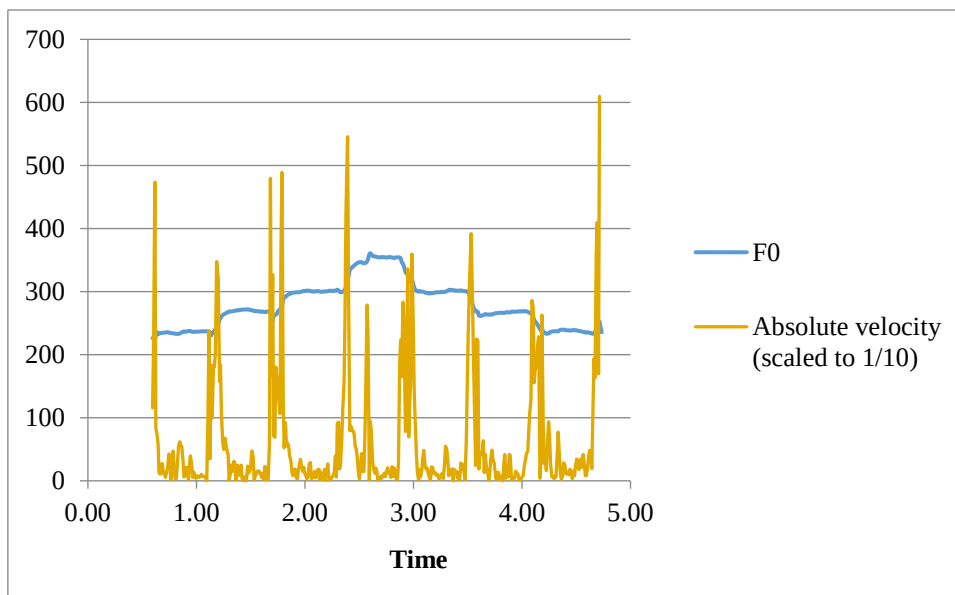


Figure 6.9. Fundamental frequency and absolute f_0 velocity profiles of a trial from Sing The Tune Task (1st novel melody; see **Figure 5.11a**, p. 128).

b) Determining the segmentation threshold

Thresholding is a well-established area in the field of image processing; many thresholding algorithms have been developed to automatically convert greyscale images into binary (e.g., black and white) images according to the threshold determined by the algorithm. In view of the similar nature of binary image thresholding with the current aim of finding a threshold to differentiate the high and low f_0 velocity regions, the efficacy of various image thresholding algorithms was explored (for a comprehensive review of image thresholding methods, see Sezgin and Sankur, 2004). One thresholding algorithm in particular, the fuzzy entropic thresholding method, consistently yielded good thresholds distinguishing the two f_0 velocity regions (Shanbhag, 1994) and was thus adopted in the fine-grained pitch segmentation process to estimate the absolute

velocity threshold. The following is an outline of Shanbhag's fuzzy entropic thresholding algorithm.

Two key definitions underpinned the algorithm:

Fuzzy: (Mathematics) maths of or relating to a form of set theory in which set membership depends on a likelihood function.

Entropy: (communication theory) a numerical measure of the uncertainty of an outcome

Essentially, this algorithm works on the principle that the absolute velocity profile comprised two fuzzy sets; one set (high V) corresponds to the high absolute velocity values and the other set (low V) corresponds to the low values. For a certain threshold T which segregates the two sets, membership values were calculated for all the absolute velocity values (rounded up to the closest integer) inside each set, to reflect the degree of likelihood that a particular absolute velocity value belongs to the set. In the current algorithm, the membership value of a particular absolute velocity value i is dependent on the proximity of i to the threshold T . The further i is away from T , the greater the degree of certainty that it belongs to the current set.

As an illustration, **Figure 6.10** showed an example of a horizontal number line representing the absolute velocity values from $V_{\min}$ to $V_{\max}$. A threshold T segregates the velocity values into high V and low V regions. It can be recognised that a velocity value at threshold T has an equal 50% chance or maximum uncertainty of being assigned to the high V region or the low V region, while an absolute velocity value of $V_{\min}$ would have 100% probability or maximum certainty of belonging to the low V region (and the velocity value of $V_{\max}$ has 100% probability of belonging to the high V region). Therefore, it follows that the membership values within a region span from 0.5 to 1.



Figure 6.10. An illustration of the two fuzzy sets of absolute velocity regions (low and high) and how the membership value (M_L or M_H) of a particular velocity value varies from 0.5 to 1 depending on its position in the set.

In the current algorithm, the membership value M_L for an absolute velocity value i in the low V region is determined by the following equation

$$M_L = 0.5 + \frac{0.5 \times \sum_{k=i}^T p(k)}{\sum_{k=1}^T p(k)}$$

where $p(k)$ is the relative frequency of an absolute velocity value k occurring in the phrase.

The membership value M_H of an absolute velocity value j in the high V region is computed by the following equation

$$M_H = 0.5 + \frac{0.5 \times \sum_{k=T+1}^j p(k)}{\sum_{k=T+1}^{V_{\max}} p(k)}$$

where $V_{\max}$ is the maximum absolute velocity value rounded up to the closest integer.

The entropy E_L associated with the low V region below threshold T will then be

$$E_L = - \sum_{k=1}^T \frac{p(k)}{\sum_{i=1}^T p(i)} \times \log(M_L)$$

Similarly, the entropy E_H associated with the high V region above threshold T can be shown as

$$E_H = - \sum_{k=T+1}^{Vmax} \frac{p(k)}{\sum_{i=T+1}^{Vmax} p(i)} \times \log(M_H)$$

In this algorithm, the optimum threshold is where E_L is approximately equal to E_H , which indicates that an absolute velocity value at the optimum T threshold has almost equal average uncertainty of being in low V region as in the high V region. Therefore, by iteratively setting T from the minimum to the maximum absolute velocity values, the optimum T is selected where $|E_L - E_H|$ is the minimum.

For Sing The Tune task example in **Figure 6.9**, an optimum threshold of 80 was found using the fuzzy entropic thresholding algorithm. As can be seen from **Figure 6.11**, the chosen threshold T is effective in segregating the high and low f_0 velocity regions.

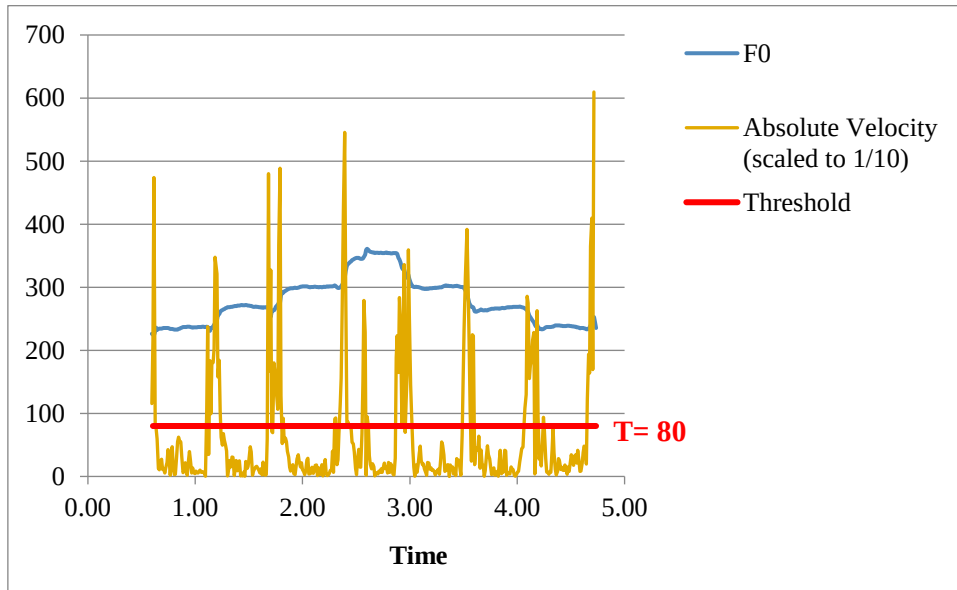


Figure 6.11. Fundamental frequency and absolute f_0 velocity profiles of a trial from Sing The Tune Task (1st novel melody), with the threshold (T=80) determined by Shanbhag's fuzzy entropic thresholding algorithm.

c) Refined pitch boundary segmentation

Using the optimum segmentation threshold for the phrase, iterative searches were conducted from both ends of each coarsely demarcated pitch segment to identify more precise boundaries of each segment. The 5-step procedure is as follows:

- i. From the beginning of the coarse segment till $\frac{1}{3}$ of the segment, search for the first absolute velocity value for which the value as well as the succeeding two absolute velocity values all fall below the optimum threshold. The time corresponding to that absolute velocity value will be established as the onset of the refined pitch segment.
- ii. If no suitable candidate is found from (i), from the same search area in (i), find the first absolute velocity value for which the value and the next absolute velocity value both fall below the optimum threshold. Set the corresponding sampled time as the refined pitch segment onset.
- iii. If no suitable candidate is found after (i) and (ii), repeat the search in the search area for the first absolute velocity value which falls below the segmentation threshold and set the corresponding sampled time as the refined pitch segment onset.
- iv. If there is no absolute velocity value below the segmentation threshold within the search area, find the lowest absolute velocity value within the search segment and set the corresponding sampled time as the refined pitch segment onset.
- v. Repeat the same procedure for the end of the coarse segment.

After experimenting with search areas of varying widths, it was found that setting the search area to occur $\frac{1}{3}$ from the beginning or the end of the coarse pitch segments yielded more reliable results. If the search area was set too wide (e.g., from the beginning to the middle of the segment), the resultant refined pitch segment might be too narrow (since absolute velocity values toward the middle of the pitch segment tend to be lower and have greater likelihood of fulfilling the (i) criterion). The narrow refined pitch segment, however, would not be fully representative of the pitch sung by the

participant, especially if the participant had difficulty holding the pitch steady (e.g., the fourth pitch segment in **Figure 6.11**). Conversely, if the search area was set to be less than 1/3, there would be a greater likelihood that the absolute velocities considered in the search area were all above the optimum threshold, rendering the iterative search less effective.

After the new boundaries for all the pitch segments in the phrase were determined by the refined segmentation procedure, a graph displaying the f_0 curve, absolute f_0 velocities (scaled by 1/10), the optimum threshold as well as the onsets and offsets of the refined pitch segments was generated for the phrase (**Figure 6.12**). Additionally, median f_0 , mean f_0 , standard deviation and durations of the refined pitch segments were computed and displayed on the Excel spreadsheet.

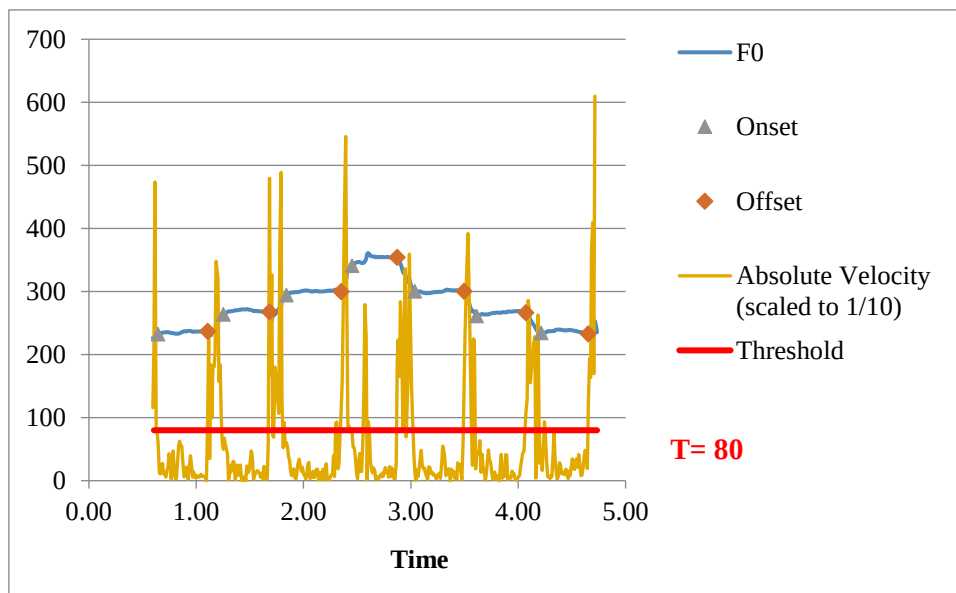


Figure 6.12. Fundamental frequency and absolute f_0 velocity profiles of a trial from Sing The Tune Task (1st novel melody), with onset and offset of each refined pitch segment displayed.

The suitability of the refined boundaries in a phrase were examined from the graph generated. If certain boundaries were deemed unsatisfactory, a section of the VBA code for the segmentation procedure was modified to manually select more appropriate boundaries based on visual inspection of the graph and f_0 velocity information. A new graph was then generated and computations pertaining to the refined pitch segments recalculated.

The procedure for setting the pitch boundaries in Sing The Note Task was more straightforward than the above described pitch segmentation procedure for the melodic singing tasks. While the data from Sing The Note Task also underwent the pitch segment labelling and f_0 estimation processes detailed in **Sections 6.2.2.1** and **6.2.2.2** (pp. 157-164), determining the optimum threshold and refining the pitch segmentation boundaries were unnecessary for this task. This is because in each trial of the task, the first two seconds of vocalisation were selected as the final pitch segment to be analysed.

The rationale for selecting the first two seconds of vocalisation related to the notion that variability in participants' task performance was likely to be evident in the first two seconds. Consider the example of a participant who was initially inaccurate in matching the target pitch but gradually slid up to the correct pitch in the middle of the vocalisation. Computing the mean or median f_0 from the two-second pitch segment would judiciously reflect the pitch inaccuracy, whereas taking the mean or median f_0 from the entire five seconds of vocalisation would understate the pitch inaccuracy at the beginning, causing the participant to appear more accurate than in reality.

The VBA macro for the fine-grained segmentation procedure of Happy Birthday Singing Task is available in **Appendix C-3** (p. 319). As the fine-grained segmentation procedure of Sing The Tune Task is exactly the same, the macro for the task not included.

6.2.2.4 Computing the median f_0

After all the recordings from the singing tasks were processed using the procedure described above, the median f_0 values computed from the refined pitch segments were transferred to specially formatted spreadsheet templates to compute the task measures, with one spreadsheet for each task.

Although both mean and median f_0 were computed for the tasks, median f_0 was ultimately chosen to represent the pitch height of a pitch segment as it was comparatively more robust against extreme values of f_0 within a pitch segment due to potential artifacts in the Praat-estimated f_0 curve (Dalla Bella, 2015).

6.2.3 Data processing for the tongue twister task

In the Praat environment, after appropriate pitch range and other pitch parameters were determined for a tongue-twister sound file, a specially written Praat script was run to obtain the median f_0 as well as the interquartile range (5th to 95th percentiles) of the vocalisation (**Appendix C-4**, p. 340). This information was saved to a text file and then subsequently transferred to a central excel spreadsheet containing all the participants' tongue-twister median f_0 and speech ranges.

6.2.4 Re-identification of participants

After all the data processing for the singing tasks and the tongue-twister task was completed blind, the participants were re-identified by their Twin IDs, such that the processed data could now be grouped by twin pairs. Questionnaire data and Match The Note Task data were then exported from the text files to the respective Excel spreadsheets. Once all the participants' data was transferred to the appropriate spreadsheets, each twin pair's zygosity was finally revealed. Data of twin pairs was then grouped according to zygosity.

Finally, Excel VBA macros were run to transfer all the twin data from the various zygosity groups into one central data spreadsheet in Excel, one row per twin, to facilitate subsequent analyses in the SPSS and R environments. In the central data spreadsheet, fields with missing data were coded "9999", while empty fields due to non-applicable questions (e.g., questions about music training for non-musically trained participants) were coded "-9".

6.2.5 Issues encountered during data processing

Several issues were observed while processing participants' data and thus, the following measures were taken to mitigate each of these issues.

6.2.5.1 Octave error in Sing The Note and Sing The Tune Tasks

In Sing The Note Task and Sing The Tune Task, it was observed that a few participants made octave errors when matching the pitch or melodic stimuli. Special considerations

were given to participants who made consistent octave errors throughout all trials of a task. In such instances, their f_0 data was adjusted higher or lower by one octave so that they were of the same register as the target pitches. This would prevent them from being excessively penalised by the pitch deviation measure (see **Section 6.3.1**, p. 175).

However, in instances where the octave errors made throughout the task appeared to be random and inconsistent, no adjustments were made to the f_0 data.

6.2.5.2 Failure to adhere to task instructions

Although the participants were asked to sing on “la” in the final two paced trials of Happy Birthday Singing Task, some participants sang with lyrics instead. In total, approximately 19% of the final two paced trials were sung with lyrics. Data processing of these trials proceeded as normal because the pitch segmentation process could still be applied successfully on songs with lyrics.

For Sing The Tune Task, as the melody was presented twice in each trial, some participants misunderstood and sang the melody twice in a row. In such cases, only their first attempt at the melody was processed, as these participants might have become more accurate during the second performance due to practice effects.

For Sing The Note Task, instead of following the instructions to hold the pitch steady for five seconds, some participants only held it steady for a shorter duration (e.g., 0.5 s or 1 s). As the duration in such cases was less than the intended two-second duration required for analysis, the entire vocalisation was used for the computation of the median f_0 .

6.2.5.3 Missing data due to human error or poor recording quality of the sound data

Some participants started singing before or while they pressed the record button. As a result, the first few notes of their singing performance might be missing from the sound file. Some participants also inadvertently pressed the record and stop button in quick succession, and therefore failed to record their singing attempt during a trial successfully. There were also some participants who laughed or spoke during a recording, which meant that Praat was unable to reliably estimate the f_0 in those sections

of the recording. Across the three singing tasks, the percentages of missing notes due to these user end errors ranged from 0.25% to 1.74%.

In addition, some of the participants' sound data was of poor quality due to their computer recording device, which caused systematic partial corruption to occur in every sound file (i.e., consistently in its front, middle or at the end). This resulted in partial loss of f_0 data from each trial.

In the case of partially missing f_0 data, during the initial pitch segment labelling process, only the intact pitch segments were labelled according to their expected order in the phrase. For example, if the first note of every trial in Sing The Tune Task was consistently missing due to a recording problem, the remaining pitch segments would be labelled from 2 to 7, and not from 1 to 6. This ensured that the f_0 data would be correctly exported and compared with the corresponding pitch targets in the specially formatted Excel spreadsheets for the tasks.

6.2.5.4 Missing data due to technical issues

Some of the participants experienced technical issues such as freezing of the program or an intermittent internet connection when they attempted the online study. As a result, the amount of data available from each participant for processing and analysis varied from task to task. Out of the total number of 216 participants, 215 of them had singing data available for Happy Birthday Singing Task, whereas 214 and 209 had data from Sing The Note Task and Sing The Tune Task, respectively. As for Match The Note Task, 211 participants' data were available. Across the four tasks, 3.8% of data were missing due to technical issues. Specifically, the percentage of files missing from Happy Birthday Singing Task, Sing The Note Task, Sing The Tune Task and Match The Note Task were 1.7%, 3.2%, 5.0% and 2.3%, respectively.

6.3 Performance Measures

The following section describes the performance measures used to assess the ability of the participants on music and singing tasks, as well as the tongue twister task.

6.3.1 Pitch deviation (PD)

In all the musical and singing tasks, the pitch deviation (PD) measure was used to assess pitch accuracy by summing and averaging the absolute differences between the produced pitches and the target pitches. The measure was expressed in cents, the logarithmic unit of measure for musical intervals. It is more perceptually and musically relevant to express pitch differences in cents since human perception of pitch differences is not linear but logarithmic with respect to fundamental frequency. In equal temperament tuning, the octave is divided into twelve semitones where each semitone is equivalent to 100 cents.

The pitch deviation (in cents) was computed using the following equation

$$PD = \frac{\sum_{i=1}^n \left| 1200 \times \log_2 \frac{f_i}{r_i} \right|}{n}$$

where f_i is the fundamental frequency (in Hz) of the i^{th} pitch produced by the participant, r_i is the fundamental frequency of the corresponding reference pitch, and n is the total number of trials in the task. The smaller the PD, the better the pitch accuracy.

The reason for averaging across absolute differences instead of signed differences was to prevent pitch deviations that were in opposite directions from cancelling each other out, thereby under-penalising a participant's pitch errors.

Unlike the other musical and singing tasks which have prescribed target pitches or melodies, it was more challenging to compute the PD for Happy Birthday Singing Task, as the participants could begin the song in whatever pitch they chose. Thus, it was necessary to include a preliminary step to extrapolate the target pitches of *Happy Birthday* from the participants' singing, by using pitch information from the first phrase sung, as well as the intervallic information from the melody of *Happy Birthday*.

As the first, second and fourth notes of the first phrase of *Happy Birthday* are the same pitch, the average f_0 (in Hz) of these three notes (in Hz) was computed to serve as the starting reference pitch. Instead of basing the starting reference pitch on only the first

note, using an average of the three notes was considered more appropriate as it could yield a more stable estimate of the starting pitch and help prevent minor inflections in the first note from skewing the subsequent reference pitches and unnecessarily penalising the participants for pitch deviation errors. Using the known intervallic information of *Happy Birthday*, the subsequent reference pitches could be derived using the following equation:

$$r_i = 2^{\frac{int}{12}} \times r_{i-1}$$

where r_i is the fundamental frequency (in Hz) of the reference pitch in the i^{th} position of the song, r_{i-1} is the fundamental frequency of the preceding reference pitch, and int is the interval (in semitones) between the current and previous reference pitches. For illustration purposes, **Figure 6.13** shows *Happy Birthday* and the intervallic relationships between the adjacent pitches of the song.



Figure 6.13. *Happy Birthday* presented in F major. The numbers below show the intervallic relationship (in semitones) between two adjacent pitches. The 1st, 2nd and 4th pitches from a participant's recorded attempt were averaged to form the starting reference pitch, from which other pitches were computed using the known intervals of the song.

The PD measure is particularly useful for Happy Birthday Singing Task as it was sensitive to transposition errors made by participants to a different key in the middle of the song.

6.3.2 Interval deviation (ID)

For the melodic singing tasks (i.e., Happy Birthday Singing Task and Sing The Tune Task), it was important to assess intervallic accuracy given that actively maintaining the correct interval relationships between adjacent pitches is integral to success in these

tasks. Therefore, in addition to PD, interval deviation (ID) was computed by averaging the absolute differences between the produced intervals and the reference intervals of the target pitches.

The interval deviation (in cents) for each trial was therefore computed as follows

$$ID_{trial} = \frac{\sum_{i=2}^n |produced\ interval_i| - |reference\ interval_i|}{n}$$

$$= \frac{\sum_{i=2}^n \left| 1200 \times \log_2 \frac{f_i}{f_{i-1}} \right| - \left| 1200 \times \log_2 \frac{r_i}{r_{i-1}} \right|}{n}$$

where f_i is the fundamental frequency (in Hz) of the i^{th} pitch produced by the participant, r_i is the fundamental frequency of the corresponding reference pitch of the stimulus, and n is the total number of pitches in the stimulus of the task. Averaging ID_{trial} across the total number of trials in the task would yield ID, with a small ID reflecting good melodic accuracy.

Interval deviation has been used as an objective measure of pitch accuracy in numerous studies (Berkowska & Dalla Bella, 2009b; Dalla Bella & Berkowska, 2009; Dalla Bella et al., 2007; Peter Q. Pfordresher, Steven Brown, Kimberly M. Meier, Michel Belyk, & Mario Liotti, 2010). Its ecological validity has been shown in a recent study, where a high and significant correlation was observed between interval deviation and the subjective perceptual ratings of expert singing judges (Larrouy-Maestri et al., 2013).

ID alone however, is not adequate as a measure of pitch accuracy, as it does not sufficiently penalise cases where participants transposed to another key in the middle of a melody. As an example, consider the situation where a participant sang *Happy Birthday* in F major and then transposed to C major two notes into the third phrase (**Figure 6.14**).

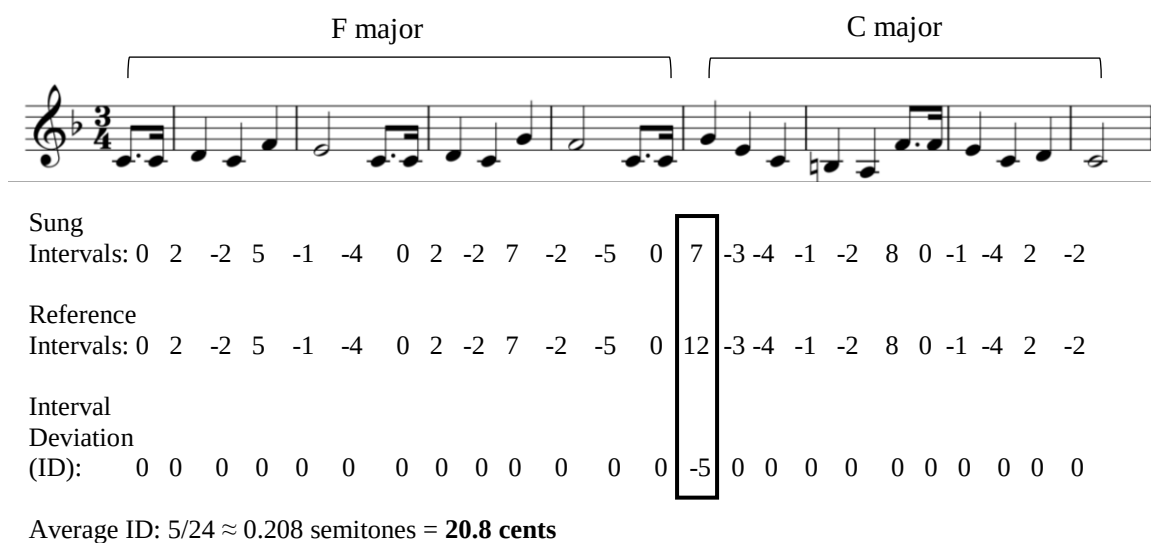


Figure 6.14. *Happy Birthday* with a transposition error in Bar 5. The numbers below show the intervallic relationship (in semitones) between two adjacent pitches, for both the actual intervals sung by the participant and the reference intervals.

As can be observed, there was only one interval error (5 semitones or 500 cents) made at the point of transposition. The ID in this case was thus 20.8 cents (500 cents averaged across 24 intervals), which was less than a quarter tone. This measure would therefore give the false impression that the participant was an accurate singer, although any judge who listened to the recording would have likely given a low rating due to the transposition error.

In contrast, the measure PD would consider the last 11 pitches to each have deviated five semitones (500 cents) from the corresponding reference pitches in the accurate version of *Happy Birthday* (**Figure 6.15**), thus yielding a PD of 220 cents

$\left(\frac{500 \text{ cents} \times 11 \text{ pitches}}{25 \text{ pitches}} \right)$. This indicates that the participant, on average, made pitch

deviation errors of 2.2 semitones, thereby correctly demonstrating that the participant was not an accurate singer. Due to the above considerations, it is therefore essential to include PD as a measure of melodic singing tasks, to detect whether a consistent tonal centre is maintained and to penalise accordingly.



Figure 6.15. The first melody is *Happy Birthday* performed by a participant with a transposition error in Bar 5. The second melody is the reference melody. The numbers below show the pitch differences (in semitones) between the participant's pitch and the corresponding reference pitch.

6.3.3 Key deviation (KD)

Another measure useful for evaluating key transposition error in Happy Birthday Singing Task is key deviation (KD). Similar to the tonal centre deviation measure detailed by Larrouy-Maestri and Morsomme (2014), four notes that are important to the tonal hierarchy of the melody form the basis of the computation of KD: the first notes of the first three phrases and the final note of the melody. For ease of reference, these four notes will be called Note 1, Note 2, Note 3 and Note 4 subsequently (**Figure 6.16**). Notes 1, 2 and 3 constitute the dominant of the key while Note 4 is the tonic. Together, the four notes are able to provide clues to any shift of tonal centre, phrase by phrase.

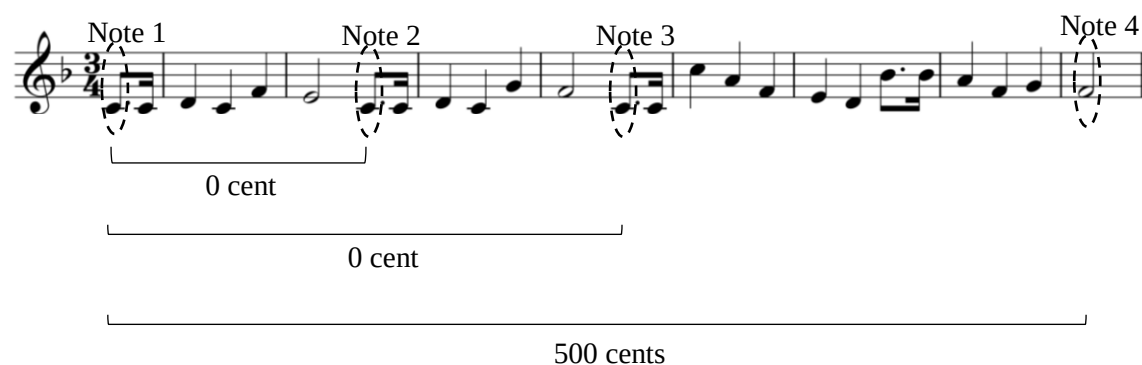


Figure 6.16. The four notes considered for the computation of the key deviation (KD) measure in Happy Birthday Singing Task. The expected intervals between Notes 2 and 1, Notes 3 and 1, and Notes 4 and 1 are 0, 0 and 500 cents, respectively.

The intervals between Note 2 and Note 1, Note 3 and Note 1, and Note 4 and Note 1 were therefore calculated and compared to the expected intervals of these notes according to the melody of *Happy Birthday*. It is clear from **Figure 6.16** that Notes 1, 2 and 3 are expected to be the same pitches, and so the expected interval between these notes is 0. In contrast, the expected interval between Note 4 and Note 1 is five semitones (i.e., 500 cents).

The key deviation (KD) measure was thus the average of the absolute differences between the produced intervals and the expected intervals and was computed as follows

$$KD = \frac{\left| 1200 \times \log_2 \frac{\text{Note 2}}{\text{Note 1}} \right| + \left| 1200 \times \log_2 \frac{\text{Note 3}}{\text{Note 1}} \right| + \left| 1200 \times \log_2 \frac{\text{Note 4}}{\text{Note 1}} - 500 \right|}{3}$$

where Notes 1, 2, 3 and 4 represent the fundamental frequencies (in Hz) of the four notes

In the transposed example from **Figure 6.14**, the KD was calculated to be

$$\frac{0+0+|0-500|}{3} = \frac{500}{3} = 166.67 \text{ cents (Figure 6.17), thereby demonstrating that this}$$

measure is able to penalise key transposition error appropriately.

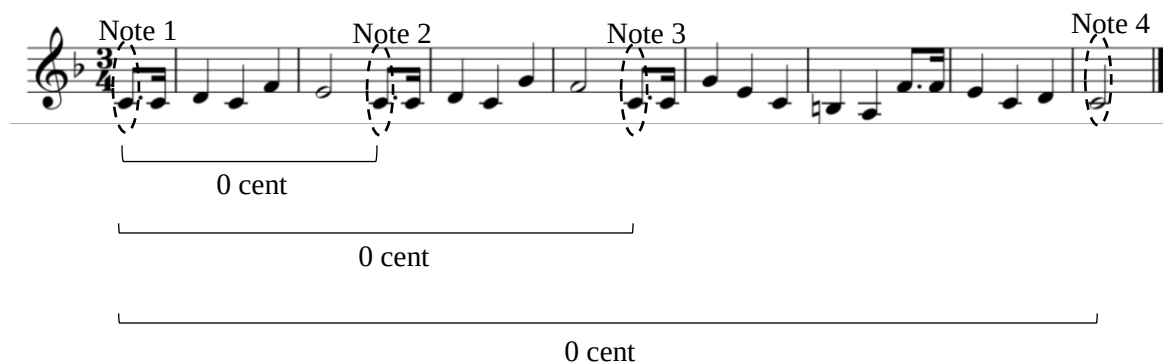


Figure 6.17. The transposed *Happy Birthday* example from **Figure 6.14**. The interval between Note 1 and Note 4 was 0 cents instead of 500 cents due to the transposition.

6.3.4 Categorical measures

In addition to the three types of continuous measures described above, categorical measures were also constructed from the continuous measures using a 50-cent cutoff criterion. Specifically, participants with mean deviation less than 50 cent in a continuous measure were classified as Category 1, participants with mean deviation between 50 to 100 cents were classified as Category 2, and participants with mean deviation 100 cents and above were classified as Category 3. By this definition, Category 1 were the accurate singers, Category 2 were the moderately inaccurate singers, Category 3 were the highly inaccurate singers. The rationale for having categorical measures alongside continuous measures was to better compare the incidence of accurate and inaccurate singers using the accuracy categories. In addition, categorical measures might be deemed ‘coarser’ estimates of pitch accuracy, it had been previously reported that most people can only reliably discern pitch deviations in singing that exceeded 50 cents while pitch errors as high as 40 cents were not reliably judged as out of tune (Hutchins et al., 2012; Vurma & Ross, 2006). As such, using categorical measures to characterise singing proficiency might correspond better with perceptual judgment of singing accuracy.

6.3.5 Measures for the tongue twister task

A number of studies on poor-pitch singing have observed that some poor-pitch singers show little or no variation in pitch (Blind, 1938; Joyner, 1969; Roberts & Davies, 1975), while speech range and speech fundamental frequency has emerged as strong predictor of pitch-matching accuracy in preschool children (Trollinger, 2003). Therefore, measures for speech fundamental frequency (f_0) and speech range were computed for this task.

The median speech fundamental frequency (in Hz) was used as a measure for speech fundamental frequency. Median was preferred over mean in this case since the quality of the speech recordings was largely dependent on the participants’ recording devices and the environment they undertook the online assessment. Thus, it was possible that the quality of some of the speech data would be degraded due to noise introduced by the recording devices or background noise. These noises, interspersed amid the tongue

twister recording, might be spuriously represented as outlier fundamental frequencies by Praat. The mean fundamental frequency computed across the entire tongue twister recording would therefore be unduly influenced by these pitch outliers. In contrast, the median fundamental frequency is a more robust measure against noisy recordings.

Due to the same considerations, instead of simply taking the difference between the maximum and minimum fundamental frequency detected for the tongue twister recording as the measure of pitch range, a more robust 5%-95% interquantile range (IQR), i.e., the difference (in cents) between the fundamental frequencies at the 95th percentile and the 5th percentile, was used as the speech range measure (Goldman, 2007).

In addition to computing the above two measures for the two paced trials (by averaging across the two trials), both measures were also computed for the unpaced trial.

6.3.6 Summary of task measures

Table 6.6 summarises the measures used in the various objective music and singing tasks.

Table 6.6. Measures Used to Assess Performance in the Music, Singing and Tongue-Twister Tasks

Match The Note Task	Sing The Note Task	Happy Birthday Singing Task	Sing The Tune Task	Tongue-twister
MatchTheNote PD	SingTheNote PD	HappyBirthday PD	SingTheTune PD	median speech f_0
MatchTheNote PD (category)	SingTheNote PD (category)	HappyBirthday PD (category)	SingTheTune PD (category)	5%-95% IQR
		HappyBirthday ID	SingTheTune ID	
		HappyBirthday ID (category)	SingTheTune ID (category)	
		HappyBirthday KD		
		HappyBirthday KD (category)		

Note. PD: pitch deviation; ID: interval deviation; KD: key deviation; f_0 : fundamental frequency; IQR: interquantile range

In addition, a combined singing score (SINGCOMB) was constructed by averaging all the continuous measures from the three singing tasks. A categorical SINGCOMB measure was then constructed from the continuous SINGCOMB measure, in the same manner as described in **Section 6.3.4** (p. 181).

6.4 Proposed Statistical Analyses

6.4.1 Investigate the genetic basis of singing ability (Aim 1)

6.4.1.1 Descriptive statistics of singing task performance

In order to address the first aim, descriptive statistics of the singing task measures were first computed to investigate how the singing proficiency of the sample varied according to each task or measure. Although several studies have asserted that non-normality of variables generally do not affect the robustness of structural equation modelling using maximum likelihood estimation methods (which would be employed for the current study's genetic analyses) (Iacobucci, 2010; Lei & Lomax, 2005; Olsson, Foss, Troye, & Howell, 2000), for the sake of caution, transformation would be performed if the distribution of any measure was considerably skewed or kurtotic.

The general consensus within the field of structural equation modelling research is that absolute skewness and kurtosis values less than 1 indicate slight non-normality, between 1.0 to around 2.3 indicate moderate non-normality and above 2.3 indicate severe non-normality (Lei & Lomax, 2005). In view of this, task measures with absolute skewness and kurtosis values above 1.0 were transformed.

In addition to the singing task measures, descriptive statistics were also computed for MatchTheNote PD as well as self-rated singing ability, singing interest, music ability and music interest. Bivariate correlations between the task measures were also computed.

6.4.1.2 Univariate genetic analyses

The following procedure were then undertaken to test each hypothesis in Aim 1:

- 1) Compute the intraclass correlations for the MZ twins (r_{MZ}) and the DZ twins (r_{DZ}) separately for each of the continuous and categorical singing task measure (SINGCOMB, SingTheNote PD, HappyBirthday PD, HappyBirthday ID, HappyBirthday KD, SingTheTune PD and SingTheTune ID). Similarly, compute the r_{MZ} and r_{DZ} for self-rated singing ability.
- 2) For each measure, determine whether r_{MZ} is significantly higher than r_{DZ} using Fisher's r to Z transformation. Significantly higher r_{MZ} would suggest a sizeable genetic component for the measure.
- 3) After ensuring the assumptions of equality of means, variances and covariances were met, conduct univariate genetic modelling to estimate the additive genetic (A), common environmental (C) and unique environmental (E) components of each task measure.

All the above proposed genetic analyses were performed in the R environment (version 3.2.1) using the OpenMx package (version 2.2.4). The univariate genetic models were estimated based on raw data using full information maximum likelihood (FIML) modelling, which is the generally preferred approach for model estimation, as it is able to utilise datasets with missing values automatically and flexibly (OpenMx Development Team, 2015).

When computing the intraclass correlations and conducting the univariate genetic modelling, as best practice, all the measures were adjusted for age and sex effects to prevent biased estimation of the twin correlations and model parameters (McGue & Bouchard Jr, 1984). In addition, to control for possible birth order effects, the ordering of a twin pair as twin 1 and twin 2 was randomised for the same sex twin groups (MZ_F, MZ_M, DZ_F, DZ_M). In the DZ_O group, the female twin was always assigned as twin 1 while the male was assigned as twin 2, in accordance to standard practice in twin methodology (Neale & Maes, 2004).

Besides following the above procedure to specifically test the genetic hypotheses pertaining to singing ability, the same procedure was also used to estimate the r_{MZ} , r_{DZ} ,

and *A*, *C*, *E* components of the following measures: MatchTheNote PD, self-rated singing interest, self-rated music interest and self-rated music ability.

The OpenMx scripts that were used to run the above analyses are included in **Appendix C-5** to **Appendix C-11** (pp. 342-367).

6.4.2 Investigate the genetic bases of environmental components associated with singing ability (Aim 2)

6.4.2.1 Identification of singing and music background components

Before testing the genetic hypotheses in Aim 2, underlying components in the music and singing background questionnaire were first identified by conducting principal component analysis on the Z-scores of each questionnaire item.

The following assumptions were tested prior to conducting principal component analysis:

- a) Factorability: All items correlated at least .3 with one or more other items.
- b) Sampling adequacy: Kaiser-Meyer-Olkin measure was above 0.6 and Bartlett's test of sphericity was significant. The diagonals of the anti-image correlation matrix were all above 0.5.
- c) Each item shared some common variance with other items: communalities were above 0.3 for all items.

Both varimax and oblimin rotations of the factor loading matrix were examined to investigate whether the solutions arising from both rotations were similar, and which one offered the best defined factor structure. The scree plot was also used to determine the number of components underlying the questionnaire items. To ensure that the components were reasonably well-defined, items that failed to meet a minimum criteria of having a primary factor loading of at least 0.4, and having a cross-loading of at least 0.3 with another component were removed. Suitable labels best describing the latent construct of each component were then generated.

The internal consistency of each component was also examined using Cronbach's alpha. If the removal of any questionnaire item resulted in substantial increases in a

component's alpha, it was removed to improve the internal consistency of the component. A composite score for each component was then computed by averaging the Z-scores of the questionnaire items that loaded primarily on that component.

Based on the composite scores of the underlying components, descriptive statistics were generated to investigate how the components varied within the study sample and determine whether transformation was necessary for any component that was considerably skewed or kurtotic.

6.4.2.2 Univariate genetic analyses

To test the first hypothesis in Aim 2, the procedure described in **Section 6.4.1.2** (p. 183) was used to estimate the r_{MZ} , r_{DZ} , and A , C , E components of the music and singing background components so that the genetic influences on each component could be determined.

6.4.2.3 Bivariate genetic analyses

To test the second hypothesis, bivariate genetic modelling was used to determine the extent and significance of shared additive genetic (A), common environmental (C) and unique environmental influences (E) between the singing task measures and the music and singing background components. In addition, additional bivariate genetic analyses between MatchTheNote PD and background components related to formal music training were also performed, since significant shared genetic influences between music perception ability and the amount of music practice had been previously reported (Mosing et al., 2014).

Each singing task measure and each background component were first fitted with a full bivariate Cholesky decomposition model (**Figure 6.18**). Three submodels which removed shared A , C and E influences (i.e., a_{21} , c_{21} or e_{21}) in turn from the full bivariate model were then fitted. The importance of shared additive genetic influences in explaining the association between the two variables would be demonstrated if constraining the shared additive genetic influences (a_{21}) to zero resulted in a significant deterioration in model fit as compared to the full model. In addition, the significance of

shared additive genetic influences would also be evident if the confidence interval of the additive genetic correlation did not include zero.

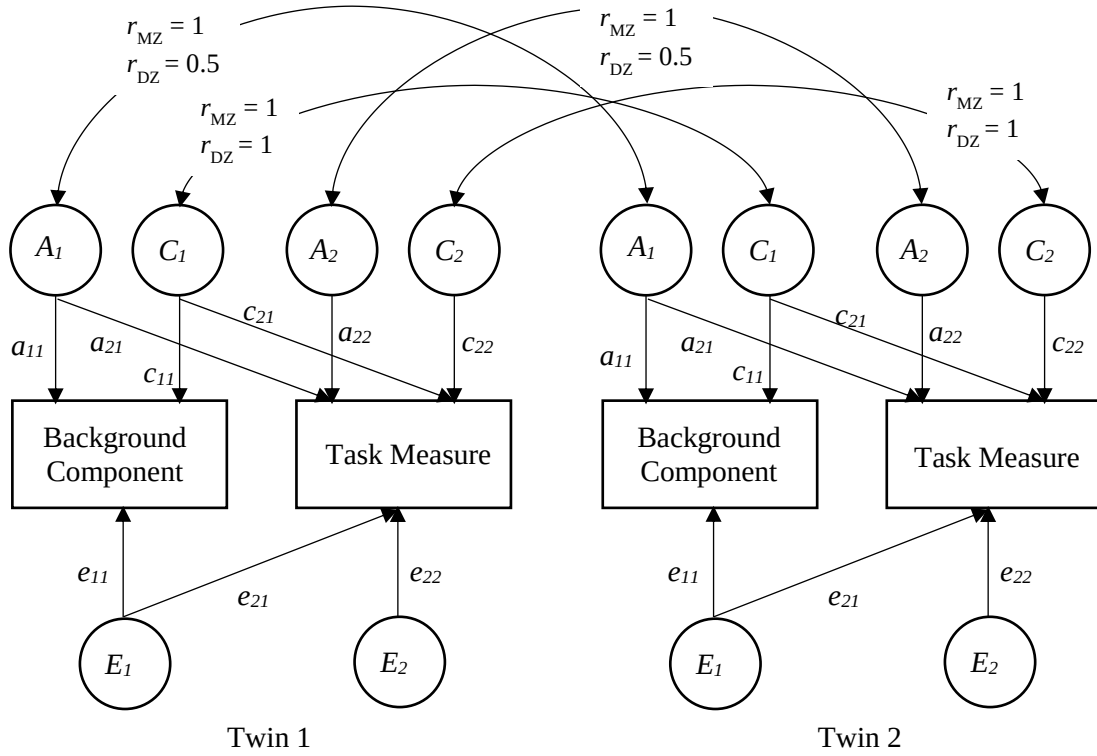


Figure 6.18. The full bivariate Cholesky model. The background component and task measure of Twin 1 and Twin 2 are shown in the boxes. a_{11} , c_{11} , e_{11} and a_{22} , c_{22} , e_{22} are the additive genetic, common environmental and unique environmental effects acting on the background component and the task measure, respectively, whereas a_{21} , c_{21} , e_{21} are the additive genetic, common environmental and unique environmental influences shared by both the component and the task measure. Three submodels were constructed by removing a_{21} , c_{21} and e_{21} from the full model, respectively.

The contributions of shared A, C, and E influences to the phenotypic correlation are computed as follows:

$$\text{Correlation due to A} = \sqrt{A_1} \times r_A \times \sqrt{A_2}$$

$$\text{Correlation due to C} = \sqrt{C_1} \times r_C \times \sqrt{C_2}$$

$$\text{Correlation due to E} = \sqrt{E_1} \times r_E \times \sqrt{E_2}$$

where r_A , r_C , and r_E are the additive genetic, common environmental and unique environmental correlations, whereas A_1 , C_1 , E_1 and A_2 , C_2 , E_2 are the univariate heritabilities of trait 1 and trait 2 in the bivariate model, respectively.

Similar to the univariate genetic analyses, all the bivariate models were also adjusted for age and sex effects. The OpenMx script used to conduct bivariate genetic modelling is available in **Appendix C-12** (p. 367).

6.4.3 Secondary analyses

To investigate potential confounding variables that might influence task performance, the following secondary analyses were performed.

Specifically, independent *t*-tests were used to compare if there were significant differences in each task measure between:

- a) Males and females
- b) Participants with and without AP
- c) Tonal language speakers and non-tonal language speakers
- d) Monolingual and bilingual participants

Simple regressions were used to investigate whether the following variables were significant predictors of each task measure:

- a) Age
- b) Years of education
- c) Self-rated interests and abilities in music and singing
- d) Parents' interests and abilities in music and singing
- e) Singing and music background components
- f) Speech range and median speaking frequency (from the tongue twister task)

Estimates of parents' music and singing abilities and interests were computed by taking the mean of the Z-scores from both twins' ratings of their parents. In cases where the rating from one twin was unavailable (due to missing data or if they rated "I don't know" for that variable), the rating score would be computed solely based on the available rating from the co-twin.

As the median speaking frequency was likely to differ in range for male and female participants, simple regressions were performed separately for male and female.

Finally, potential confounding effects of demographic variables (sex, age and years of education) on music and singing background components as well as self-rated interests and abilities in music and singing were investigated using independent *t*-tests and simple regressions.

All the descriptive statistics and secondary analyses were conducted using IBM SPSS Statistics Version 19 (IBM Corp., 2010).

To better contextualise the genetic findings that will be reported in Chapter 8, Chapter 7 will commence the results section by reporting the descriptive statistics of the task measures and questionnaire components, as well as the results from the secondary analyses which addressed potential confounding variables in the study.

7

BEHAVIOURAL FINDINGS

This chapter presents the behavioural findings, which include descriptive statistics of the task performances (**Section 7.1**), self-ratings of abilities and interests in music and singing (**Section 7.2**), as well as components extracted from the singing and music background questionnaire (**Section 7.3**). Investigation of potential confounding variables that might have influenced task performance and questionnaire responses are also reported in this chapter.

7.1 Task Performance

7.1.1 Music and singing tasks

The performances of the participants in the objective singing and music tasks are summarised in **Table 7.1**. The wide-ranging minimum and maximum deviation values for each task reveal the heterogeneity in singing and music perception abilities among the participants. A comparison of the task means and medians shows that the task median was lower than the mean in all instances, especially for Sing The Note Task and Sing The Tune Task. It was therefore deemed more appropriate to interpret group performance with the medians for the raw data.

The most accurately performed tasks were the single pitch-matching tasks, both perceptually and vocally. Match The Note Task (perceptual pitch-matching) had a median deviation of 13.76 cents whereas Sing The Note Task had a median deviation of 28.31 cents. Happy Birthday Singing Task was also relatively well performed; all three task measures (PD, ID and KD) had median deviations of approximately 40 cents. The most difficult task was Sing The Tune Task, which involves vocally matching novel short melodies. In this task, participants exhibited less pitch deviation (median = 54.03)

as compared to interval deviation (median = 65.82). For the combined singing score (SINGCOMB), the median pitch deviation was 50.90 cents, lower than Sing The Tune Task, but higher than the median deviations from Sing The Note Task and Happy Birthday Singing Task.

Table 7.1. Group Performance in the Objective Singing and Music Tasks (Untransformed)

	N* (Total = 216)	Mean (cents)	Median (cents)	SD	Min	Max	Skew- ness	Kurto- sis
SINGCOMB	208	81.43	50.90	76.68	12.49	374.10	1.73	2.30
SingTheNote PD	214	111.00	28.31	192.24	5.88	991.69	2.60	6.35
HappyBirthday PD	215	67.75	41.31	61.27	10.84	350.45	1.90	3.55
HappyBirthday ID	215	52.26	40.51	37.83	12.16	366.59	3.52	22.59
HappyBirthday KD	215	64.34	41.79	57.31	7.74	334.28	2.08	4.86
SingTheTune PD	209	97.38	54.03	110.34	9.92	646.95	2.48	7.20
SingTheTune ID	209	93.00	65.82	77.58	10.75	519.23	1.63	3.85
MatchTheNote PD	211	36.52	13.76	56.42	1.87	487.30	3.87	21.88

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* The number of analysed samples varies from task to task due to missing data (see **Sections 6.2.5.3 and 6.2.5.4**)

As evident from **Table 7.1**, the skewness and kurtosis of the task measures were indicative of non-normality: the skewness of the task measures ranged from 1.63 to 3.87 while the kurtosis ranged from 3.55 to 22.59. All the task measures thus underwent natural log (ln) transformation such that their skewness and kurtosis values fell below 1.

The descriptive statistics of the transformed continuous measures are shown in **Table 7.2**. An improvement in the normality of the measures was evident from the absolute values of the skewness and kurtosis falling below 1.

All subsequent references to the continuous task measures in this thesis refer to the transformed task measures. All subsequent references to Public Singing in this thesis refer to the transformed measure.

Table 7.2. Group Performance of the Sample in the Objective Singing and Music Tasks (Transformed)

	<i>N</i>	Mean	SD	Min	Max	Skewness	Kurtosis
SINGCOMB	208	4.05	3.94	2.53	5.92	0.48	-0.60
SingTheNote PD	214	3.72	1.30	1.77	6.90	0.86	-0.35
HappyBirthday PD	215	3.91	0.75	2.38	5.86	0.57	-0.54
HappyBirthday ID	215	3.78	0.57	2.50	5.90	0.54	0.08
HappyBirthday KD	215	3.87	0.75	2.05	5.81	0.37	-0.23
SingTheTune PD	209	4.12	0.92	2.29	6.47	0.40	-0.43
SingTheTune ID	209	4.20	0.84	2.37	6.25	-0.07	-0.76
MatchTheNote PD	211	2.91	1.10	0.63	6.19	0.61	-0.22

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

The bivariate correlations of the singing task measures are presented in **Table 7.3**. All the bivariate correlations were significant ($p < .01$). Not surprisingly, the bivariate correlations of SINGCOMB with the other singing task measures were very high, ranging from $r = .83$ to $.95$. In particular, the measures of Sing The Tune Task were comparatively more highly correlated with SINGCOMB ($r = .90$ to $.95$) than the other singing task measures ($r = .83$ to $.88$). Different measures within the same task were also highly correlated. In particular, the correlation ($r = .93$) between HappyBirthday PD and HappyBirthday KD was extremely high, as was the correlation between SingTheTune PD and SingTheTune ID ($r = .94$). The generally high correlations between SINGCOMB and the singing task measures indicate that SINGCOMB provides a good overall estimate of singing ability.

The bivariate correlations between the singing task measures were comparatively higher ($r = .60$ to $.95$) than those between the singing task measures and MatchTheNote PD ($r = .33$ to $.51$). In particular, SingTheNote PD and SINGCOMB had the highest correlations with MatchTheNote PD ($r = .51$). Similar magnitudes of correlations were also observed between MatchTheNote PD and the measures of Sing The Tune Task ($r = .49$ -. 50). The correlations between MatchTheNote PD and the Happy Birthday task measures were comparatively lower ($r = .33$ -. 40), but remained significant.

Table 7.3. Bivariate Correlations of the Objective Task Measures

	SINGCOMB	SingTheNote PD	HappyBirthday PD	HappyBirthday ID	HappyBirthday KD	SingTheTune PD	SingTheTune ID	MatchTheNote PD
SINGCOMB	1							
SingTheNote PD	.85**	1						
HappyBirthday PD	.88**	.65**	1					
HappyBirthday ID	.85**	.65**	.88**	1				
HappyBirthday KD	.83**	.60**	.93**	.80**	1			
SingTheTune PD	.95**	.76**	.76**	.76**	.71**	1		
SingTheTune ID	.90**	.64**	.72**	.73**	.67**	.94**	1	
MatchTheNote PD	.51**	.51**	.35**	.40**	.33**	.50**	.49**	1

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

** $p < .01$

Table 7.4 presents the distribution of participants in terms of the three categorical measures of performance in the various singing tasks.

Table 7.4. Singing Accuracy Distribution of the Participants by the Three Categories

	<i>N</i>	Category 1 (<i>n</i>) (<50 cents)	Category 2 (<i>n</i>) (50≤ <i>x</i> <100 cents)	Category 3 (<i>n</i>) (≥100 cents)
SINGCOMB	208	102 (49.0%)	52 (25.0%)	54 (26.0%)
SingTheNote PD	214	142 (66.4%)	19 (8.9%)	53 (24.8%)
HappyBirthday PD	215	127 (59.1%)	44 (20.5%)	44 (20.5%)
HappyBirthday ID	215	132 (61.4%)	62 (28.8%)	21 (9.8%)
HappyBirthday KD	215	126 (58.6%)	50 (23.3%)	39 (18.1%)
SingTheTune PD	209	95 (45.5%)	57 (27.3%)	57 (27.3%)
SingTheTune ID	209	79 (37.8%)	62 (29.7%)	68 (32.5%)

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

In terms of SINGCOMB, slightly less than half (49.0%) of the participants were classified as Category 1, whereas approximately one quarter of participants belonged to Category 2 and Category 3, respectively. This suggests that in the current sample, based on performance across all singing tasks, approximately 50% of the participants were accurate singers, whereas the other 50% were inaccurate singers, of which half of them were highly inaccurate, missing target notes by more than one semitone (Category 3).

The percentages of Category 1 participants (accurate singers) in the other task measures also corresponded with the descriptive statistics reported for the continuous measures (**Table 7.2**). SingTheNote PD was the most well-performed singing task measure, indicated by approximately 66% of the participants classified as Category 1, whereas 59-61% of the participants belonged to Category 1 for the various HappyBirthday task measures. In Happy Birthday Singing Task, the number of Category 1 participants was slightly greater for ID than for PD and KD, indicating that accurate interval singing was relatively easier than absolute pitch and key accuracy on this task. Sing The Tune Task was the most challenging task, with only approximately 38-46% of participants in Category 1. For this task, there were fewer Category 1 participants for ID (37.8%) compared to PD (45.5%), and there were more highly inaccurate Category 3 participants for ID (32.5%) than for PD (27.3%).

Interestingly, although Sing The Note Task had the highest percentage (66.4%) of accurate singers, it also had one of the highest proportions of Category 3 singers (24.8%). In contrast, HappyBirthday ID had the least number of Category 3 participants (9.8%), suggesting most participants were either accurate or just moderately inaccurate (Category 2) by this measure. However, HappyBirthday PD and HappyBirthday KD have approximately twice as many Category 3 participants compared to HappyBirthday ID. This strongly indicates that many participants made key transposition errors when singing a familiar tune, which detrimentally affected their accuracy in terms of PD and KD, while leaving ID relatively intact.

For Happy Birthday Melody Perception Task, out of the 193 participants who did not have missing data for this task, 100% of them identified the correct Happy Birthday melody from the other two slightly altered versions. This suggests that pitch and key deviations for Happy Birthday Singing Task do not reflect a lack of familiarity with the tune.

7.1.2 Tongue twister task

The descriptive statistics of the speech ranges and median speaking fundamental frequency (f_0) from the tongue twister task are presented in **Table 7.5**. The units of the measures are in cents and Hz.

Table 7.5. Speech Range and Median Speaking Fundamental Frequency of the Tongue Twister Task

	<i>N</i>	Mean	SD	Min	Max	Skewness	Kurtosis
Unpaced male median f_0 (Hz)	49	114.59	15.25	82.62	149.43	0.19	-0.47
Unpaced female median f_0 (Hz)	147	192.98	26.63	113.00	271.92	-0.01	0.32
Unpaced range (cents)	196	869.93	291.46	246.86	1807.85	0.52	-0.10
Paced male median f_0 (Hz)	50	119.49	18.18	92.26	170.38	0.69	0.05
Paced female median f_0 (Hz)	152	198.66	29.57	116.03	338.93	0.76	3.28
Paced range (cents)	202	743.58	265.15	153.87	1884.47	1.05	1.65

Not surprisingly, the median speaking f_0 of male participants was considerably lower than that of female participants, as confirmed by a significant independent samples t -tests comparing the two, for both unpaced and paced conditions (unpaced: $t(145.71) = 25.34, p < .001$; paced: $t(137.60) = 22.52, p < .001$).

Dependent samples t -tests comparing the speech ranges of the unpaced and paced conditions revealed significant differences in the two conditions, with wider speech ranges in the unpaced conditions, $t(193) = 8.537, p < .001$. During acoustical processing, it was observed that many of the participants tended to recite the tongue twister in a monotonous, chant-like manner during the paced condition, which could have caused the significantly lower speaking ranges in the paced condition. In view of this, the unpaced speech range was used for subsequent analyses because it was likely to be more representative of the participants' actual speech range in spontaneous speech.

7.2 Self-Reported Interests and Abilities in Music and Singing

Descriptive statistics of the participants' self-ratings for Music Interest, Music Ability, Singing Interest and Singing Ability on 7-point Likert type scales are summarised in **Table 7.6**. Of the four variables, Singing Ability had the lowest mean rating ($M = 3.66$, $SD = 1.68$), followed by Music Ability ($M = 4.03$, $SD = 1.70$), Singing Interest ($M = 4.79$, $SD = 1.89$) and Music Interest ($M = 5.68$, $SD = 1.38$). The mean ratings suggest that while participants of the present study have a generally low opinion of their singing abilities, most of them reported a high level of music interest.

Table 7.6. Descriptive Statistics of Self-Reported Music and Singing Interests and Abilities

	<i>N</i>	Mean	SD	Skewness	Kurtosis
Singing Ability	207	3.66	1.68	-0.04	-0.85
Music Ability	207	4.03	1.70	-0.28	-0.79
Singing Interest	207	4.79	1.89	-0.51	-0.91
Music Interest	207	5.68	1.38	-1.06	0.61

7.3 Singing and Music Background Components

To identify underlying components of the questionnaire items on singing and music background, principal component analysis was conducted on the Z-scores of the questionnaire items.

All 13 questionnaire items related to singing and music background correlated at least 0.30 with one or more other items, suggesting reasonable factorability. The Kaiser-Meyer-Olkin measure of sampling adequacy was .85, above the recommended value of 0.60, and Bartlett's test of sphericity was significant ($\chi^2(78) = 1296.73, p < .001$). The diagonals of the anti-image correlation matrix were also all above 0.50. The communalities were between 0.54 to 0.83, all of which were above the minimum suggested value of 0.30. This further confirmed that each item shared some common variance with other items. Fulfilment of the above criteria was used to justify that all 13 items were suitable to undergo principal components analysis.

Principal components analysis using both varimax and direct oblimin rotations were performed to identify underlying components and determine which rotation offered the best defined factor structure. The varimax and oblimin solutions were similar; both revealed the presence of four components explaining 72% of the variance, but direct oblimin rotation provided the best defined factor structure. The four factor solution was also corroborated by the 'levelling off' of eigenvalues on the scree plot after four factors. All items in this analysis had primary loadings over 0.45, which exceeded the minimum criterion of 0.40 for primary factor loading. The scree plot and the factor loading matrix for the final solution are available in **Figure D-1** and **Table D-1** of **Appendix D** (pp. 375-377).

The four extracted components were labelled 'Family Singing', 'Public Singing', 'Personal Singing' and 'Music Listening'. As evident from **Table 7.7**, Family Singing comprised questionnaire items that describe singing activities with family members, whereas Public Singing denoted current singing activities as a solo performer, in a group setting or with friends. As the third factor contained items describing singing alone during childhood and at present, it was termed Personal Singing. Finally, Music

Listening was labelled as such as it contained items that described engagement in music listening activities during one's childhood.

Internal consistency for each component was examined using Cronbach's alpha. The alphas were moderate to high: 0.87 for Family Singing (5 items), 0.78 for Public Singing (3 items), 0.77 for Music Listening (3 items) and 0.76 for Personal Singing (2 items). All items in each component were retained as the removal of any item did not cause a component's alpha to increase greatly.

In addition, a second principal components analysis was performed on participants with music training ($n = 169$) using the 13 questionnaire items mentioned above as well as 6 items related to musically trained participants' instrumental training background, in order to investigate whether there was an underlying factor for instrumental training background. All 19 items correlated at least 0.30 with one or more other items, suggesting reasonable factorability. The Kaiser-Meyer-Olkin measure of sampling adequacy was 0.84, above the recommended value of 0.60, and Bartlett's test of sphericity was significant ($\chi^2(171) = 1690.21, p < .001$). The diagonals of the anti-image correlation matrix were also all above 0.50. The communalities were between 0.38 to 0.83, all of which were above the minimum suggested value of 0.30, further confirming that each item shared some common variance with other items. Fulfilment of the above criteria indicates that all 19 items were suitable to undergo principle components analysis. Principal components analysis using both varimax and oblimin rotations indicated that all items relating to the participants' instrumental background converged to form one component. The primary loadings of items within this factor ranged from 0.57 to 0.78, using oblimin rotation. This component is therefore termed Instrumental Expertise (see **Table D-2** of **Appendix D** for the factor loading matrix for the final solution, p. 377). Internal consistency for Instrumental Expertise was examined using Cronbach's alpha. The alpha for the 6 items in Instrumental Expertise was low (0.56), indicating that the items in this factor were not internally consistent. It was observed that removing the item 'Years since last regular practice' resulted in a substantial increase in alpha to 0.81. In view of this, the above-mentioned item was removed from the Instrumental Expertise component. The questionnaire items contained in the Instrumental Expertise component are shown in **Table 7.7**.

Table 7.7. Extracted Components from the Principal Components Analyses

Component	Questionnaire items
Family Singing	In my childhood, an adult family member/s sang with me
	In my childhood, an adult family member/s sang to me
	In my childhood, an adult family member/s taught me songs
	In my childhood, I sang with my siblings/friends
	How often do you currently sing with your family?
Public Singing	How often do you currently sing in a choir/group?
	How often do you currently sing as a solo performer?
	How often do you currently sing with your friends?
Personal Singing	In my childhood, I sang by myself
	How often do you currently sing by yourself?
Music Listening	In my childhood, music was present around my home
	In my childhood, I listened to music
	In my childhood, my family attended live musical events together
Instrumental Expertise	How good are you on this instrument/voice?
	What was your level of motivation to learn this instrument/voice?
	How many days do you practise now every week?
	How many years of training have you had on this instrument/voice?
	Weekly peak practice duration (when you were most interested in learning your instrument/voice)

Composite scores were created for each of the five components by taking the average of the Z-scores of each item that had their primary loadings for the particular factor.

Descriptive statistics of the five components are presented in **Table 7.8**. Apart from Public Singing, which was positively skewed (indicating that the majority of the participants had a low degree of public singing engagement), all other components had absolute skewness and kurtosis values less than 1, which indicated only slight non-normality. Therefore, Public Singing underwent natural log transformation and the skewness and kurtosis values of the transformed measure were .51 and -.47, respectively. All subsequent references to Public Singing in this thesis refer to the transformed measure.

Table 7.8. Descriptive Statistics of the Composite Scores of the Components Derived from the Questionnaire

	<i>N</i>	Mean	SD	Min	Max	Skewness	Kurtosis
Personal Singing	207	0.00	0.90	-2.49	1.43	-0.54	-0.11
Family Singing	207	0.00	0.81	-1.90	1.81	-0.08	-0.35
Public Singing	207	0.00	0.83	-0.83	3.25	1.39	1.85
Public Singing (transformed)	207	0.52	0.41	0.00	1.63	0.51	-0.47
Music Listening	207	0.00	0.83	-1.99	1.28	-0.40	-0.83
Instrumental Expertise	169	0.04	0.75	-1.02	2.24	0.89	0.35

Table 7.9 shows the bivariate correlations of the composite scores. The correlations between the composite scores of the items were significant ($p < .01$), with correlation strengths ranging from low to moderate ($r = .30$ to $.53$). In particular, Family Singing was moderately correlated with Personal Singing ($r = .51$) and with Public Singing ($r = .53$), whereas Instrumental Expertise was less strongly correlated with Personal Singing ($r = .30$) for participants with formal music training.

Table 7.9. Bivariate Correlations of the Composite Scores of the Components

	Personal Singing	Family Singing	Public Singing	Music Listening	Instrumental Expertise
Personal Singing	1				
Family Singing	.51**	1			
Public Singing	.44**	.45**	1		
Music Listening	.46**	.53**	.37**	1	
Instrumental Expertise	.30**	.40**	.39**	.42**	1

** $p < .01$

The relationship between the background components and the objective task measures were also examined through bivariate correlations (**Table 7.10**). All the background components and singing task measures were significantly correlated ($p < .01$), with low to moderate correlation strengths ($|r| = .23$ to $.48$). Not surprisingly, MatchTheNote PD was not significantly correlated with the three singing components. However, it was significantly correlated with Music Listening and Instrumental Expertise ($p < .01$ and $p < .05$, respectively), although the size of the correlation was small ($|r| = .18$). On the whole, the significant correlations indicate that greater singing and music engagement were associated with better objective singing accuracy and music perception.

Table 7.10. Correlations between the Background Components and the Task Measures

	Personal Singing	Family Singing	Public Singing	Music Listening	Instrumental Expertise
SINGCOMB	-.35**	-.44**	-.42**	-.47**	-.39**
SingTheNote PD	-.23**	-.32**	-.32**	-.38**	-.27**
HappyBirthday PD	-.35**	-.41**	-.38**	-.43**	-.32**
HappyBirthday ID	-.38**	-.45**	-.41**	-.41**	-.28**
HappyBirthday KD	-.30**	-.35**	-.30**	-.37**	-.26**
SingTheTune PD	-.37**	-.43**	-.43**	-.48**	-.42**
SingTheTune ID	-.34**	-.42**	-.41**	-.41**	-.39**
MatchTheNote PD	-.08	-.11	-.06	-.18**	-.18*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .05$; ** $p < .01$

7.3.1 Singing and music background components

Simple regression analyses were also performed to examine whether singing and music background components significantly predict task performance. The results are summarised in **Tables 7.11** through **7.16**.

Table 7.11. Summary of Simple Regression Analysis for Personal Singing Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.32	.06	-.35	.13	28.82*	-5.37*
SingTheNote PD	206	-0.33	.10	-.23	.05	11.20*	-3.35*
HappyBirthday PD	207	-0.29	.06	-.35	.12	28.05*	-5.30*
HappyBirthday ID	207	-0.24	.04	-.38	.14	33.48*	-5.79*
HappyBirthday KD	207	-0.25	.06	-.30	.09	19.93*	-4.46*
SingTheTune PD	205	-0.38	.07	-.37	.14	32.67*	-5.72*
SingTheTune ID	205	-0.32	.06	-.34	.11	25.91*	-5.09*
MatchTheNote PD	204	-0.09	.09	-.08	.01	1.20	-1.10

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .001$

Table 7.12. Summary of Simple Regression Analysis for Family Singing Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	<i>R</i> ²	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.44	.06	-.44	.20	48.78*	-6.99*
SingTheNote PD	206	-0.51	.11	-.32	.10	23.08*	-4.80*
HappyBirthday PD	207	-0.38	.06	-.41	.16	40.20*	-6.34*
HappyBirthday ID	207	-0.32	.04	-.45	.21	53.26*	-7.30*
HappyBirthday KD	207	-0.33	.06	-.35	.13	29.32*	-5.42*
SingTheTune PD	205	-0.50	.07	-.43	.19	46.56*	-6.82*
SingTheTune ID	205	-0.44	.07	-.42	.17	42.45*	-6.52*
MatchTheNote PD	204	-0.15	.10	-.11	.01	2.47	-1.57

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

**p* < .001

Table 7.13. Summary of Simple Regression Analysis for Public Singing Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	<i>R</i> ²	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.83	.13	-.42	.18	43.17*	-6.57*
SingTheNote PD	206	-1.02	.21	-.32	.10	23.59*	-4.86*
HappyBirthday PD	207	-0.71	.12	-.38	.15	34.94*	-5.91*
HappyBirthday ID	207	-0.58	.09	-.41	.17	42.50*	-6.52*
HappyBirthday KD	207	-0.57	.12	-.30	.09	20.78*	-4.56*
SingTheTune PD	205	-0.97	.14	-.43	.18	45.23*	-6.73*
SingTheTune ID	205	-0.85	.13	-.41	.17	41.26*	-6.42*
MatchTheNote PD	204	-0.16	.19	-.06	.00	0.72	-0.85

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

**p* < .001

Table 7.14. Summary of Simple Regression Analysis for Music Listening Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	<i>R</i> ²	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.46	.06	-.47	.22	56.36**	-7.51**
SingTheNote PD	206	-0.60	.10	-.38	.15	35.33**	-5.94**
HappyBirthday PD	207	-0.39	.06	-.43	.18	45.79**	-6.77**
HappyBirthday ID	207	-0.29	.04	-.41	.17	42.42**	-6.51**
HappyBirthday KD	207	-0.34	.06	-.37	.14	33.23**	-5.76**
SingTheTune PD	205	-0.54	.07	-.48	.23	60.76**	-7.80**
SingTheTune ID	205	-0.42	.07	-.41	.17	41.06**	-6.41**
MatchTheNote PD	204	-0.24	.09	-.18	.03	7.05*	-2.66*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

p* < .01; *p* < .001

Table 7.15. Summary of Simple Regression Analysis for Instrumental Expertise Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	167	-0.40	.07	-.39	.15	25.23**	-5.46**
SingTheNote PD	168	-0.42	.12	-.27	.07	12.86**	-3.59**
HappyBirthday PD	169	-0.31	.07	-.32	.10	19.39**	-4.40**
HappyBirthday ID	169	-0.20	.06	-.28	.08	13.81**	-3.72**
HappyBirthday KD	169	-0.25	.07	-.26	.07	12.18**	-3.49**
SingTheTune PD	168	-0.49	.08	-.42	.18	35.20**	-5.93**
SingTheTune ID	168	-0.43	.08	-.39	.15	30.08**	-5.48**
MatchTheNote PD	169	-0.25	.19	-.18	.03	5.87*	-2.42*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .05$; ** $p < .001$

All the singing and music background components emerged as significant predictors of singing task measures, accounting for significant proportions of the variance in the task measures. For SINGCOMB, Music Listening accounted for the largest proportion of the variance ($R^2 = 22\%$), followed by Family Singing ($R^2 = 20\%$), Public Singing ($R^2 = 18\%$), Instrumental Expertise ($R^2 = 15\%$), and Personal Singing ($R^2 = 13\%$).

Notably, Music Listening explained a relatively greater proportion of the variance ($R^2 = 14\text{-}23\%$) in the singing task measures compared to the other components (**Table 7.14**). Personal Singing, Family Singing and Public Singing explained 5-14%, 10-21%, and 9-18% of the variances in the singing task measures, respectively (**Tables 7.11 to 7.13**). Instrumental Expertise also explained 7-18% of the variances in the singing task measures (**Table 7.15**); it accounted for relatively greater proportions ($R^2 = 15\text{-}18\%$) of the variance in the measures of Sing The Tune Task as compared to the variance ($R^2 = 7\text{-}10\%$) in the measures of Sing The Note Task and Happy Birthday Singing Task. It is possible that Sing The Tune Task was more influenced by instrumental expertise as compared to other tasks because aural skills constitute an important component of formal music training.

Not surprisingly, for MatchTheNote PD, none of the singing-related background components were significant predictors. Only Music Listening and Instrumental Expertise significantly predicted MatchTheNote PD, both explaining 3% of variance in the measure ($p < .01$ and $p < .05$, respectively).

As the regression analyses for Instrumental Expertise only applied to participants with music training, to examine the influence of formal music training on the task performance of all participants, additional regression analyses were performed with Years of Music Training as the predictor variable. Analyses revealed that Years of Music Training was a significant predictor of performance for all the task measures ($p < .001$), explaining 21% of the variance in SINGCOMB and significant proportions ($R^2 = 11\text{-}20\%$) of the variance in other measures (**Table 7.16**).

Table 7.16. Summary of Simple Regression Analysis for Years of Music Training Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	197	-0.10	.01	-.46	.21	53.00*	-7.28*
SingTheNote PD	198	-0.13	.02	-.40	.16	37.25*	-6.10*
HappyBirthday PD	199	-0.08	.01	-.42	.17	40.95*	-6.40*
HappyBirthday ID	199	-0.05	.01	-.35	.12	26.56*	-5.15*
HappyBirthday KD	199	-0.07	.01	-.36	.13	29.37*	-5.42*
SingTheTune PD	198	-0.10	.02	-.44	.20	47.38*	-6.88*
SingTheTune ID	198	-0.09	.01	-.40	.16	37.26*	-6.10*
MatchTheNote PD	199	-0.09	.02	-.33	.11	24.39*	-4.94*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .001$

7.4 Potential Confounding Variables Influencing Task Performance

7.4.1 Demographic variables: Sex, age, years of education

Independent samples *t*-tests revealed that males generally performed more poorly on all of the transformed task measures (**Table 7.17**). Female participants performed significantly better than male participants on most of the task measures ($p < .05$), except for SingTheTune ID and HappyBirthday KD, both of which also approached significance ($p < .1$). The effect sizes of the significant sex differences were small to medium, however, ranging from .19 to .25.

Table 7.17. Results of *t*-tests and Descriptive Statistics for Task Performances by Males and Females

Task measure	Group						95% CI for Mean Difference		<i>t</i>	df	Sig.	<i>r</i>
	Males			Females								
	<i>M</i>	<i>SD</i>	<i>n</i>	<i>M</i>	<i>SD</i>	<i>n</i>						
SINGCOMB	4.31	0.78	49	3.97	0.80	159	0.08, 0.59	2.59	206	.01	.18	
SingTheNote PD	4.23	1.22	51	3.56	1.28	163	-1.06, -0.26	-3.26	212	.00	.22	
HappyBirthday PD	4.16	0.67	51	3.83	0.76	164	-0.56, -0.09	-2.75	213	.01	.19	
HappyBirthday ID	4.03	0.56	51	3.70	0.54	164	-0.51, -0.16	-3.78	213	.00	.25	
HappyBirthday KD	4.04	0.68	51	3.81	0.77	164	-0.46, 0.01	-1.88	213	.06	.13	
SingTheTune PD	4.38	0.89	49	4.04	0.92	160	0.04, 0.63	2.24	207	.03	.15	
SingTheTune ID	4.38	0.79	49	4.15	0.85	160	-0.04, 0.50	1.70	207	.09	.12	
MatchTheNote PD	3.40	1.21	50	2.76	1.02	161	-0.98, -0.29	-3.67	209	.00	.25	

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score
 Variables with significant task differences are in bold

Simple linear regressions were performed on each task measure with age and years of education. Age was found to be a significant predictor for the MatchTheNote PD. The older the participant, the greater the mean pitch deviation, $\beta = .31$, $t(209) = 4.71$, $p < .01$ (**Table 7.18**). A significant proportion of the variance in this measure was explained by age, as evident from the significant F value ($F(1, 209) = 22.1$) and R^2 effect size ($R^2 = .10$), $p < .001$. Age was not a significant predictor for all the other task measures ($p > .05$). Similarly, Years of Education was not a significant predictor for any of the task measure ($p > .05$; **Table 7.19**).

Table 7.18. Summary of Simple Regression Analysis for Age Predicting Task Performance

	N	B	$SE\ B$	β	R^2	F	t
SINGCOMB	208	0.01	.01	.10	.01	2.00	1.41
SingTheNote PD	214	0.01	.01	.07	.01	1.17	1.08
HappyBirthday PD	215	0.00	.00	.01	.00	0.03	0.18
HappyBirthday ID	215	0.00	.00	.08	.01	1.51	1.23
HappyBirthday KD	215	0.00	.00	.02	.00	0.07	0.27
SingTheTune PD	209	0.01	.01	.13	.02	3.38	1.84
SingTheTune ID	209	0.01	.01	.13	.02	3.50	1.87
MatchTheNote PD	211	0.03	.00	.31	.10	22.10**	4.71**

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

** $p < .01$

Table 7.19. Summary of Simple Regression Analysis for Years of Education Predicting Task Performance

	N	B	$SE\ B$	β	R^2	F	t
SINGCOMB	207	0.00	.02	.01	.00	0.01	0.07
SingTheNote PD	211	-0.03	.04	-.06	.00	0.76	-0.87
HappyBirthday PD	212	0.01	.02	.03	.00	0.13	0.37
HappyBirthday ID	212	0.01	.02	.03	.00	0.17	0.41
HappyBirthday KD	212	0.01	.02	.04	.00	0.39	0.62
SingTheTune PD	208	0.01	.03	.01	.00	0.04	0.19
SingTheTune ID	208	0.00	.02	.01	.00	0.01	0.09
MatchTheNote PD	209	-0.03	.03	-.06	.00	0.75	-0.87

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

$p > .05$ for all measures

7.4.2 Absolute pitch ability

Independent samples *t*-tests showed that self-reported AP possessors achieved significantly better performance than non-AP possessors in SINGCOMB, Happy Birthday Singing Task and Sing The Tune Task. In particular, large effect sizes ($r = .84$ to $.88$) were observed for SINGCOMB and the measures of Happy Birthday Singing Task (**Table 7.20**).

7.4.3 Self-reported abilities and interests in singing and music

Simple regressions revealed that all four self-ratings of abilities and interests were significant predictors of the performance on all of the task measures (**Tables 7.21-7.24**). In general, self-rated abilities explained a greater proportion of the variance in the task performances compared to self-rated interests. Specifically, self-rated singing ability explained 42% of the variance in SINGCOMB, thus suggesting that self-perceived singing ability is a reliable indicator of objective singing ability. Similarly, self-rated music ability explained 41% of the variance in SINGCOMB, whereas self-rated singing and music interests only explained 27% and 23%, respectively. For the Happy Birthday task measures, self-rated singing ability explained 31% to 39% of the variance while self-rated music ability explained 27% to 35% of the variance. Self-rated singing interest also explained a relatively higher proportion ($R^2 = 18$ -25%) of the variance in the Happy Birthday task measures than self-rated music interest ($R^2 = 13$ -16%). For Sing The Tune Task, self-rated singing and music abilities explained substantial proportions ($R^2 = 33$ -39%) of the variance in the measures, while self-rated singing and music interests explained comparatively smaller proportions ($R^2 = 21$ -28%).

Compared to the two melodic singing tasks, self-rated singing and music abilities explained relatively smaller proportions ($R^2 = 29$ -30%) of the variance in SingTheNote PD, whereas self-rated singing and music interests explained an even smaller proportion ($R^2 = 15$ -16%) of the variance.

Table 7.20. Results of *t*-tests and Descriptive Statistics for Task Performances by AP/Non-AP Possessors

Task measure	Group						95% CI for				
	AP possessors			Non-AP possessors			Mean Difference	<i>t</i>	df	Sig.	<i>r</i>
	<i>M</i>	<i>SD</i>	<i>n</i>	<i>M</i>	<i>SD</i>	<i>n</i>					
SINGCOMB	3.32	0.37	8	4.08	0.81	196	-1.09, -0.44	-5.28*	9.91	.00	.86
SingTheNote PD	3.27	0.72	8	3.75	1.31	198	-0.44, 1.40	1.03	204	.30	.07
HappyBirthday PD	3.32	0.30	8	3.93	0.77	199	0.35, 0.87	5.18*	11.25	.00	.84
HappyBirthday ID	3.28	0.20	8	3.80	0.57	199	0.34, 0.70	6.31*	12.15	.00	.88
HappyBirthday KD	3.20	0.28	8	3.89	0.76	199	0.44, 0.94	6.05*	11.60	.00	.87
SingTheTune PD	3.27	0.69	8	4.16	0.92	197	-1.54, -0.24	-2.71	203	.01	.19
SingTheTune ID	3.29	0.51	8	4.23	0.84	197	-1.54, -0.36	-3.18	203	.00	.22
MatchTheNote PD	2.56	1.29	8	2.92	1.09	196	-0.43, 1.13	0.90	202	.37	.06

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

Variables with significant task differences are in bold

*Satterthwaite approximation employed due to unequal group variances.

Table 7.21. Summary of Simple Regression Analysis for Self-Rated Singing Ability Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.31	.03	-.65	.42	146.40**	-12.10**
SingTheNote PD	206	-0.41	.05	-.53	.29	81.19**	-9.01**
HappyBirthday PD	207	-0.28	.03	-.62	.39	128.59**	-11.34**
HappyBirthday ID	207	-0.20	.02	-.60	.35	112.07**	-10.59**
HappyBirthday KD	207	-0.25	.03	-.56	.31	91.30**	-9.56**
SingTheTune PD	205	-0.34	.03	-.62	.39	128.69**	-11.34**
SingTheTune ID	205	-0.29	.03	-.58	.33	101.99**	-10.10**
MatchTheNote PD	204	-0.12	.05	-.18	.03	6.57*	-2.56*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .05$; ** $p < .001$

Table 7.22. Summary of Simple Regression Analysis for Self-Rated Music Ability Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.30	.03	-.64	.41	139.22**	-11.80**
SingTheNote PD	206	-0.42	.05	-.55	.30	87.36**	-9.35**
HappyBirthday PD	207	-0.26	.03	-.59	.35	108.67**	-10.43**
HappyBirthday ID	207	-0.18	.02	-.52	.27	76.56**	-8.75**
HappyBirthday KD	207	-0.24	.03	-.54	.29	82.69**	-9.09**
SingTheTune PD	205	-0.34	.03	-.62	.39	127.45**	-11.29**
SingTheTune ID	205	-0.28	.03	-.57	.33	99.81**	-9.99**
MatchTheNote PD	204	-0.15	.04	-.24	.06	12.20*	-3.49*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .001$; ** $p < .001$

Table 7.23. Summary of Simple Regression Analysis for Self-Rated Singing Interest Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	204	-0.22	.03	-.52	.27	74.84**	-8.65**
SingTheNote PD	206	-0.27	.04	-.39	.16	37.39**	-6.12**
HappyBirthday PD	207	-0.20	.022	-.50	.25	68.98**	-8.31**
HappyBirthday ID	207	-0.15	.02	-.49	.24	63.62**	-7.97**
HappyBirthday KD	207	-0.17	.03	-.43	.18	46.33**	-6.81**
SingTheTune PD	205	-0.25	.03	-.51	.26	69.81**	-8.36**
SingTheTune ID	205	-0.22	.03	-.49	.24	65.50**	-8.09**
MatchTheNote PD	204	-0.09	.04	-.16	.02	5.05*	-2.25*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .05$; ** $p < .001$

Table 7.24. Summary of Simple Regression Analysis for Self-Rated Music Interest Predicting Task Measures

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	204	-.28	.04	-.48	.23	61.05**	-7.81**
SingTheNote PD	206	-.36	.06	-.38	.15	34.59**	-5.88**
HappyBirthday PD	207	-.22	.04	-.40	.16	39.56**	-6.29**
HappyBirthday ID	207	-.16	.03	-.38	.15	34.81**	-5.90**
HappyBirthday KD	207	-.20	.04	-.36	.13	30.96**	-5.56**
SingTheTune PD	205	-.35	.04	-.53	.28	78.74**	-8.87**
SingTheTune ID	205	-.28	.04	-.46	.21	53.04**	-7.28**
MatchTheNote PD	204	-.13	.06	-.16	.03	5.50*	-2.35*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .05$; ** $p < .001$

While the self-rated abilities and interests were also significant predictors of MatchTheNote PD, the proportions of variance explained by the self-ratings for this measure were considerably smaller as compared to the singing tasks. Among all the self-ratings, self-rated music ability explained 6% of the variance in MatchTheNote PD. The other self-ratings, however, only explained 2-3% of the variance for this measure.

7.4.4 Parents' abilities and interests in singing and music

Results showed that the participants' perceptions of their parents' abilities and interests in singing and music were significant predictors of the participants' combined singing score, explaining 9% to 20% of the variance, $p < .001$. From **Table 7.25**, it can be observed that while all the predictors were significant, the perceived abilities and interests of mothers appeared to explain greater proportions (16% to 20%) of the variance in SINGCOMB compared to those of fathers (9% to 16%). For both parents, singing ability explained relatively greater proportions of participants' SINGCOMB, while music interest explained a smaller proportion. The fact that parents' singing abilities were relatively strong predictors of SINGCOMB provide support that singing ability has a heritable component.

Table 7.25. Summary of Simple Regression Analysis for Parents' Interests and Abilities in Singing and Music Predicting SINGCOMB

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
Singing Ability (Mum)	200	-.40	.06	-.45	.20	49.38*	-7.03*
Music Ability (Mum)	206	-.38	.06	-.43	.19	47.30*	-6.88*
Singing Interest (Mum)	204	-.38	.06	-.43	.18	44.85*	-6.70*
Music Interest (Mum)	206	-.35	.06	-.40	.16	39.08*	-6.25*
Singing Ability (Dad)	197	-.34	.06	-.40	.16	35.96*	-6.00*
Music Ability (Dad)	206	-.28	.06	-.34	.11	25.86*	-5.09*
Singing Interest (Dad)	204	-.31	.06	-.37	.14	31.94*	-5.65*
Music Interest (Dad)	206	-.25	.06	-.30	.09	19.73*	-4.44*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .001$

7.4.5 Speech and language characteristics

7.4.5.1 Median speaking fundamental frequency and speech range

Regression analyses revealed that with the exception of HappyBirthday PD and HappyBirthday KD, male median speaking fundamental frequency (f_0) in the tongue-twister task was a significant predictor of performance of the majority of the singing task measures, explaining 8% to 13% of the variance, $p < .05$ (Table 7.26). Specifically, lower median speaking f_0 was associated with larger deviations in the measures. In contrast, for female participants, median speaking f_0 was not a significant predictor of any of the singing task measures (Table 7.27). The findings suggest a link between low median speaking f_0 and low pitch accuracy in singing in male participants.

Table 7.26. Summary of Simple Regression Analysis for Median Speaking Fundamental Frequency Predicting Singing Task Measures of Males

	<i>n</i>	<i>B</i>	<i>SE B</i>	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	48	-0.02	.01	-.33	.11	5.51*	-2.35*
SingTheNote PD	49	-0.03	.01	-.33	.11	5.87*	-2.42*
HappyBirthday PD	49	-0.01	.01	-.19	.04	1.69	-1.30
HappyBirthday ID	49	-0.01	.01	-.29	.08	4.24*	-2.06*
HappyBirthday KD	49	-0.01	.01	-.13	.02	0.78	-0.88
SingTheTune PD	48	-0.02	.01	-.36	.13	6.89*	-2.63*
SingTheTune ID	48	-0.02	.01	-.31	.09	4.79*	-2.19*

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

* $p < .05$

Table 7.27. Summary of Simple Regression Analysis for Median Speaking Fundamental Frequency Predicting Singing Task Measures of Females

	<i>n</i>	B	SE B	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	146	0.00	.00	-.05	.00	0.37	-0.61
SingTheNote PD	146	0.00	.00	-.06	.00	0.47	-0.68
HappyBirthday PD	147	0.00	.00	.01	.00	0.01	0.07
HappyBirthday ID	147	0.00	.00	-.01	.00	0.02	-0.15
HappyBirthday KD	147	0.00	.00	-.03	.00	0.09	-0.30
SingTheTune PD	147	0.00	.00	-.03	.00	0.09	-0.31
SingTheTune ID	147	0.00	.00	-.03	.00	0.16	-0.40

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score
 $p > .05$

On the other hand, unpaced speech range from the tongue twister task was not found to be a significant predictor of any of the singing task measures, $p > .05$ (**Table 7.28**).

Table 7.28. Summary of Simple Regression Analysis for Unpaced Speech Range Predicting Singing Task Measures

	<i>N</i>	B	SE B	β	R^2	<i>F</i>	<i>t</i>
SINGCOMB	194	0.00	0.00	.00	.00	0.00	0.05
SingTheNote PD	195	0.00	0.00	.00	.00	0.00	0.04
HappyBirthday PD	196	0.00	0.00	-.05	.00	0.43	-0.65
HappyBirthday ID	196	0.00	0.00	.05	.00	0.43	0.65
HappyBirthday KD	196	0.00	0.00	-.01	.00	0.01	-0.12
SingTheTune PD	195	0.00	0.00	.00	.00	0.00	0.06
SingTheTune ID	195	0.00	0.00	.04	.00	0.36	0.60

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score
 $*p < .05$

7.4.5.2 Language characteristics

Independent samples *t*-tests revealed that in general, there were no significant differences between tonal language speakers and non-tonal language speakers on the various singing task measures. A significant group difference ($p = .04$) was observed for SingTheTune ID in favour of tonal language speakers, but the effect size was small ($r = .14$; **Table 7.29**). Independent samples *t*-tests comparing monolingual and bilingual participants revealed no significant difference on all the singing task measures. For SingTheTune ID however, there appeared to be a trend ($p = .07$) in favour of bilingual participants (**Table 7.30**).

Table 7.29. Results of *t*-tests and Descriptive Statistics for Task Performances by Tonal/Non-Tonal Language Speakers

Task measure	Group						95% CI for Mean Difference				
	Tonal language speakers			Non-tonal language speakers			<i>t</i>	df	Sig.	<i>r</i>	
	<i>M</i>	<i>SD</i>	<i>n</i>	<i>M</i>	<i>SD</i>	<i>n</i>					
MatchTheNote (PD)	2.87	0.85	25	2.92	1.14	184	-0.42, 0.51	0.19	207	.08	.01
SingTheNote PD	3.61	1.17	25	3.75	1.31	186	-0.40, 0.69	0.53	209	.36	.04
HappyBirthday PD	3.75	0.82	25	3.93	0.75	187	-0.13, 0.50	1.14	210	.25	.08
HappyBirthday ID	3.67	0.52	25	3.80	0.57	187	-0.12, 0.36	1.02	210	.31	.07
HappyBirthday KD	3.68	0.82	25	3.89	0.75	187	-0.10, 0.53	1.33	210	.70	.09
SingTheTune PD	3.83	0.95	24	4.16	0.92	184	-0.73, 0.06	-1.66	206	.10	.11
SingTheTune ID	3.87	0.79	24	4.24	0.84	184	-0.73, -0.02	-2.07	206	.04	.14
SINGCOMB	3.80	0.81	24	4.09	0.81	183	-0.63, 0.06	-1.63	205	.11	.11

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score. Variable with significant task differences is in bold.

Table 7.30. Results of *t*-tests and Descriptive Statistics for Task Performances by Monolingual/ Bilingual Participants

Task measure	Group						95% CI for Mean Difference	<i>t</i>	df	Sig.	<i>r</i>
	Monolingual			Bilingual							
	<i>M</i>	<i>SD</i>	<i>n</i>	<i>M</i>	<i>SD</i>	<i>n</i>					
MatchTheNote PD	2.92	1.14	151	2.90	1.02	58	-0.32, 0.35	0.09	207	0.93	.01
SingTheNote PD	3.73	1.31	153	3.76	1.26	58	-0.42, 0.37	-0.14	209	0.89	.01
HappyBirthday PD	3.92	0.74	153	3.88	0.81	59	-0.19, 0.27	0.33	210	0.74	.02
HappyBirthday ID	3.80	0.58	153	3.72	0.52	59	-0.09, 0.25	0.93	210	0.35	.06
HappyBirthday KD	3.87	0.75	153	3.85	0.78	59	-0.21, 0.25	0.19	210	0.85	.01
SingTheTune PD	4.19	0.91	151	3.97	0.96	57	-0.06, 0.50	1.55	206	0.12	.11
SingTheTune ID	4.27	0.84	151	4.03	0.84	57	-0.02, 0.50	1.84	206	0.07	.13
SINGCOMB	4.09	0.80	150	3.96	0.83	57	-0.13, 0.37	0.97	205	0.33	.07

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

7.4.6 Potential confounds in self-ratings and background components

Independent samples *t*-tests and simple regression analyses were conducted to examine whether demographic factors might have potentially confounded responses to the questionnaire, such as self-rated abilities and interests in singing and music, as well as the singing and music background components identified from the principal components analyses. Results are presented in **Tables 7.31-7.33**.

No significant sex differences were found for the self-ratings, Years of Music Training, Instrumental Expertise, and Public Singing, although a trend towards significance ($p = .052$) was observed for self-rated Singing Interest, where male participants had a lower mean rating for self-rated Singing Interest (**Table 7.31**). Males also had significantly lower means than females for Personal Singing, Family Singing and Music Listening. The effect sizes were small for Music Listening and Personal Singing ($r = .20$), and medium for Family Singing ($r = .29$).

Years of Education emerged as a significant predictor for self-rated Music Interest, Personal Singing, and Family Singing ($p < .05$), explaining 2%, 6% and 3% of the variance in these variables, respectively (**Table 7.32**). The more years of education a participant has, the lower the self-rated Music Interest, Personal Singing and Family Singing components. Age, on the other hand, did not significantly predict any of the questionnaire responses (**Table 7.33**).

Table 7.31. Results of *t*-tests and Descriptive Statistics for the Questionnaire Responses of Males and Females

Questionnaire measure	Group						95% CI for Mean Difference				
	Males			Females				<i>t</i>	df	Sig.	<i>r</i>
	<i>M</i>	<i>SD</i>	<i>n</i>	<i>M</i>	<i>SD</i>	<i>n</i>					
Music Interest	5.64	1.40	50	5.69	1.38	157	-0.28, 0.36	-0.24	205	.81	.02
Music Ability	3.94	1.70	50	4.06	1.71	157	-0.25, 0.39	-0.42	205	.67	.03
Singing Interest	4.34	1.78	50	4.94	1.91	157	0.00, 0.63	-1.95	205	.05	.14
Singing Ability	3.38	1.54	50	3.75	1.71	157	-0.10, 0.54	-1.37	205	.17	.10
Personal Singing	-0.32	1.03	50	0.10	0.83	157	0.14, 0.71	2.98	205	.00	.20
Family Singing	-0.42	0.80	50	0.13	0.77	157	-0.80, -0.30	-4.37	205	.00	.29
Public Singing	0.51	0.43	50	0.52	0.40	157	-0.13, 0.13	0.05	205	.96	.00
Music Listening	-0.30	0.76	50	0.09	0.83	157	0.13, 0.65	2.97	205	.00	.20
Instrumental Expertise	-0.03	0.73	40	0.06	0.76	129	-0.36, 0.17	-0.69	167	.49	.05
Years of Music Training	4.67	4.63	47	4.65	3.78	152	-1.33, 1.30	-0.03	197	.98	.00

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score
 Variables with significant task differences are in bold.

Table 7.32. Summary of Simple Regression Analysis for Years of Education Predicting Questionnaire Responses

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	<i>R</i> ²	<i>F</i>	<i>t</i>	<i>Sig.</i>
Singing Ability	207	-.02	.03	-.06	.00	0.69	-0.83	.41
Music Ability	207	-.01	.03	-.02	.00	0.11	-0.33	.74
Singing Interest	207	-.03	.03	-.08	.01	1.17	-1.08	.28
Music Interest	207	-.05	.03	-.14	.02	3.93*	-1.98*	.05
Personal Singing	207	-.09	.02	-.25	.06	13.05*	-3.61*	.00
Family Singing	207	-.05	.02	-.17	.03	6.05*	-2.46*	.02
Public Singing	207	-.02	.01	-.12	.02	3.11	-1.77	.08
Music Listening	207	-.03	.02	-.09	.01	1.79	-1.34	.18
Instrument Expertise	169	-.01	.02	-.04	.00	0.29	-0.54	.59
Years of Music Training	199	.19	.11	.12	.02	2.96	1.72	.09

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

**p* < .05

Table 7.33. Summary of Simple Regression Analysis for Age Predicting Questionnaire Responses

	<i>N</i>	<i>B</i>	<i>SE B</i>	β	<i>R</i> ²	<i>F</i>	<i>t</i>
Singing Ability	207	.00	.01	.02	.00	0.10	0.31
Music Ability	207	-.00	.01	-.03	.00	0.24	-0.49
Singing Interest	207	.00	.01	.03	.00	0.14	0.38
Music Interest	207	-.01	.01	-.06	.00	0.84	-0.92
Personal Singing	207	-.01	.01	-.07	.01	1.01	-1.01
Family Singing	207	-.01	.01	-.12	.01	2.91	1.60
Public Singing	207	-.00	.00	-.12	.01	1.13	-1.06
Music Listening	207	-.00	.01	-.04	.00	0.29	-0.54
Instrument Expertise	169	-.01	.01	-.16	.03	4.57	2.26
Years of Music Training	199	-.05	.02	-.14	.02	3.76	-1.94

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score

p > .05

7.5 Summary of Key Behavioural Findings

Key behavioural findings presented in this chapter are summarised as follows in point form:

- The majority of the participants performed well on the objective singing and music tasks, as evident from the positively skewed distributions of the continuous measures.
- The most accurately performed tasks (in terms of lower median deviations) were the perceptual and vocal pitch-matching tasks, followed by Happy Birthday Singing Task, and the melody imitation task.
- Opposite trends of task measure proficiency were observed for the two melodic singing tasks. While participants performed better on ID as compared to PD for Happy Birthday Singing Task, for Sing The Tune Task, better performance was observed for PD than ID. This suggests that the participants were focusing on different aspects of the melodies for these two tasks.
- All singing task measures were significantly correlated ($p < .01$). The bivariate correlations of SINGCOMB with the other singing task measures were very high, ranging from $r = .83$ to $.95$, of which the correlations with SingTheTune PD and SingTheTune ID were comparatively higher ($r = .90$ to $.95$). Different measures within the same singing task were also highly correlated ($r = .88$ to $.94$). The significant correlations across the various singing task measures suggest that performance across the tasks reflects general singing ability. Hence, SINGCOMB is a useful combined measure to assess the impact of other variables on general singing ability.
- In terms of the SINGCOMB categorical measure, the incidence of accurate singers (Category 1: < 50 cents deviation) was nearly 50% of the study sample. Approximately 25% of the sample were moderately inaccurate (Category 2: between 50 and 100 cents deviation), while the remaining participants were highly inaccurate singers (Category 3: > 100 cents deviation) (**Table 7.4**).

- Based on self-reported abilities and interests in singing and music, participants of the present study generally reported low levels of perceived singing ability ($M = 3.66$, $SD = 1.68$), and high levels of music interest ($M = 5.68$, $SD = 1.38$).
- MatchTheNote PD was significantly correlated with the singing task measures ($p < .01$). In particular, MatchTheNote PD was most highly correlated with SingTheNote PD and SINGCOMB ($r = .51$), followed by SingTheTune PD and SingTheTune ID ($r = .49-.50$). The correlations with the Happy Birthday task measures were relatively lower ($r = .33-.40$).
- The following variables were found to influence task performance:
 - **Sex:** Female participants performed significantly better than male participants on the majority of singing task measures (except for HappyBirthday KD and SingTheTune ID), with small to medium effect sizes ($r = .15-.25$).
 - **Age:** Age was a significant predictor of MatchTheNote PD task ($R^2 = 10\%$), with older participants being less accurate on the task.
 - **Self-reported AP ability:** Self-reported AP possessors performed significantly better than non-AP possessors in SINGCOMB and the melodic singing tasks (Happy Birthday Singing Task and Sing The Tune Task), with especially large effect sizes for SINGCOMB and the Happy Birthday task measures ($r = .84-.88$).
 - **Self-rated abilities and interests in music and singing:** Self-rated singing and music abilities explained 41-42% of the variance in SINGCOMB, whereas self-rated singing and music interests explained 23-27% of the variance.
 - **Perception of parents' abilities and interests in singing and music:** Perception of parents' abilities and interests in singing and music explained 9-20% of the variance in SINGCOMB. Perceived abilities and interests of mother in singing and music explained greater proportions (16-20%) of the variance in SINGCOMB compared to those of the father (9-16%).

- **Singing and music background components** (Personal Singing, Family Singing, Public Singing, Music Listening, Instrumental Expertise and Years of Music Training): The six background components explained 13-22% of the variance in SINGCOMB. Among them, Music Listening, Years of Music Training and Family Singing explained the largest proportions of the variance (20-22%).
- **Male median speaking frequency:** Median speaking frequency of male participants in the tongue twister recitation task was a significant predictor of the majority of singing task measures, explaining 8% to 13% of the variance.
- **Tonal language:** Tonal language speakers had significantly better performance on SingTheTune ID than non-tonal language speakers, although the effect size was small ($r = .14$).
- The following variables were found to influence self-ratings of abilities and interests and singing and music background components:
 - **Sex:** Female participants had significantly higher means for Personal Singing, Family Singing and Music Listening. The effect sizes for the sex differences were small to moderate ($r = .19-.29$).
 - **Years of Education:** Years of Education was a significant predictor for self-rated Music Interest, Personal Singing and Family Singing ($R^2 = 2-6\%$), whereby participants with more years of education had lower means for these variables.

8

DISCUSSION OF BEHAVIOURAL FINDINGS

This chapter will discuss the key behavioural findings from Chapter 7. Specifically, the singing proficiency of the participants demonstrated in various task measures will be discussed and compared with relevant findings from previous studies. The relationship between self-rated abilities and interests in singing and music and objectively assessed singing ability will also be considered. Finally, the confounding variables that influenced task performance will also be discussed.

8.1 Task Measures

In this sample, the distributions of all of the objective singing task measures were positively skewed and departed from normality. This indicates that the majority of the participants were reasonably proficient at the singing tasks, while a smaller proportion were less accurate. Although a possible explanation for the general proficiency could be that the majority of the participants (85.9%) were musically trained, with over 4 years of music training on average ($M = 4.66$; $SD = 3.98$), similar positively-skewed distributions in singing and music ability were observed in a sample of 50 occasional singers with no formal music training (Berkowska & Dalla Bella, 2013). The similar distributions across studies, therefore, suggest that the current study sample is representative of the general population in terms of singing proficiency. This is also in line with previous studies that have shown that the majority of the general population can sing in tune (Dalla Bella & Berkowska, 2009; Dalla Bella et al., 2007; Pfordresher & Steven, 2007).

In terms of singing proficiency across all task measures (represented by the categorical measure of SINGCOMB), it was demonstrated that nearly half (49%) of the participants

were accurate singers by the 50-cent criterion (i.e., Category 1). Based on the 100-cent criterion (i.e., Category 1 and Category 2), however, the percentage of accurate singers increased to nearly three-quarters (74%) of the sample (**Table 7.4**, p. 194). This indicates that 26% of the participants were deemed inaccurate singers by the 100-cent criterion, which is higher than the 10-15% incidence of inaccurate singers reported by other studies using the same criterion (Dalla Bella & Berkowska, 2009; Dalla Bella et al., 2007; Pfordresher & Brown, 2007). It is possible that the singing tasks used in the current study were more challenging than those in the previous studies, which increased the percentage of inaccurate singers. In particular, participants were least successful on Sing The Tune Task, which in turn detrimentally affected SINGCOMB, since the correlations between SINGCOMB and measures of Sing The Tune Task were comparatively higher than SINGCOMB's correlations with other singing task measures.

Among the singing tasks, Sing The Note Task was the most accurately performed task in terms of median deviation (28.31 cents) and percentage of accurate singers by the 50-cent criterion (Category 1: 66.4%). The mean PD (111 cents) for the entire sample was substantially larger than the median, however, which suggests that the mean PD was skewed upwards by a minority who performed poorly on the task. Other studies using similar vocal pitch-matching tasks have reported mean pitch deviations ranging from 38 to 140 cents for non-musicians, and 17 to 50 cents for musicians (Amir et al., 2003; Berkowska & Dalla Bella, 2013; Hutchins, Larrouy-Maestri, & Peretz, 2014; Hutchins & Peretz, 2012). The mean PD for Sing The Note Task therefore fell within the range of the mean pitch deviation for non-musicians in similar tasks, whereas the median PD for Sing The Note Task was of similar magnitude as the mean pitch deviations for musicians. Notably, similar to Sing The Note Task, Amir et al. (2003) also used sine tones as stimuli and obtained a mean PD of 50 cents for musicians and 130 cents for non-musicians, which were very similar in order of magnitudes with the median PD (28.31) and mean PD (111 cents) of Sing The Note Task, respectively.

For the melodic singing tasks, participants performed better on Happy Birthday Singing Task than Sing The Tune task, especially in terms of ID. The mean and median ID for Happy Birthday Singing Task (52.26 and 40.51 cents, respectively) were comparable to the mean interval deviations reported in other studies investigating proficiency in singing familiar songs, which ranged from approximately 44 to 60 cents for non-

musicians, and 30 to 62 cents for musicians (Berkowska & Dalla Bella, 2013; Dalla Bella et al., 2007; Hutchins et al., 2014; Larrouy-Maestri & Morsomme, 2014). In the only other study which utilised key deviation (referred to as tonal centre deviation) as a measure for singing a familiar song, the mean KD reported by Larrouy-Maestri and Morsomme (2014) for non-musicians singing *Happy Birthday* was 42.33 cents, whereas trained singers had a mean KD of approximately 26 cents. The mean KD ($M = 64.34$ cents) of the current study was therefore higher than the values reported for both non-musicians and trained singers in Larrouy-Maestri and Morsomme (2014), but the median KD obtained in the current study (41.79 cents) was comparable to the mean KD of non-musicians in that study. It is possible that the relatively better key accuracy in Larrouy-Maestri and Morsomme (2014) might be due to the fact that they only included non-musicians who did not make any contour errors in their analyses, whereas in the current study no such provisions were made.

Although the median ID and KD for Happy Birthday Singing Task were similar in magnitude in the current sample, there was greater variability for KD performance as evident from its wider standard deviation. Moreover, the incidence of inaccurate singing for the two measures differed considerably. Using the 100-cent criterion, only approximately 10% of the participants were inaccurate in singing *Happy Birthday* (Category 3) in terms of ID, whereas the estimate of inaccurate singers increased by nearly twofold (18.1%) if KD was considered. This serves to demonstrate the sensitivity of the KD measure in identifying key transposition errors that were otherwise undetected by interval deviation. Apart from ID and KD, the inclusion of pitch deviation (PD) as an additional measure for Happy Birthday Singing Task remained expedient, nonetheless, as it facilitated comparisons with other singing tasks that typically use PD as an accuracy measure.

Based on the 100-cent criterion (Category 3), the incidence of inaccurate singers as defined by PD, ID and KD of Happy Birthday Singing Task ranged from 9.8% to 20.5%, which is in line with the 10% to 20% prevalence of poor-pitch singing in the general population estimated by previous studies (Dalla Bella & Berkowska, 2009; Dalla Bella et al., 2007; Pfordresher & Brown, 2007, 2009; Pfordresher et al., 2010) . However, using the 50-cent criterion (Categories 2 and 3), the percentage of inaccurate

singers defined by the various Happy Birthday task measures was considerably higher, at approximately 40%.

On the other hand, using the 50-cent criterion, an even higher percentage of participants (54.5-62.2%) were inaccurate for Sing The Tune Task, demonstrating this task's higher difficulty level compared to the other singing tasks. Incidentally, the proportion of inaccurate singers for Sing The Tune Task was strikingly close to the percentage of university students (59%) who self-reported that they could not accurately imitate melodies (Pfordresher & Brown, 2007). The mean PD ($M = 97.38$ cents) obtained for Sing The Tune Task was lower than the mean pitch deviations reported for non-musicians in similar tasks imitating four-note and six-note novel melodies ($M = 123.58$ to 126.40 cents) (Berkowska & Dalla Bella, 2013; Pfordresher & Brown, 2007). On the other hand, the median PD for Sing The Tune Task (54.03 cents) was comparable but slightly higher than the mean pitch deviation ($M \approx 40$ cents) for musically-trained participants (mean years of formal music training = 4.65) in another study which used five-note melodic stimuli (Wise & Sloboda, 2008). In particular, the median PD and ID values for Sing The Tune Task (54.03 and 65.82cents, respectively) were also higher than those reported by Berkowska and Dalla Bella (2013), which examined non-musicians' ability to imitate six-note novel melodies (34.4 and 74.4 cents, respectively). The higher median deviations observed in the current study could be due to the longer length (seven notes) of the melodic stimuli, which might have increased the task difficulty and made the task challenging even for participants with prior music training. Wise and Sloboda (2008) had shown that novel melody length negatively impacted singing accuracy. In addition, several studies on pitch memory have demonstrated that melody length has an effect on pitch memory (Boh, Herholz, Lappe, & Pantev, 2011; Kumar et al., 2013). Therefore, using seven-note melodies for Sing The Tune Task possibly imposed a greater memory load and had a greater impact on the accuracy of recall and pitch-matching. Even though the length of the novel melodic stimuli in the current study presumably fell within the average working memory span of seven plus minus two (Miller, 1994), empirical studies have demonstrated that the melodic memory capacity for most people is limited to four different pitches (Boh et al., 2011). However, behavioural and electrophysiological evidence have also indicated that musically trained participants were able to encode tonal sequences with up to 8 different pitches (Boh et al., 2011).

Memory demands have not been considered a major cause for inaccurate singing in some previous studies (e.g., Pfordresher & Brown, 2007, Hutchins & Peretz, 2011), possibly because the novel melodic stimuli used in these studies have not been sufficiently complex to induce memory-related vocal imitation inaccuracies (Hutchins & Peretz, 2012). In the present study, the use of seven-note novel melodies comprising a comprehensive range of interval sizes was likely challenging enough to impact pitch recall and in turn, pitch-matching ability. This was supported by the observation that some participants had problems recalling the correct length of the melodies and either shortened or lengthened the melodies during the task.

As the two melodic singing tasks differentially enlisted the long-term and short-term auditory memory systems, comparison of the performance measures for the two tasks may reveal some important differences concerning how melodic information is encoded and represented in long-term and short-term memory. A comparison of the categorical measures of the two tasks shows that using either the 50-cent or 100-cent criterion, the percentage of participants deemed accurate for HappyBirthday ID was higher than the percentage for HappyBirthday PD, whereas the percentage of accurate participants for SingTheTune PD was higher than that for SingTheTune ID (see **Table 7.4**, p. 194). These results are in line with those of Berkowska and Dalla Bella (2013) when the median ID and PD values (referred to as the relative and absolute pitch accuracy values) of the familiar song (ID: 44.2; PD: 126.4) and novel melody-matching tasks (ID: 74.7; PD: 34.4) were compared.

The opposite effects of proficiency for the two tasks may stem from the different salience of interval information in short-term and long-term memory. It has been demonstrated in several studies that interval information is not readily processed and represented in short-term memory (Dowling, 1978; Dowling & Bartlett, 1981). Instead, increasing evidence shows that novel melodies are likely to be encoded in short-term memory in terms of absolute pitch levels (Attneave & Olson, 1971; Deutsch, 1978; Dowling, 1999), contour (Dowling & Bartlett, 1981) and possibly key (Bartlett & Dowling, 1980). In contrast, interval information is a salient property of melodies in long-term memory, as indicated by several studies (Deutsch, 1972; Dowling & Bartlett, 1981; Dowling, Kwak, & Andrews, 1995; Dowling, Tillman, & Ayers, 2002), as well as the observation that even non-musicians can transpose familiar melodies to other keys

while maintaining the correct intervallic relationships between notes (Attneave & Olson, 1971; Dowling, 1978; Dowling & Fujitani, 1971). The disparity between the salience of interval information in short-term and long-term memory may suggest that interval information takes time and repeated exposure to be consolidated in the memory system (Andrews & Dowling, 1991; Creel & Tumlin, 2012; Patel, 2008).

Animal studies with birds and monkeys have shown that species other than humans tend to encode sounds predominantly in terms of absolute pitch and are generally insensitive to relative pitch cues. In contrast, humans show relative pitch processing ability even from infancy (Chang & Trehub, 1977; Cohen, Thorpe, & Trehub, 1987; Plantinga & Trainor, 2005; Trainor & Trehub, 1992; Trehub, 2001; Trehub, Thorpe, & Morrongiello, 1985; Trehub & Trainor, 1990, 1993; Trehub, Trainor, & Unyk, 1993), suggesting that relative pitch encoding is a more cognitively sophisticated ability than absolute pitch encoding (Honing, 2014; Hulse, Takeuchi, & Braaten, 1992; Izumi, 2001; Plantinga & Trainor, 2005). Although there is evidence that absolute pitch information is also stored in long-term memory (Halpern, 1988; Levitin, 1994), it has also been shown that relative pitch information nonetheless serves as a more prominent cue for melody recognition (Creel & Tumlin, 2012).

In light of these findings, the better retained relative pitch information in long-term memory may explain why participants were more accurate in terms of ID in Happy Birthday Singing Task. On the other hand, the tendency for short-term memory to encode melodic information more strongly in terms of absolute pitch levels may conceivably explain the relatively better PD performance in Sing The Tune Task.

Another possible explanation for these opposite effects in task performance could be that PD and ID were differentially sensitive in the two melodic singing tasks. Participants might have been more accurate in terms of HappyBirthday ID because it was not as sensitive in detecting key transposition error as HappyBirthday PD or KD, as explained previously in **Section 6.3.2** (p. 176). Similarly, the larger SingTheTune ID relative to SingTheTune PD could be due to ID incurring a higher penalty than PD in the event that a participant made pitch errors in the middle of a melody. One example involved an instance where a participant was asked to imitate Tune 5 (**Figure 8.1a**) but inadvertently made a mistake in the penultimate pitch (**Figure 8.1b**). The average

deviation in terms of PD is $\frac{2 \text{ semitones}}{7 \text{ notes}} \approx 29$ cents, whereas the average deviation in terms of ID is $\frac{2+2 \text{ semitones}}{6 \text{ intervals}} \approx 66$ cents. The disparity in the two measures is even greater if a participant made note-switching errors, such as the one shown in **Figure 8.1c**. In terms of PD, the average deviation is $\frac{3+3 \text{ semitones}}{7 \text{ notes}} \approx 85$ cents, whereas for ID, the average deviation becomes $\frac{3+6+3 \text{ semitones}}{6 \text{ intervals}} \approx 200$ cents, which is quite severe for a relatively minor error. It was observed during data processing that these types of errors were not uncommon, therefore it is possible that the difference in computation for these two measures resulted in worse performance for ID in Sing The Tune Task. However, the fact that such errors occurred in Sing The Tune Task may point to a relatively weak representation of relative pitch information in short-term memory compared to the representation of absolute pitch information.



Absolute PD: 0 0 0 0 0 2 0
Average PD: 2/7 ST ≈ 29 cents

Absolute ID 0 0 0 0 2 2
Average ID: 4/6 ST ≈ 66 cents



Absolute PD: 0 0 3 3 0 2 0
Average PD: 6/7 ST ≈ 85 cents

Absolute ID 0 3 6 3 0 0
Average ID: 12/6 ST ≈ 200 cents

Figure 8.1. Illustration of how interval deviation (ID) might incur a greater penalty than pitch deviation (PD) on singing inaccuracies. Fig. 8.1(a) shows the reference melody (Tune 5). Fig. 8.1(b) illustrates a pitch error in the penultimate note. Fig. 8.1(c) illustrates a note switching error (between the 3rd and 4th notes).

Finally, across all tasks, the participants were most proficient in perceptual pitch-matching (MatchTheNote PD). Their performance in perceptual pitch-matching was superior to vocal pitch-matching (SingTheNote PD), although the two pitch-matching tasks were moderately correlated ($r = .51, p < .01$). The sizeable yet non-perfect correlation between perceptual and vocal pitch-matching tasks suggests that accurate vocal pitch-matching is not simply dependent on pitch perception ability. This is consistent with the vocal sensorimotor loop (VSL) described in **Section 4.2.1** (p. 86) which highlights the importance of other functional components such as auditory-motor mapping and motor planning in singing ability.

Several other studies that used both perceptual and vocal pitch-matching tasks have reported similar positive relationship between the two tasks (Amir et al., 2003; Hutchins et al., 2014; Hutchins & Peretz, 2012). In particular, the perceptual pitch-matching task in the present study was similar to the one used in studies by Hutchins and colleagues (Hutchins et al., 2014; Hutchins & Peretz, 2012), albeit in their study, synthesised voice timbre was used. The mean PD for Match The Note Task was considerably higher than the mean deviations reported for both musicians ($M \leq 2$ cents) and non-musicians ($M = 10-13$ cents) in the aforementioned studies by Hutchins and colleagues. Interestingly, the median PD for Match The Note Task (13.76 cents) corresponded well with the mean deviation of non-musicians in those studies. In addition, the mean PD for Match The Note Task was of similar magnitude as the mean pitch deviation ($M = 44$ cents) reported in another perceptual pitch-matching study which used bassoon timbre for the stimuli (Demorest, 2001).

Conceivably, the superior performance of both non-musicians and musicians in the studies by Hutchins and colleagues may be due to the use of synthesised voice timbre, which might sound more familiar to participants than sine tones, thereby enhancing their pitch-matching accuracy. On the other hand, the sine tones used in the current study and the bassoon timbre used in Demorest (2001) might be less familiar to the study participants and hence reduced the mean pitch-matching accuracy in these studies. Another possible explanation could be the difference in age range of the sample. The age range of the participants in Hutchins and Peretz (2012) was 18 to 30, whereas the age range of the current sample was 15 to 80. Age was found to be a significant predictor of MatchTheNote PD performance, where older participants made larger pitch

deviation errors. This could be indicative of an age-related hearing deterioration that affected the older participants' task performance. While the study information clearly stipulated that only individuals with no diagnosed hearing deficits could participate, it was not possible to screen for such deficits in an online study. Further, the online nature of the study made it difficult to prevent user-end error or ensure that the study setting was uniform for all participants. For instance, some participants might have used a laptop touchpad to move the onscreen slider, which could result in less precision compared to using a mouse. The similar order of magnitudes between the current perceptual pitch-matching results and other laboratory-based pitch-matching studies nonetheless supports the viability of online studies for collecting large amount of participant data on such tasks.

In general, it appears that for the majority of the task measures in the current study, the mean values were often in keeping with the mean values reported for non-musicians using similar measures, whereas the median values were similar to the mean values reported for musicians. Conceivably, non-musically trained participants in the current sample might have performed considerably poorer than those with musical training, which caused the mean values of the task measures to be unduly inflated, even though the median values and the highly skewed distributions of the task measures suggest that most of the participants performed well for the objective tasks. Post-hoc analyses were therefore conducted to compare the differences in task performances between musicians and non-musicians in the current sample with those from other studies that used similar tasks and measures. To ensure that the musician and non-musician groups in the current study were matched with those of previous studies, the definitions of musicians and non-musicians from the aforementioned studies were adopted when computing task measure means for the two groups, that is, musicians are those who received seven years of music training or more, and non-musicians as those who received less than a year of formal music training. **Table 8.1** shows a comparison of the task performances by the musicians and non-musicians in the current sample with those from previous studies.

It can be observed from **Table 8.1** that the task measure means of the musician group in the current study corresponded closely with the median values of the overall current study sample. This serves to confirm that formal music training indeed contributed to

the low median values observed across the tasks. In contrast, the non-musician group of the current study appeared to have substantially higher means than the mean values obtained by non-musicians from other studies. This suggests that the non-musicians from the current sample were generally less proficient in the objective tasks than the non-musician samples from similar studies.

Table 8.1. Comparison of Task Performance by Musician and Non-Musicians in Previous Studies and Current Study

Task measures	Previous studies		Current study		
	Non-musicians	Musicians	Non-musicians (<i>n</i> = 33)	Musicians (<i>n</i> = 52)	Overall mean and median (<i>N</i> = 216)
MatchTheNote PD	<i>M</i> = 10-44	<i>M</i> < 2	<i>M</i> = 78.08	<i>M</i> = 20.21	<i>M</i> = 36.52; <i>Mdn</i> = 13.76
SingTheNote PD	<i>M</i> = 38-140	<i>M</i> = 17-50	<i>M</i> = 265.34	<i>M</i> = 39.08	<i>M</i> = 111.00; <i>Mdn</i> = 28.31
HappyBirthday ID	<i>M</i> = 44-60	<i>M</i> = 30-62	<i>M</i> = 73.37	<i>M</i> = 43.30	<i>M</i> = 52.26; <i>Mdn</i> = 40.51
HappyBirthday KD	<i>M</i> ≈ 42	<i>M</i> ≈ 26	<i>M</i> = 99.73	<i>M</i> = 43.03	<i>M</i> = 64.34; <i>Mdn</i> = 41.79
SingTheTune PD	<i>M</i> = 124-126 <i>Mdn</i> ≈ 34.4	<i>M</i> ≈ 40	<i>M</i> = 173.75	<i>M</i> = 48.15	<i>M</i> = 97.38; <i>Mdn</i> = 54.03
SingTheTune ID	<i>M</i> ≈ 40 <i>Mdn</i> ≈ 74.4	-	<i>M</i> = 141.67	<i>M</i> = 60.40	<i>M</i> = 93.00; <i>Mdn</i> = 65.82

Note. Musicians: ≥ 7 years of formal music training; Non-musicians: < 1 year of formal music training; *M*: mean; *Mdn*: median.

8.2 Self-Rated Abilities and Interests in Singing and Music

While the positively skewed distributions of the task measures clearly indicated the generally high performance of participants in the singing and music perception tasks, it is interesting to note from the subjective ratings that the participants generally held conservative perceptions of their own music and singing abilities. This was evident from the mean self-rated singing and music abilities being slightly above and below the midpoint of the 7-point Likert scale (3.66 and 4.03, respectively), while their mean self-rated singing and music interests were considerably higher (4.79 and 5.68, respectively). Interestingly, the mean self-rating for singing ability obtained in this study was very

similar to the ratings of self-declared tone-deaf participants in Wise and Sloboda (2008) when asked to rate their performance on singing tasks using a 7-point Likert scale ($M = 3.69$). The observation that objectively assessed singing ability was better than self-reported singing ability corroborates with past findings showing that most people actually sing better than they believe they can (Dalla Bella et al., 2007; Pfordresher & Brown, 2007).

Regression results showed that all four self-ratings were nonetheless significant predictors of objective singing task performance. In particular, self-rated singing and music abilities were able to explain as much as 41-42% of the variance in SINGCOMB, whereas self-rated singing and music interests explained smaller proportions (27% and 23%, respectively). This suggests that the current sample of participants were relatively reliable in their self-assessments of abilities.

8.3 Confounding Variables Influencing Task Performance

An interesting observation arising from the findings was that female participants performed significantly better than male participants on most of the task measures, even though the effect sizes were small to medium ($r = .15-.25$). These differences in task performance were unlikely to be due to sex differences in formal music training, as there were no significant sex differences for either Instrumental Expertise or Years of Music Training. However, males were observed to have significantly lower scores for Personal Singing, Family Singing and Music Listening than females, which may account for their generally poorer performance in the singing and music tasks. It is possible that lower engagement in music listening and singing activities can have a negative impact on singing ability and music perception.

As expected, the performance of self-reported AP possessors on the music and singing tasks was found to be significantly superior to non-AP possessors, with especially large effect sizes for the Happy Birthday task measures and SINGCOMB ($r = .84$ to $.88$). The facilitation of performance of Happy Birthday Singing Task by AP ability may be explained by the notion that AP is an ability rooted in long-term memory, which enables

the recognition and labelling of pitch height based on internal absolute pitch representations (Levitin, 1999). As Happy Birthday Singing Task appeared to rely more heavily on accessing melodic information from long-term memory, it is possible that the long-term memory representations of absolute pitches conferred an advantage for AP possessors to perform accurately for this task. For instance, the AP possessors may have had an advantage over non-AP possessors in remembering the most optimal key or the ideal starting pitch to sing *Happy Birthday*, which would allow them to successfully navigate the octave leap in the third phrase.

Importantly, participants' estimates of their parents' music and singing interests and abilities also emerged as significant predictors of SINGCOMB. This may be indicative of a potential genetic transmission of singing and music abilities from parents to offspring. It is also possible that parental interests and abilities in music and singing were crucial in shaping a musical home environment, which in turn, influence their children's musical skills, as several studies have demonstrated (Brand, 1986; Ilari, Moura, & Bourscheidt, 2011; McPherson, 2009; Zdzinski, 1996). Although it was not possible to determine whether genes or environment exert a stronger influence on singing ability through simple regression analyses, this could be addressed by subsequent genetic analyses which would disentangle the relative contributions of genetic and environmental components on singing ability. The observation that mothers' ratings explained a greater proportion (16-20%) of SINGCOMB compared to fathers' ratings (9-16%) may also suggest that mothers play a bigger role in creating a musically-rich home environment than fathers. Although gender differences in musical parenting have not been well-researched, the ubiquitous nature of maternal singing across all cultures (Trehub & Schellenberg, 1995; Trehub & Trainor, 1998), and anecdotal accounts of maternal influence on children's musical outcomes indicate that this is an area worthy of further investigation (Petersen, 2012).

While all five components (Personal Singing, Family Singing, Public Singing, Music Listening, Instrumental Expertise) that emerged from the singing and music background questionnaire were significant predictors of the singing task measures, it is of interest that Music Listening and Family Singing accounted for large proportion of the variance in SINGCOMB (20-22%) and also generally explained a greater proportion of each singing task measure than the other components. As these two components comprised

questions mostly pertaining to music listening, music exposure and engagement in singing activities with family members during childhood, this finding may be indicative of the importance of exposure to music and singing during the formative years in shaping singing ability. On the other hand, Instrumental Expertise and Public Singing accounted for 15% and 18% of the variance in SINGCOMB, respectively, while Personal Singing accounted for the least proportion (13%) among all components. In particular, Instrumental Expertise was able to explain a relatively greater proportion of the variance of measures for Sing The Tune Task (15-18%) compared to the measures for the other two singing tasks (7-10%), suggesting that instrumental training is especially advantageous for imitating novel melodies. This suggestion is consistent with the observation that perceiving and imitating novel melodies constitute part of the aural training for musicians.

Evidence from several studies corroborate this finding. Short-term and long-term music training have been demonstrated to enhance the ability to encode melodies and detect deviant tones (Fujioka, Trainor, Ross, Kakigi, & Pantev, 2004; Herholz, Lappe, & Pantev, 2009; Lappe, Herholz, Trainor, & Pantev, 2008; Van Zuijen, Simoens, Paavilainen, Naatanen, & Tervaniemi, 2006; Van Zuijen, Sussman, Winkler, Näätänen, & Tervaniemi, 2005). Pitch imagery acuity was also stronger in participants with longer music training (Janata & Paroo, 2006). A link between auditory working memory and vocal production has been proposed by Schulze and Koelsch (2012), whereby sensorimotor codes that guide vocal production are implicated in the representation and rehearsal of auditory information in working memory. This proposition may serve to explain the influence of short-term pitch memory on the performance of Sing The Tune Task.

Interestingly, Years of Music Training, one of the items that constituted Instrumental Expertise, was able to explain a greater proportion of the variance in SINGCOMB (21%) and all the task measures (11-20%) as compared to Instrumental Expertise (3-18%; **Tables 7.15** and **7.16**; pp. 203-204). This suggests that other constituents of Instrumental Expertise may be less strongly associated with singing task performance than Years of Music Training. For both melodic singing tasks, the influence of Years of Music Training on the PD measures were greater than its effect on the ID measures. This observation is in line with a study which reported that musical experience has a

smaller effect on relative pitch judgments than absolute pitch judgments (Dowling, 1978). Similar to Instrumental Expertise, Years of Music Training explained a relatively greater proportion of the variance of Sing The Tune Task (16-20%) than other singing tasks (12-17%).

Intriguingly, Years of Education was a significant predictor of self-rated Music Interest, Personal Singing and Family Singing, with a negative relationship between Years of Education and these variables. This suggests that participants with more years of education tended to score lower on these variables. The current findings appear to be at odds with past evidence demonstrating significant positive correlations between education level and interest in classical music (McManus & Furnham, 2006), as well as between familial music and singing frequency and academic performance (Maule & Hilpold, 2013). Although Years of Education was a significant predictor, it is worth noting that Years of Education explained only a small proportion of the variance in these variables (2-6%).

Another intriguing finding is that tonal language speakers performed significantly better than non-tonal language speakers in terms of SingTheTune ID, albeit only with a small effect size ($r = .14$). This finding may point to facilitation of relative pitch processing by tonal languages, which is in keeping with past research showing an ethnicity effect for relative pitch processing (Hove et al., 2010).

Also interesting was the finding that the median speaking fundamental frequency (f_0) of male participants in the tongue-twister task was a significant predictor of most of the singing task measures, explaining 8% to 13% of the variance in these measures. Specifically, male participants with lower median speaking f_0 tended to perform less accurately. While the relationship between singing accuracy and speech range or speaking frequency in adults has not been well explored, Trollinger (2003) found that speaking f_0 was a significant predictor of vocal pitch-matching accuracy in pre-schoolers. More investigation is warranted to examine whether male participants with median lower speaking f_0 had a motor control deficit that may have impacted on both their speaking f_0 as well as other singing ability. As lower pitches are typically produced with thicker and more relaxed vocal folds and higher pitches are produced by stretching and increasing the tension on vocal folds, it may be possible that some male participants

with lower speaking f_0 lacked the motor coordination skills to manipulate the tension of their vocal folds effectively to sing in tune. As speech range was not observed to be a significant predictor of singing accuracy in the current sample, it is presumed that the potential issue with controlling the vocal folds' tension have lesser impact on male participants' speaking range than singing range, since singing range is usually much wider and requires more precise control of the vocal folds to produce and sustain a desired pitch.

8.4 Summary of Discussion

On the whole, most participants performed well on the singing and music tasks, as evident from the positively skewed distributions of the continuous measures, which were consistent with findings from previous studies that demonstrate that the majority of the general population can sing in tune. In particular, the mean values of the task measures were considerably larger than the median values, and were mostly comparable to the mean values for non-musicians using similar task measures. On the other hand, the median values of the task measures were generally consistent with the mean values for musicians in previous studies that used similar tasks. This suggests that the large variability and highly skewed distributions observed for the various task measures in the current study are due in part to differences in formal music training. The comparable magnitudes of task measures between current and previous findings demonstrates the viability of running objective singing and music tasks through online programs.

The large significant bivariate correlations of SINGCOMB with the other singing task measures ($r = .83$ to $.95$) demonstrate that SINGCOMB reliably reflects general singing ability across all tasks and is therefore a useful combined measure to assess the impact of other variables on general singing ability. The incidence of inaccurate singers as measured by the SINGCOMB categorical measure was 51% and 26% by the 50-cent and 100-cent criteria, respectively. These estimates of inaccurate singers were much higher than the 10-20% prevalence of poor-pitch singing in the general population estimated by previous studies, even though the majority of the participants (85.9%) in this study had music training. The higher prevalence of inaccurate singers may be due to relatively higher difficulty of the singing tasks in this study, especially for Sing The

Tune Task, where 54.5% to 62.2% of the sample were inaccurate singers by the 50-cent criterion.

Notably, large proportion of variance ($R^2 = 42\%$) in SINGCOMB can be explained by self-reported singing ability, which indicates that participants were relatively reliable in their self-assessment of singing ability, thereby lending credence to the reliability of similar studies that were based on perceived music and singing abilities.

Looking at specific task measures, it was observed that there were opposite trends in behavioural performance for PD and ID measures of the two melodic singing tasks (Happy Birthday Singing Task and Sing The Tune Task). This may be explained by the different manner in which melodic information is encoded in short-term and long-term memory. In long-term memory, melodies are more strongly represented in terms of their relative pitch information, which may have resulted in the superior ID performance for Happy Birthday Singing Task. In short-term memory, interval information appears to be processed secondary to absolute pitch information, which may serve to explain the relatively better PD performance in Sing The Tune Task.

A significant and moderate correlation was observed between Match The Note Task and its vocal counterpart, Sing The Note Task ($r = .51$). This was consistent with evidence from several previous studies that also used perceptual and vocal pitch-matching tasks and found a positive relationship between the two tasks. While the correlation between the two tasks were sizeable, the non-perfect correlation suggests that accurate vocal pitch-matching is not solely dependent on pitch perception ability. This is consistent with the vocal sensorimotor loop (VSL) described in **Section 4.2.1** (p. 86) which highlights the importance of other components such as auditory-motor mapping and motor planning in singing ability.

Several variables were found to influence task performance. In particular, male participants performed significantly worse than female participants on the majority of singing task measures, which could be due to the significantly lower engagement in Personal Singing, Family Singing and Music Listening by male participants. All singing and music background components (Personal Singing, Family Singing, Public Singing, Music Listening, Instrumental Expertise and Years of Music Training) were significant predictors of SINGCOMB, explaining 13-22% of the variance. Among them, Music

Listening, Years of Music Training and Family Singing explained the largest proportions of the variance (20-22%). The finding that Music Listening and Family Singing accounted for a greater proportion of the variance in SINGCOMB supports the importance of familial exposure to singing and music during the formative years in shaping singing ability. Moreover, the observation that Instrumental Expertise explained a relatively greater proportion of the variance in Sing The Tune Task (15-18%) than the other singing tasks (7-10%) is consistent with previous findings demonstrating the enhancement of melody encoding ability, pitch imagery acuity and auditory working memory by music training.

Perception of parents' abilities and interests in singing and music were also significant predictors of SINGCOMB and explained 9-20% of the variance. As the significant relationship between singing ability and perceived abilities and interests of parents might reflect either genetic or environmental influences on singing ability, genetic modelling of the singing data of twins would therefore be beneficial in disentangling the relative contributions of genes and the environment. The genetic findings from the twin analyses are reported in the next chapter.

9

GENETIC FINDINGS

The genetic findings presented in this chapter address the two main aims of the study, namely, to estimate the genetic component of singing ability, and to investigate the genetic bases of environmental components that were associated with singing ability.

9.1 The Genetic Basis of Singing Ability

9.1.1 Intraclass correlations

9.1.1.1 Task measures

Table 9.1 presents the intraclass correlations (ICC) of the MZ and DZ groups for the continuous and categorical measures of the objective tasks (see **Section 6.3** for description of measures, p. 174). All the measures were adjusted for the effects of age and sex via regression to prevent biased estimation of the twin correlations and model parameters.

The MZ twins exhibited considerably higher similarity than the DZ twins on all of the continuous task measures ($r_{MZ} = .63-.82$; $r_{DZ} = -.02-.48$). In particular, the ICCs of the MZ twins were significantly larger than those of the DZ twins for SINGCOMB, SingTheNote PD, HappyBirthday ID, SingTheTune PD and MatchTheNote PD, as demonstrated by the Fisher's r to Z transformation ($p < .01$) for all effects.

As for the categorical measures, r_{MZ} was significantly higher than r_{DZ} for all measures, apart from SingTheTune ID. This indicates that compared to the continuous measures, a greater number of categorical measures showed significant differences in r_{MZ} and r_{DZ} .

Table 9.1. Intraclass Correlations of the MZ and DZ Groups for the Objective Tasks

Task measure	<i>N</i>	<i>r</i> _{MZ}	<i>r</i> _{DZ}	<i>Z</i>
SINGCOMB	100	.82 [.73, .89]	.41 [.11, .64]	3.34**
SINGCOMB (category)	100	.81 [.62, .92]	.43 [.04, .71]	3.09**
SingTheNote PD	106	.71 [.57, .81]	.06 [-.25, .37]	3.92**
SingTheNote PD (category)	106	.83 [.61, .94]	.24 [-.24, .64]	4.47**
HappyBirthday PD	107	.73 [.60, .83]	.48 [.20, .69]	1.94
HappyBirthday PD (category)	107	.78 [.56, .90]	.51 [.11, .78]	2.31*
HappyBirthday ID	107	.69 [.54, .79]	.29 [-.03, .55]	2.63**
HappyBirthday ID (category)	107	.74 [.50, .88]	.08 [-.35, .48]	4.16**
HappyBirthday KD	107	.65 [.48, .76]	.46 [.17, .68]	1.33
HappyBirthday KD (category)	107	.79 [.58, .91]	.41 [.01, .70]	3.04**
SingTheTune PD	101	.74 [.61, .83]	.31 [-.01, .56]	2.92**
SingTheTune PD (category)	101	.72 [.49, .86]	.36 [-.03, .67]	2.46*
SingTheTune ID	101	.66 [.50, .78]	.47 [.17, .68]	1.31
SingTheTune ID (category)	101	.62 [.37, .79]	.36 [-.05, .68]	1.62
MatchTheNote PD	103	.63 [.46, .75]	-.02 [-.34, .30]	3.58**

Note. DZ: Dizygotic twins; ID: Interval deviation; KD: Key deviation; MZ: Monozygotic twins; *N*: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Task measures with category in parentheses refer to the categorical task measures (see Section 6.3.4, p. 181). Values in brackets are the 95% confidence intervals.

Measures where differences between *r*_{MZ} and *r*_{DZ} are statistically significant are shown in bold.

p* < .05; *p* < .01.

9.1.1.2 Self-reported interests and abilities in singing and music

Table 9.2 presents the ICCs for the self-ratings of the MZ and DZ groups.

Table 9.2. Intraclass Correlations of MZ and DZ Groups for Self-Ratings of Abilities and Interests (*N* = 99)

Self-ratings	<i>r</i> _{MZ}	<i>r</i> _{DZ}	<i>Z</i>
Singing Ability	.87 [.77, .93]	.54 [.22, .76]	3.36**
Music Ability	.83 [.72, .90]	.35 [.01, .62]	3.80**
Singing Interest	.76 [.61, .86]	.14 [-.21, .45]	3.95**
Music Interest	.74 [.56, .85]	.10 [-.28, .46]	3.92**

Note. DZ: Dizygotic twins; MZ: Monozygotic twins; *N*: Number of twin pairs

Values in brackets are the 95% confidence intervals.

Measures where differences between *r*_{MZ} and *r*_{DZ} are statistically significant are shown in bold.

***p* < .01.

MZ twins were significantly more alike than DZ twins for self-reported singing ability (*r*_{MZ} = .87; *r*_{DZ} = .54), self-reported music ability (*r*_{MZ} = .83; *r*_{DZ} = .35), and music and singing interests (*r*_{MZ} = .74-.76; *r*_{DZ} = .10-.14). In both MZ and DZ groups, the ICCs for the self-reported abilities were higher than the ICCs for self-reported interests.

Taken together, the MZ group exhibited significantly higher ICCs than the DZ group across a range of variables. These greater similarities between MZ twin pairs relative to DZ twin pairs are indicative of genetic influences. Genetic structural equation modelling (SEM) was thus performed to determine the relative genetic and environmental contributions to the measures with greater precision.

9.1.2 Preliminary testing of the equality of covariances, means and variances

Prior to conducting univariate analyses to test the hypotheses of the first aim, preliminary testing of the equality of covariances between sexes of the same zygosity (i.e., between MZF and MZM; between DZF, DZM and DZO) were tested for all the objective singing and music measures and the self-ratings of interests and abilities. In addition, equality of means and variances within twin pairs and across zygosity (i.e., between Twin 1 and Twin 2; between MZ and DZ) were also tested for the continuous task measures. For ordinal variables such as the categorical measures of the singing tasks and self-rated interests and abilities, equality of thresholds were tested instead of equality of means and variances. Effects of age and sex on the variables were adjusted via regression.

9.1.2.1 Testing equality of covariances between sexes of the same zygosity

The likelihood ratio chi-square values for the tests of equality of covariances are presented in **Table 9.3**. The detailed fit statistics are available in **Appendices E-1** (p. 379), **E-3** (p. 381), and **E-5** (p. 383).

For the continuous task measures and the self ratings, covariances of MZF and MZM twin pairs could be equated without significant deterioration of fit, as could the covariances of the DZF, DZM and DZO twin pairs. This indicates the absence of quantitative and qualitative sex differences, thus supporting subsequent genetic analyses for these variables to be performed using one MZ group and one DZ group.

Table 9.3. Likelihood Ratio Chi-Square Values ($\Delta\chi^2$) for Tests of Equality of Covariances

Variables	N	Equality of Covariances Between		
		MZF & MZM	MZF & MZM; DZF & DZM	MZF & MZM; DZF, DZM & DZO
SINGCOMB	100	0.01	0.08	0.00
SINGCOMB (category)	100	0.01	0.18	0.00
SingTheNote PD	106	0.06	0.51	0.25
SingTheNote PD (category)	106	0.09	0.86	2.04
HappyBirthday PD	107	0.79	0.12	0.16
HappyBirthday PD (category)	107	4.48*	1.05	0.27
HappyBirthday ID	107	0.04	0.35	0.09
HappyBirthday ID (category)	107	1.73	0.07	1.29
HappyBirthday KD	107	2.58	0.52	0.12
HappyBirthday KD (category)	107	4.64*	0.36	0.01
SingTheTune PD	101	0.05	1.58	0.00
SingTheNote PD (category)	101	0.09	0.86	2.04
SingTheTune ID	101	0.04	0.02	0.01
SingTheTune PD (category)	101	1.00	0.02	0.47
MatchTheNote PD	103	0.14	0.01	0.01
Singing Ability	99	1.16	0.88	1.44
Music Ability	99	0.07	1.34	1.22
Singing Interest	99	0.31	0.87	0.71
Music Interest	99	1.61	0.05	2.22

Note. DZF: Dizygotic female twins; DZM: Dizygotic male twins; DZO: Dizygotic opposite sex twins;

ID: Interval deviation; KD: Key deviation; MZF: Monozygotic female twins; MZM: Monozygotic male twins

N: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Task measures with category in parentheses refer to the categorical task measures (see Section 6.3.4, p. 181).

* $p < .05$.

For the singing task accuracy categories, there was significant deterioration of fit for HappyBirthday PD and HappyBirthday KD when equating the covariances of MZF and MZM twin pairs ($p = 0.03$). However, given the multiple comparisons made (3 comparisons per measure), the adjusted p value after applying Bonferroni correction was $p = \frac{0.05}{3} \approx 0.017$. In other words, if the adjusted p value was considered, there would not be a significant deterioration of fit for the two categorical measures. As the covariances could be equated between sexes of the same zygosity for most of the variables, quantitative and qualitative sex limitation effects were therefore not modelled, and the genetic modelling for each variable was conducted with one MZ group and one DZ group.

9.1.2.2 Testing equality of means and variances or equality of thresholds within twin pairs and across zygositys

The likelihood ratio chi-square values for the tests of equality of means and variances and equality of thresholds are presented in **Table 9.4** and **Table 9.5**, respectively. The detailed fit statistics are available in **Tables E-2** (p. 380), **E-4** (p. 382), and **E-6** (p. 384) in **Appendix E**.

Table 9.4. Likelihood Ratio Chi-Square Values ($\Delta\chi^2$) for Tests of Equality of Means and Variances for Continuous Variables

Variables	<i>N</i>	Equality of means across twin order	Equality of means & variances across twin order	Equality of means & variances across zygositys
SINGCOMB	100	0.61	0.70	1.82
SingTheNote PD	106	2.18	0.42	0.47
HappyBirthday PD	107	1.14	0.55	2.15
HappyBirthday ID	107	0.93	3.03	2.76
HappyBirthday KD	107	0.06	3.18	3.16
SingTheTune PD	101	0.73	1.46	2.16
SingTheTune ID	101	0.90	2.33	1.51
MatchTheNote PD	103	0.59	0.33	0.07

Note. ID: Interval deviation; KD: Key deviation; *N*: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.
 $p > .05$.

Table 9.5. Likelihood Ratio Chi-Square Values ($\Delta\chi^2$) for Tests of Equality of Thresholds for Ordinal Variables

Variables	<i>N</i>	Equality of thresholds across twin order	Equality of thresholds across zygositys
SINGCOMB (category)	100	1.70	1.38
SingTheNote PD (category)	106	7.95	0.42
HappyBirthday PD (category)	107	3.21	3.11
HappyBirthday ID (category)	107	4.30	2.20
HappyBirthday KD (category)	107	2.24	2.22
SingTheTune PD (category)	101	3.30	1.73
SingTheTune ID (category)	101	2.18	1.07
Singing Ability	99	17.63	6.34
Music Ability	99	15.97	7.42
Singing Interest	99	6.21	7.07
Music Interest	99	19.45	6.75

Note. ID: Interval deviation; KD: Key deviation; *N*: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Task measures with category in parentheses refer to the categorical task measures (see Section 6.3.4, p. 181).

$p > .05$.

No significant deterioration of model fit was observed for any of the continuous or ordinal variables when means and variances or thresholds were equated within twin pairs and across zygosity. Univariate genetic analyses were thus performed on all variables.

9.1.3 Univariate genetic analyses

As the small sample size of the current twin study offered little statistical power, this may potentially lead to biased heritability estimates in the reduced models, especially for the ordinal measures (Medland & Hatemi, 2009; Sullivan & Eaves, 2002). In view of this limitation, only full ACE model results will be discussed.

9.1.3.1 Task measures

The parameter estimates derived from the univariate genetic modelling performed on the continuous and categorical task measures are shown in **Table 9.6**. Effects of age and sex were adjusted via regression. The detailed fit statistics are presented in **Tables E-9 and E-10** in **Appendix E** (pp. 387-388).

Table 9.6 shows that apart from HappyBirthday KD and SingTheTune ID, all the other continuous task measures had significant heritability estimates (as shown by confidence intervals that excluded zero) of moderate to large magnitudes, and negligible to moderate common environmental influences ($A = 44\text{-}71\%$, $C = 0\text{-}29\%$). Unique environmental influences were significant for all measures ($E = 19\text{-}48\%$).

In particular, the additive genetic influences for SINGCOMB were large, explaining 69% of the variance, while common and unique environmental influences only accounted for 11% and 19% of the variance, respectively.

The heritability estimates for SingTheNote PD, SingTheTune PD and HappyBirthday ID were similarly high ($A = 68\text{-}71\%$). Interestingly, the estimated heritabilities for different measures of the same singing task tended to vary considerably. For Happy Birthday Singing Task, additive genetic influences on HappyBirthday ID were considerably greater ($A = 68\%$) than those on HappyBirthday PD ($A = 44\%$) and

HappyBirthday KD ($A = 26\%$). As for Sing The Tune Task, SingTheTune PD had a significant and substantial additive genetic component ($A = 71\%$) whereas SingTheTune ID had a moderate heritability estimate ($A = 28\%$). As mentioned earlier, the heritability estimates of HappyBirthday KD and SingTheTune ID did not reach statistical significance.

A large genetic component ($A = 60\%$) was also estimated for perceptual pitch-matching (MatchTheNote PD). For both perceptual and vocal pitch-matching (i.e., Match The Note Task and Sing The Note Task), the confidence intervals of the heritability estimates did not overlap with those of the common environment estimates. This supports the prevailing importance of additive genetic influences compared to environmental influences in explaining the variance observed for these two tasks.

Table 9.6. Results of Univariate Genetic Modelling Showing Genetic (A), Common Environmental (C), and Unique Environmental (E) Influences on Continuous and Categorical Measures of Singing and Music Tasks

Task Measure	N	A	C	E
SINGCOMB	100	.69 [.27, .87]	.11 [.00, .52]	.19 [.13, .29]
SINGCOMB (category)	100	.70 [.04, .90]	.09 [.00, .67]	.21 [.10, .40]
SingTheNote PD	106	.69 [.54, .79]	.00 [.00, .24]	.31 [.21, .46]
SingTheNote PD (category)	106	.79 [.19, .91]	.00 [.00, .52]	.21 [.09, .44]
HappyBirthday PD	107	.44 [.11, .80]	.29 [.00, .65]	.28 [.19, .40]
HappyBirthday PD (category)	107	.59 [.00, .90]	.20 [.00, .75]	.21 [.09, .42]
HappyBirthday ID	107	.68 [.27, .78]	.00 [.00, .38]	.32 [.22, .46]
HappyBirthday ID (category)	107	.72 [.29, .87]	.00 [.00, .34]	.28 [.13, .53]
HappyBirthday KD	107	.26 [.00, .72]	.37 [.00, .68]	.37 [.26, .53]
HappyBirthday KD (category)	107	.72 [.03, .90]	.06 [.00, .67]	.22 [.10, .42]
SingTheTune PD	101	.71 [.31, .80]	.01 [.00, .50]	.29 [.20, .42]
SingTheTune PD (category)	101	.63 [.00, .84]	.07 [.00, .69]	.30 [.16, .53]
SingTheTune ID	101	.28 [.00, .73]	.36 [.00, .69]	.36 [.25, .52]
SingTheTune ID (category)	101	.57 [.00, .79]	.05 [.00, .64]	.37 [.21, .63]
MatchTheNote PD	103	.60 [.34, .74]	.00 [.00, .20]	.40 [.26, .59]

Note. ID: Interval deviation; KD: Key deviation; N : Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score. Task measures with category in parentheses refer to the categorical task measures (see Section 6.3.4, p. 181).

Values in brackets are the 95% confidence intervals.

Significant parameter estimates (whose interval values do not pass through zero) are shown in bold.

A comparison of the *ACE* estimates of the continuous task measures (**Table 9.6**) and the corresponding categorical measures showed that the heritability estimates for the categorical measures were generally higher than the continuous measures (apart from SingTheTune PD), albeit with wider confidence intervals due to reduced statistical power for ordinal measures. Nonetheless, SingTheNote PD, HappyBirthday ID, HappyBirthday KD and SINGCOMB had non-zero-crossing confidence intervals for their heritability estimates, indicating significant genetic components.

The relative sizes of genetic influences across tasks were generally consistent between the continuous and categorical singing task measures. In particular, both the continuous and categorical measures for SINGCOMB yielded similar heritability estimates ($A = 69\text{--}70\%$). In contrast, the heritability estimate for HappyBirthday KD (category) was substantially higher ($A = 72\%$) than the corresponding continuous HappyBirthday KD ($A = 26\%$). SingTheTune ID (category) also had a larger additive genetic component ($A = 57\%$) than the continuous measure of SingTheTune ID ($A = 28\%$). Contrastingly, SingTheTune PD (category) had a smaller genetic component ($A = 63\%$) than SingTheTune PD ($A = 71\%$).

9.1.3.2 Self-reported interests and abilities in music and singing

The estimates from the full *ACE* models of the self-ratings are shown in **Table 9.7**. Effects of age and sex were adjusted via regression. The detailed fit statistics are presented in **Table E-11** in **Appendix E** (p. 389).

Table 9.7. Results of Univariate Genetic Modelling Showing Genetic (*A*) Common Environmental (*C*), and Unique Environmental (*E*) Influences on Self-Rated Abilities and Interests in Music and Singing ($N = 99$)

Self-rating	<i>A</i>	<i>C</i>	<i>E</i>
Singing Ability	.72 [.27, .91]	.13 [.00, .56]	.15 [.09, .25]
Music Ability	.81 [.40, .88]	.00 [.00, .39]	.19 [.12, .31]
Music Interest	.65 [.15, .78]	.00 [.00, .45]	.35 [.22, .54]
Singing Interest	.72 [.35, .95]	.00 [.00, .33]	.28 [.05, .44]

Note. Values in brackets are the 95% confidence intervals.

Significant parameter estimates (whose interval values do not pass through zero) are shown in bold.

A large genetic component was estimated for self-rated singing ability ($A = 72\%$), with low common and unique environmental influences ($C = 13\%$; $E = 15\%$). Similar heritability was estimated for self-rated singing interest ($A = 72\%$), with the latter having a negligible common environmental component.

Self-rated music ability had the highest heritability estimate of all four self-ratings ($A = 81\%$) while self-rated music interest had a relatively lower heritability than the other three self-ratings ($A = 65\%$). Nonetheless, for all four self-ratings, both additive genetic influences as well as unique environmental influences were significant, as evident from the confidence intervals that did not contain zero. Common environmental influences (C) did not reach statistical significance for any of the variables. In particular, the 95% confidence intervals of A and C did not overlap for self-rated singing interest and music ability, highlighting the importance of additive genetic influences for these two variables.

9.2 The Genetic Bases of Environmental Components Associated with Singing Ability

To investigate the genetic basis of environmental components associated with singing ability, the five singing and music background components (i.e., Personal Singing, Family Singing, Public Singing, Music Listening, and Instrumental Expertise) were examined. As Instrumental Expertise only applied to participants with music training, non-musically trained participants were excluded from the genetic analyses performed on this component. In view of this, Years of Music Training (which was collected for both the musically and non-musically trained participants) was also examined in the genetic analyses, serving as a proxy for Instrumental Expertise.

9.2.1 Intraclass correlations of environmental components

Table 9.8 presents the age-and sex-corrected ICCs for the singing and music background components for the MZ and DZ groups.

Table 9.8. Intraclass Correlations of MZ and DZ Groups for Singing and Music Background Components

Components	<i>N</i>	<i>r</i> _{MZ}	<i>r</i> _{DZ}	<i>Z</i>
Personal Singing	99	.53 [.33, .69]	.43 [.13, .66]	0.60
Family Singing	99	.63 [.45, .76]	.65 [.42, .80]	-0.16
Public Singing	99	.72 [.57, .82]	.25 [-.09, .54]	3.01**
Music Listening	99	.64 [.46, .76]	.54 [.26, .73]	0.71
Instrument Expertise	74	.72 [.55, .83]	.19 [-.19, .51]	2.82**
Years of Music Training	106	.86 [.78, .92]	.55 [.28, .74]	3.04**

Note. Values in brackets are the 95% confidence intervals.

Measures where differences between *r*_{MZ} and *r*_{DZ} are statistically significant are shown in bold.

***p* < .01.

MZ twins were significantly more alike than DZ twins for Years of Music Training, Instrumental Expertise, and Public Singing (*p* < .01; *r*_{MZ} = .72-.86; *r*_{DZ} = .19-.55), as demonstrated by the significant *Z* scores derived from Fisher's *r* to *Z* transformation. This indicates that these variables were likely to have sizeable genetic influences. For Music Listening and Personal Singing, MZ twins were also more alike than DZ twins, but to a degree that did not reach statistical significance (*r*_{MZ} = .53-.64; *r*_{DZ} = .43-.54). Interestingly, MZ twins and DZ twins exhibited comparable similarity in Family Singing (*r*_{MZ} = .63; *r*_{DZ} = .65), which suggested that a negligible genetic component could be expected for this component.

9.2.2 Preliminary testing of the equality of covariances, means and variances

Prior to performing univariate genetic modelling on the environmental components, preliminary testing of the equality of covariances between sexes of the same zygosity (i.e., between MZF and MZM; between DZF, DZM and DZO) were conducted. In addition, equality of means and variances within twin pairs and across zygosity (i.e., between Twin 1 and Twin 2; between MZ and DZ) were also tested for the environmental components. Effects of age and sex were adjusted via regression.

9.2.2.1 Testing equality of covariances across sexes within the same zygosity

The likelihood ratio chi-square values for the tests of equality of covariances are presented in **Table 9.9**. The detailed fit statistics are available in **Table E-7** in **Appendix E** (p. 385).

For all the environmental components, covariances of MZF and MZM twin pairs could be equated without significant deterioration of fit, as could the covariances of the DZF, DZM and DZO twin pairs. This indicates the absence of quantitative and qualitative sex differences, supporting subsequent genetic analyses for these variables to be performed using one MZ group and one DZ group.

Table 9.9. Likelihood Ratio Chi-Square Values ($\Delta\chi^2$) for Tests Concerning Equality of Covariances of the Environmental Components

Variables	N	Equality of Covariances Between		
		MZF & MZM	MZF & MZM; DZF & DZM	MZF & MZM; DZF, DZM & DZO
Personal Singing	99	0.76	0.17	0.16
Family Singing	99	1.53	1.00	0.10
Public Singing	99	0.01	0.47	2.06
Music Listening	99	3.45	0.98	0.58
Instrumental Expertise	74	0.00	0.64	1.57
Years of Music Training	106	1.23	1.41	0.98

Note. DZF: Dizygotic female twins; DZM: Dizygotic male twins; DZO: Dizygotic opposite sex twins;
MZF: Monozygotic females; MZM: Monozygotic males; N: Number of twin pairs
 $p > .05$.

9.2.2.2 Testing equality of means and variances or equality of thresholds within twin pairs and across zygositys

The likelihood ratio chi-square values for the tests of equality of means and variances of the environmental components are presented in **Table 9.10**. The detailed fit statistics are presented in **Table E-8** in **Appendix E** (p. 386). The means and variances of all the environmental components could be equated within twin pairs and across zygositys without significant deterioration of fit, thus indicating that all the preliminary conditions were fulfilled and univariate genetic analyses could be conducted on all the variables.

Table 9.10. Likelihood Ratio Chi-Square Values ($\Delta\chi^2$) for Tests Concerning Equality of Means and Variances of the Environmental Components

Variables	<i>N</i>	Equality of means across twin order	Equality of means & variances across twin order	Equality of means & variances across zygositys
Personal Singing	99	3.04	0.37	4.42
Family Singing	99	1.22	0.06	1.61
Public Singing	99	4.87	0.44	5.92
Music Listening	99	3.63	0.10	0.45
Instrumental Expertise	74	5.29	3.89	3.17
Years of Music Training	106	4.70	1.87	2.04

Note. *N*: Number of twin pairs. $p > .05$.

9.2.3 Univariate genetic analyses of environmental components

The estimates from the full ACE models for the singing and music background components are shown in **Table 9.11**. Effects of age and sex were adjusted via regression. The detailed fit statistics are presented in **Table E-12** in **Appendix E** (p. 390).

Table 9.11. Results of Univariate Genetic Modelling Showing Additive Genetic (*A*), Common Environmental (*C*), and Unique Environmental (*E*) Influences on Music and Singing Background Components

Variables	<i>N</i>	<i>A</i>	<i>C</i>	<i>E</i>
Personal Singing	99	.33 [.00, .69]	.23 [.00, .60]	.44 [.30, .64]
Family Singing	99	.00 [.00, .40]	.63 [.25, .74]	.37 [.26, .50]
Public Singing	99	.66 [.09, .78]	.03 [.00, .55]	.32 [.22, .46]
Music Listening	99	.14 [.00, .69]	.49 [.00, .71]	.38 [.26, .53]
Instrumental Expertise	74	.68 [.20, .80]	.00 [.00, .44]	.32 [.20, .48]
Years of Music Training	106	.46 [.14, .88]	.38 [.00, .69]	.15 [.10, .23]

Note. Values in brackets are the 95% confidence intervals. Significant parameter estimates (whose interval values do not pass through zero) are shown in bold.

The heritability estimates of the singing and music background components were wide ranging: Family Singing has negligible genetic influences ($A = 0\%$), Music Listening has a low heritability estimate ($A = 14\%$), Personal Singing and Years of Music Training have moderate estimates ($A = 33\%$ and 46%), and Public Singing and Instrumental Expertise have substantial genetic influences ($A = 66\%$ and 68%). Among

the variables, only the heritability estimates of Public Singing, Instrumental Expertise and Years of Music Training reached statistical significance, as demonstrated by the confidence intervals shown in **Table 9.11**. While the common environmental influences were minimal for Public Singing and Instrumental Expertise, the variances in Music Listening and Family Singing were largely explained this ($C = 49\%$ and 63% , respectively). In particular, Family Singing was the only variable with a significant common environmental component.

9.2.4 Bivariate genetic analyses of singing ability and environmental components

Bivariate genetic analyses were conducted to examine the relationship between each singing task measure and each environmental component associated with singing ability. The bivariate model-fitting results for the preliminary tests of equality of means and variances within and across twins and zygosity are presented in **Tables E-14 to E-19 of Appendix E** (pp. 392-397). For the bivariate model between Instrumental Expertise and HappyBirthday ID, there was significant deterioration of fit from the saturated bivariate model when means and variances were equated across MZ and DZ ($p = .04$; see **Table E-14 in Appendix E**, p. 392). However, given the multiple comparisons made (3 comparisons per measure), the adjusted p value after applying Bonferroni correction was $p = \frac{0.05}{3} \approx 0.017$. In other words, if the adjusted p value was considered, there would not be a significant deterioration of fit for this bivariate model. Bivariate genetic analyses were therefore performed to investigate the association between each singing task measure and environmental component.

Results of bivariate genetic analyses testing the correlations between every music and singing background component and the task measures are shown in **Tables 9.12 through 9.23**. For each component, the table outlining the contribution of shared additive genetic, common environmental and unique environmental influences to the association between the component and the task measures is presented first, followed by the table detailing the bivariate model fitting results. As evident from the wide confidence intervals of the genetic and environmental correlations presented, the small sample size of the present study lacked the power to determine the magnitudes of these correlations with greater precision. In view of this, the reporting and the subsequent interpretation of

the bivariate genetic results will place greater emphasis on the statistical significance rather than the magnitude of the genetic and environmental correlations.

As Instrumental Expertise and Years of Music Training were of direct relevance to the hypotheses relating to Aim 2, the bivariate modelling findings related to these two components are presented first, followed by the other four components.

9.2.4.1 Instrumental Expertise and the objective task measures

Notably, Instrumental Expertise had significant additive genetic correlations with all of the singing task measures as well as MatchTheNote PD (**Table 9.12**). Specifically, the correlations due to additive genetic influences between Instrumental Expertise and the task measures ranged from **-.28** (SingTheNotePD and MatchTheNote PD) to **-.52** (SingTheTune PD), and were observed to predominantly account for the phenotypic correlations.

Table 9.12. Proportions of the Phenotypic Correlations between Instrumental Expertise and the Objective Task Measures due to *A*, *C* and *E*

Task Measure	<i>N</i>	Phenotypic correlation			
		Due to Additive Genetic (<i>A</i>)	Due to Common Environment (<i>C</i>)	Due to Unique Environment (<i>E</i>)	Total
SINGCOMB	72	-.50 [-.67, -.17]	.08 [-.24, .22]	.00 [-.08, .07]	-.42**
SingTheNote PD	73	-.28 [-.44, -.09]	.00 [-.19, .16]	-.04 [-.14, .04]	-.32**
HappyBirthday PD	74	-.47 [-.63, -.13]	.08 [-.25, .23]	.03 [-.06, .11]	-.36**
HappyBirthday ID	74	-.30 [-.55, -.01]	.03 [-.23, .22]	-.03 [-.14, .07]	-.30**
HappyBirthday KD	74	-.44 [-.59, -.15]	.09 [-.20, .23]	.06 [-.03, .15]	-.29**
SingTheTune PD	73	-.52 [-.67, -.18]	.07 [-.24, .19]	.01 [-.08, .09]	-.44**
SingTheTune ID	73	-.49 [-.63, -.19]	.07 [-.22, .19]	.01 [-.08, .09]	-.41**
MatchTheNote PD	74	-.28 [-.49, -.04]	.00 [-.19, .15]	.02 [-.07, .11]	-.26*

Note. ID: Interval deviation; KD: Key deviation; *N*: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

* $p < .05$; ** $p < .01$.

In addition, reduced bivariate models which constrained additive genetic correlations to zero all resulted in significant worsening of model fit when compared to the full bivariate models (**Table 9.13**), thereby demonstrating the central role of shared additive genetic influences in explaining the associations between Instrumental Expertise and the

task measures. In contrast, both common and unique environmental correlations were not statistically significant.

Table 9.13. Bivariate Model-Fitting Results for the Associations between Instrumental Expertise and the Objective Task Measures

Associated trait	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	ACE	15	738.77	362	14.77	-	-	-	-
	$r_A = 0$	14	747.79	363	21.79	9.01	1	0.00**	ACE
	$r_C = 0$	14	739.12	363	13.12	0.35	1	0.56	ACE
	$r_E = 0$	14	738.79	363	12.79	0.01	1	0.91	ACE
SingTheNote PD	ACE	15	996.56	368	260.56	-	-	-	-
	$r_A = 0$	14	1001.51	369	263.51	4.95	1	0.03*	ACE
	$r_C = 0$	14	996.56	369	258.56	0.00	1	1.00	ACE
	$r_E = 0$	14	997.73	369	259.73	1.17	1	0.28	ACE
HappyBirthday PD	ACE	15	744.41	369	6.41	-	-	-	-
	$r_A = 0$	14	751.95	370	11.95	7.54	1	0.01*	ACE
	$r_C = 0$	14	744.67	370	4.67	0.26	1	0.61	ACE
	$r_E = 0$	14	744.90	370	4.90	0.49	1	0.48	ACE
HappyBirthday ID	ACE	15	639.60	369	-98.40	-	-	-	-
	$r_A = 0$	14	643.57	370	-96.43	3.97	1	0.05*	ACE
	$r_C = 0$	14	639.68	370	-100.32	0.08	1	0.77	ACE
	$r_E = 0$	14	640.06	370	-99.94	0.46	1	0.50	ACE
HappyBirthday KD	ACE	15	765.87	369	27.87	-	-	-	-
	$r_A = 0$	14	773.08	370	33.08	7.21	1	0.01*	ACE
	$r_C = 0$	14	766.36	370	26.36	0.49	1	0.48	ACE
	$r_E = 0$	14	767.74	370	27.74	1.88	1	0.17	ACE
SingTheTune PD	ACE	15	820.15	363	94.15	-	-	-	-
	$r_A = 0$	14	829.18	364	101.18	9.03	1	0.00**	ACE
	$r_C = 0$	14	820.48	364	92.48	0.33	1	0.56	ACE
	$r_E = 0$	14	820.16	364	92.16	0.02	1	0.90	ACE
SingTheTune ID	ACE	15	791.04	363	65.04	-	-	-	-
	$r_A = 0$	14	799.95	364	71.95	8.92	1	0.00**	ACE
	$r_C = 0$	14	791.33	364	63.33	0.29	1	0.59	ACE
	$r_E = 0$	14	791.13	364	63.13	0.09	1	0.77	ACE
MatchTheNote PD	ACE	15	937.15	365	207.15	-	-	-	-
	$r_A = 0$	14	942.25	366	210.25	5.10	1	0.02*	ACE
	$r_C = 0$	14	937.15	366	205.15	0.00	1	1.00	ACE
	$r_E = 0$	14	937.34	366	205.34	0.18	1	0.67	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$; ** $p < .01$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

9.2.4.2 Years of Music Training and the objective task measures

Similar to Instrumental Expertise, Years of Music Training also had significant additive genetic correlations with all of the singing task measures and MatchTheNote PD, albeit with the exception of HappyBirthday ID (**Table 9.14**). The magnitude of the correlations due to shared additive genetic influences between Years of Music Training and the task measures ranged from -.27 (SingTheNote PD) to -.44 (SingTheTune PD), accounting for a large proportion of the phenotypic correlations. All the common and unique environmental correlations were not statistically significant.

Table 9.14. Proportions of Phenotypic Correlations between Years of Music Training and the Objective Task Measures due to *A*, *C* and *E*

Task Measure	<i>N</i>	Phenotypic correlation			
		Due to Additive Genetic (<i>A</i>)	Due to Common Environment (<i>C</i>)	Due to Unique Environment (<i>E</i>)	Total
SINGCOMB	91	-.38 [-.65, -.07]	-.07 [-.38, .20]	-.01 [-.06, .04]	-.46**
SingTheNote PD	92	-.27 [-.51, -.01]	-.10 [-.35, .12]	-.02 [-.09, .04]	-.39**
HappyBirthday PD	93	-.39 [-.66, -.09]	-.04 [-.35, .23]	.02 [-.04, .07]	-.42**
HappyBirthday ID	93	-.26 [-.52, .05]	-.05 [-.36, .19]	-.03 [-.10, .03]	-.34**
HappyBirthday KD	93	-.32 [-.62, -.01]	-.08 [-.39, .22]	.05 [-.02, .11]	-.35**
SingTheTune PD	92	-.44 [-.65, -.10]	.03 [-.32, .22]	-.02 [-.08, .04]	-.43**
SingTheTune ID	92	-.39 [-.64, -.10]	.00 [-.31, .24]	.00 [-.06, .06]	-.39**
MatchTheNote PD	93	-.30 [-.53, -.05]	-.06 [-.30, .15]	.02 [-.05, .09]	-.34**

Note. ID: Interval deviation; KD: Key deviation; *N*: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

** $p < .01$.

The importance of shared additive genetic influences in explaining the relationship between Years of Music Training and the task measures (except for HappyBirthday ID) was also evident from the significant deterioration in model fit when additive genetic correlations were constrained to zero (**Table 9.15**). The results therefore demonstrated that the associations between Years of Music Training and the task measure were significantly mediated by shared additive genetic influences.

Table 9.15. Bivariate Model-Fitting Results for the Associations between Years of Music Training and the Objective Task Measures

Associated trait	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	ACE	15	1404.73	392	620.73	-	-	-	-
	$r_A = 0$	14	1411.01	393	625.01	6.28	1	0.01*	ACE
	$r_C = 0$	14	1404.85	393	618.85	0.12	1	0.73	ACE
	$r_E = 0$	14	1405.02	393	619.02	0.29	1	0.59	ACE
SingTheNote PD	ACE	15	1658.67	398	862.67	-	-	-	-
	$r_A = 0$	14	1663.00	399	865.00	4.33	1	0.04*	ACE
	$r_C = 0$	14	1659.26	399	861.26	0.59	1	0.44	ACE
	$r_E = 0$	14	1659.31	399	861.31	0.64	1	0.42	ACE
HappyBirthday PD	ACE	15	1410.20	399	612.20	-	-	-	-
	$r_A = 0$	14	1417.03	400	617.03	6.83	1	0.01*	ACE
	$r_C = 0$	14	1410.25	400	610.25	0.05	1	0.82	ACE
	$r_E = 0$	14	1410.52	400	610.52	0.32	1	0.57	ACE
HappyBirthday ID	ACE	15	1307.46	399	509.46	-	-	-	-
	$r_A = 0$	14	1310.00	400	510.00	2.54	1	0.11	ACE
	$r_C = 0$	14	1307.55	400	507.55	0.09	1	0.76	ACE
	$r_E = 0$	14	1308.66	400	508.66	1.2	1	0.27	ACE
HappyBirthday KD	ACE	15	1436.65	399	638.65	-	-	-	-
	$r_A = 0$	14	1440.62	400	640.62	3.97	1	0.05*	ACE
	$r_C = 0$	14	1436.86	400	636.86	0.20	1	0.65	ACE
	$r_E = 0$	14	1438.42	400	638.42	1.77	1	0.18	ACE
SingTheTune PD	ACE	15	1490.09	393	704.09	-	-	-	-
	$r_A = 0$	14	1496.90	394	708.90	6.81	1	0.01*	ACE
	$r_C = 0$	14	1490.11	394	702.11	0.01	1	0.90	ACE
	$r_E = 0$	14	1490.43	394	702.43	0.34	1	0.56	ACE
SingTheTune ID	ACE	15	1466.10	393	680.10	-	-	-	-
	$r_A = 0$	14	1473.01	394	685.01	6.91	1	0.01*	ACE
	$r_C = 0$	14	1466.10	394	678.10	0.00	1	1.00	ACE
	$r_E = 0$	14	1466.10	394	678.10	0.00	1	0.96	ACE
MatchTheNote PD	ACE	15	1587.52	395	797.52	-	-	-	-
	$r_A = 0$	14	1593.19	396	801.19	5.67	1	0.02*	ACE
	$r_C = 0$	14	1587.79	396	795.79	0.27	1	0.61	ACE
	$r_E = 0$	14	1587.86	396	795.86	0.34	1	0.56	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

9.2.4.3 Personal Singing and the singing measures

For Personal Singing, only the additive genetic correlations with SINGCOMB, SingTheTune PD and SingTheTune ID were significant, ranging from -.41 to -.49 (**Table 9.16**). In keeping with these findings, constraining the additive genetic correlation between Personal Singing and these three measures to zero resulted in significant deterioration in model fit from the full bivariate ACE models (**Table 9.17**). This highlights the importance of shared additive genetic influences in explaining the associations between these measures and Personal Singing.

All the other genetic and environmental correlations between Personal Singing and the task measures were not found to be significant, even though in terms of their magnitude. The correlations due to additive genetic influences appeared to explain a considerable proportion of the phenotypic correlations between Personal Singing and various measures (**Table 9.16**).

Table 9.16. Proportions of the Phenotypic Correlations between Personal Singing and the Singing Measures due to A, C and E

Task Measure	N	Phenotypic correlation			
		Due to Additive Genetic (A)	Due to Common Environment (C)	Due to Unique Environment (E)	Total
SINGCOMB	97	-.44 [-.60,-.10]	.11 [-.22,.25]	-.02 [-.10,.04]	-.35**
SingTheNote PD	98	-.10 [-.36,.20]	-.06 [-.32,.16]	-.06 [-.16,.02]	-.22**
HappyBirthday PD	99	-.30 [-.56,.06]	.02 [-.31,.25]	-.06 [-.16,.02]	-.34**
HappyBirthday ID	99	-.21 [-.53,.13]	-.12 [-.41,.16]	-.05 [-.15,.04]	-.38**
HappyBirthday KD	99	-.25 [-.52,.12]	-.03 [-.37,.22]	-.01 [-.12,.08]	-.29**
SingTheTune PD	98	-.49 [-.60,-.23]	.15 [-.10,.23]	-.04 [-.12,.03]	-.38**
SingTheTune ID	98	-.41 [-.58,-.10]	.07 [-.23,.22]	.00 [-.09,.08]	-.34**

Note. ID: Interval deviation; KD: Key deviation; N: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

** $p < .01$.

Table 9.17. Bivariate Model-Fitting Results for the Associations between Personal Singing and the Singing Measures

Associated trait	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	ACE	15	904.24	400	104.24	-	-	-	-
	$r_A = 0$	14	910.38	401	108.38	6.13	1	0.01*	ACE
	$r_C = 0$	14	904.61	401	102.61	0.36	1	0.55	ACE
	$r_E = 0$	14	904.61	401	102.61	0.37	1	0.55	ACE
SingTheNote PD	ACE	15	1165.49	406	353.49	-	-	-	-
	$r_A = 0$	14	1165.88	407	351.88	0.39	1	0.53	ACE
	$r_C = 0$	14	1165.68	407	351.68	0.19	1	0.67	ACE
	$r_E = 0$	14	1167.56	407	353.56	2.07	1	0.15	ACE
HappyBirthday PD	ACE	15	907.43	407	93.43	-	-	-	-
	$r_A = 0$	14	910.10	408	94.10	2.67	1	0.10	ACE
	$r_C = 0$	14	907.44	408	91.44	0.01	1	0.93	ACE
	$r_E = 0$	14	909.29	408	93.29	1.86	1	0.17	ACE
HappyBirthday ID	ACE	15	794.29	407	-19.71	-	-	-	-
	$r_A = 0$	14	795.58	408	-20.42	1.3	1	0.25	ACE
	$r_C = 0$	14	794.70	408	-21.30	0.41	1	0.52	ACE
	$r_E = 0$	14	795.39	408	-20.61	1.11	1	0.29	ACE
HappyBirthday KD	ACE	15	930.94	407	116.94	-	-	-	-
	$r_A = 0$	14	932.70	408	116.70	1.76	1	0.18	ACE
	$r_C = 0$	14	930.98	408	114.98	0.04	1	0.84	ACE
	$r_E = 0$	14	931.03	408	115.03	0.09	1	0.77	ACE
SingTheTune PD	ACE	15	980.58	401	178.58	-	-	-	-
	$r_A = 0$	14	989.74	402	185.74	9.15	1	0.00**	ACE
	$r_C = 0$	14	981.70	402	177.70	1.12	1	0.29	ACE
	$r_E = 0$	14	981.67	402	177.67	1.09	1	0.30	ACE
SingTheTune ID	ACE	15	956.75	401	154.75	-	-	-	-
	$r_A = 0$	14	963.51	402	159.51	6.76	1	0.01*	ACE
	$r_C = 0$	14	956.91	402	152.91	0.16	1	0.69	ACE
	$r_E = 0$	14	956.75	402	152.75	0.00	1	0.95	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

* $p < .05$; ** $p < .01$.

9.2.4.4 Family Singing and the singing measures

In contrast with the bivariate genetic modelling results reported thus far, the associations between Family Singing and all the singing task measures were demonstrated to be significantly mediated by shared common environmental influences, ranging from -.27 (SingTheNote PD) to -.46 (HappyBirthday PD and HappyBirthday KD) (**Table 9.18**). This was also evident from the significant fit deterioration in the reduced models that constrained the shared common environmental correlations between Family Singing and the singing measures to zero (**Table 9.19**).

Table 9.18. Proportions of the Phenotypic Correlations between Family Singing and the Singing Measures due to *A*, *C* and *E*

Task Measure	<i>N</i>	Phenotypic correlation			
		Due to Additive Genetic (<i>A</i>)	Due to Common Environment (<i>C</i>)	Due to Unique Environment (<i>E</i>)	Total
SINGCOMB	97	.03 [-.23,.19]	-.43 [-.59,-.16]	-.05 [-.11,.01]	-.45**
SingTheNote PD	98	-.01 [-.27,.19]	-.27 [-.46,-.01]	-.03 [-.11,.04]	-.31**
HappyBirthday PD	99	.10 [-.15,.22]	-.46 [-.59,-.21]	-.04 [-.12,.03]	-.40**
HappyBirthday ID	99	.00 [-.30,.18]	-.37 [-.55,-.09]	-.07 [-.15,.00]	-.44**
HappyBirthday KD	99	.10 [-.17,.21]	-.46 [-.59,-.19]	.00 [-.08,.09]	-.36**
SingTheTune PD	98	-.05 [-.35,.14]	-.37 [-.56,-.07]	-.02 [-.10,.05]	-.44**
SingTheTune ID	98	-.02 [-.32,.16]	-.41 [-.60,-.10]	.00 [-.09,.08]	-.43**

Note. ID: Interval deviation; KD: Key deviation; *N*: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals.

***p* < .01. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

Table 9.19. Bivariate Model-Fitting Results for the Associations between Family Singing and the Singing Measures

Associated trait	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	ACE	15	825.14	400	25.14	-	-	-	-
	$r_A = 0$	14	825.23	401	23.23	0.09	1	0.77	ACE
	$r_C = 0$	14	833.62	401	31.62	8.48	1	0.00**	ACE
	$r_E = 0$	14	827.54	401	25.54	2.40	1	0.12	ACE
SingTheNote PD	ACE	15	1088.57	406	276.57	-	-	-	-
	$r_A = 0$	14	1088.57	407	274.57	0.00	1	0.96	ACE
	$r_C = 0$	14	1092.80	407	278.80	4.23	1	0.04*	ACE
	$r_E = 0$	14	1089.25	407	275.25	0.68	1	0.41	ACE
HappyBirthday PD	ACE	15	832.56	407	18.56	-	-	-	-
	$r_A = 0$	14	833.43	408	17.43	0.87	1	0.35	ACE
	$r_C = 0$	14	842.20	408	26.20	9.64	1	0.00**	ACE
	$r_E = 0$	14	833.97	408	17.97	1.41	1	0.23	ACE
HappyBirthday ID	ACE	15	716.80	407	-97.20	-	-	-	-
	$r_A = 0$	14	716.80	408	-99.20	0.00	1	1.00	ACE
	$r_C = 0$	14	723.00	408	-93.00	6.20	1	0.01*	ACE
	$r_E = 0$	14	720.37	408	-95.63	3.57	1	0.06	ACE
HappyBirthday KD	ACE	15	851.93	407	37.93	-	-	-	-
	$r_A = 0$	14	852.50	408	36.50	0.56	1	0.45	ACE
	$r_C = 0$	14	861.05	408	45.05	9.11	1	0.00**	ACE
	$r_E = 0$	14	851.93	408	35.93	0.00	1	0.99	ACE
SingTheTune PD	ACE	15	908.00	401	106.00	-	-	-	-
	$r_A = 0$	14	908.16	402	104.16	0.16	1	0.69	ACE
	$r_C = 0$	14	913.71	402	109.71	5.71	1	0.02*	ACE
	$r_E = 0$	14	908.44	402	104.44	0.45	1	0.50	ACE
SingTheTune ID	ACE	15	878.61	401	76.61	-	-	-	-
	$r_A = 0$	14	878.62	402	74.62	0.02	1	0.90	ACE
	$r_C = 0$	14	884.76	402	80.76	6.16	1	0.01*	ACE
	$r_E = 0$	14	878.62	402	74.62	0.01	1	0.90	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$; ** $p < .01$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

9.2.4.5 Public Singing and the singing measures

While Public Singing had moderate and significant phenotypic correlations with the singing task measures ($r = -.30$ to $-.44$), only the correlation due to shared unique environmental influences between Public Singing and SingTheTune ID was statistically significant (**Table 9.20**). This was also demonstrated in **Table 9.21**, whereby constraining the unique environmental correlation to zero caused significant worsening of model fit from the full model. All the other genetic and environmental correlations were not statistically significant.

For most of the task measures, the contribution of shared environmental influences to the correlation with Public Singing was generally larger than the contribution of additive genetic influences (except for SingTheNote PD and HappyBirthday ID).

Table 9.20. Portions of the Phenotypic Correlations between Public Singing and the Singing Measures due to A, C and E

Task Measure	N	Phenotypic correlation			
		Due to Additive Genetic (A)	Due to Common Environment (C)	Due to Unique Environment (E)	Total
SINGCOMB	97	-.12 [-.48,.14]	-.27 [-.52,.04]	-.03 [-.10,.03]	-.42**
SingTheNote PD	98	-.14 [-.41,.18]	-.13 [-.43,.06]	-.05 [-.13,.03]	-.32**
HappyBirthday PD	99	-.18 [-.52,.09]	-.23 [-.48,.09]	.03 [-.05,.10]	-.38**
HappyBirthday ID	99	-.26 [-.53,.06]	-.15 [-.45,.08]	-.03 [-.11,.05]	-.44**
HappyBirthday KD	99	-.06 [-.42,.19]	-.28 [-.51,.05]	.04 [-.05,.13]	-.30**
SingTheTune PD	98	-.15 [-.48,.16]	-.22 [-.51,.06]	-.06 [-.14,.01]	-.43**
SingTheTune ID	98	.01 [-.38,.22]	-.35 [-.56,.02]	-.08 [-.18,-.01]	-.42**

Note. ID: Interval deviation; KD: Key deviation; N: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals.

** $p < .01$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

Table 9.21. Bivariate Model-Fitting Results for the Associations between Public Singing and the Singing Measures

Associated trait	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	ACE	15	555.76	400	-244.24	-	-	-	-
	$r_A = 0$	14	556.45	401	-245.55	0.69	1	0.41	ACE
	$r_C = 0$	14	557.66	401	-244.34	1.90	1	0.17	ACE
	$r_E = 0$	14	557.01	401	-244.99	1.25	1	0.26	ACE
SingTheNote PD	ACE	15	816.24	406	4.24	-	-	-	-
	$r_A = 0$	14	816.83	407	2.83	0.59	1	0.44	ACE
	$r_C = 0$	14	816.64	407	2.64	0.40	1	0.53	ACE
	$r_E = 0$	14	817.65	407	3.65	1.41	1	0.23	ACE
HappyBirthday PD	ACE	15	560.10	407	-253.90	-	-	-	-
	$r_A = 0$	14	561.72	408	-254.28	1.62	1	0.20	ACE
	$r_C = 0$	14	561.84	408	-254.16	1.73	1	0.19	ACE
	$r_E = 0$	14	560.55	408	-255.45	0.44	1	0.51	ACE
HappyBirthday ID	ACE	15	443.33	407	-370.67	-	-	-	-
	$r_A = 0$	14	445.65	408	-370.35	2.32	1	0.13	ACE
	$r_C = 0$	14	443.84	408	-372.16	0.51	1	0.47	ACE
	$r_E = 0$	14	443.74	408	-372.26	0.42	1	0.52	ACE
HappyBirthday KD	ACE	15	586.31	407	-227.69	-	-	-	-
	$r_A = 0$	14	586.49	408	-229.51	0.18	1	0.67	ACE
	$r_C = 0$	14	588.90	408	-227.10	2.59	1	0.11	ACE
	$r_E = 0$	14	587.00	408	-229.00	0.69	1	0.40	ACE
SingTheTune PD	ACE	15	637.28	401	-164.72	-	-	-	-
	$r_A = 0$	14	638.06	402	-165.94	0.79	1	0.38	ACE
	$r_C = 0$	14	638.33	402	-165.67	1.05	1	0.30	ACE
	$r_E = 0$	14	640.03	402	-163.97	2.75	1	0.10	ACE
SingTheTune ID	ACE	15	608.95	401	-193.05	-	-	-	-
	$r_A = 0$	14	608.96	402	-195.04	0.00	1	0.95	ACE
	$r_C = 0$	14	612.35	402	-191.65	3.40	1	0.07	ACE
	$r_E = 0$	14	613.32	402	-190.68	4.37	1	0.04*	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

9.2.4.6 Music Listening and task measures

Similar to the bivariate modelling results between Personal Singing and the singing task measures, Music Listening also demonstrated significant additive genetic correlations with SingTheTune PD, SingTheTune ID and SINGCOMB, ranging from -.33 (SINGCOMB) to -.49 (SingTheTune PD) (**Table 9.22**). In keeping with this, there was significant deterioration of model fit when the correlations due to shared additive genetic influences between Music Listening and these three measures were constrained to zero (**Table 9.23**).

All the other genetic and environmental correlations were not statistically significant, even though there were significant and moderate phenotypic correlations ($r = -.37$ to $-.48$) between Music Listening and all the singing task measures.

Table 9.22. Portions of the Phenotypic Correlations between Music Listening and the Singing Measures due to A, C and E

Task Measure	N	Phenotypic correlation			
		Due to Additive Genetic (A)	Due to Common Environment (C)	Due to Unique Environment (E)	Total
SINGCOMB	97	-.33 [-.63,.00]	-.09 [-.41,.19]	-.04 [-.12,.02]	-.46**
SingTheNote PD	98	-.18 [-.45,.12]	-.12 [-.40,.12]	-.07 [-.16,.01]	-.37**
HappyBirthday PD	99	-.24 [-.59,.08]	-.14 [-.44,.19]	-.03 [-.12,.04]	-.41**
HappyBirthday ID	99	-.18 [-.53,.13]	-.18 [-.48,.14]	-.04 [-.12,.04]	-.40**
HappyBirthday KD	99	-.16 [-.53,.16]	-.20 [-.49,.16]	-.01 [-.10,.08]	-.37**
SingTheTune PD	98	-.49 [-.65,-.16]	.03 [-.30,.17]	-.02 [-.10,.05]	-.48**
SingTheTune ID	98	-.37 [-.62,-.07]	-.04 [-.34,.20]	-.01 [-.09,.06]	-.42**

Note. ID: Interval deviation; KD: Key deviation; N: Number of twin pairs; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals.

** $p < .01$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

Table 9.23. Bivariate Model-Fitting Results for the Associations between Music Listening and the Singing Measures

Associated trait	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	ACE	15	836.91	400	36.91	-	-	-	-
	$r_A = 0$	14	840.80	401	38.80	3.89	1	0.05*	ACE
	$r_C = 0$	14	837.13	401	35.13	0.22	1	0.64	ACE
	$r_E = 0$	14	838.80	401	36.80	1.89	1	0.17	ACE
SingTheNote PD	ACE	15	1096.92	406	284.92	-	-	-	-
	$r_A = 0$	14	1098.22	407	284.22	1.30	1	0.25	ACE
	$r_C = 0$	14	1097.68	407	283.68	0.76	1	0.38	ACE
	$r_E = 0$	14	1100.29	407	286.29	3.37	1	0.07	ACE
HappyBirthday PD	ACE	15	848.60	407	34.60	-	-	-	-
	$r_A = 0$	14	850.69	408	34.69	2.10	1	0.15	ACE
	$r_C = 0$	14	849.20	408	33.20	0.61	1	0.44	ACE
	$r_E = 0$	14	849.31	408	33.31	0.72	1	0.40	ACE
HappyBirthday ID	ACE	15	737.60	407	-76.40	-	-	-	-
	$r_A = 0$	14	738.70	408	-77.30	1.10	1	0.29	ACE
	$r_C = 0$	14	738.60	408	-77.40	1.00	1	0.32	ACE
	$r_E = 0$	14	738.38	408	-77.62	0.78	1	0.38	ACE
HappyBirthday KD	ACE	15	871.67	407	57.67	-	-	-	-
	$r_A = 0$	14	872.66	408	56.66	0.99	1	0.32	ACE
	$r_C = 0$	14	872.97	408	56.97	1.31	1	0.25	ACE
	$r_E = 0$	14	871.69	408	55.69	0.02	1	0.88	ACE
SingTheTune PD	ACE	15	913.21	401	111.21	-	-	-	-
	$r_A = 0$	14	921.76	402	117.76	8.55	1	0.00**	ACE
	$r_C = 0$	14	913.23	402	109.23	0.02	1	0.89	ACE
	$r_E = 0$	14	913.52	402	109.52	0.31	1	0.58	ACE
SingTheTune ID	ACE	15	895.03	401	93.03	-	-	-	-
	$r_A = 0$	14	901.22	402	97.22	6.20	1	0.01*	ACE
	$r_C = 0$	14	895.07	402	91.07	0.04	1	0.84	ACE
	$r_E = 0$	14	895.11	402	91.11	0.09	1	0.77	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$; ** $p < .01$. Significant genetic and environmental correlations (confidence intervals do not include zero) are shown in bold.

9.3 Summary of Key Genetic Findings

The key genetic findings presented in this chapter are summarised in point form below.

9.3.1 Results pertaining to the genetic basis of singing ability

- For SINGCOMB, r_{MZ} (.81-.82) was significantly higher than r_{DZ} (.41-.43) for both the continuous and categorical measures. Univariate genetic modelling estimated a significant and substantial genetic component for SINGCOMB: $A = 69\%$ (continuous measure); $A = 70\%$ (categorical measure).
- Univariate genetic modelling estimated significant genetic components for the following continuous measures, with moderate to high heritability estimates: SingTheNote PD, HappyBirthday PD, HappyBirthday ID and SingTheTune PD ($A = 44-71\%$). Significant genetic components were also estimated for SingTheNote PD (category), HappyBirthday ID (category) and HappyBirthday KD (category), with high heritability estimates ($A = 72-79\%$).
- The heritability estimate of HappyBirthday ID ($A = 68\%$) was higher than that of HappyBirthday PD ($A = 44\%$), whereas the reverse was observed in Sing The Tune Task, where the heritability estimate of SingTheTune PD ($A = 71\%$) was higher than SingTheTune ID ($A = 28\%$). In both tasks, the singing measure with the higher heritability estimate was also observed to have relatively better behavioural performance.
- The heritability estimates for the categorical measures of HappyBirthday KD and SingTheTune ID were much higher ($A = 72\%$ and 57%) than the heritability estimates for the corresponding continuous measures ($A = 26\%$ and 28%).
- For MatchTheNote PD, r_{MZ} was also significantly higher than r_{DZ} . Univariate genetic modelling estimated a significant and substantial genetic component for MatchTheNote PD: $A = 60\%$.

- For self-reported singing ability, r_{MZ} (.87) was significantly higher than r_{DZ} (.54). Univariate genetic modelling estimated a significant and substantial genetic component for self-reported singing ability: $A = 72\%$.
- For self-reported music ability, music interest and singing interest, r_{MZ} was also significantly higher than r_{DZ} . Significant and substantial heritabilities were also estimated for these measures ($A = 65-81\%$).

9.3.2 Results pertaining to the genetic bases of environmental components associated with singing ability

- For music and singing background components, r_{MZ} was significantly higher than r_{DZ} for Instrumental Expertise, Years of Music Training and Public Singing. Significant and substantial heritabilities ($A = 46-68\%$) were estimated for these measures based on univariate genetic modelling. On the other hand, significant common environmental influences were estimated for Family Singing ($C = 63\%$).
- Bivariate genetic analyses showed that significant shared additive genetic influences mediated the associations between:
 - Instrumental Expertise and all the singing task measures.
 - Years of Music Training and all the singing task measures (except HappyBirthday ID).
- Bivariate genetic analyses also showed that significant shared additive genetic influences mediated the associations between:
 - Personal Singing and the task measures SINGCOMB, SingTheTune PD, and SingTheTune ID.
 - Music Listening and the task measures SINGCOMB, SingTheTune PD, and SingTheTune ID.
 - Instrumental Expertise and MatchTheNote PD.
 - Years of Music Training and MatchTheNote PD.

- Bivariate genetic analyses also showed that significant shared common environmental influences mediated the associations between:
 - Family Singing and all the singing task measures.

10

DISCUSSION OF GENETIC FINDINGS

This chapter discusses the genetic findings in light of the two main aims outlined in **Section 4.6**, namely, to investigate the genetic basis of singing ability and the genetic bases of environmental components associated with singing ability. The discussion will also examine whether the findings confirmed the hypotheses stipulated *a priori* and whether the findings corroborate with evidence from previous studies.

10.1 Investigating the Genetic Basis of Singing Ability

10.1.1 Objectively-assessed singing ability across all tasks

Overall, the significantly larger ICC in MZ twins compared to DZ twins for SINGCOMB and the large genetic contribution ($A = 69\text{-}70\%$) on SINGCOMB confirmed the first hypothesis of the primary aim of the study. In particular, the findings provide strong evidence that there are substantial genetic influences underlying the variation of singing ability in the current twin sample, when singing proficiency across all tasks is considered as a collective whole. Notably, the heritability estimates of SINGCOMB using either continuous or categorical measures were highly consistent with each other ($A = 69\%$ to 70%), thus further strengthening the evidence for the genetic basis of singing ability.

Univariate genetic modelling conducted on each of the singing task measures also showed significant genetic influences for most tasks, with moderate to large heritabilities ($26\text{-}71\%$) and negligible to moderate common environmental influences ($0\text{-}37\%$). These heritability estimates were also corroborated by the significantly larger ICCs in MZ twins compared to DZ twins for most of the task measures. In the

subsequent sections, the genetic influences on each singing task will be discussed in greater detail.

10.1.2 Sing The Note Task

The significantly higher ICCs of the MZ twins relative to the DZ twins as well as the substantial genetic influences ($A = 69\%$) estimated for SingTheNote PD served to demonstrate that the ability to vocally match single pitches has a significant genetic component, thus confirming part (a) of the first hypothesis. Moreover, the additive genetic contribution (A) to variances in Sing The Note Task were significantly greater than the contribution of common environmental (C) influences, which supports the role played by genetic factors in influencing basic vocal pitch-matching ability.

Apart from the current study, only one other genetic study has assessed vocal pitch-matching ability (Park et al., 2012). In their pedigree study of a Mongolian population, Park et al. (2012) reported a moderate heritability of 40% of pitch-matching ability. The relatively lower heritability estimate in Park et al. (2012) compared to the current study may reflect their use of a different measure for pitch accuracy (i.e., difference limen instead of average pitch deviation). In addition, the pitch stimuli used in their study comprised complex tones instead of sine tones used in the current study. Another feasible explanation could be a possible Gene $\times$ Practice interaction effect on singing ability. Hambrick and Tucker-Drob (2014) previously demonstrated a Gene $\times$ Practice interaction effect on music accomplishment, where participants with more practice were observed to have a considerably larger genetic component for music accomplishment than participants who did not report any music practice. Conceivably, the high percentage (86%) of musically trained participants in the current sample may have contributed to the higher heritability estimate for Sing The Note Task, whereas the lower heritability estimate in Park et al. (2012) may be due to the minimal out-of-school music training undertaken by most of the participants.

In the same study, Park et al. (2012) identified chromosomal loci 4q23, 4q26 and the gene *UGT8* as potential genetic correlates for vocal pitch-matching ability. This finding is promising in light of the evidence from previous molecular genetic studies implicating the nearby locus 4q22 in music perception ability (e.g., Pulli et al., 2008;

Oikkonen et al., 2014). Given that unimpaired perception of external pitch stimuli is important for accurate vocal imitation of pitch, it is thus plausible that music perception and vocal pitch-matching may share a common genetic locus on chromosome 4q.

As vocal pitch-matching is a fundamental skill for singing, the large heritable component estimated for SingTheNote PD serves to bolster the case for a genetic basis of singing ability.

10.1.3 Happy Birthday Singing Task

In general, the MZ and DZ ICCs and results of univariate genetic modelling on the various measures of Happy Birthday Singing Task provided support for part (b) of the first hypothesis, which predicted a significant genetic contribution underlying the ability to sing a familiar song accurately.

In terms of the continuous measures, HappyBirthday ID yielded a high heritability estimate ($A = 68\%$), whereas HappyBirthday PD and HappyBirthday KD showed moderate genetic influences of 44% and 26%, respectively. It is worth noting that the heritability estimates appeared to correspond with performance on the task measures: the measure with the highest heritability estimate (ID) was the best performed measure, while the measure with the lowest heritability estimate (KD) was the least well-performed measure (in terms of median deviation; see **Table 7.1**, p. 191).

In **Section 8.1** (p. 225), it was argued that the relatively better performance of HappyBirthday ID may be due to greater salience of relative pitch information in long-term memory as compared to absolute pitch information (Deutsch, 1972; Dowling & Bartlett, 1981; Dowling et al., 1995; Dowling et al., 2002). Conceivably, the differential heritability estimates of the various measures of Happy Birthday Singing Task may reflect how familiar melodies are encoded and represented in long-term memory, with stronger music cues in long-term memory (i.e., relative pitch cues) underpinned by greater genetic influences. Following this line of reasoning, the fact that significant and moderate genetic influences were also estimated for HappyBirthday (PD) is consistent with past evidence indicating that absolute pitch information is stored in long-term music memory (Halpern, 1988; Levitin, 1994), albeit occupying less prominence than

relative pitch information (Creel & Tumlin, 2012). The larger genetic effects on HappyBirthday ID may therefore imply that ID is a more well-defined phenotypic marker for the ability to sing familiar songs, and thus can be used by future molecular genetic studies to investigate the possibility genetic substrates underlying this type of singing ability. The suitability of ID as a phenotype for singing familiar songs is also supported by a previous behavioural finding which demonstrated that mean absolute interval deviation significantly and highly correlated with subjective expert ratings of pitch accuracy for *Happy Birthday* (Larrouy-Maestri et al., 2013).

Intriguingly, while the genetic influences for the continuous measure of HappyBirthday KD were moderate ($A = 26\%$) and statistically insignificant, the heritability estimate for the corresponding categorical measure for KD was significant and markedly higher ($A = 72\%$). This suggests that the similarity between identical twins was substantially greater when the ability to stay in key was considered in terms of three broad accuracy or expertise categories rather than as a continuous measure. Although the heritabilities for the categorical measures of HappyBirthday PD and HappyBirthday ID were also higher than their continuous counterparts, the differences between continuous and categorical measures for PD and ID were not as large.

Being the first study to estimate the heritabilities of melodic singing tasks, there are no previous genetic studies with which the current findings can be compared in order to make inferences about the discrepant heritability estimates between the continuous and categorical KD measures. Previous behavioural studies have however reported that most listeners, even those with music training, are only able to discern pitch deviations in singing that exceed 50 cents; even pitch errors as high as 40 cents are not reliably judged as out of tune (Hutchins et al., 2012; Vurma & Ross, 2006). In addition, Mauch, Frieler, and Dixon (2014) has noted that even in a sample of accurate singers, a median absolute intonation drift (i.e., key deviation) of 11 cents was observed during the course of the recording where participants were asked to sing *Happy Birthday* accompanied thrice in a row. Collectively, the aforementioned evidence indicates that slight deviation in key centre is inevitable even in accurate singers, and average key deviations below 50 cents may be too subtle to be deemed inaccurate by subjective perceptual judgment. As such, the categorical KD measure may be a more ecologically valid measure to assess the ability to maintain a reliable tonal centre than the continuous KD measure. If this is

true, based on the categorical KD measure, the ability to maintain a consistent tonal centre may have a significant and sizeable genetic component. This finding is preliminary and needs to be replicated by future genetic research using larger samples of participants.

This interpretation is consistent with previous work showing that the ability to perceive a distortion of the tonal centre of a familiar song is genetically influenced. Using a distorted tunes test that required participants to judge whether familiar song fragments were in-tune or had been distorted melodically (i.e., an abrupt shift of tonal centre in the middle of the fragment), Drayna et al. (2001) found large genetic influences ($A = 71\%$) explaining the variation of task performance in a female twin sample. This heritability estimate for tonal perception ability of familiar songs is strikingly similar to the current heritability estimate for the ability to maintain a stable tonal centre while singing a familiar song. Given the possibility of a common genetic locus for single pitch discrimination and vocal pitch-matching on chromosome 4q, it is conceivable that the perception and production of tonal centre may also have a shared genetic basis. More in-depth genetic investigations are warranted to investigate this idea further.

10.1.4 Sing The Tune Task

Finally, part (c) of the first hypothesis was supported by the significantly higher MZ relative to DZ ICC and large heritability estimate of SingTheTune PD.

The findings indicate that in the current sample, genetic factors were important in explaining the variation observed in the ability to imitate novel melodies.

Similar to Happy Birthday singing task, the heritabilities estimated for the task measures from Sing The Tune Task were also very different. In terms of the continuous measures, although SingTheTune PD demonstrated significant and large genetic influences ($A = 71\%$) similar to those of SingTheNote PD and HappyBirthday ID, the genetic influences estimated for SingTheTune ID were moderate ($A = 28\%$) and failed to reach significance.

Importantly, as with Happy Birthday singing task, the magnitudes of the heritability estimates for Sing The Tune Task were observed to correspond with the behavioural

performance. Participants, on the whole, showed better performance in terms of SingTheTune PD than SingTheTune ID. Correspondingly, the heritability estimate for SingTheTune PD was higher than that of SingTheTune ID. Following the same line of explanation as that proposed for the measures in Happy Birthday Singing Task, it is possible that the disparity between the heritability estimates of PD and ID in Sing The Tune Task point to preferential encoding of novel melodies in terms of absolute pitches rather than intervals in short-term memory, before interval information undergoes consolidation in long-term memory (see Section 8.1, p. 225). The large heritability estimate for SingTheTune PD may therefore be indicative of a strong genetic component underlying the superiority of absolute pitch encoding mechanisms in the short-term retention of music. Furthermore, the sizeable genetic component may suggest that SingTheTune PD is a more suitable phenotypic marker for the ability to sing novel tunes which can facilitate the identification of accurate genotype for this type of singing ability.

While no genetic studies to date have investigated the heritability of the ability to vocally imitate novel melodies, two twin studies have reported high heritability estimates (58-59%) for the perception of novel melodies using paired discrimination tasks (Mosing, Madison, et al., 2014; Seesjärvi et al., 2015). As perceiving and encoding novel melodies with high integrity in short-term memory is a pre-requisite for subsequent effective manipulation of the melodic information in the working memory, the substantial genetic influences found for these tasks may be an indication of a sizeable genetic component for short-term music memory. Provisional evidence of possible genetic correlates for short-term music memory can be seen in a candidate gene study which showed that certain polymorphisms of the genes *AVPR1A* and *SLC6A4* were associated with short-term music memory (Granot et al., 2007). The link between *AVPR1A* polymorphisms and short-term music memory was also supported by evidence from Ukkola et al. (2009), who reported associations between *AVPR1A* gene polymorphisms and other music perception tasks such as pitch, rhythm and music pattern discrimination.

10.1.5 Self-reported abilities and interests in singing and music

As the validity of self-report data has been questioned, the presence of both objectively-assessed singing ability and self-reported singing ability allowed the current study the unique opportunity to compare the estimated genetic influences of both. Remarkably, the heritability estimates of self-rated singing ability and SINGCOMB corresponded extremely well ($A = 72\%$ and 69% , respectively), even down to the confidence interval ranges. The congruent heritabilities suggest that in this sample, subjectively-assessed singing ability was a reliable reflection of objectively-assessed singing ability of the participants, which was corroborated by simple regression analyses that established self-reported singing ability as a significant predictor of SINGCOMB. The significant and large heritability estimate of self-rated singing ability thus served to confirm the second hypothesis of the primary aim of the study (see **Section 4.6**, p. 108).

Univariate genetic modelling performed on self-rated music ability and self-rated singing and music interests also revealed that significant genetic influences explained the variance in these self-ratings, with high heritability estimates ranging from 65% (Music Interest) to 81% (Music Ability) and statistically insignificant common environmental influences.

The high heritability estimate obtained for self-reported music ability in the current study appears to contradict the findings from two twin studies that have used the Loehlin and Nichols National Merit Twin Sample (Coon & Carey, 1989; Hambrick & Tucker-Drob, 2014). Both studies reported that music accomplishments were influenced predominantly by common environmental influences. Hambrick and Tucker-Drob (2014) did find, however, an interaction effect between genes and practice whereby the effect of genetic influences on music accomplishments was reported to be larger than that of a common environment for musically trained participants who reported practising ($A = 59\%$; $C = 27\%$), while the reverse was true for trained participants who did not practise ($A = 1\%$; $C = 76\%$). On the other hand, Vinkhuyzen et al. (2009) also found considerable genetic influences ($A = 66\%$) for self-rated music aptitude in male twins and moderate genetic influences ($A = 30\%$) in females. Interestingly, when self-rated exceptional music aptitude was assessed as a dichotomous variable (outstanding

vs. normal) in their study, a substantial genetic component ($A = 86\%$) was reported, which is similar to the heritability estimate for self-rated music ability in the current study.

Presumably, the difference in heritability estimates for self-reported music ability of the present study and those reported by Coon & Carey (1989) and Hambrick & Tucker-Drob (2014) stemmed from the use of different constructs to represent music ability. While the current study asked the participants to rate their perceived music ability on a 7-point Likert scale, music ability in Coon & Carey (1989) was based on vocational interest in music, instrumental music experience, engagement in non-amateur musical performances, and music prizes received. Hambrick and Tucker-Drob (2014), on the other hand, used endorsement of one or more questionnaire items pertaining to music prizes received or out-of-school music performance experience to construct a dichotomous music accomplishment variable (see **Section 2.4.3**, p. 58). In contrast, the self-rated exceptional music aptitude in Vinkhuyzen et al. (2009) and the self-rated music ability of the current study are probably tapping into similar constructs, which may explain the congruence in the heritability of self-reported music ability in these two studies.

While no previous genetic studies have looked specifically at the heritability of self-rated singing ability and interest, the large genetic component found for singing interest ($A = 72\%$) in the current study is comparable to the heritability estimate reported by Coon and Carey (1989) for singing participation in male twins ($A = 71\%$). In contrast, singing participation in female twins in that study had a larger contribution of common environmental factors relative to genetic factors ($A = 20\%$; $C = 59\%$). The large disparity in heritability estimates between the current sample and the female twins in the study by Coon and Carey (1989) is somewhat surprising, especially considering the current sample has a large percentage of female twins (76.4%). A possible explanation is that the measures in the two studies assessed different constructs; while the current study explicitly asked the participants about their level of interest in singing, the singing-related questions in Coon and Carey (1989) typically asked participants about their level of involvement in singing activities such as singing in choirs or small groups and taking voice lessons. These authors suggest that the gender stereotyping of singing activities as feminine activities could have resulted in the higher heritability estimate for

male twins, as more inherent interest in singing might be essential for males to participate in singing activities (Coon and Carey, 1989). On the other hand, peer influence might have prompted female twins to engage in singing, even if they might not be inclined to do so by nature, thereby resulting in the larger common environmental influences. When understood in this context, the current study finding of a large heritability estimate for singing interest corroborates previous research.

10.1.6 Match The Note Task

Similar to its vocal counterpart (i.e., SingTheNote PD), variation in perceptual pitch-matching ability was also demonstrated to be explained by a significant and large additive genetic component ($A = 60\%$) and a moderate unique environmental component ($E = 40\%$), as measured by MatchTheNote PD. Strong evidence for a substantial genetic basis for pitch perception ability comes from the observation that even by considering the lower bound of the confidence interval (i.e., 34%) as a conservative estimate for heritability, it can still be argued that genetic influences moderate in magnitude were important for pitch perception. In addition, the non-overlapping confidence intervals between the estimates for genetic (A) and common (C) environmental influences further demonstrate the importance of genetic influences in explaining the variance in pitch perception ability.

A possible genetic basis for fine pitch discrimination was previously proposed by Cebrian and Janata (2010), who observed that the acuity of auditory mental representations of pitches in the working memory of many participants without music training were comparable to those of participants with substantial music training. Two genetic studies provided evidence of significant genetic influences for pitch perception ability using tasks involving paired pitch discrimination judgment. While Mosing, Madison, et al. (2014) found significant yet modest genetic influences ($A = 30\%$) for the pitch perception of female twins, a number of large Finnish pedigree studies reported high heritability estimates ranging from 52% to 68% in their pedigree sample (Oikkonen et al., 2014; Pulli et al., 2008; Ukkola et al., 2009). The large heritability estimate of MatchTheNote PD obtained in the current study is therefore consistent with the findings from the majority of studies using similar tasks, suggesting a sizeable genetic component underlying basic pitch discrimination ability.

Several chromosomal loci containing genes implicated in the auditory pathway have been identified as possible genetic substrates for pitch perception in various molecular genetic studies (Kanduri, Raijas, et al., 2015; Liu et al., 2016; Oikkonen et al., 2014; Ukkola et al., 2009). For instance, the chromosome region 3q21.3 was shown to be strongly associated with Seashore pitch test and the combined music perception score in a genome-wide linkage and association study (Oikkonen et al., 2014). Located near this region is the *GATA2* gene, a transcription factor whose function includes regulating the development of the inner ear and the inferior colliculus (Haugas et al., 2010; Lahti et al., 2013), which in turn are implicated in tonotopic mapping. This makes *GATA2* a likely candidate gene for basic pitch discrimination ability. The *PCDH7* gene (protocadherin 7) at 4p15.1, which is located next to the best linkage evidence for Seashore Pitch Test (4p14), was also demonstrated to play a role in cochlear development (Lin et al., 2012). Similarly, a recent genome-wide study found positive selection of genes related to auditory pathway development (e.g., *GPR98* at 5q14.3 and *USH2A* at 1q32.3-41) in participants with high combined music perception scores (Liu et al., 2016).

Importantly, increasing evidence has emerged for the involvement of chromosome 4q in music ability. A wide linkage region spanning 4p15 to 4q24 was observed for pitch and rhythm discrimination as well as auditory structuring ability (Oikkonen et al., 2014), which partially replicated an earlier study finding relating to the contribution of chromosome 4q22 in music perception (Pulli et al., 2008). Interestingly, chromosome 4q22 harbours the gene *SNCA*, which is regulated by the aforementioned *GATA2* gene and was shown to be increasingly expressed in musically-trained participants after listening to classical music (see **Section 2.4.1.1**, p. 33).

10.2 Investigating the Genetic Bases of Environmental Components Associated with Singing Ability

10.2.1 Components related to formal music training

Both Instrumental Expertise and its subcomponent Years of Music Training were demonstrated to have significant genetic components with moderate to large heritability estimates ($A = 68\%$ and 46% , respectively). This confirmed the first hypothesis of the

second aim of the study, which predicted a significant genetic contribution for environmental components related to formal music training. As Years of Music Training is clearly related to and may be regarded as a coarser indicator of the amount of accumulated music practice, the moderate heritability estimate for Years of Music Training in the current study corroborates two recent twin studies that have reported moderate to large heritabilities ($A = 38\%$ to 69%) for music practice (Hambrick & Tucker-Drob, 2014; Mosing, Madison, et al., 2014)

Although common environmental influences were not statistically significant for both variables, the moderate magnitude of the common environmental component ($C = 38\%$) suggests that common environmental factors are also necessary to explain the variation in Years of Music Training in the sample. The proposed importance of common environmental influences is reasonable, because in the case of music training, parents would usually let both twins take music lessons, instead of depriving one of them the opportunity.

It is interesting to note, however, that genetic influences were larger than common environmental influences, indicating that identical twin pairs correlate more highly than non-identical twins in terms of the duration of formal music training. This suggests that there is a genetic basis for persisting with music training, which may in turn be linked to one's interest and motivation towards music learning. It is possible that the motivation to learn music might have stemmed from sibling rivalry, which, incidentally, was reported to have a substantial genetic component ($A = 52\%$) in a previous twin study (Pike & Atzaba-Poria, 2003). The sizeable heritability estimate for self-reported music interest lends support to this claim. In addition, the relatively higher heritability estimate for Instrumental Expertise, which comprised items such as motivation level for instrumental learning and peak weekly practice duration, as compared to Years of Music Training, also gives credence to the importance of these factors in influencing the genetic contribution to Years of Music Training. Furthermore, music flow (i.e., the state of total absorption in musical activity) was demonstrated to have a moderate heritable component ($A = 40\%$) and substantial shared genetic influences with accumulated music practice in a recent study (Butkovic et al., 2015). Thus, it is possible that the genetic influences underlying music flow might also contribute to the genetic component of Years of Music Training.

The predominant influence of genetic factors on Instrumental Expertise, however, was contrary to the findings of Coon and Carey (1989) for instrumental music engagement, which was reported to have low to moderate genetic influences and substantial common environmental influences. One possible explanation could be that the Instrumental Expertise component in the present study included items such as self-rated instrumental ability and motivation level for instrumental learning, whereas instrumental music engagement in Coon and Carey (1989) primarily reflected involvement and participation only, without personal assessment of expertise and motivation. As involvement does not necessarily imply expertise, it is reasonable to consider Instrumental Expertise as a better gauge of a participant's instrumental training.

Notably, bivariate genetic analyses also demonstrated that Instrumental Expertise and Years of Music Training have significant shared additive genetic influences with the singing task measures, which confirmed the second hypothesis of the second aim of the study. This predicted a partially shared genetic basis between these components and singing ability. The current study is the first to demonstrate that the association between formal music training and singing ability is significantly mediated by shared genetic influences. In addition, the significant genetic overlap between formal music training and music perception ability (as measured by MatchTheNote PD) observed in the current study is consistent with previous evidence of significant genetic correlations between accumulated music practice and music perception ability (Mosing, Madison, et al., 2014).

Collectively, the findings appear to corroborate molecular genetic evidence of a putative common genetic locus at 4q22-23 for music aptitude (as measured by music perception ability) and vocal pitch-matching accuracy (Oikkonen et al., 2014; Park et al., 2012; Pulli et al., 2008). It is possible that an underlying common genetic factor predisposes both pitch perception and production ability, which may also enable one's music ability to be better facilitated by music training. Interestingly, unlike additive genetic influences, neither common nor unique environmental influences were statistically significant in explaining the associations between formal music training and the task measures. This suggests that the environmental effects influencing singing ability may be different from those influencing instrumental music training. It is also possible that

the current study is underpowered to detect significant environmental correlations between the two.

10.2.2 Singing-related components

Of the three singing-related background components, only Public Singing had a significant and large genetic component ($A = 66\%$), albeit with a wide confidence interval. As the items constituting Public Singing include singing together with or in the presence of others (e.g., with friends, in a choir or as a soloist), Public Singing may be reflective of a social component. Sociability has been previously demonstrated to have significant additive and dominant genetic components in a twin study (Olson, Vernon, Harris, & Jang, 2001). In addition, a polymorphism of *SLC6A4* which was associated with cooperative behaviour (Saiz et al., 2010) was found to be associated with choir participation in a candidate gene study (Morley et al., 2012). These findings support the possibility that the social aspects of singing may account for the significant genetic influences observed for Public Singing.

Bivariate genetic analyses did not reveal any significant shared genetic and environmental influences between Public Singing and the singing tasks, except for the significant unique environmental correlation with SingTheTune ID. This was somewhat intriguing, especially considering the significant and high heritability estimate of Public Singing in univariate genetic modelling. Besides the possibility that the small sample size lacked the statistical power to detect significant genetic or environmental correlations between Public Singing and most of the task measures, another possibility is that the genetic influences underlying singing accuracy are distinct from those underlying Public Singing, which relates more to social factors. This is somewhat in line with the findings from Morley et al. (2012), who reported no significant association between choir participation and the *AVPR1A* polymorphisms, which were reportedly associated with music perception ability (Ukkola et al., 2009). The researchers conjectured that the significant association of choir participation with *SLC64* may suggest a predisposition to group activity. It is thus plausible that in the current study, Public Singing may be a phenotype for social singing behaviour rather than a phenotype for singing ability *per se*, which may have therefore resulted in distinct genetic influences for the two variables.

Conversely, Family Singing had a significant and substantial common environmental component ($C = 63\%$) and an insignificant, negligible genetic component. This result suggests that identical and non-identical twins raised in the same homes probably experienced equally similar family music and singing environment in childhood. Importantly, this result supports the validity of the equal-environment assumption, which is a crucial assumption for the classical twin design (Rijsdijk & Sham, 2002). The equal-environment assumption stipulates that identical and non-identical twin pairs are similarly correlated in experiencing environmental conditions that are important to the trait of interest. As Family Singing mostly consisted of items pertaining to childhood engagement in singing activities with one's family, it can be considered as a trait-relevant environmental exposure for subsequent singing ability.

Interestingly, Family Singing was shown to have significant shared common environmental influences with all the singing task measures. This points to the importance of a conducive family singing environment in shaping a child's subsequent singing ability. As mentioned in **Section 3.3** (p. 68), numerous studies have already detailed how a musically rich family environment can positively impact on the musical outcome of children (Brand, 1986; Custodero, Rebello Britto, & Brooks-Gunn, 2003; Ilari et al., 2011; McPherson, 2009; Zdzinski, 1996).

Univariate genetic modelling revealed that neither additive genetic nor common environmental influences were statistically significant in explaining the variance in Personal Singing; only unique environmental influences were significant ($E = 44\%$). Despite having a moderate heritability estimate ($A = 33\%$), the non-significance of the genetic influences was somewhat surprising, as one might have expected the heritability estimates of Personal Singing and self-reported singing interest to be similar. As Personal Singing only contains two components that asked participants to indicate how often they sang by themselves in childhood as well as currently, it is possible that this component is not a good indicator of singing interest because having a twin sibling might mean that there was little opportunity for twins to sing by themselves during childhood, and hence most twins might not have rated this component highly. It is also possible that the small twin sample was underpowered to detect the significance of the genetic contribution on Personal Singing through univariate genetic analysis.

10.2.3 Music Listening

Apart from Family Singing, among the music and singing background components, Music Listening had the lowest heritability estimate ($A = 14\%$) and was not statistically significant. It is interesting to note that Music Listening and Family Singing were the two most important predictors of SINGCOMB among the background components, yet both variables had the lowest heritability estimates. In a similar fashion to Family Singing, Music Listening may be reflecting, in part, the childhood family music environment which helped shape subsequent singing ability. The low and statistically insignificant genetic influences on Music Listening thus served to bolster the equal-environment assumption, confirming that identical and non-identical twin pairs were similarly correlated in terms of childhood music environment. Fulfilling the equal-environment assumption in turn affirms that the greater MZ twin similarity relative to DZ twin similarity on the objective task measures truly reflects genetic influences, thus giving credence to the genetic findings of the current study (Rijsdijk & Sham, 2002).

In the present study, the Music Listening component likely represents a passive music listening behaviour during childhood that was determined mostly by the parents or other family members. It is possible that the heritability estimate for music listening may have been higher if the music background questionnaire contained questions asking participants about their current or lifelong music listening frequency, and differentiated clearly between active and passive music listening. Ukkola-Vuoti et al. (2011) reported that current active listening and active listening across the lifetime were significantly associated with music perception ability and the *AVPR1A* haplotypes, whereas passive music listening (current or over the lifetime) was not significantly associated with music discrimination. Furthermore, Kanduri, Raijas, et al. (2015) observed an upregulation of the gene *SNCA* in musically-trained participants after listening to classical music. *SNCA* is located at 4q22, which has been proposed along with nearby loci to be a putative chromosomal region important for music aptitude (Oikkonen et al., 2014; Park et al., 2012; Pulli et al., 2008). Interestingly, other genes that were increasingly expressed include *HDAC4* (2q37.3) and *FAM49B* (8q24.21), both of which have been suggested to be potentially linked to absolute pitch ability (Gervain et al., 2013; Theusch et al., 2009).

Bivariate genetic analyses revealed that both Music Listening and Personal Singing have significant genetic correlations with Sing The Tune task measures and SINGCOMB. This means that some genetic influences which bear on the performance in Sing The Tune Task (and the combined singing score in general) may also predispose the frequency with which participants listened to music during childhood, and the frequency with which they sang or currently sing by themselves. As Sing The Tune Task requires good pitch and melodic processing ability and the ability to translate melodic information into appropriate vocal-motor codes, it is conceivable that inherent abilities or inclinations for music listening and exploring one's own singing voice may partially contribute to the genetic component for the Sing The Tune task measures.

10.3 Summary of Discussion

In relation to the primary aim of the study (i.e., determining whether there is a sizeable genetic component for singing ability), genetic analyses revealed that there are substantial genetic influences underlying the variance of singing proficiency across all singing tasks, as shown by the large genetic contribution ($A = 69-70\%$) on SINGCOMB, thus confirming the first hypothesis of the primary aim. In addition, sub-hypotheses were confirmed as significant genetic influences were estimated for some of the singing measures used to assess the abilities to vocally match single pitches ($A = 69\%$), sing a familiar song ($A = 44-72\%$), and imitate novel melodies ($A = 71\%$)

For each of the two melodic singing tasks, it was observed that the singing measure with relatively better behavioural performance also had a correspondingly higher heritability estimate compared to other measures of the same task. It was speculated that the better behavioural performance and higher heritability estimates reflect the preferential encoding of relative pitch and absolute pitch in long-term and short-term music memory, respectively.

The second hypothesis of the primary aim was confirmed by the significant genetic component estimated for subjectively-assessed singing ability based on self-report ($A = 72\%$). The similarity in the heritability estimates of self-rated singing ability and

SINGCOMB suggests that in this sample, self-reported singing ability was a reliable reflection of objectively-assessed singing ability of participants.

Finally, the significant and considerable genetic influences estimated for perceptual and vocal pitch-matching were consistent with previous findings from behavioural and molecular genetic studies.

With reference to the second aim of the study (i.e., determining the genetic basis of environmental components associated with singing ability), significant genetic influences were estimated for environmental components related to formal music training (i.e., Instrumental Expertise and Years of Music Training). The findings were in line with two recent twin studies that have reported moderate to large heritabilities ($A = 38\%$ and 69%) for music practice. Bivariate genetic analyses also revealed a partially shared genetic basis between these components related to music training and singing ability. Similarly, the associations between music perception ability and these training-related components were demonstrated to be mediated by significant shared additive genetic influences. The findings are in line with previous evidence of significant genetic correlations between music perception ability and accumulated music practice (Mosing, Madison, et al., 2014).

As for other singing and music background components, the large genetic component ($A = 66\%$) for Public Singing might be reflective of the social aspect of singing, rather than a phenotype for singing ability *per se*. The negligible genetic influences for Family Singing and Music Listening suggest that identical and non-identical twin pairs were similarly correlated in terms of childhood singing and music environment. These results provide promising evidence for the equal-environment assumption, which is a crucial assumption for the classical twin design.

The significant shared common environmental influences between Family Singing and all the singing task measures may point to the importance of a conducive family singing environment in shaping subsequent singing ability of children. Finally, Sing The Tune Task and SINGCOMB had significant genetic correlations with Personal Singing and Music Listening, which led to the speculation that inherent abilities or inclinations for

music listening and singing by oneself may partially contribute to the genetic components of these singing measures.

11

CONCLUSION

11.1 Summary of Thesis

Singing ability is probably the most universal and multi-faceted form of music making that encompasses a range of music perception and production subskills. Investigating the genetic basis of singing ability is thus an important step towards developing a greater understanding of the genetic basis of music ability.

In this thesis, the genetic basis of singing ability was examined using a twin study design, which is effective in disentangling the relative contributions of genetic and environmental influences on the variation of a trait in a population.

The study sought to interrogate two main research questions: 1) Is there a sizeable genetic component for singing ability?; 2) Is there evidence of genetic influences on the environmental components associated with singing ability?

To answer the first question, singing ability was both objectively and comprehensively assessed using three singing tasks, as well as subjectively-assessed based on self-reports. Univariate genetic analyses confirmed the main study hypothesis by demonstrating the presence of significant and substantial genetic influences ($A = 69\text{--}70\%$) underlying the variation in singing ability across all tasks. In particular, there were evidence of significant genetic contribution to the ability to vocally match single pitches ($A = 69\%$), to sing a familiar song ($A = 44\text{--}68\%$) and to sing novel melodies ($A = 71\%$), although the heritability estimates in each task varied depending on the task measure used. The significant and large heritability estimate for self-rated singing ability ($A = 72\%$) was consistent with the sizeable genetic influences found for objectively-assessed singing ability, thereby strengthening the case for the genetic basis of singing ability. In addition, the congruent heritability estimates between self-rating and objective

assessment lend support to the reliability of findings from previous genetic studies that utilised self-report measures (Vinkhuyzen et al., 2009).

The second research question was addressed by identifying environmental components associated with singing ability from a singing and music background questionnaire and estimating the genetic influences on these components using univariate genetic analyses. The significant genetic components ($A = 46\%$ and 68%) estimated for Years of Music Training and Instrumental Expertise confirmed the study hypothesis which predicted a significant genetic contribution for environmental components related to formal music training. Moreover, bivariate genetic analyses demonstrating significant genetic correlations between the two components and singing ability also supported the second hypothesis which predicted a partially shared genetic basis between formal music training and singing ability. While significant genetic correlations between music perception ability and accumulated music practice have been previously reported, this study was the first to report a similar finding for singing ability and formal music training. These promising results therefore help establish the genetic bases of environmental components associated with singing ability.

11.2 Implications for Research

For a long time, in the field of developmental psychology and music education research, many have argued in favour of the overriding importance of nurture in the development of music ability (Howe et al., 1998; Lehmann, 1997; Sloboda, 1996), to the extent that the importance of nature has not been given its due consideration. In line with recent music genetic research (Mosing, Madison, et al., 2014; Oikkonen et al., 2014; Park et al., 2012; Pulli et al., 2008; Ukkola et al., 2009), the current twin study challenged this prevailing view and demonstrated that both singing ability and music perception ability have substantial genetic components. Moreover, the study showed that some ostensibly “environmental” variables that were associated with singing and music perception were also significantly influenced by genetic factors. The undeniable role played by genes in influencing music and singing ability was further strengthened by the evidence that the associations between the singing task measures and environmental components relating to formal music training were significantly mediated by shared additive genetic

influences. These findings give clear indication that an extreme “environmentalist” account of music and singing development is untenable. The importance of genetic influences is unlikely to be limited to merely conferring innate anatomical or physiological advantages that enable some individuals to become expert singers and musicians. Rather, according to the current findings and other recent genetic research, the impact of genes in shaping music and singing ability is likely to be much more far-reaching.

In view of this, it is hoped that the findings from the current study will attract more research efforts into uncovering the genetic basis of other music abilities and music-related traits, such as those pertaining to individual differences in learning and motivation. In this respect, behavioural genetics is especially valuable in interrogating the interplay between genes and the environment and how this affects individual differences in musical traits. The utility of behavioural genetics in disentangling genetic, common environmental and unique environmental influences may sway researchers to put aside their “nurture bias” and give greater consideration to the impact of genetic influences by measuring environmental effects using genetically sensitive research designs. For instance, potential gene-environment correlations between music ability and related environmental variables can be detected through bivariate twin modelling, as was demonstrated in the present study.

Linking the genetic findings of the current study back to the vocal sensorimotor loop (VSL) proposed by Dalla Bella (see **Section 4.2.1**, p. 86), it can be observed that the current findings provide preliminary evidence of genetic influences on several components of the VSL. For instance, the genetic influences on Match The Note Task demonstrate the heritability of the pitch perception component of the VSL. The memory components (both long-term and short-term) of the VSL are also likely to be underpinned by genetic factors, as reflected by the genetic influences on vocal imitation tasks that rely on short-term music memory system (i.e., Sing The Note Task and Sing The Tune Task), and familiar song recall task (Happy Birthday Singing Task) that recruits long-term memory. The genetic effects were particularly salient for task measures (SingTheTune PD, HappyBirthday ID) that correspond with the preferential encoding of music in terms of absolute pitch and relative pitch information in short-term and long-term memory systems, respectively, thereby providing support that the large

genetic influences are likely to pertain to the memory components of the VSL. It is also possible, however, that the other components further down the loop (e.g., auditory-motor mapping and motor planning) were genetically influenced. This may be indicated by the large heritable component estimated for SINGCOMB, which considered the overall singing accuracy across all singing tasks, regardless of the memory system enlisted. It may be possible for subsequent behavioural genetic studies with larger sample sizes to shed light on the heritability of each VSL component using multivariate genetic models that estimate the proportion of genetic influences shared among different singing measures, and the proportion that is unique to a particular measure. For instance, given that Sing The Note Task is the vocal counterpart of Match The Note Task, the estimated shared genetic influences between the two measures probably reflect the genetic influences on music perception, which is common to both tasks, whereas the genetic influences specific to Sing The Note Task possibly indicate the genetic effects on the auditory-motor mapping and motor planning components. Findings from behavioural genetic research thus help form a strong basis for conducting molecular studies aimed at discovering the genetic correlates of various music and singing abilities.

Molecular genetic investigations can uncover the actual genetic mechanism by which gene expression may be conditional on environmental factors, and how gene expression in turn affects neurophysiological processes and ultimately influences musical behaviour. As music ability is likely to be influenced by multiple genes of small effect, elucidation of the actual genetic mechanisms of singing ability is expected to be challenging, since small genetic effects are usually hard to be detected reliably. It is thus all the more necessary to encourage more research efforts into such genetic investigations in order to advance understanding of the complexity of genotype-phenotype relationships in music ability, and how genetic influences may explain the heterogeneity of music learning outcomes both within and across individuals. The selection of suitable phenotypic markers is integral to the identification of more accurate and precise genotypes through molecular studies. As discussed in **Section 9.1** (p. 237), based on heritability estimates obtained in the current study, mean absolute pitch deviation appears to be a good phenotypic marker for singing ability in tasks that enlist short-term music memory (i.e., single pitch-matching and melody imitation tasks), whereas mean absolute interval deviation may be a suitable marker for the ability to

sing familiar songs, due to the salience of interval information in long-term music memory. The behavioural genetic findings of the current study therefore provide a useful point of departure for future research that is interested to investigate the molecular basis of singing.

Ultimately, it is hoped that molecular genetics and neuroscientific research may eventually provide substantive evidence for inherent musical capacity in human beings.

11.3 Implications for Music Education

Recognising the importance of genetic influences in explaining individual differences in singing and music ability has important implications for music education. The current findings and other similar recent work serves to encourage music educators to take into account the role of genes when devising music teaching strategies. Some music pedagogues may be uncomfortable with accepting the influence of genetic factors in the acquisition of music ability because of erroneous beliefs that this may promote social inequality through selective allocation of resources to certain individuals while depriving others of the opportunities (Kovas, Tikhomirova, Selita, Tosto, & Malykh, 2016). In reality, however, genetic information can potentially be used to optimise music learning for everyone by devising more informed and well-tailored music education and intervention programs that recognise individual differences in musical strengths and weaknesses and are suited to each individual's musical capacity.

Despite the well-documented benefits and value of music education, the Commonwealth Government's National Review of Music Education revealed that the situation in Australian music education has reached a "critical point" (Pascoe et al., 2005), with a dearth of music education opportunities in Australian schools and communities. The review received one of the largest public responses to a government inquiry, and established an immediate priority for improving and sustaining the quality and status of music education in schools. Such effort is especially critical in view of the fact that active music participation has declined among Australian adults. It is conceivable that "one-size-fits-all" music education approach may not be effective in eliciting the same degree of learning outcomes or fostering positive music and singing

experiences in everyone, which in turn may diminish interest and motivation in music learning and engagement.

To develop teaching strategies that will maximise music learning success for each person, a better understanding of the roles played by genes and environment in the aetiology of music ability is thus necessary. It is hoped that continued research efforts in this field will eventually lead to the identification of genetic and environmental markers that can account for individual differences in music ability. Based on the preliminary findings from this study, the numerous singing task measures showing sizeable genetic influences can potentially be used as phenotypic markers for singing ability. Subsequent genetic studies can explore possible gene $\times$ environment interactions to determine whether the genetic effects on these phenotypic markers vary as a function of putative environmental markers, such as Family Singing, Music Listening and Years of Music Training, as identified in the current study. For instance, gene $\times$ environment interactions may reveal that the genetic influences on one singing phenotype may diminish as instrumental expertise increases, whereas the genetic influences on another aspect of singing ability may become less important as the amount of music listening increases. Understanding the interplay between genetic and environmental influences would therefore help music educators or parents to develop teaching strategies that will be particularly effective to address a certain area of singing or music ability, according to a child's need. Moreover, understanding how genetic influences on a music or singing phenotype may vary with age will help parents and music educators to know the time window during which an ability will be most malleable to intervention or training strategies. For example, if the genetic influences on a certain music or singing skill are demonstrated to increase with age in a manner similar to the heritability of IQ, until a plateau is reached at some point, it is likely that implementing early childhood intervention or training would be especially beneficial for the development and acquisition of this particular skill.

The above examples serve to demonstrate how genetic knowledge can be beneficial for improving the music learning outcomes of all children through the joint efforts of scientists, educators and policy makers in integrating music-related genetic, neuroscientific and educational research findings to develop and implement more efficacious music teaching methods.

11.4 Study Limitations

While the current study has reported many promising findings, there are a number of limitations. First, as noted in **Section 6.1.1** (p. 148), the response rate to the online twin study was extremely low, with a recruitment rate of approximately 7% from the Australian Twin Registry. As a result, the sample size for the current twin study was comparatively smaller than other recent twin studies (Hambrick & Tucker-Drob, 2014; Mosing, Madison, et al., 2014), albeit comparable in size with that of Seesjärvi et al. (2015). Although this causes overall power limitations, significant genetic influences remained evident across various tasks and measures. Moreover, the significantly different ICCs between MZ and DZ twins across the majority of the task measures demonstrated the importance of genetic influences in explaining the variation in singing and music perception abilities.

Second, the majority of the current sample was female (76.4%). While no sex-limitation effects were detected prior to genetic modelling (see **Section 9.1.2**, p. 239), and sex was also included as a covariate in the genetic models, it is conceivable that the findings of the current study are more applicable to females rather than being representative of the general population. A larger sample of male twins is necessary to reliably test for sex-limitation effects and explore whether the relative contribution of genetic and environmental influences in task variance may differ between males and females.

Third, although it was indicated in the invitation email and information sheet that no prior singing and music background was required to participate in the study, musically-trained participants still constituted approximately 86% of the final sample (**Table 6.1**, p. 146). There is potentially a selection bias, whereby the current sample was more musically inclined than the general population. This, however, is unlikely to have significant bearing on the observed main findings. Although not reported in Chapter 9, univariate genetic analyses that adjusted for the effects of age, sex and years of music training were initially conducted for all the objective task measures. After bivariate genetic analyses revealed that most of the task measures and years of music training had significant shared genetic influences, the abovementioned univariate genetic modelling results were excluded from the main findings because the partially shared genetic basis between the task measures and years of music training implies that adjusting for the

effects of years of music training may cause the genetic influences on the age, sex and music training-adjusted task measures to be underestimated. Despite the likely underestimation of genetic effects, apart from Sing The Tune Task, most of the measures of other music and singing tasks as well as the combined singing score still showed significant genetic influences after adjusting for the effects of years of music training (see **Table E-13** in **Appendix E**, p. 391). These results therefore attest to the importance of genetic factors in the variation of singing and music abilities.

Finally, the online nature of the twin study meant that it was not conducted in a carefully controlled laboratory setting. Although pre-emptive measures were undertaken during program development to mitigate potential issues that arise from conducting a study online (see **Section 5.3.1**, p. 126), it was not possible to control for every factor.

11.5 Future Directions

In light of the limitation in sample size of the current study, larger twin studies should be conducted in the future to confirm the positive findings from the present study. It is hoped that the larger sample would comprise more male twins, more non-musically trained participants, and a more even distribution of MZ and DZ twin pairs. Replication of the positive findings from the current study by a larger twin study would establish, beyond question, that singing ability has a substantial genetic component.

Moreover, a larger twin sample likely provides sufficient power to run more complex genetic analyses and allow more meaningful interpretations to be drawn from the results. For example, the shared genetic and environmental influences mediating the associations between the task measures and environmental variables could be more reliably estimated, which would include determining the extent (in terms of percentage) to which genetic or environmental factors were shared. In addition, a larger-scaled twin study would also make it possible to conduct multivariate genetic modelling and examine how much genetic or environmental factors are shared among different singing task measures, among singing tasks and music perception tasks, or among the task measures and other related traits such as cognitive ability or motivation.

A larger twin sample also increases the utility of running other sophisticated genetic models. For example, univariate genetic models with age as the moderating variable could help to investigate how the relative contribution of genetic and environmental factors to music and singing abilities may vary at different ages or stages of development. Similarly, potential variation in genetic and environmental influences due to differences in music training duration could be explored by using years of music training as a moderating variable. Such investigations may enable a better understanding of the non-static nature of genetic effects on trait variation and help identify interesting trends in the variation of heritability and environmental influences with age or with level of music expertise.

Furthermore, subsequent behavioural genetic investigations into singing and music abilities would be enhanced if twin registries from other countries or cultures could be utilised in order to study the effects of socio-cultural environment on the heritability estimates of music abilities and music-related traits. As compared to what was observed in the current study, it is conceivable that singing or music ability may be subjected to a stronger environmental component relating to the cultural environment, which incorporates singing and music making activities into everyday community living, such as the African culture (Blacking, 1995; Primos, 2002).

Prior to the current twin study, few genetic studies had investigated the genetic basis of music production ability. It is therefore hoped that the promising results from the present study will become a driving force for subsequent twin studies to explore the genetic basis of other music production abilities. If more behavioural genetic studies are able to demonstrate consistent genetic influences for various music abilities and determine the degree of shared genetic influence among these traits, this will support subsequent research efforts to conduct molecular genetic studies to identify the genetic determinants and mechanisms of singing and music abilities.

11.6 Conclusion

The current twin study is the first to investigate and establish the genetic basis of singing ability by objectively assessing singing accuracy across a comprehensive set of

singing tasks. The substantial genetic component found for objectively-assessed singing ability was also supported by subjectively-assessed singing ability, which revealed a heritability estimate of similar magnitude. In addition, the study provided novel evidence for a partially shared genetic basis between singing ability and formal music training. These findings set a valuable background for subsequent behavioural and molecular genetic studies to continue the investigation of the role of genetic factors in influencing various forms of music ability.

While the current findings highlight the importance of genetic influences on singing ability, it should be recognised that the results do not in any way negate the value and necessity of conducive home and formal music learning environments in the development of music and singing ability. Parents and music educators are still obliged to create environments that will be favourable for music development, with due consideration of individual differences in music ability and interest, so as to optimise music learning experiences and outcomes. Ultimately, by gaining a more complete picture of the contributions and interplay of genes and environment in the neurobiology of music learning and music ability, the current study and other music genetic studies hope to enable more people to enjoy and maintain lifelong singing and music engagement, so as to reap the physical, mental, emotional and social benefits singing and music have to offer. This captures the ethos that was elegantly expressed by William Byrd, the Renaissance English composer in 1588, in the preface of his songbook *Psalms, Sonnets and Songs*,

“Since singing is so good a thing, I wish all men would learn to sing.”

Appendices

Appendix A

RECRUITMENT

INFORMATION

Appendix A-1 Recruitment Email for ATR Twins

Your ATR ID Number:

email address:



Why Do We Need To Sing?

Dear Twin,

Did you know that singing enhances our wellbeing and affords benefits to our speech and cognitive development, improving our quality of life? It is not well understood though how this ability emerges and develops. This study seeks to understand the role of genes in singing ability.

About the Project

We are currently inviting our twin members to take part in a fun and engaging interactive online singing survey – it is also the world's first twin study to deal with singing.

All twin pairs who complete the survey will be eligible for a lucky draw to win two iPad minis - one each! (see [Terms & Conditions](#) for more details).

All twins aged 15 and above with access to a computer with Adobe Flash Player, active internet connection and a computer microphone are welcome to participate in the study (click [here](#) for more details about required equipment). *Smart phones, Tablets and iPads will not be able to load the study.*

Participation in this study does not require any musical experience, nor do you need to know how to sing.

What is Involved

Participation involves completing an online assessment, comprising of 6 main singing related tasks and a questionnaire. Completion of the tasks should take approximately 30 minutes.

To read more about what is involved, please see the attached [information sheet](#). We have also included some information designed to assist you should you encounter any difficulties completing the online test.

If you are willing to take part in the study, please click

[HERE](#)

At the beginning of the assessment, you will be asked to enter your ATR ID for identification purposes of the study. (As a reminder, your ATR ID is «TwinID»).

(If the link does not activate, cut and paste the following into your web browser: <http://twinsing.solvswweb.com/>)

Alternatively, you can choose to complete the online assessment at the University of Melbourne Parkville campus. To arrange a session time or for more information, please contact the student researcher Yi Ting Tan (Phone: 0434 498 242; Email: yitt@student.unimelb.edu.au).

This project has been independently reviewed and approved by the ATR as having significant scientific value and meeting the necessary ethical requirements. The ATR has ethical approval from the University of Melbourne's Human Research Ethics ([Confidentiality and Ethics](#)).

We appreciate your consideration and thank you in advance of receiving your response.

Many thanks,
John Hopper, Director

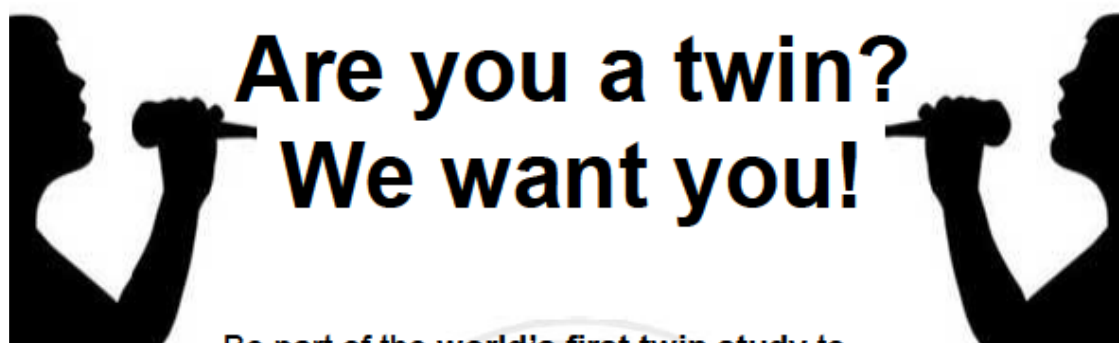
[Update your contact details](#)



The Australian Twin Registry is supported by an Enabling Grant from the National Health and Medical Research Council administered by the University of Melbourne

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Appendix A-2 Recruitment Poster for On-Campus Participant Recruitment



Be part of the world's first twin study to investigate how genes influence singing ability.

You will get to do a series of fun, online interactive music tasks*!

You and your twin could each win an iPad mini with retina display!

Even if you think you can't sing, we want you!

For more information, please contact Yi Ting Tan at:
yitt@student.unimelb.edu.au or 0434 498 242

*You can opt to either do the online study on your computer or arrange a session time with us to do the online study on-campus.

(Ethics approval number: HREC 1238728.3)

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Appendix A-3 Pre-Screening Zygoty Questionnaire for Non-ATR Twins

1. Are you part of a set of:
 - a) Twins
 - b) Triplets
 - c) Quadruplets
 - d) Quintuplets
 - e) Septuplets
 - f) Octuplets
 - g) Others
 2. Gender: Male/Female
 3. Date of Birth (DD/MM/YYYY): _____
 4. Which country were you and your twin born in? _____
 5. (If country of birth was Australia) Which State or Territory were you and your twin born in?
 6. Are you the older twin? Yes/No
 7. First Name: _____ Preferred Name: _____
 8. Surname: _____ Previous Surname: _____
- Contact details** (please provide at least one of the following)
9. Home Phone: _____
 10. Mobile: _____
 11. Email: _____
 12. Are you and your twin IDENTICAL or NON-IDENTICAL?
 - a) Identical
 - b) Non-identical
 - c) Not sure

13. How did you find out you were IDENTICAL or NON-IDENTICAL?

- a) We think of ourselves this way
- b) We were always told we were by our parents
- c) We had a DNA test
- d) The Doctor/Obstetrician/Midwife told us/our parents
- e) We are male/female twins
- f) Other reasons: _____

14. Do you and your twin have the same eye colour? Yes/No

15. Do you and your twin have similar height, weight and natural hair colour and texture? Yes/No

16. Were you and your twin usually mistaken for one another by non-family members as children? Yes/No

Appendix A-4 Study Information Sheet



Dear Twin Registry Member,

We would like to invite you and your twin to participate in an online assessment for our study: *Investigating the Genetic Basis of Singing Ability: A Twin Study*. This project will form part of Ms Yi Ting Tan's doctoral dissertation.

What is the study about?

Nature or nurture? For centuries, many have been intrigued by the expression of musical abilities. Singing behaviour is ideal for such investigation because it is a universal trait present in all human societies and emerges early in human development. Interestingly, singing ability varies across individuals. We have all heard accounts of “singing families” whose family members appear to possess naturally good singing abilities. On the other hand, there are also people who cannot seem to carry a tune, even though they may have other forms of musical abilities, such as playing musical instruments or appreciating music. Brain research has already shown how the “singing network” in our brain varies with singing ability. This means it is possible that there is a genetic component to singing ability.

Our study will be the world's first twin study to investigate the genetic basis of singing ability through an interactive online assessment. It aims to explore the relative contributions of genetic and environmental components to singing ability. The online assessment is designed to be fun and engaging, and you can perform the simple tasks in the comfort and privacy of your own home. Participating in this study does not require any singing or musical experience. Rather, we invite people from all musical backgrounds to participate. This will allow us to have a representative set of results to conduct meaningful analyses.

Who is eligible?

We are seeking the participation of identical and non-identical twins aged 15 and above, with no diagnosed hearing deficits or vocal cord lesions (e.g., nodules, polyps and cysts), no current mental illness (excluding anxiety and/or depression), and no history of brain injury, stroke, genetic or neurological disorders.

Please note that you will need access to a computer with Adobe Flash Player (this is free and easy to download on all types of computers), a computer microphone (inbuilt or external; e.g., webcam or computer headset), and internet capability to participate. Tablets, iPads and smart phones are unable to be used for the online assessment.

What is involved?

Participation involves the completion of an online assessment, comprising of 6 main singing related tasks and a questionnaire.

The singing related section consists of:

Brief background questionnaire - includes general questions about your name, gender, date of birth, first language and ethnicity, and education and employment level.

Familiar song singing task - sing a familiar song in several different conditions (e.g., at a self-determined pace or a prescribed pace, with or without lyrics), starting at any pitch that is most comfortable for you.

Manual pitch-matching task - match a series of pitches by moving a pitch slider.

Vocal pitch-matching task - sing a series of pitches that have been played to you.

Vocal melody-matching task - sing several short melodies that have been played to you.

Tongue twister task - one-phrase tongue twister in unpaced and paced conditions.

Distorted tune task - identify the correct version of a familiar song from several mistuned versions.

The questionnaire component includes questions about your childhood musical environment, musical expertise, interest in singing and self-assessment of singing ability.

Your responses to certain tasks will be audio-recorded for subsequent data analysis. You will be shown how to do this by the online program. We estimate that the total time commitment required of you will take approximately **30 minutes**.

What are the benefits of taking part in the study and what kind of feedback will be provided to the participants?

We hope that you will find the online singing assessment fun and engaging, and that you will enjoy being able to help our study, which may eventually lead to the development of more sophisticated classroom singing training programs that take into account differences between individuals, such as musical ability. Once the study arising from this research has been completed, a brief summary of the findings will be available to you. It is also possible that the results will be presented at scientific conferences and scientific journals.

Every twin pair where both twins have completed the entire online singing ability survey will also be eligible to enter a **lucky draw** at the end of the recruitment period. Each twin from the winning twin pair will be awarded an **iPad mini with retina display**. For more information about the lucky draw, please refer to the [iPad mini lucky draw terms and conditions](#).

As an exclusive promotion in line with the 2015 Twins Plus Festival, **the first 40 pairs of twins** who both complete the entire online singing ability survey between 10AM AEST Sunday 22 March 2015 and 11:59PM AEST Sunday 5 April 2015, will be entitled to receive a **\$40 WISH eGift card**, one for each twin. For more information about the promotion, please refer to the [\\$40 WISH eGift card Promotion terms and conditions](#).

Participation is voluntary.

You are under no obligation to take part in this study and you are free to withdraw at any stage. You may ask questions and request written information about the study at any time. Should you wish to withdraw at any stage, or to withdraw any unprocessed data you have supplied, you are free to do so without prejudice.

How will my confidentiality be protected?

All data collected for the study will remain confidential. It will be used only for the purposes of investigating singing ability. It will be stored securely, with access limited to members of the research team. The information you provide to the study will not be made available to anyone outside of the research team and the Australian Twin Registry without your consent.

The research team will not share personal information among family members without the approval of the individual concerned. The results of the research will be published in a form that will not allow individuals to be identified.

Where can I get further information?

Should you require any further information, or have any concerns, please do not hesitate to contact Ms Yi Ting Tan on 0434 498 242 or via e-mail yitt@student.unimelb.edu.au, or Prof Sarah Wilson on (03) 8344 7391 or via e-mail sarahw@unimelb.edu.au, or Prof Gary McPherson on (03) 8344 7889 or via email g.mcpherson@unimelb.edu.au. Should you have any concerns about the conduct of the project, you are welcome to contact the Executive Officer, Human Research Ethics, The University of Melbourne, on ph: 8344 2073, or fax: 9347 6739.

Thank you for taking the time to consider this study.

Sincerely,

Ms Yi Ting Tan

BMus (Hons)

PhD candidate in Musicology

Melbourne Conservatorium of Music

Prof Sarah Wilson

Bsc (Hons), PhD, MAPS, CCN

Professor & Deputy Head of School,

Melbourne School of Psychological Sciences

Prof Gary McPherson

DipMusEd, MMusEd, PhD

Ormond Chair and Director,

Melbourne Conservatorium of Music

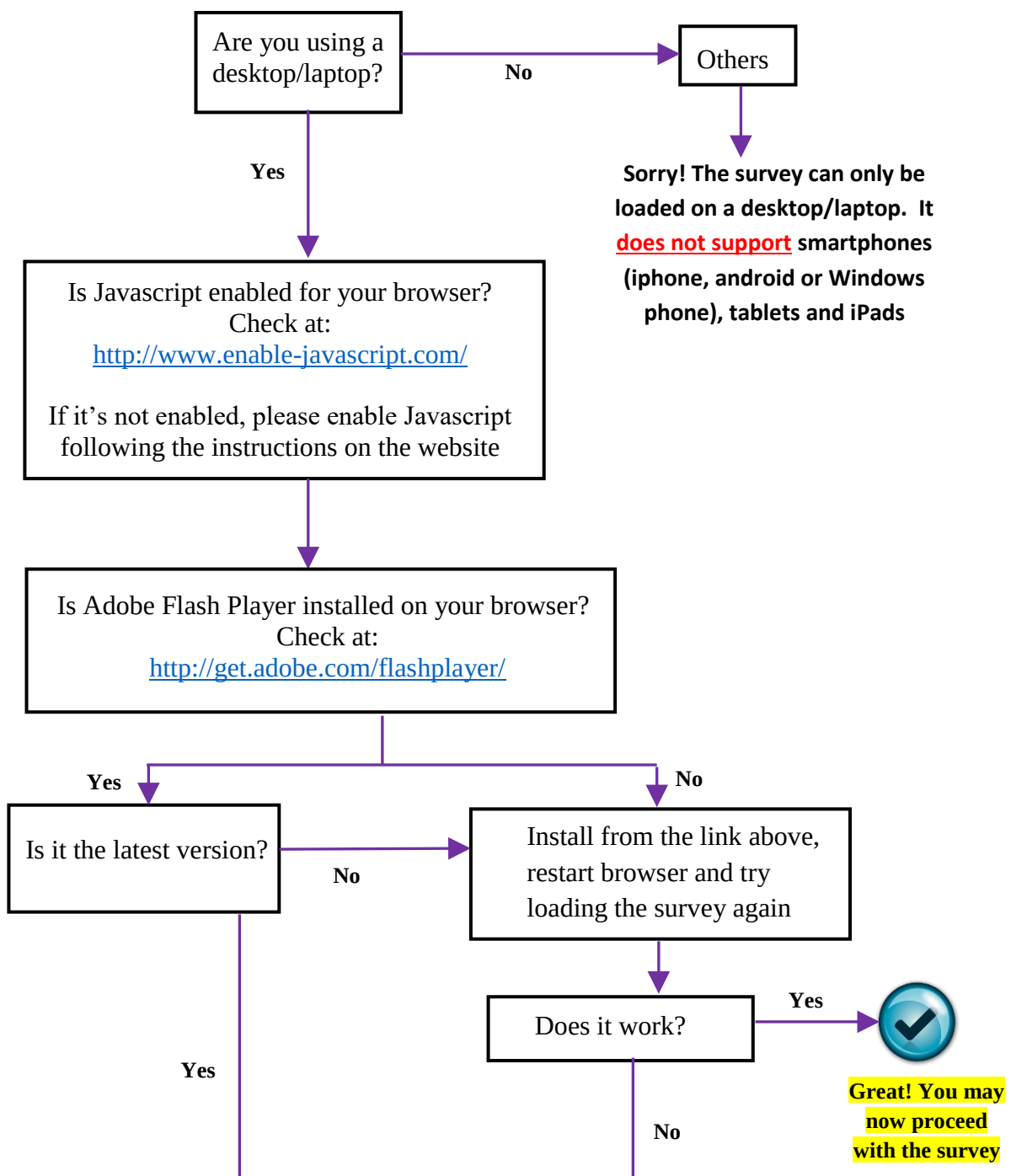
Appendix B

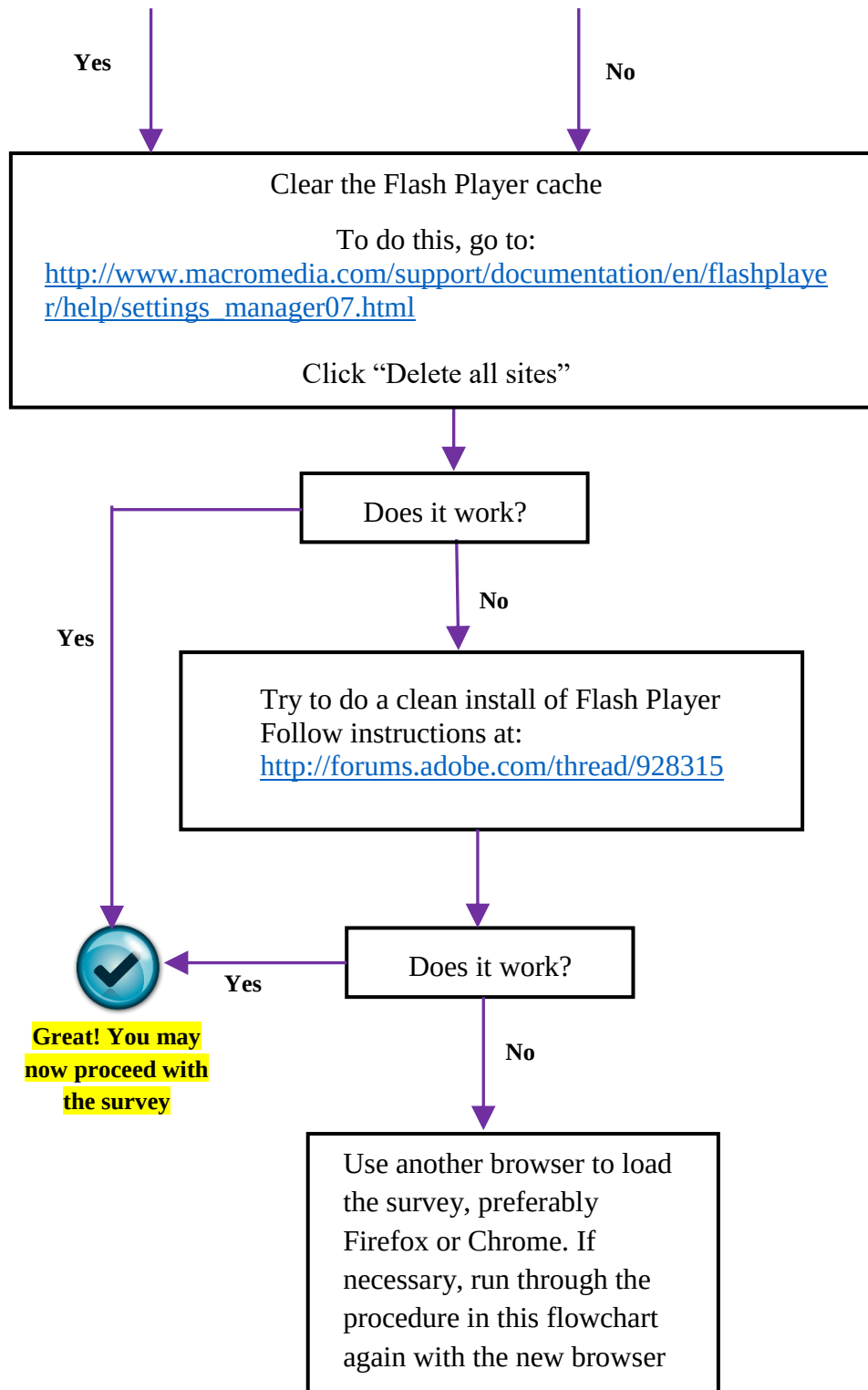
TROUBLESHOOTING INSTRUCTIONS

Appendix B-1 Troubleshooting Instructions for Problem with Loading the Program

Having problems? You can contact Yi Ting, the researcher of this study at: 0434498242 (mobile) or yitt@student.unimelb.edu.au (email) for troubleshooting assistance.

Or you can follow the flowchart below to self-troubleshoot:





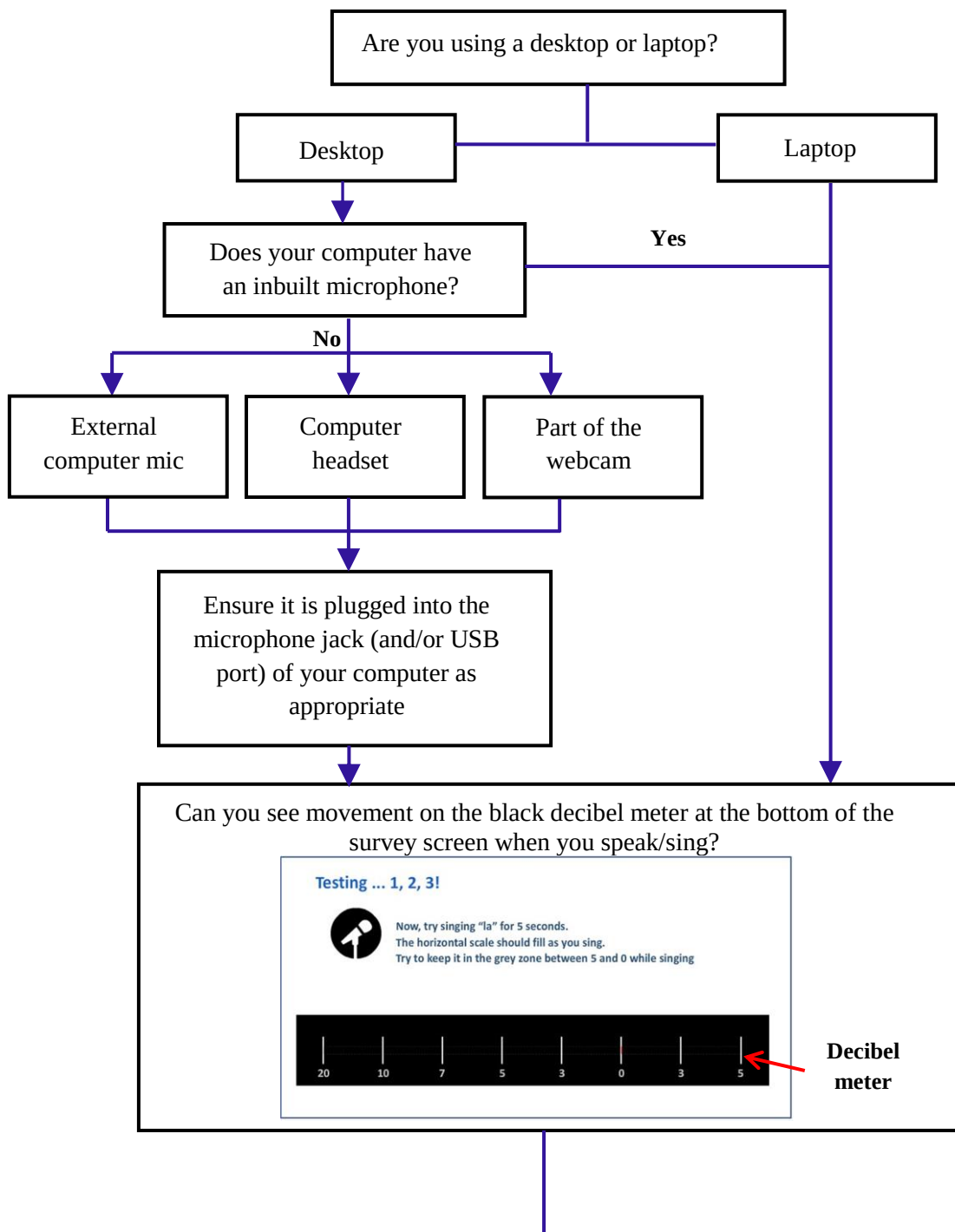
Still not working?

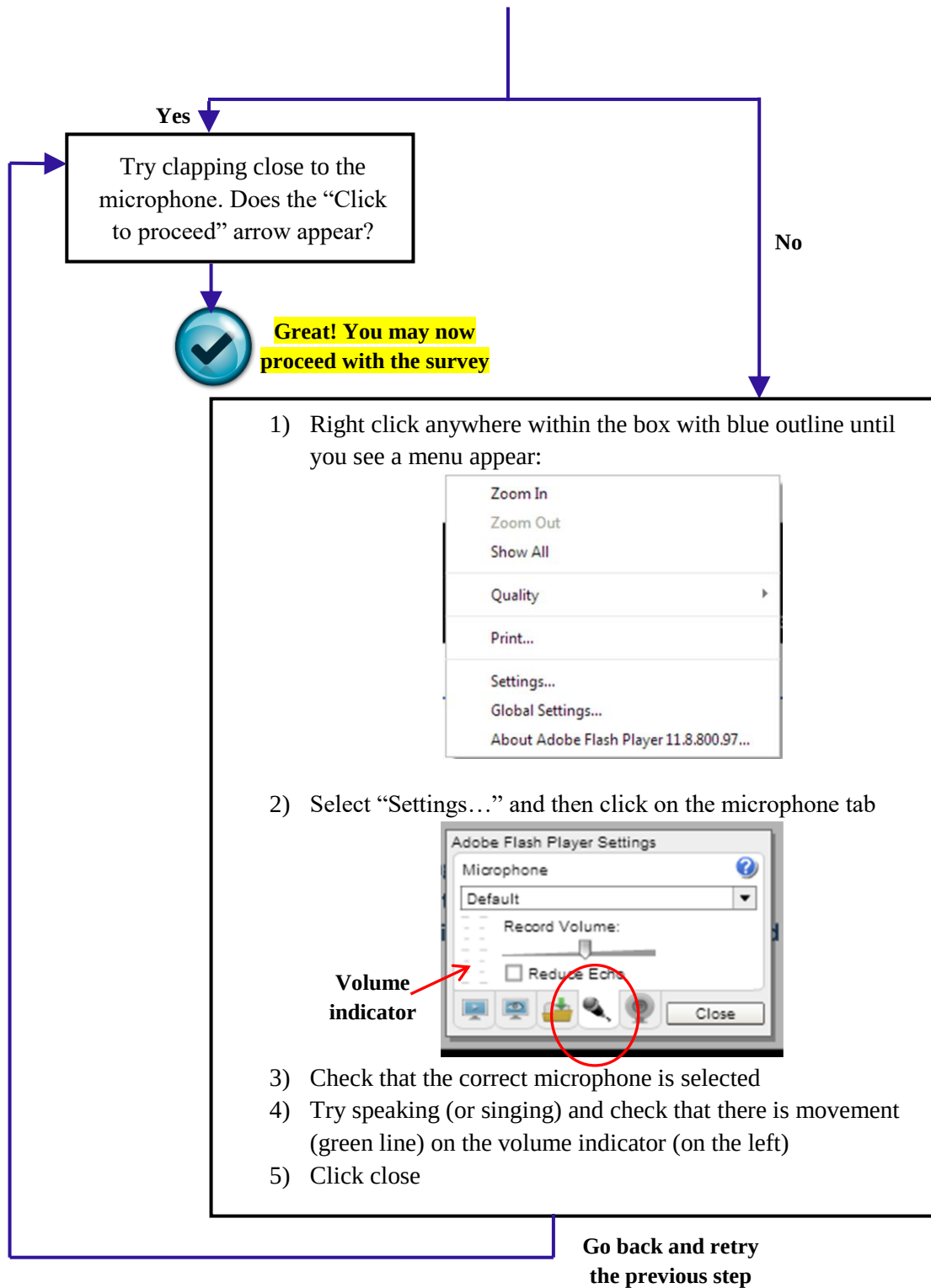
For technical assistance, please contact Yi Ting using the contact information above the flowchart

Appendix B-2 Troubleshooting Instructions for Microphone Detection Problem

Having problems? You can contact Yi Ting, the researcher of this study at: 0434498242 (mobile) or yitt@student.unimelb.edu.au (email) for troubleshooting assistance.

Or you can follow the flowchart below to self-troubleshoot:





Appendix C

PROGRAMMING CODES

Appendix C-1 Praat script for estimating f_0 values

```
# This Praat script gets the sampled  $f_0$  values estimated by Praat and
output the values in a text file
# Note: TextGrid and WAV files must have the same file names and be in
the same directory.

form Get F0

    comment Directory of sound files
    text sound_directory F:\participant\folder\number\
    sentence Sound_file_extension .wav
    comment Directory of TextGrid files
    text textGrid_directory F:\participant\folder\number\
    sentence TextGrid_file_extension .label

    comment Pitch analysis parameters
    positive time_step 0.01
    positive minimum_pitch 200
    positive maximum_pitch 600
    positive voicing_threshold 0.45
    positive silence_threshold 0.03
    positive octave_jump_cost 0.35
    positive octave_cost 0.01

endform

#Read all files in a folder
Create Strings as file list... list
'sound_directory$'*'sound_file_extension$'
numberOfFiles = Get number of strings

for ifile to numberOfFiles

# Extract sampled  $f_0$  using the specified pitch settings
filename$ = Get string... ifile
Read from file... 'sound_directory$/'filename$'
soundname$ = selected$ ("Sound",1)
To Pitch (ac)... time_step minimum_pitch 15 no silence_threshold
voicing_threshold octave_cost octave_jump_cost 0.14 maximum_pitch
Rename: "pitch"

#Delete any existing old  $f_0$  files with the same name
filedelete 'sound_directory$'soundname$.samplef0

# Write-out the header (copy if necessary)
resultfile$ = "'sound_directory$'soundname$.samplef0"
titleline$ = "intervalname'tab$'SampleTime'tab$'F0 (Hz)'newline$"
fileappend "'resultfile$'" 'titleline$'

# Open a TextGrid by the same name:
gridname$ =
"textGrid_directory$'soundname$'textGrid_file_extension$"
if fileReadable (gridname$)
Read from file... 'gridname$'
    numberOfIntervals = Get number of intervals... 1

# Get the sampled  $f_0$  from each labelled segment
```



```

for k from 1 to numberOfIntervals
select TextGrid 'soundname$'
  label$ = Get label of interval... 1 'k'
  if label$ <> ""

    # calculates the onset and offset
    onset = Get starting point... 1 'k'
    offset = Get end point... 1 'k'

    #Get sampled  $f_0$  at 0.01 s intervals
    for i to (offset-onset)/0.01
      time = onset + i*0.01
      selectObject: "Pitch pitch"
      pitch = Get value at time: time, "Hertz", "Linear"

      # Save result to text file:
      resultline$ =
        ""label$""tab$""time""tab$""pitch""newline$""
      fileappend ""resultfile$"" 'resultline$'
    endfor
  endif
endfor

# Remove the TextGrid object from the object list
select TextGrid 'soundname$'
Remove

endif

# Remove the temporary objects from the object list
select Sound 'soundname$'
Remove
select Strings list
# and move on to the next sound file
endfor

# clean up
select all
Remove

```

Appendix C-2 VBA macro to export f_0 data from .sampledf0 files onto Excel spreadsheet

```

Sub ReadSamplef0 ()

'====reading samplef0 files from a participant's folder for all
three tasks

Const adOpenStatic = 3
Const adLockOptimistic = 3
Const adCmdText = &H1

Dim intRow As Integer
Dim num As Integer
Dim ctr As Integer
Dim fileCtr As Integer
Dim cellAlpha As String
Dim refcol As Integer
Dim currFile As String
Dim currfolder As String
Dim file1 As String
Dim filefront As String
Dim fileHBD As String
Dim fileSTN As String
Dim fileSTT As String

Dim taskCtr As Integer
Dim taskName As String
Dim trialNo As String
Dim gender As String

Dim FilePath As String
Dim fileName As String
Dim lineCtr As Integer

currfolder = "216" '====Change accordingly
gender = "female" '====Change accordingly

'====file destination
filefront = "F:\PhDstuff\complete pairs analysis\2015 New Proc\"

'====file names for the exported  $f_0$ , organised by tasks
fileHBD = filefront & currfolder & "\" & currfolder & "_HBDraw.xlsx"
fileSTN = filefront & currfolder & "\" & currfolder & "_STNraw.xlsx"
fileSTT = filefront & currfolder & "\" & currfolder & "_STTraw.xlsx"

file1 = ".samplef0"

For taskCtr = 1 To 3

'====Happy Birthday Singing Task
If taskCtr = 1 Then

    Workbooks.Add
    ActiveWorkbook.SaveAs fileName:= _

```

```

fileHBD, _
FileFormat:=xlOpenXMLWorkbook, CreateBackup:=False

Set wbl = Workbooks(currfolder & "_HBDDraw.xlsx")

'#To read the  $f_0$  data of the four trials one by one
For fileCtr = 1 To 4

    If fileCtr = 1 Then
        Set curr_ws = wbl.Sheets(1) 'change accordingly
        curr_ws.Activate
        curr_ws.Name = "1"
        currFile = "song1"
    ElseIf fileCtr = 2 Then
        Set curr_ws = wbl.Sheets(2) 'change accordingly
        curr_ws.Activate
        curr_ws.Name = "2"
        currFile = "song2"
    ElseIf fileCtr = 3 Then
        Set curr_ws = wbl.Sheets(3) 'change accordingly
        curr_ws.Activate
        curr_ws.Name = "3"
        currFile = "song3"
    ElseIf fileCtr = 4 Then
        Set curr_ws = wbl.Sheets(4) 'change accordingly
        curr_ws.Activate
        curr_ws.Name = "3a"
        currFile = "song3a"
    End If

    strpathtotextFile = "F:\PhDstuff\deidentifiedpairs\" &
currfolder

    ' =====creating the schema.ini file
    FilePath = strpathtotextFile & "\Schema.ini"
    Open FilePath For Output As #1

        fileName = "[" & currFile & file1 & "]"
        Print #1, fileName
        fileName = ""

        Line1 = "Format = TabDelimited"
        Print #1, Line1

        Line2 = "Col1 = rowLabel Text"
        Print #1, Line2

        Line3 = "Col2=SampleTime Double"
        Print #1, Line3

        Line4 = "Col3=F0 Double"
        Print #1, Line4

    Close #1

    Set objConnection = CreateObject("ADODB.Connection")
    Set objRecordSet = CreateObject("ADODB.Recordset")

    objConnection.Open "Provider=Microsoft.Jet.OLEDB.4.0;" & _

```

```

        "Data Source=" & strpathtoTextFile & ";" & _
        "Extended
Properties=""text;HDR=YES;FMT=Delimited""

objRecordSet.Open "SELECT * FROM " & currFile & file1, _
objConnection, adOpenStatic, adLockOptimistic,
adCmdText

'#Write the f0 values of each of the 4 phrases into separate columns
For ctr = 1 To 4

    If ctr = 1 Then
        cellAlpha = "A"
    ElseIf ctr = 2 Then
        cellAlpha = "I"
    ElseIf ctr = 3 Then
        cellAlpha = "Q"
    ElseIf ctr = 4 Then
        cellAlpha = "Y"
    End If

    refcol = Range(cellAlpha & 1).Column

    intRow = 51

    If ctr = 1 Or ctr = 2 Or ctr = 3 Then

        Do While objRecordSet(0) <> "p"
            Cells(intRow, refcol) = objRecordSet(0)
            Cells(intRow, refcol + 1) = objRecordSet(1)
            Cells(intRow, refcol + 2) = objRecordSet(2)

            intRow = intRow + 1
            objRecordSet.MoveNext
        Loop

        Do Until objRecordSet(0) <> "p"
            objRecordSet.MoveNext
        Loop

    ElseIf ctr = 4 Then

        Do Until objRecordSet.EOF
            Cells(intRow, refcol) = objRecordSet(0)
            Cells(intRow, refcol + 1) = objRecordSet(1)
            Cells(intRow, refcol + 2) = objRecordSet(2)

            intRow = intRow + 1
            objRecordSet.MoveNext
        Loop

    End If

    Next ctr    '#go to the next phrase in the trial

objRecordSet.Close
objConnection.Close

Set objRecordSet = Nothing
Set objConnection = Nothing

```

```

        If fileCtr < 4 Then
            Sheets.Add after:=ActiveSheet
        End If

    Next fileCtr    '#go to the next trial

    wb1.Save

    '====Sing The Note Task
    ElseIf taskCtr = 2 Then

        Workbooks.Add
        ActiveWorkbook.SaveAs fileName:= _
        fileSTN, _
        FileFormat:=xlOpenXMLWorkbook, CreateBackup:=False

        Set wb2 = Workbooks(currfolder & "_STNraw.xlsx")

        taskName = "singTheNote_" & gender    'female/male

        If gender = "female" Then
            '#Info from each of the 5 pitch stimuli saved on a
            separate spreadsheet
            For fileCtr = 1 To 5

                If fileCtr = 1 Then
                    Set curr_ws = wb2.Sheets(1) 'change accordingly
                    curr_ws.Activate
                    curr_ws.Name = "B3"
                    currFile = "B3"

                ElseIf fileCtr = 2 Then
                    Set curr_ws = wb2.Sheets(2) 'change accordingly
                    curr_ws.Activate
                    curr_ws.Name = "CS4"
                    currFile = "CS4"

                ElseIf fileCtr = 3 Then
                    Set curr_ws = wb2.Sheets(3) 'change accordingly
                    curr_ws.Activate
                    curr_ws.Name = "DS4"
                    currFile = "DS4"

                ElseIf fileCtr = 4 Then
                    Set curr_ws = wb2.Sheets(4) 'change accordingly
                    curr_ws.Activate
                    curr_ws.Name = "F4"
                    currFile = "F4"

                ElseIf fileCtr = 5 Then
                    Set curr_ws = wb2.Sheets(5) 'change accordingly
                    curr_ws.Activate
                    curr_ws.Name = "G4"
                    currFile = "G4"

                End If

                strpathtoTextFile = "F:\PhDstuff\deidentifiedpairs\" &
currfolder

```

```

'#For each stimulus, f0 data of each of the 3 trials saved in
separate columns
    For ctr = 1 To 3

        If ctr = 1 Then 'trial a
            trialNo = "_1"
            cellAlpha = "A"
        ElseIf ctr = 2 Then 'trial b
            trialNo = "_2"
            cellAlpha = "I"
        ElseIf ctr = 3 Then 'trial c
            trialNo = "_3"
            cellAlpha = "Q"
        End If

        '==== creating the schema.ini file

        FilePath = strpathtoTextFile & "\Schema.ini"
        Open FilePath For Output As #1

            fileName = "[" & taskName & currFile & trialNo &
file1 & "]"

            Print #1, fileName
            fileName = ""

            Line1 = "Format = TabDelimited"
            Print #1, Line1

            Line2 = "Col1 = rowLabel Text"
            Print #1, Line2

            Line3 = "Col2=SampleTime Double"
            Print #1, Line3

            Line4 = "Col3=F0 Double"
            Print #1, Line4

        Close #1

        '=====

        Set objConnection = CreateObject("ADODB.Connection")
        Set objRecordSet = CreateObject("ADODB.Recordset")

        objConnection.Open "Provider=Microsoft.Jet.OLEDB.4.0;"
& _
            "Data Source=" & strpathtoTextFile & ";" & _
            "Extended
Properties="""text;HDR=YES;FMT=Delimited"""

        objRecordSet.Open "SELECT * FROM " & taskName &
currFile & trialNo & file1, _
            objConnection, adOpenStatic,
adLockOptimistic, adCmdText

        refcol = Range(cellAlpha & 1).Column

        intRow = 51

        Do Until objRecordSet.EOF

```

```

        Cells(intRow, refcol) = objRecordSet(0)
        Cells(intRow, refcol + 1) = objRecordSet(1)
        Cells(intRow, refcol + 2) = objRecordSet(2)

        intRow = intRow + 1
        objRecordSet.MoveNext
    Loop

    objRecordSet.Close
    objConnection.Close

    Set objRecordSet = Nothing
    Set objConnection = Nothing

Next ctr

If fileCtr < 5 Then
    Sheets.Add after:=ActiveSheet
End If

Next fileCtr

ElseIf gender = "male" Then
    ' if male
    For fileCtr = 1 To 5

        If fileCtr = 1 Then
            Set curr_ws = wb2.Sheets(1) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "B2"
            currFile = "B2"

        ElseIf fileCtr = 2 Then
            Set curr_ws = wb2.Sheets(2) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "CS3"
            currFile = "CS3"

        ElseIf fileCtr = 3 Then
            Set curr_ws = wb2.Sheets(3) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "DS3"
            currFile = "DS3"

        ElseIf fileCtr = 4 Then
            Set curr_ws = wb2.Sheets(4) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "F3"
            currFile = "F3"

        ElseIf fileCtr = 5 Then
            Set curr_ws = wb2.Sheets(5) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "G3"
            currFile = "G3"

        End If

        strpathtoTextFile = "F:\PhDstuff\deidentifiedpairs\" &
currfolder

```

```

For ctr = 1 To 3

    If ctr = 1 Then 'trial a
        trialNo = "_1"
        cellAlpha = "A"
    ElseIf ctr = 2 Then 'trial b
        trialNo = "_2"
        cellAlpha = "I"
    ElseIf ctr = 3 Then 'trial c
        trialNo = "_3"
        cellAlpha = "Q"
    End If

    '==== creating the schema.ini file

    FilePath = strpathtoTextFile & "\Schema.ini"
    Open FilePath For Output As #1

        fileName = "[" & taskName & currFile & trialNo
& file1 & "]"

        Print #1, fileName
        fileName = ""

        Line1 = "Format = TabDelimited"
        Print #1, Line1

        Line2 = "Col1 = rowLabel Text"
        Print #1, Line2

        Line3 = "Col2=SampleTime Double"
        Print #1, Line3

        Line4 = "Col3=F0 Double"
        Print #1, Line4

    Close #1

    '=====

    Set objConnection =
CreateObject("ADODB.Connection")
    Set objRecordSet = CreateObject("ADODB.Recordset")

    objConnection.Open
"Provider=Microsoft.Jet.OLEDB.4.0;" & _
        "Data Source=" & strpathtoTextFile & ";"
& _
        "Extended
Properties="""text;HDR=YES;FMT=Delimited"""

    objRecordSet.Open "SELECT * FROM " & taskName &
currFile & trialNo & file1, _
        objConnection, adOpenStatic,
adLockOptimistic, adCmdText

    refcol = Range(cellAlpha & 1).Column

    intRow = 51

```



```

        Do Until objRecordSet.EOF
            Cells(intRow, refcol) = objRecordSet(0)
            Cells(intRow, refcol + 1) = objRecordSet(1)
            Cells(intRow, refcol + 2) = objRecordSet(2)

            intRow = intRow + 1
            objRecordSet.MoveNext
        Loop

        objRecordSet.Close
        objConnection.Close

        Set objRecordSet = Nothing
        Set objConnection = Nothing

    Next ctr

    If fileCtr < 5 Then
        Sheets.Add after:=ActiveSheet
    End If

    Next fileCtr

End If

wb2.Save

'====Sing The Tune Task
    ElseIf taskCtr = 3 Then

        Workbooks.Add
        ActiveWorkbook.SaveAs fileName:= _
            fileSTT, _
            FileFormat:=xlOpenXMLWorkbook, CreateBackup:=False
    ,

    Set wb3 = Workbooks(currfolder & "_STTraw.xlsx")

    taskName = "singTheTune_" & gender

    '#f0 data of each of the five novel tunes read into separate
spreadsheet
    For fileCtr = 1 To 5

        If fileCtr = 1 Then
            Set curr_ws = wb3.Sheets(1) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "3"
            currFile = "3"

        ElseIf fileCtr = 2 Then
            Set curr_ws = wb3.Sheets(2) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "6"
            currFile = "6"

        ElseIf fileCtr = 3 Then
            Set curr_ws = wb3.Sheets(3) 'change accordingly
            curr_ws.Activate
            curr_ws.Name = "8"
            currFile = "8"

```

```

ElseIf fileCtr = 4 Then
    Set curr_ws = wb3.Sheets(4) 'change accordingly
    curr_ws.Activate
    curr_ws.Name = "11"
    currFile = "11"

ElseIf fileCtr = 5 Then
    Set curr_ws = wb3.Sheets(5) 'change accordingly
    curr_ws.Activate
    curr_ws.Name = "15"
    currFile = "15"

End If

currfolder    strpathtoTextFile = "F:\PhDstuff\deidentifiedpairs\" &

'#The three trials of a stimulus read into 3 separate
columns on the spreadsheet
For ctr = 1 To 3
    If ctr = 1 Then 'trial a
        trialNo = "_1"
        cellAlpha = "A"
    ElseIf ctr = 2 Then 'trial b
        trialNo = "_2"
        cellAlpha = "I"
    ElseIf ctr = 3 Then 'trial c
        trialNo = "_3"
        cellAlpha = "Q"
    End If

'==== creating the schema.ini file

FilePath = strpathtoTextFile & "\Schema.ini"
Open FilePath For Output As #1

    fileName = "[" & taskName & currFile & trialNo & file1
& "]"

    Print #1, fileName
    fileName = ""

    Line1 = "Format = TabDelimited"
    Print #1, Line1

    Line2 = "Col1 = rowLabel Text"
    Print #1, Line2

    Line3 = "Col2=SampleTime Double"
    Print #1, Line3

    Line4 = "Col3=F0 Double"
    Print #1, Line4

Close #1

'=====

Set objConnection = CreateObject("ADODB.Connection")
Set objRecordSet = CreateObject("ADODB.Recordset")

```

```

        objConnection.Open "Provider=Microsoft.Jet.OLEDB.4.0;" & _
            "Data Source=" & strpathtoTextFile & ";" & _
            "Extended
Properties="""text;HDR=YES;FMT=Delimited"""

        objRecordSet.Open "SELECT * FROM " & taskName & currFile &
trialNo & file1, _
            objConnection, adOpenStatic, adLockOptimistic,
adCmdText

        refcol = Range(cellAlpha & 1).Column

        intRow = 51

        Do Until objRecordSet.EOF
            Cells(intRow, refcol) = objRecordSet(0)
            Cells(intRow, refcol + 1) = objRecordSet(1)
            Cells(intRow, refcol + 2) = objRecordSet(2)

            intRow = intRow + 1
            objRecordSet.MoveNext
        Loop

        objRecordSet.Close
        objConnection.Close

        Set objRecordSet = Nothing
        Set objConnection = Nothing

    Next ctr

    If fileCtr < 5 Then
        Sheets.Add after:=ActiveSheet
    End If

    Next fileCtr

    wb3.Save

End If

Next taskCtr

End Sub

```

Appendix C-3 VBA macro for fine-grained pitch segmentation for Happy Birthday Singing Task

```
Sub HappyBirthdayPitchSegmentation()  
  
    Dim S1a As Integer 'row number of start of segment  
    Dim S1b As Integer 'row number of end of segment  
    Dim S2a As Integer  
    Dim S2b As Integer  
    Dim S3a As Integer  
    Dim S3b As Integer  
    Dim S4a As Integer  
    Dim S4b As Integer  
    Dim S5a As Integer  
    Dim S5b As Integer  
    Dim S6a As Integer  
    Dim S6b As Integer  
    Dim S7a As Integer  
    Dim S7b As Integer  
    Dim S8a As Integer 'just in case it goes up to 8 notes per phrase  
    Dim S8b As Integer  
  
    Dim S1m As Integer  
    Dim S2m As Integer  
    Dim S3m As Integer  
    Dim S4m As Integer  
    Dim S5m As Integer  
    Dim S6m As Integer  
    Dim S7m As Integer  
    Dim S8m As Integer  
  
    Dim S1r As Integer  
    Dim S2r As Integer  
    Dim S3r As Integer  
    Dim S4r As Integer  
    Dim S5r As Integer  
    Dim S6r As Integer  
    Dim S7r As Integer  
    Dim S8r As Integer  
  
    Dim S1s As Integer  
    Dim S2s As Integer  
    Dim S3s As Integer  
    Dim S4s As Integer  
    Dim S5s As Integer  
    Dim S6s As Integer  
    Dim S7s As Integer  
    Dim S8s As Integer  
  
    Dim transDur As Double  
  
    Dim frontnum As Integer  
    Dim backnum As Integer  
    Dim initFront As Integer  
    Dim initBack As Integer  
  
    Dim refcol As Integer  
    Dim rownum As Integer
```

```

Dim p60 As Double    'name of best threshold determined

Dim cellAlpha As String

Dim a As Integer
Dim b As Integer
Dim c As Integer
Dim d As Integer
Dim e As Integer
Dim F As Integer

Dim i As Integer
Dim j As Integer
Dim sumV As Double
Dim avgV As Double
Dim sdV As Double
Dim sdF As Double
Dim avgF As Double
Dim medF As Double

Dim ctr As Integer
Dim folderCtr As Integer

Dim firstRow As Integer
Dim lastRow As Integer
Dim SA As Integer
Dim SB As Integer
Dim SM As Integer
Dim SN As Integer

Dim roundNo As Integer
Dim count As Integer

Dim velArr() As Double
Dim currVal As Integer

Dim lastX As Integer

Dim lowH As Double
Dim highH As Double
Dim currLM As Double
Dim currHM As Double
Dim currLPG As Double
Dim currHPG As Double
Dim currH As Double
Dim minH As Double
Dim bestT As Integer
Dim totalItem As Integer

Dim signchange As Integer
Dim currCell As Double
Dim currsign As Integer

'change to the Excel file with the sampled  $f_0$  data
Set wb = Workbooks("240_HBDraw.xlsx")

For folderCtr = 1 To 4    'process the  $f_0$  data from each trial one by
one

Set curr_ws = wb.Sheets(folderCtr)

```

```

curr_ws.Activate

For count = 1 To 4           'process each phrase of the trial one by one

    If count = 1 Then
        cellAlpha = "a"
    ElseIf count = 2 Then
        cellAlpha = "i"
    ElseIf count = 3 Then
        cellAlpha = "q"
    ElseIf count = 4 Then
        cellAlpha = "y"
    End If

S1a = 0
S1b = 0
S2a = 0
S2b = 0
S3a = 0
S3b = 0
S4a = 0
S4b = 0
S5a = 0
S5b = 0
S6a = 0
S6b = 0
S7a = 0
S7b = 0
S8a = 0
S8b = 0

S1r = 0
S1s = 0
S2r = 0
S2s = 0
S3r = 0
S3s = 0
S4r = 0
S4s = 0
S5r = 0
S5s = 0
S6r = 0
S6s = 0
S7r = 0
S7s = 0
S8r = 0
S8s = 0

refcol = Range(cellAlpha & 1).Column

Cells(49, refcol).Value = count
Cells(50, refcol).Value = "rowLabel"
Cells(50, refcol + 1).Value = "SampleTime"
Cells(50, refcol + 2).Value = "F0"
Cells(50, refcol + 3).Value = "F0 (semitone) "
Cells(50, refcol + 4).Value = "velocity"
Cells(50, refcol + 5).Value = "abs velocity(/10) "
Cells(50, refcol + 6).Value = "Threshold"

```

```

firstRow = 51
lastRow = Range(cellAlpha & Rows.count).End(xlUp).Offset(0).Row
'last row

'to pad all the f0 values in 'g' segments with 0
i = firstRow
    Do While i <= lastRow

        If Range(cellAlpha & i).Value = "g" Then
            Cells(i, refcol + 2).Value = 0
        End If

        i = i + 1

    Loop

'and delete all the undefined values in the numbered segments
i = firstRow
    Do While i <= lastRow

        If ((Range(cellAlpha & i).Value = "1" Or Range(cellAlpha &
i).Value = "2" Or Range(cellAlpha & i).Value = "3" Or Range(cellAlpha
& i).Value = "4" Or Range(cellAlpha & i).Value = "5" Or
Range(cellAlpha & i).Value = "6" Or Range(cellAlpha & i).Value = "7")
And IsEmpty(Cells(i, refcol + 2).Value) = True) Or Range(cellAlpha &
i).Value = "n" Then
            Range(Cells(i, refcol), Cells(i, refcol + 7)).Delete
(xlShiftUp)
        Else
            i = i + 1
        End If

    Loop

'recalculate lastRow again after the shifts
lastRow = Range(cellAlpha & Rows.count).End(xlUp).Offset(0).Row
'last row

'to find the start and end of each coarse segment (a to b)
For ctr = 1 To 8
    i = firstRow
    Do While Cells(i, refcol).Value <> ctr And i <= lastRow
        i = i + 1
    Loop

    'if i already reaches Lastrow + 1. means there's no such segment
    If i = lastRow + 1 Then
        frontnum = 0
        backnum = 0
    Else
        frontnum = i
        Do While Cells(i, refcol).Value = ctr
            i = i + 1
        Loop

        backnum = i - 1
    End If

    If ctr = 1 Then
        Sla = frontnum
    End If

```

```

        S1b = backnum
    ElseIf ctr = 2 Then
        S2a = frontnum
        S2b = backnum
    ElseIf ctr = 3 Then
        S3a = frontnum
        S3b = backnum
    ElseIf ctr = 4 Then
        S4a = frontnum
        S4b = backnum
    ElseIf ctr = 5 Then
        S5a = frontnum
        S5b = backnum
    ElseIf ctr = 6 Then
        S6a = frontnum
        S6b = backnum
    ElseIf ctr = 7 Then
        S7a = frontnum
        S7b = backnum
    ElseIf ctr = 8 Then
        S8a = frontnum
        S8b = backnum
    End If

Next ctr

For ctr = 1 To 8

    If ctr = 1 Then
        rownum = S1a
    ElseIf ctr = 2 Then
        rownum = S2a
    ElseIf ctr = 3 Then
        rownum = S3a
    ElseIf ctr = 4 Then
        rownum = S4a
    ElseIf ctr = 5 Then
        rownum = S5a
    ElseIf ctr = 6 Then
        rownum = S6a
    ElseIf ctr = 7 Then
        rownum = S7a
    ElseIf ctr = 8 Then
        rownum = S8a
    End If

    If rownum <> 0 Then

        Range(Cells(rownum, refcol), Cells(rownum, refcol + 6)).Select

'color the beginning of segment.
        With Selection.Interior
            .Pattern = xlSolid
            .PatternColorIndex = xlAutomatic
            .Color = 65535
            .TintAndShade = 0
            .PatternTintAndShade = 0
        End With

    End If

End For

```



```

Next ctr

'=====

'convert  $f_0$  in Hz into semitones
For rownum = firstRow To lastRow

    If Cells(rownum, refcol + 2).Value = 0 Then
        Cells(rownum, refcol + 3).Value = 0
    Else
        Cells(rownum, refcol + 3).Value = 1200 * Log(Cells(rownum,
refcol + 2).Value) / Log(2) 'semitone  $f_0$  of the next row
    End If

Next rownum

'calculate absolute  $f_0$  velocity
For rownum = firstRow + 1 To lastRow

    If Cells(rownum, refcol + 2).Value = 0 Or Cells(rownum - 1, refcol
+ 2).Value = 0 Or Cells(rownum + 1, refcol + 2).Value = 0 Then 'if
current row, prev row or next row has  $f_0 = 0$  (i.e., g segment), assign
velocity as NULL
        Cells(rownum, refcol + 4).Value = ""
    Else 'compute  $f_0$  velocity according to central differentiation only
when the next row and the previous row don't have 0.
        Cells(rownum, refcol + 4).Value = (Cells(rownum + 1, refcol +
3).Value - Cells(rownum - 1, refcol + 3).Value) / (Cells(rownum + 1,
refcol + 1).Value - Cells(rownum - 1, refcol + 1).Value)
    End If

    If Cells(rownum, refcol + 4).Value <> "" Then
        Cells(rownum, refcol + 5).Value = Abs(Cells(rownum, refcol +
4).Value) / 10 'absolute  $f_0$  velocity (divided by 10 to scale it such
that it fits on the same graph as the  $f_0$  graph)
    End If

Next rownum

'===Using Shanbhag's fuzzy entropy method to find the best threshold
to separate high  $f_0$  velocity regions from low velocity regions in each
phrase
totalItem = WorksheetFunction.CountA(Range(Cells(firstRow + 1, refcol
+ 5), Cells(lastRow - 1, refcol + 5)))
lastX = Int(WorksheetFunction.Max(Range(Cells(firstRow + 1, refcol +
5), Cells(lastRow - 1, refcol + 5)))) + 1 'the last filled bin

minH = 1000000

ReDim velArr(lastX, 3)

'read the  $f_0$  velocity values (as Integer type) into the respective
array bins - first dimension of the array
'to compute the frequency of all the rounded off  $f_0$  velocity values
For i = firstRow + 1 To lastRow - 1
    If Cells(i, refcol + 5).Value <> "" Then 'to prevent counting all
the 0 empty values

```

```

        currVal = Int(Cells(i, refcol + 5).Value) + 1 'round the
current  $f_0$  velocity to the next largest integer.
    Else
        currVal = 0
    End If

    velArr(currVal, 2) = velArr(currVal, 2) + 1 'histogram value
Next i

'compute incidence (frequency/total number of  $f_0$  velocity values) in
column 2 and cumulative precentage in column 3
For i = 1 To lastX
    velArr(i, 1) = i
    velArr(i, 2) = velArr(i, 2) / totalItem
    For j = 1 To i
        velArr(i, 3) = velArr(i, 3) + velArr(j, 2)
    Next j
    velArr(i, 3) = velArr(i, 3) 'convert to cumulative percentage
Next i

'let threshold value vary from 1 to the maximum absolute  $f_0$  velocity
value, and iteratively search for the best threshold using Shanbhag
entropy method
For i = 1 To lastX
    lowH = 0 'reset everything to 0
    highH = 0
    currH = 0

    'to prevent them from selecting the extreme  $f_0$  velocity values
(front and end)
    If velArr(i, 3) > 0 And velArr(i, 3) < 1 Then

        For j = 1 To i
            currLPG = velArr(j, 2)

            currLM = 0.5 + (velArr(i, 3) - velArr(j, 3)) / (2 *
velArr(i, 3)) 'low membership value

            lowH = lowH - (currLPG / velArr(i, 3)) * Log(currLM)
        Next j

        For k = i + 1 To lastX
            currHPG = velArr(k, 2)

            currHM = 0.5 + (velArr(k, 3) - velArr(i, 3)) / (2 * (1 -
velArr(i, 3))) 'high membership value

            highH = highH - (currHPG / (1 - velArr(i, 3))) *
Log(currHM)
        Next k

        currH = lowH - highH

        If currH < minH Then
            minH = currH
            bestT = i
        End If
    End If
Next i

```

```

End If

Next i

Cells(firstRow, refcol + 7).Value = bestT
Cells(firstRow + 1, refcol + 7).Value = velArr(bestT, 3) 'cumulative
percentage
Cells(firstRow + 2, refcol + 7).Value = minH
Cells(firstRow + 3, refcol + 7).Value = totalItem

Erase velArr

p60 = bestT

For rownum = firstRow + 1 To lastRow

'to fill the last column of the phrase with the threshold value
Cells(rownum, refcol + 6).Value = p60

Next rownum

'=====
'Use the best threshold to determine the onset and offset of the
stable segments one by one
'frontnum and backnum = the best onset and offset values
'S1 to S8

For ctr = 1 To 8

If ctr = 1 Then
    SA = S1a + 1 'S1a+1 is the first cell with abs velocity value
    SB = S1b
ElseIf ctr = 2 Then
    SA = S2a
    SB = S2b
ElseIf ctr = 3 Then
    SA = S3a
    SB = S3b
ElseIf ctr = 4 Then
    SA = S4a
    SB = S4b
ElseIf ctr = 5 Then
    SA = S5a
    SB = S5b
ElseIf ctr = 6 Then
    SA = S6a
    SB = S6b
ElseIf ctr = 7 Then
    SA = S7a
    SB = S7b
ElseIf ctr = 8 Then
    SA = S8a
    SB = S8b
End If

frontnum = 0
backnum = 0 'resetting to 0

If SA <> 0 And SB <> 0 Then

```

```

frontnum = SA
backnum = SB
initFront = SA
initBack = SB

'If the frontnum or backnum happens to not have an absolute  $f_0$ 
velocity value (e.g., when the segment is next to a gap)
If IsEmpty(Cells(frontnum, refcol + 5)) Then
    frontnum = SA + 1
    initFront = SA + 1
End If

If IsEmpty(Cells(backnum, refcol + 5)) Then
    backnum = SB - 1
    initBack = SB - 1
End If

SM = frontnum + CInt((backnum - frontnum + 1) / 3) - 1
SN = backnum - CInt((backnum - frontnum + 1) / 3) + 1

'color the SM and SN cells (the end points of the onset and
offset search boundaries in each segment)
Range(Cells(SM, refcol), Cells(SM, refcol + 6)).Select
With Selection.Interior
    .Pattern = xlSolid
    .PatternColorIndex = xlAutomatic
    .Color = 4891391 'orange in decimal
    .TintAndShade = 0
    .PatternTintAndShade = 0
End With

Range(Cells(SN, refcol), Cells(SN, refcol + 6)).Select
With Selection.Interior
    .Pattern = xlSolid
    .PatternColorIndex = xlAutomatic
    .Color = 14204670 'light pink
    .TintAndShade = 0
    .PatternTintAndShade = 0
End With

Range(Cells(frontnum, refcol), Cells(frontnum, refcol +
6)).Select 'color the beginning of segment.
With Selection.Interior
    .Pattern = xlSolid
    .PatternColorIndex = xlAutomatic
    .Color = 65535
    .TintAndShade = 0
    .PatternTintAndShade = 0
End With

'to determine the stable segment onset (i.e., frontnum)
For roundNo = 1 To 3

    If roundNo = 1 Then
        Do Until frontnum = SM Or Abs(Cells(frontnum, refcol +
5).Value) <= p60 And Abs(Cells(frontnum + 1, refcol + 5).Value) <= p60
And Abs(Cells(frontnum + 2, refcol + 5).Value) <= p60
            frontnum = frontnum + 1
        Loop
    End If

```

```

        'if the end of the search boundary is reached without
        finding a suitable candidate, start from the beginning of the search
        boundary and begin round 2 of search
        If frontnum = SM And Not (Abs(Cells(frontnum, refcol +
5).Value) <= p60 And Abs(Cells(frontnum + 1, refcol + 5).Value) <= p60
And Abs(Cells(frontnum + 2, refcol + 5).Value) <= p60) Then
            frontnum = initFront

        End If

        ElseIf roundNo = 2 Then
            Do Until frontnum = SM Or Abs(Cells(frontnum, refcol +
5).Value) <= p60 And Abs(Cells(frontnum + 1, refcol + 5).Value) <= p60
                frontnum = frontnum + 1
            Loop

            'if the end of the search boundary is reached without
            finding a suitable candidate, start from the beginning of the search
            boundary and begin round 3 of search
            If frontnum = SM And Not (Abs(Cells(frontnum, refcol +
5).Value) <= p60 And Abs(Cells(frontnum + 1, refcol + 5).Value) <=
p60) Then
                frontnum = initFront

            End If

            ElseIf roundNo = 3 Then
                Do Until frontnum = SM Or Abs(Cells(frontnum, refcol +
5).Value) <= p60
                    frontnum = frontnum + 1
                Loop

                'if the end of the search boundary is reached without
                finding a suitable candidate, let best onset be the smallest value in
                the search boundary, if all are above T
                If frontnum = SM And Not (Abs(Cells(frontnum, refcol +
5).Value) <= p60) Then
                    frontnum = initFront +
WorksheetFunction.Match(WorksheetFunction.Min(Range(Cells(initFront,
refcol + 5), Cells(SM, refcol + 5))), Range(Cells(initFront, refcol +
5), Cells(SM, refcol + 5)), 0) - 1

                End If

            End If

        Next roundNo

        'to determine the stable segment offset (i.e., backnum)
        For roundNo = 1 To 3

            If roundNo = 1 Then
                Do Until backnum = SN Or Abs(Cells(backnum, refcol +
5).Value) <= p60 And Abs(Cells(backnum - 1, refcol + 5).Value) <= p60
And Abs(Cells(backnum - 2, refcol + 5).Value) <= p60
                    backnum = backnum - 1
                Loop
            End If
        Next roundNo

```

```

        If backnum = SN And Not (Abs(Cells(backnum, refcol +
5).Value) <= p60 And Abs(Cells(backnum - 1, refcol + 5).Value) <= p60
And Abs(Cells(backnum - 2, refcol + 5).Value) <= p60) Then 'reached
the end
            backnum = initBack 'reset backnum to original
value

        End If

        ElseIf roundNo = 2 Then
            Do Until backnum = SN Or Abs(Cells(backnum, refcol +
5).Value) <= p60 And Abs(Cells(backnum - 1, refcol + 5).Value) <= p60
                backnum = backnum - 1
            Loop

            If backnum = SN And Not (Abs(Cells(backnum, refcol +
5).Value) <= p60 And Abs(Cells(backnum - 1, refcol + 5).Value) <= p60)
Then 'reached the end
                backnum = initBack 'reset backnum to original
value

            End If

            ElseIf roundNo = 3 Then
                Do Until backnum = SN Or Abs(Cells(backnum, refcol +
5).Value) <= p60
                    backnum = backnum - 1
                Loop

                If backnum = SN And Not (Abs(Cells(backnum, refcol +
5).Value) <= p60) Then 'reached the end

                    backnum = SN +
WorksheetFunction.Match(WorksheetFunction.Min(Range(Cells(SN, refcol +
5), Cells(initBack, refcol + 5))), Range(Cells(SN, refcol + 5),
Cells(initBack, refcol + 5)), 0) - 1
                    'let backnum be the smallest value in the range,
if all are above T

                End If

            End If

        Next roundNo

        'color the frontnum and backnum cells

        Range(Cells(frontnum, refcol), Cells(frontnum, refcol +
6)).Select
        With Selection.Interior
            .Pattern = xlSolid
            .PatternColorIndex = xlAutomatic
            .Color = 14599344 'steel gray
            .TintAndShade = 0
            .PatternTintAndShade = 0
        End With

        Range(Cells(backnum, refcol), Cells(backnum, refcol +
6)).Select

```

```

        With Selection.Interior
            .Pattern = xlSolid
            .PatternColorIndex = xlAutomatic
            .Color = 15631086 'magenta
            .TintAndShade = 0
            .PatternTintAndShade = 0
        End With

        'S_r and S_s store the best onset and offset of each segment,
        respectively
        If ctr = 1 Then
            S1r = frontnum
            S1s = backnum
        ElseIf ctr = 2 Then
            S2r = frontnum
            S2s = backnum
        ElseIf ctr = 3 Then
            S3r = frontnum
            S3s = backnum
        ElseIf ctr = 4 Then
            S4r = frontnum
            S4s = backnum
        ElseIf ctr = 5 Then
            S5r = frontnum
            S5s = backnum
        ElseIf ctr = 6 Then
            S6r = frontnum
            S6s = backnum
        ElseIf ctr = 7 Then
            S7r = frontnum
            S7s = backnum
        ElseIf ctr = 8 Then
            S8r = frontnum
            S8s = backnum
        End If

    End If

Next ctr

'#####

'insert any modifications for R values here.e.g., S3r = 173
'S1r = S1a
'S2r = S2a
'S3r = S3a
'S4r = S4a
'S5r = S5a
'S6r = S6a
'S7r = S7a

'insert any modifications for S values here.e.g., S3s = 173
'S5s = 217
'S2s = 91
'S7r = 266
'S7s = 280

'#####

```

'display the following variables on the spreadsheet

```
Cells(1, refcol).Value = "Point r"
Cells(1, refcol + 1).Value = "Time"
Cells(1, refcol + 2).Value = " $f_0$ "
Cells(1, refcol + 3).Value = "Point s"
Cells(1, refcol + 4).Value = "Time"
Cells(1, refcol + 5).Value = " $f_0$ "
Cells(2, refcol).Value = 1
Cells(3, refcol).Value = 2
Cells(4, refcol).Value = 3
Cells(5, refcol).Value = 4
Cells(6, refcol).Value = 5
Cells(7, refcol).Value = 6
Cells(8, refcol).Value = 7
Cells(9, refcol).Value = 8

Cells(11, refcol).Value = "Stable"
Cells(11, refcol + 1).Value = "mean  $f_0$ "
Cells(11, refcol + 2).Value = "sd"
Cells(11, refcol + 3).Value = "median  $f_0$ "
Cells(11, refcol + 4).Value = "Transition"
Cells(11, refcol + 5).Value = "sd"
Cells(11, refcol + 6).Value = "duration"
Cells(12, refcol).Value = 1
Cells(13, refcol).Value = 2
Cells(14, refcol).Value = 3
Cells(15, refcol).Value = 4
Cells(16, refcol).Value = 5
Cells(17, refcol).Value = 6
Cells(18, refcol).Value = 7
Cells(19, refcol).Value = 8
Cells(20, refcol).Value = "mean sd"

Cells(12, refcol + 4).Value = 1
Cells(13, refcol + 4).Value = 2
Cells(14, refcol + 4).Value = 3
Cells(15, refcol + 4).Value = 4
Cells(16, refcol + 4).Value = 5
Cells(17, refcol + 4).Value = 6
Cells(18, refcol + 4).Value = 7
Cells(19, refcol + 4).Value = 8
Cells(20, refcol + 4).Value = "mean sd"

Cells(22, refcol).Value = "Stable"
Cells(22, refcol + 1).Value = "mean abs vel"
Cells(22, refcol + 2).Value = "sd"
Cells(22, refcol + 3).Value = "Zero crossings"
Cells(22, refcol + 4).Value = "mean abs vel"
Cells(22, refcol + 5).Value = "sd"
Cells(22, refcol + 6).Value = "Zero crossings"

Cells(23, refcol).Value = 1
Cells(24, refcol).Value = 2
Cells(25, refcol).Value = 3
Cells(26, refcol).Value = 4
Cells(27, refcol).Value = 5
```



```

Cells(28, refcol).Value = 6
Cells(29, refcol).Value = 7
Cells(30, refcol).Value = 8
Cells(31, refcol).Value = "average"

i = 2
For ctr = 1 To 8

    If ctr = 1 Then
        frontnum = S1r
        backnum = S1s
    ElseIf ctr = 2 Then
        frontnum = S2r
        backnum = S2s
    ElseIf ctr = 3 Then
        frontnum = S3r
        backnum = S3s
    ElseIf ctr = 4 Then
        frontnum = S4r
        backnum = S4s
    ElseIf ctr = 5 Then
        frontnum = S5r
        backnum = S5s
    ElseIf ctr = 6 Then
        frontnum = S6r
        backnum = S6s
    ElseIf ctr = 7 Then
        frontnum = S7r
        backnum = S7s
    ElseIf ctr = 8 Then
        frontnum = S8r
        backnum = S8s
    End If

    If frontnum <> 0 And backnum <> 0 Then

        sdF = WorksheetFunction.StDev(Range(Cells(frontnum, refcol +
3), Cells(backnum, refcol + 3)))
        avgV = WorksheetFunction.Average(Range(Cells(frontnum, refcol
+ 5), Cells(backnum, refcol + 5)))
        sdV = WorksheetFunction.StDev(Range(Cells(frontnum, refcol +
5), Cells(backnum, refcol + 5)))

        Cells(i, refcol + 1).Value = Cells(frontnum, refcol + 1).Value
'time of r
        Cells(i, refcol + 4).Value = Cells(backnum, refcol + 1).Value
'time of s
        Cells(i, refcol + 2).Value = Cells(frontnum, refcol + 2).Value
'f0 for r
        Cells(i, refcol + 5).Value = Cells(backnum, refcol + 2).Value
'f0 for s

        avgF = WorksheetFunction.Average(Range(Cells(frontnum, refcol
+ 2), Cells(backnum, refcol + 2)))
        medF = WorksheetFunction.Quartile(Range(Cells(frontnum, refcol
+ 2), Cells(backnum, refcol + 2)), 2)

        Cells(i + 10, refcol + 1).Value = avgF
        Cells(i + 10, refcol + 3).Value = medF

```

```

Cells(i + 10, refcol + 2).Value = sdF
Cells(i + 21, refcol + 1).Value = avgV * 10 'rescale it back
by 10
Cells(i + 21, refcol + 2).Value = sdV * 10

End If

i = i + 1

Next ctr

'the transition regions seg 1 to 7

For ctr = 1 To 7

If ctr = 1 Then

a = S1s
b = S1b
c = S2a
d = S2r

If c = 0 Then 'if there's a missing segment
If S3a <> 0 Then
c = S3a
d = S3r
ctr = ctr + 1
ElseIf S4a <> 0 Then
c = S4a
d = S4r
ctr = ctr + 2
ElseIf S5a <> 0 Then
c = S5a
d = S5r
ctr = ctr + 3
ElseIf S6a <> 0 Then
c = S6a
d = S6r
ctr = ctr + 4
ElseIf S7a <> 0 Then
c = S7a
d = S7r
ctr = ctr + 5
ElseIf S8a <> 0 Then
c = S8a
d = S8r
ctr = ctr + 6
Else
Exit For
End If
End If

ElseIf ctr = 2 Then

a = S2s
b = S2b
c = S3a
d = S3r

```

'if the next segment is missing, let the next nonzero segment
be the new c and d and jump to the next ctr

```
If c = 0 Then
    If S4a <> 0 Then
        c = S4a
        d = S4r
        ctr = ctr + 1
    ElseIf S5a <> 0 Then
        c = S5a
        d = S5r
        ctr = ctr + 2
    ElseIf S6a <> 0 Then
        c = S6a
        d = S6r
        ctr = ctr + 3
    ElseIf S7a <> 0 Then
        c = S7a
        d = S7r
        ctr = ctr + 4
    ElseIf S8a <> 0 Then
        c = S8a
        d = S8r
        ctr = ctr + 5
    Else
        Exit For
    End If
End If

ElseIf ctr = 3 Then

    a = S3s
    b = S3b
    c = S4a
    d = S4r
```

'if the next segment is missing, let the next nonzero segment
be the new c and d and jump to the next ctr

```
If c = 0 Then
    If S5a <> 0 Then
        c = S5a
        d = S5r
        ctr = ctr + 1
    ElseIf S6a <> 0 Then
        c = S6a
        d = S6r
        ctr = ctr + 2
    ElseIf S7a <> 0 Then
        c = S7a
        d = S7r
        ctr = ctr + 3
    ElseIf S8a <> 0 Then
        c = S8a
        d = S8r
        ctr = ctr + 4
    Else
        Exit For
    End If
End If

ElseIf ctr = 4 Then
```

```

a = S4s
b = S4b
c = S5a
d = S5r

'if the next segment is missing, let the next nonzero segment
be the new c and d and jump to the next ctr
If c = 0 Then
    If S6a <> 0 Then
        c = S6a
        d = S6r
        ctr = ctr + 1
    ElseIf S7a <> 0 Then
        c = S7a
        d = S7r
        ctr = ctr + 2
    ElseIf S8a <> 0 Then
        c = S8a
        d = S8r
        ctr = ctr + 3
    Else
        Exit For
    End If
End If

ElseIf ctr = 5 Then

a = S5s
b = S5b
c = S6a
d = S6r

'if the next segment is missing, let the next nonzero segment
be the new c and d and jump to the next ctr
If c = 0 Then
    If S7a <> 0 Then
        c = S7a
        d = S7r
        ctr = ctr + 1
    ElseIf S8a <> 0 Then
        c = S8a
        d = S8r
        ctr = ctr + 2
    Else
        Exit For
    End If
End If

ElseIf ctr = 6 Then

a = S6s
b = S6b
c = S7a
d = S7r

'if the next segment is missing, let the next nonzero segment
be the new c and d and jump to the next ctr
If c = 0 Then
    If S8a <> 0 Then
        c = S8a
        d = S8r

```

```

        ctr = ctr + 1
    Else
        Exit For
    End If
End If

ElseIf ctr = 7 Then

    a = S7s
    b = S7b
    c = S8a
    d = S8r

End If

'if the current segment and the next segment are both present
If b <> 0 And c <> 0 Then

    sdF = WorksheetFunction.StDev(Range(Cells(a, refcol + 3),
Cells(b, refcol + 3)), Range(Cells(c, refcol + 3), Cells(d, refcol +
3)))

    avgV = WorksheetFunction.Average(Range(Cells(a, refcol +
5), Cells(b, refcol + 5)), Range(Cells(c, refcol + 5), Cells(d, refcol +
5)))

    sdV = WorksheetFunction.StDev(Range(Cells(a, refcol + 5),
Cells(b, refcol + 5)), Range(Cells(c, refcol + 5), Cells(d, refcol +
5)))

    transDur = Cells(d, refcol + 1).Value - Cells(a, refcol +
1).Value

    Cells(ctr + 11, refcol + 5).Value = sdF
    Cells(ctr + 11, refcol + 6).Value = transDur
    Cells(ctr + 22, refcol + 4).Value = avgV * 10
    Cells(ctr + 22, refcol + 5).Value = sdV * 10

End If

Next ctr

'mean sd for f0 in stable segment
Cells(20, refcol + 2).Value =
WorksheetFunction.Average(Range(Cells(12, refcol + 2), Cells(19,
refcol + 2)))

'mean sd for f0 in transition area (between one stable segment to the
next)
If WorksheetFunction.CountA(Range(Cells(12, refcol + 5), Cells(19,
refcol + 5))) <> 0 Then
    Cells(20, refcol + 5).Value =
WorksheetFunction.Average(Range(Cells(12, refcol + 5), Cells(19,
refcol + 5)))
End If

'mean duration for transition areas
If WorksheetFunction.CountA(Range(Cells(12, refcol + 6), Cells(19,
refcol + 6))) <> 0 Then
    Cells(20, refcol + 6).Value =
WorksheetFunction.Average(Range(Cells(12, refcol + 6), Cells(19,
refcol + 6)))

```

```

End If

'mean absolute velocity in stable segments
Cells(31, refcol + 1).Value =
WorksheetFunction.Average(Range(Cells(23, refcol + 1), Cells(30,
refcol + 1)))

'mean absolute velocity in transition areas
If WorksheetFunction.CountA(Range(Cells(23, refcol + 4), Cells(30,
refcol + 4))) <> 0 Then
    Cells(31, refcol + 4).Value =
WorksheetFunction.Average(Range(Cells(23, refcol + 4), Cells(30,
refcol + 4)))
End If

'mean sd for abs vel in stable segments
Cells(31, refcol + 2).Value =
WorksheetFunction.Average(Range(Cells(23, refcol + 2), Cells(30,
refcol + 2)))

'mean sd for abs vel in transition areas
If WorksheetFunction.CountA(Range(Cells(23, refcol + 5), Cells(30,
refcol + 5))) <> 0 Then
    Cells(31, refcol + 5).Value =
WorksheetFunction.Average(Range(Cells(23, refcol + 5), Cells(30,
refcol + 5)))
End If

'====draw the  $f_0$  and the absolute  $f_0$  velocity (scaled by 1/10) graphs

Dim r1 As Range 'the freq (y axis)
Dim r2 As Range
Dim r3 As Range
Dim r4 As Range
Dim r5 As Range

Dim xr1 As Range 'the time (x axis)
Dim xr2 As Range
Dim xr3 As Range

Set r1 = ActiveSheet.Range(Cells(firstRow, refcol + 2), Cells(lastRow,
refcol + 2)) 'f0 values
Set r2 = ActiveSheet.Range(Cells(2, refcol + 2), Cells(9, refcol + 2))
'R values
Set r3 = ActiveSheet.Range(Cells(2, refcol + 5), Cells(9, refcol + 5))
'S values
Set r4 = ActiveSheet.Range(Cells(firstRow + 1, refcol + 5),
Cells(lastRow, refcol + 5)) 'abs vel values
Set r5 = ActiveSheet.Range(Cells(firstRow, refcol + 6), Cells(lastRow,
refcol + 6)) 'threshold values

Set xr1 = ActiveSheet.Range(Cells(firstRow, refcol + 1),
Cells(lastRow, refcol + 1))
Set xr2 = ActiveSheet.Range(Cells(2, refcol + 1), Cells(9, refcol +
1)) 'time at onset
Set xr3 = ActiveSheet.Range(Cells(2, refcol + 4), Cells(9, refcol +
4)) 'time at offset

ActiveSheet.Shapes.AddChart.Select
ActiveChart.ChartType = xlXYScatterLinesNoMarkers

```

```

ActiveChart.SeriesCollection.NewSeries
ActiveChart.SeriesCollection(1).Name = ""F0""
ActiveChart.SeriesCollection(1).XValues = xr1
ActiveChart.SeriesCollection(1).Values = r1

ActiveChart.SeriesCollection.NewSeries
ActiveChart.SeriesCollection(2).Name = ""S""
ActiveChart.SeriesCollection(2).XValues = xr3
ActiveChart.SeriesCollection(2).Values = r3
ActiveChart.SeriesCollection(2).ChartType = xlXYScatter

ActiveChart.SeriesCollection.NewSeries
ActiveChart.SeriesCollection(3).Name = ""R""
ActiveChart.SeriesCollection(3).XValues = xr2
ActiveChart.SeriesCollection(3).Values = r2
ActiveChart.SeriesCollection(3).ChartType = xlXYScatter

ActiveChart.SeriesCollection.NewSeries
ActiveChart.SeriesCollection(4).Name = ""absVel(/10)""
ActiveChart.SeriesCollection(4).XValues = xr1
ActiveChart.SeriesCollection(4).Values = r4
ActiveChart.SeriesCollection(4).ChartType =
xlXYScatterLinesNoMarkers

ActiveChart.SeriesCollection.NewSeries
ActiveChart.SeriesCollection(5).Name = ""p60""
ActiveChart.SeriesCollection(5).XValues = xr1
ActiveChart.SeriesCollection(5).Values = r5
ActiveChart.SeriesCollection(5).ChartType =
xlXYScatterLinesNoMarkers

ActiveChart.SeriesCollection(2).Select
With Selection
    .MarkerStyle = 2
    .MarkerSize = 6
End With

ActiveChart.SeriesCollection(4).Select
With Selection.Format.Line
    .Visible = msoTrue
    .Weight = 1.25
End With

ActiveChart.Axes(xlCategory).MinimumScale = Int(Cells(firstRow,
refcol + 1).Value)

ActiveChart.Parent.Cut
DoEvents
Cells(33, refcol).Select
ActiveSheet.Paste

Application.CutCopyMode = False

Next count

Range("AF1").Value = "Song Duration"
Range("AF2").Value = "1st sampled time"
Range("AF3").Value = "last sampled time"
Range("AF4").Value = "duration"
Range("AF5").Value = "bpm"

```

```

Range("AG2").Value = Range("B51").Value
Range("AG3").Value = Cells(lastRow, refcol + 1).Value
Range("AG4").Value = Range("AG3").Value - Range("AG2").Value
Range("AG5").Value = 25 / (Range("AG4").Value / 60)

Range("AG8").Value = "mean stable sd"
Range("AG9").Value = WorksheetFunction.Average(Range("C12:C17"),
Range("K12:K17"), Range("S12:S18"), Range("AA12:AA17"))

Range("AG11").Value = "mean transition sd"
Range("AG12").Value = WorksheetFunction.Average(Range("F12:F17"),
Range("N12:N17"), Range("V12:V18"), Range("AD12:AD17"))

Next folderCtr

wb.Save

End Sub

```


Appendix C-4 Praat script for Computing Tongue Twister Measures

```

form ReadTongueTwisterData
#to compute median pitch and 5th to 95th quantile of speaking range in
tongue twister

    comment Directory of sound files
    text sound_directory F:\PhDstuff\deidentifiedpairs\230\
    positive time_step 0.01
    positive minimum_pitch 120
    positive maximum_pitch 400
    positive voicing_threshold 0.4
    positive silence_threshold 0.03
    positive octave_jump_cost 0.9
    positive octave_cost 0.01

endform

# Write-out the header (copy if necessary)
resultfile$ = "'sound_directory$tongueTwisterinfo.txt"
appendFileLine: "'resultfile$'", "Legend: median q5 q10 q90 q95
90%range 80%range"
appendFileLine:
"'resultfile$'", "'minimum_pitch'tab$'maximum_pitch'tab$'voicing_th
reshold'tab$'silence_threshold'tab$'octave_jump_cost'tab$'octave
_cost'"

tmin = 0
tmax = 0

appendFileLine: "'resultfile$'", "'tmin'tab$'tmax'tab$'"

n = numberOfSelected ("Sound")

for i to n
    sound [i] = selected ("Sound", i)
endfor

# Median pitches of all selected sounds:
for i to n
    selectObject: sound [i]
    To Pitch (ac)... time_step minimum_pitch 15 no silence_threshold
voicing_threshold octave_cost octave_jump_cost 0.14 maximum_pitch

fileappend "'resultfile$'" 'i''newline$'

#   appendFileLine: "'resultfile$'", "timeStart: 'tmin'"
#   appendFileLine: "'resultfile$'", "timeEnd: 'tmax'"

median = Get quantile: tmin, tmax, 0.50, "Hertz"
q05 = Get quantile: tmin, tmax, 0.05, "Hertz"
q10 = Get quantile: tmin, tmax, 0.10, "Hertz"
q90 = Get quantile: tmin, tmax, 0.90, "Hertz"
q95 = Get quantile: tmin, tmax, 0.95, "Hertz"

range90 = q95-q05

```

```

    range80 = q90-q10

    appendFileLine:
    "'resultfile$',"'"median'"tab$'"q05'"tab$'"q10'"tab$'"q90'"tab$'"q95'"
    tab$'"range90'"tab$'"range80'"newline$"

    Remove

endfor

# Restore selection:
selectObject ( ) ; deselect all objects
for i from 1 to n
    plusObject: sound [i]
endfor

```

Appendix C-5 OpenMx Script for Testing Equality of Covariances for Continuous Measure

```
# -----
# Adapted from twinHetAceCon.R by Hermine Maes (09 21 2014)
# Univariate Heterogeneity Twin Analysis model to estimate causes of
# variation
# Matrix style model - Raw data - Continuous data
# -----|-----|-----|-----|-----|-----|-----
#read output into text file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/Het5Sat_AS_lnNewSingComb.txt", append=TRUE, split=TRUE)

# Load Library
require(OpenMx)
require(psych)

# -----
# PREPARE DATA

#=====
cat("\n")

# Select Variable for Analysis
Vars <- 'var1'
combVars <- c('Age', 'Sex', Vars) #,'yrsTraining'
nvInit <- 3
nv <- 1 # number of variables
ntv <- nv*2 # number of total variables
selVars <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")
#eg c('ht1', 'wt1', 'ht2', 'wt2')

#Select Data for Analysis
mzfData <- subset(twinData2015, ZygosityGrp==1, selVars)
dzfData <- subset(twinData2015, ZygosityGrp==2, selVars)
mzmData <- subset(twinData2015, ZygosityGrp==3, selVars)
dzmData <- subset(twinData2015, ZygosityGrp==4, selVars)
dzoData <- subset(twinData2015, ZygosityGrp==5, selVars)

colnames(mzfData)=colnames(dzfData)=colnames(mzmData)=colnames(dzmData
)=colnames(dzoData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', 't2')

#if error message says that the starting values are infeasible try to
#scale the values up.
# mzfData[,3] <- mzfData[,3]*5
# dzfData[,3] <- dzfData[,3]*5
# dzoData[,3] <- dzoData[,3]*5
# mzmData[,3] <- mzmData[,3]*5
# dzmData[,3] <- dzmData[,3]*5
#
# mzfData[,6] <- mzfData[,6]*5
# dzfData[,6] <- dzfData[,6]*5
# dzoData[,6] <- dzoData[,6]*5
# mzmData[,6] <- mzmData[,6]*5
# dzmData[,6] <- dzmData[,6]*5

describe(mzfData)
describe(dzfData)
```

```

describe(mzmData)
describe(dzmData)
describe(dzoData)

# Generate Descriptive Statistics
colMeans(mzfdData, na.rm=TRUE)
colMeans(dzfdData, na.rm=TRUE)
colMeans(mzmData, na.rm=TRUE)
colMeans(dzmData, na.rm=TRUE)
colMeans(dzoData, na.rm=TRUE)
cat("\n")
cov(mzfdData, use="complete")
cov(dzfdData, use="complete")
cov(mzmData, use="complete")
cov(dzmData, use="complete")
cov(dzoData, use="complete")
cat("\n")

# Set Starting Values
svMe      <- 3      # start value for means
svVa      <- 5      # start value for variance
lbVa      <- 0.0001  # start value for lower bounds
svVas     <- diag(svVa, ntv, ntv)    # assign start values to diagonal
of matrix
lbVas     <- diag(lbVa, ntv, ntv)    # assign lower bounds values to
diagonal of matrix

# -----
# PREPARE MODEL

# Saturated Model
# Algebra for expected Mean Matrices in MZ & DZ twins

# Matrix for expected Mean
intercept_mzm      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values= svMe,
labels=c("mMZm1", "mMZm2"), name="MeanMzm" )
intercept_mzf      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values= svMe,
labels=c("mMZf1", "mMZf2"), name="MeanMzf" )
intercept_dzm      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values= svMe,
labels=c("mDZm1", "mDZm2"), name="MeanDzm" )
intercept_dzf      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values= svMe,
labels=c("mDZf1", "mDZf2"), name="MeanDzf" )
intercept_dzo      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values= svMe,
labels=c("mDZo1", "mDZo2"), name="MeanDzo" )

# Matrix for moderating/interacting variable
defSex      <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
labels=c("data.Sex1", "data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for covariate
B_Sex      <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,

```

```

        values= .01, label="betaSex", name="bSex" )

meanSex    <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge     <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                        labels=c("data.Age1","data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for covariate
B_Age      <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                        values= .01, label="betaAge", name="bAge" )

meanAge    <- mxAlgebra( bAge%*%Age, name="AgeR")

#*****
# Algebra for expected Mean and Variance/Covariance Matrices in MZ &
# DZ twins

meanGMZf   <- mxAlgebra( MeanMzf + AgeR + SexR , name="expMeanGMZf")
meanGDZf   <- mxAlgebra( MeanDzf + AgeR + SexR , name="expMeanGDZf")
meanGMZm   <- mxAlgebra( MeanMzm + AgeR + SexR , name="expMeanGMZm")
meanGDZm   <- mxAlgebra( MeanDzm + AgeR + SexR , name="expMeanGDZm")
meanGDZo   <- mxAlgebra( MeanDzo + AgeR + SexR , name="expMeanGDZo")

defs_mzm    <- list( intercept_mzm, defSex, B_Sex, meanSex, defAge,
                    B_Age, meanAge)
defs_mzf    <- list( intercept_mzf, defSex, B_Sex, meanSex, defAge,
                    B_Age, meanAge)
defs_dzm    <- list( intercept_dzm, defSex, B_Sex, meanSex, defAge,
                    B_Age, meanAge)
defs_dzf    <- list( intercept_dzf, defSex, B_Sex, meanSex, defAge,
                    B_Age, meanAge)
defs_dzo    <- list( intercept_dzo, defSex, B_Sex, meanSex, defAge,
                    B_Age, meanAge)

# Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
covMZf      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svVas, lbound=lbVas, labels=c("vMZf1","cMZf21","vMZf2"),
                        name="covMZf" )
covDZf      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svVas, lbound=lbVas, labels=c("vDZf1","cDZf21","vDZf2"),
                        name="covDZf" )
covMZm      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svVas, lbound=lbVas, labels=c("vMZm1","cMZm21","vMZm2"),
                        name="covMZm" )
covDZm      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svVas, lbound=lbVas, labels=c("vDZm1","cDZm21","vDZm2"),
                        name="covDZm" )
covDZo      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svVas, lbound=lbVas, labels=c("vDZo1","cDZo21","vDZo2"),
                        name="covDZo" )

# Expectation objects for Multiple Groups
expMZf      <- mxExpectationNormal( covariance="covMZf",
                        means="expMeanGMZf", dimnames=c('t1','t2') )
expDZf      <- mxExpectationNormal( covariance="covDZf",
                        means="expMeanGDZf", dimnames=c('t1','t2') )
expMZm      <- mxExpectationNormal( covariance="covMZm",
                        means="expMeanGMZm", dimnames=c('t1','t2') )

```

```

expDZm      <- mxExpectationNormal( covariance="covDZm",
means="expMeanGDZm", dimnames=c('t1','t2') )
expDZo      <- mxExpectationNormal( covariance="covDZo",
means="expMeanGDZo", dimnames=c('t1','t2') )
funML       <- mxFitFunctionML()

# Data objects for Multiple Groups
dataMZf <- mxData(subset(mzfData,
(!is.na(mzfData$t1)!!is.na(mzfData$t2))), "raw")
dataDZf <- mxData(subset(dzfData,
(!is.na(dzfData$t1)!!is.na(dzfData$t2))), "raw")
dataMZm <- mxData(subset(mzmData,
(!is.na(mzmData$t1)!!is.na(mzmData$t2))), "raw")
dataDZm <- mxData(subset(dzmData,
(!is.na(dzmData$t1)!!is.na(dzmData$t2))), "raw")
dataDZo <- mxData(subset(dzoData,
(!is.na(dzoData$t1)!!is.na(dzoData$t2))), "raw")

# Combine Groups
modelMZf <- mxModel( defs_mzf, meanGMZf, covMZf, dataMZf, expMZf,
funML, name="MZf" )
modelDZf <- mxModel( defs_dzf, meanGDZf, covDZf, dataDZf, expDZf,
funML, name="DZf" )
modelMZm <- mxModel( defs_mzm, meanGMZm, covMZm, dataMZm, expMZm,
funML, name="MZm" )
modelDZm <- mxModel( defs_dzm, meanGDZm, covDZm, dataDZm, expDZm,
funML, name="DZm" )
modelDZo <- mxModel( defs_dzo, meanGDZo, covDZo, dataDZo, expDZo,
funML, name="DZo" )
fitML <-
mxFitFunctionMultigroup(c("MZf.fitfunction","DZf.fitfunction","MZm.fit
function","DZm.fitfunction", "DZo.fitfunction"))
HetSatConModel <- mxModel( "HetSat", modelMZf, modelDZf, modelMZm,
modelDZm, modelDZo, fitML )

# -----
# RUN MODEL

# Run Saturated Model
HetSatConFit      <- mxRun( HetSatConModel, intervals=F )
HetSatConSum      <- summary( HetSatConFit )
HetSatConSum
round(HetSatConFit$output$estimate,4)
cat("\n")

# Generate Saturated Model Output
HetSatConFit$MZf.covMZf$values
HetSatConFit$DZf.covDZf$values
HetSatConFit$MZf.MeanMzf$values
HetSatConFit$DZf.MeanDzf$values
HetSatConFit$DZo.MeanDzf$values
cat("\n")
HetSatConFit$MZm.covMZm$values
HetSatConFit$DZm.covDZm$values
HetSatConFit$MZm.MeanMzm$values
HetSatConFit$DZm.MeanDzm$values
HetSatConFit$DZo.MeanDzm$values
cat("\n")
HetSatConSum$observedStatistics

```

```

length(HetSatConSum$parameters[[1]])
HetSatConSum$degreesOfFreedom
HetSatConFit$output$Minus2LogLikelihood
HetSatConSum$AIC

cat("\n")
# Use Helper Functions
parameterSpecifications(HetSatConFit)
tableFitStatistics(HetSatConFit)
mxCompare(HetSatConFit)
cat("\n")

# -----
# RUN SUBMODELS

#TESTING EQUALITY OF COVARIANCES
#constrain covariances of MZF and MZM to be equal
eqcMZModel <- mxModel(HetSatConFit, name="eqcMZ" )
eqcMZModel <- omxSetParameters(eqcMZModel, label =
c("cMZf21","cMZm21"),free=TRUE, values = 0, newlabels = 'cMZ21')
eqcMZFit <- mxRun( eqcMZModel, intervals=F )
mxCompare(HetSatConFit, eqcMZFit)
cat("\n")

#constrain covariances of MZF and MZM to be equal, and DZF and DZM to
be equal
eqcDZModel <- mxModel(eqcMZFit, name="eqcDZ" )
eqcDZModel <- omxSetParameters(eqcDZModel , label =
c("cDZf21","cDZm21"),free=TRUE, values = 0, newlabels = 'cDZ21')
eqcDZFit <- mxRun( eqcDZModel , intervals=F )
mxCompare(eqcMZFit, eqcDZFit)
cat("\n")

# constrain covariances of MZF and MZM to be equal, and DZO to be
equal to those of DZM and DZF.
eqMZDZAllModel <- mxModel(eqcMZFit, name="eqMZDZAll" )
eqMZDZAllModel <- omxSetParameters(eqMZDZAllModel, label =
c("cDZf21","cDZm21","cDZo21"),free=TRUE, values = 0, newlabels =
'cDZ21')
eqMZDZAllFit <- mxRun( eqMZDZAllModel, intervals=F )
mxCompare(eqcDZFit, eqMZDZAllFit)
cat("\n")

# # -----
# # Print Comparative Fit Statistics
SatNested <-
list(eqMeansTwinFit,eqMeansSSZygFit,eqMeansAllZygFit,eqVarsTwinFit,
eqVarsSSZygFit, eqVarsAllZygFit, eqcMZFit,eqcDZFit,eqMZDZAllFit)
mxCompare(HetSatConFit, SatNested)
cat("\n")

sink()

```

Appendix C-6 OpenMx Script for Testing Equality of Means and Variances for Continuous Measure

```
# -----
# Adapted from twinSatCon.R by Hermine Maes (08 28 2014)
#
# Univariate Twin Saturated model to estimate means and (co)variances
across multiple groups
# Matrix style model - Raw data - Continuous data
# -----|-----|-----|-----|-----|-----|
#read output into text file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/twinSatAgeSexMZDZallobjTasks.txt", append=TRUE,
split=TRUE)

# Load Libraries
library(OpenMx)
library(psych)

# -----
# PREPARE DATA

# Load Data

#change Vars to variable of interest
Vars <- 'var1'
combVars <- c('Age', 'Sex', Vars)
nvInit <- 3
nv <- 1 # number of variables
ntv <- nv*2 # number of total variables
selVars <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")
#eg c('ht1', 'wt1', 'ht2', 'wt2')

#Select Data for Analysis
mzData <- subset(twinData2015, Zygosity==1, selVars)
dzData <- subset(twinData2015, Zygosity==2, selVars)

colnames(mzData)=colnames(dzData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', '
t2')

cat("mzData\n")
describe(mzData)
cat("\n")
cat("\n")
cat("dzData\n")
describe(dzData)
cat("\n")
cat("\n")

# Set Starting Values
svMe <- 0 # start value for means
svVa <- 1 # start value for variance
lbVa <- 0.0001 # start value for lower bounds
svVas <- diag(svVa, ntv, ntv) # assign start values to diagonal
of matrix
lbVas <- diag(lbVa, ntv, ntv) # assign lower bounds values to
diagonal of matrix
```



```

# -----
# PREPARE MODEL
intercept_mz      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
                                free=TRUE,
                                values= svMe, labels=c("mMZ1","mMZ2"),
                                name="meanMZ" )
intercept_dz      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
                                free=TRUE,
                                values= svMe, labels=c("mDZ1","mDZ2"),
                                name="meanDZ" )

# Matrix for covariate: sex
defSex            <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                                labels=c("data.Sex1","data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for covariate
B_Sex            <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                                values= .01, label="betaSex", name="bSex" )

meanSex          <- mxAlgebra( bSex%*%Sex, name="SexR")

#Matrix for covariate: age
defAge           <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                                labels=c("data.Age1","data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for covariate
B_Age           <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                                values= .01, label="betaAge", name="bAge" )

meanAge         <- mxAlgebra( bAge%*%Age, name="AgeR")

#*****
# Algebra for expected Mean and Variance/Covariance Matrices in MZ &
# DZ twins

meanGMZ         <- mxAlgebra( meanMZ + AgeR + SexR , name="expMeanGMZ")
meanGDZ         <- mxAlgebra( meanDZ + AgeR + SexR , name="expMeanGDZ")

defs_mz         <- list( intercept_mz, defSex, B_Sex, meanSex, defAge,
                        B_Age, meanAge)
defs_dz         <- list( intercept_dz, defSex, B_Sex, meanSex, defAge,
                        B_Age, meanAge)

# Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
covMZ           <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                                values=svVas, lbound=lbVas, labels=c("vMZ1","cMZ21","vMZ2"),
                                name="covMZ" )
covDZ           <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                                values=svVas, lbound=lbVas, labels=c("vDZ1","cDZ21","vDZ2"),
                                name="covDZ" )

# Expectation objects for Multiple Groups
expMZ           <- mxExpectationNormal( covariance="covMZ",
                                means="expMeanGMZ", dimnames=c('t1','t2') )
expDZ           <- mxExpectationNormal( covariance="covDZ",
                                means="expMeanGDZ", dimnames=c('t1','t2') )

# Data objects for Multiple Groups
dataMZ          <- mxData( observed=mzData, type="raw" )
dataDZ          <- mxData( observed=dzData, type="raw" )

```

```

funML      <- mxFitFunctionML()

modelMZ    <- mxModel( defs_mz, meanGMZ, covMZ, dataMZ, expMZ, funML,
name="MZ" )
modelDZ    <- mxModel( defs_dz, meanGDZ, covDZ, dataDZ, expDZ, funML,
name="DZ" )

fitML      <-
mxFitFunctionMultigroup(c("MZ.fitfunction","DZ.fitfunction"))

ciCov      <- mxCI( c('MZ.covMZ','DZ.covDZ' ) )
ciMean     <- mxCI( c('MZ.meanMZ','DZ.meanDZ' ) )
twinSatConModel <- mxModel( "twinSatCon", modelMZ, modelDZ, fitML,
ciCov, ciMean )

# -----
# RUN MODEL
# Run Saturated Model
twinSatConFit    <- mxRun( twinSatConModel, intervals=F )
twinSatConSum    <- summary( twinSatConFit )
twinSatConSum
round(twinSatConFit$output$estimate,4)

# Generate Saturated Model Output
twinSatConFit$MZ.covMZ$values
twinSatConFit$DZ.covDZ$values
twinSatConFit$MZ.MeanMz$values
twinSatConFit$DZ.MeanDz$values

twinSatConSum$observedStatistics
length(twinSatConSum$parameters[[1]])
twinSatConSum$degreesOfFreedom
twinSatConFit$output$Minus2LogLikelihood
twinSatConSum$AIC

# Use Helper Functions
parameterSpecifications(twinSatConFit)
tableFitStatistics(twinSatConFit)
mxCompare(twinSatConFit)

# -----
# RUN SUBMODELS

# Constrain expected Means to be equal across twin order
eqMeansTwinModel <- mxModel(twinSatConFit, name="eqMeansTwin" )
eqMeansTwinModel <- omxSetParameters( eqMeansTwinModel,
label=c("mMZ1","mMZ2"), free=TRUE, values=svMe, newlabels='mMZ' )
eqMeansTwinModel <- omxSetParameters( eqMeansTwinModel,
label=c("mDZ1","mDZ2"), free=TRUE, values=svMe, newlabels='mDZ' )

eqMeansTwinFit    <- mxRun( eqMeansTwinModel, intervals=F )
eqMeansTwinSum    <- summary( eqMeansTwinFit )
eqMeansTwinLLL    <- eqMeansTwinFit$output$Minus2LogLikelihood

twinSatConLLL     <- twinSatConFit$output$Minus2LogLikelihood
chi2Sat_eqM       <- eqMeansTwinLLL-twinSatConLLL
pSat_eqM          <- pchisq( chi2Sat_eqM, lower.tail=F, 2)
chi2Sat_eqM; pSat_eqM
mxCompare(twinSatConFit, eqMeansTwinFit)

# Constrain expected Means and Variances to be equal across twin order

```

```

eqMVarsTwinModel      <- mxModel(eqMeansTwinFit, name="eqMVarsTwin" )
eqMVarsTwinModel      <- omxSetParameters( eqMVarsTwinModel,
label=c("vMZ1","vMZ2"), free=TRUE, values=svVa, newlabels='vMZ' )
eqMVarsTwinModel      <- omxSetParameters( eqMVarsTwinModel,
label=c("vDZ1","vDZ2"), free=TRUE, values=svVa, newlabels='vDZ' )

eqMVarsTwinFit        <- mxRun( eqMVarsTwinModel, intervals=F )
eqMVarsTwinSum         <- summary( eqMVarsTwinFit )
eqMVarsTwinLLL         <- eqMVarsTwinFit$output$Minus2LogLikelihood
tableFitStatistics(eqMeansTwinFit, eqMVarsTwinFit)
tableFitStatistics(twinSatConFit, eqMVarsTwinFit)
subs <- list(eqMeansTwinFit, eqMVarsTwinFit)
mxCompare(twinSatConFit, subs)

# Constrain expected Means and Variances to be equal across twin order
# and zygosity
eqMVarsZygModel       <- mxModel(eqMVarsTwinModel, name="eqMVarsZyg" )
eqMVarsZygModel       <- omxSetParameters( eqMVarsZygModel,
label=c("mMZ","mDZ"), free=TRUE, values=svMe, newlabels='mZ' )
eqMVarsZygModel       <- omxSetParameters( eqMVarsZygModel,
label=c("vMZ","vDZ"), free=TRUE, values=svVa, newlabels='vZ' )

eqMVarsZygFit         <- mxRun( eqMVarsZygModel, intervals=F )
eqMVarsZygSum          <- summary( eqMVarsZygFit )
eqMVarsZygLLL         <- eqMVarsZygFit$output$Minus2LogLikelihood
mxCompare(eqMVarsTwinFit, eqMVarsZygFit)

# -----

# Print Comparative Fit Statistics
SatNested <- list(eqMeansTwinFit, eqMVarsTwinFit, eqMVarsZygFit)
mxCompare(twinSatConFit, SatNested)

sink()

```

Appendix C-7 OpenMx Script for Testing Equality of Covariances for Categorical Measure

```
# -----
# Adapted from twinSatOrd.R by Hermine Maes (09 08 2015)
# -----|-----|-----|-----|-----|-----|-----

#read output into text file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/SatordACEHet5_AS_crd.txt", append=TRUE, split=TRUE)

# Load Library
require(OpenMx)
require(psych)

# # -----
# Select variable for analysis
Vars      <- 'var1'

combVars   <- c('Age', 'Sex', Vars)
nvInit     <- 3
nv         <- 1      # number of variables
ntv        <- nv*2    # number of total variables
selVars    <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")
#eg c('ht1', 'wt1', 'ht2', 'wt2')

nth         <- 2      # number of thresholds; change accordingly

mzfData     <- subset(twinData2015, ZygotityGrp==1, selVars)
dzfData     <- subset(twinData2015, ZygotityGrp==2, selVars)
mzmData     <- subset(twinData2015, ZygotityGrp==3, selVars)
dzmData     <- subset(twinData2015, ZygotityGrp==4, selVars)
dzoData     <- subset(twinData2015, ZygotityGrp==5, selVars)

colnames(mzfData)=colnames(dzfData)=colnames(mzmData)=colnames(dzmData)
)=colnames(dzoData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', 't2')

mzfData[,3] <- mxFactor( x=mzfData[,3], levels=c(1:3) ) #change
accordingly
mzfData[,6] <- mxFactor( x=mzfData[,6], levels=c(1:3) )

dzfData[,3] <- mxFactor( x=dzfData[,3], levels=c(1:3) )
dzfData[,6] <- mxFactor( x=dzfData[,6], levels=c(1:3) )

mzmData[,3] <- mxFactor( x=mzmData[,3], levels=c(1:3) ) #change
accordingly
mzmData[,6] <- mxFactor( x=mzmData[,6], levels=c(1:3) )

dzmData[,3] <- mxFactor( x=dzmData[,3], levels=c(1:3) )
dzmData[,6] <- mxFactor( x=dzmData[,6], levels=c(1:3) )

dzoData[,3] <- mxFactor( x=dzoData[,3], levels=c(1:3) )
dzoData[,6] <- mxFactor( x=dzoData[,6], levels=c(1:3) )

# Set Starting Values
svLTh      <- -3      # start value for first threshold
svITH      <- 1       # start value for increments
svTh       <- matrix(rep(c(svLTh, (rep(svITH, nth-1)))), nrow=nth, ncol=nv)
```

```

# start value for thresholds
lbTh      <- matrix(rep(c(-3, (rep(0.001, nth-1))), nv), nrow=nth, ncol=nv)
# lower bounds for thresholds
svCor     <- .5      # start value for correlations
lbCor     <- -0.99   # lower bounds for correlations
ubCor     <- 0.99    # upper bounds for correlations

labThMZf   <-
c(paste("t", 1:nth, "MZf1", sep=""), paste("t", 1:nth, "MZf2", sep=""))
labThDZf   <-
c(paste("t", 1:nth, "DZf1", sep=""), paste("t", 1:nth, "DZf2", sep=""))
labThMZm   <-
c(paste("t", 1:nth, "MZm1", sep=""), paste("t", 1:nth, "MZm2", sep=""))
labThDZm   <-
c(paste("t", 1:nth, "DZm1", sep=""), paste("t", 1:nth, "DZm2", sep=""))
labThDZo   <-
c(paste("t", 1:nth, "DZo1", sep=""), paste("t", 1:nth, "DZo2", sep=""))

# -----
# PREPARE MODEL
# Saturated Model

# Matrix for covariates
#sex
defSex     <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                        labels=c("data.Sex1", "data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for sex covariate
B_Sex     <- mxMatrix( type="Full", nrow=nth, ncol=1, free=TRUE,
                        values= .01, label="betaSex", name="bSex" )

meanSex    <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge     <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                        labels=c("data.Age1", "data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for age covariate
B_Age     <- mxMatrix( type="Full", nrow=nth, ncol=1, free=TRUE,
                        values= .01, label="betaAge", name="bAge" )

meanAge    <- mxAlgebra( bAge%*%Age, name="AgeR")

#*****
# Algebra for expected Mean and Threshold Matrices in MZ & DZ twins
defs      <- list( defSex, B_Sex, meanSex, defAge, B_Age, meanAge)
meanG     <- mxMatrix( type="Zero", nrow=1, ncol=ntv, name="meanG" )
thinMZf   <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThMZf, name="thinMZf" )
thinDZf   <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThDZf, name="thinDZf" )
thinMZm   <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThMZm, name="thinMZm" )
thinDZm   <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThDZm, name="thinDZm" )
thinDZo   <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThDZo, name="thinDZo" )

inc       <- mxMatrix( type="Lower", nrow=nth, ncol=nth, free=FALSE,
                        values=1, name="inc" )
threMZf   <- mxAlgebra( expression= inc %*% thinMZf, name="threMZf" )

```

```

threDZf    <- mxAlgebra( expression= inc %*% thinDZf, name="threDZf" )
threMZm    <- mxAlgebra( expression= inc %*% thinMZm, name="threMZm" )
threDZm    <- mxAlgebra( expression= inc %*% thinDZm, name="threDZm" )
threDZo    <- mxAlgebra( expression= inc %*% thinDZo, name="threDZo" )

threCMZf <- mxAlgebra( expression = threMZf + SexR + AgeR, name =
"threCMZf") #with covariates
threCDZf <- mxAlgebra( expression = threDZf + SexR + AgeR, name =
"threCDZf") #with covariates
threCMZm <- mxAlgebra( expression = threMZm + SexR + AgeR, name =
"threCMZm") #with covariates
threCDZm <- mxAlgebra( expression = threDZm + SexR + AgeR, name =
"threCDZm") #with covariates
threCDZo <- mxAlgebra( expression = threDZo + SexR + AgeR, name =
"threCDZo") #with covariates

# Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
corMZf    <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
values=svCor, lbound=lbCor, ubound=ubCor, labels="rMZf",
name="corMZf" )
corDZf    <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
values=svCor, lbound=lbCor, ubound=ubCor, labels="rDZf",
name="corDZf" )
corMZm    <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
values=svCor, lbound=lbCor, ubound=ubCor, labels="rMZm",
name="corMZm" )
corDZm    <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
values=svCor, lbound=lbCor, ubound=ubCor, labels="rDZm",
name="corDZm" )
corDZo    <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
values=svCor, lbound=lbCor, ubound=ubCor, labels="rDZo",
name="corDZo" )

# Data objects for Multiple Groups
dataMZf    <- mxData( observed=mzfData, type="raw" )
dataDZf    <- mxData( observed=dzfData, type="raw" )
dataMZm    <- mxData( observed=mzmData, type="raw" )
dataDZm    <- mxData( observed=dzmData, type="raw" )
dataDZo    <- mxData( observed=dzoData, type="raw" )

# Objective objects for Multiple Groups
expMZf    <- mxExpectationNormal( covariance="corMZf", means="meanG",
dimnames=c('t1','t2'), thresholds="threCMZf" )
expDZf    <- mxExpectationNormal( covariance="corDZf", means="meanG",
dimnames=c('t1','t2'), thresholds="threCDZf" )
expMZm    <- mxExpectationNormal( covariance="corMZm", means="meanG",
dimnames=c('t1','t2'), thresholds="threCMZm" )
expDZm    <- mxExpectationNormal( covariance="corDZm", means="meanG",
dimnames=c('t1','t2'), thresholds="threCDZm" )
expDZo    <- mxExpectationNormal( covariance="corDZo", means="meanG",
dimnames=c('t1','t2'), thresholds="threCDZo" )

funML      <- mxFitFunctionML()

# Combine Groups
modelMZf    <- mxModel( "MZf",defs, meanG, corMZf, thinMZf, inc,
threMZf, threCMZf, dataMZf, expMZf, funML )
modelDZf    <- mxModel( "DZf", defs, meanG, corDZf, thinDZf, inc,
threDZf, threCDZf, dataDZf, expDZf, funML )
modelMZm    <- mxModel( "MZm",defs, meanG, corMZm, thinMZm, inc,
threMZm, threCMZm, dataMZm, expMZm, funML )

```

```

modelDZm <- mxModel( "DZm", defs, meanG, corDZm, thinDZm, inc,
threDZm, threCDZm, dataDZm, expDZm, funML )
modelDZo <- mxModel( "DZo", defs, meanG, corDZo, thinDZo, inc,
threDZo, threCDZo, dataDZo, expDZo, funML )

multi <-
mxFitFunctionMultigroup( c("MZf.fitfunction","DZf.fitfunction","MZm.fi
tfunction","DZm.fitfunction","DZo.fitfunction") )
ciCor <-
mxCI( c('MZf.corMZf','DZf.corDZf','MZm.corMZm','DZm.corDZm','DZo.corDZ
o' ))
#ciThre <- mxCI( c('MZ.threMZ','DZ.threDZ' ))
twinSatOrdModel <- mxModel( "twinSatOrd", modelMZf, modelDZf,
modelMZm, modelDZm, modelDZo, multi, ciCor)

# -----
# RUN MODEL

# Run Saturated Model
twinSatOrdFit <- mxRun( twinSatOrdModel, intervals=T )
twinSatOrdSum <- summary( twinSatOrdFit, verbose = TRUE )
twinSatOrdSum
round(twinSatOrdFit$output$estimate,4)

mxCompare(twinSatOrdFit)
cat("\n")
# -----
#TESTING EQUALITY OF COVARIANCES WITH SUBMODELS
#constrain covariances of MZF and MZM
eqcMZModel <- mxModel(twinSatOrdFit, name="eqcMZ" )
eqcMZModel <- omxSetParameters(eqcMZModel, label =
c("rMZf","rMZm"),free=TRUE, values = 0, newlabels = 'rMZ')
eqcMZFit <- mxRun( eqcMZModel, intervals=F )
mxCompare(twinSatOrdFit, eqcMZFit)
cat("\n")

#constrain covariances of MZF and MZM, DZF and DZM
eqcDZModel <- mxModel(eqcMZFit, name="eqcDZ" )
eqcDZModel <- omxSetParameters(eqcDZModel , label =
c("rDZf","rDZm"),free=TRUE, values = 0, newlabels = 'rDZ')
eqcDZFit <- mxRun( eqcDZModel , intervals=F )
mxCompare(eqcMZFit, eqcDZFit)
cat("\n")

# #constrain covariances of MZF and MZM; DZF, DZM and DZO
eqMZDZAllModel <- mxModel(eqcMZFit, name="eqMZDZAll" )
eqMZDZAllModel <- omxSetParameters(eqMZDZAllModel, label =
c("rDZf","rDZm","rDZo"),free=TRUE, values = 0, newlabels = 'rDZ')
eqMZDZAllFit <- mxRun( eqMZDZAllModel, intervals=F )
mxCompare(eqcDZFit, eqMZDZAllFit)
cat("\n")

# -----

# Print Comparative Fit Statistics
SatNested <- list(eqcMZFit, eqcDZFit,eqMZDZAllFit)
mxCompare(twinSatOrdFit, SatNested)

sink()

```

Appendix C-8 OpenMx Script for Testing Equality of Means and Variances and Computing Intraclass Correlations for Categorical Measure

```
# -----
# Adapted from twinSatOrd.R by Hermine Maes (09 08 2015)
# Univariate Twin Saturated model to estimate thresholds and
# intraclass correlations across multiple groups
# Matrix style model - Raw data - Ordinal data
# -----|-----|-----|-----|-----|-----

#read output into text file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/SatordACE_AS_crd.txt", append=TRUE, split=TRUE)

# Load Library
require(OpenMx)
require(psych)
# # -----
# specify variable for analysis
Vars      <- 'var1'
combVars  <- c('Age', 'Sex', Vars)  #, 'yrsTraining'
nvInit    <- 3
nv        <- 1      # number of variables
ntv       <- nv*2    # number of total variables
selVars   <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")

nth       <- 2      # number of thresholds; change accordingly

mzData    <- subset(twinData2015, Zygosity==1, selVars)  #MZ
dzData    <- subset(twinData2015, Zygosity==2, selVars)  #DZ

colnames(mzData)=colnames(dzData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', '
t2')

# Select Data for Analysis
mzData[,3] <- mxFactor( x=mzData[,3], levels=c(1:3) )  #change
accordingly
mzData[,6] <- mxFactor( x=mzData[,6], levels=c(1:3) )

dzData[,3] <- mxFactor( x=dzData[,3], levels=c(1:3) )
dzData[,6] <- mxFactor( x=dzData[,6], levels=c(1:3) )

# Set Starting Values
svLTh     <- -3      # start value for first threshold
svITH     <- 1       # start value for increments
svTh      <- matrix(rep(c(svLTh, (rep(svITH, nth-1)))), nrow=nth, ncol=nv)
# start value for thresholds
lbTh      <- matrix(rep(c(-3, (rep(0.001, nth-1))), nv), nrow=nth, ncol=nv)
# lower bounds for thresholds
svCor     <- .5      # start value for correlations
lbCor     <- -0.99   # lower bounds for correlations
ubCor     <- 0.99    # upper bounds for correlations

labThMZ   <-
c(paste("t", 1:nth, "MZ1", sep=""), paste("t", 1:nth, "MZ2", sep=""))
labThDZ   <-
c(paste("t", 1:nth, "DZ1", sep=""), paste("t", 1:nth, "DZ2", sep=""))
```



```

# -----
# PREPARE SATURATED MODEL
# Algebra for expected Mean & Threshold Matrices in MZ & DZ twins
# Matrices for covariates
defSex      <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                        labels=c("data.Sex1","data.Sex2"), name="Sex")

B_Sex       <- mxMatrix( type="Full", nrow=nth, ncol=1, free=TRUE,
                        values= .01, label="betaSex", name="bSex" )

meanSex     <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge      <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                        labels=c("data.Age1","data.Age2"), name="Age")

B_Age       <- mxMatrix( type="Full", nrow=nth, ncol=1, free=TRUE,
                        values= .01, label="betaAge", name="bAge" )

meanAge     <- mxAlgebra( bAge%*%Age, name="AgeR")
#*****
defs_mz     <- list( defSex, B_Sex, meanSex, defAge, B_Age, meanAge)
defs_dz     <- list( defSex, B_Sex, meanSex, defAge, B_Age, meanAge)

meanG       <- mxMatrix( type="Zero", nrow=1, ncol=ntv, name="meanG" )
thinMZ      <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThMZ, name="thinMZ" )
thinDZ      <- mxMatrix( type="Full", nrow=nth, ncol=ntv, free=TRUE,
                        values=svTh, lbound=lbTh, labels=labThDZ, name="thinDZ" )
inc         <- mxMatrix( type="Lower", nrow=nth, ncol=nth, free=FALSE,
                        values=1, name="inc" )
threMZ      <- mxAlgebra( expression= inc %*% thinMZ, name="threMZ" )
threDZ      <- mxAlgebra( expression= inc %*% thinDZ, name="threDZ" )

threCMZ <- mxAlgebra( expression = threMZ + SexR + AgeR, name =
"threCMZ") #with covariates
threCDZ <- mxAlgebra( expression = threDZ + SexR + AgeR, name =
"threCDZ") #with covariates

# Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
# Intraclass correlations of MZ and DZ twins
corMZ       <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svCor, lbound=lbCor, ubound=ubCor, labels="rMZ", name="corMZ" )
corDZ       <- mxMatrix( type="Stand", nrow=ntv, ncol=ntv, free=TRUE,
                        values=svCor, lbound=lbCor, ubound=ubCor, labels="rDZ", name="corDZ" )

# Data objects for Multiple Groups
dataMZ      <- mxData( observed=mzData, type="raw" )
dataDZ      <- mxData( observed=dzData, type="raw" )

# Objective objects for Multiple Groups
expMZ       <- mxExpectationNormal( covariance="corMZ", means="meanG",
                        dimnames=c('t1','t2'), thresholds="threCMZ" )
expDZ       <- mxExpectationNormal( covariance="corDZ", means="meanG",
                        dimnames=c('t1','t2'), thresholds="threCDZ" )
funML       <- mxFitFunctionML()

# Combine Groups
modelMZ     <- mxModel( "MZ",defs_mz, meanG, corMZ, thinMZ, inc, threMZ,
                        threCMZ, dataMZ, expMZ, funML )

```

```

modelDZ    <- mxModel( "DZ", defs_dz, meanG, corDZ, thinDZ, inc,
threDZ, threCDZ, dataDZ, expDZ, funML )
multi      <-
mxFitFunctionMultigroup( c("MZ.fitfunction","DZ.fitfunction") )
ciCor      <- mxCI( c('MZ.corMZ','DZ.corDZ' ))
twinSatOrdModel    <- mxModel( "twinSatOrd", modelMZ, modelDZ, multi,
ciCor)

# -----
# Run Saturated Model
twinSatOrdFit      <- mxRun( twinSatOrdModel, intervals=T )
twinSatOrdSum      <- summary( twinSatOrdFit, verbose = TRUE )
twinSatOrdSum
round(twinSatOrdFit$output$estimate,4)

mxCompare(twinSatOrdFit)

# -----
# RUN SUBMODELS
# Constrain expected Thresholds to be equal across twin order
eqThresTwinModel    <- mxModel(twinSatOrdFit, name="eqThresTwin" )
eqThresTwinModel    <- omxSetParameters( eqThresTwinModel,
label=c("t1MZ1","t1MZ2"), free=TRUE, values=svLTh, newlabels='t1MZ' )
  for (i in 2:nth) { eqThresTwinModel    <-
omxSetParameters( eqThresTwinModel,
label=c(paste("t",i,"MZ1",sep=""),paste("t",i,"MZ2",sep="")),
free=TRUE, values=svITh, newlabels=paste("t",i,"MZ",sep="") ) }

eqThresTwinModel    <- omxSetParameters( eqThresTwinModel,
label=c("t1DZ1","t1DZ2"), free=TRUE, values=svLTh, newlabels='t1DZ' )
  for (i in 2:nth) { eqThresTwinModel    <-
omxSetParameters( eqThresTwinModel,
label=c(paste("t",i,"DZ1",sep=""),paste("t",i,"DZ2",sep="")),
free=TRUE, values=svITh, newlabels=paste("t",i,"DZ",sep="") ) }

eqThresTwinFit      <- mxRun( eqThresTwinModel, intervals=F )
eqThresTwinSum      <- summary( eqThresTwinFit )
eqThresTwinLLL      <- eqThresTwinFit$output$Minus2LogLikelihood
mxCompare(twinSatOrdFit, eqThresTwinFit)

# Constrain expected Thres to be equal across twin order and zygosity
eqThresZygModel     <- mxModel(eqThresTwinModel, name="eqThresZyg" )
eqThresZygModel     <- omxSetParameters( eqThresZygModel,
label=c("t1MZ","t1DZ"), free=TRUE, values=svLTh, newlabels='t1Z' )
  for (i in 2:nth) { eqThresZygModel     <-
omxSetParameters( eqThresZygModel,
label=c(paste("t",i,"MZ",sep=""),paste("t",i,"DZ",sep="")), free=TRUE,
values=svITh, newlabels=paste("t",i,"Z",sep="") ) }

eqThresZygFit       <- mxRun( eqThresZygModel, intervals=F )
eqThresZygSum       <- summary( eqThresZygFit )
eqThresZygLLL       <- eqThresZygFit$output$Minus2LogLikelihood
mxCompare(eqThresTwinFit, eqThresZygFit)

# -----
# Print Comparative Fit Statistics
SatNested <- list(eqThresTwinFit, eqThresZygFit)
mxCompare(twinSatOrdFit, SatNested)

sink()

```

Appendix C-9 OpenMx Script for Computation of Intraclass Correlations of Continuous Measures

```

sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/rMZrDZ_AS_var.txt", append=TRUE, split=TRUE)

require(OpenMx)
require(psych)

#change to variable of interest
Vars <- 'var1'
combVars <- c('Age', 'Sex', Vars)
nvInit <- 3
nv <- 1 # number of variables
ntv <- nv*2 # number of total variables
selVars <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")
#eg c('ht1', 'wt1', 'ht2', 'wt2')

# Select Data for Analysis
mzData <- subset(twinData2015, Zygoty==1, selVars) #MZ
dzData <- subset(twinData2015, Zygoty==2, selVars) #DZ

colnames(mzData)=colnames(dzData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', '
t2')

mzdat = mxData(mzData, "raw")
dzdat = mxData(dzData, "raw")

defnvars <- mxMatrix(type="Full", nrow=1, ncol=4, free=F,

labels=c("data.Age1", "data.Sex1", "data.Age2", "data.Sex2"), name="xdef")

Beta0mz <-
mxMatrix(type="Full", nrow=1, ncol=1, free=T, values=1, labels="beta0mz", na
me="Beta0mz")
Beta0dz <-
mxMatrix(type="Full", nrow=1, ncol=1, free=T, values=1, labels="beta0mz", na
me="Beta0dz") #Same by zyg.
Betage <-
mxMatrix(type="Full", nrow=1, ncol=1, free=T, values=0, labels="betage", nam
e="Betage")
Betasex <-
mxMatrix(type="Full", nrow=1, ncol=1, free=T, values=0, labels="betasex", na
me="Betasex")

Mzcor <-
mxMatrix(type="Stand", nrow=2, ncol=2, free=T, values=0.5, labels="mzcor", n
ame="Mzcor")
Dzcor <-
mxMatrix(type="Stand", nrow=2, ncol=2, free=T, values=0.5, labels="dzcor", n
ame="Dzcor")

Mzsds <-
mxMatrix(type="Full", nrow=2, ncol=1, free=T, values=1, labels="mzsd", lboun
d=0.0001, name="Mzsds")

```

```

Dzsds <-
mxMatrix(type="Full",nrow=2,ncol=1,free=T,values=1,labels="dzsd",lboun
d=0.0001,name="Dzsds")

Mzvar <- mxAlgebra(Mzcor * (Mzsds %*% t(Mzsds)), name="Mzvar",
dimnames=list(c('t1','t2'),c('t1','t2')))
Dzvar <- mxAlgebra(Dzcor * (Dzsds %*% t(Dzsds)), name="Dzvar",
dimnames=list(c('t1','t2'),c('t1','t2')))

Mzmeans <-
mxAlgebra(cbind(Beta0mz+(Betage*xdef[1,1])+(Betasex*xdef[1,2]),
Beta0mz+(Betage*xdef[1,3])+(Betasex*xdef[1,4])), name="Mzmeans",
dimnames=list(NULL,c('t1','t2')))
Dzmeans <-
mxAlgebra(cbind(Beta0dz+(Betage*xdef[1,1])+(Betasex*xdef[1,2]),
Beta0dz+(Betage*xdef[1,3])+(Betasex*xdef[1,4])), name="Dzmeans",
dimnames=list(NULL,c('t1','t2')))

objMZ <- mxExpectationNormal( covariance="Mzvar", means="Mzmeans",
dimnames=c('t1','t2') )
objDZ <- mxExpectationNormal( covariance="Dzvar", means="Dzmeans",
dimnames=c('t1','t2') )

funML <- mxFitFunctionML()

Mzmodel <-
mxModel("MZtwins",Beta0mz,Betage,Betasex,Mzcor,Mzmeans,Mzsds,Mzvar,def
nvars,mzdat,
objMZ,funML)
Dzmodel <-
mxModel("DZtwins",Beta0dz,Betage,Betasex,Dzcor,Dzmeans,Dzsds,Dzvar,def
nvars,dzdat,
objDZ,funML)

fitML <-
mxFitFunctionMultigroup(c("MZtwins.fitfunction","DZtwins.fitfunction")
)

Allmodell <-
mxModel("All",Mzmodel,Dzmodel,fitML,mxCI(c("mzcor","dzcor")))
Allrun1 <- mxRun(Allmodell, intervals=T)
( Allsumml <- summary(Allrun1) )

#Covariance matrices:
Allrun1$MZtwins.Mzvar@result
Allrun1$DZtwins.Dzvar@result

#Intraclass correlations of MZ and DZ groups
#Correlation matrices:
Allrun1$MZtwins.Mzcor@values
Allrun1$DZtwins.Dzcor@values

sink()

```

Appendix C-10 OpenMx Script for Univariate Genetic

Modelling of Continuous Measure

```
# -----
# Adapted from twinAceCon.R by Hermine Maes (02 14 2012)
# Univariate Twin Analysis model to estimate causes of variation
# -----|-----|-----|-----|-----|-----|-----

#Read output into file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/uniACE_AS_lnHBDcd.txt", append=TRUE, split=TRUE)

# Load Library
require(OpenMx)
require(psych)

# Select Variables for Analysis
Vars <- 'var1'
combVars <- c('Age', 'Sex', Vars)
nvInit <- 3
nv <- 1 # number of variables
ntv <- nv*2 # number of total variables
selVars <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")
#eg c('ht1', 'wt1', 'ht2', 'wt2')

#=====
# Select Data for Analysis

#Load Data
mzData <- subset(twinData2015, Zygosity==1, selVars) #MZ
dzData <- subset(twinData2015, Zygosity==2, selVars) #DZ
colnames(mzData)=colnames(dzData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', 't2')

# Generate Descriptive Statistics
colMeans(mzData, na.rm=TRUE)
colMeans(dzData, na.rm=TRUE)
cov(mzData, use="complete")
cov(dzData, use="complete")

mzData = mxData(mzData, "raw")
dzData = mxData(dzData, "raw")

# -----
# PREPARE MODEL
# ACE Model
pathA <- mxMatrix( type="Full", nrow=nv, ncol=nv, free=TRUE,
  values=.6, label="a11", name="a" )
pathC <- mxMatrix( type="Full", nrow=nv, ncol=nv, free=TRUE,
  values=.6, label="c11", name="c" )
pathE <- mxMatrix( type="Full", nrow=nv, ncol=nv, free=TRUE,
  values=.6, label="e11", name="e" )

covA <- mxAlgebra( a %*% t(a), name="A" )
covC <- mxAlgebra( c %*% t(c), name="C" )
covE <- mxAlgebra( e %*% t(e), name="E" )
covP <- mxAlgebra( A+C+E, name="V" )
```

```

# Matrix for expected Mean
intercept      <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE,
                             values= 5, label="mean", name="Mean" )
#####

# Matrix for covariates: Age and Sex
defSex         <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                             labels=c("data.Sex1","data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for covariate sex
B_Sex          <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                             values= .01, label="betaSex", name="bSex" )

meanSex        <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge         <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
                             labels=c("data.Age1","data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for covariate age
B_Age          <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                             values= .01, label="betaAge", name="bAge" )

meanAge        <- mxAlgebra( bAge%*%Age, name="AgeR")

#####
expMean        <- mxAlgebra( Mean + AgeR + SexR , name="expMean")

defs           <- list( intercept, defSex, B_Sex, meanSex, defAge, B_Age,
                        meanAge)

covMZ          <- mxAlgebra(
  rbind( cbind(A+C+E , A+C),
          cbind(A+C , A+C+E)), name="expCovMZ" )

covDZ          <- mxAlgebra(
  rbind( cbind(A+C+E, 0.5x%A+C),
          cbind(0.5x%A+C , A+C+E)), name="expCovDZ" )

# Objective objects for Multiple Groups
objMZ          <- mxExpectationNormal(covariance="expCovMZ",
  means="expMean", dimnames=c('t1','t2'))
objDZ          <- mxExpectationNormal(covariance="expCovDZ",
  means="expMean", dimnames=c('t1','t2'))

funML <- mxFitFunctionML()

rowVars        <- rep('vars',nv)
colVars        <- rep(c('A','C','E','SA','SC','SE'),each=nv)
estVars        <- mxAlgebra(cbind(A,C,E,A/V,C/V,E/V), name="Vars",
                             dimnames=list(rowVars,colVars))

parameters    <- list( pathA, pathC, pathE, covA, covC, covE, covP,
                        estVars)

modelMZ        <- mxModel( parameters, defs, expMean, covMZ, mzData, objMZ,
                        funML,
                             name="MZ" )

```

```

modelDZ    <- mxModel( parameters, defs, expMean, covDZ, dzData, objDZ,
funML,
                                name="DZ" )

fitML    <-
mxFitFunctionMultigroup(c("MZ.fitfunction","DZ.fitfunction"))

AceModel  <- mxModel( "ACE", parameters, modelMZ, modelDZ, fitML,
mxCI(c("Vars[1,4:6]")))
# -----
# RUN MODEL
# Run ACE model
AceFit_cov    <- mxRun(AceModel,intervals = T)
AceFitsumm    <- summary(AceFit_cov)
AceFitsumm

SatCon <- mxRefModels(AceFit_cov, run=TRUE)
mxCompare(SatCon,AceFit_cov)
# -----
# FIT SUBMODELS

# Run AE model
AeModel    <- mxModel( AceFit_cov, name="AE" )
AeModel    <- omxSetParameters( AeModel, labels="c11", free=FALSE,
values=0 )
AeFit_cov    <- mxRun(AeModel,intervals=T)
AeFitsumm    <- summary(AeFit_cov)
AeFitsumm

mxCompare(AceFit_cov,AeFit_cov)

# Run CE model
CeModel    <- mxModel( AceFit_cov, name="CE" )
CeModel    <- omxSetParameters( CeModel, labels="a11", free=FALSE,
values=0 )
CeFit_cov    <- mxRun(CeModel,intervals=T)
CeFitsumm    <- summary(CeFit_cov)
CeFitsumm

mxCompare(AceFit_cov,CeFit_cov)

# Run E model
EModel    <- mxModel( AeFit_cov, name="E" )
EModel    <- omxSetParameters( EModel, labels="a11", free=FALSE,
values=0 )
EFit_cov    <- mxRun(EModel,intervals=T)
EFitsumm    <- summary(EFit_cov)
EFitsumm

mxCompare(AceFit_cov,EFit_cov)

AceNested <- list(AeFit_cov,CeFit_cov,EFit_cov)
mxCompare(AceFit_cov,AceNested)

sink()

```

Appendix C-11 OpenMx Script for Univariate Genetic Modelling of Categorical Measure

```
# -----
# Adapted from twinAceOrdS.R by Hermine Maes (09 08 2015)
# Univariate Twin Analysis model to estimate causes of variation
# Matrix style model - Raw data - Ordinal data
# -----|-----|-----|-----|-----|-----|-----

#read output into text file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/ordACE_AS_var1.txt", append=TRUE, split=TRUE)

# Load Library
require(OpenMx)
require(psych)

# Specify Variables for Analysis
Vars <- 'var1'
combVars <- c('Age', 'Sex', Vars) #,'yrsTraining'
nvInit <- 3
nv <- 1 # number of variables
ntv <- nv*2 # number of total variables
selVars <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")
#eg c('ht1', 'wt1', 'ht2', 'wt2')

nth <- 2 # number of thresholds ; change accordingly

mzData <- subset(twinData2015, Zygosity==1, selVars) #note if it's
Zygosity or ZygosityGrp
dzData <- subset(twinData2015, Zygosity==2, selVars)

describe(mzData)
describe(dzData)

colnames(mzData)=colnames(dzData)=c('Age1', 'Sex1', 't1', 'Age2', 'Sex2', '
t2')

mzData[,1] <- mzData[,1]/100 #divide age by 100 to avoid program
error
mzData[,4] <- mzData[,4]/100

dzData[,1] <- dzData[,1]/100
dzData[,4] <- dzData[,4]/100

mzData[,3] <- mxFactor( x=mzData[,3], levels=c(1:3) )
mzData[,6] <- mxFactor( x=mzData[,6], levels=c(1:3) )

dzData[,3] <- mxFactor( x=dzData[,3], levels=c(1:3) )
dzData[,6] <- mxFactor( x=dzData[,6], levels=c(1:3) )

# Set Starting Values
svLTh <- -3 # start value for first threshold
svITH <- 1 # start value for increments
svTh <- matrix(rep(c(svLTh, (rep(svITH, nth-1)))), nrow=nth, ncol=nv)
# start value for thresholds
lbTh <- matrix(rep(c(-3, (rep(0.001, nth-1))), nv), nrow=nth, ncol=nv)
svCor <- .5 # start value for correlations
lbCor <- -0.99 # lower bounds for correlations
```



```

ubCor      <- 0.99      # upper bounds for correlations
labThZ     <- c(paste("t",1:nth,"Z",sep=""),paste("t",1:nth,"Z",sep=""))

# Set Starting Values
svPa       <- .6       # start value for path coefficients
# -----
# PREPARE MODEL
# ACE Model
# Matrices declared to store a, c, and e Path Coefficients
pathA      <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
values=0, label="a11", name="a" )
pathC      <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
values=0, label="c11", name="c" )
pathE      <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
values=1, label="e11", name="e" )

# Matrices generated to hold A, C, and E computed Variance Components
covA       <- mxAlgebra( expression=a %*% t(a), name="A" )
covC       <- mxAlgebra( expression=c %*% t(c), name="C" )
covE       <- mxAlgebra( expression=e %*% t(e), name="E" )

# Matrix for covariates
#sex
defSex     <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
labels=c("data.Sex1","data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for sex covariate
B_Sex     <- mxMatrix( type="Full", nrow=nth, ncol=1, free=TRUE,
values=.1, label="betaSex", name="bSex" )

meanSex    <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge     <- mxMatrix( type="Full", nrow=1, ncol=2, free=FALSE,
labels=c("data.Age1","data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for age covariate
B_Age     <- mxMatrix( type="Full", nrow=nth, ncol=1, free=TRUE,
values=.1, label="betaAge", name="bAge" )

meanAge    <- mxAlgebra( bAge%*%Age, name="AgeR")

#*****

defs       <- list( defSex, B_Sex, meanSex, defAge, B_Age, meanAge)

# Matrix & Algebra for expected means vector and expected thresholds
meanG     <- mxMatrix( type="Zero", nrow=1, ncol=ntv, name="expMean" )
threG     <- mxMatrix( type="Full", nrow=nth, ncol=nv, free=TRUE,
values=svTh, lbound=lbTh, labels=labThZ, name="Thre" )
inc       <- mxMatrix( type="Lower", nrow=nth, ncol=nth, free=FALSE,
values=1, name="Inc" )
threT     <- mxAlgebra( expression= cbind(Inc %*% Thre,Inc %*% Thre),
name="expThre" )
threC     <- mxAlgebra( expression = expThre + SexR + AgeR, name =
"expThreC") #with covariates

# Algebra to compute total variances and standard deviations (diagonal
only)
covP      <- mxAlgebra( expression=A+C+E, name="V" )

```

```

# Algebras generated to hold Parameter Estimates and Derived Variance
Components
rowVars <- rep('vars',nv)
colVars <- rep(c('A','C','E','SA','SC','SE'),each=nv)
estVars <- mxAlgebra( expression=cbind(A,C,E,A/V,C/V,E/V),
name="Vars", dimnames=list(rowVars,colVars))

# Algebra for expected Mean and Variance/Covariance Matrices in MZ &
DZ twins
covMZ <- mxAlgebra( expression= rbind( cbind(V, A+C), cbind(A+C,
V)), name="expCovMZ" )
covDZ <- mxAlgebra( expression= rbind( cbind(V, 0.5x%A+C),
cbind(0.5x%A+C, V)), name="expCovDZ" )

# Constraint on variance of Ordinal variables
matUnv <- mxMatrix( type="Unit", nrow=nv, ncol=1, name="Unv1" )
var1 <- mxConstraint( expression=diag2vec(V)==Unv1, name="Var1" )

# Data objects for Multiple Groups
dataMZ <- mxData( observed=mzData, type="raw" )
dataDZ <- mxData( observed=dzData, type="raw" )

# Objective objects for Multiple Groups
expMZ <- mxExpectationNormal( covariance="expCovMZ",
means="expMean", dimnames=c('t1','t2'), thresholds="expThreC" )
expDZ <- mxExpectationNormal( covariance="expCovDZ",
means="expMean", dimnames=c('t1','t2'), thresholds="expThreC" )
funML <- mxFitFunctionML()
ci <- mxCI(c("Vars[1,4:6]"))

# Combine Groups
pars <- list( pathA, pathC, pathE, covA, covC, covE, covP, inc,
matUnv, estVars )
modelMZ <- mxModel( pars, defs, meanG, threG, threT, threC, covMZ,
dataMZ, expMZ, funML, name="MZ" )
modelDZ <- mxModel( pars, defs, meanG, threG, threT, threC, covDZ,
dataDZ, expDZ, funML, name="DZ" )
multi <- mxFitFunctionMultigroup( c("MZ","DZ") )
AceModel <- mxModel( "ACE", pars, var1, modelMZ, modelDZ, multi, ci )

# -----
# RUN MODELS

# Run ACE Model
#AceFit <- mxRun(AceModel, unsafe=T)
AceFit <- mxRun(AceModel, intervals=T)
AceSumm <- summary(AceFit, verbose = T)
AceSumm
round(AceFit$output$estimate,4)
cat("\n")
round(AceFit$Vars$result,4)

cat("\n")
AceFit$MZ$expThre
cat("\n")

# Run AE model
AeModel <- mxModel( AceFit, name="AE" )
AeModel <- omxSetParameters( AeModel, labels="c11", free=FALSE,
values=0 )
AeFit <- mxRun(AeModel, intervals=T)

```

```

AeSumm  <- summary(AeFit, verbose = T)
AeSumm
cat("\n")
round(AeFit@output$estimate,4)
cat("\n")
round(AeFit$Vars@result,4)

# Run CE model
CeModel  <- mxModel( AceFit, name="CE" )
CeModel  <- omxSetParameters( CeModel, labels="all", free=FALSE,
values=0 )
CeFit    <- mxRun(CeModel, intervals=T)
CeSumm   <- summary(CeFit, verbose = T)
CeSumm
cat("\n")
round(CeFit@output$estimate,4)
cat("\n")
round(CeFit$Vars@result,4)

# Run E model
eModel   <- mxModel( AceFit, name="E" )
eModel   <- omxSetParameters( eModel, labels="all", free=FALSE,
values=0 )
eFit     <- mxRun(eModel, intervals=T)
eSumm    <- summary(eFit, verbose = T)
eSumm
cat("\n")
round(eFit@output$estimate,4)
cat("\n")
round(eFit$Vars@result,4)

# -----

# Print Comparative Fit Statistics
AceNested <- list(AeFit, CeFit, eFit)
mxCompare(AceFit,AceNested)
cat("\n")
round(c(AceFit@output$estimate,AeFit@output$estimate,CeFit@output$esti
mate,eFit@output$estimate),4)
cat("\n")
round(rbind(AceFit$Vars@result,AeFit$Vars@result,CeFit$Vars@result,eFi
t$Vars@result),4)

sink()

```

Appendix C-12 OpenMx Script for Bivariate Genetic Modelling of Continuous Measures

```
# -----
# Adapted from twinBivAceCon.R by Hermine Maes and Elizabeth Prom-
# Wormley (10 20 2014)
#
# Bivariate Twin Analysis model to estimate causes of variation
# Matrix style model - Raw data - Continuous data
# -----|-----|-----|-----|-----|-----|-----
#read output into text file
sink("F:/PhDstuff/complete pairs analysis/2015 New
Proc/AceOutput/BivAce_var1var2.txt", append=TRUE, split=TRUE)
source('F:/PhDstuff/complete pairs analysis/#Stats/codes/R
codes/GenEpiHelperFunctions.R')

# Load Library
require(OpenMx)
require(psych)

# -----
# PREPARE DATA

# Specify Variables for Analysis
# Vars: Singing and Background Component; PVars: Singing task measure
Vars <- 'var1'
PVars <- 'var2'

combVars      <- c('Age', 'Sex', Vars, PVars)
nvInit        <- 4
nv            <- 2      # number of variables
ntv          <- nv*2    # number of total variables
selVars       <- paste(combVars, c(rep(1, nvInit), rep(2, nvInit)), sep="")

mzData <- subset(twinData2015, Zygosity==1, selVars) #MZ
dzData <- subset(twinData2015, Zygosity==2, selVars) #DZ
colnames(mzData)=colnames(dzData)=c('Age1', 'Sex1', 'Vars1', 'PVars1', 'Ag
e2', 'Sex2', 'Vars2', 'PVars2')

describe(mzData)
describe(dzData)

cat("\n")
# Generate Descriptive Statistics
colMeans(mzData, na.rm=TRUE)
colMeans(dzData, na.rm=TRUE)
cov(mzData, use="complete")
cov(dzData, use="complete")
cor(mzData, use="complete")
cor(dzData, use="complete")
cat("\n")
```

```

# -----

# PREPARE SATURATED MODEL

# Fit Bivariate Saturated Model
# Set Starting Values
svMe      <- c(0,0)          # start value for means
laMeMZ    <-
c('Vars1_MeanMZ','PVars1_MeanMZ','Vars2_MeanMZ','PVars2_MeanMZ')
laMeDZ    <-
c('Vars1_MeanDZ','PVars1_MeanDZ','Vars2_MeanDZ','PVars2_MeanDZ')
svVa      <- c(0.5,0.8)     # start value for variances
svVas     <- diag(svVa,ntv,ntv)
laCvMZ    <- paste("covMZ",rev(ntv+1-
sequence(1:ntv)),rep(1:ntv,ntv:1),sep="_")
laCvDZ    <- paste("covDZ",rev(ntv+1-
sequence(1:ntv)),rep(1:ntv,ntv:1),sep="_")

intercept_mz      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values=svMe, labels=laMeMZ,
name="MeanMZ" )

intercept_dz      <- mxMatrix( type="Full", nrow=1, ncol=ntv,
free=TRUE,
                                values=svMe, labels=laMeDZ,
name="MeanDZ" )

# Matrix for covariates
# sex
defSex    <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=FALSE,
labels=c("data.Sex1","data.Sex1","data.Sex2","data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for sex covariate
B_Sex     <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                        values= .01, label="betaSex", name="bSex" )
meanSex    <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge     <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=FALSE,
labels=c("data.Age1","data.Age1","data.Age2","data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for age covariate
B_Age     <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                        values= .01, label="betaAge", name="bAge" )
meanAge    <- mxAlgebra( bAge%*%Age, name="AgeR")

#*****
# Algebra for expected Mean and Variance/Covariance Matrices in MZ &
DZ twins

meanGMZ    <- mxAlgebra( MeanMZ + AgeR + SexR , name="expMeanMZ")
meanGDZ    <- mxAlgebra( MeanDZ + AgeR + SexR , name="expMeanDZ")

defs_MZ    <- list( intercept_mz, defSex, B_Sex, meanSex, defAge,
B_Age, meanAge)
defs_DZ    <- list( intercept_dz, defSex, B_Sex, meanSex, defAge,
B_Age, meanAge)

```

```

# Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
covMZ      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
values=svVas, labels=laCvMZ, name="expCovMZ" )
covDZ      <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
values=svVas, labels=laCvDZ, name="expCovDZ" )

# Expectation objects for Multiple Groups
expMZ      <- mxExpectationNormal( covariance="expCovMZ",
means="expMeanMZ", c('Vars1','PVars1','Vars2','PVars2') )
expDZ      <- mxExpectationNormal( covariance="expCovDZ",
means="expMeanDZ", c('Vars1','PVars1','Vars2','PVars2') )
funML      <- mxFitFunctionML()

# Data objects for Multiple Groups
dataMZ     <- mxData(mzData, "raw")
dataDZ     <- mxData(dzData, "raw")

# Combine Groups
SatmodelMZ <- mxModel( defs_MZ, meanGMZ, covMZ, dataMZ, expMZ, funML,
name="MZ" )
SatmodelDZ <- mxModel( defs_DZ, meanGDZ, covDZ, dataDZ, expDZ, funML,
name="DZ" )
fitML     <-
mxFitFunctionMultigroup(c("MZ.fitfunction","DZ.fitfunction"))
bivTwinSatModel <- mxModel( "bivTwinSat", SatmodelMZ, SatmodelDZ,
fitML )

bivTwinSatFit <- mxRun(bivTwinSatModel)
bivTwinSatSumm <- summary(bivTwinSatFit)
bivTwinSatSumm

# Generate Saturated Output
# -----
parameterSpecifications(bivTwinSatFit)
expectedMeansCovariances(bivTwinSatFit)
tableFitStatistics(bivTwinSatFit)

# -----
# RUN SATURATED SUBMODELS
# Fit Bivariate Model with Equal Means & Variances across Twin Order
and Zygoty
# -----
# Constrain expected means and variances to be equal across twin order
equateMeansTwinModel <- mxModel(bivTwinSatFit, name="equateMeansTwin",

mxConstraint( expression=MZ.expMeanMZ[1,1:nv]==MZ.expMeanMZ[1,(nv+1):n
tv], name="MeanMZt1eqt2"),

mxConstraint( expression=DZ.expMeanDZ[1,1:nv]==DZ.expMeanDZ[1,(nv+1):n
tv], name="MeanDZt1eqt2")
)
equateMeansTwinFit <- mxRun(equateMeansTwinModel)

tableFitStatistics(bivTwinSatFit, equateMeansTwinFit)

equateMeansVarsTwinModel <- mxModel(equateMeansTwinFit,
name="equateMeansVarsTwin",

mxAlgebra( expression=t(diag2vec(MZ.expCovMZ)), name="expVarMZ"),

```

```

mxAlgebra( expression=t(diag2vec(DZ.expCovDZ)), name="expVarDZ"),

mxConstraint( expression=expVarMZ[1,1:nv]==expVarMZ[1,(nv+1):ntv],
name="VarMZt1eqt2"),

mxConstraint( expression=expVarDZ[1,1:nv]==expVarDZ[1,(nv+1):ntv],
name="VarDZt1eqt2")
)
equateMeansVarsTwinFit <- mxRun(equateMeansVarsTwinModel)
tableFitStatistics(bivTwinSatFit, equateMeansVarsTwinFit)

# Constrain expected means and variances to be equal across twin order
and zygosity
equateMeansVarsTwinZygModel <- mxModel(equateMeansVarsTwinFit,
name="equateMeansVarsTwinZyg",

mxConstraint( expression=expVarMZ[1,1:nv]==expVarDZ[1,1:nv],
name="VarMZeqDZ"),

mxConstraint( expression=MZ.expMeanMZ[1,1:nv]==DZ.expMeanDZ[1,1:nv],
name="MeanMZeqDZ")
)
equateMeansVarsTwinZygFit <- mxRun(equateMeansVarsTwinZygModel)
mxCompare(equateMeansVarsTwinFit,equateMeansVarsTwinZygFit)
tableFitStatistics(bivTwinSatFit, list(equateMeansTwinFit,
equateMeansVarsTwinFit, equateMeansVarsTwinZygFit))

# -----
# PREPARE ACE MODEL

# Set Starting Values
svMe      <- c(0,0)          # start value for means
laMe      <- c('Vars1_Mean','PVars1_Mean','Vars2_Mean','PVars2_Mean')
svPa      <- .6              # start value for parameters
svPas     <- diag(svPa,nv,nv)
laA       <- paste("a",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")
# c("a11","a21","a22")
laD       <- paste("d",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")
laC       <- paste("c",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")
laE       <- paste("e",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")

# Matrices declared to store a, c, and e Path Coefficients
pathA     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE,
values=svPas, label=laA, name="a" )
pathD     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=FALSE,
values=0, label=laD, name="d" )
pathC     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE,
values=svPas, label=laC, name="c" )
pathE     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE,
values=svPas, label=laE, name="e" )

# Matrices generated to hold A, C, and E computed Variance Components
covA      <- mxAlgebra( expression=a %*% t(a), name="A" )
covD      <- mxAlgebra( expression=d %*% t(d), name="D" )
covC      <- mxAlgebra( expression=c %*% t(c), name="C" )
covE      <- mxAlgebra( expression=e %*% t(e), name="E" )

# Algebra to compute total variances and standard deviations (diagonal
only)
covP      <- mxAlgebra( expression=A+D+C+E, name="V" )

```

```

matI      <- mxMatrix( type="Iden", nrow=nv, ncol=nv, name="I")
invSD     <- mxAlgebra( expression=solve(sqrt(I*V)), name="iSD")
#this is to help to get stdized paths

# Algebras generated to hold Parameter Estimates and Derived Variance
Components
rowVars   <- rep('vars',nv)
colVars   <- rep(c('A','D','C','E','SA','SD','SC','SE'),each=nv)

#each variable is repeated, A of Var1, A of var2, D of Var1, D of Var2
estVars   <- mxAlgebra( expression=cbind(A,D,C,E,A/V,D/V,C/V,E/V) ,
name="Vars", dimnames=list(rowVars,colVars))

SA <- mxAlgebra(expression=A/V, name="SA")
SD <- mxAlgebra(expression=D/V, name="SD")
SC <- mxAlgebra(expression=C/V, name="SC")
SE <- mxAlgebra(expression=E/V, name="SE")

# Algebra for expected Mean and Variance/Covariance Matrices in MZ &
DZ twins

intercept <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE,
                        values=svMe, labels=laMe, name="Mean" )

# Matrix for moderating/interacting variable
defSex    <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=FALSE,

labels=c("data.Sex1","data.Sex1","data.Sex2","data.Sex2"), name="Sex")

# Matrices declared to store linear Coefficients for covariate
B_Sex     <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                        values= .01, label="betaSex", name="bSex" )

meanSex    <- mxAlgebra( bSex%*%Sex, name="SexR")

#age
defAge     <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=FALSE,

labels=c("data.Age1","data.Age1","data.Age2","data.Age2"), name="Age")

# Matrices declared to store linear Coefficients for covariate
B_Age     <- mxMatrix( type="Full", nrow=1, ncol=1, free=TRUE,
                        values= .01, label="betaAge", name="bAge" )

meanAge    <- mxAlgebra( bAge%*%Age, name="AgeR")

#*****
# Algebra for expected Mean and Variance/Covariance Matrices in MZ &
DZ twins

meanT     <- mxAlgebra( Mean + AgeR + SexR , name="expMean")
defs      <- list( intercept, defSex, B_Sex, meanSex, defAge, B_Age,
meanAge)

covMZ      <- mxAlgebra( expression= rbind( cbind(V , A+D+C),
cbind(A+D+C , V)), name="expCovMZ" )
covDZ      <- mxAlgebra( expression= rbind( cbind(V,
0.5%x%A+0.25%x%D+C), cbind(0.5%x%A+0.25%x%D+C ,V)), name="expCovDZ" )

```



```

# Calculate genetic and environmental correlations
corA      <- mxAlgebra( expression=solve(sqrt(I*A))%&%A, name ="rA" )
corC      <- mxAlgebra( expression=solve(sqrt(I*C))%&%C, name ="rC" )
corE      <- mxAlgebra( expression=solve(sqrt(I*E))%&%E, name ="rE" )

#calculate genetic and environmental correlations due to A, D, C and E
corrA <- mxAlgebra(expression = sqrt(SA[1,1])*rA[2,1]*sqrt(SA[2,2]),
name="corrA")
corrC <- mxAlgebra(expression = sqrt(SC[1,1])*rC[2,1]*sqrt(SC[2,2]),
name="corrC")
corrE <- mxAlgebra(expression = sqrt(SE[1,1])*rE[2,1]*sqrt(SE[2,2]),
name="corrE")

ci <- mxCI
(c("SA[1,1]", "SA[2,2]", "SD[1,1]", "SD[2,2]", "SC[1,1]", "SC[2,2]", "SE[1,1]",
"SE[2,2]", "rA[2,1]", "rC[2,1]", "rE[2,1]", "corrA", "corrC", "corrE"))

# Expectation objects for Multiple Groups
expMZ      <- mxExpectationNormal( covariance="expCovMZ",
means="expMean", c('Vars1','PVars1','Vars2','PVars2') )
expDZ      <- mxExpectationNormal( covariance="expCovDZ",
means="expMean", c('Vars1','PVars1','Vars2','PVars2') )
funML      <- mxFitFunctionML()

# Data objects for Multiple Groups
dataMZ <- mxData(mzData, "raw")
dataDZ <- mxData(dzData, "raw")

# Combine Groups
pars      <- list( pathA, pathD, pathC, pathE, SA,SD,SC,SE,covA, covD,
covC, covE, covP, matI, invSD, estVars, corA, corC, corE, corrA,
corrC, corrE)
modelMZ   <- mxModel( pars, defs, meanT, covMZ, dataMZ, expMZ, funML,
name="MZ" )
modelDZ   <- mxModel( pars, defs, meanT, covDZ, dataDZ, expDZ, funML,
name="DZ" )
fitML     <-
mxFitFunctionMultigroup(c("MZ.fitfunction", "DZ.fitfunction"))

BivAceModelci <- mxModel( "BivACE", pars, modelMZ, modelDZ, fitML,ci)
BivAceModel <- mxModel( "BivACE", pars, modelMZ, modelDZ, fitML)

# -----
# RUN MODEL

# Run Bivariate ACE model
BivAceFitci <- mxRun(BivAceModelci,intervals=T)
BivAceFit <- mxRun(BivAceModel)

#Rerun the model to avoid the optimality prob.
BivAceFitciAgain <- mxRun(BivAceFitci,intervals=T)
BivAceSumm <- summary(BivAceFitciAgain, verbose = T)
BivAceSumm

# Generate List of Parameter Estimates and Derived Quantities using
formatOutputMatrices
ACEpathMatrices <- c("a","c","e","iSD","iSD %%% a","iSD %%%
c","iSD %%% e","(iSD %%% a)*(iSD %%% a)","(iSD %%% c)*(iSD %%%
c)","(iSD %%% e)*(iSD %%% e)")

```

```

ACEpathLabels <-
c("pathEst_a","pathEst_d","pathEst_e","isd","stPathEst_a","stPathEst_c",
"stPathEst_e", "st2PathEst_a","st2PathEst_c","st2PathEst_e")
formatOutputMatrices(BivAceFit,ACEpathMatrices,ACEpathLabels,Vars,4)

ACEcovMatrices <- c("A","C","E","V","A/V","C/V","E/V")
ACEcovLabels <-
c("covComp_A","covComp_C","covComp_E","Var","stCovComp_A","stCovComp_C",
"stCovComp_E")
formatOutputMatrices(BivAceFit,ACEcovMatrices,ACEcovLabels,Vars,4)

ACEcorMatrices <- c("rA","rC","rE","corrA","corrC","corrE")
ACEcorLabels <- c("rA","rC","rE","corrA","corrC","corrE")
formatOutputMatrices(BivAceFit,ACEcorMatrices,ACEcorLabels,Vars,4)

#Generate submodels: constrain a21, c21, and e21 to 0, respectively
BivAceModelna21 <- mxModel( BivAceFitci, name="ACEna21" )
BivAceModelna21 <- omxSetParameters( BivAceModelna21,
labels=c("a21"), free=FALSE, values=0 )
BivAcena21Fit <- mxRun(BivAceModelna21, intervals=T)
BivAcena21Summ <- summary(BivAcena21Fit)

BivAceModelnc21 <- mxModel( BivAceFitci, name="ACEnc21" )
BivAceModelnc21 <- omxSetParameters( BivAceModelnc21,
labels=c("c21"), free=FALSE, values=0 )
BivAcenc21Fit <- mxRun(BivAceModelnc21, intervals=T)
BivAcenc21Summ <- summary(BivAcenc21Fit)

BivAceModelne21 <- mxModel( BivAceFitci, name="ACEna21" )
BivAceModelne21 <- omxSetParameters( BivAceModelne21,
labels=c("e21"), free=FALSE, values=0 )
BivAcene21Fit <- mxRun(BivAceModelne21, intervals=T)
BivAcene21Summ <- summary(BivAcene21Fit)

BivAceNested <- list(BivAcena21Fit, BivAcenc21Fit, BivAcene21Fit)
tableFitStatistics(BivAceFit,BivAceNested)

#Generate the output of the first submodel: ACEna21
BivAcena21Summ

# Generate List of Parameter Estimates and Derived Quantities using
formatOutputMatrices
ACEpathMatrices <- c("a","c","e","isd","isd %%% a","isd %%%
c","isd %%% e","(isd %%% a)*(isd %%% a)","(isd %%% c)*(isd %%%
c)","(isd %%% e)*(isd %%% e)")
ACEpathLabels <-
c("pathEst_a","pathEst_d","pathEst_e","isd","stPathEst_a","stPathEst_c",
"stPathEst_e", "st2PathEst_a","st2PathEst_c","st2PathEst_e")
formatOutputMatrices(BivAcena21Fit,ACEpathMatrices,ACEpathLabels,Vars,
4)

ACEcovMatrices <- c("A","C","E","V","A/V","C/V","E/V")
ACEcovLabels <-
c("covComp_A","covComp_C","covComp_E","Var","stCovComp_A","stCovComp_C",
"stCovComp_E")
formatOutputMatrices(BivAcena21Fit,ACEcovMatrices,ACEcovLabels,Vars,4)

ACEcorMatrices <- c("rA","rC","rE","corrA","corrC","corrE")
ACEcorLabels <- c("rA","rC","rE","corrA","corrC","corrE")
formatOutputMatrices(BivAcena21Fit,ACEcorMatrices,ACEcorLabels,Vars,4)

```

```

#Generate the output of the second submodel: ACEnc21
BivAcenc21Summ

# Generate List of Parameter Estimates and Derived Quantities using
formatOutputMatrices
ACEpathMatrices <- c("a","c","e","isd","isd %*% a","isd %*%
c","isd %*% e","(isd %*% a)*(isd %*% a)","(isd %*% c)*(isd %*%
c)","(isd %*% e)*(isd %*% e)")
ACEpathLabels <-
c("pathEst_a","pathEst_d","pathEst_e","isd","stPathEst_a","stPathEst_c
","stPathEst_e","st2PathEst_a","st2PathEst_c","st2PathEst_e")
formatOutputMatrices(BivAcenc21Fit,ACEpathMatrices,ACEpathLabels,Vars,
4)

ACEcovMatrices <- c("A","C","E","V","A/V","C/V","E/V")
ACEcovLabels <-
c("covComp_A","covComp_C","covComp_E","Var","stCovComp_A","stCovComp_C
","stCovComp_E")
formatOutputMatrices(BivAcenc21Fit,ACEcovMatrices,ACEcovLabels,Vars,4)

ACEcorMatrices <- c("rA","rC","rE","corrA","corrC","corrE")
ACEcorLabels <- c("rA","rC","rE","corrA","corrC","corrE")
formatOutputMatrices(BivAcenc21Fit,ACEcorMatrices,ACEcorLabels,Vars,4)

#Generate the output of the third submodel: ACEnc21
BivAcene21Summ

# Generate List of Parameter Estimates and Derived Quantities using
formatOutputMatrices
ACEpathMatrices <- c("a","c","e","isd","isd %*% a","isd %*%
c","isd %*% e","(isd %*% a)*(isd %*% a)","(isd %*% c)*(isd %*%
c)","(isd %*% e)*(isd %*% e)")
ACEpathLabels <-
c("pathEst_a","pathEst_d","pathEst_e","isd","stPathEst_a","stPathEst_c
","stPathEst_e","st2PathEst_a","st2PathEst_c","st2PathEst_e")
formatOutputMatrices(BivAcene21Fit,ACEpathMatrices,ACEpathLabels,Vars,
4)

ACEcovMatrices <- c("A","C","E","V","A/V","C/V","E/V")
ACEcovLabels <-
c("covComp_A","covComp_C","covComp_E","Var","stCovComp_A","stCovComp_C
","stCovComp_E")
formatOutputMatrices(BivAcene21Fit,ACEcovMatrices,ACEcovLabels,Vars,4)

ACEcorMatrices <- c("rA","rC","rE","corrA","corrC","corrE")
ACEcorLabels <- c("rA","rC","rE","corrA","corrC","corrE")
formatOutputMatrices(BivAcene21Fit,ACEcorMatrices,ACEcorLabels,Vars,4)

sink()

```

Appendix D

INFORMATION FROM THE PRINCIPAL COMPONENTS ANALYSES

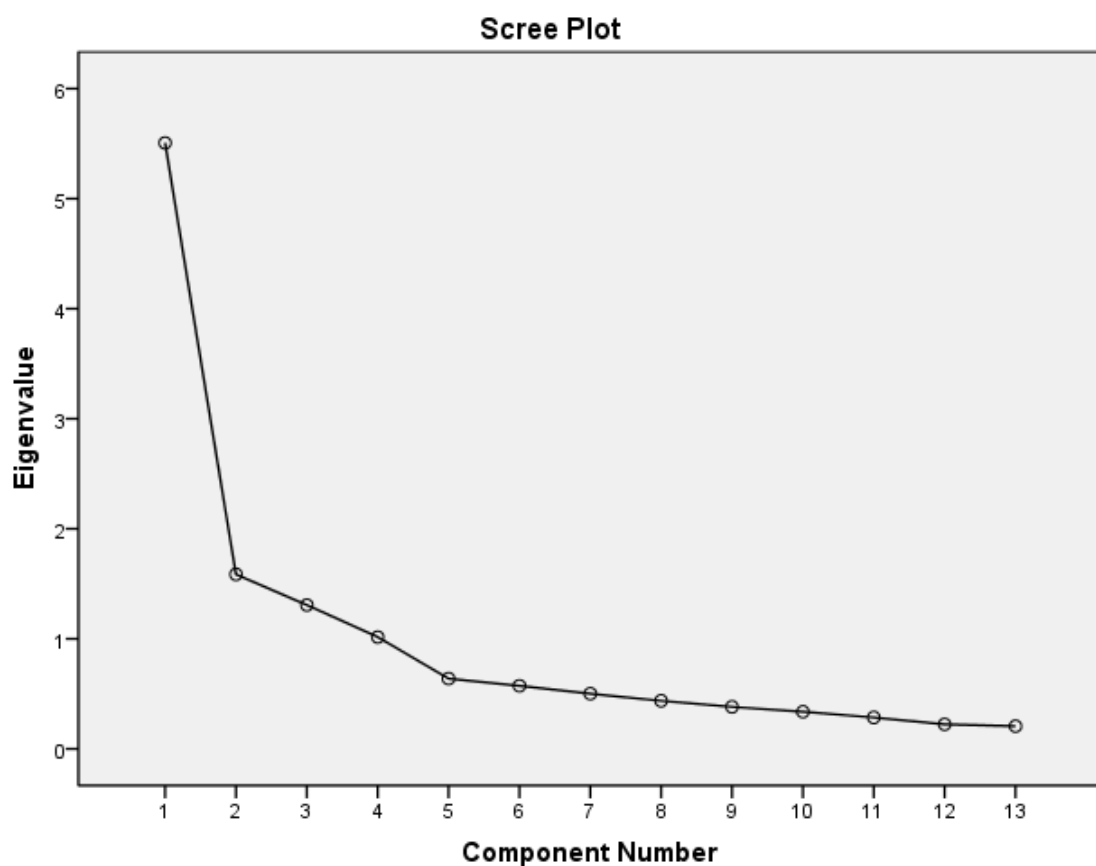


Figure D-1. Scree plot of the first principal components analysis using direct oblimin rotation.

Table D-1. Factor Loadings for the First Principal Components Analysis Using Direct Oblimin Rotation

Item	Personal Singing	Family Singing	Public Singing	Music Listening
In my childhood, I sang by myself	-.82	.02	.06	.08
How often do you currently sing by yourself?	-.73	.10	.07	.10
In my childhood, an adult family member/s sang with me	.05	.90	.00	.05
In my childhood, an adult family member/s sang to me	-.07	.87	-.06	.02
In my childhood, an adult family member/s taught me songs	.04	.86	-.01	.06
How often do you currently sing with your family?	-.38	.52	.09	-.09
In my childhood, I sang with my siblings/friends	-.36	.45	.14	.13
How often do you currently sing in a choir/group?	.08	-.08	.95	-.03
How often do you currently sing as a solo performer?	-.04	-.08	.86	.01
How often do you currently sing with your friends?	-.16	.22	.61	.03
In my childhood, music was present around my home	-.01	.12	-.01	.86
In my childhood, I listened to music	-.33	-.21	-.04	.82
In my childhood, my family attended live musical events together	.25	.30	.17	.65

Note. Factor loadings > .40 are in bold.

Table D-2. Factor Loadings for the Second Principal Components Analysis Using Direct Oblimin Rotation

Item	Personal Singing	Family Singing	Public Singing	Music Listening	Instrumental Expertise
In my childhood, I sang by myself	-.67	.19	.11	.12	-.11
How often do you currently sing by yourself?	-.54	.29	.16	.22	.05
In my childhood, an adult family member/s sang with me	.08	.91	-.08	.04	-.09
In my childhood, an adult family member/s sang to me	-.03	.90	-.05	.02	-.04
In my childhood, an adult family member/s taught me songs	.05	.87	.00	.04	.08
How often do you currently sing with your family?	-.30	.61	.08	-.09	-.09
In my childhood, I sang with my siblings/friends	-.26	.48	.16	.17	-.11
How often do you currently sing in a choir/group?	.07	-.13	.92	.02	-.04
How often do you currently sing as a solo performer?	.00	-.08	.85	.00	-.09
How often do you currently sing with your friends?	-.16	.29	.61	-.01	.01
In my childhood, music was present around my home	-.09	.07	.07	.88	.09
In my childhood, I listened to music	-.48	-.16	-.09	.68	-.24
In my childhood, my family attended live musical events together	.15	.29	.15	.65	.09
Years since last regular practice	.20	.01	.00	.20	.77
How good are you on this instrument/voice?	.10	.17	.19	.03	-.76
What was your level of motivation to learn this instrument/voice?	.02	.02	.26	.09	-.73
How many days do you practise now every week?	-.12	-.03	.05	-.02	-.72
How many years of training have you had on this instrument/voice?	.40	.21	-.01	.17	-.62
Weekly peak practice duration	.17	-.01	-.08	.34	-.44

Note. Factor loadings > .40 are in bold.

Appendix E

SEM FIT STATISTICS

Table E-1. Univariate Model-Fitting Results Testing Equality of Covariances for Continuous Task Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	1	27	393.30	181	31.30	-	-	-	-
	2	26	393.31	182	29.31	0.01	1	0.92	1
	3	25	393.39	183	27.39	0.08	1	0.78	2
	4	24	393.40	184	25.40	0.00	1	0.95	3
SingTheNote PD	1	27	643.81	187	269.81	-	-	-	-
	2	26	643.87	188	267.87	0.06	1	0.80	1
	3	25	644.38	189	266.38	0.51	1	0.48	2
	4	24	644.63	190	264.63	0.25	1	0.61	3
HappyBirthday PD	1	27	395.90	188	19.90	-	-	-	-
	2	26	396.70	189	18.70	0.79	1	0.37	1
	3	25	396.82	190	16.82	0.12	1	0.73	2
	4	24	396.97	191	14.97	0.16	1	0.69	3
HappyBirthday ID	1	27	276.76	188	-99.24	-	-	-	-
	2	26	276.81	189	-101.19	0.04	1	0.84	1
	3	25	277.16	190	-102.84	0.35	1	0.55	2
	4	24	277.25	191	-104.75	0.09	1	0.76	3
HappyBirthday KD	1	27	417.07	188	41.07	-	-	-	-
	2	26	419.64	189	41.64	2.58	1	0.11	1
	3	25	420.16	190	40.16	0.52	1	0.47	2
	4	24	420.28	191	38.28	0.12	1	0.73	3
SingTheTune PD	1	27	481.96	182	117.96	-	-	-	-
	2	26	482.01	183	116.01	0.05	1	0.83	1
	3	25	483.59	184	115.59	1.58	1	0.21	2
	4	24	483.59	185	113.59	0.00	1	0.96	3
SingTheTune ID	1	27	452.99	182	88.99	-	-	-	-
	2	26	453.03	183	87.03	0.04	1	0.84	1
	3	25	453.05	184	85.05	0.02	1	0.88	2
	4	24	453.05	185	83.05	0.01	1	0.94	3
MatchTheNote PD	1	27	565.85	184	197.85	-	-	-	-
	2	26	565.99	185	195.99	0.14	1	0.71	1
	3	25	566.00	186	194.00	0.01	1	0.91	2
	4	24	566.01	187	192.01	0.01	1	0.94	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Saturated univariate model (means, variances and covariances of twins are allowed to freely vary);

Model 2: Univariate model constraining covariances of MZM and MZF to be equal;

Model 3: Univariate model constraining covariances between MZM and MZF, as well as between DZM and DZF to be equal;

Model 4: Univariate model constraining covariances between MZM and MZF, as well as between DZM, DZF and DZO to be equal

Table E-2. Univariate Model-Fitting Results Testing Equality of Means and Variances for Continuous Task Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	1	12	411.48	196	19.48	-	-	-	-
	2	10	412.09	198	16.09	0.61	2	0.74	1
	3	8	412.79	200	12.79	0.70	2	0.70	2
	4	6	414.61	202	10.61	1.83	2	0.40	3
SingTheNote PD	1	12	654.36	202	250.36	-	-	-	-
	2	10	656.54	204	248.54	2.18	2	0.34	1
	3	8	656.95	206	244.95	0.41	2	0.81	2
	4	6	657.43	208	241.43	0.47	2	0.79	3
HappyBirthday PD	1	12	413.33	203	7.33	-	-	-	-
	2	10	414.47	205	4.47	1.14	2	0.57	1
	3	8	415.02	207	1.02	0.55	2	0.76	2
	4	6	417.17	209	-0.83	2.15	2	0.34	3
HappyBirthday ID	1	12	296.26	203	-109.74	-	-	-	-
	2	10	297.18	205	-112.82	0.93	2	0.63	1
	3	8	300.22	207	-113.78	3.04	2	0.22	2
	4	6	302.98	209	-115.02	2.76	2	0.25	3
HappyBirthday KD	1	12	430.23	203	24.22	-	-	-	-
	2	10	430.28	205	20.28	0.06	2	0.97	1
	3	8	433.47	207	19.47	3.19	2	0.20	2
	4	6	436.63	209	18.63	3.16	2	0.21	3
SingTheTune PD	1	12	493.48	197	99.48	-	-	-	-
	2	10	494.21	199	96.21	0.73	2	0.70	1
	3	8	495.66	201	93.66	1.45	2	0.48	2
	4	6	497.82	203	91.82	2.16	2	0.34	3
SingTheTune ID	1	12	465.41	197	71.41	-	-	-	-
	2	10	466.31	199	68.31	0.90	2	0.64	1
	3	8	468.64	201	66.64	2.33	2	0.31	2
	4	6	470.15	203	64.15	1.51	2	0.47	3
MatchTheNote PD	1	12	572.93	199	174.93	-	-	-	-
	2	10	573.52	201	171.52	0.59	2	0.74	1
	3	8	573.85	203	167.85	0.33	2	0.85	2
	4	6	573.92	205	163.92	0.07	2	0.97	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Saturated univariate model (means and variances of twins are allowed to freely vary);

Model 2: Univariate model constraining means within twin pairs to be equal;

Model 3: Univariate model constraining means and variances within twin pairs to be equal;

Model 4: Univariate model constraining means and variances across zygosity to be equal.

Table E-3. Univariate Model-Fitting Results Testing Equality of Covariances for Categorical Singing Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB (Category)	1	27	372.43	181	10.43	-	-	-	-
	2	26	372.44	182	8.44	0.01	1	0.94	1
	3	25	372.62	183	6.62	0.18	1	0.67	2
	4	24	372.62	184	4.62	0.00	1	0.99	3
SingTheNote PD (Category)	1	27	302.40	187	-71.60	-	-	-	-
	2	26	302.49	188	-73.51	0.09	1	0.77	1
	3	25	303.34	189	-74.66	0.86	1	0.36	2
	4	24	305.39	190	-74.61	2.04	1	0.15	3
HappyBirthday PD (Category)	1	27	347.01	188	-28.99	-	-	-	-
	2	26	351.49	189	-26.51	4.48	1	0.03*	1
	3	25	352.54	190	-27.46	1.05	1	0.31	2
	4	24	352.81	191	-29.19	0.27	1	0.60	3
HappyBirthday ID (Category)	1	27	325.40	188	-50.60	-	-	-	-
	2	26	327.13	189	-50.87	1.73	1	0.19	1
	3	25	327.21	190	-52.79	0.07	1	0.79	2
	4	24	328.50	191	-53.50	1.29	1	0.26	3
HappyBirthday KD (Category)	1	27	352.86	188	-23.14	-	-	-	-
	2	26	357.50	189	-20.50	4.64	1	0.03*	1
	3	25	357.86	190	-22.14	0.36	1	0.55	2
	4	24	357.87	191	-24.13	0.01	1	0.92	3
SingTheTune PD (Category)	1	27	399.44	182	35.44	-	-	-	-
	2	26	400.44	183	34.44	1.00	1	0.32	1
	3	25	400.45	184	32.45	0.02	1	0.90	2
	4	24	400.92	185	30.92	0.47	1	0.49	3
SingTheTune ID (Category)	1	27	417.20	182	53.20	-	-	-	-
	2	26	418.55	183	52.55	1.34	1	0.25	1
	3	25	419.69	184	51.69	1.14	1	0.29	2
	4	24	419.71	185	49.71	0.03	1	0.87	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Saturated univariate ordinal model (threshold levels and covariances of twins are allowed to freely vary);

Model 2: Univariate ordinal model constraining covariances of MZM and MZF to be equal;

Model 3: Univariate ordinal model constraining covariances between MZM and MZF, as well as between DZM and DZF to be equal;

Model 4: Univariate ordinal model constraining covariances between MZM and MZF, as well as between DZM, DZF and DZO to be equal.

* $p < .05$

Table E-4. Univariate Model-Fitting Results Testing Equality of Means and Variances for Categorical Singing Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB (Category)	1	12	388.99	196	-3.01	-	-	-	-
	2	8	390.69	200	-9.31	1.70	4	0.79	1
	3	6	392.07	202	-11.93	1.38	2	0.50	2
SingTheNote PD (Category)	1	12	314.69	202	-89.31	-	-	-	-
	2	8	322.64	206	-89.36	7.95	4	0.09	1
	3	6	323.06	208	-92.94	0.42	2	0.81	2
HappyBirthday PD (Category)	1	12	366.89	203	-39.11	-	-	-	-
	2	8	370.09	207	-43.91	3.21	4	0.52	1
	3	6	373.21	209	-44.79	3.11	2	0.21	2
HappyBirthday ID (Category)	1	12	344.81	203	-61.19	-	-	-	-
	2	8	349.11	207	-64.89	4.30	4	0.37	1
	3	6	351.31	209	-66.69	2.20	2	0.33	2
HappyBirthday KD (Category)	1	12	372.07	203	-33.93	-	-	-	-
	2	8	374.32	207	-39.68	2.24	4	0.69	1
	3	6	376.53	209	-41.47	2.22	2	0.33	2
SingTheTune PD (Category)	1	12	408.99	197	14.99	-	-	-	-
	2	8	412.29	201	10.29	3.30	4	0.51	1
	3	6	414.02	203	8.02	1.73	2	0.42	2
SingTheTune ID (Category)	1	12	431.76	197	37.76	-	-	-	-
	2	8	433.93	201	31.93	2.18	4	0.70	1
	3	6	435.00	203	29.00	1.07	2	0.59	2

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Saturated univariate ordinal model (threshold levels of twins are allowed to freely vary);

Model 2: Univariate ordinal model constraining threshold levels within twin pairs to be equal;

Model 3: Univariate ordinal model constraining threshold levels across zygosity to be equal.

**p* < .05

Table E-5. Univariate Model-Fitting Results Testing Equality of Covariances for Self-Rated Interests and Abilities in Singing and Music

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
Singing Ability	1	67	627.82	140	347.82	-	-	-	-
	2	66	628.97	141	346.97	1.16	1	0.28	1
	3	65	629.85	142	345.85	0.88	1	0.35	2
	4	64	631.29	143	345.29	1.44	1	0.23	3
Music Ability	1	67	638.57	140	358.57	-	-	-	-
	2	66	638.64	141	356.64	0.07	1	0.79	1
	3	65	639.98	142	355.98	1.34	1	0.25	2
	4	64	641.20	143	355.20	1.22	1	0.27	3
Singing Interest	1	67	665.45	140	385.45	-	-	-	-
	2	66	665.76	141	383.76	0.31	1	0.58	1
	3	65	666.63	142	382.63	0.87	1	0.35	2
	4	64	667.34	143	381.34	0.71	1	0.40	3
Music Interest	1	67	544.67	140	264.67	-	-	-	-
	2	66	546.28	141	264.28	1.61	1	0.20	1
	3	65	546.32	142	262.32	0.05	1	0.83	2
	4	64	548.54	143	262.54	2.22	1	0.14	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test. Model 1: Saturated univariate ordinal model (threshold levels and covariances of twins are allowed to freely vary); Model 2: Univariate ordinal model constraining covariances of MZM and MZF to be equal; Model 3: Univariate ordinal model constraining covariances between MZM and MZF, as well as between DZM and DZF to be equal; Model 4: Univariate ordinal model constraining covariances between MZM and MZF, as well as between DZM, DZF and DZO to be equal.

Table E-6. Univariate Model-Fitting Results Testing Equality of Means and Variances for Self-Rated Interests and Abilities in Singing and Music

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
Singing Ability	1	28	657.84	179	299.84	-	-	-	-
	2	16	675.47	191	293.47	17.63	12	0.13	1
	3	10	681.81	197	287.81	6.34	6	0.39	2
Music Ability	1	28	676.41	179	318.41	-	-	-	-
	2	16	692.38	191	310.38	15.97	12	0.19	1
	3	10	699.80	197	305.80	7.42	6	0.28	2
Singing Interest	1	28	709.23	179	351.23	-	-	-	-
	2	16	715.44	191	333.44	6.21	12	0.91	1
	3	10	722.50	197	328.50	7.07	6	0.31	2
Music Interest	1	28	579.66	179	221.66	-	-	-	-
	2	16	599.11	191	217.11	19.45	12	0.08	1
	3	10	605.86	197	211.86	6.75	6	0.34	2

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test. Model 1: Saturated univariate ordinal model (threshold levels of twins are allowed to freely vary);

Model 2: Univariate ordinal model constraining threshold levels within twin pairs to be equal;

Model 3: Univariate ordinal model constraining threshold levels across zygosity to be equal.

Table E-7. Univariate Model-Fitting Results Testing Equality of Covariances for Singing and Music Background Components

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
Personal Singing	1	27	476.82	180	116.82	-	-	-	-
	2	26	477.59	181	115.59	0.76	1	0.38	1
	3	25	477.76	182	113.76	0.17	1	0.68	2
	4	24	477.92	183	111.92	0.16	1	0.69	3
Family Singing	1	27	414.36	180	54.36	-	-	-	-
	2	26	415.88	181	53.88	1.53	1	0.22	1
	3	25	416.88	182	52.88	1.00	1	0.32	2
	4	24	416.98	183	50.98	0.10	1	0.75	3
Public Singing	1	27	128.16	180	-231.84	-	-	-	-
	2	26	128.17	181	-233.83	0.01	1	0.91	1
	3	25	794.95	182	430.95	0.47	1	0.49	2
	4	24	797.01	183	431.01	2.06	1	0.15	3
Music Listening	1	27	423.56	180	63.56	-	-	-	-
	2	26	427.01	181	65.01	3.45	1	0.06	1
	3	25	428.00	182	64.00	0.98	1	0.32	2
	4	24	428.57	183	62.57	0.58	1	0.45	3
Instrumental Expertise	1	27	316.35	142	32.35	-	-	-	-
	2	26	316.35	143	30.35	0.00	1	0.95	1
	3	25	317.00	144	29.00	0.64	1	0.42	2
	4	24	318.57	145	28.57	1.57	1	0.21	3
Years of Music Training	1	27	77.03	172	-266.97	-	-	-	-
	2	26	78.26	173	-267.74	1.23	1	0.27	1
	3	25	79.67	174	-268.33	1.41	1	0.24	2
	4	24	997.08	175	647.08	0.98	1	0.32	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test. Model 1: Saturated univariate model (means, variances and covariances of twins are allowed to freely vary); Model 2: Univariate model constraining covariances of MZM and MZF to be equal; Model 3: Univariate model constraining covariances between MZM and MZF, as well as between DZM and DZF to be equal; Model 4: Univariate model constraining covariances between MZM and MZF, as well as between DZM, DZF and DZO to be equal.

Table E-8. Univariate Model-Fitting Results Testing Equality of Means and Variances for Singing and Music Background Components

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
Personal Singing	1	12	496.93	195	106.93	-	-	-	-
	2	10	499.97	197	105.97	3.04	2	0.22	1
	3	8	500.35	199	102.35	0.38	2	0.83	2
	4	6	504.76	201	102.76	4.42	2	0.11	3
Family Singing	1	12	425.85	195	35.85	-	-	-	-
	2	10	427.07	197	33.07	1.22	2	0.54	1
	3	8	427.13	199	29.13	0.06	2	0.97	2
	4	6	428.74	201	26.74	1.61	2	0.45	3
Public Singing	1	12	156.61	195	-233.39	-	-	-	-
	2	10	161.48	197	-232.52	4.87	2	0.09	1
	3	8	161.92	199	-236.08	0.44	2	0.80	2
	4	6	167.84	201	-234.16	5.92	2	0.05	3
Music Listening	1	12	451.80	195	61.80	-	-	-	-
	2	10	455.43	197	61.43	3.63	2	0.16	1
	3	8	455.52	199	57.52	0.09	2	0.95	2
	4	6	455.97	201	53.97	0.45	2	0.80	3
Instrumental Expertise	1	12	329.43	157	15.43	-	-	-	-
	2	10	334.72	159	16.72	5.29	2	0.07	1
	3	8	338.62	161	16.62	3.90	2	0.14	2
	4	6	341.78	163	15.78	3.17	2	0.21	3
Years of Music Training	1	12	97.17	187	-276.83	-	-	-	-
	2	10	101.87	189	-276.13	4.70	2	0.10	1
	3	8	103.74	191	-278.26	1.87	2	0.39	2
	4	6	105.78	193	-280.22	2.04	2	0.36	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Saturated univariate model (means and variances of twins are allowed to freely vary);

Model 2: Univariate model constraining means within twin pairs to be equal;

Model 3: Univariate model constraining means and variances within twin pairs to be equal;

Model 4: Univariate model constraining means and variances across zygosity to be equal.

Table E-9. Univariate Model-Fitting Results for Continuous Task Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	ACE	7	414.61	202	10.61	-	-	-	-
	AE	6	414.78	203	8.78	0.17	1	0.68	ACE
	CE	6	427.51	203	21.51	12.90	1	0.00**	ACE
	E	6	492.30	204	84.30	77.69	2	0.00**	ACE
SingTheNote PD	ACE	7	660.29	208	244.29	-	-	-	-
	AE	6	660.29	209	242.29	0.00	1	1.00	ACE
	CE	6	674.85	209	256.85	14.57	1	0.00**	ACE
	E	6	706.61	210	286.61	46.33	2	0.00**	ACE
HappyBirthday PD	ACE	7	417.17	209	-0.83	-	-	-	-
	AE	6	418.35	210	-1.65	1.18	1	0.28	ACE
	CE	6	421.55	210	1.55	4.38	1	0.04*	ACE
	E	6	478.89	211	56.89	61.71	2	0.00**	ACE
HappyBirthday ID	ACE	7	303.10	209	-114.90	-	-	-	-
	AE	6	303.10	210	-116.90	0.00	1	1.00	ACE
	CE	6	312.15	210	-107.85	9.05	1	0.00**	ACE
	E	6	349.78	211	-72.22	46.68	2	0.00**	ACE
HappyBirthday KD	ACE	7	436.63	209	18.63	-	-	-	-
	AE	6	438.30	210	18.30	1.68	1	0.20	ACE
	CE	6	437.74	210	17.74	1.12	1	0.29	ACE
	E	6	482.18	211	60.18	45.56	2	0.00**	ACE
SingTheTune PD	ACE	7	497.82	203	91.82	-	-	-	-
	AE	6	497.82	204	89.82	0.00	1	0.98	ACE
	CE	6	505.61	204	97.61	7.79	1	0.01**	ACE
	E	6	551.72	205	141.72	53.90	2	0.00**	ACE
SingTheTune ID	ACE	7	470.15	203	64.15	-	-	-	-
	AE	6	471.72	204	63.72	1.57	1	0.21	ACE
	CE	6	471.42	204	63.42	1.27	1	0.26	ACE
	E	6	514.59	205	104.59	44.44	2	0.00**	ACE
MatchTheNote PD	ACE	7	578.55	205	168.55	-	-	-	-
	AE	6	578.55	206	166.55	0.00	1	1.00	ACE
	CE	6	589.78	206	177.78	11.23	1	0.00**	ACE
	E	6	605.81	207	191.81	27.26	2	0.00**	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

p* < .05; *p* < .01.

Table E-10. Univariate Model-Fitting Results for Categorical Singing Task Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	ACE	7	392.07	202	-11.93	-	-	-	-
	AE	6	392.12	203	-13.88	0.05	1	0.82	ACE
	CE	6	396.41	203	-9.59	4.34	1	0.04*	ACE
	E	6	396.41	203	-9.59	4.34	1	0.04*	ACE
SingTheNote PD	ACE	7	323.75	208	-92.25	-	-	-	-
	AE	6	323.75	209	-94.25	0.00	1	1.00	ACE
	CE	6	329.75	209	-88.25	6.00	1	0.01*	ACE
	E	6	329.75	209	-88.25	6.00	1	0.01*	ACE
HappyBirthday PD	ACE	7	373.21	209	-44.79	-	-	-	-
	AE	6	373.53	210	-46.47	0.32	1	0.57	ACE
	CE	6	376.32	210	-43.68	3.11	1	0.08	ACE
	E	6	376.32	210	-43.68	3.11	1	0.08	ACE
HappyBirthday ID	ACE	7	353.42	209	-64.58	-	-	-	-
	AE	6	353.42	210	-66.58	0.00	1	1.00	ACE
	CE	6	361.08	210	-58.92	7.66	1	0.01*	ACE
	E	6	361.08	210	-58.92	7.66	1	0.01*	ACE
HappyBirthday KD	ACE	7	376.53	209	-41.47	-	-	-	-
	AE	6	376.56	210	-43.44	0.03	1	0.87	ACE
	CE	6	380.70	210	-39.30	4.17	1	0.04*	ACE
	E	6	380.70	210	-39.30	4.17	1	0.04*	ACE
SingTheTune PD	ACE	7	414.02	203	8.02	-	-	-	-
	AE	6	414.04	204	6.04	0.03	1	0.87	ACE
	CE	6	416.62	204	8.62	2.61	1	0.11	ACE
	E	6	416.62	204	8.62	2.61	1	0.11	ACE
SingTheTune ID	ACE	7	435.00	203	29.00	-	-	-	-
	AE	6	435.02	204	27.02	0.02	1	0.89	ACE
	CE	6	437.03	204	29.03	2.03	1	0.15	ACE
	E	6	437.03	204	29.03	2.03	1	0.15	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$.

Table E-11. Univariate Model-Fitting Results for Self-rated Abilities and Interests

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
Singing Ability	ACE	11	681.81	197	287.81	-	-	-	-
	AE	10	681.99	198	285.99	0.17	1	0.68	ACE
	CE	10	694.36	198	298.36	12.55	1	0.00**	ACE
	E	10	694.36	198	298.36	12.55	1	0.00**	ACE
Music Ability	ACE	11	700.07	197	306.07	-	-	-	-
	AE	10	700.07	198	304.07	0.00	1	1.00	ACE
	CE	10	714.57	198	318.57	14.49	1	0.00**	ACE
	E	10	714.57	198	318.57	14.49	1	0.00**	ACE
Singing Interest	ACE	11	723.90	197	329.90	-	-	-	-
	AE	10	723.90	198	327.90	0.00	1	1.00	ACE
	CE	10	734.48	198	338.48	10.58	1	0.00**	ACE
	E	10	734.48	198	338.48	10.58	1	0.00**	ACE
Music Interest	ACE	11	606.84	197	212.84	-	-	-	-
	AE	10	606.84	198	210.84	0.00	1	1.00	ACE
	CE	10	612.65	198	216.65	5.81	1	0.02*	ACE
	E	10	612.65	198	216.65	5.81	1	0.02*	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$; ** $p < .01$.

Table E-12. Univariate Model-Fitting Results for Singing and Music Background Components

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
Personal Singing	ACE	6	504.76	201	102.76	-	-	-	-
	AE	5	505.47	202	101.47	0.71	1	0.40	ACE
	CE	5	506.11	202	102.11	1.35	1	0.25	ACE
	E	4	532.83	203	126.83	28.07	2	0.00**	ACE
Family Singing	ACE	6	428.89	201	26.89	-	-	-	-
	AE	5	436.47	202	32.47	7.58	1	0.01*	ACE
	CE	5	428.89	202	24.89	0.00	1	1.00	ACE
	E	4	478.07	203	72.07	49.19	2	0.00**	ACE
Public Singing	ACE	6	167.84	201	-234.16	-	-	-	-
	AE	5	167.84	202	-236.16	0.01	1	0.94	ACE
	CE	5	173.24	202	-230.76	5.41	1	0.02*	ACE
	E	4	213.57	203	-192.43	45.73	2	0.00**	ACE
Music Listening	ACE	6	455.97	201	53.97	-	-	-	-
	AE	5	459.06	202	55.06	3.09	1	0.08	ACE
	CE	5	456.29	202	52.29	0.32	1	0.57	ACE
	E	4	499.57	203	93.57	43.60	2	0.00**	ACE
Instrumental Expertise	ACE	6	342.11	163	16.11	-	-	-	-
	AE	5	342.11	164	14.11	0.00	1	1.00	ACE
	CE	5	349.28	164	21.28	7.17	1	0.01*	ACE
	E	4	376.71	165	46.71	34.59	2	0.00**	ACE
Years of Music Training	ACE	6	1022.21	193	636.21	-	-	-	-
	AE	5	1024.39	194	636.39	2.17	1	0.14	ACE
	CE	5	1031.51	194	643.51	9.30	1	0.00**	ACE
	E	4	1109.75	195	719.75	87.54	2	0.00**	ACE

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

* $p < .05$; ** $p < .01$.

Table E-13. Results of Univariate Genetic Modelling Showing Genetic (*A*), Common Environmental (*C*), and Unique Environmental (*E*) Influences on Continuous Measures (Adjusted for Age, Sex and Years of Music Training)

Task Measure	<i>A</i>	<i>C</i>	<i>E</i>
SINGCOMB	.58 [.11, .82]	.16 [.00, .57]	.26 [.17, .40]
SingTheNote PD	.64 [.36, .77]	.00 [.00, .23]	.36 [.23, .54]
HappyBirthday PD	.38 [.00, .78]	.31 [.00, .68]	.32 [.21, .48]
HappyBirthday ID	.65 [.14, .77]	.00 [.00, .44]	.35 [.23, .51]
HappyBirthday KD	.27 [.00, .73]	.36 [.00, .68]	.38 [.25, .56]
SingTheTune PD	.52 [.00, .75]	.12 [.00, .59]	.36 [.25, .52]
SingTheTune ID	.07 [.00, .65]	.49 [.00, .67]	.45 [.30, .62]
MatchTheNote PD	.52 [.28, .69]	.00 [.00, .22]	.48 [.31, .56]

Note. ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score.

Values in brackets are the 95% confidence intervals.

Significant parameter estimates (whose interval values do not pass through zero) are shown in bold.

Table E-14. Bivariate Model-Fitting Results Testing Equality of Means and Variances Within Twin Pairs and Across Zygosity for Instrumental Expertise and the Objective Task Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	1	30	714.50	347	20.50	-	-	-	-
	2	30	719.74	351	17.74	5.24	4	0.26	1
	3	30	725.53	355	15.53	5.79	4	0.22	2
	4	30	732.07	359	14.07	6.54	4	0.16	3
SingTheNote PD	1	30	976.16	353	270.16	-	-	-	-
	2	30	984.18	357	270.18	8.02	4	0.09	1
	3	30	989.18	361	267.18	5.00	4	0.29	2
	4	30	992.58	365	262.58	3.40	4	0.49	3
HappyBirthday PD	1	30	718.30	354	10.30	-	-	-	-
	2	30	724.93	358	8.93	6.63	4	0.16	1
	3	30	729.67	362	5.67	4.73	4	0.32	2
	4	30	738.96	366	6.96	9.30	4	0.05	3
HappyBirthday ID	1	30	604.94	354	-103.06	-	-	-	-
	2	30	611.79	358	-104.21	6.85	4	0.14	1
	3	30	618.99	362	-105.01	7.20	4	0.13	2
	4	30	628.99	366	-103.01	10.0	4	0.04*	3
HappyBirthday KD	1	30	738.31	354	30.31	-	-	-	-
	2	30	745.68	358	29.68	7.37	4	0.12	1
	3	30	752.29	362	28.29	6.61	4	0.16	2
	4	30	761.08	366	29.08	8.78	4	0.07	3
SingTheTune PD	1	30	792.80	348	96.80	-	-	-	-
	2	30	798.54	352	94.54	5.74	4	0.22	1
	3	30	805.49	356	93.49	6.96	4	0.14	2
	4	30	811.54	360	91.54	6.04	4	0.20	3
SingTheTune ID	1	30	762.14	348	66.14	-	-	-	-
	2	30	768.26	352	64.26	6.12	4	0.19	1
	3	30	775.94	356	63.94	7.68	4	0.10	2
	4	30	781.84	360	61.84	5.9	4	0.21	3
MatchTheNote PD	1	30	913.12	350	213.12	-	-	-	-
	2	30	920.69	354	212.69	7.57	4	0.11	1
	3	30	926.44	358	210.44	5.75	4	0.22	2
	4	30	931.89	362	207.89	5.45	4	0.24	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Bivariate saturated model (means and variances of twins are allowed to freely vary);

Model 2: Bivariate model constraining means within twin pairs to be equal;

Model 3: Bivariate model constraining means and variances within twin pairs to be equal;

Model 4: Bivariate model constraining means and variances across zygosity to be equal

* $p < .05$

Table E-15. Bivariate Model-Fitting Results Testing Equality of Means and Variances Within Twin Pairs and Across Zygositys for Years of Music Training and the Objective Task Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	1	30	1391.68	377	637.68	-	-	-	-
	2	30	1397.04	381	635.04	5.36	4	0.25	1
	3	30	1401.05	385	631.05	4.01	4	0.40	2
	4	30	1404.36	389	626.36	3.31	4	0.51	3
SingTheNote PD	1	30	1644.35	383	878.35	-	-	-	-
	2	30	1651.13	387	877.13	6.78	4	0.15	1
	3	30	1654.87	391	872.87	3.74	4	0.44	2
	4	30	1657.08	395	867.08	2.21	4	0.70	3
HappyBirthday PD	1	30	1397.01	384	629.01	-	-	-	-
	2	30	1402.83	388	626.83	5.82	4	0.21	1
	3	30	1406.16	392	622.16	3.34	4	0.50	2
	4	30	1410.58	396	618.58	4.41	4	0.35	3
HappyBirthday ID	1	30	1284.13	384	516.13	-	-	-	-
	2	30	1289.62	388	513.62	5.49	4	0.24	1
	3	30	1295.99	392	511.99	6.37	4	0.17	2
	4	30	1300.36	396	508.36	4.37	4	0.36	3
HappyBirthday KD	1	30	1419.45	384	651.45	-	-	-	-
	2	30	1424.53	388	648.53	5.07	4	0.28	1
	3	30	1430.44	392	646.44	5.92	4	0.21	2
	4	30	1435.03	396	643.03	4.59	4	0.33	3
SingTheTune PD	1	30	1474.35	378	718.35	-	-	-	-
	2	30	1480.57	382	716.57	6.21	4	0.18	1
	3	30	1485.50	386	713.50	4.94	4	0.29	2
	4	30	1489.14	390	709.14	3.63	4	0.46	3
SingTheTune ID	1	30	1449.19	378	693.19	-	-	-	-
	2	30	1455.92	382	691.92	6.73	4	0.15	1
	3	30	1461.31	386	689.31	5.39	4	0.25	2
	4	30	1464.52	390	684.52	3.21	4	0.52	3
MatchTheNote PD	1	30	1568.25	380	808.25	-	-	-	-
	2	30	1575.04	384	807.04	6.79	4	0.15	1
	3	30	1578.84	388	802.84	3.80	4	0.43	2
	4	30	1583.62	392	799.62	4.77	4	0.31	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Bivariate saturated model (means and variances of twins are allowed to freely vary);

Model 2: Bivariate model constraining means within twin pairs to be equal;

Model 3: Bivariate model constraining means and variances within twin pairs to be equal;

Model 4: Bivariate model constraining means and variances across zygositys to be equal

Table E-16. Bivariate Model-Fitting Results Testing Equality of Means and Variances Within Twin Pairs and Across Zygosity for Personal Singing and the Singing Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	1	30	886.14	385	116.14	-	-	-	-
	2	30	890.83	389	112.83	4.69	4	0.32	1
	3	30	892.06	393	106.06	1.23	4	0.87	2
	4	30	898.77	397	104.77	6.71	4	0.15	3
SingTheNote PD	1	30	1150.77	391	368.77	-	-	-	-
	2	30	1158.01	395	368.01	7.24	4	0.12	1
	3	30	1158.72	399	360.72	0.71	4	0.95	2
	4	30	1164.14	403	358.14	5.42	4	0.25	3
HappyBirthday PD	1	30	892.74	392	108.74	-	-	-	-
	2	30	897.86	396	105.86	5.12	4	0.28	1
	3	30	898.89	400	98.89	1.03	4	0.91	2
	4	30	903.85	404	95.85	4.96	4	0.29	3
HappyBirthday ID	1	30	775.85	392	-8.15	-	-	-	-
	2	30	781.65	396	-10.35	5.80	4	0.21	1
	3	30	784.45	400	-15.55	2.80	4	0.59	2
	4	30	790.93	404	-17.07	6.48	4	0.17	3
HappyBirthday KD	1	30	913.54	392	129.54	-	-	-	-
	2	30	917.99	396	125.99	4.44	4	0.35	1
	3	30	921.31	400	121.31	3.33	4	0.50	2
	4	30	927.21	404	119.21	5.90	4	0.21	3
SingTheTune PD	1	30	961.40	386	189.40	-	-	-	-
	2	30	966.80	390	186.80	5.40	4	0.25	1
	3	30	968.77	394	180.77	1.96	4	0.74	2
	4	30	976.65	398	180.65	7.89	4	0.10	3
SingTheTune ID	1	30	936.65	386	164.65	-	-	-	-
	2	30	942.34	390	162.34	5.69	4	0.22	1
	3	30	945.20	394	157.20	2.86	4	0.58	2
	4	30	952.00	398	156.00	6.80	4	0.15	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Bivariate saturated model (means and variances of twins are allowed to freely vary);

Model 2: Bivariate model constraining means within twin pairs to be equal;

Model 3: Bivariate model constraining means and variances within twin pairs to be equal;

Model 4: Bivariate model constraining means and variances across zygosity to be equal

Table E-17. Bivariate Model-Fitting Results Testing Equality of Means and Variances Within Twin Pairs and Across Zygosity for Family Singing and the Singing Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	1	30	804.29	385	34.29	-	-	-	-
	2	30	809.13	389	31.13	4.85	4	0.30	1
	3	30	810.04	393	24.04	0.90	4	0.92	2
	4	30	813.53	397	19.53	3.49	4	0.48	3
SingTheNote PD	1	30	1073.30	391	291.30	-	-	-	-
	2	30	1079.84	395	289.84	6.54	4	0.16	1
	3	30	1080.12	399	282.12	0.28	4	0.99	2
	4	30	1082.51	403	276.51	2.39	4	0.66	3
HappyBirthday PD	1	30	817.46	392	33.46	-	-	-	-
	2	30	823.52	396	31.52	6.06	4	0.19	1
	3	30	824.05	400	24.05	0.53	4	0.97	2
	4	30	827.40	404	19.40	3.35	4	0.50	3
HappyBirthday ID	1	30	700.03	392	-83.97	-	-	-	-
	2	30	705.21	396	-86.79	5.18	4	0.27	1
	3	30	707.59	400	-92.41	2.38	4	0.67	2
	4	30	711.81	404	-96.19	4.22	4	0.38	3
HappyBirthday KD	1	30	833.07	392	49.07	-	-	-	-
	2	30	836.80	396	44.80	3.72	4	0.44	1
	3	30	839.40	400	39.40	2.61	4	0.63	2
	4	30	843.69	404	35.69	4.29	4	0.37	3
SingTheTune PD	1	30	886.39	386	114.39	-	-	-	-
	2	30	890.54	390	110.54	4.15	4	0.39	1
	3	30	892.15	394	104.15	1.61	4	0.81	2
	4	30	896.06	398	100.06	3.92	4	0.42	3
SingTheTune ID	1	30	853.72	386	81.72	-	-	-	-
	2	30	857.73	390	77.73	4.01	4	0.40	1
	3	30	860.13	394	72.13	2.40	4	0.66	2
	4	30	863.22	398	67.22	3.09	4	0.54	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Bivariate saturated model (means and variances of twins are allowed to freely vary);

Model 2: Bivariate model constraining means within twin pairs to be equal;

Model 3: Bivariate model constraining means and variances within twin pairs to be equal;

Model 4: Bivariate model constraining means and variances across zygosity to be equal

Table E-18. Bivariate Model-Fitting Results Testing Equality of Means and Variances Within Twin Pairs and Across Zygositys for Public Singing and the Singing Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	p-value	Comparison model
SINGCOMB	1	30	535.18	385	-234.82	-	-	-	-
	2	30	541.89	389	-236.11	6.71	4	0.15	1
	3	30	542.86	393	-243.14	0.97	4	0.91	2
	4	30	550.59	397	-243.41	7.74	4	0.10	3
SingTheNote PD	1	30	792.88	391	10.88	-	-	-	-
	2	30	803.11	395	13.11	10.23	4	0.04	1
	3	30	803.72	399	5.72	0.61	4	0.96	2
	4	30	810.41	403	4.41	6.69	4	0.15	3
HappyBirthday PD	1	30	540.29	392	-243.71	-	-	-	-
	2	30	547.78	396	-244.22	7.49	4	0.11	1
	3	30	548.66	400	-251.34	0.88	4	0.93	2
	4	30	556.8	404	-251.20	8.13	4	0.09	3
HappyBirthday ID	1	30	418.54	392	-365.46	-	-	-	-
	2	30	425.49	396	-366.51	6.94	4	0.14	1
	3	30	428.25	400	-371.75	2.77	4	0.60	2
	4	30	436.53	404	-371.47	8.28	4	0.08	3
HappyBirthday KD	1	30	562.1	392	-221.90	-	-	-	-
	2	30	568.29	396	-223.71	6.20	4	0.18	1
	3	30	571.68	400	-228.32	3.39	4	0.49	2
	4	30	581.07	404	-226.93	9.38	4	0.05	3
SingTheTune PD	1	30	616.8	386	-155.20	-	-	-	-
	2	30	623.01	390	-156.99	6.22	4	0.18	1
	3	30	624.75	394	-163.25	1.73	4	0.79	2
	4	30	632.94	398	-163.06	8.20	4	0.08	3
SingTheTune ID	1	30	588.68	386	-183.32	-	-	-	-
	2	30	594.83	390	-185.17	6.15	4	0.19	1
	3	30	597.28	394	-190.72	2.45	4	0.65	2
	4	30	604.43	398	-191.57	7.15	4	0.13	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Bivariate saturated model (means and variances of twins are allowed to freely vary);

Model 2: Bivariate model constraining means within twin pairs to be equal;

Model 3: Bivariate model constraining means and variances within twin pairs to be equal;

Model 4: Bivariate model constraining means and variances across zygositys to be equal

Table E-19. Bivariate Model-Fitting Results Testing Equality of Means and Variances Within Twin Pairs and Across Zygositys for Music Listening and the Singing Measures

Measure	Model	EP	-2LL	df	AIC	$\Delta\chi^2$	Δdf	<i>p</i> -value	Comparison model
SINGCOMB	1	30	824.59	385	54.59	-	-	-	-
	2	30	829.13	389	51.13	4.53	4	0.34	1
	3	30	829.99	393	43.99	0.86	4	0.93	2
	4	30	832.63	397	38.63	2.64	4	0.62	3
SingTheNote PD	1	30	1085.48	391	303.48	-	-	-	-
	2	30	1093.99	395	303.99	8.51	4	0.07	1
	3	30	1094.23	399	296.23	0.24	4	0.99	2
	4	30	1095.62	403	289.62	1.39	4	0.85	3
HappyBirthday PD	1	30	836.86	392	52.86	-	-	-	-
	2	30	841.69	396	49.69	4.83	4	0.31	1
	3	30	842.23	400	42.23	0.54	4	0.97	2
	4	30	846.13	404	38.13	3.90	4	0.42	3
HappyBirthday ID	1	30	721.85	392	-62.15	-	-	-	-
	2	30	727.46	396	-64.54	5.62	4	0.23	1
	3	30	729.78	400	-70.22	2.31	4	0.68	2
	4	30	733.97	404	-74.03	4.20	4	0.38	3
HappyBirthday KD	1	30	856.31	392	72.31	-	-	-	-
	2	30	860.15	396	68.15	3.85	4	0.43	1
	3	30	863.10	400	63.10	2.94	4	0.57	2
	4	30	867.37	404	59.37	4.27	4	0.37	3
SingTheTune PD	1	30	898.91	386	126.91	-	-	-	-
	2	30	903.43	390	123.43	4.52	4	0.34	1
	3	30	905.21	394	117.21	1.78	4	0.78	2
	4	30	907.94	398	111.94	2.73	4	0.60	3
SingTheTune ID	1	30	875.99	386	103.99	-	-	-	-
	2	30	880.77	390	100.77	4.78	4	0.31	1
	3	30	883.45	394	95.45	2.68	4	0.61	2
	4	30	885.72	398	89.72	2.27	4	0.67	3

Note. AIC: Akaike's Information Criterion; df: Degrees of freedom; EP: Estimated parameters; ID: Interval deviation; KD: Key deviation; PD: Pitch deviation; SINGCOMB: Combined singing score; -2LL: -2 log likelihood; Δdf : Change in degrees of freedom; $\Delta\chi^2$: Change in chi-square test.

Model 1: Bivariate saturated model (means and variances of twins are allowed to freely vary);

Model 2: Bivariate model constraining means within twin pairs to be equal;

Model 3: Bivariate model constraining means and variances within twin pairs to be equal;

Model 4: Bivariate model constraining means and variances across zygositys to be equal

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