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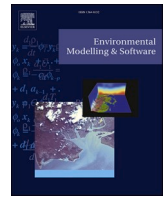
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A generalised and scalable framework for modelling incursions, surveillance and control of plant and environmental pests

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ABSTRACT

Invasive plant and environmental pests can seriously impact environment, economy, health and amenity. It is challenging to form response policies given the diversity of pest species; complex spatiotemporal interplay between arrival, spread, surveillance, and control; and limited field data when pests are rare/absent. Models can provide useful decision support through the exploration of incursion pathways and comparison of surveillance and control strategies. However, increased use of quantitative models to inform pest management requires adaptable modelling frameworks. The new Australian Priority Pest and Disease modelling framework (APPDIS) allows pest models to be constructed through user configuration choices for a broad range of different pest types. Pest populations may be defined as point incursions, established populations, or estimated mechanistically from environmental criteria. Spread occurs at multiple scales, through either simple mathematical kernels, or more complex spatial pathways, depending on data availability and pest type. Useful experiments can be conducted on general surveillance, specific surveillance, and treatment regimes. Control activities are dynamically resource-constrained and costed for relative comparisons in terms of benefit and cost. A case study on a tramp ant incursion is provided for illustrative purposes.

1. Introduction

Plant and environmental pests can inflict serious damage to the economy, environment, human health, and social amenity (Davis, 2009). It typically falls to government to construct and fund robust policies for the early detection of, and response to, harmful invasive pests. However, it can be challenging to form cost effective policies given the inherent uncertainty of, and complex spatiotemporal interplay between, the arrival, spread, detection and control of exotic pests (Schmidt et al., 2010; Keith and Spring, 2013). Further, when a pest is rare or absent there may be limited local experience and field data to inform policies for surveillance and control/eradication. Models can help policy makers explore:

- potential entry points and arrival rates of invasive pests (Douma et al., 2016; Sikes et al., 2018; Faulkner et al., 2020; Camac et al., 2020),
- potential distribution of a pest species in an environment (Sutherst et al., 1999; Phillips et al., 2006; Deutsch et al., 2008; Aurambout

et al., 2009; De Meyer et al., 2010; Yang et al., 2013; De Villiers et al., 2015),

- potential spread of a pest (Renton et al., 2011; Rebaudo et al., 2011; Adeva et al., 2012; Rasmussen and Hamilton, 2012; Lustig et al., 2017; Cook et al., 2019; Briscoe et al., 2019),
- surveillance and treatment strategies (Parry et al., 2006; Keith and Spring, 2013; Parnell et al., 2014; Baxter et al., 2017),
- the effect of resource and/or cost constraints on surveillance and treatment (Bogich et al., 2008; Kompas and Che, 2009; Hauser and McCarthy, 2009; Rout et al., 2011; Kompas et al., 2016; Spring et al., 2017).

It is, however, very difficult to encompass all aspects of an invasive pest incursion into a single decision support model. The challenge of modelling population spread and control is magnified by the diversity of plant and environmental pests, modes of dispersal, and availability of data for estimating biophysical and economic relationships in detection and control. A detailed spatially-explicit model of an individual pest may capture life-cycle and ecological specifics, and take into account

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environmental heterogeneity, but can be complex and expensive to construct, and may not readily translate to other pests. Generalised mathematical models are simpler and cheaper to build but may not capture pest-specific ecological nuances and environmental heterogeneity.

These challenges in pest spread modelling have resulted in a lack of general-purpose modelling frameworks, despite the large number of problem-specific models that have been developed. It has been argued that spread simulation models with the capacity to capture complex spatio-temporal processes, such as human-assisted and vector-borne spread, have prohibitive time and resource costs in developing, parameterizing, and testing the models (Robinet et al., 2012). This reflects an assumption that biosecurity management personnel may lack the time and/or expertise to conduct such analyses. Most general-purpose modelling frameworks for informing pest risk analysis have consequently focused on capturing simpler processes governing pest arrival and spread (Rafoss, 2003; Robinet et al., 2012; Kehlenbeck et al., 2012). There remains a need for general-purpose modelling platforms with the capacity to capture complex spatio-temporal processes.

The Australian Priority Pest and Disease modelling framework (APPDIS) is an attempt to incorporate the key aspects of invasive pest arrival, spread, detection and control in a pragmatic ‘middle ground’ modelling approach – incorporating both generalised and pest-specific techniques. An APPDIS user can create a variety of pest-specific models by supplying datasets and parameter values (ie., model creation is largely a configuration activity that does not require specialised mathematical reformulation and/or recoding). When field or environmental data is scarce or unreliable, APPDIS can be configured to spread a pest through simple aggregative mathematical pathways. Alternatively, data permitting, APPDIS can be configured to spread a pest through individual data-driven pathways that consider pest ecological nuances and environmental heterogeneities.

Effective early detection surveillance can pre-emptively lower a country’s potential liability for incursion costs. Modelling approaches need to consider the likely points where a pest can establish and potential spread in relation to surveillance intensity and extent. Scenarios need to consider the likely success of response activities at the initial detection in order to identify the value of surveillance. An APPDIS model allows a pest to be introduced anywhere in the study area at any point in time. Once established, a pest population spreads over time and space according to environmental suitability, via both natural and assisted spread pathways. The simulated initial detection of a pest may arise from general surveillance or early detection surveillance via a permanent trapping grid. APPDIS allows useful experimentation on the cost effectiveness of a trapping grid design (via configurable trap locations, spacings, lure types, costs, and sensitivity/specificity), and the implications of early versus late detection.

Containment and eradication of a pest relies upon adequate delimitation of an incursion. It can be challenging to estimate the distribution of a pest in relation to presence and absence data, particularly for pests with broad host ranges, complex spread pathways, and poor detectability. There are options to either increase surveillance to better understand the extent of the incursion or to increase treatment intensity and extent in order to cover uncertainty. Even for well-studied pests, there can be gaps in the understanding of ecology, surveillance efficacy, and control strategies. The significance of uncertainty is often not appreciated until viewed in the context of a control and containment program. Spatiotemporal models can be useful for testing scenarios with complex relationships that are subject to a great deal of uncertainty. APPDIS allows useful experimentation on the cost effectiveness of delimiting surveillance and post-treatment surveillance (via configurable trap spacings, lure types, costs, and sensitivity/specificity), and treatment (via configurable treatment schedules, efficacy and cost). All control actions simulated by APPDIS have user-defined durations, costs, and resource requirements. This allows investigation into the impact of

resource shortfalls on the efficacy and cost of managing an incursion.

A case study on the potential eradication of an established tramp ant population illustrates the steps in configuring an APPDIS pest model and provides some examples of model use. Firstly, the tramp ant population is allowed to spread unchecked and emergent spread rates are compared with field observations. Secondly, surveillance and treatment options are enabled and a sensitivity analysis is conducted on the effect of trap spacing on the cost effectiveness of eradication. It is important to note that the purpose of the case study is to demonstrate configuration and use of the modelling framework, and is not intended to inform policy on potential eradication of the pest in question.

2. Methods

2.1. The APPDIS modelling framework

APPDIS is a new modelling framework that can be used to instantiate models of the spread and control of plant and environmental pests. It is the Plant Health equivalent of the Australian animal disease modelling framework AADIS (Bradhurst et al., 2015), which can be used to instantiate models of livestock disease such as foot-and-mouth disease, bluetongue, classical swine fever and African swine fever.

APPDIS pest models are stochastic discrete-event simulations similar to geographic automata (Torrens and Benenson, 2005; Laffan et al., 2007). The study area of interest is represented by a grid delineated by lines of latitude and longitude. The modelling unit of interest is a cell within the grid. Each cell has environmental attributes (such as elevation, average weekly temperature, annual rainfall, human population density, vegetation index, land use category and average weekly wind speed), that can be used to estimate the spatiotemporal habitat suitability of the cell for a pest of interest.

The problem of modelling the incursion, spread, detection, and control of a pest in a gridded environment is reduced to seven separate sub-problems:

- which cells are initially populated with the pest?
- how does the within-cell abundance of the pest change over time?
- when/how might the pest population spread between cells?
- how cost effective are surveillance activities at detecting the pest?
- how cost effective are treatment programs at controlling/eradicating the pest?
- how cost effective are post-treatment surveillance activities at detecting residual pest populations?
- how do resource constraints affect surveillance, treatment and post-treatment activities?

2.1.1. Definition of an initial pest population

The grid extent and cell dimensions of an APPDIS model are user configurable and facilitate regional studies (inside a localised grid) up to national-scale studies (inside a much larger grid). The choice of cell size will largely depend on the pest being modelled, the extent of the study area, and the granularity of the relevant environmental data. A large cell size may not capture within-cell spatial heterogeneities in vegetation, land use, elevation, temperature, etc. A small cell size captures spatial temperature heterogeneities (data granularity permitting) but comes with a computational overhead for large grids. It is advisable to restrict the total number of grid cells to under 1,048,576 so that the raster data input comma-separated value (CSV) file (which is indexed row-major order on cell ID), can be opened by a standard desktop spreadsheet program.

APPDIS provides three ways for a user to define the initial pest population in the grid:

- point incursion – one or more cells may be explicitly seeded with a pest propagule. This represents an undetected post-border arrival of an exotic pest, for example, at a port.
- established population – an established pest population can be defined via pre-defined population densities or counts per cell, perhaps informed by field data.
- built-in mechanistic species distribution model – the location of the initial pest population can be automatically estimated by the model based on configurable ranges of environmental criteria such as temperature, vegetation, water sources, elevation, rainfall, land use, etc.

2.1.2. Within-cell abundance of a pest

Each infested cell agent has an embedded population model that estimates the population density of a pest within a cell over time, for example, via logistic growth (Kingsland, 1982; Kehlenbeck et al., 2012; Law et al., 2003). This represents how a pest population in a naive cell may initially grow exponentially, but then growth will slow as the population approaches the carrying capacity of the cell (Roughgarden, 1975). The carrying capacity of a cell is derived from user-defined habitat suitability data specific to the pest being modelled. This allows pest abundance to vary across the model grid based on environmental variables such as temperature, elevation, land use, rainfall, and vegetation).

A logistic population growth rate is unlikely to be a static value, and actual population values may not be available from empirical studies. APPDIS allows the growth rate to vary with temperature, perhaps informed by laboratory data on pest development and mortality response to temperature. This approach allows colder temperatures to be associated with negative growth rates and trigger seasonal declines of a population. Fig. 1 illustrates how a logistic function can have a constant growth rate R or a variable growth rate R(τ) that depends on temperature τ.

The logistic growth model for a temperature-dependent growth rate is given by Equation (1).

$$d(t) = \frac{K}{1 + \left\{ \frac{K}{d(t-1)} - 1 \right\} e^{-R(\tau)}} \quad (\text{Eqn. 1})$$

where

- d(t) = pest population density on day t (normalised with respect to carrying capacity K)
- K = carrying capacity of the cell (normalised across all cells)
- R(τ) = pest population growth rate for temperature τ

If the population in a cell falls below a configurable threshold it becomes quiescent and declines to extinction over a configurable period. This approximates an Allee effect (Stephens and Sutherland, 1999) whereby small or sparse populations (represented by very low cell population densities), can suffer from reduced population growth that leads to extinction.

Although not yet investigated, it would be possible for a cell agent to have multiple population models, each corresponding to a distinct species. This functionality could be useful for exploring interspecific mutualism with respect to presence and abundance.

2.1.3. Between cell spread of a pest

As the within-cell population density of a pest increases or decreases over time (per the embedded population model), the rising or falling ‘dispersal pressure’ within the infested cell affects the probability of between-cell spread. The steady short-range spread of a pest between adjoining cells is modelled by a diffusion pathway. The sporadic longer-range spread of a pest between cells is modelled by one or more jump pathways.

2.1.3.1. Diffusive spread between adjoining cells. The progressive spread of a pest from an infested cell into an adjoining candidate cell is modelled with a stochastic diffusion process that considers:

- the infested cell’s pest population density
- the infested cell’s environmental conditions (e.g., certain wind and/or temperature criteria may be required for diffusion to occur) (optional)
- the environmental suitability of the candidate cell (so that more suitable cells will have a higher probability of pest incursion than less suitable cells) (optional)
- the elevation gradient between the centroids of the source and candidate cell (optional)

Daily decisions as to whether an infested cell diffuses into the

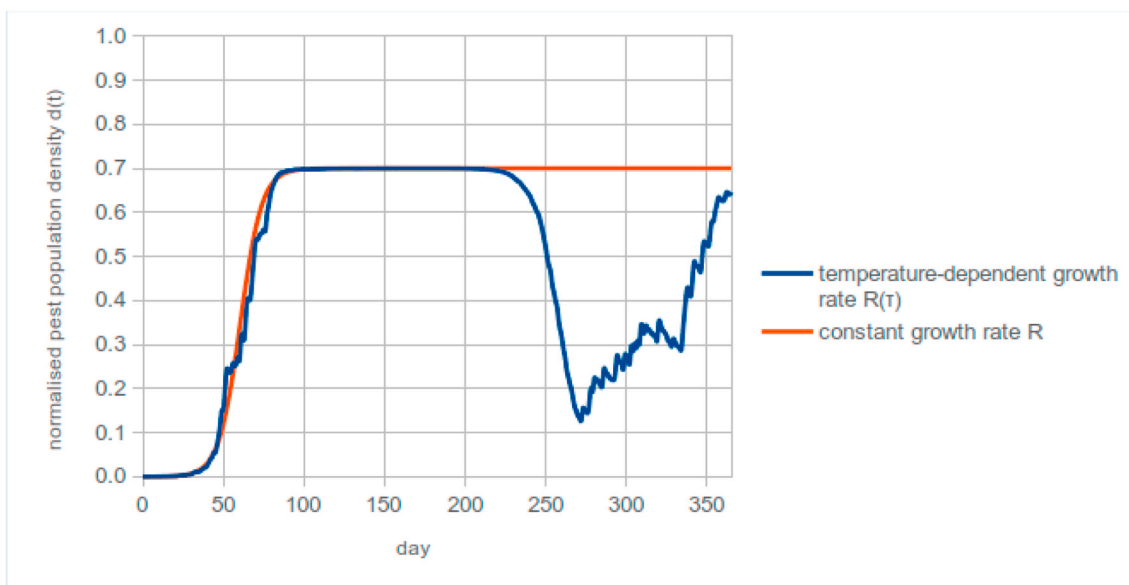


Fig. 1. A logistic growth function with a constant growth rate (R = 0.15) compared to one with a temperature-dependent growth rate R(τ). In both cases the normalised carrying capacity K is 0.7.

adjoining candidate cells are made by sampling from binomial distributions of the probability of diffusion (Equation (2)).

$$p_d(t) = 1 - \{1 - P_d S \delta \lambda \varepsilon\}^{d(t)} \quad (\text{Eqn. 2})$$

where

$p_d(t)$ = probability of diffusion occurring on day t
 P_d = baseline daily probability of diffusion of a viable number of pests from an infested cell into another cell (configurable per land use category of the infested cell)
 S = relative suitability of the candidate cell (normalised across all cells) (optional)
 δ = distance weight for the infested and candidate cells (optional)
 λ = temperature weight of the infested cell (optional)
 ε = elevation weight for the infested and candidate cells (optional)

The (optional) distance weight δ is a simple relative measure of distance between the centroids of the source infested cell and the adjoining candidate cells, and dampens the probability of diffusion into the north-west, south-west, north-east and south-east neighbours ($\delta = 0.7$), as opposed to the north, south, west, and east neighbours ($\delta = 1.0$).

The (optional) temperature weight λ is derived from the relationship between the average weekly temperature τ for the infested cell and four configured temperature thresholds for pest activity: min, optimal_lower, optimal_upper and max.

$\lambda = 0$ (for $\tau < \text{min}$)
 $\lambda = \text{linear increase from 0 to 1}$ (for $\text{min} \leq \tau \leq \text{optimal_lower}$)
 $\lambda = 1$ (for $\text{optimal_lower} \leq \tau \leq \text{optimal_upper}$)
 $\lambda = \text{linear decrease 1 to 0}$ (for $\text{optimal_upper} \leq \tau \leq \text{max}$)
 $\lambda = 0$ (for $\tau > \text{max}$)

The (optional) elevation weight ε is derived from the gradient between the centroids of the infested cell and the candidate cell. It allows the user to increase/decrease the probability of diffusion uphill/downhill (per 100 m difference in elevation).

The baseline daily probability of diffusion P_d includes the probability of post-dispersal establishment in the candidate cell. A diffusion event conveys a user-defined propagule from the source infested cell to the destination cell. If the destination cell is naïve then it acquires an equation-based population model (Equation (1)) with the propagule as the initial population. If the destination cell is already infested, then the propagule is added to the population and the population model recalculated. A cell can receive multiple diffusion events over the course of a simulation. APPDIS allows environmental criteria (temperature, habitat suitability, elevation, etc.) to be disabled, in which case diffusion is driven purely by the daily probability P_d , which in turn can be estimated by reverse engineering observed spread velocities of the pest.

2.1.3.2. Jump spread between cells. Invasive pest populations may spread over multiple scales. Whilst natural dispersal may result in short-range diffusive spread, less predictable mechanisms such as windborne spread and human-mediated dispersal can lead to longer-range jumps (Robinet et al., 2009; Gippet et al., 2019). The sporadic longer-range spread of a pest from an infested cell into non-adjoining cells is modelled with one or more stochastic jump processes that consider:

- the infested cell's pest population density
- the infested cell's environmental conditions (e.g., certain wind and/or temperature criteria may be required for a jump to occur) (optional)
- the environmental suitability of the candidate destination cell (optional)
- the human population density of the infested cell (optional)
- the land use of the infested cell (optional)

- the land use of the candidate destination cell (optional)
- waterways in the infested and candidate destination cells (optional)

Daily decisions as to whether an infested cell disperses into a distant cell are made by sampling from a binomial distribution of the probability of a jump event (Equation (3)).

$$p_j(t) = 1 - \{1 - P_j \omega \lambda\}^{d(t)} \quad (\text{Eqn. 3})$$

where

$p_j(t)$ = probability of a jump occurring on day t
 P_j = baseline daily probability of a jump occurring
 ω = human population density of the infested cell (normalised across all cells) (optional)
 λ = temperature weight of the infested cell (optional)

The jump direction may be random, influenced by the land use category of the source and destination cells, or influenced by the weekly prevailing wind direction. The jump distance is determined by sampling from a BetaPERT (Vose, 2008) distance distribution. A catchment area of cells is formed at the site of the jump landing based on either a user-defined Moore neighbourhood range or radial distance. The jump destination cell is then selected from the candidates within the catchment area either randomly or based on suitability criteria.

As per diffusion, the baseline daily probability P_j of a jump occurring includes the probability of post-dispersal establishment in the candidate cell. A jump event conveys a user-defined propagule from the source infested cell to the destination cell. If the destination cell is naïve then it acquires an equation-based population model with the propagule as the initial population. If the destination cell is already infested, then the propagule is added to the population and the population model recalculated. A cell can receive multiple jump events over the course of a simulation. P_j can be estimated either from expert opinion or the frequency that satellite pest colonies are observed arising unexpectedly some distance from a known infested area.

2.1.4. General surveillance

General surveillance by members of the public is an important means of early detection of plant and environmental pests (Cacho et al., 2010; Hester and Cacho, 2017; Wilson et al., 2004). All cells that have both a pest population and a human population are scanned daily for detections by a stochastic process that considers:

- the infested cell's pest population density
- the infested cell's human population density
- the sensitivity of the observer

The probability of a general surveillance detection event occurring on any given day is adapted from Sharov et al. (1998) and Bogich et al. (2008), and is given by Equation (4).

$$p_{TP}(t) = 1 - e^{-d(t) \omega S_e} \quad (\text{Eqn. 4})$$

where

$p_{TP}(t)$ = probability of a true positive detection occurring on day t
 ω = human population density of the infested cell (normalised across all cells)
 S_e = sensitivity of the observer

The observer sensitivity for unmanaged cells is defined separately to that for managed cells. A managed cell is defined as any cell that is undergoing, or has undergone, delimiting surveillance or treatment. The model provides the option of the first general surveillance detection occurring on a fixed day rather than on a stochastically determined day.

This allows useful experimentation on the impact of ‘time to detection’ on incursion severity and cost. Fig. 2 uses Equation (4) (with $Se = 0.70$), to illustrate how the probability of a general surveillance detection varies with respect to the normalised pest population density and the normalised human population density.

2.1.5. Early detection surveillance

There is considerable interest in the cost effectiveness of surveillance strategies for invasive species (Field et al., 2004; Gerber et al., 2005; Bogich et al., 2008; Hauser and McCarthy, 2009; Kompas and Che, 2009; Cacho et al., 2010; Epanchin-Niell et al., 2014; Holden et al., 2016). APPDIS allows the user to define a permanent trapping grid of geo-located traps with specified lure types. All cells that have both a pest population and a permanent trap location are scanned daily for active detections. The detection of a pest population is modelled with a stochastic process that considers:

- the infested cell’s pest population density
- the lure type and spacing of traps in the infested cell
- the sensitivity of the surveillance process (traps and personnel)
- the specificity of the surveillance process (traps and personnel)

The probability of a true positive detection occurring on day t is adapted from Sharov et al. (1998) and Bogich et al. (2008), and is given by Equation (5).

$$p_{TP}(t) = 1 - e^{-a(t) \varphi S_e} \tag{Eqn. 5}$$

where

- $p_{TP}(t)$ = probability of a true positive detection on day t
- $a(t)$ = pest area of the infested cell in hectares on day t
- φ = trap density (traps per hectare) in the infested cell ($= 10,000/(\text{trap spacing in metres})^2$)
- S_e = sensitivity of the surveillance process (traps and personnel)

As the pest area $a(t)$ of an infested cell is not actually known (as cells are atomic), it is proxied by multiplying the normalised population density of the cell $d(t)$ by the cell area in hectares. The model also provides the option of the first early detection occurring on a fixed day rather than on a stochastically determined day. This allows useful experimentation on the impact of ‘time to detection’ on incursion severity and cost. Fig. 3 uses Equation (5) with $Se = 0.96$ to illustrate how the probability of early detection inside a 10-ha cell varies with the normalised pest population density and trap spacing.

If a surveyed cell does not yield a true positive result, then it is

checked for a false positive result. The probability of a false positive detection occurring is given by Equation (6).

$$p_{FP} = 1 - S_p \tag{Eqn. 6}$$

where

- p_{FP} = probability of a false positive detection
- S_p = specificity of the surveillance process (traps and personnel)

If a surveyed cell does not yield a positive result, then a true/false negative result is assigned according to the actual absence/presence of the pest in the cell.

2.1.6. Delimiting surveillance

After a pest population has been detected in a cell, the surrounding cells undergo delimiting surveillance. Delimiting surveillance comprises a configurable number of periodic surveillance visits. Delimiting surveillance operates in either Moore mode (where the cells in the Moore neighbourhood of the detected cell are surveyed), or Radial mode (where all cells within a configurable distance of the detected cell are surveyed). The detection of a pest population through delimiting surveillance is modelled by a stochastic process that considers:

- the surveyed cell’s pest population density
- trap spacing in the surveyed cell
- the sensitivity of the surveillance process (traps and personnel)
- the specificity of the surveillance process (traps and personnel)

The daily probability of a true positive detection is given by Equation (5). If a cell does not yield a true positive result it is then checked for a false positive detection (Equation (6)). A positive surveillance result triggers a treatment program. If a cell does not yield a positive result, then a true/false negative result is assigned according to the actual absence/presence of the pest in the cell. The pest is deemed absent from a cell once a configurable number of consecutive negative surveillance results has been reached.

2.1.7. Treatment

All cells that have yielded a positive result (true or false), from general surveillance, early detection surveillance, or delimiting surveillance, undergo a treatment program. A treatment program comprises a configurable number of treatments, conducted at a configurable period. Each treatment reduces the population by a percentage amount (determined stochastically between a configured minimum and maximum reduction). A pest population is deemed extinct if a treatment

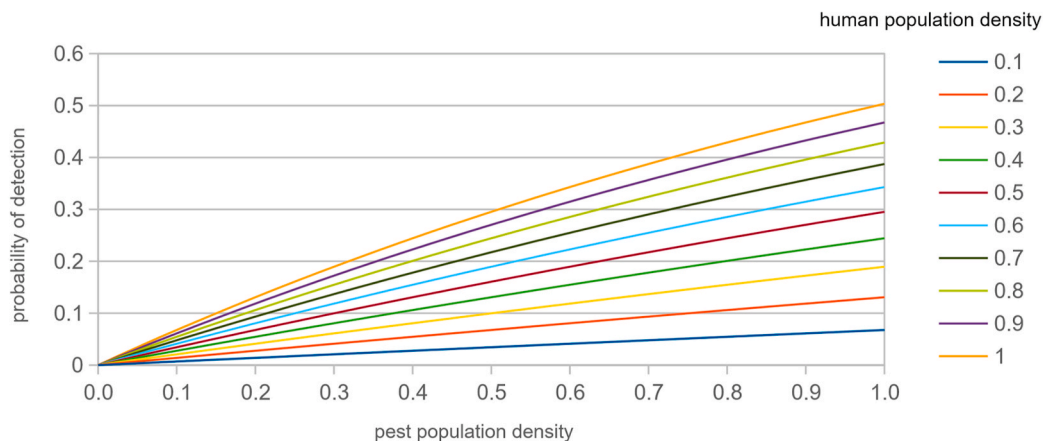


Fig. 2. Probability of general surveillance detection with respect to pest population density and human population density.

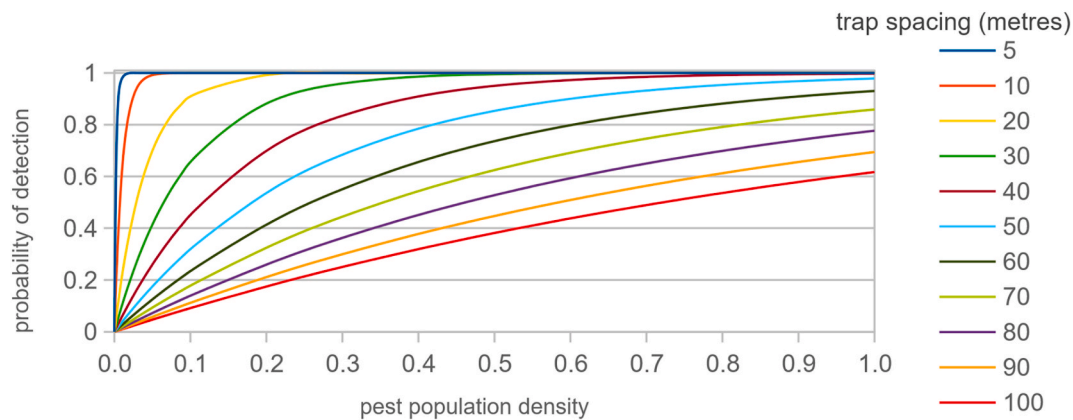


Fig. 3. Probability of specific surveillance detection in relation to pest population density and trap spacing.

program reduces it to below the configured minimum population size. A treatment program may operate in Spot mode (where only the detected cell is treated), Moore mode (where all cells in the Moore neighbourhood of the detected cell are treated), or Radial mode (where all cells within a configurable distance of the detected cell are treated).

2.1.8. Post-treatment surveillance

Post-treatment surveillance commences at a configurable period after the completion of the last scheduled treatment. A post-treatment surveillance program comprises a configurable number of periodic surveillance visits. Post-treatment surveillance is modelled with a stochastic process that considers:

- the surveyed cell's pest population density
- the trap spacing in the surveyed cell
- sensitivity of the surveillance process (traps and personnel)
- specificity of the surveillance process (traps and personnel)

As per delimiting surveillance, the daily probability of a true positive detection is given by Equation (5). If a cell does not yield a true positive result it is then checked for a false positive detection (Equation (6)). A positive post-treatment surveillance result triggers another treatment program. If a cell does not yield a positive result, then a true/false negative result is assigned according to the actual absence/presence of the pest in the cell. A cell is deemed free of the pest after a configurable number of consecutive negative surveillance results.

2.1.9. Resourcing

The active surveillance and treatment of plant and environmental pests are typically resource-constrained processes (Rout et al., 2011; McCarthy et al., 2012). An APPDIS 'resource' is abstract in the sense that it is a (user-defined) set of personnel/equipment/supplies required to carry out a specific job. The model maintains pools for each resource type (early detection surveillance, delimiting surveillance, treatment, and post-treatment surveillance). The resourcing profile for each pool is configurable as to whether resource levels are fixed or vary over time.

When a field operation is scheduled a resource is requested from the corresponding pool. If a resource is available, then it is 'borrowed' from the pool and the field operation commences. If a resource is not available, then the field operation is queued until such time as the required resource becomes available. Once a field operation has completed, the resource is 'returned' to the pool.

The model reports the daily resource usage for early detection surveillance, delimiting surveillance, treatment, and post-treatment surveillance. Resource pools can be configured to be 'unlimited' in which case resources are always immediately granted upon request. In this mode the resourcing profile of an outbreak is a model output instead of a model input that constrains the efficacy of the control program.

2.1.10. Implementation highlights

The APPDIS modelling framework utilises an agent-based modelling platform (Bradhurst, 2015) which can operate in four modes: contagious livestock disease, vector-borne livestock disease, plant/environmental pests, and human disease. When modelling the spread and control of contagious disease in livestock, the agents are herds, farms (containers of one or more herds), saleyards and abattoirs. When modelling the spread and control of plant and environmental pests, the agents are cells in a lattice environment. When modelling the spread and control of insect vector-borne livestock disease (such as bluetongue), the agents are herds, farms, saleyards, abattoirs, and cells. When modelling the spread and control of human disease the agents are people. Descriptions of the vector-borne livestock and human disease modes will appear in future papers. The modelling behaviour (livestock disease, plant/environmental pests, or human disease) of an instantiated model is purely determined by the configuration files and database loaded.

An APPDIS agent can have an embedded population model of the within-agent abundance over time. For example, when modelling an exotic fruit fly incursion each infested cell agent has an embedded temperature-dependent logistic growth model that predicts the within-cell population over time. An agent can also have an embedded infection model of the within-agent prevalence of a pathogen in the population. For example, when modelling the spread of a contagious disease in feral pigs each infected cell agent has an embedded SEIRD (Susceptible, Exposed, Infectious, Recovered, Deceased) compartmental disease model (implemented as a system of ordinary differential equations), that predicts the within-cell infected and infectious prevalence of the disease over time. The interplay between a cell agent's population and infection models will be described in a separate paper. The details of the population and infection models are private to the agent, which means that alternate within-cell models can be used without impacting the greater model.

APPDIS models scale well as the agents are threadless and lightweight. APPDIS agents interact in a spatially-explicit disaggregated environment comprised of threaded 'components' that operate concurrently and independently (Bradhurst, 2015). Examples of components relevant to contagious livestock disease include local spread, direct spread, saleyard spread, indirect spread, airborne spread, movement restrictions, surveillance, tracing, vaccination, stamping out and post-outbreak surveillance (Bradhurst et al., 2015). Examples of components relevant to plant/environmental pests include unaided diffusive spread, human-mediated hitchhiking spread, wind-assisted airborne spread, early detection surveillance, general surveillance, delimiting surveillance, treatment, and post-treatment surveillance. All APPDIS components are independent and can be separately enabled/disabled. As the implementation of each component is private, alternate components can be swapped in and out. For example, the implementation of a treatment component can completely change without impacting the rest

of the model.

APPDIS has a concurrent software architecture that allows it to take advantage of the cheap parallelism available with multi-core personal computers. This, together with other design efficiencies, such as an in-memory database and grid-based spatial indexing, allow APPDIS to efficiently conduct national-scale simulations (Bradhurst et al., 2016). Further details on the underlying model and software architecture can be found in Bradhurst (2015) and Bradhurst et al. (2016).

The primary APPDIS outputs are CSV files which can be post-processed statistically. APPDIS also provides a graphical user interface for interacting with the model and dynamic visualisation of incursions as they unfold. The ability for APPDIS to convey incursion and management concepts visually may suit it to classroom use. Fig. 4 is a screenshot of APPDIS depicting a hitchhiking escape of a tramp ant population from within the managed area. The population model of any cell can be visualised, for example, Fig. 4 depicts the population of cell 70814 being knocked down over the course of a treatment program and the residual population recovering over time.

2.1.11. Verification and validation

The APPDIS and AADIS modelling frameworks have a common underlying software baseline (Bradhurst, 2015). APPDIS thus inherits from previous AADIS verification and validation activities, and modelling studies (Bradhurst, 2015; Bradhurst et al., 2015; Bradhurst et al., 2016; Garner et al., 2016; Bradhurst et al., 2019; Firestone et al., 2019; Bradhurst et al., 2021; Firestone et al., 2020).

APPDIS models were instantiated for *Anoplolepis gracilipes* (yellow crazy ant) and *Bactrocera dorsalis* (Oriental fruit fly) case studies during development of the framework. A model has also been developed of the spread of disease in feral pigs. The yellow crazy ant model is described in this paper, and the Oriental fruit fly and feral pig models will be described in separate future papers. APPDIS validation will be an ongoing process as each new pest (or pest group) model instantiation will require separate validation.

2.1.12. Hardware and platform specifications, and software availability

APPDIS is written in Java (Oracle, 2020), and employs open-source products such as SQL Power Architect (SQL Power Group, 2020), PostgreSQL (2020), OpenMap (BBN, 2016) and Log4j (Apache, 2020). APPDIS runs under either Linux™ or Windows™ with a recommended minimum hardware configuration of a quad-core processor, 16 GB RAM and a 1920 × 1080 display resolution. The model is available at no cost for non-commercial use under a licensing agreement with the Australian Department of Agriculture, Water and the Environment.

2.2. Case study: Established population of tramp ants

Tramp ants are a diverse group of invasive ant species that can severely impact native species and habitats, agriculture, forestry, human health and social amenity. If introduced they can rapidly establish and spread through natural and human-mediated dispersal (Abbott, 2005; Hoffman, 2014).

An example of a tramp ant that is a concern to Australia is *Anoplolepis gracilipes* (yellow crazy ant (YCA)). YCA causes severe ecological damage (Abbott, 2005, 2006), and can affect the horticulture industry by farming sap-sucking scale insects for honeydew. This can lead to larger infestations of pests on host plants (Haines and Haines, 1978b; Lach and Barker, 2013; Helms, 2013), and an increase in the risk of disease being transmitted to plants through insect vectors. Supercolonies are formed through colony budding and the absence of intraspecific aggression (O'Dowd et al., 1999).

2.2.1. Model setup

2.2.1.1. Study area. This study area for this case study was approximately 18,724 km² (bounded by latitudes -16.450 to -17.941 and longitudes 145.090 to 146.149). A cell size of 10 ha was chosen to reflect the observation that a YCA supercolony spanning an area less than 10 ha tends to be a single contiguous population, whereas a supercolony spanning an area greater than 10 ha tends to be comprised of fragmented

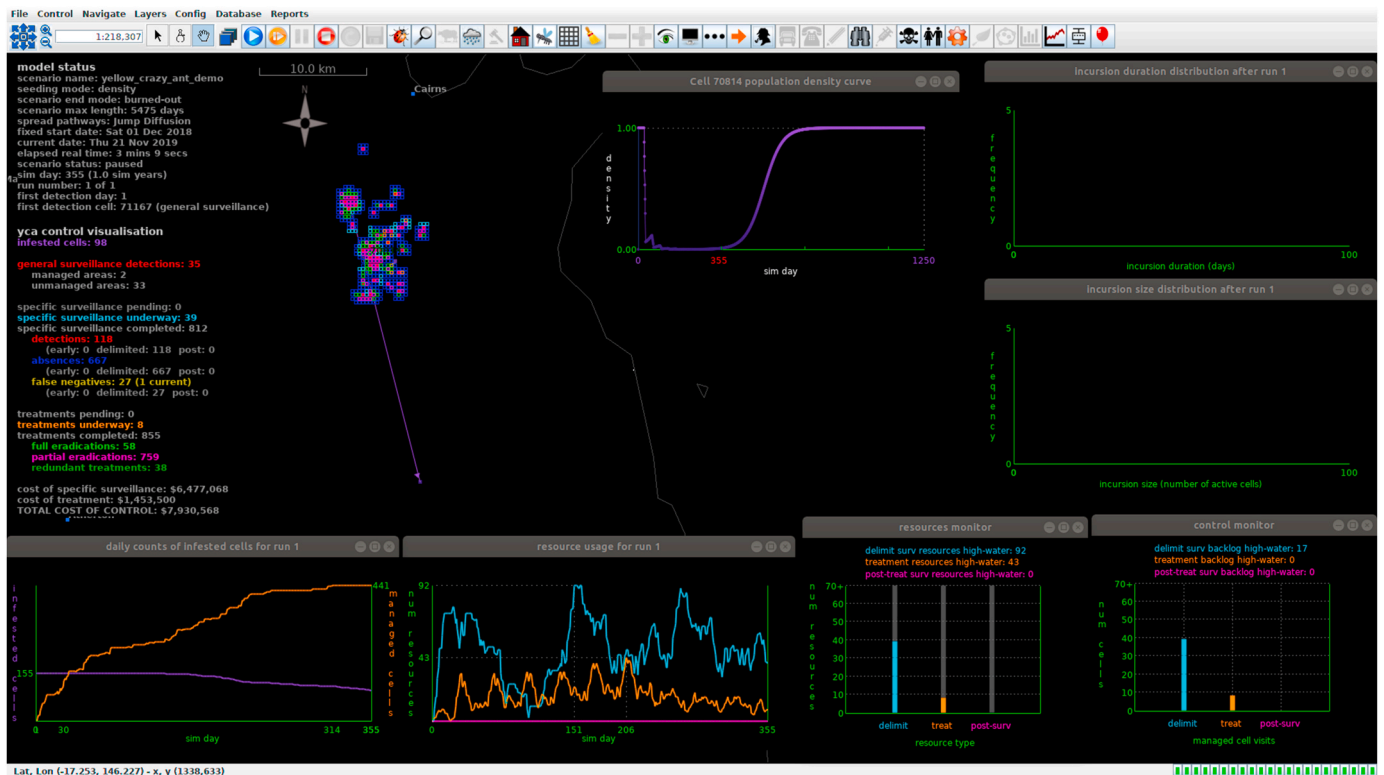


Fig. 4. APPDIS spread and control visualisation.

populations (Hoffmann, 2014).

APPDIS raster data layers were defined for:

- land use (sugar cane farms, sugar cane railway corridors, managed land, natural areas)
- watercourses
- elevation
- human population density
- YCA habitat suitability (land = suitable, sea/lakes = unsuitable)

YCA densities have previously been estimated at between 0.2 million and 3.5 million per hectare (Haines and Haines, 1978a), and up to 20 million per hectare (Abbott, 2005). As the habitat suitability data layer for this study was very simple, a conservative grid-wide carrying capacity of 2 million YCA per hectare was chosen. This means that every land cell is deemed equally suitable for YCA with a nominal carrying capacity of 20 million. This simplistic assumption could be improved with a richer habitat suitability layer that incorporates variables such as rugosity and food sources in the determination of cell suitability, which in turn would provide heterogeneity in cell carrying capacity.

The initial YCA population (Fig. 5) spanned 154 cells. Cell population densities were synthesized, graduating from a population of 20 million in cells at the centre of large clusters, down to 2000 in cells at the edge of clusters. This resulted in an overall initial YCA population of

approximately 310 million across 1540 ha. The initial YCA population of any subsequently infested cell was an arbitrary propagule, deemed to comprise 24 workers and 1 queen.

2.2.1.2. Within-cell abundance. The abundance of the YCA population within an infested cell over time was represented by a deterministic logistic growth function (Equation (1)) with a temperature-independent population growth rate $R(\tau) = 0.025$ based on the assumption that for an ideally suitable 10 ha cell, an uncontrolled YCA population will take approximately 2 years to grow from a single propagule ($n = 25$) to 99% of the cell carrying capacity ($n = 19.8M$). This implies that 50% of the carrying capacity is reached after 454 days. Natural contractions of YCA populations (Abbott, 2006) were not modelled.

2.2.1.3. Diffusive spread of YCA between adjoining cells. An APPDIS diffusion spread pathway was instantiated to model the steady spread of YCA over time to adjoining cells. The baseline daily probability of diffusion P_d (required for Equation (2)), depends on the land use category of the infested cell (Table 1). This allows heterogeneity in the diffusive behaviour. For example, diffusion in a cane farm cell (where natural budding is perhaps augmented by short-range movements arising from within-farm activities such as harvesting), is assumed to be more vigorous than diffusion in a national park cell (that is primarily due to natural budding).

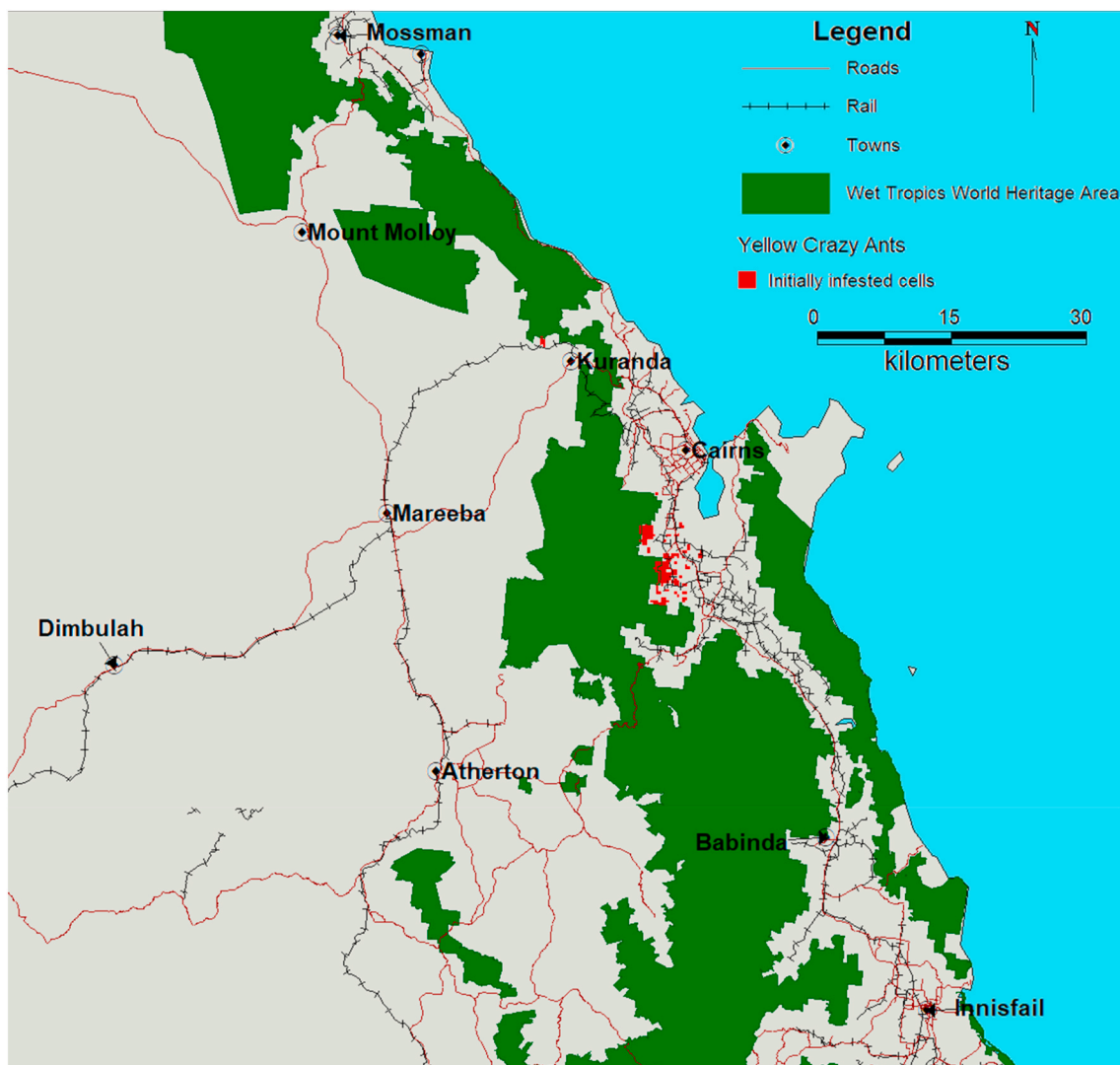


Fig. 5. Initial yellow crazy ant population.

Table 1
Selected parameterisation of the YCA diffusion pathway.

Parameter	Value
Dependent on land use	true
Daily diffusion baseline probability P_d on a cane farm	0.000445 ¹
Daily diffusion baseline probability P_d in a railway corridor	0.000083 ²
Daily diffusion baseline probability P_d in managed land	0.000083 ²
Daily diffusion baseline probability P_d in a natural area	0.000028 ³

¹ based on the assumption that a cane farm cell with maximal YCA population (i.e., at carrying capacity), has a 15% chance of diffusing into another cell within a year, i.e., $P_d = 1 - (1-0.15) (1/365)$.

² Based on the assumption that a cell with maximal YCA population (i.e., at carrying capacity), in a railway corridor or on managed land, has a 3% chance of diffusing into another cell within a year, i.e., $P_d = 1 - (1-0.03) (1/365)$.

³ Based on the assumption that a cell with maximal YCA population (i.e., at carrying capacity), in a natural area, has a 1% chance of diffusing into another cell within a year, i.e., $P_d = 1 - (1-0.01) (1/365)$.

2.2.1.4. Spread between non-adjoining cells due to sugar cane farming activities. An APPDIS jump spread pathway was instantiated to model the sporadic spread of YCA due to medium-range hitchhiking from sugar cane farming activities. Jumps were parameterised to only originate from cells containing sugar cane farms, and only end in cells that had either sugar cane farms or railway corridors. The ability to define the baseline daily probability P_j (Equation (3)) per land use category allows heterogeneity in the jumping frequency (Table 2). For example, jumps between cane farms (brought about by harvesting activities spanning multiple farms), can be defined differently to jumps from cane farms to cane railway corridors (brought about by cane rail transportation).

Seasonal variations in cane farming activities were not modelled, i.e., the pathway represents average cane jumps over the course of a year.

2.2.1.5. Spread between cells due to human-mediated hitchhiking. An APPDIS jump spread pathway was instantiated to model the sporadic spread of YCA via human-mediated hitchhiking (unrelated to cane farming activities). Jumps were parameterised to only involve cells with a non-zero human population density (Table 3). Although the model allows a proportion of jumps to end in non-populated cells (simulating for example, movements into natural areas), the feature was not enabled for this case study.

2.2.1.6. Spread between cells due to rafting. An APPDIS jump spread pathway was instantiated to model the sporadic spread of YCA due to rafting. Jumps were parameterised to only originate from cells containing watercourses, and only end in lower elevation cells that contain watercourses (Table 4).

2.2.1.7. General surveillance. An APPDIS general surveillance component was instantiated per Table 5.

2.2.1.8. Specific surveillance and treatment. APPDIS delimiting surveillance, treatment, and post-treatment components were instantiated per Table 6.

Table 2
Selected parameterisation of the YCA sugar cane farming jump pathway.

Parameter	Value
Dependent on land use	true
Daily jump baseline probability P_j onto a cane farm	0.000289 ¹
Daily jump baseline probability P_j into a railway corridor	0.000289 ¹
Jump distance (minimum, most likely, maximum) (km)	BetaPERT ² (0.5, 2, 20)

¹ based on the assumption that a cell with maximal YCA population (i.e., is at carrying capacity), has a 10% chance of a sugar-cane farming hitchhiking jump into another cell within a year, i.e., $P_j = 1 - (1-0.1) (1/365)$

² Vose (2008).

Table 3
Selected parameterisation of the YCA human-mediated hitchhiking jump pathway.

Parameter	Value
Dependent on human population density	true
Daily jump baseline probability P_j	0.000289 ¹
Proportion of jumps allowed into non-populated areas	0.0
Jump distance (minimum, most likely, maximum) (km)	BetaPERT (0.5, 10, 75)

¹ based on the assumption that a cell with maximal YCA population (i.e., is at carrying capacity), and maximal human population (i.e., normalised human population density of 1.0), has a 30% chance of a human-mediated hitchhiking jump into another cell within a year, i.e., $P_j = 1 - (1-0.3) (1/365)$

Table 4
Selected parameterisation of the YCA sugar cane farming jump pathway.

Parameter	Value
Dependent on land use	false
Dependent on human population density	false
Dependent on temperature	false
Dependent on gradient	true
Dependent on watercourses	true
Daily jump baseline probability P_j	0.000141 ¹
Jump distance (minimum, most likely, maximum) (km)	BetaPERT (0.5, 0.5, 5)

Seasonal variations in rafting likelihood were not modelled, i.e., the pathway represents average rafting jumps over the course of a year.

¹Based on the assumption that a cell with maximal YCA population (i.e., is at carrying capacity), has a 5% chance of rafting jump into another cell within a year, i.e., $P_j = 1 - (1-0.05) (1/365)$

Table 5
YCA general surveillance parameterisation.

Parameter	Value
General surveillance mode	Passive
Observer sensitivity S_e in managed areas	0.60
Observer sensitivity S_e in unmanaged areas	0.25

Table 6
YCA specific surveillance and treatment parameterisation.

Parameter	Delimiting surveillance	Treatment	Post-treatment surveillance
Mode	Moore	Spot	Spot
Visit duration (per cell)	21 days	7 days	21 days
Trap spacing	10 m	N/A	10 m
Sensitivity S_e	0.99	N/A	0.99
Specificity S_p	1.00	N/A	1.00
Effectiveness	N/A	0.8 to 0.95	N/A
Visit cost	A\$10 per trap	A\$1700 per cell	A\$10 per trap
Interval between visits	90 days	28 days	180 days
Minimum number of visits	8	6	4

2.2.1.9. Resources. The APPDIS resources component was set to Unlimited i.e., surveillance and treatment activities were not resource constrained.

2.2.2. Scenario 1 - uncontrolled spread

The established YCA population (Fig. 5) was allowed to spread without surveillance or treatment for 30 years and the emergent rates and extent of spread recorded. The scenario was repeated 50 times.

2.2.3. Scenario 2 – sensitivity of delimiting surveillance trap spacing

The established YCA population (Fig. 5) was allowed to spread in

conjunction with surveillance and treatment programs. The delimiting surveillance trap spacing parameter (Table 6) was systematically varied between 2 and 100 m, while the post-treatment surveillance trap spacing was held constant at 10 m. 500 iterations of the scenario were run for each trap spacing. The maximum length of a scenario was limited to 15 years (5475 days).

2.2.4. Scenario 3 - sensitivity of post-treatment surveillance trap spacing

The established YCA population (Fig. 5) was allowed to spread in conjunction with surveillance and treatment programs. The post-treatment surveillance trap spacing parameter (Table 6) was systematically varied between 2 and 100 m, while the delimiting surveillance trap spacing was held constant at 10 m. 500 iterations of the scenario were run for each trap spacing. The maximum length of a scenario was limited to 15 years (5475 days).

3. Results

3.1. Scenario 1 results - uncontrolled spread

Table 7 provides a summary of uncontrolled YCA spread over 30 years.

Convergence estimates the percentage standard error E of the sample mean with 95% confidence for a given number of iterations (Equation (7)) (Driels and Shin, 2004).

$$E = \frac{100z_c S_x}{\bar{x}\sqrt{n}} \quad (\text{Eqn. 7})$$

where

- E = percentage standard error of the sample mean
- z_c = confidence coefficient (1.96 = 95%)
- S_x = sample standard deviation
- \bar{x} = sample mean
- n = number of runs

Fig. 6 provides a snippet of the yearly spread report for the case study. The model outputs the population density for each active cell at the end of every year, for each simulation run.

The model creates a pest distribution risk map that represents how often a cell was infested across all iterations of a particular scenario. Fig. 7 presents a colour-coding of cells in the study area where the most frequently infested cells are encoded in red and the least frequently infested cells in yellow.

3.2. Scenario 2 results - sensitivity of delimiting surveillance trap spacing

Table 8 and Figs. 8 and 9 summarise the effect of delimiting

Table 7

Simulation results for 50 iterations of 30 years of uncontrolled yellow crazy ant spread.

Model outcome	Value
YCA population increase ¹	310 million → 124 billion
Initial infestation area increase ¹	154 cells (1540 ha) → 6936 cells (69,360 ha)
Final infestation area convergence ²	2.90%
Number of diffusion events ¹	105 per year
Managed land diffusion rate ¹	119 m per year
Cane farm diffusion rate ¹	132 m per year
Cane railway diffusion rate ¹	90 m per year
Natural area diffusion rate ¹	68 m per year
Cane-related jump rate ¹	41 jumps per year
Human-mediated jump rate ¹	16 jumps per year
Rafting jump rate ¹	13 jumps per year

¹ averaged over 50 runs.

² percentage standard error of the sample mean (95% confidence).

surveillance trap spacing on the average cost and effectiveness of control/eradication.

3.3. Scenario 3 results - sensitivity of post-outbreak surveillance trap spacing

Table 9 and Figs. 10 and 11 summarise the effect of post-treatment surveillance trap spacing on the average cost and effectiveness of control/eradication.

4. Discussion

4.1. Uncontrolled spread

The average YCA diffusion rate over a 30-year period ranged from 68 m/year in natural areas up to 132 m/year in cane farming areas. This is broadly in line with reported budding distances of 125 m/year on average (range 37–402) (Haines and Haines, 1978a), and up to 182 m per year (Abbott, 2006). Note that cells may have multiple land uses (e. g. cane + managed, railway + managed) and each cell diffuses based on its highest risk land use. This can artificially boost the diffusion rate for the lower risk land use of the cell (e. g. a managed cell with cane fields contributes correctly to the overall cane diffusion rate but over-contributes to the overall managed land diffusion rate).

Dispersion via winged flight of queens (fission) was not explicitly modelled as it is unclear whether this is an important means of dispersal for YCA (Rao et al., 1991; Haines et al., 1994; O'Dowd et al., 1999; Abbott et al., 2014; Hoffmann, 2014). It would have been possible, data permitting, to include a fission jump pathway as the model supports multiple concurrent jump spread pathways.

Longer range sporadic spread of YCA via hitchhiking is more unpredictable and harder to quantify than steady diffusive spread. The probability of spread via human-mediated hitchhiking is influenced by an infested cell's pest population density and human population density, however, the frequency and distance of such jumps is largely driven by expert opinion and inference from unexpected satellite colonies. For example, an unexpected appearance of YCA in Russett Park, Queensland (30 km from the nearest known infestation near Cairns, Queensland), was attributed to hitchhiking via the transportation of landscaping materials.

As illustrated in Fig. 7, one of the outputs of APPDIS is a risk map of spread – driven by the number of times a cell is infested over a series of scenario runs. The land uses of the resultant infested cells can be analysed to provide an estimation of the potential long-term impact on agricultural, residential, and environmentally sensitive areas. This case study strongly suggests that 30 years of uncontrolled spread of YCA would lead to significant incursions into the Wet Tropics World Heritage Area.

The simulation produced very good convergence (2.90%) of the mean number of infested cells after 50 iterations. This implies there is 95% confidence of only 2.90% standard error in the distribution of the sample mean.

4.2. Sensitivity of surveillance trap spacing

The cost of control was largely independent of delimiting surveillance trap spacings greater than 20 m, but rose steeply for trap spacings less than 20 m (Fig. 8). The cost of control was weakly dependent on post-treatment surveillance trap spacings greater than 10 m, and rose steeply for trap spacings less than 10 m (Fig. 10).

The effectiveness of control (measured by population reduction and incursion duration), was far more sensitive to post-treatment surveillance trap spacing than delimiting surveillance trap spacing. Figs. 8 and 9 shows how the YCA population was reduced by 99% within 15 years for all delimiting surveillance trap spacings. In contrast, only post-treatment surveillance trap spacings between 2 and 10 m resulted in a

run	sim_day	calendar_date	cell_ID	latitude	longitude	infest day	pathway	Source ID	pest density	population
1	3650	Sun 29 Nov 2026	38667	-16.7785	145.65851	3203	hitchhiking	67996	0.0819	1637160
1	3650	Sun 29 Nov 2026	40417	-16.793499	145.6135	3242	budding	40769	0.0325	650698
1	3650	Sun 29 Nov 2026	40762	-16.796501	145.58951	3147	budding	40763	0.2655	5310817
1	3650	Sun 29 Nov 2026	40763	-16.796501	145.5925	1777	budding	41117	1	20000000
1	3650	Sun 29 Nov 2026	40764	-16.796501	145.59549	0	seed	0	1	20000000
1	3650	Sun 29 Nov 2026	40765	-16.796501	145.59851	2508	budding	41117	1	19999994
1	3650	Sun 29 Nov 2026	40768	-16.796501	145.6075	3477	budding	40769	0.0001	1889
1	3650	Sun 29 Nov 2026	40769	-16.796501	145.6105	1559	rafting	41472	1	20000000
1	3650	Sun 29 Nov 2026	41117	-16.7995	145.59549	0	seed	0	1	20000000
1	3650	Sun 29 Nov 2026	41118	-16.7995	145.59851	0	seed	0	1	20000000
1	3650	Sun 29 Nov 2026	41119	-16.7995	145.6015	3148	budding	40765	0.2607	5213876
1	3650	Sun 29 Nov 2026	41470	-16.802502	145.59549	0	seed	0	1	20000000
1	3650	Sun 29 Nov 2026	41471	-16.802502	145.59851	0	seed	0	1	20000000
1	3650	Sun 29 Nov 2026	41472	-16.802502	145.6015	318	budding	41118	1	20000000
1	3650	Sun 29 Nov 2026	41474	-16.802502	145.6075	2213	rafting	41472	1	20000000
1	3650	Sun 29 Nov 2026	41475	-16.802502	145.6105	185	rafting	41824	1	20000000
1	3650	Sun 29 Nov 2026	41481	-16.802502	145.62851	3273	rafting	41826	0.0153	305133
1	3650	Sun 29 Nov 2026	41816	-16.8055	145.5745	2293	hitchhiking	68702	1	20000000
1	3650	Sun 29 Nov 2026	41822	-16.8055	145.5925	2442	budding	41823	1	19999999
1	3650	Sun 29 Nov 2026	41823	-16.8055	145.59549	178	budding	41824	1	20000000
1	3650	Sun 29 Nov 2026	41824	-16.8055	145.59851	0	seed	0	1	20000000
1	3650	Sun 29 Nov 2026	41826	-16.8055	145.60449	2661	rafting	41823	1	19999707
1	3650	Sun 29 Nov 2026	42169	-16.808498	145.5745	3398	budding	41816	0.0007	13605
1	3650	Sun 29 Nov 2026	42176	-16.808498	145.59549	1233	budding	41824	1	20000000
1	3650	Sun 29 Nov 2026	44615	-16.829498	145.49951	2465	hitchhiking	65867	1	19999998
1	3650	Sun 29 Nov 2026	46762	-16.8475	145.5865	2804	hitchhiking	63756	0.9995	19989563
1	3650	Sun 29 Nov 2026	46775	-16.8475	145.62549	1615	hitchhiking	68702	1	20000000
1	3650	Sun 29 Nov 2026	47128	-16.8505	145.62549	2579	budding	46775	1	19999962
1	3650	Sun 29 Nov 2026	47469	-16.8535	145.58951	2465	hitchhiking	60933	1	19999998
1	3650	Sun 29 Nov 2026	49568	-16.8715	145.5325	3606	hitchhiking	60225	0	75
1	3650	Sun 29 Nov 2026	51405	-16.886501	145.7485	1448	cane jump	65877	1	20000000
1	3650	Sun 29 Nov 2026	51709	-16.8895	145.6015	2739	hitchhiking	66575	0.9999	19997944
1	3650	Sun 29 Nov 2026	52062	-16.8925	145.6015	3503	budding	51709	0	986
1	3650	Sun 29 Nov 2026	52148	-16.8925	145.8595	2038	hitchhiking	41470	1	20000000

Fig. 6. Yellow crazy ant simulation spread report (snippet only).

99% population reduction within 15 years (Figs. 10 and 11). The effectiveness of control decreased markedly as post-treatment surveillance trap spacing increased, with a trap spacing of 100 m yielding no net population reduction after 15 years. This suggests that the effectiveness of post-treatment surveillance is a vital aspect of pest eradication. Fig. 10 indicates that a post-treatment surveillance trap spacing of 18 m minimised the cost of control at approximately A\$23.5M and resulted in an average 95% population reduction. However, to achieve an average 99.99% population reduction, the required 2-m post-treatment surveillance trap spacing would, however, incur a much higher cost of approximately A\$163M.

The decrease in control effectiveness with increased post-treatment surveillance trap spacing is also reflected by the average model runtime per iteration. In scenario 2 where the post-delimiting surveillance trap spacing was held steady at 10 m while the delimiting surveillance trap spacing was varied, the average model runtime (per scenario iteration) was reasonably stable (average = 60.50 s, standard deviation = 9.68) (Table 8). In scenario 3 where the delimiting surveillance trap spacing was held steady at 10 m while the post-outbreak surveillance trap spacing was varied, the average model runtime (per scenario iteration) was strongly dependent on trap spacing (ranging from 28.04 to 141.75 s). This is due to the additional treatment and post-treatment surveillance activities (and hence simulation processing) required when the surveillance strategy is less effective (reflected by higher false negative results (Table 9)).

The high sensitivity of control cost-effectiveness to post-treatment surveillance trap spacing is perhaps because post-treatment surveillance is typically conducted in cells with very small pest densities. As

shown in Fig. 3, the model's implementation of specific surveillance is highly sensitive to trap spacing at low pest population densities. An incorrect determination of pest absence in a treated cell (after 4 successive false negative results), leads to cell populations that will recover over time. In the absence of an early detection surveillance system, the subsequent detection of a residual population relies on general surveillance. The probability of a general surveillance detection is, however, greatly reduced at low pest and human population densities (Fig. 2).

The simulations produced very good convergence for the mean total cost of control (<1.7%). This implies 95% confidence that there is at most 1.7% standard error in the distribution of the sample mean, and that 500 iterations of the scenarios were sufficient.

4.3. Advantages and limitations of the APPDIS modelling approach

Decision support tools that represent the spread of a pest in an environment range from simple aggregative mathematical models to complex pest-specific spatial simulations. Aggregative mathematical models generally do not take host and environmental heterogeneity into account, but are concise, easy to parameterise, scalable, computationally efficient, and may be readily extensible to other pests. They can be very useful for the fast prototyping of incursion dynamics, especially when data is scarce or unreliable. Detailed spatially explicit and pest-specific simulations can capture environmental and host heterogeneities, but are data dependent, can be complicated to construct and parameterise, may not scale well computationally, and may not be readily extensible to other pests.

The APPDIS modelling framework attempts to find a pragmatic

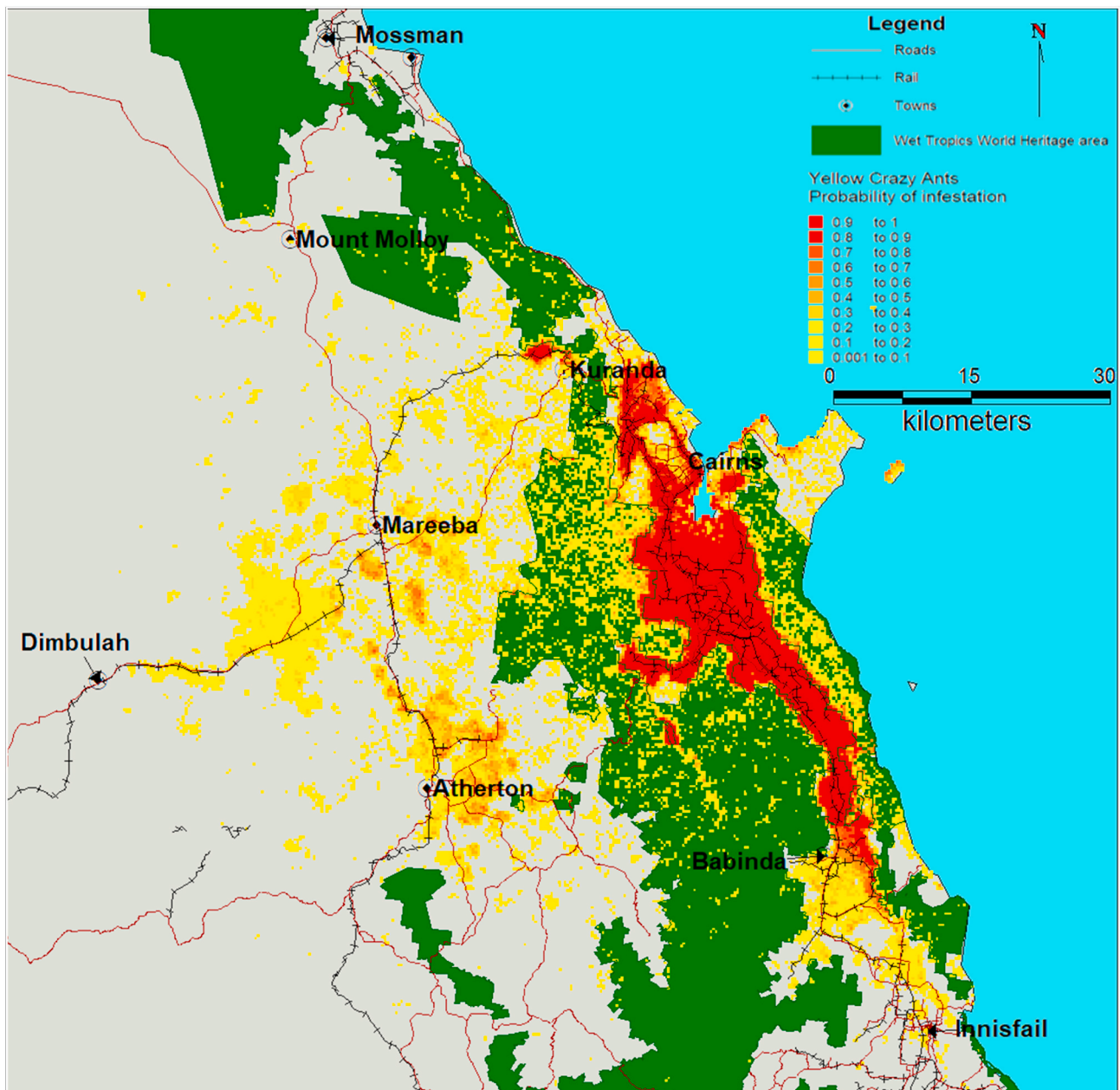


Fig. 7. Projected yellow crazy ant distribution after 30 years of uncontrolled spread.

Table 8
Average effect of delimiting surveillance trap spacing on control effectiveness and cost.

Trap spacing (metres)	Outbreak length (days)	Delimiting surveillance cost (A \$ million)	Treatment cost (A\$ million)	Post-treatment surveillance cost (A \$ million)	Total cost of control convergence	Delimiting surveillance false negatives	Reduction in infested cells	Average model runtime per iteration (secs)
2	4113	504.64	0.27	6.34	0.50%	0.58	99.25%	64.25
5	4182	80.54	0.26	6.35	0.27%	7.59	99.50%	45.98
8	4227	31.65	0.27	6.46	0.45%	17.90	99.14%	44.2
10	4281	20.31	0.27	6.51	0.31%	23.28	99.16%	54.73
15	4255	9.05	0.27	6.68	0.26%	34.59	99.20%	56.23
20	4354	5.10	0.27	6.79	0.26%	45.29	99.12%	51.91
30	4431	2.28	0.27	6.99	0.24%	61.73	99.07%	52.75
40	4469	1.28	0.27	7.09	0.23%	75.37	98.99%	58.46
50	4471	0.82	0.27	7.14	0.24%	86.22	99.13%	72.05
60	4490	0.57	0.27	7.21	0.26%	95.89	98.84%	66.25
70	4455	0.41	0.27	7.21	0.24%	103.26	99.13%	71.67
80	4474	0.31	0.27	7.22	0.26%	110.18	98.85%	70.91
90	4508	0.25	0.27	7.22	0.25%	115.87	99.03%	68.00
100	4434	0.19	0.27	7.22	0.24%	120.49	99.16%	69.59

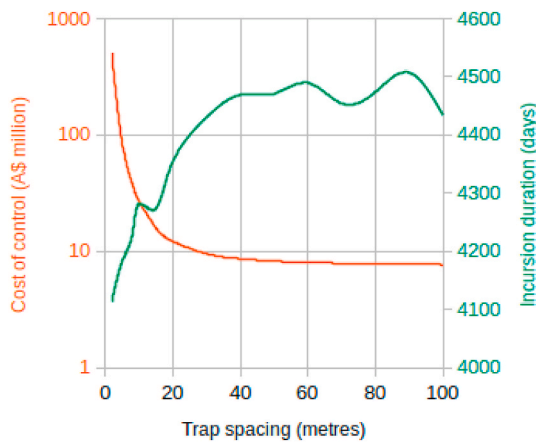


Fig. 8. Effect of delimiting surveillance trap spacing on incursion duration and control cost.

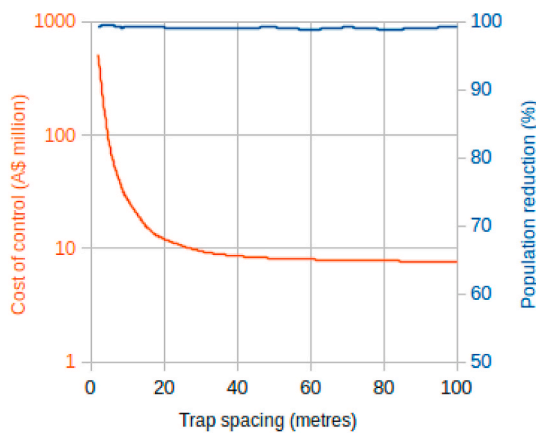


Fig. 9. Effect of delimiting surveillance trap spacing on control effectiveness and cost.

middle ground between the biological and ecological fidelity of a complex pest-specific spatial model, and the extensibility of a generalised mathematical model. APPDIS is flexible in that a user can configure either simple or complex spread models. In studies where field data is scarce or unreliable, a simple mathematical spread model is obtained by disabling the environmental data layers and configuring an aggregative diffusion kernel based on predicted spread rates. A complex spread model can be achieved by enabling environmental data layers and

configuring individual spread pathways that consider heterogeneities in elevation, temperature, wind speed, vegetation, land use, human population density, etc.

Once a model is spreading a pest in a way that is congruent with available field data and expert opinion, a decision support tool should allow useful experimentation with surveillance and control strategies. A further design tension exists between implementing detailed pest specific detection/control options that may not be readily extensible to

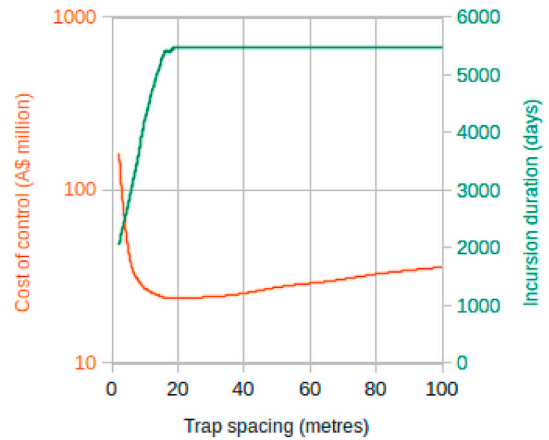


Fig. 10. Effect of post-treatment surveillance trap spacing on incursion duration and control cost.

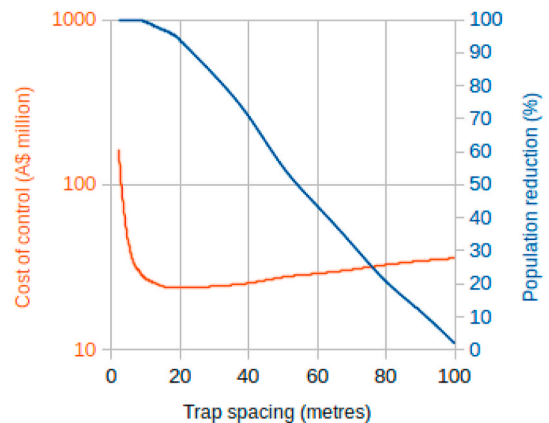


Fig. 11. Effect of post-treatment surveillance trap spacing on control effectiveness and cost.

Table 9

Average effect of post-treatment surveillance trap spacing on control effectiveness and cost.

Trap spacing (metres)	Outbreak length (days)	Delimiting surveillance cost (A\$ million)	Treatment cost (A\$ million)	Post-treatment surveillance cost (A\$ million)	Total cost of control convergence	Post-treatment surveillance false negatives	Reduction in infested cells	Average model runtime per iteration (secs)
2	2049	20.07	0.26	143.39	0.10%	0.05	99.99%	28.04
5	2796	20.10	0.26	23.57	0.14%	10.29	99.90%	34.37
8	3611	20.18	0.26	9.74	0.21%	31.56	99.64%	40.74
10	4233	20.27	0.27	6.51	0.25%	48.59	99.31%	49.00
15	5262	20.73	0.27	3.24	0.46%	97.29	96.95%	60.69
20	5470	21.36	0.27	2.03	0.60%	151.01	93.78%	58.94
30	5475	22.87	0.28	1.09	0.73%	269.86	83.12%	74.41
40	5475	24.37	0.29	0.69	0.86%	378.37	70.68%	94.89
50	5475	26.72	0.31	0.49	0.92%	481.37	55.37%	109.78
60	5475	28.30	0.32	0.36	1.07%	566.74	43.54%	117.59
70	5475	29.99	0.33	0.28	1.33%	650.54	32.11%	123.97
80	5475	32.17	0.34	0.22	1.51%	718.66	20.69%	131.17
90	5475	33.92	0.36	0.19	1.66%	780.78	11.66%	136.57
100	5475	35.36	0.37	0.15	1.48%	836.07	1.87%	141.75

other pests and/or jurisdictions, and implementing generalised detection/control options that may not be detailed enough for the pest under study. Again, APPDIS attempts to find a pragmatic middle ground by providing detection/control options that are detailed enough to be useful yet abstract enough to extend to a range of pests. Surveillance and treatment regimes are configurable by the user in generalised terms such as duration, cost, resource requirements, efficacy, sensitivity, and specificity. As the underlying pest spread mechanisms are stochastic, a control policy can be trialed against a distribution of plausible incursions. In this way, despite inherent uncertainty in how an exotic pest population may spread, confidence can be gained as to the likelihood of a particular policy to achieve the desired control/eradication outcome.

Configuring an APPDIS model for a pest (or pest group) requires personnel versed in pest ecology, plant health policy, and the APPDIS modelling platform (including the assembly of supporting data, parameterisation, designing and running incursion scenarios, and statistical interpretation of simulation results). The configuration effort required when employing disaggregated (data-driven) spread pathways is considerably more than that required for aggregative mathematical pathways. An advantage of a disaggregated approach to modelling spread (by simulating each spread pathway separately), is that control measures can be applied to specific spread pathways. For example, consider a pest that spreads through a windborne pathway and a market-driven pathway. With a disaggregated modelling approach, it is easy to test the effect of movement restrictions on the market-driven pathway whilst still allowing the airborne pathway to spread the pest. This is more difficult when all spread pathways are aggregated into a single mathematical spread mechanism.

A disadvantage of grid-based modelling approaches is that point-based agricultural entities such as orchards, nurseries and markets are not represented. It would be possible to extend APPDIS to include point-based entities and directed spread pathways (as is the case with the AADIS framework), however this would require further development of the framework and consultation with domain experts to ensure that entities and networks are captured in an abstract way that extends to as many pest species as possible.

Whilst models can assist with preparedness and planning for incursions and in some cases response, they can suffer silently from poor assumptions, sub-standard data, inadequate validation, and improper use. Flawed models have the potential to mislead rather than inform, particularly when modelling outputs are detailed and appear definitive. APPDIS is primarily a data-driven model and as such, relies heavily on the quality of the underlying data and parameterisation. Each instantiation of APPDIS for a new pest species (or pest species group), will require a separate validation process that fosters user trust in the model assumptions, data, parameterisation, and capabilities. APPDIS models are best suited to relative comparisons between control and resourcing strategies, rather than predicting incursion outcomes in absolute terms.

4.4. Conclusions

APPDIS is a general-purpose plant and environmental pest modelling framework that is extensible (not tied to a specific pest), scalable (operable regionally and nationally), and flexible (offering simple equation-based spread pathways or complex data-driven pathways that capture heterogeneity in the host environment). APPDIS allows relative comparisons of strategies for early detection surveillance, delimiting surveillance, treatment, and post-treatment surveillance, with respect to efficacy, resource usage and cost. The case study has demonstrated the potential for APPDIS to assist with decision support for both plant pests and environmental pests. Importantly, APPDIS is extensible to a range of pests via user configurable parameters (i.e., without the need for specialised mathematical reformulation and/or computer programming).

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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