1 INTRODUCTION

This thesis presents the Australian Animal DISease (AADIS) model - a new disease modelling approach to support emergency livestock disease preparedness and planning in Australia. Although the AADIS model architecture supports any pathogen, foot-and mouth disease (FMD) is the test case owing to its international importance, complex epidemiology and economic significance to Australia.

1.1 The importance of emergency disease in livestock

Agriculture is an important aspect of the Australian economy and directly accounts for approximately 3% of GDP. The annual gross value of farm production is $53.36 billion AUD with livestock and livestock products amounting to $23.22 billion AUD. Annual exports of livestock and livestock products are valued at $18.33 billion AUD, of which $15.40 billion AUD is attributable to the major livestock industries of cattle, sheep and pigs (Australian Bureau of Agricultural and Resource Economics and Sciences, 2014).

An emergency animal disease (EAD) is a disease with the potential to severely impact trade, livestock production, the environment, or human health (Department of Primary Industries, 2014). Australia is free of most EADs, including, FMD, sheep and goat pox, Rift Valley fever (RVF), African swine fever (ASF), classical swine fever (CSF), rabies, screw-worm fly and transmissible spongiform encephalopathy. An epidemic of an EAD in a livestock population would have serious economic and social impacts.

A particularly important EAD is FMD, a highly contagious viral disease of cloven-hoofed animals including cattle, sheep, pigs and goats. An outbreak of FMD in an FMD-free country triggers loss of access to international markets for livestock and livestock products (Matthews, 2011). This would have serious consequences for a country such as Australia where exports account for approximately 60% of the gross value of livestock production (Australian Bureau of Agricultural and Resource

Economics and Sciences, 2014). Domestic markets would be greatly weakened from excess supply, and potential consumer resistance to livestock and livestock products in the face of an FMD outbreak. A range of industries including livestock, livestock products and genetic material would experience severe production and income losses. The present value of total direct economic losses from an outbreak of FMD in Australia was recently estimated at up to $52.2 billion AUD over 10 years, depending on the size of the outbreak and the effectiveness of control (Buetre et al., 2013). This figure includes export losses and the costs of controlling and eradicating the disease (for example, quarantining of infected premises, culling and disposal of affected livestock, decontamination of premises, and vaccination supplies).

A large outbreak of FMD would also have a considerable indirect impact on support industries such as livestock services, supplies and transportation, flow-on industries such as wool and leather processing, and tourism (Rich, 2005; Buetre et al., 2013). For example, the 2001 outbreak of FMD in the UK impacted the tourism industry by £2.7 to £3.2 billion, approximately equivalent to the impact of the outbreak on the agriculture and food chain industries (Thompson et al., 2002). It is estimated that previously FMD-free countries suffered losses of around $25 billion USD (in 2011 US dollars), from incursions over the last 15 years (Knight-Jones and Rushton, 2013). Examples include the 2010-11 outbreak in South Korea with an impact of $2.87 billion USD and the 2010 outbreak in Japan with an impact of $568 million USD (in 2011 US dollars) (Knight-Jones and Rushton, 2013). The 2000-02 outbreak of FMD in Argentina affected 2519 herds (Perez et al., 2004), and had an economic impact of between $1.6 billion USD and 2.1 billion USD (Gallacher, 2007). The 2001 outbreak of FMD in Uruguay affected 2057 farms and had a total economic impact of $243.6 million USD (Spickler et al., 2010).

Due to the serious economic impact and highly contagious nature of FMD, a control program in an FMD-free country is aimed at containing and eradicating the disease as quickly as possible. Generally this is based on the 'stamping out' of infection through

culling of infected and exposed animals, disposal of carcasses, and decontamination of infected premises and materials, in conjunction with the establishment of controlled areas to restrict movements of livestock and livestock products. Other control measures may include surveillance, tracing the movements of livestock and livestock products, and vaccination (OIE, 2012; OIE, 2013). A large outbreak of FMD can require a control program on a massive scale, for example, during the 2001 UK FMD outbreak, 6,456,000 sheep, cattle and pigs were destroyed for disease control and welfare purposes (Anderson, 2002) (Figure 1.1). The tally is conservative as it excludes still-suckling animals, and may even be as high as 10 million (Campbell and Lee, 2003; Kitching et al., 2006). To put these numbers into perspective, the 2000 UK agricultural census reports a total population of 55 million sheep, cattle and pigs (Bourn, 2002). The culling and disposal of such vast numbers of animals created major logistical problems, and raised concerns on the environmental impact of large-scale funeral pyres and burial pits (Scudamore et al., 2002; Hickman and Hughes, 2002). Other examples of the potential scale of an FMD control program are the 2010-11 outbreak in Korea where 3.47 million animals were culled, and the 1997 outbreak in Taiwan where 4 million animals were culled (Knight-Jones and Rushton, 2013).

Figure 1.1. Funeral pyres during the 2001 UK FMD outbreak (MacLeod, 2001)

Those involved in FMD control operations such as disease managers, veterinarians, culling teams, disposal teams and police, are subject to considerable mental health stresses from the intensive and disturbing nature of the work (Productivity Commission, 2002; Convery et al., 2007). Of the 10,157 premises on which culling occurred in the UK in 2001, only 2026 were confirmed infected premises. The remaining 8,131 premises (4,762 dangerous contact premises and 3,369 contiguous premises), were culled pre-emptively (Anderson, 2002). The policy of pre-emptive culling places operational personnel in the highly distressing situation of potentially destroying large numbers of animals that otherwise might have remained healthy (Productivity Commission, 2002; Whiting and Marion, 2011).

Figure 1.2. Quarantined premises during the 2001 UK FMD outbreak (MacLeod, 2001)

Approximately 312,800 people are directly employed in the Australian rural sector (Australian Bureau of Agricultural and Resource Economics and Sciences, 2014). An outbreak of FMD would have severe social impacts on owners and workers in the affected livestock industries. Major psychosocial stresses can arise from the isolation of quarantine (Figure 1.2), marginalisation of owning/working on infected premises, loss of self-determination and trauma from the imposition of culling, loss of livelihood, and uncertainty about the future (Productivity Commission, 2002; Van

Haaften et al., 2004; Peck, 2005; Mort et al., 2005; Olff et al., 2005; Cohen et al., 2007). Farmers impacted by an FMD outbreak and personnel involved in the control program may experience trauma during the outbreak, as well as ongoing post-traumatic stress after the outbreak (Olff et al., 2005; Convery et al., 2007).

1.2 Modelling to inform animal health policy and disease planning

Disease managers are faced with a variety of challenges when responding to an outbreak of exotic disease. These include: what control measures to adopt; trade and economic implications of control measures; management of finite resources such as personnel, equipment and vaccine; animal welfare issues; potential risks to public health; and consumer concerns (Garner et al., 2007; Buetre et al., 2013). The control program for an epidemic can be a compromise between the need for a large-scale implementation and what is logistically and economically feasible (Morris et al., 2002; Tildesley et al., 2006). It is a complex task to efficiently contain a highly contagious disease whilst minimising the impact of the control program on non-infected areas, the environment, export markets, and society in general (Scudamore and Harris, 2002; Buetre et al., 2013).

Epidemics can be difficult to study empirically, particularly if a pathogen is dangerous, rare, or not present in a country. FMD, for example, was last suspected (on clinical grounds), in Australia in 1872 (Bunn et al., 1998). During a disease response, animal health personnel are largely restricted to enacting established policies that leave little scope for the trialing of new control strategies (Animal Health Australia, 2014a). Disease models are increasingly being employed as decision support tools to inform planning and policy development for exotic animal diseases (Bates et al., 2003a; Dubé et al., 2007a; Garner et al., 2007; Garner and Hamilton, 2011). An epidemiological model provides a safe and low-cost means of studying the potential spread of disease and the cost-benefit of control measures (Miller, 1976). A model is useful for conducting 'what-if scenarios', for example: the influence of early/late detection on outbreak severity (Ward et al., 2009); the augmentation of a stamping out control policy with suppressive ring vaccination (Hagerman et al., 2012); the benefits

of rapid effective tracing of livestock movements in the event of an outbreak (Hagerman et al., 2013); and the impact of human resourcing levels on the effectiveness of a control program (Roche et al., 2014). Models can also be used to inform risk analysis on the introduction and establishment of disease (East et al., 2013); assess the economic impact of disease outbreaks and control programs (Garner and Lack, 1995; Abdalla et al., 2002; Buetre et al., 2013); study the role of wild and feral animals in livestock epidemiology (Pech and Hone, 1988; Doran and Laffan, 2005; Ward et al., 2015); and assist in the training of disease managers (Taylor, 2003).

Models can be used retrospectively or prospectively (Woolhouse, 2004). A retrospective model is 'fitted' to data from past outbreaks, and used to better understand that particular outbreak's dynamics (Taylor, 2003). For example, alternative control strategies can be trialed to determine whether the historical outcome could have been improved upon (Keeling et al., 2001; Mangen et al., 2001). A prospective model is typically used to explore hypothetical outbreak scenarios, for example, as part of animal health policy development (Garner et al., 2007; Roche et al., 2014).

Due to the serious economic and social consequences of emergency diseases like FMD, Australia invests considerable time and resources in prevention and contingency planning (Animal Health Australia, 2014b). Models of disease spread and control are increasingly recognised as cost-effective and informative tools to support policy development and EAD planning.

1.3 Modelling FMD in Australia

AusSpread is a regional-based model of FMD spread and control developed by the Australian Government Department of Agriculture and Water Resources to assist with EAD planning (Garner, 2004; Garner and Beckett, 2005; Beckett and Garner 2007). AusSpread is based on the MapBasic/MapInfo geographic information system (GIS) platform (Pitney Bowes, 2014), which allows spatially explicit representation of

entities such as farms, saleyards, weather stations, local government areas and states. Seven farm types are defined (specialist beef, dairy, sheep, pig, mixed beef-sheep, smallholders and feedlots), with also the option of user-defined farm types. The transmission of disease between farms is simulated through discrete spread 'pathways'. Control measures are implemented per Australia's emergency animal disease response policy – the Australian Veterinary Emergency Plan (AUSVETPLAN) (Section 2.3), and can be customised to facilitate a range of what-if scenarios. AusSpread has been used in a variety of FMD studies including: airborne spread (Gloster et al., 2010), the potential economic impact of an FMD epidemic (Buetre et al., 2013), the impact of resource constraints on the efficacy of an FMD control program (Roche et al., 2014; Garner et al., 2014), animal welfare implications of an FMD control program (East et al., 2014b), and evaluation of vaccination strategies (Roche et al., 2015). Although operating within a GIS environment provides considerable advantages in terms of model development and visualisation, runtime computational constraints effectively limit AusSpread's practical use to studying disease at a regional level.

A national-scale FMD model is needed to study the consequences of inter-region livestock movements while taking into account regional differences in environment, livestock production and marketing systems. Disease control in Australia is managed by individual states and territories according to agreed policies and guidelines (Animal Health Australia, 2014a). A national-scale model thus also needs to take into account jurisdictional differences in the implementation of control programs.

1.4 Aims of the PhD project

The goal of the PhD project is to develop the Australian Department of Agriculture and Water Resources' next-generation epidemiological model of national-scale, using FMD as the test case disease. To support EAD planning and response, a disease model needs to be able to represent the host population, and the spread and control of disease across the environment. The aims of the project are identified below.

The unit of interest for an epidemiological model can be the animal, the herd (a same-species group of animals managed as a distinct unit), or the farm (premises that contain one or more herds). The choice of modelling unit of interest is a trade-off between the desired modelling granularity, availability of data, and computational overhead.

> ***Aim 1**: Determine the most appropriate modelling unit of interest for an FMD model of national scale.*

FMD can spread through a number of mechanisms including movement of infected animals (Green et al., 2006); contact with contaminated material, products and equipment (Bates et al., 2001); and under appropriate conditions, viral plumes (Donaldson et al., 2001).

> ***Aim 2**: Model the transmission of disease between herds/farms across spread pathways appropriate to FMD.*

The transmission of FMD is a multi-scale process in that the spread of disease within a herd/farm proceeds under different circumstances and rates to the spread of disease between herds/farms (Carpenter et al., 2003; Kitching et al., 2006; Balcan et al., 2010).

> ***Aim 3**: Capture the multi-scale nature of the spread of FMD by considering both within-herd/farm and between-herd/farm spread mechanisms.*

Australia is a large country with diverse livestock production systems, marketing systems, geography and climate, all of which potentially influence the spread of FMD (Animal Health Australia 2014b).

> ***Aim 4**: Capture heterogeneities of species, environment, region, production systems and marketing systems that influence the spread of FMD.*

While national policy for the control and eradication of FMD is outlined in AUSVETPLAN (Animal Health Australia, 2014a), Australia is a federation and disease control is implemented under individual state/territory legislation.

> *__Aim 5__: Model all key control measures used in the control and eradication of FMD in Australia, taking into account jurisdictional heterogeneities in both policy implementation and resourcing.*

Epidemiological models of large populations can be computationally intensive and may require custom software implementations (Parker and Epstein, 2011), and highly parallel platforms such as high-performance computing clusters (Germann et al., 2006). The target hardware for the PhD project is, however, limited to a standard desktop computer. Also, the software must be standalone (i.e., not reliant on external servers and services).

> *__Aim 6__: The model is computationally efficient such that national-scale simulations of FMD spread and control can be conducted on a standard desktop computer.*

An important role of epidemiological models is to explore hypothetical outbreak scenarios, for example, as part of animal health policy development (Kao, 2002; Garner et al., 2007). Accordingly, a model should be flexible and user-configurable.

> *__Aim 7__: The model has a high level of configurability so that a range of what-if scenarios can be conducted on the spread and control of FMD.*

Although the test case disease for AADIS is FMD, other livestock diseases are to be modelled in the future. The model should have the ability to incorporate a range of data sources such as weather, vegetation and feral animal ranges.

> *__Aim 8__: The model has an extensible model architecture and software architecture.*

It is vital that epidemiological models are carefully validated as fit for purpose (Taylor, 2003). A model that is not properly verified and validated is nothing more than 'an exercise in mathematical sophistry' (Kitching et al., 2006). Expected users of the AADIS model may include animal health policy officers, disease managers and veterinary epidemiologists from both the public and private sectors.

> ***Aim 9**: **Users have confidence that the model is fit for the purpose of supporting the development of animal health policy.***

There are a range of FMD models already described in the scientific literature. The project will review and draw upon existing work while seeking innovative ways to improve performance and functionality.

> ***Aim 10**: **The project produces an epidemiological model that advances the field of computational science in the context of veterinary epidemiology.***

1.5 Thesis outline

- Chapter 1 introduces the AADIS project by explaining the motivation for modelling the spread and control of emergency disease in livestock, and the nature and significance of foot-and-mouth disease in Australia. The aims for the project are stated.

- Chapter 2 provides background information on FMD, livestock production systems in Australia and how EADs are managed in Australia. Population-based and individual-based epidemiological modelling approaches are reviewed in order to provide context for the AADIS hybrid modelling approach.

- Chapter 3 describes the AADIS hybrid model architecture and the underlying epidemiology, algorithms and formulae for each disease spread pathway and control measure.

- Chapter 4 provides an overview of the AADIS software architecture and some implementation highlights. Examples of the user interface are provided to illustrate the capabilities of the model.

- Chapter 5 describes the verification and validation of AADIS. Testing of the grid-based spatial-indexing system is used as an example of verification. Validation activities include cross-model comparisons with the well-published AusSpread and InterSpread Plus models, a parameter sensitivity analysis, and an independent assessment of AADIS by the University of Melbourne.

- Chapter 6 presents three small case studies. Firstly, AADIS is used to assess the benefits of augmenting a stamping out control policy with suppressive ring vaccination. Secondly, an analysis of the number of runs required for model outcomes to converge is conducted. Thirdly, model performance is compared between a regional-scale simulation and a national-scale simulation.

- Chapters 7 and 8 discuss findings and draw conclusions. The aims of the PhD project are re-examined to assess if they have been met.

- The appendices contain a glossary of acronyms, the relational database schema, summaries of the model input and output files, and the University of Melbourne report.

2 REVIEW OF FMD EPIDEMIOLOGY AND MODELLING APPROACHES

2.1 Aetiology and epidemiology of FMD

FMD is an acute, extremely contagious viral disease of domestic and wild cloven-hoofed animals, including cattle, sheep, goats, swine, deer, Bactrian camel, buffalo, bison, moose and antelope. The FMD virus (FMDV) is a member of the *Picornaviridae* family of RNA viruses and has seven serotypes: A, O, C, Asia 1, and South African Territories (SAT) 1, 2 and 3. Each FMDV serotype exhibits a wide variety of antigenic characteristics which adds complexity to diagnosis, and the development and availability of vaccines (Grubman and Baxt, 2004; Merck, 2012).

FMD is clinically characterised by fever and the formation of vesicles and erosions in the mouth and nostrils, on the teats, and on the skin between and above the hoofs (Meyer and Knudsen, 2001; Donaldson, 2004). The manifestation of the disease varies between species, for example, sheep typically exhibit mild clinical signs that can be difficult to detect and may be mistaken for less serious conditions (Grubman and Baxt, 2004). FMD does not typically kill adult animals although mortality rates in young animals can be very high. Infected animals become debilitated with loss of appetite, weight loss, lameness, weakness and significantly reduced milk yield (Animal Health Australia, 2014a). FMDV replicates in the nasopharynx, and epithelium of the tongue, nose, muzzle, and coronary bands. Infectious animals release virus in exhaled air, vesicular fluid, saliva, milk, sweat, semen, faeces and urine (Meyer and Knudsen, 2001). The concentration of viral particles in exhaled air is species dependent, for example, pigs can shed over a thousand times more viral particles from the respiratory tract than cattle (Donaldson and Alexandersen, 2002).

Transmission of FMD generally occurs through direct contact between infected and susceptible animals (Kitching, 2011). A susceptible animal can become infected via inhalation, ingestion, artificial or natural breeding, and through skin abrasions and mucous membranes (Grubman and Baxt, 2004). The incubation period varies with host species, dose of virus, strain, and route of infection. An infected preclinical animal can shed large amounts of virus, for example, the milk from an infected cow can contain virus up to four days before the onset of clinical signs (Animal Health Australia, 2014a). This is epidemiologically significant as infectious animals may be unwittingly moved and/or sold. Infected animals tend to stop shedding virus within six days of the appearance of vesicles (Animal Health Australia, 2014a).

FMDV can survive for long periods outside a host cell, for example, up to 50 days in water, up to 74 days on pasture, up to 90 days in faeces, and up to 200 days in soil. Viable virus has been recovered from milk and butter for up to 45 days, from bacon for up to 190 days, and from bovine semen stored at -50ºC for 320 days (Animal Health Australia, 2014a; Center for Food Security and Public Health, 2014). FMD thus poses a serious threat of indirect spread through animal products, by-products, fomites and vectors.

Under favourable climactic conditions aerosolised FMDV can travel substantial distances. The extent of an aerosol plume depends on the concentration of the viral source, the virus strain, whether the plume is over land or water, wind speed and stability, relative humidity and temperature (Donaldson and Alexandersen, 2002; Animal Health Australia, 2014a). Although it is suspected that in 1981 FMDV was conveyed over 250 km from France to the UK, it is generally accepted that airborne spread poses a risk over land at shorter distances of up to say 20 km (Gloster et al., 2006; Schley et al., 2009).

Whilst Australia has been free of FMD since 1872 (Bunn et al., 1998), it is endemic in approximately 50 countries across Africa, the Middle East, Asia and South America (Kitching, 2011) (Figure 2.1).

Figure 2.1. Conjectured world status of FMD (Kitching, 2011)
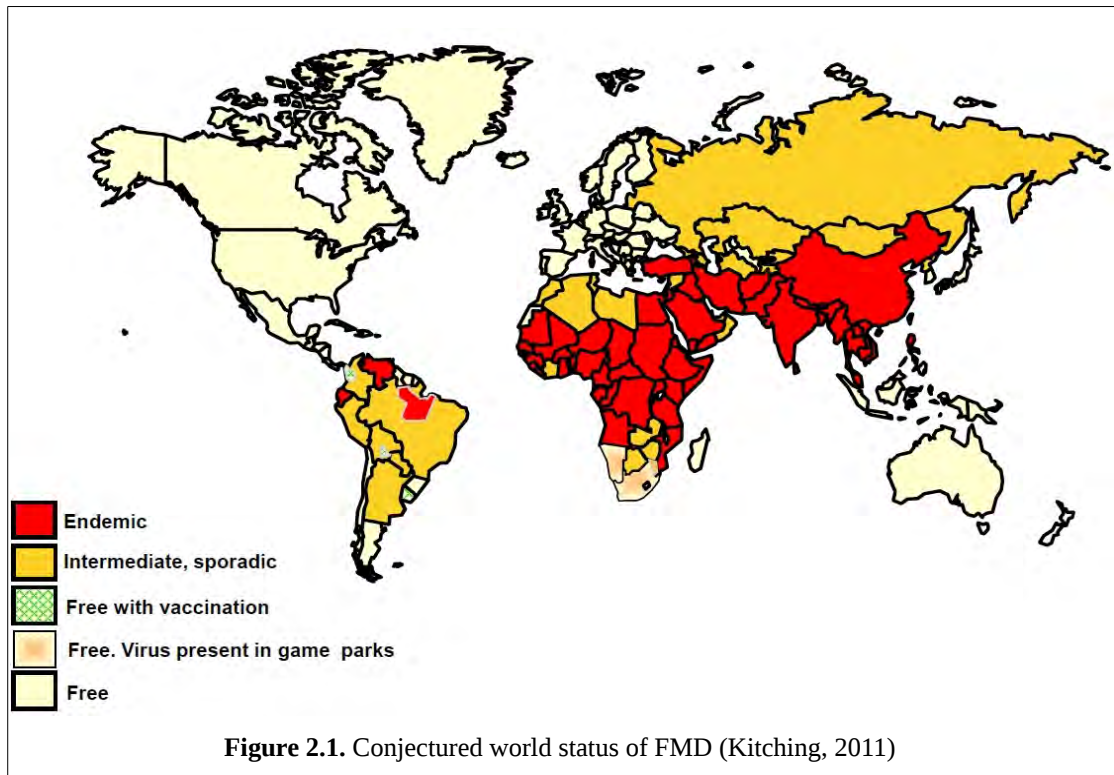
FMD is one of the most infectious diseases known (Grubman and Baxt, 2004; Rushton et al., 2012), with the basic reproduction number R_0 (the expected number of new infections arising from one infected animal in a fully susceptible population), estimated as high as 70 (Woolhouse et al., 1996), and high morbidity rates in susceptible populations (Geering et al., 1995). Live FMDV is strictly regulated in FMD-free countries such as Australia and the USA. For example, research involving live FMDV is not permitted in Australia (Jeggo and Griffiths, 2010), and is only allowed in the USA in the high-security Plum Island Animal Disease Center (Department of Homeland Security, 2015).

The epidemiology of FMD is complex as the virus is highly contagious, multi-serotype, multi-host and can spread via multiple pathways. FMD is the most

significant threat to the Australian livestock sector due to its economic importance and presence in regional neighbours (Matthews, 2001; Animal Health Australia, 2014a).

2.2 Australian livestock production systems

Livestock production in Australia is largely based on extensive grazing of cattle and sheep, with smaller intensive poultry, pig, fisheries and aquaculture industries (Australian Bureau of Statistics, 2014; Australian Bureau of Agricultural and Resource Economics and Sciences, 2014). The beef cattle industry also has intensive lotfeeding and finishing components (Meat and Livestock Australia, 2014c). The main industries vulnerable to an FMD outbreak are beef, dairy, wool, sheepmeat, and pigs. Australia has approximately 76 million sheep, 29 million cattle and 2 million pigs on approximately 78,000 commercial farms (Australian Bureau of Statistics, 2014). Commercial farms in Australia vary greatly in size, ranging from, for example, small piggeries in the intensively farmed Goulburn Valley (Regional Development Victoria, 2010), up to extensive cattle stations such as the 23,677 km^2 Anna Creek Station in remote outback South Australia (Kidman, 2015). Farms may consist of more than one herd of the same or different species, for example, mixed beef-sheep farms.

The 'smallholder' category of premises includes hobby/lifestyle farms and farms where the primary activity is unrelated to livestock. A typical smallholder has under 50 animals of mixed species on a small acreage of under 20 hectares (Department of Primary Industries, 2006; Hernández-Jover et al., 2014). Unlike commercial farming enterprises, there is far less data available on small holdings of livestock. It is estimated that there are over 100,000 smallholder premises in Australia (Roche, 2013), with the majority occupying peri-urban regions (Aslin et al., 2004; Department of Primary Industries, 2006).

The Australian livestock industry is geographically diverse and spread across temperate regions in the south-west and south-east, desert and grassland regions in the centre, subtropical regions in the north-east, and tropical regions in the north. For the

purposes of studying disease outbreaks and assessing control measures, it is convenient to partition Australia into reasonably homogeneous regions on the basis of geography, environment, livestock production and marketing practices. The regions provide a useful framework for the spatiotemporal characterisation of livestock movements. The 12 beef production regions (AusVet Animal Health Services, 2006) are provided as an example in Figure 2.2.

Figure 2.2. Australian beef regions (Department of Agriculture and Water Resources, 2015)
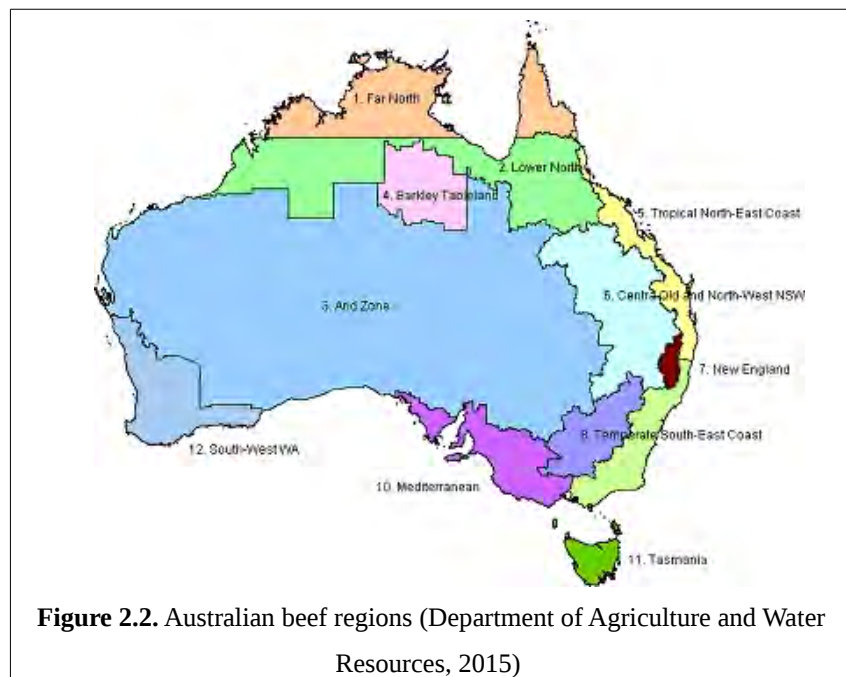
There is considerable heterogeneity in the movement patterns of Australian livestock. Sheep movements typically occur within 200km of the home premises but may range up to 500km for stud animals (Hassall and Associates, 2006). Beef cattle in the high-density eastern and south-eastern regions tend to undergo high frequency and short distance movements (Durr et al., 2010). Beef cattle in the low density central and northern regions tend to undergo low frequency and long distance movements, ranging up to over 3000 km between Queensland and the Northern Territory (AusVet Animal Health Services, 2006).

Livestock movements can facilitate the rapid spread of infectious disease, especially early in an outbreak prior to detection (Gibbens et al., 2001). The rapid escalation of

the 2001 UK FMD outbreak is attributed to movements of infected sheep to and from markets prior to the establishment of movement controls (Ferguson et al., 2001; Kao, 2002; Mansley et al., 2003; Mansley et al., 2011). Routine long distance movements from home premises to places of finishing and/or slaughter are of epidemiological interest as preclinical infectious animals can potentially develop expansive contact networks. The broad range of movement patterns in the Australian livestock industries contrasts to those in countries such as Denmark and the Netherlands where livestock industries are generally based on small farms, intensive production systems, and short-range livestock movements (Bigras-Poulin et al., 2006; Backer et al., 2012a).

2.3 Management of emergency animal disease in Australia

Australia is a federation made up of six states and two mainland territories. The Australian Government is responsible for quarantine, disease reporting, export certification and international trade. State and territory governments are responsible for animal health services within their respective jurisdictions. This means that while there are national policies for managing notifiable diseases such as FMD, the actual control measures are administered by the jurisdictions under their own legislation (Animal Health Australia, 2014b). The Emergency Animal Disease Response Agreement (EADRA) defines how the cost of an EAD control program is shared between federal, state and industry stake-holders (Animal Health Australia, 2014d). In the event of an EAD outbreak, all parties must agree on the infected jurisdiction's disease management plans.

Australian policy for the control and eradication of FMD is outlined in AUSVETPLAN (Animal Health Australia, 2014a; Animal Health Australia, 2014c). In brief, the policy is to eradicate the disease as quickly as possible using stamping out, which involves culling and disposal of infected and exposed animals. Upon confirmation of FMD, mandatory control strategies include:

- The establishment of a national livestock standstill that imposes total movement controls on all species susceptible to FMD for a minimum of three days.

- Quarantine and movement controls of animals, animal products and fomites in declared areas in order to minimise the spread of infection. A restricted area (RA) of minimum radius 3km is established around each infected premises (IP) and dangerous contact premises (DCP). An RA imposes the highest levels of surveillance and movement controls. Premises within an RA that have not yet been formally assessed are termed at-risk premises (ARPs). A control area (CA) of minimum radius 10km is also established around each IP and DCP. A CA is intended to be a disease-free buffer between the (known-to-be infected) RAs and (the believed to be uninfected) areas outside the controlled areas. A CA imposes lower levels of surveillance and movement controls than an RA. Premises within a CA and outside an RA that have not yet been formally assessed are termed premises of relevance (PORs). The area outside the RAs and CAs is not a declared area and is referred to as the outside area (OA). Premises in the OA are still subject to surveillance and movement restrictions.

- Tracing and surveillance to determine the source and extent of infection. A trace premises (TP) is a temporary classification for a premises that has been identified through tracing has having been potentially exposed to FMDV, and is awaiting surveillance. A suspect premises (SP) is a temporary classification for a premises that has been reported as containing susceptible animal(s) that are exhibiting clinical signs consistent with FMD, and is awaiting surveillance.

- Valuation and destruction of animals on IPs and potentially on DCPs.

- Disposal of destroyed animals and infected animal products, and decontamination of depopulated premises. An IP is re-classified as a resolved premises (RP) when all IP operations have been completed.

Optional control strategies include:

- Vaccination to reduce susceptibility of animals to infection and clinical disease, and potentially reduce virus excretion. A farm on which vaccination has been completed is referred to as a vaccinated premises (VP).

- Pre-emptive destruction of susceptible animals in order to minimise the spread of infection.

- Zoning and/or compartmentalisation (to support trade).

- Risk-based movement controls.

Refer to Animal Health Australia (2014a and 2014c), for further details of the Australian policy for the control and eradication of FMD.

2.4 Approaches to modelling the spread and control of disease

Models of disease spread can be distinguished on the basis of how they handle time (discrete/continuous), space (spatially-explicit/non-spatial), and variability, chance and uncertainty (deterministic/stochastic) (Taylor, 2003). However, these criteria do not lend themselves to a taxonomy. For example, a stochastic model may or may not be spatial, and a deterministic model may view time discretely or continuously. Another way of viewing models is whether they are population-based or individual-based. A population-based model is formulated from the top down with population-level relationships that predict individual-level states. Individual-level models are formulated from the bottom-up, whereby population-level relationships emerge organically from the aggregation of individual-level behaviours. Similar distinctions between the top-down mathematical emphasis of population-based approaches and the bottom-up ecological emphasis of individual-based approaches have been made by Fahse and colleagues (1998), Kostova-Vassilevska, (2004) and Grimm and Railsback (2005). A hybrid model combines population-based and individual-based approaches in order to exploit the strengths of both approaches.

The classification of modelling approaches in Figure 2.3 provides context for the AADIS hybrid model architecture and is not intended to be an overarching taxonomy.

Figure 2.3. Modelling approaches for the spread of disease
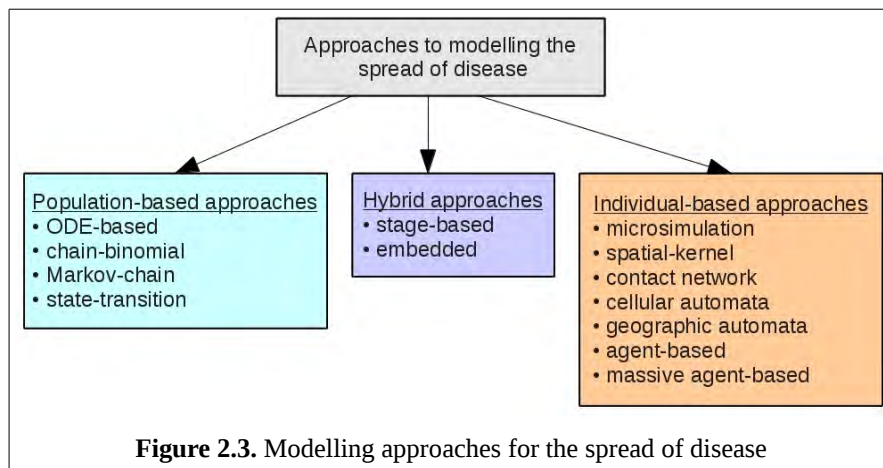
2.4.1 Population-based modelling

A population-based model views a population as homogeneous, i.e., individuals within the population mix uniformly and randomly, and have an equal likelihood of contracting a disease (Hethcote, 2000). Population-level relationships are formulated from the top down (for example, a system of equations), in order to predict individual-level states (such as the proportion of the population that is infected over time).

Earn (2008) provides an interesting introduction to population-based modelling of epidemics by analysing historical data on bubonic plague in 17th century London and measles in 20th century New York. Plague deaths and measles cases are plotted to yield curves that illustrate how an epidemic waxes and wanes over time (Figure 2.4). Earn explores how well the classic Susceptible-Infected-Recovered (SIR) mass-action model (Section 2.4.1.1) fits the empirical data. The goal of mathematical epidemiological modelling is to quantify empirical trends in order to arrive at reusable formulations and principles.
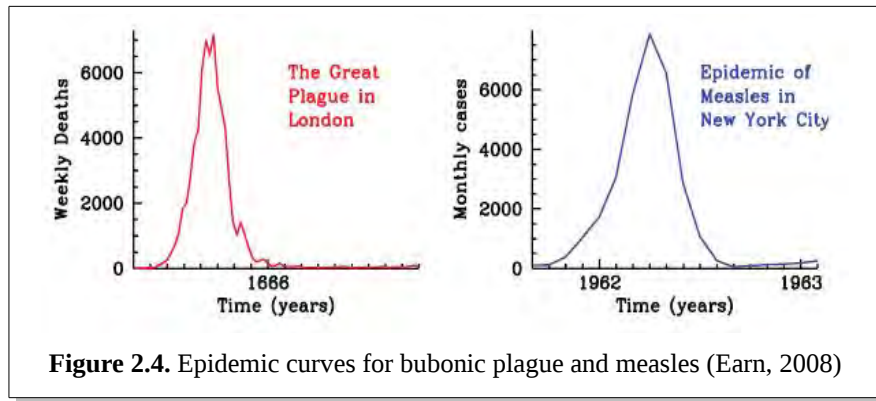
Figure 2.4. Epidemic curves for bubonic plague and measles (Earn, 2008)

Population-based models of disease spread have been in use since at least Bernoulli in the 18th century (Dietz and Heesterbeek, 2002; Blower and Bernoulli, 2004). Seminal contributions from the early 20th century include:

- Hamer's and Soper's observations on the periodicity of measles outbreaks, which led to the understanding of epidemic thresholds and herd immunity (Jacquez, 1987; Fine, 1993; Heesterbeek, 2005),

- Ordinary differential equation (ODE)-based mass-action models by Kermack and McKendrick, and Ross and Hudson (Diekmann et al., 1995; Heesterbeek, 2005; Earn, 2008),

- The Greenwood and Reed-Frost chain-binomial models (Abbey, 1952; Fine, 1977; Jacquez, 1987).

The continuous-time ODE-based SIR mass-action model and the discrete-time Reed-Frost chain-binomial model laid important foundations for subsequent modelling efforts. They are briefly described below to set the scene for the AADIS hybrid approach. Broader coverage of population-based modelling techniques can be found in texts such as Murray (2002) and Keeling and Rohani (2008).

2.4.1.1   ODE-based mass-action models

The genre of mass-action models of disease spread is generally credited to the independent teams of Kermack and McKendrick, and Ross and Hudson (Heesterbeek, 2005). Epidemiological mass-action is analogous to the 'law of mass-action' in

chemical kinetics, where the rate of a chemical reaction between two reactants in a 'well stirred' reaction vessel is proportional to the concentrations of the reactants (Heesterbeek, 2005). The rate of transmission from infectious to susceptible individuals is proportional to the product of the densities of the infectious and susceptible sub-populations (Heesterbeek, 2005). Mass-action epidemiological models assume a homogeneous ('well stirred') population, i.e., the population mixes uniformly and randomly, and individuals have an equal likelihood of contracting a disease (Hethcote, 2000). Mass-action disease transmission is also referred to as frequency-dependent, i.e., the per-capita force of infection is proportional to the 'frequency' of infectious individuals (where frequency is the ratio of infectious individuals to the population size). This implies that the contact rate between infectious and susceptible individuals is constant and thus independent of the population density (Begon et al., 2002). (The alternative is density-dependent transmission where the contact rate is proportional to the population density.)

$$\frac{dS}{dt} = -\beta S I \qquad (2.1)$$

$$\frac{dI}{dt} = \beta S I - \gamma I \quad (2.2)$$

$$\frac{dR}{dt} = \gamma I \qquad (2.3)$$

$where\ S$ = proportion of animals in the herd that are susceptible
I = proportion of animals in the herd that are infected
R = proportion of animals in the herd that are recovered
β = effective contact rate (contact rate $\times$ transmission probability)
γ = recovery rate

Figure 2.5. Simple SIR ODE-system

A classic example of a mass-action equation-based model (EBM) is provided in Figure 2.5. The system of ODEs deterministically and dynamically disaggregates a population into logical, non-spatial compartments (susceptible, infected, and recovered), according to infection state. The expression βSI in Equation 2.1 is referred to as the transmission term as it describes the rate at which susceptible individuals

become infected (Murray, 2002). The ODE system is solved numerically to yield compartment proportions over a solution time interval. (For illustrative purposes, the solution to the related Susceptible-Exposed-Infectious-Recovered (SEIR) ODE-system is provided in Figure 2.6. In this case, the Infected compartment is sub-divided into Exposed and Infectious compartments – this is covered in Section 3.4). A mass-action model describes how the population 'flows' between compartments during an outbreak.

Figure 2.6. Web utility for solving an SEIR ODE system (Nesse, 2012)
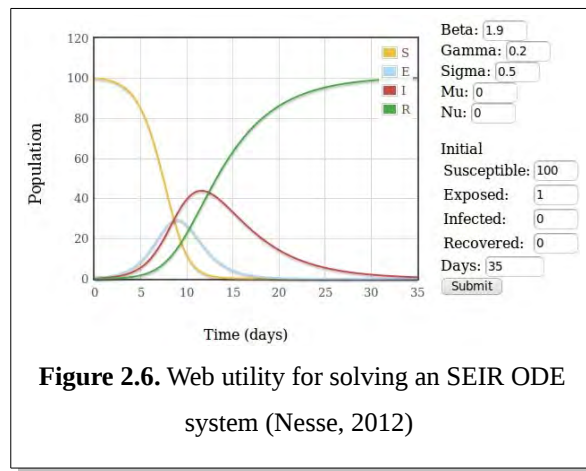
2.4.1.2   Reed-Frost chain-binomial model

The flow of a population between compartments can also be dictated by probabilities derived from sources such as the current epidemic state, livestock movement patterns, historical data and expert opinion (Miller, 1976). The Reed-Frost model (Abbey, 1952), is a discrete-time model where the infection state transitions are governed by probabilities that depend on contact rates and population size (see Figure 2.7).

Consider a closed population of size N with one infectious individual and N-1 susceptible individuals. Let t = the time period for the simulation.
Let k = the number of contacts that the infectious individual has with susceptible individuals per time period.
The probability p that an arbitrary susceptible individual comes into contact with the infected individual in a given time period is given by:

       $p = k / (N-1)$ (2.4)

Let q = the probability that contact does not occur in the given time period.

       $q = 1 - [k / (N-1)]$ (2.5)

Let I_t = the number of infectious individuals in the population at time period t.
Contacts between individuals are independent events. The probability that an arbitrary susceptible individual does not come into contact with any infectious individuals in a given time period t is thus q^{It}.

The probability that an arbitrary susceptible individual does come into contact with an infectious individual in a given time period t is thus $1 - q^{It}$.

Let S_t = the number of susceptible individuals in the population at time period t.
The expected number of new latent cases arising during time period t is thus $S_t [1 - q^{It}]$.
Thus, the number of new latent cases at the conclusion of time period t (i.e., in time period t + 1) is

$$L_{t+1} = S_t [1 - q^{It}] \qquad (2.6)$$

Let D = the mean duration of disease latency expressed in the same units as the time period.
The number of infectious individuals in the population in any given time period t is calculated by summing the set of new latent cases, (i.e., L_t), that have progressed into the infectious state.

$$I_t = \sum_{i=0}^{i=t-D} L_i \qquad (2.7)$$

Equations 2.6 and 2.7 form the Reed-Frost model.

Figure 2.7. Reed-Frost model (Abbey, 1952; Bates et al., 2003a)

Population-based models have been widely used to study a range of animal diseases. Some examples are highly pathogenic avian influenza (HPAI) (Arino et al., 2006; Bavinck et al., 2009; Pandit et al., 2013), CSF (Stegeman et al., 1999), bovine tuberculosis (Perez et al., 2002) and FMD (Miller, 1976; Haydon et al., 1997; Howard and Donnelly, 2000; Ferguson et al., 2001; Kao, 2002; Thornley and France, 2009).

2.4.1.3 Population-based models of FMD

Complex biological/environmental/economic systems are typically multi-scale and non-linear - characteristics that are ill-suited to a simple population-based modelling approach (Baroni and Richiardi, 2007; Bansal et al., 2007; D'Souza et al., 2009; Grassly and Fraser, 2008; Parker and Epstein, 2011; Vincenot et al., 2011). The parameters in a basic compartmental model are fixed over the solution interval. This is not realistic as variables such as weather, biosecurity procedures and resource constraints on the implementation of control, dynamically reshape an outbreak of disease (Donaldson et al., 2001; Caraco et al., 2001; Keeling et al., 2001; Campbell and Lee, 2003; Hagenaars et al., 2004; Galvani and May, 2005; Lloyd-Smith et al.,

2005; Kitching et al., 2006; Bansal et al., 2007; James et al., 2007; Mansley et al., 2011; Garner and Hamilton, 2011).

Miller (1976) provides an example of how a discrete state-transition FMD model can be augmented to better reflect outbreak dynamics. The herd population is disaggregated into four compartments based on infection state: susceptible, infectious, immune and removed. The proportion of the population in each of the four compartments is determined probabilistically in discrete time steps of a week. The probability of a susceptible herd becoming infected during week *n* depends on the number of infected herds in week *n - 1* and the 'dissemination rate', a measure of the average number of herds that an infectious herd comes into contact with. The dissemination rate varies weekly reflecting the dynamic influence of factors such as quarantines, restrictions on the movement of live animals, and increased awareness of the outbreak. A dynamic dissemination rate provides more granular disease dynamics than a constant contact rate such as that used in the Reed-Frost model. A compartmental approach scales well with population size as individual herd states are not calculated, just the proportion of the population in each of the infection states. As such, the Miller model is a computationally efficient means of modelling the spread of FMD across the continental USA.

Population-based models are generally concise and easy to parameterise. They can be useful for fast prototyping of disease dynamics, for example, early in an outbreak when the data needed to parameterise a more complicated individual-based model may not yet be available (Keeling, 2005; Arino et al., 2006). During the early stages of the 2001 UK FMD outbreak, an ODE-based mass action model (Ferguson et al., 2001), was able to be quickly parameterised from the limited outbreak data that was available (Keeling, 2005). The more complex individual-based models that were also used (Keeling et al., 2001; Morris et al., 2001), required far greater data and effort to parameterise (Kao, 2002; Keeling, 2005). Population-based models can also serve as

useful benchmarks to test the broad validity of more complex models (Heesterbeek, 2005; Skvortsov et al., 2007).

The traditional simple ODE-based mass action model can be augmented to include: the clustering effect of short range infection (Ferguson et., 2001; Kao, 2002); within-farm transmission (Thornley and France, 2009); the appearance of clinical signs (Thornley and France, 2009); and control measures such as stamping out, pre-emptive culling (Matthews et al., 2003) and vaccination (Thornley and France, 2009). Haydon and colleagues (1997) employ a discrete-time SEIR compartmental model to estimate how the transmission rate β and basic reproduction number R_0 varied over time during the 1967 outbreak of FMD in the UK. Howard and Donnelly (2000) employ a similar method to estimate how the transmission rate varied during the 1967 UK and 1997 Taiwan outbreaks. The derived values are then used to retrospectively simulate the outbreaks in order to conduct what-if scenarios on the impact of delays between diagnosis and culling. A population-based model can, however, become very complex and less tractable as more variables are factored into the mathematical abstraction (Miller, 1976; Parunak et al., 1998; Bobashev et al., 2007). As the mathematics driving a model becomes more sophisticated, it risks becoming a 'black box' to non-mathematicians.

Livestock disease outbreak dynamics are influenced by heterogeneities in region, environment, species, herd size, and farming practices (Keeling et al., 2001). Take for example, an outbreak of FMD within an extensive beef farm in remote northern Australian, compared to one in an intensive dairy farm in southern Australia. Despite the same pathogen and species, there are quite distinct disease spread dynamics and control environments for each region. This is due to heterogeneities in livestock density, farming practices, market systems, climate, probability of disease detection and reporting (based on the level of contact between owners/inspectors and livestock), and jurisdiction-dependent disease control policies and resourcing. The homogeneous 'well-mixed' assumption of aggregated population-based models is quite a limitation if

the population is heterogeneous and mixes heterogeneously (Hethcote, 2000; Keeling et al., 2001; Kitching et al., 2006; Bansal et al., 2007; Grassly and Fraser, 2008). This is especially the case with a disease such as FMD where infectivity and susceptibility varies significantly between the affected species (Kitching et al., 2006). In a simple compartmental model such as the SIR EBM in Figure 2.5, individuals within a compartment are indiscernible. A population-based approach cannot account for the impact of singular individuals such as super-spreaders (Lloyd-Smith et al., 2005), and the influence that the spatial distribution of a population has on disease transmission (Matthews et al., 2003).

2.4.2 Individual-based modelling

Individual-based models are formulated from the bottom-up. The modelling focus is the natural behaviour of individuals and how they interact with each other, and with the environment. Population-level relationships emerge over time as opposed to a population-based model where the relationships are prescribed as inputs. The notion of a population of synergistic individuals is flexible, for example, buyers and sellers in a market (Heppenstall et al., 2005), bacteria and immune cells in tissue (D'Souza et al., 2009), or the occupants of a city (Colizza and Vespignani, 2008). The population-level outcomes that emerge from individual-based models are free from the 'aggregation bias' that can occur from the implicit statistical averaging of population-based models (Baroni and Richiardi, 2007). A shift has been observed from a population-based approach towards an individual-based approach in the economic (Birkin and Wu, 2012), geographical (Crooks and Heppenstall, 2012), ecological (Parry and Evans, 2008), and animal health policy (Garner and Hamilton, 2011) modelling domains.

Individual-based models have a natural affinity for capturing population heterogeneity, stochasticity, spatial relationships, adaptivity, social systems and policy elements (Parunak et al., 1998; Davidsson, 2001; Hare and Deadman, 2004; Bithell et al., 2008; Perez and Dragicevic, 2009; Carpenter, 2011; Parker and Epstein, 2011). An individual-based modelling approach is well suited to the heterogeneous environment

in which a livestock epidemic operates (Kao, 2002). Significant heterogeneities may exist in host species, production systems, market practices, geography, climate and jurisdiction-dependent policies. The ability to distinguish between individuals in a population is useful during the initial and final stages of an outbreak when the number of infected animals is low and the averaged approach of population-based models may not be accurate (Teclaw, 1979; Germann et al., 2006; Bansal et al., 2007).

2.4.2.1 Emergence

Emergence is the aggregation of individual-level behaviours that forms population-level behaviour, in the absence of a centralised controlling entity. The emergent population-level behaviour cannot be directly inferred from the behaviour of the individuals – it only arises organically from the synergistic interaction between individuals, and between individuals and the environment (Grimm and Railsback, 2005). Examples of emergence are tropical cyclones (Figure 2.8), termite mounds (Figure 2.9), the stock market, the schooling of fish (Figure 2.10), the swarming of insects, and the flocking of birds (Figure 2.11).
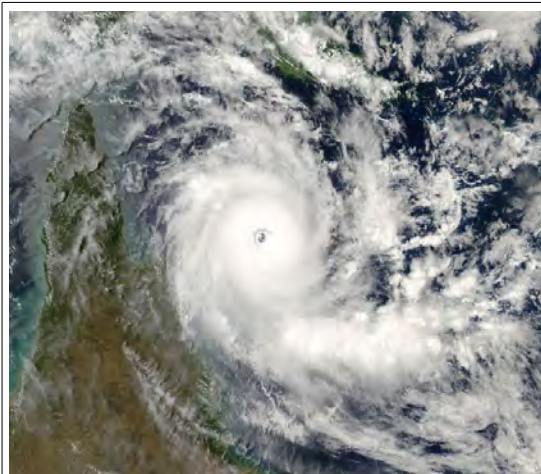

Figure 2.8. Tropical cyclone Ingrid off the Queensland coast (Descloitres, 2005)

Figure 2.9. Termite mound in Litchfield National Park, Australia (Bradhurst, 2008)

Figure 2.10. Blue jack mackerel bait ball (Swann, 2014)

Figure 2.11. Simulated flocking of starlings in Rome (Feder, 2007)

Feder (2007) uses stereoscopic cameras to capture 3D images of starlings flocking in Rome. The data reveals that a bird's speed and heading is influenced by six to seven of its neighbours. The interactions are anisotropic, in that neighbours on either side of a bird exert more influence than neighbours at the front and rear. Further, the interactions are not dependent on distance between the subject bird and its neighbours. These observations are perhaps related to the wide field of view and limited depth perception of monocular bird vision. The distance-independent relationship between neighbours allow a flock's density to vary, yet the flock remain cohesive, whilst responding to an external stimuli such as the detection of a predator. Each bird is modelled with a software entity that dynamically calculates a heading based on its neighbours. For simplicity, all birds are assumed to maintain a constant velocity. Individual birds autonomously carry out simple rules such as maintaining a heading/speed that is compatible with immediate neighbours, whilst watching out for environmental obstacles and predators. At a population level, complex and dynamic 3D flocking patterns emerge with no centralised coordination (Figure 2.11).

2.4.2.2 Microsimulations

One of the earliest examples of a disaggregated approach to modelling is the Orcutt socio-economic system (Orcutt, 1957; Orcutt et al., 1961). Orcutt focuses on the role of individual decision-makers in an economy such as people, households and

companies, as opposed to the traditional economic sector-based aggregated approach. The behaviours and responses of individuals depend on the current state of the system, and are evaluated at discrete time steps (e.g., weekly). Individual-level behaviour may be deterministic, or stochastic via sampling from probability distributions (Vose, 2008). As the system evolves, so too do the probabilities governing individual behaviours, until such time as an overall system 'solution' emerges. Model parameterisation is varied in order to investigate the impact of economic policies on the population. Sensitivity/uncertainty analysis (Taylor, 2003), is used to isolate the parameters that strongly influence model outputs.

In general, microsimulation models (MSMs), simulate the states, behaviours, interactions and evolution of individual units in an environment (Baroni and Richiardi, 2007). Microsimulations are a useful mechanism to study the impact of policy on a population, at both the individual level and the population level (Boman and Holm, 2005; Baroni and Richiardi, 2007; Birkin and Wu, 2012). Early microsimulations were non-spatial and represented individuals with simple data structures (Elveback et al., 1971). Microsimulations later evolved to include the spatial aspects of a population through integration with GIS platforms.

Microsimulations are able to model the ecological elements of an epidemic separately. This approach offers more transparency and control than a population-based model that has complex aggregated formulations. An example is AusSpread, a spatially-explicit state-transition microsimulation based on the MapBasic/MapInfo GIS platform (Pitney Bowes, 2014). The 'policies' of disease transmission (via direct contact, saleyard spread, indirect contact and airborne spread), are applied to the population of susceptible farms. Policies of disease control and eradication (movement restrictions, tracing, surveillance, IP operations and vaccination), are applied during the control program. AusSpread operates in discrete time steps of a day and uses Markov chain Monte-Carlo (MCMC) methods (Hamra et al., 2013), to represent the natural stochasticity of disease spread and control. The values for

fluctuating, uncertain, or unknown parameters are dynamically sampled from probability distributions. An outbreak scenario is run hundreds of times with the same initial conditions in order to produce probability distributions of possible outcomes. Outbreak metrics include number of infected premises, outbreak duration, infected area, number of culled animals, number of vaccinated animals, and cost of the control program. AusSpread has been used to study the spread and control of FMD in Australia (Garner and Lack, 1995; Beckett and Garner, 2007; Buetre et al., 2013; Garner et al., 2014; Roche et al., 2014; East et al., 2014b), and the United States (Ward et al., 2009; Hagerman et al., 2012; Hagerman et al., 2013), and has also been adapted to study other diseases including CSF (Cowled et al., 2012).

InterSpread Plus (Stevenson et al., 2013), Exodis (Risk Solutions, 2005a), and the North American Animal Disease Spread Model (NAADSM) (Harvey et al., 2007) are also spatially-explicit, stochastic, state-transition microsimulations. They have been used to study the spread and control of FMD in Canada (Sanson et al., 2014), Denmark (Halasa et al., 2014), Korea (Yoon et al., 2006), New Zealand (Owen et al., 2011), Switzerland (Bachman et al., 2005), the United Kingdom (Keeling, 2005) and the United States (Cozzens et al., 2010; McReynolds et al., 2014), and have also been adapted to study other animal diseases including ASF (Nigsch et al., 2013), CSF (Jalvingh et al., 1999; Ribbens et al., 2012), Equine Influenza (Garner et al., 2011; Rosanowski, 2012) and HPAI (Vandendriessche et al., 2009; Longworth et al., 2014). Microsimulations such as AusSpread, InterSpread Plus, Exodis and NAADSM have proven useful as decision support tools for FMD planning and policy development (Garner et al., 2007). By varying model parameterisation, what-if scenarios can be conducted across a variety of outbreak scenarios and control strategies. The emergent behaviour of such models is the spatiotemporal spread of disease across the population, waxing and waning as the epidemic unfolds and control measures are deployed.

Complex individual-based models (such as AusSpread, InterSpread Plus, Exodis and NAADSM), that endeavour to explicitly capture the heterogeneities of an epidemic can have extensive configuration data. This may include livestock demographics, livestock movements, weather and pathogen strain specifics. The suitability of data-driven models for a study depends on the availability and quality of supporting data (Green and Medley, 2002; Kao, 2002; Keeling, 2005; Kitching et al., 2006; Dubé et al., 2007a). Inadequate data can be replaced with assumptions/expert opinion but this has the potential to introduce bias into a model. The parameterisation of complex spatially-explicit models can be time consuming and require a good understanding of the epidemiological system being modelled (Woolhouse, 2004; Keeling, 2005). This can make them less agile than simpler population-based models (Kao, 2002; Arino et al., 2006). There is a risk that incorrect parameterisation of a complex individual-based model may actually mislead rather than inform (Thornley et al., 2009).

2.4.2.3   Spatial-kernel models

A spatial-kernel (or transmission kernel), is a means of deriving probabilities of transmission between infectious and susceptible individuals in a population, based on the distances between them (Hayama et al., 2013). An example of a model that employs this approach is the 'Cambridge-Edinburgh' model (Keeling et al., 2001), used during the 2001 outbreak of FMD in the UK. The farm population is derived from UK census data on farm locations and livestock holdings. The probability that an infected farm transmits disease to a susceptible farm is based on species, number of animals on the farms, and a transmission kernel that relates infectivity to the distance between the farms. Monte-Carlo methods drive the transition of farms through susceptible, incubating, infectious, and culled states. FMD studies that employ the Cambridge-Edinburgh model or its derivatives include Keeling and colleagues (2003), Tildesley and colleagues (2006), Tildesley and Keeling (2008), Tildesley and colleagues (2009) and Porphyre and colleagues (2013).

The spatial-kernel approach aggregates the various FMD spread mechanisms at work (direct contacts, indirect contacts and aerosols), into a simple tractable formulation.

Kitching and colleagues (2006), however, warn that the spatial-kernel approach may over-emphasise the importance of short-range transmission, with models tending to spread disease radially in short-distance increments from infected premises. The disaggregated approach of a microsimulation such as AusSpread and InterSpread Plus avoids this phenomena as distinct transmission 'policies' (such as long range livestock movements), are applied across the population.

The aggregation of spread mechanisms in a spatial-kernel approach results in simple parameterisation. During the UK 2001 outbreak, the Cambridge-Edinburgh model was able to be quickly parameterised from contact tracing data collected early in the outbreak (Keeling, 2005). In contrast, the disaggregated approach of InterSpread Plus required much more detailed parameterisation. This illustrates the fine balance between a model being detailed enough that it is granular and realistic, yet not so complex that its usability is hampered by lack of supporting data and complex parameterisation (Keeling, 2005).

2.4.2.4 Cellular and geographic automata

A cellular automaton (CA) is an individual-based model that discretises a spatial environment into a lattice of cells (Iltanen, 2012). Individuals (sometimes referred to as agents), occupy at most one cell at a time. Agents have internal states, and rules that govern interactions with other agents and with the environment. The rules may be deterministic or stochastic and typically depend on the current states of neighbouring agents. Agents may be static and confined to a home cell, or mobile across the environment. Time is also discretised in that the rules are triggered *en masse* at periodic intervals. The states and/or positions of the agents evolve over time and the CA may exhibit emergent behaviour. A simple example of the CA concept is Conway's game of 'Life' (Gardner, 1970). Cellular automata are computationally efficient, and relatively straight forward to build and understand. Over the years, they have evolved into a sophisticated modelling technique ranging from micro-environments such as the spread of bacteria within tissue (Alber et al., 2003), right up to macro-environments such as viral spread across a population (Doran and Laffan,

2005). Cellular automata have been used to study a range of animal diseases including CSF (Milne et al., 2008), rabies (Thulke et al., 1999), HPAI (Situngkir, 2004) and FMD (Morley and Chang, 2003; Doran and Laffan, 2005),

Doran and Laffan (2005) employ a CA to study the potential spread of FMD between feral pigs and unfenced livestock in Queensland, Australia (Figure 2.12). A lattice with cell dimensions of 5.385 x 5.385 km is superimposed over the study area. The resulting 29 km^2 cell area represents a typical home range for feral pigs in tropical Australia. Feral pig densities and distributions across the lattice are synthesised from aerial surveys, questionnaires and expert opinion. Livestock densities and distributions are synthesised from census data.

Figure 2.12. Feral pigs interacting with domestic cattle in Australia (Wishart, 2011)

The agent population is comprised of feral pig herds and 'pig-equivalent' herds. A pig-equivalent herd is an artificial construct representing livestock, but expressed in terms of pigs. The translation takes into account variability between species with respect to virus shedding, and susceptibility to infection. A sheep flock is deemed equivalent to 0.5 pig herds, while a cattle herd is deemed equivalent to 0.64 pig herds. This tactic allows the model to simplify disease spread as being between homogeneous herds.

Herds are assumed to mix homogeneously within a cell. Intra-cell disease spread is handled by a deterministic, state-transition Susceptible, Exposed, Infectious, Recovered, Susceptible (SEIRS) model. An infected feral pig herd is assumed to roam within its home cell and have an effective contact with a susceptible herd within one to six days. Exposed herds transition to infectious, recovered and susceptible again based on model parameterisation. A cell is deemed to be completely infected at most six days from the first infection of a herd, after which it starts participating in the inter-cell spread of disease. Inter-cell spread of disease is represented by a stochastic distance kernel, defined in terms of cells. The only susceptible cells at risk from an infected cell are those in the immediate Moore neighbourhood (Weisstein, 2015). The probability of infection depends on the density of susceptible herds and the cell location relative to the infected cell. The diagonal cells (north-west, north-east, south-west and south-east), are seen as 71% less likely to become infected than the adjacent cells (north, south, east and west).

A geographic automaton (GA) is an evolution of cellular automata. Whereas a CA environment is defined rigidly in terms of a lattice, a GA has a fully geographic environment, typically through integration with a GIS platform (Torrens and Benenson, 2005; Ward et al., 2007; Laffan et al., 2007; Yassemi et al., 2008; Highfield et al., 2008; Ward et al., 2011). An example of a GA is Sirca (Laffan et al., 2007), which builds upon the Doran and Laffan (2005) CA. Sirca allows herd neighbours (for the purposes of inter-herd spread), to be defined as a function of geography (e.g. distance), as opposed to purely in terms of neighbouring cells. While a geographical environment is conducive to higher quality simulated contacts, it is typically accompanied by an increased computational overhead from the geographic queries. Techniques such as spatial-indexing can ease this burden (Kennedy et al., 2009).

2.4.2.5   Agent-based models

An agent (Franklin and Graesser, 1997; Boman and Holm, 2005; Macal and North, 2010), is generally regarded as having the following characteristics:

- self-contained with respect to state, logic and goals,

- the ability to detect and interact with other agents and/or the environment,

- autonomy/authority to react/interact without external prompting,

- adapts/evolves/learns over time as a consequence of interactions.

Autonomy is perhaps the single most important characteristic of an agent (Macal and North, 2010). An agent can independently react to a variety of stimuli, for example, other agents, the environment, the passing of time, and progression through space. In contrast, traditional microsimulations tend to have populations of passive individuals upon which external 'policies' are applied.

An agent-based model (ABM) is a system of autonomous, self-organising agents that interact in the context of an environment. Agents need not be homogeneous and so ABMs are naturally suited to modelling heterogeneous populations. An agent can represent a discrete individual or abstract a group of individuals such as a herd. An ABM is a continuation along the CA/GA evolutionary path. Whereas a CA environment is constrained to a lattice of cells, and a GA environment is constrained by geography, an ABM environment is generalised. Agents may interact over a variety of topologies, including lattices, Euclidean 2D/3D space, contact networks, GIS and aspatial 'soup' (Macal and North, 2010). As with other individual-level models, population-level behaviour emerges over time from the collective states of agents and the environment of an ABM (Macal and North, 2010). There are several alternative terms for similar concepts such as multi-agent system, agent-based simulation, multi-agent-based system, individual-based model, and complex adaptive systems (Hare and Deadman, 2004; Boman and Holm, 2005; Macal and North, 2010). The variety of terminology perhaps reflects the breadth of research domains interested in agent-based modelling and simulation. There are several programming languages, frameworks, integrated development environments, and distributed platforms specific to the development of ABMs (Bordini et al., 2006; Railsback et al., 2006; Allan, 2010). The Foundation for Intelligent Physical Agents (FIPA) defines a standard for the creation, management and interoperation of heterogeneous agents (IEEE, 2014).

ABM frameworks generally provide standard infrastructure such as agent communication, discrete time management, and agent scheduling. Popular examples include NetLogo (Wilensky, 1999), JADE (Bellifemine et al., 2001), MASON (Luke et al., 2005), Swarm (Minar et al., 1996), Repast Simphony (North et al., 2013), GAMA (Grignard et al., 2013) and D-MASON (Cordasco et al., 2013). ABMs have been used to study a variety of animal diseases, including FMD (Dion et al., 2011; Ariuntsetseg and Yom, 2013), bovine tuberculosis (Ross et al., 2011), RVF (Paul et al., 2014), and HPAI (Amouroux et al., 2008; Kim et al., 2010; Roche et al., 2011).

EPIFMD (Dion et al., 2011) is an example of an ABM used in the study of FMD. It models the effect of landscape heterogeneities on the potential spread of FMD between African buffalo in the Kruger National Park and domestic cattle adjoining the park. Three FMD serotypes are endemic in South Africa, and buffalo can carry FMDV with minimal clinical signs. Domestic cattle are typically managed in a traditional communal manner, which involves daily herding between village enclosures and unfenced grazing/water resources. Whilst Kruger is in theory enclosed by a fence, in practice, the fence has unpredictable integrity due to large animals, poachers, floods, wear and tear, and gates being left open. Cattle based near Kruger are thus at risk of contracting FMD through direct contact with buffalo at shared watering holes and grazing areas. As such, cattle are vaccinated against FMD twice a year and subjected to weekly inspections by government veterinarians. The buffalo population is synthesised from park census data and ranger observations. A buffalo agent is a small group of buffaloes that moves stochastically around the environment based on census data and ranger observations. Whether or not a buffalo agent leaves the park (and poses a risk to cattle), depends on the state of the nearby fence. The uncertainty of fence disrepair and repair are factored into the model stochastically based on fence maintenance, survey data, and surrounding land features. The cattle population is synthesised from survey data and livestock register reports. Each herd of cattle is modelled by an agent that stochastically moves around the environment according to survey data and GPS-derived grazing patterns. The EPIFMD environment is GIS-based and includes features such as land cover, water resources,

climate, land use, villages, roads and park fences. The movements of animal agents are influenced by seasonal environmental variables including temperature, precipitation, water resources and vegetation. A lattice with cell dimensions of 100 metres x 100 metres is superimposed over the environment. A cattle agent and a buffalo agent are deemed to be in contact when they occupy the same cell. As EPIFMD is stochastic, the model outputs are spatiotemporal distributions of cattle and buffalo movements to and from grazing/water resources, buffalo excursions from the park, and direct contacts between buffalo and cattle. EPIFMD only models contacts that may lead to the transmission of FMD, not the actual transmission of FMD. Indirect contacts are not modelled as the national park and surrounding villages do not typically share vehicles, equipment, personnel. Airborne 'contacts' are also not modelled due to the low numbers of (virus shedding) pigs in the area, and the Kruger climate generally not being conducive to virus remaining viable in a plume (Donaldson and Alexandersen, 2002). The parameterisation of EPIFMD can be varied to study the extent to which factors such as landscape heterogeneities, population distributions and densities, population demographics, movement patterns, fence integrity, climate, and seasonal variations, influence the location and frequency of direct contacts. EPIFMD is an example of how the individual-level approach of an ABM is a natural fit for capturing the complexities of a heterogeneous environment.

2.4.2.6　　　Massive Agent-based models

A massive agent-based model (MABM) is an expansion of an ABM to handle very large populations. The distinction between an ABM and a MABM is somewhat arbitrary. However, for illustrative purposes, an ABM has up to thousands, or perhaps hundreds of thousands of agents, while a MABM may run into the millions, or even billions of agents. The explicit modelling of individuals in a large population can be computationally intensive and MABMs are generally not suitable for desktop computers and off-the-shelf ABM frameworks. In particular, some simple ABM frameworks employ a thread of execution per agent which imposes limits on the maximum number of agents that a platform can support (Krzywicki et al., 2015). This limitation is addressed by frameworks such as D-MASON (Cordasco et al., 2013) that

support distributed ABMs. Large populations may require specialised implementation strategies such as lightweight agents that share pools of threads (Kim et al., 2007), custom memory management (Parker and Epstein, 2011), or aggregated 'super-individuals' (Scheffer et al., 1995; Parry and Evans, 2008). MABMs typically require a highly parallel platform such as high-performance computing (HPC) clusters (Carley et al., 2006; Germann et al., 2006; Stroud et al., 2007; Yamamoto et al., 2007; Macal and North, 2008; Aleman et al., 2009; Parker and Epstein, 2011), which tends to confine them to university, defense and scientific research environments. GPGPU (General Purpose computing on Graphics Processing Units) is a low cost alternative parallel platform (Lysenko and D'Souza, 2008; D'Souza et al., 2009; Richmond et al., 2009; Welch et al., 2014).

An example of a MABM is the Global Scale Agent Model (GSAM) (Parker and Epstein, 2011). GSAM is a distributed modelling platform capable of simulating pandemics across populations of several billion agents. Disease may spread from an infectious agent to a susceptible agent as a consequence of family contacts, coworker/classmate contacts or random contacts. Agents transition through infection states according to the disease being modelled. GSAM is written in Java and employs a highly optimised distributed software architecture that is portable across both operating systems and hardware platforms. GSAM is typically hosted on an HPC cluster with each node dedicated to processing an assigned spatial compartment. Inter-node communication is queued and carried out in periodic bursts in order to reduce latency. GSAM efficiently simulates the global propagation of a variety of diseases. An example run-time performance is 2.4 billion infections across a population of 6.5 billion agents in 7.8 hours (on a 32 node HPC UNIX cluster).

2.4.2.7 Network-based models

Individuals in a population can be abstracted as nodes in a network. An edge between two nodes represents an interaction between individuals (or direct contact), that may facilitate the transmission of disease (Bansal et al., 2007). A network-based model extends the spatial-kernel approach (Section 2.4.2.3), with a data-driven contact

network that defines the set of potential paths over which disease may propagate. The level of realism of the contact network depends on the available data in the modelling domain. Human contact networks are irregular and heterogeneous, and so large network-based models of human disease such as influenza, often employ generalised contact patterns derived from sources such as surveys and census data (Bansal et al., 2007).

The notion of a network-based model extends to metapopulations (Hess, 1996). In this case, the nodes are sub-populations and the contact network describes the movement of individuals between sub-populations (Colizza and Vespignani, 2008). This type of network-based model is well suited to livestock with farms as the nodes in the network and a contact network derived from recorded livestock movements. In countries where agriculture and biosecurity is of great importance to the economy, there is an increasing availability of data on the movement of livestock and livestock products. An example is the Australian National Livestock Identification System (NLIS) which tracks livestock from property of birth to place of slaughter/export (Durr et al., 2010; Meat and Livestock Australia, 2014a). The NLIS database is a rich source of data on cattle movements that take into account species, production system and region, and can be used to derive realistic livestock movement patterns on a per-consignment basis. Green and colleagues (2006) use the UK equivalent Cattle Tracing System (CTS) to derive a realistic contact network based on inter-farm movements and consignments to and from markets. Their FMD model is then able to take into account temporal heterogeneities such as season-based movements, and spatial heterogeneities such as market catchment areas. Green and colleagues also model the clustering of infected farms through a fixed-rate local spread mechanism.

2.4.3 Hybrid models

Hybrid epidemiological models incorporate a population-based approach and an individual-based approach into a single model in order to harness the strengths of both approaches.

2.4.3.1 Stage-based

A stage-based (or threshold) hybrid model is modal in that simulation is conducted at any given time by either a population-level model (such as an EBM), *or* an individual-level model (such as an ABM). Bobashev and colleagues (2007) describe a stage-based hybrid model of global human influenza that dynamically switches between an ABM and an EBM, based on the number of cases. Within-city spread is initially modelled with an ABM in order to capture subtle interactions between individuals early in an epidemic. The ABM is halted when a cases threshold is reached and a snapshot of agent states is used as the initial conditions for an EBM. Although the granularity of modelling decreases to population-level, it occurs at a point in the outbreak when the number of cases is sufficient to support a population-averaged approach. Moreover, the overall performance of the model is maintained due to the computationally efficient EBM. The model switches back to an ABM when the number of cases in a city falls below a threshold value in order to capture subtle interactions between individuals as the epidemic wanes.

2.4.3.2 Embedded

An embedded hybrid model extends both the spatial-kernel (Section 2.4.2.3) and network-based (Section 2.4.2.7) approaches with the addition of explicit modelling of the spread of disease within a sub-population. An individual-based model simulates the spread of disease between sub-populations, and a population-based model simulates the spread of disease within sub-populations. This approach captures the multi-scale nature of an epidemic in that the mechanisms and rates of disease spread within sub-populations are often quite distinct from those between sub-populations (Balcan et al., 2010). A population-based approach is appropriate when a sub-population can be simplified as closed and homogeneous. An individual-based approach captures heterogeneity across the meta-population and in the environment.

Embedded models have been used to study large scale human epidemics, with realistic mobility networks characterised from data sources such as censuses, surveys, the International Air Transport Association (IATA) database and the Official Airline

Guide (OAG) database (Bansal et al., 2007; Balcan et al., 2009; Yu et al., 2010; Van den Broeck et al., 2011; Parker and Epstein, 2011; Yoneyama et al., 2012). An example of a large-scale embedded model is the Global Epidemic and Mobility Model (GLEaM) (Balcan et al., 2009). The global land surface is decomposed into sub-populations based on Voronoi polygons that enclose IATA-indexed airports. The spread of disease within a sub-population is modelled by a pathogen-specific, stochastic, SEIR-based, compartmental EBM that assumes homogeneous mixing. The spread of disease between sub-populations is driven by a two-layer mobility network. Short-range commuting patterns between sub-populations are characterised from census data and represented by a gravity law. Longer-range air travel patterns between sub-populations are characterised from historical IATA data on commercial air traffic and represented by stochastic variables that follow a multinomial distribution. The mobility network is multi-scale, reflecting how the commuting flow between sub-populations is an order of magnitude heavier than longer haul air traffic flows between sub-populations. Disease pathways form stochastically between sub-populations as infectious individuals travel and come into contact with susceptible individuals. Ajelli and colleagues (2010), compare the GLEaM metapopulation hybrid model with a matched MABM. They report that GLEaM is computationally more efficient than the MABM yet produces broadly comparable modelling outcomes.

An embedded approach is a good match for a livestock disease model due to the distinct dynamics of within-farm and between-farm disease spread (Carpenter et al., 2003; Chis Ster et al., 2012; Backer et al., 2012a). Once infection is introduced into a farm the rate of within-farm spread is dependent on the specifics of the pathogen and the farm. Factors may include the host species, livestock density, livestock numbers, production system, and biosecurity measures. The spread of disease between farms is influenced by more irregular factors such as contact networks between farms (direct and indirect), market practices, distance between farms, and environmental conditions such as weather. Embedded models have been used to study a range of animal diseases, including FMD (Kim et al., 2012; LaBute et al., 2014), HPAI (Nickbakhsh et al., 2013; LaBute et al., 2014), CSF (Holmstrom, 2008), Mycobacterium avium

subspecies paratuberculosis (Teose et al., 2011), and swine vesicular disease and vesicular stomatitus (Eisinger, 2012).

The Davis Animal Disease Simulation (DADS) (Bates et al., 2003a) is a stochastic model of the spread and control of FMD in Californian livestock. DADS extends the spatial-kernel approach (Section 2.4.2.3), by embedding a Reed-Frost chain binomial model (Section 2.4.1.2), to represent the spread of disease within a herd. The probabilities of adequate contacts between infectious and susceptible animals in the same herd are obtained through daily Monte Carlo sampling of Beta-PERT distributions that factor in herd type and transmission mode (direct, low risk indirect and high risk indirect). Between-herd spread is handled by a stochastic spatial transmission kernel that takes into account the probability of adequate contact per transmission mode, the infectiousness of infectious herds (as calculated by the within-herd spread model), and the distance between infectious and candidate susceptible herds. The inter-herd transmission modes are characterised from realistic direct/indirect contact rates and movement distances (Bates et al., 2001). Studies that have used DADS include: the spread and control of FMD in Californian livestock (Bates et al., 2003a; Bates et al., 2003b; Dickey et al., 2008); the spread of FMD from wild pigs to Californian cattle and evaluation of control strategies (Pineda-krch et al., 2010); the economic importance of early detection of FMD in Californian livestock (Carpenter et al., 2011); and an evaluation of vaccination as a response to an FMD outbreak in Switzerland (Dürr et al., 2014).

The Multiscale Epidemiologic/Economic Simulation and Analysis (MESA) decision support system is a national-scale model of livestock disease spread and control. It employs an SEIR-based approach to represent the spread of disease within herds, and an agent-based approach to model the direct and indirect spread of disease between herds (Speck, 2008). Various control measures are incorporated including quarantine, movement controls, tracing, vaccination and depopulation. An economic module assesses the impact of an outbreak including the cost of control strategies and loss of

trade. It has been used to study livestock diseases including CSF (Holmstrom, 2008) and FMD (Hullinger, 2008). The MESA model is no longer being funded, development has stopped and it has not been used for several years (P. Hullinger, personal communication, 30 May 2015).

The Technical University of Denmark - Davis Animal Disease Simulation (DTU-DADS) (Boklund et al., 2013) is an adaption of the DADS model to the spread and control of FMD in Denmark. Apart from migration to the Danish livestock population and movement patterns, DTU-DADS incorporates local spread within a 3km radius of infectious herds and airborne spread beyond the local spread radius. Surveillance and tracing are included, and movement restrictions, depopulation of infected herds, and vaccination are modified to match European Union and Danish regulations. FMD studies that have used DTU-DADS include Boklund and colleagues (2013), Halasa and colleagues (2013), and Halasa and colleagues (2014).

The Netherlands FMD model (Backer et al., 2012a), extends the spatial-kernel approach (Section 2.4.2.3), by embedding an SEIR-based EBM to represent the spread of disease within a herd. Between-herd spread is handled by a spatial-kernel that is driven by the distance between infectious and susceptible herds, the infection pressure of an infectious herd (as determined by the EBM), and the types of the infectious and susceptible herds. The spatial-kernel is parameterised with data from the 2001 FMD outbreak in the Netherlands. The model simulates various control strategies including stamping out, pre-emptive ring culling and suppressive ring vaccination. FMD studies that make use of the Netherlands model include Backer and colleagues (2012b), and Bergevoet and Asseldonk (2014).

2.4.4 Summary

Section 2.4 illustrates the range of approaches used in the modelling of FMD spread, control and eradication. There are advantages and disadvantages with both the population-based and individual-based approaches. Population-based models are

mathematically based and tend to be concise, relatively easy to parameterise and computationally efficient. This makes them useful for fast prototyping of disease dynamics especially when outbreak data is scarce. Population-based models carry an assumption that the population is homogeneous and 'well-mixed', which is a limitation if the population is heterogeneous and mixes heterogeneously. Individual-based models tend to be ecologically based and focus on the role and contribution of an individual in the environment. They have a natural affinity for capturing heterogeneity, stochasticity and spatial relationships. Individual-based models are often data-driven, have extensive parameterisation and may not scale well with population size. A hybrid modelling approach combines the strengths of population and individual-based approaches into a single model.

In the next chapter a case is put forward as to why the hybrid embedded approach is a good match for modelling FMD on a national-scale in Australia.

3 MODEL ARCHITECTURE AND DESCRIPTION

Chapter 2 illustrated that there are a variety of approaches to the modelling of infectious livestock diseases such as FMD. The choice of modelling approach is perhaps influenced by the background of the modellers, the availability of data, and the purpose of the model. For example, in a situation where data is limited and there is a need to quickly characterise outbreak dynamics, a simple population-based approach is far more agile than a complex individual-based approach (Section 2.4.1.3). As another example, the explicit simulation of individual spread pathways and control measures (Section 2.4.2.2), provides much greater flexibility when conducting policy-driven what-if scenarios than an aggregated mathematical approach such as that of spatial-kernel models (Section 2.4.2.3). When deciding upon a modelling approach it is important to take into account a range of factors such as scalability for the required population size, availability and quality of data, and how the model is to be used.

This chapter explores why a hybrid embedded modelling approach is suitable for a national-scale model of FMD in Australia. Firstly, the most appropriate epidemiological modelling unit of interest is determined. Secondly, the Australian population of FMD-susceptible animals is characterised in terms of the chosen modelling unit of interest. Thirdly, the AADIS model architecture is described. Finally, the epidemiology, algorithms and formulae for the spread and control of disease are outlined.

3.1 Epidemiological unit of interest

There are three options for the modelling unit of interest: the animal, the herd and the farm. The most granular choice is modelling on a per-animal basis, which in Australia yields a population of over 100,000,000 individuals. This option would place AADIS

in the company of large scale network-based models and MABMs (Sections 2.4.2.6 and 2.4.2.7).

It is theoretically possible to construct a national contact-network based on actual cattle movements in Australia (Happold et al., 2010; Donald et al., 2010). The NLIS database on cattle movements is highly accurate due to mandatory tagging of each animal with a radio frequency identification (RFID) ear tag or rumen bolus. However, movement data for sheep and pigs is less accurate as there are still visual and manual components in the tracking system (Schembri et al., 2007; Hernández-Jover et al., 2009; Australian Bureau of Agricultural and Resource Economics and Sciences, 2013; Meat and Livestock Australia, 2014b). There are also variations between jurisdictions in the accuracy of premises data (Durr et al., 2010), and the accuracy of movement data (Hernández-Jover et al., 2009; Australian Bureau of Agricultural and Resource Economics and Sciences, 2013). Inconsistencies in the quality of premises and movement data (across jurisdictions and between species), are problematic for a national-scale epidemiological model as they weaken the realism of simulated direct contacts and traces.

Apart from the computational burden, modelling disease on a per-animal basis is arguably overkill for a livestock model of national scale. As a counter-example, consider the spread of disease between humans. Each person has a distinct contact network of family, friends, classmates, colleagues, team mates and fellow commuters. (Colizza and Vespignani, 2010). An infectious individual can set off a chain reaction of infection rippling across their personal contact network. Livestock, on the other hand, are typically managed in a relatively structured way as groups that effectively share a single contact network whilst on a farm (Kostova-Vassilevska, 2004). An epidemiological unit of interest of the herd or the farm is thus appropriate for modelling the spread of livestock disease on a national scale.

Modelling the spread of disease on a per-herd basis captures heterogeneity within multi-species farms. For example, farms that manage both sheep and cattle can be modelled as two independent herds with distinct disease dynamics and animal management practices. This approach allows more granular modelling of disease transmission than models such as AusSpread and InterSpread Plus that use the farm as the base modelling unit. This leads to the decision for AADIS to adopt the herd as the epidemiological unit of interest for disease transmission. A herd is assumed to be homogeneous with respect to species and farming practices, and well-mixed from a disease transmission point of view. This implies that any one member of a herd has the same likelihood of contracting a disease as any other member.

For the purposes of disease control and eradication, however, the unit of interest is the farm (Animal Health Australia, 2014a). This stems from the policy of applying control measures to all herds on a farm of interest. This leads to the innovative choice of dual modelling units of interest for AADIS: the herd for the spread of disease, and the farm for the control of disease.

3.2 Livestock population

Commercial animals in Australia that are susceptible to FMD include sheep, cattle, pigs, goats, camels, alpaca, llama, deer and bison (Animal Health Australia, 2014a). For modelling purposes, the national livestock population of FMD-susceptible animals is simplified to only comprise sheep, cattle and pigs as they are by far the predominant commercial species (Australian Bureau of Agricultural and Resource Economics and Sciences, 2014). Wild and feral animals that are susceptible to FMD include pigs, goats, deer, buffalo, camels and some marsupials (Animal Health Australia, 2014a). The potential role of wild and feral animals in the spread of FMD is an ongoing area of research (Doran and Laffan, 2005; Ward et al., 2015). In the interests of simplicity, and assuming that wild and feral populations pose a low risk of transmitting FMD to livestock (Animal Health Australia, 2014a), the initial focus of AADIS is commercial animals only.

The Australian population of over 107 million FMD-susceptible livestock is aggregated into herds and farms based on species and farming practices. As the availability and quality of data varies between jurisdictions, the national dataset used in this study is derived from a blend of agricultural census data, industry reports and expert opinion (Department of Primary Industries, 2006; Australian Bureau of Statistics, 2014; Roche, 2013; Hernández-Jover et al., 2014). This results in a national herd population of 235,668 herds across 10 herd types (Table 3.1). A herd has static attributes (ID, type, size, latitude and longitude, state/territory jurisdiction, local government area, region and nearest weather station), and dynamic attributes describing infection status. The herd dataset is stored in a relational database (Section 4.2.1, and Appendices B and C). A farm can have one or more herds, resulting in a national farm population of 202,775 farms across 9 farm types (Table 3.1). A farm has static attributes (ID, type and constituent herd IDs), and dynamic attributes describing disease control and eradication status. AADIS spatially identifies a farm and its constituent herds as a single point of latitude and longitude.

Table 3.1. AADIS farm and herd types

| Farm type	Number of farms	Number of animals mean (min - max)	Herd type	Number of herds
Extensive beef	1331	1909 (1200 – 46,575)	Extensive beef	3993
Intensive beef	51,383	280 (30 – 7436)	Intensive beef	51,383
Feedlot	508	1825 (100 – 39,963)	Feedlot	508
Mixed beef/sheep	21,556	242 (30 – 5700)	Mixed beef	21,556
			Mixed sheep	21,556
Dairy	8675	298 (40 – 2742)	Dairy	8675
Small pigs	1873	244 (40 – 4850)	Small pigs	1873
Large pigs	333	4922 (1000 – 17,896)	Large pigs	333
Sheep	22,150	1649 (20 – 44,000)	Sheep	22,150
Smallholder	103,641	5 (1 – 14)	Smallholder	103,641
Total	**202,775**			**235,668**

3.3 The AADIS hybrid modelling approach

The choice of a hybrid embedded modelling approach for AADIS is driven by the purpose of the model – to support emergency livestock disease preparedness and planning in Australia. Spatially-explicit microsimulations such as AusSpread, InterSpread Plus and NAADSM are highly configurable so that a range of what-if scenarios can be conducted, specifically to assist with the development of animal health policy. The explicit representation of individual spread pathways and control measures (Section 2.4.2.2), provides a framework for detailed policy experimentation on both a spatial and temporal basis. For example: what-if scenarios on quarantine and movement restriction policies can be conducted and the impact on the direct spread, indirect spread and saleyard spread pathways assessed; what-if scenarios involving biosecurity measures can be conducted and the impact on the local spread pathway assessed; what-if scenarios involving weather variations can be conducted and the impact on the airborne spread pathway assessed; what-if scenarios involving seasonal/regional variations can be conducted and the impact on the direct and saleyard spread pathways assessed. This level of granularity is not available when a model aggregates the various means by which disease spreads between herds into a spatial-kernel (Section 2.4.2.3), or does not take into account spatial heterogeneities in the population and environment (Section 2.4.1).

A shortcoming of the microsimulation approach is limited representation of within-herd disease dynamics as disease spread 'policies' are typically applied upon a cohort of farms (Section 2.4.2.2). Techniques such as 'probability of transmission' lookup tables (Section 5.2.3), can provide a degree of intra-farm disease dynamics, but a more complete solution is the explicit modelling of within-herd spread. This is a feature of hybrid embedded models (Section 2.4.3.2), such as DADS and DTU-DADS where within-herd spread is handled by a Reed-Frost model, and the Netherlands FMD model which employs an SEIR mass-action model to represent within-herd spread. The decoupling of within-herd spread and between-herd spread reflects the multi-scale nature of livestock epidemics (Carpenter et al., 2003). Whereas the spread

of disease within a homogeneous herd is governed by species, pathogen and production system, the spread of disease between farms is influenced by more heterogeneous and irregular factors such as contact networks, market practices, distance between farms, geography and weather.

AADIS borrows from both the microsimulation approach of AusSpread, InterSpread Plus, Exodis and NAADSM, and the embedded approach of the DADS, MESA, DTU-DADS and the Netherlands models. AADIS models the spread of disease within a herd with a deterministic mass-action SEIR model. A population-based approach such as this is well-suited to modelling the spread of disease within a herd, when the herd can be assumed to be homogeneous and well-mixed. Whilst a herd is viewed as a population for the purposes of within-herd disease spread (Figure 3.1), it is (somewhat paradoxically), also viewed as an atomic individual participating in an ABM (Figure 3.2).

Figure 3.1. Herd agent with embedded EBM   **Figure 3.2.** Network of herd agents.
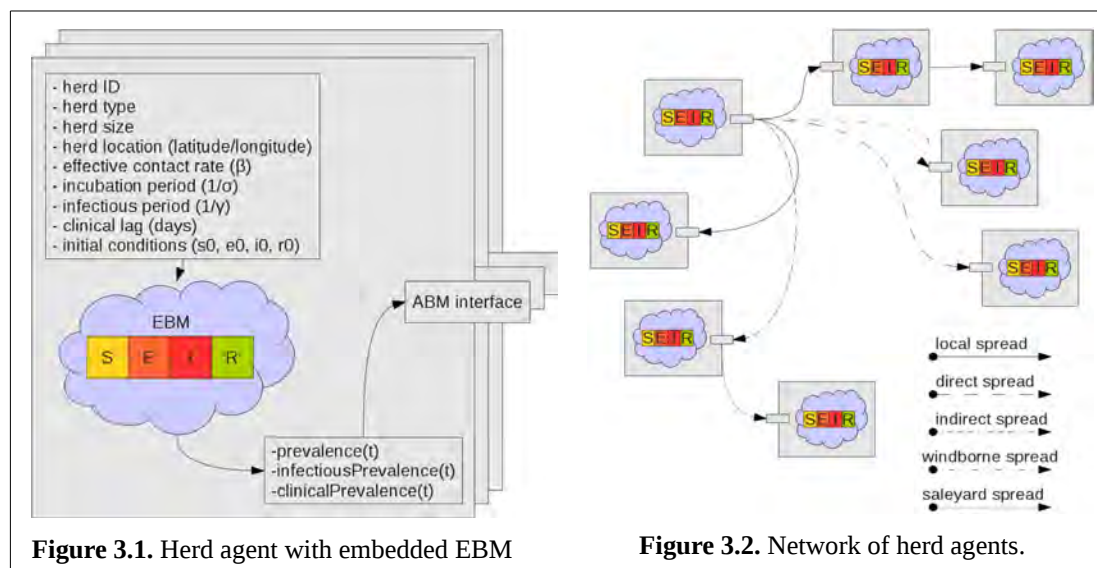
The EBM generates herd-level infected, infectious and clinical prevalence which are used by the ABM when modelling the spread of disease between herds. The ABM is also responsible for modelling the control and eradication of disease – which is conducted in the context of heterogeneous environment of jurisdiction-dependent policy and resourcing. An individual-based model has an affinity for capturing

heterogeneities in host species, production systems, market practices, geography, climate and jurisdiction-dependent policies. The emergent behaviour of the AADIS ABM is the spatiotemporal waxing of disease across the population and the subsequent waning due to control and eradication processes.

The AADIS ABM environment is comprised of disease spread pathways (direct, indirect, local, airborne, saleyard), and control measures (detection, movement restrictions, surveillance, direct tracing, indirect tracing, suspect premises reporting, infected premises operations and vaccination). The spread pathways and control measures can be thought of as *components* of the ABM environment. Each component operates independently and concurrently. The AADIS embedded hybrid architecture is a generalisation of the hybrid embedded approach as an ABM is the most flexible form of an individual-based model. For example, an ABM can represent distinct spread pathways like a microsimulation and a network-based model, *or* aggregate spread mechanisms like a spatial-kernel model.

3.4 Within-herd disease spread

AADIS employs a non-spatial, deterministic SEIR compartmental approach to model within-herd spread of FMD (Figure 3.3). Although this introduces additional complexity and computational overhead compared to a pure individual-based approach such as a microsimulation, it captures the multi-scale nature of livestock outbreaks (Section 3.3). For a model of national-scale it is important to be able to distinguish between micro-level disease dynamics (for example, within an intensive feedlot), and those on a macro-level (for example, stemming from very long range livestock movements (Section 2.2)).

$$\frac{dS}{dt} = \mu - \beta I S - \mu S \qquad (3.1)$$

$$\frac{dE}{dt} = \beta I S - \mu E - \sigma E \qquad (3.2)$$

$$\frac{dI}{dt} = \sigma E - \mu I - \gamma I \qquad (3.3)$$

$$\frac{dR}{dt} = \gamma I - \mu R \qquad (3.4)$$

where S = proportion of the herd that are susceptible
E = proportion of the herd that are exposed
I = proportion of the herd that are infectious
R = proportion of the herd that are recovered
$\frac{1}{\mu}$ = average natural lifespan of the host, (μ = birth rate = natural mortality rate)
β = effective contact rate (contact rate $\times$ transmission probability)
$\frac{1}{\sigma}$ = average duration of the latent period, (σ = progression rate from exposed to infectious)
$\frac{1}{\gamma}$ = average duration of the infectious period, (γ = recovery rate)

Figure 3.3. The AADIS EBM ODE system

Each herd is represented by an ODE-based EBM that takes into account the herd type, herd size and the pathogen under study. The rate of animals joining a herd via births and transfers in, is assumed equal to the rate of animals leaving a herd via natural deaths and transfers out. The assumption of a constant herd size, although not quantifiable, is a reasonable concession when modelling on a large-scale. Modelling the spread of disease within a herd deterministically is reasonable for such a highly contagious disease as FMD, that once introduced into a susceptible herd will typically progress unchecked (Meyer and Knudsen, 2001; Carpenter et al., 2003, Kostova-Vassilevska, 2004).

The parameterisation of the EBM ODE system is dependent on the strain of FMD, the relative infectiousness and susceptibility of the species, and the production system (which influences the degree of contact between animals). The baseline ODE configuration is derived from various FMD studies (Carpenter et al., 2004; Orsel et al., 2005; Orsel et al., 2007a; Orsel et al., 2007b; Goris et al., 2009; Orsel et al., 2009; Brito et al., 2011), taking into account characteristics of Australian production

systems. The ODE configuration in Table 3.2 corresponds to the Ebm database table (Section 4.2.1 and Appendices B and C).

Table 3.2. Sample EBM parameterisation

Herd type	Effective contact rate (β)	Latent period (days)	Infectious period (days)	R_0 (derived)	Clinical period (days)	Clinical signs lag (days)	Clinical signs damping	Immune period (days)
Extensive beef	0.7	2	4	2.8	12	5	1	180
Intensive beef	2	2	4	8	12	5	1	180
Feedlot	8	2	4	32	12	5	1	120
Mixed beef	2	2	4	8	12	5	1	180
Mixed sheep	0.8	2	7	5.6	5	5	0.5	180
Dairy	6	2	4	24	12	5	1	180
Small pigs	6	1	4	24	10	4	1	90
Large pigs	8	1	4	32	10	4	1	90
Sheep	0.8	2	7	5.6	5	5	0.5	180
Smallholder	2	2	5	10	9	5	0.75	180

When a susceptible herd becomes infected the ODE system is solved numerically via a 4th-order Runge Kutta method (Cash and Karp, 1990), to yield the SEIR compartmental proportions over time. The EBM further divides the Recovered compartment into the proportion of animals that are naturally immune, vaccine immune or culled. The number of animals in a particular state is obtained by multiplying the compartment proportion by the herd size and rounding to the nearest whole animal. Infected prevalence is defined as the proportion of the herd that is carrying the virus, i.e., the sum of the Exposed and Infectious compartment proportions. Infectious prevalence is defined as the proportion of the herd that is infectious, i.e., the Infectious compartment proportion. Figure 3.4 illustrates how the EBM-generated prevalence curves vary per herd type (using example SEIR initial values of 0.9, 0.1, 0, 0). Clinical prevalence is defined as the proportion of the herd that is exhibiting clinical signs. The clinical prevalence curve (Figure 3.5) is derived from the infected prevalence curve and takes into account a species-dependent lag

between infection and the appearance of clinical signs, and a species-dependent clinical signs damping factor (representing, for example, how sheep exhibit milder clinical signs than cattle) (Table 3.2).

Figure 3.4. EBM infected prevalence per herd type

Figure 3.5. EBM clinical prevalence per herd type
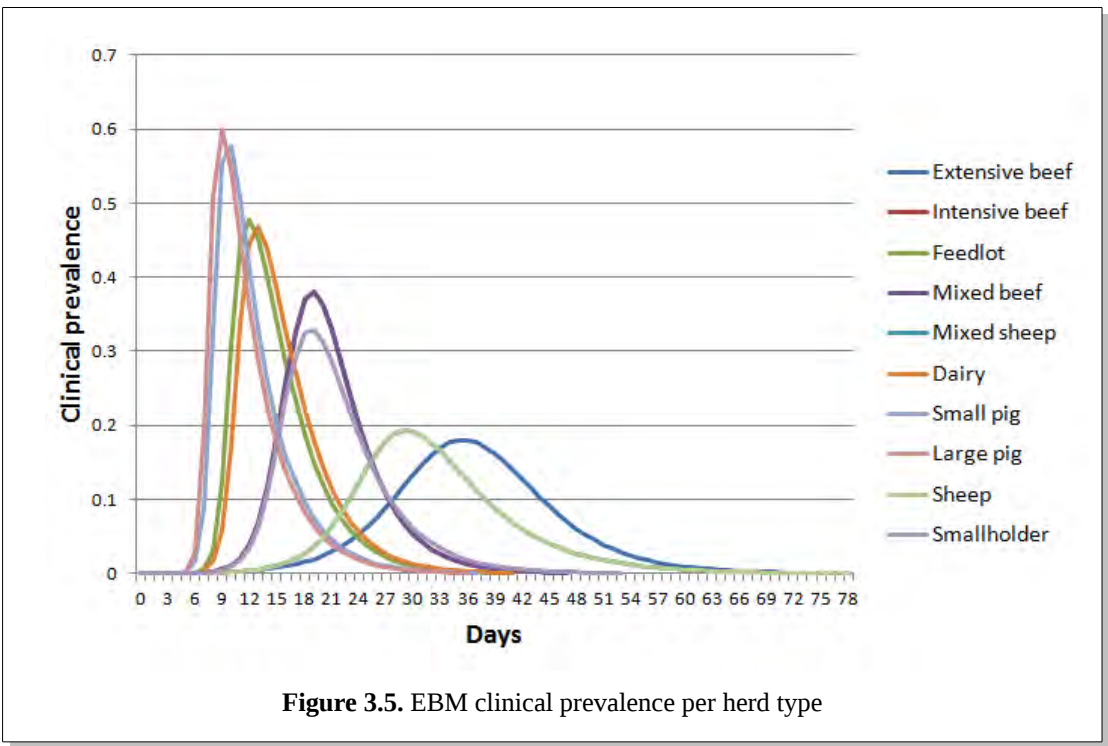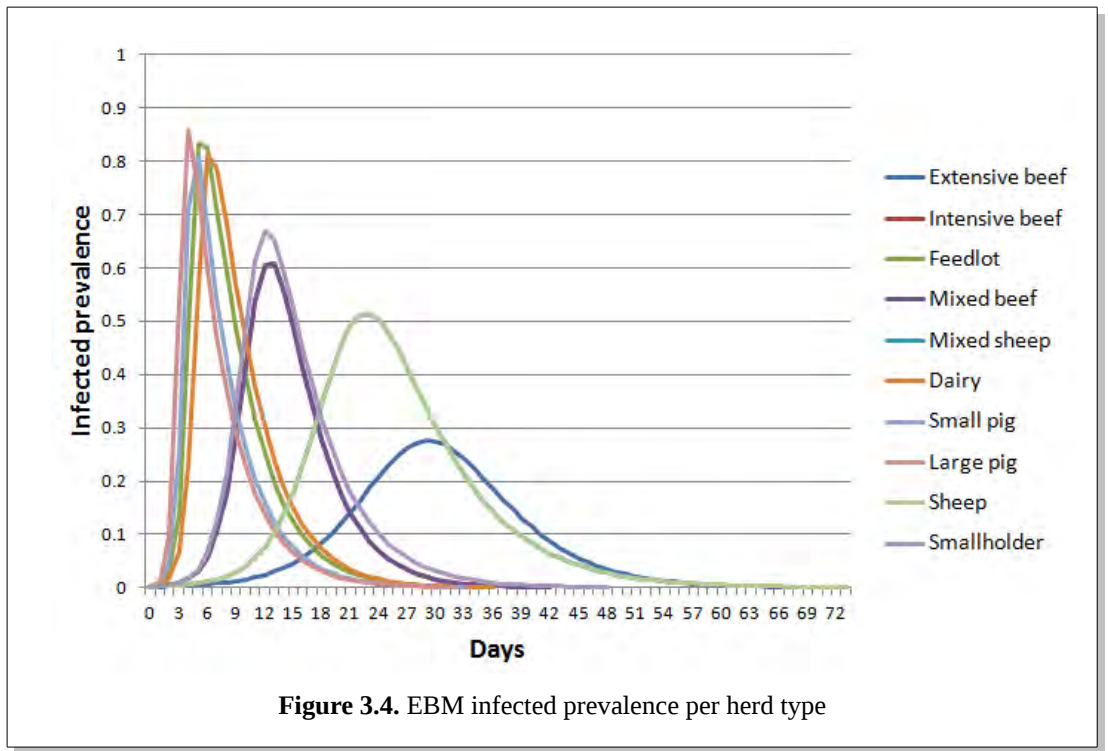
The SEIR ODE-based model was chosen for AADIS as it is well-understood, and easily solved using standard numerical techniques. An ODE-based EBM is computationally efficient as the system is solved once to yield compartment proportions over the entire solution interval. The solution remains in place up until an external event (such as culling or vaccination), acts upon the herd. For example, if a herd is vaccinated the EBM reacts by resolving the ODE system to reflect increasing levels of immunity from the day of inoculation through to effective immunity. The EBM thus *adapts* and provides a dynamic representation of the within-herd infected, infectious and clinical prevalence.

The EBM-generated prevalence curves may be displayed for any infected herd and depict infected prevalence (heat-colours), clinical prevalence (blue), and the normalised infectious prevalence (red) (Figures 3.6, 3.7 and 6.3).
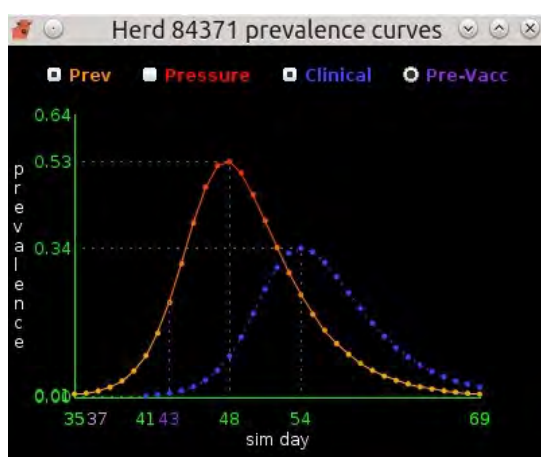
Figure 3.6. Pre-vaccination prevalence curves
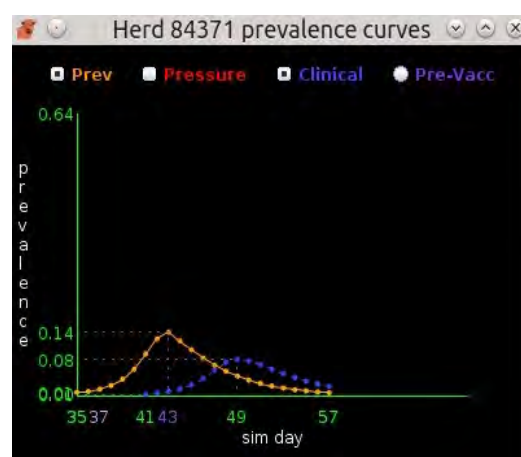
Figure 3.7. Post-vaccination prevalence curves

The prevalence curves in Figure 3.6 depict the EBM solution for a beef herd on simulation day 37 prior to vaccination. Infection started on day 35, peaks with 53% infected prevalence on day 48 and ends on day 69. The prevalence curves in Figure 3.7 shows the same herd, but this time with vaccination occurring on day 37 (light purple). Susceptible animals in the herd achieve immunity on day 43 (dark purple)

resulting in a greatly diminished peak infected prevalence of 14% and an earlier end to infection on day 57.

3.5 Between-herd disease spread

The ABM models the spread of disease between herds through the following pathways:

- Direct contact spread – movement of live animals between premises,

- Saleyard spread – movement of live animals in and out of saleyards/markets,

- Indirect contact spread – movement of animal products, by-products or fomites,

- Local spread – proximity-based contact (e.g., over a boundary fence),

- Airborne transmission – viral plumes conveyed on the wind.

Each spread pathway has an independent algorithm that determines on any given simulation day whether or not disease transfers from an infectious herd to susceptible herd(s). AADIS introduces stochasticity through Monte-Carlo sampling of probability distribution functions (Vose, 2008). The pseudo-code provided in this section conveys the high-level logic for each disease spread component of the ABM environment.

3.5.1 Direct contact spread

FMD can spread when a susceptible animal comes into direct contact with an infectious animal. For example, respiratory transmission can occur between animals sharing a paddock, yard or pen. In the context of the spread of FMD between herds, direct contact through the relocation of live animals is often reported as the most significant means of FMD transmission (Gibbens et al., 2001; Donaldson et al., 2001; Kao, 2002; Green et al., 2006; Kao et al., 2006; Kao et al., 2007; Lindström et al., 2009; Kitching, 2011).

The expected number, size and destination of daily movements into and out of herds, stratified by month, is derived from the NLIS, and various reports and industry

sources (AusVet Animal Health Services, 2005 and 2006; Kokic and Mues, 2006; Hassall and Associates, 2006; Cutler and Holyoake, 2007; East and Foreman, 2011; Hernández-Jover et al., 2014; East et al., 2014a; Wicks and East, 2014). Movements can occur from farms to abattoirs, and between farms. Only movements between farms are potential conduits for disease spread, i.e., movements to abattoirs are considered 'dead-ends' with respect to disease transmission. AADIS only models movements from infected herds since it would be computationally prohibitive to consider all movements from all herds. For each infected herd, the daily likelihood of a movement, the type of herd the movement is directed to, and the movement distance and direction is determined stochastically. This is based on configuration data that includes movement frequencies, distance distributions and contact matrices. Transmission depends on the prevalence of infection in the source herd and the consignment size (Equation 3.5).

$$p_i = 1 - [1 - p(t)]^n \tag{3.5}$$

where

p_i = probability that the consignment contains at least one exposed or infectious animal

$p(t)$ = prevalence of infection in the source herd at time t, where prevalence is defined as the proportion of infectious and exposed animals in the herd (as calculated by the source herd's EBM)

n = consignment size

When a susceptible herd becomes infected an EBM is created and solved with initial conditions based on the proportion of infectious and exposed animals in the consignment, and the size of the destination herd (Equations 3.6 to 3.9).

$$E_d = E_s\, n\, / \,(N_d + n) \tag{3.6}$$
$$I_d = I_s\, n\, / \,(N_d + n) \tag{3.7}$$
$$R_d = 0 \tag{3.8}$$
$$S_d = 1 - E_d - I_d \tag{3.9}$$

where

E_d = proportion of exposed animals in the destination herd

E_s = proportion of exposed animals in the source herd

I_d = proportion of infectious animals in the destination herd

I_s = proportion of infectious animals in the source herd

R_d = proportion of infectious animals in the destination herd

S_d = proportion of susceptible animals in the destination herd
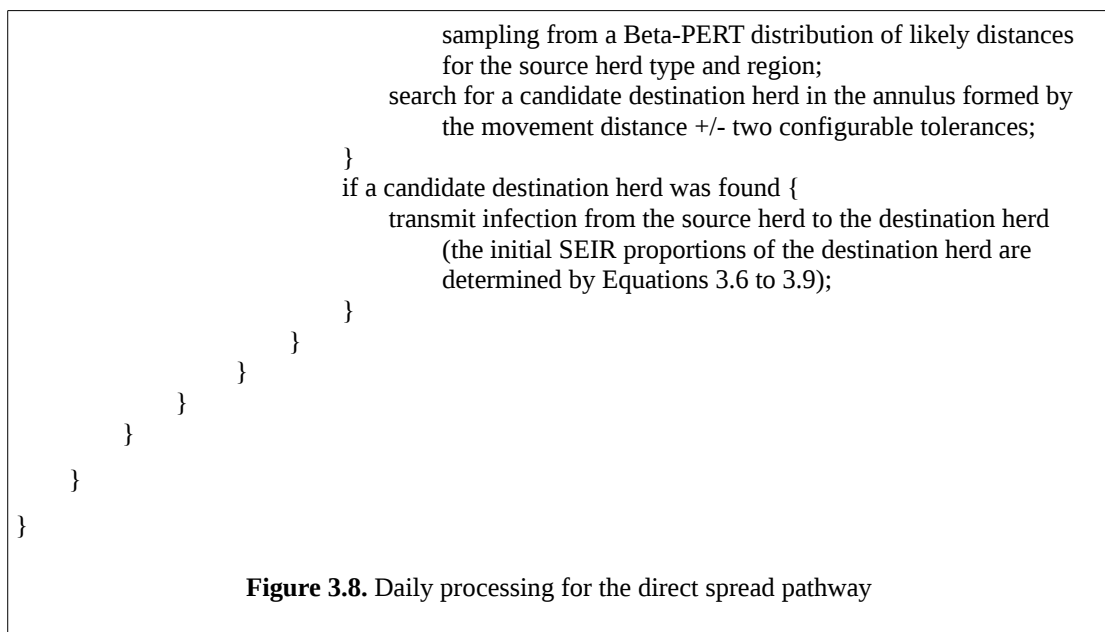
N_d = number of animals in the destination herd

n = number of animals in the consignment

The pseudo-code for the daily processing of the Direct Spread component is presented in Figure 3.8.

```
for (each infected herd) {
    determine if one or more consignments leave the herd by sampling from a Poisson distribution
        of the average number of daily movements for the herd type for the current month;
    for (each consignment) {
        determine the consignment size by sampling from a Beta-PERT distribution of the expected
            consignment size for the herd type and herd size;
        calculate probability $p_i$ that the consignment contains at least one infected animal
            (Equation 3.5);
        determine if the consignment is infected by sampling from a Binomial distribution of $p_i$;
        if (the consignment is infected) {
            if (direct-driven saleyard spread is enabled (Section 3.5.5)) {
                determine the destination premises type by sampling from a cumulative
                    probability distribution of the likely destination type (abattoir, farm or
                    saleyard) for the source herd type;
            } else {
                determine the destination premises type by sampling from a cumulative
                    probability distribution of the likely destination type (abattoir or farm)
                    for the source herd type;
            }
            if (the consigment is destined for a farm) {
                while (a dest herd has not been found within configurable number of attempts) {
                    determine the destination herd type by sampling from a cumulative
                        probability distribution of the likely destination herd types for the
                        source herd type;
                    determine the destination region by sampling from a cumulative probability
                        distribution of the likely destination regions for the source herd type;
                    if (the consignment is intra-region) {
                        determine the movement distance for the consignment by sampling
                            from a Beta Pert distribution of likely distances for the source
                            herd type and source region;
                        search for a candidate destination herd in the annulus formed by the
                            movement distance +/- two configurable search tolerances;
                    } else if (the consignment is inter-region) {
                        search for a candidate destination herd in the destination region;
                    }
                }
                if a candidate destination herd was found {
                    transmit infection from the source herd to the destination herd (with initial
                        SEIR proportions of the destination herd per Equations 3.6 to 3.9);
                }
            } else if (the consignment is destined for a saleyard) {
                determine the number of consignments leaving the saleyard by sampling from a
                    Beta-PERT distribution of the expected number for the source herd type;
                for (each outgoing consignment) {
                    determine the consignment size by sampling from a Beta-PERT distribution
                        of the expected consignment size for the source herd type and size;
                    determine if consignment is destined for a farm by sampling from a
                        binomial distribution of the likelihood based on the source herd type;
                    if (the consignment is destined for a farm) {
                        while (dest herd not found within a configurable num of attempts) {
                            determine the destination herd type by sampling from a
                                cumulative probability distribution of likely destination herd
                                types for the source herd type;
                            determine the movement distance for the consignment by
```

```
                        sampling from a Beta-PERT distribution of likely distances
                            for the source herd type and region;
                        search for a candidate destination herd in the annulus formed by
                            the movement distance +/- two configurable tolerances;
                }
                if a candidate destination herd was found {
                        transmit infection from the source herd to the destination herd
                            (the initial SEIR proportions of the destination herd are
                            determined by Equations 3.6 to 3.9);
                }
            }
        }
      }
    }
  }
}
```

Figure 3.8. Daily processing for the direct spread pathway

3.5.2 Indirect contact spread

Indirect contact transmission arises from the movement between herds of contaminated animal products, by-products, and fomites such as equipment, people and vehicles. Potential sources include veterinarians, shearing contractors, artificial insemination technicians, milk tankers, and feed delivery vehicles. Indirect contacts can be categorised as high, medium or low according to their potential for transmitting infection (Nielen et al., 1996; Bates et al., 2001; Sanson, 2005; Nöremark et al., 2013). In the interests of computational efficiency, AADIS only uses a single category of indirect contacts with a specified average (baseline) probability of transmission. The user can parameterise this to represent different risk profiles. Compared to direct contacts, there is limited data on indirect contacts. The type and location of exposed herds is determined stochastically using a contact matrix and distance distributions by herd type. The indirect spread pathway does not operate inside the local spread area (default 3km radius around each infected herd). This is because the local spread pathway is a proximity-based catchall and aggregates various spread mechanisms such as short-range aerosols, equipment sharing, and boundary fences (Section 3.5.3).

If a herd is exposed through indirect contact, the probability of transmission p_i depends on the infectious prevalence of the source herd, the relative infectiousness of the source herd (based on species and herd size), environmental conditions that influence virus survival, biosecurity practices, and relative susceptibility of the exposed herd (based on species and herd size) (Equation 3.10).

$$p_i = P_b \ p(t) \ w_i \ w_s \ w_b \ w_x \qquad\qquad (3.10)$$

where

> p_i = probability that the indirect contact results in an infection
> P_b = baseline probability that any indirect contact results in infection
> $p(t)$ = normalised infectious prevalence of the source herd at time t
> w_i = infectivity weight of the source herd
> w_s = susceptibility weight of the destination herd
> w_b = biosecurity weight of the destination herd
> w_x = seasonal weight

Tildesley and colleagues (2012), found that a non-linear relationship between herd size and infectivity/susceptibility better described data from the 2001 UK FMD outbreak than a linear relationship. AADIS provides modelling flexibility with user-configurable power law parameters P_i and P_s that specify the level of influence that a herd's size has on infectivity and susceptibility.

Infectivity weights depend on species and herd size, and are normalised across the herd population (Equation 3.11). The relative infectivity constants S_i specify the infectivity of a species to FMD, relative to sheep (Risk Solutions, 2005b). They are defined in the Species database table (Appendices B and C), with default values of cattle = 1.82, sheep = 1, pigs = 1.3, smallholders = 1.11 (Risk Solutions, 2005b). The infectivity powers P_i allow per-species tuning of the effect of herd size on infectivity ($0 \leq P_i \leq 1$, where a value of 0 specifies no effect and a value of 1 specifies a linear relationship). They are defined in the model configuration file with default values of 1.

$$w_i = (S_i \ n^{P_i}) \ / \ population\_mean(S_i \ n^{P_i}) \qquad (3.11)$$

where

> w_i = infectivity weight
> S_i = species relative infectivity (configurable)
> n = herd size
> P_i = infectivity power (configurable)

Susceptibility weights depend on species and herd size, and are normalised across the herd population (Equation 3.12). The relative susceptibility constants S_s indicate the susceptibility of a species to FMD, relative to sheep (Risk Solutions, 2005b). They are defined in the Species database table (Appendices B and C), with default values of cattle = 15.2, sheep = 1, pigs = 0.5, smallholders = 5.7 (Risk Solutions, 2005b). The susceptibility powers P_s allow per-species tuning of the effect of herd size on susceptibility ($0 \leq P_s \leq 1$, where a value of 0 specifies no effect and a value of 1 specifies a linear relationship). They are defined in the model configuration file with default values of 1.

$$w_s = (S_s \; n^{P_s}) \, / \, population\_mean(S_s \; n^{P_s}) \qquad (3.12)$$
where
w_s = susceptibility weight
S_s = species relative susceptibility (configurable)
n = herd size
P_s = susceptibility power (configurable)

The pseudo-code for the daily processing of the Indirect Spread component is presented in Figure 3.9.

```
for (each infected herd) {
      determine if one or more indirect movements occur from the herd by sampling from a Poisson
            distribution of the average number of daily movements for the herd type for the current
            season;
      for (each movement) {
            while (a destination herd has not been found within a configurable number of attempts) {
                  determine the destination herd type by sampling from a cumulative probability
                        distribution of the likely destination herd types for the source herd type;
                  determine the movement distance by sampling from a Beta-PERT distribution of likely
                        distances for the source herd type and source region;
                  search for a candidate destination herd in the annulus formed by the
                        movement distance +/- two configurable search tolerances;
            }
            if (a candidate destination herd was found) {
                  calculate the probability pᵢ that the indirect contact results in an infection (Equation
                        3.10);
                  determine whether the destination herd becomes infected by sampling from a
                        Binomial distribution of the probability of infection pᵢ;
                  if (infection occurs) {
                        determine n = the number of animals infected in the destination herd by
                              sampling from a Beta-PERT distribution of the likely number of infections;
                        transmit infection from the source herd to the destination herd (with initial
                              SEIR proportions of the destination herd per Equations 3.13 to 3.16);
                  }
            }
      }
}
```

Figure 3.9. Daily processing for the indirect spread pathway

When a susceptible herd becomes infected an EBM is created and solved with initial conditions based on the estimated number of exposed animals in the destination herd and the size of the destination herd (Equations 3.13 to 3.16).

$$E_d = n / N_d \qquad (3.13)$$
$$I_d = 0 \qquad (3.14)$$
$$R_d = 0 \qquad (3.15)$$
$$S_d = 1 - E_d \qquad (3.16)$$

where

E_d = proportion of exposed animals in the destination herd
I_d = proportion of infectious animals in the destination herd
R_d = proportion of recovered animals in the destination herd
S_d = proportion of susceptible animals in the destination herd
N_d = number of animals in the destination herd
n = estimated number of exposed animals in destination herd

3.5.3 Local spread

Local spread covers the short-range transmission of disease from an infected herd to neighbouring susceptible herds (Sanson, 1994). Local spread is an important pathway for FMD, particular in high-density farming areas, for example, the majority of the cases in the 2001 UK FMD outbreak were attributed to local spread (Gibbens et al., 2001). The mechanism of local transmission is poorly understood, and could include: short-range aerosol spread across fences; direct spread via the straying of stock; and indirect spread via vehicles, people, surface runoff, and sharing of equipment between neighbours (Gibbens et al., 2001; Kitching et al., 2006). AADIS represents local spread with a spatial kernel that aggregates all spread mechanisms inside a circular area enclosing each infected herd (default radius 3km). The direct, indirect, saleyard and airborne spread pathways do not operate inside the local spread area. All susceptible herds inside a local spread area are deemed at-risk, with the probability of transmission influenced by the distance between an infected herd and a susceptible herd.

The daily processing for the Local Spread component is provided in Figure 3.10.

```
for (each infected herd) {
    for (each susceptible herd within the local spread radius r) {
        calculate the probability pᵢ that the local contact results in an infection (Equation 3.17);
        determine whether the destination herd becomes infected by sampling from a Binomial
            distribution of the probability of infection pᵢ;
        if (infection occurs) {
            determine n = the number of animals infected in the destination herd by sampling
                from a Beta-PERT distribution of the likely number of infections;
            transmit infection from the source herd to the destination herd with the initial infection
                conditions of the destination herd determined by Equations 3.19 to 3.22.
        }
    }
}
```

Figure 3.10. Daily processing for the local spread pathway

The probability of transmission p_i from an infected 'source' herd to each at-risk 'destination' herd is decided stochastically, taking into account: infectious prevalence in the source herd; infectivity of the source herd (based on species and size);

susceptibility of the destination herd; biosecurity measures in place at the destination premises; and the distance between the source and destination herd (Equation 3.17).

$$p_i = P_b \; p(t) \; w_i \; w_s \; w_b \; w_x \; w_d \; w_n \qquad (3.17)$$

where

p_i = probability that the local contact results in an infection

P_b = baseline probability that a local contact between farms results in infection

$p(t)$ = normalised infectious prevalence of the source herd at time t

w_i = infectivity weight of the source herd (Equation 3.11)

w_s = susceptibility weight of the destination herd (Equation 3.12)

w_b = biosecurity weight of the destination herd (depends on herd type)

w_x = seasonal weight (depends on herd type)

w_d = distance weight (Equation 3.18)

w_n = detection weight (reflecting that local spread may organically dampen once an outbreak has been declared due to an increased awareness of risk, and decreased movements of people and vehicles)

The local spread radius, and the probabilities and weights used to calculate the probability of transmission are all configurable (Appendices C and D). Default values are derived from published studies (Sanson, 1993; Gibbens et al., 2001; Honhold et al., 2004; Risk Solutions, 2005a; Risk Solutions, 2005b; Garner and Beckett, 2005; Backer et al., 2012a), taking Australian conditions into account.

Local spread can also occur between herds that are co-resident on the same farm. In this case the baseline probability of transmission P_b (Equation 3.17), is increased to reflect the higher potential for local contact between herds managed on the same farm. The influence of distance between the source herd and target herds is described by a simple linear decay function (Equation 3.18). The closer a herd is to the source, the greater the distance weight w_d and hence the greater the probability of transmission p_i (Equation 3.17).

$$w_d = 1 - (d \, / \, r) \qquad (3.18)$$

where

w_d = distance weight

d = distance from the source herd to the destination herd

r = local spread radius

When a susceptible herd becomes infected, an EBM is created and solved with initial conditions based on the estimated number of exposed animals in the destination herd and the size of the destination herd (Equations 3.19 to 3.22).

$$E_d = n / N_d \qquad (3.19)$$
$$I_d = 0 \qquad (3.20)$$
$$R_d = 0 \qquad (3.21)$$
$$S_d = 1 - E_d \qquad (3.22)$$

where

E_d = proportion of exposed animals in the destination herd
I_d = proportion of infectious animals in the destination herd
R_d = proportion of recovered animals in the destination herd
S_d = proportion of susceptible animals in the destination herd
N_d = number of animals in the destination herd
n = estimated number of exposed animals in destination herd

3.5.4 Airborne spread

Airborne spread is the infection of susceptible animals by virus conveyed on the wind. Pigs pose the greatest threat for airborne spread because of their potential to excrete large quantities of virus relative to other species (Donaldson and Alexandersen, 2002; Alexandersen et al., 2003). The extent of a viral plume depends on the concentration of virus in the source herd, weather conditions and the strain of virus (Donaldson et al., 2001; Donaldson and Alexandersen, 2002; Gloster et al., 2006).

The AADIS approach to airborne spread is similar to that taken by AusSpread (Garner et al., 2006). The Australian Bureau of Meteorology records weather data at a range of weather stations located across Australia (Australian Bureau of Meteorology, 2013). These data are used to create probabilities of the likelihood of airborne spread of FMD per weather station, per month. The most favourable meteorological conditions for airborne spread are: constant wind direction, wind speed of 5 metres/second, high atmospheric stability, no precipitation, and relative humidity greater than 55% (Donaldson et al., 2001). Only pig herds are considered capable of transmitting FMD by airborne spread beyond the local spread area. (Aerosol transmissions within the local spread area are captured by the local spread pathway). For each simulation day, the weather station closest to each infected pig herd is queried as to whether

conditions are suitable for airborne spread. For each pig herd that is deemed to be shedding virus, a sector is constructed in the prevailing wind direction, subtended by a configurable angle of default size 30° (i.e., $\theta=15°$ on either side of the wind direction vector) (Figure 3.11).

Figure 3.11. Airborne spread sector
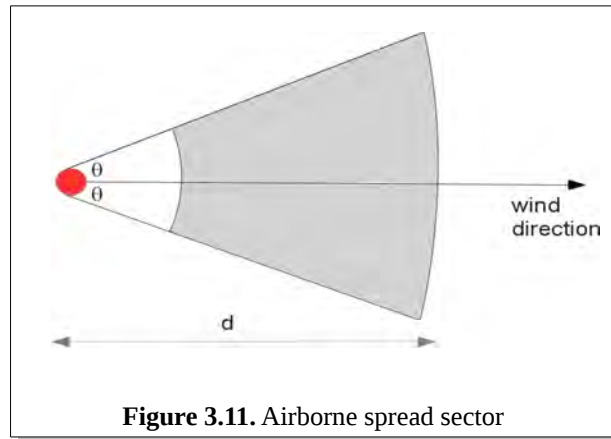
The maximum extent d of a plume depends on the number of infectious pigs in the source herd. Equation 3.23 is derived from data from a study by Donaldson and colleagues (2001), that relates the number of virus-shedding pigs to the distance downwind that cattle and sheep are at risk. The data are based on the type O Pan Asia strain of FMDV that caused the UK 2001 FMD outbreak. The coefficients A and B are configurable and depend on the strain of virus being modelled. Topographical features such as mountains, lakes and forests that might influence a plume are not considered. Although there have been reports of FMD plumes travelling substantial distances in ideal conditions over open water (Donaldson et al., 1982), the anticipated maximum extent of a plume over land is in the vicinity of 10 to 20 km (Mikkelsen et al., 2003; Gloster et al., 2006; Schley et al., 2009). The model constrains the maximum plume distance to a configurable value M (with a default value of 20km).

$$d = \max(A\, e^{B \log n}, M) \qquad\qquad (3.23)$$

where

d = distance of the viral plume

n = the number of infectious pigs in the source herd

$A = 0.113$ (configurable)

$B = 1.367$ (configurable)

M = maximum distance of the viral plume (configurable with default 20km)

Susceptible herds within the airborne spread sector are identified, excluding those within the local spread area (Figure 3.11). The probability of transmission (Equation 3.24), takes into account the susceptible herd species, the size of the susceptible herd, and the distance of the susceptible herd from the infected herd (Donaldson et al., 2001; Garner et al., 2006).

$$p_i = [1 - (1 - P_{sp})^n]\, w_d \qquad\qquad (3.24)$$

where

    p_i = probability that a susceptible herd will become infected

    P_{sp} = probability that a single animal of the susceptible species will become infected. The values are configurable with defaults cattle=0.03, sheep=0.003, pigs=0.00012 and smallholder herds=0.003 (Garner et al., 2006)

    n = size of the susceptible herd

    w_d = distance weight (Equation 3.25 or Equation 3.26)

The distance weight w_d represents the diffusion of a plume with distance from the source herds, and hence the diminishing risk of transmission. Distance weight is configurable as having either linear decay (Equation 3.25), or exponential decay (Equation 3.26). The value of the exponential decay constant C is configurable, with a default value of -6.900776 (obtained by solving Equation 3.27 for a weight w decaying over distance d).

$$w_d = 1 - (h\,/\,d) \qquad \text{(linear decay)} \qquad (3.25)$$
$$w_d = e^{\,(C\,*\,d\,/\,h)} \qquad \text{(exponential decay)} \qquad (3.26)$$

where

    w_d = distance weight

    C = decay constant

    h = distance from the source herd to the destination herd

    d = extent of the viral plume (Equation 3.23)

$$\frac{dw}{dd} = -C\,w \qquad\qquad (3.27)$$

The pseudo-code for the daily processing of the Airborne Spread component is presented in Figure 3.12.

```
for (each infected pig herd) {
      retrieve the weather data for the current month from the nearest weather station;
      determine whether the pig herd is a potential source of airborne spread by sampling from
            a Binomial distribution of the probability of suitable weather conditions;
      if (weather conditions are conducive to airborne spread) {
            calculate the distance that a viral plume may reach from the infected herd (Equation 3.23);
            estimate the bearing that a viral plume may have from the infected herd (Figure 3.11) by
                  sampling from a Beta-PERT distribution of likely bearings for the current month;
            for (each susceptible herd within the airborne spread sector) {
                  calculate the distance from the infected herd;
                  if (the susceptible herd lies within the plume distance) {
                        calculate the bearing from the infected herd;
                        if (the susceptible herd lies within the plume bearing +/- configurable tolerance) {
                              calculate the probability $p_i$ that transmission occurs (Equation 3.24);
                              determine whether the destination herd becomes infected by sampling
                                    from a Binomial distribution of the probability of infection $p_i$;
                              if (infection occurs) {
                                    determine $n$ = the number of animals infected in the dest herd by
                                          sampling from a Beta-PERT distribution of the likely number
                                          of infections;
                                    transmit infection from the source herd to the destination herd with
                                          initial infection conditions per Equations 3.19 to 3.22;
                              }
                        }
                  }
            }
      }
}
```

Figure 3.12. Daily processing for the airborne spread pathway

3.5.5 Saleyard spread

Markets and saleyards have the potential to greatly amplify an outbreak prior to the disease being recognised and controls implemented (Gibbens et al., 2001). The transmission of disease is facilitated by the stresses of transit and handling, large numbers of susceptible animals, and the mixing and partitioning of stock into consignments. Further, outgoing consignments can potentially carry infection to widely dispersed locations (Durr et al., 2010). The rapid escalation of the 2001 UK FMD outbreak is attributed to the unwitting movement of infected sheep to and from markets (Ferguson et al., 2001; Kao, 2002; Mansley et al., 2003; Mansley et al., 2011). A modelling study by Green and colleagues (2006) suggests that the number of infected saleyards strongly influences the eventual outbreak size.

Selling animals through saleyards is an important feature of livestock production in Australia, especially for cattle and sheep (Hassall and Associates, 2007). AADIS saleyard spread is driven by simulated sales of livestock at individual saleyards. The type, frequency and timing of sale events are derived from industry reports (Hassall and Associates, 2007; Durr et al., 2010) and are thus realistic. If a sale happens to involve an infected herd, then a series of stochastic decisions are made to determine the number of outgoing infected consignments, the consignment destination types (herd, feedlot or abattoir), and destination locations. Infection is transmitted to the destination herds with a force relative to the viral load in the consignment.

The pseudo-code for the daily processing of the Saleyard Spread component is presented in Figure 3.13. The vendor 85% catchment is the area relative to a saleyard (in terms of distance and direction), in which 85% of vendor herds are located. The vendor 100% catchment is the area relative to a saleyard (in terms of distance), in which 100% of vendor herds are located. The buyer catchment is the area relative to a saleyard (in terms of distance and direction), in which 100% of buyer herds are located.

```
retrieve the set of sales scheduled for the current day;
for (each sale) {
      search for potential vendors in the vendor 85% catchment area;
      if (insufficient vendors were found) {
            search for potential vendors in the vendor 100% catchment area;
      }

      for (each potential vendor, up until the maximum potential vendors for the current sale) {
            if (the vendor is infected) {
                  determine if the potential vendor contributes animals to the sale by sampling from a
                        binomial distribution based on total number of vendors in the catchment area;
                  if (the vendor contributes animals to the sale) {
                        determine the destination premises type by sampling from a cumulative
                              probability distribution of the likely destination type (abattoir, farm,
                              feedlot) for the sale;
                        if (the destination premises type is farm or feedlot) {
                              determine the number of outgoing consignments for the sale by
                                    sampling from a Beta-PERT distribution of the likely number
                                    for the source herd type;
                              for (each outgoing consignment) {
                                    randomly choose a buyer in the buyer catchment area;
                                    transmit infection from the consignment to the destination herd using
                                          initial SEIR proportions from the vendor herd;
                              }
                        }
                  }
            }
      }
}
```

Figure 3.13. Daily processing for the saleyard spread pathway

AADIS also provides a simplified means of simulating saleyard spread when there is insufficient saleyard or sale data to explicitly represent individual sales. The simplified module is part of the direct spread pathway (Section 3.5.1), and takes into account the frequency and destination of consignments leaving different herd types. On any given day the likelihood that an infected herd sends animals to a saleyard is determined stochastically. Each infected consignment to a saleyard generates multiple infected outgoing consignments based on Beta-PERT distributions. This takes into account disease spread that may occur at the saleyard as well as the splitting and mixing of incoming consignments containing infected animals.

3.6 Disease control and eradication

AADIS has been designed to incorporate the range of control measures defined in Australia's FMD strategy AUSVETPLAN (Animal Health Australia, 2014a; Section 2.3). The ABM models the control and eradication of disease in farms through the following components:

- First IP detection – detection and reporting of the index case,

- Movement Restrictions – establishment of the national livestock standstill, quarantine and controlled areas,

- Surveillance – inspection of DCPs, SPs, TPs and ARPs close to IPs in order to identify infection,

- Tracing – identification of potentially infectious movements on and off infected premises of interest,

- SP Reporting – adhoc reporting of suspicious clinical signs by owners or inspectors,

- IP Operations – depopulation of infected premises, disposal of carcasses and decontamination of premises,

- Vaccination – suppressive vaccination of susceptible animals in infected areas or protective vaccination of susceptible animals in non-infected areas,

- Resources – dynamic allocation of surveillance, culling, disposal, disinfection and vaccination teams on a per jurisdiction basis.

Each control measure component has an independent algorithm that determines on any given simulation day whether or not a control or eradication action is required. The pseudo-code provided in this section conveys the high-level logic for each control measure component of the ABM environment.

3.6.1 First IP detection

The control and eradication phase of an outbreak commences after the declaration of the first infected premises. First IP detection is the means by which AADIS transitions

from the 'silent spread' of disease to the control phase. There are two modes of first IP detection: fixed and passive. Fixed first IP detection is pre-set to occur on a fixed day at a specific or randomly selected farm. Passive first IP detection uses pre-configured probabilities of reporting by herd type, and clinical prevalence to stochastically determine the first day of the detection. Daily processing for first IP detection (Figures 3.14 and 3.15), only occurs up until the first IP has been detected.

3.6.1.1 Fixed detection

Fixed first IP detection occurs on a configured simulation day. This option is useful when comparing alternate control strategies. The detected herd can be:

- specified by ID,

- chosen randomly from all clinically prevalent herds, or

- chosen randomly from a prioritised set of clinically prevalent herds based on species.

Fixed first IP detection is configured via the model configuration file (Appendix D).

```
if (the fixed detection day has been reached and fixed detection has not yet occurred) {
    if (fixed detection is via herd ID) {
        if (the configured herd is or was infected) {
            set the herd's farm classification to IP;
        } else {
            display an error message;
        }
    } else if (fixed detection is via species) {
        build a prioritised herd type list per the configured species priorities;
        while (a target herd has not yet been selected) {
            for (each herd type) {
                if (there are clinically prevalent herds of the desired type) {
                    randomly select a target herd;
                    break;
                }
            }
        }
        if (a target herd has not yet been selected) {
            randomly select a target herd from the set of clinically prevalent herds;
        }
        if (a target herd has not yet been selected) {
            randomly select a target herd from the set of recovered herds;
        }
        if (a target herd was not selected) {
            display an error message;
        }
    } else {
        randomly select a target herd from the set of clinically prevalent herds;
        if (a target herd has not yet been selected) {
            randomly select a target herd from the set of recovered herds;
        }
        if (a target herd was not selected) {
            display an error message;
        }
    }
}
```

Figure 3.14. Daily processing for fixed first IP detection

3.6.1.2   Passive Detection

Passive first IP detection comprises two stochastic processes: detection and reporting. Detection is defined as inspecting stock (on a farm, at a saleyard or in an abattoir), noticing clinical signs and consulting a veterinarian. An infected herd is only a candidate for detection if it meets the minimum clinical prevalence level configured for the herd type. Reporting is defined as a veterinarian suspecting FMD, sending samples to a lab, FMD being confirmed and the Chief Veterinary Officer (CVO) being notified. The detection and reporting probabilities are defined per herd type, per

premises type, in the Passive Reporting database table (Appendices B and C). There is a configurable lag (in days), between the start of the reporting phase and the declaration of the premises as an IP. The confirmation lags are defined in the model configuration file (Appendix D).

```
if (passive detection has not yet occurred) {
    while (not all of the premises types (farms, saleyards, abattoirs) have been checked) {
        randomly choose one of the premises types;
        // NB: detection at an abattoir or saleyard is conditional on animals from an infected
        // herd having being sent there, whereas detection on a farm is a simple daily probability.
        assemble the set of candidate herds exhibiting the minimum clinical prevalence;
        shuffle the set of candidate herds;
        for (each candidate herd) {
            look up the probability of detection for the herd type in the database;
            decide if detection occurs by sampling from a binomial distribution;
             if (clinical signs are detected){
                look up the probability of reporting for herd type in the database;
                decide if reporting occurs by sampling a binomial distribution;
            if (the case is reported) {
                look up the confirmation lag in the model configuration file;
                confirmation day = today + a configurable confirmation lag;
                schedule the transition of the herd's farm to IP;
            }
        }
    }
}
```

Figure 3.15. Daily processing for passive first IP detection

3.6.2 Movement restrictions

A national livestock standstill (minimum of three days), is implemented immediately following detection of the first IP (Animal Health Australia, 2014a). AADIS models livestock standstill by throttling the direct and saleyard spread pathways. The level of restriction depends on standstill status, type of control area, and the spread pathway being throttled. A compliance percentage for each pathway is defined in the AADIS configuration data to allow for the possibility of illegal movements during the standstill. The AADIS configuration data defines the length of the national standstill by jurisdiction. This reflects how individual jurisdictions may extend a standstill beyond the initial three-day national period.

Controlled areas are established around each infected premises in order to restrict the movement of livestock, products and other material. The controlled areas are defined and enforced per-jurisdiction, and may be designated areas (e.g., local government, state/territory), or radius-based around each IP. There are two levels of control: Restricted Areas (RAs) that immediately enclose IPs, and Control Areas (CAs) that enclose RAs. RAs have the highest level of control while CAs have a lower level of control (Animal Health Australia, 2014a). AADIS models the imposition of controlled areas in a staged manner.

Larger controlled areas are enforced at the start of an outbreak. As the control program progresses, the dimensions of the controlled areas are reduced according to configured preferences. Radius-based controlled areas are clipped to fall within the jurisdictional boundaries of the subject IP.
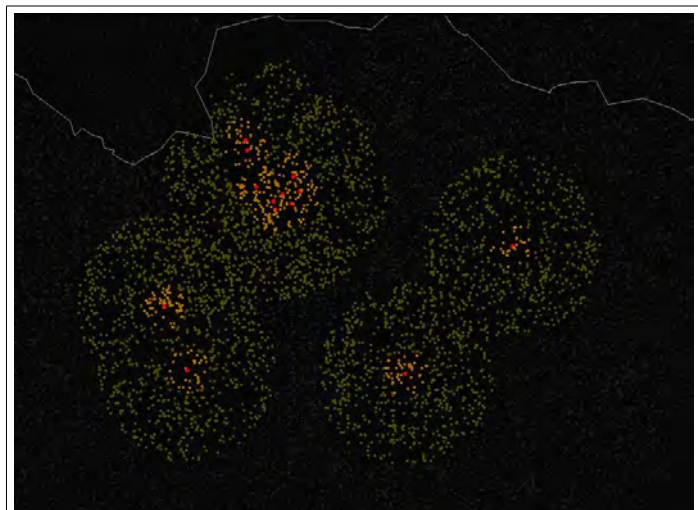
Figure 3.16. Controlled areas enclosing IPs

When IPs are clustered a meta-RA and meta-CA are formed from the union of the constituent RAs and CAs (Figure 3.16). Premises inside an RA and not already classified as an IP, DCP, SP or TP, are designated as ARPs. Premises inside a CA (but outside an RA), and not already classified as an IP, DCP, SP or TP, are designated as PORs (Section 2.3). Spread pathway throttling is described in Figure 3.17. Although the throttling rates are user configurable via the Movement Restrictions database table (Appendices B and C), specific values are used to assist readability.

```
if (jurisdiction has controlled areas) {
        if (RA) {
                throttle direct spread pathway by 98%;
                throttle indirect spread pathway by 85%;
                throttle saleyard spread pathway by 100%;
        } else if (CA) {
                throttle direct spread pathway by 98%;
                throttle indirect spread pathway by 50%;
                throttle saleyard spread pathway by 100%;
        } else { // OA
                if (SP or TP or DCP or VP) {
                        throttle direct spread pathway by 98%;
                        throttle indirect spread pathway by 50%;
                        throttle saleyard spread pathway by 100%;
                } else if (standstill in effect) {
                        throttle direct spread pathway by 98%;
                        throttle indirect spread pathway by 0%;
                        throttle saleyard spread pathway by 100%;
                }
        }
} else { // non-infected jurisdiction
        if (SP or TP or DCP or VP) {
                throttle direct spread pathway by 98%;
                throttle indirect spread pathway by 50%;
                throttle saleyard spread pathway by 100%;
        } else if standstill in effect {
                throttle direct spread pathway by 98%;
                throttle indirect spread pathway by 0%;
                throttle saleyard spread pathway by 100%;
        }
}
```

Figure 3.17. Spread pathway throttling

The Movement Restrictions component is responsible for:

- declaration of the start/end of the national livestock standstill,

- declaration and maintenance of RAs and CAs,

- designation of premises as ARPs and PORs,

- enabling/disabling of movement restrictions.

The pseudo-code for the daily processing of the Movement Restrictions component is provided in Figure 3.18.

```
for (each declared IP) {
        if (this is the first declared IP) {
                declare national standstill with duration per database table;
                initiate movement restrictions per database table;
        }
        create/update RAs around each IP per database table;
        create/update CAs around each RA per database table;
        assign all non-declared premises inside RAs as ARPs;
        assign all non-declared premises outside RAs and inside CAs as PORs;
        if (national standstill has expired) then {
                flag end of national standstill;
                lift movement restrictions for non-infected jurisdictions per database table;
                // note that individual jurisdictions may continue a standstill beyond this point
        }
}
for (each declared RP) {
        if (movement restrictions are due to be lifted per the configurable 'RP lifting delay') {
                remove the RA/CA enclosing the RP;
        }
}
```

Figure 3.18. Daily processing for movement restrictions

When IP operations have completed on an IP it transitions to an RP. Movement restrictions are retained for an RP for a configurable period defined in the model configuration file (Appendix D).

3.6.3 Surveillance

Surveillance is the process by which new infections are identified and declared. During an FMD outbreak, surveillance is used to detect new outbreaks, define the extent of infection, and demonstrate freedom in uninfected areas (Animal Health Australia, 2014a). The Surveillance component carries out visits to DCPs, SPs, TPs and local ARPs. An ARP is local when it is within a configurable distance of an IP (per the model configuration file). The process is labour intensive and is typically limited by the available resources – especially during an extensive outbreak. Resources in demand may include veterinarians, assistants, laboratories and laboratory staff.

Premises that require surveillance are identified through tracing, reporting of suspect premises, and active inspection of premises within RAs. Surveillance visits are prioritised according to risk (Animal Health Australia, 2014a). In AADIS, the priority of a visit is determined by the premises classification and the declared area, and is defined in the Surveillance database table (Appendices B and C). The priority can change dynamically if the status of a premises changes or a pending visit reaches an overdue threshold (defined in the model configuration file). AADIS maintains resource-constrained prioritised queues of premises awaiting a surveillance visit. If multiple premises have the same priority, then arbitration is based on how long a premises has been waiting for a visit. The visit duration (based on herd type), visit frequency (based on priority), and overall surveillance period are configurable. If laboratory samples are required then the result of the surveillance visit is delayed by a configurable period.

AADIS also models the active inspection of premises within RAs. All farms within a designated distance of IPs are subject to a configurable inspection schedule (number and frequency of inspections). The pseudo-code for the daily processing of the Surveillance component is provided in Figure 3.19.

```
for (each surveillance visit currently in progress) { // check for completion
    if (the visit is due to complete today) {
        if (the clinical prevalence of any herd meets the configurable minimum OR any herd
            has been infected for at the least the configurable minimum days) {
            set the premises classification to IP;
        } else {
            if (the subject premises is an SP or DCP) {
                assign premises as ARP/POR/UP per its declared area;
            } else if (the subject premises is a TP) {
                if (today is still within the configurable surveillance period) {
                    schedule the next surveillance visit;
                } else {
                    assign premises as ARP/POR/UP per declared area;
                }
            }
        }
        return the surveillance team to the resource pool;
    }
}

for (each premises queued for a surveillance visit) { // perform queue housekeeping
    if (the premises is now an IP, POR, UP, RP, VP or non-local ARP) {
        remove the premises from the pending list;
    } else if (the premises' current priority has changed) {
        update the premises current priority (and thus where it is in the queue);
    } else if (the premises has been waiting longer than the configurable threshhold) {
        if (the premises is a DCP, SP or TP) {
            increase the premises current priority (and thus where it is in the queue);
        } else if (the premises is an ARP) {
            remove the premises from the pending list;
        }
    }
}

for (each DCP, SP, TP and local ARP) { // check if surveillance is required
    if (the premises is not already under surveillance and not undergoing IP operations) {
        determine the visit priority and frequency per the configuration data;
        schedule a surveillance visit (by adding the premises to the pending queue);
    }
}

while (there are pending visits queued AND a surveillance team is available) { // start visits
    retrieve the highest priority pending visit from the queue;
    request a surveillance team from the resource pool;
    calculate the visit completion date per configuration data;
    update the premises surveillance status as 'visit in progress';
}
```

Figure 3.19. Daily processing for surveillance

3.6.4 Tracing

Tracing is the process of identifying movements on to and off IPs in order to ascertain where infection may have come from, or gone to (Durr et al., 2010). AUSVETPLAN provides minimum periods over which tracing should be carried out (Animal Health Australia, 2014a). Tracing includes animals, products, equipment, vehicles and people. Traced premises may be true cases (and thus infected), or false (not infected). AADIS can readily identify true traces by following infection chains during a simulation, allowing for variable tracing effectiveness by herd type and pathway (direct contact versus indirect contact), and tracing duration. False forward traces are obtained by applying the direct and indirect spread pathways to a premises of interest within the forward tracing window. False backward traces are obtained by reversing the direct and indirect spread pathways over the backwards tracing window (i.e., modelling movements on to the premises of interest). This approach results in a set of plausible false traces, i.e., premises of a suitable type and location that could well have been sources or destinations of movements of concern. TPs that are considered to represent a high risk of having become infected are designated as DCPs, and depending on the control policy may be pre-emptively culled or put under surveillance (Section 3.6.3).

The pseudo-code for the daily processing of the Tracing component is provided in Figure 3.20.

```
for (each IP, DCP and RP) {
        if (the subject premises has not already been traced) {
                determine the trace duration in days (ʙᴇᴛᴀ-PERT distribution based on species);
                determine the trace effectiveness (binomial distribution based on species);
                // conduct true backwards tracing
                if (infection was via the direct/indirect spread pathways AND
                        the 'movement on' occurred inside the backwards tracing window AND
                        the trace was effective) {
                        set the classification of the source premises to true TP;
                }

                // conduct true forwards tracing
                if (the subject premises infected other premises via the direct/indirect pathways
                        AND the 'movement off' occurred inside the forwards tracing window
                        AND the trace was effective) {
                        set the classification of the destination premises to true TP;
                }

                // conduct false backwards tracing
                while (number of trace days < backwards tracing window)) {
                        stochastically decide if the subject premises received a movement;
                        if (a movement occurred) then {
                                stochastically choose a source herd type, source region and
                                        movement distance;
                                find all candidate source herds within the chosen distance;
                                stochastically choose a source herd from the candidate herds;
                                flag the source premises as a false TP;
                                set the source premises as the new subject premises;
                        }
                        number trace days++;
                }

                // conduct false forwards tracing
                reset number of trace days;
                while (number of trace days < forwards tracing window)) {
                        stochastically decide if the subject premises initiated a movement;
                        if (a movement occurred) then {
                                stochastically choose a destination herd type, destination region
                                        and movement distance;
                                find all candidate destination herds within the chosen distance;
                                stochastically choose a destination herd from the candidate herds;
                                flag the destination premises as a false TP;
                                set the destination premises as the new subject premises;
                        }
                        number trace days++;
                }
        }
}
```

Figure 3.20. Daily processing for tracing

3.6.5 SP reporting

AADIS models the ad hoc reporting of suspect cases by owners, inspectors and others. This represents one of the most important mechanisms for identifying new IPs (McLaws et al., 2007). AADIS commences suspect case reporting the day after the first IP has been declared and allows for both true positive and false positive reports. True reports are generated stochastically based on an infected herd's clinical prevalence, the probability of reporting and the expected time to report. The latter two parameters are defined per herd-type in the SP Reporting database table (Appendices B and C). False reports pertain to herds that are showing clinical signs but are not actually infected with FMD. The number of false reports generated is proportional to an n-day (default 3), moving average number of true reports. The ratio of false to true reports is defined in the model configuration file with a default value of 2.34 (McLaws et al., 2007). False reports are assigned to random non-infected herds. The location mix of the false reports is user configurable, for example, 60% in RAs, 30% in CAs and 10% in the OA.

The modelling of both true and false reports allows for more realistic modelling of surveillance. It reflects how team resources are consumed regardless of whether a surveillance visit yields a positive assessment or not.

The pseudo-code for the daily processing of the SP Reporting component is provided in Figure 3.21.

```
if (control has commenced) {
    assemble and shuffle the set of candidate herds with clinical prevalence > 0;
    for (each candidate herd) {
        // conduct true SP processing
        if ((the herd is not on an SP, IP or DCP) and (the herd is not undergoing
            vaccination or IP operations)) {
            lookup min, mode and max 'days taken to report' for herd type in db table;
            calculate reporting probability by sampling a triangular distribution;
            lookup reporting proportion for herd type in the db table;
            decide if reporting occurs by sampling a binomial distribution;
            if (the case was reported) {
                set the herd's farm classification to true SP;
            }
        }
    }
    // conduct false SP processing
    calculate the n-day moving average number of true SPs per configuration data;
    calculate today's expected number of false reports per configuration data;
    calculate today's actual number of false reports by sampling from a Poisson distribution;
    apportion the false reports to RA/CA/OA per configuration data;
    assemble candidate ARPs that are not undergoing vaccination or IP operations;
    randomly assign the required number of RA-located false SPs;
    assemble candidate PORs that are not undergoing vaccination or IP operations;
    randomly assign the required number of CA-located false SPs;
    assemble candidate UPs that are not undergoing vaccination or IP operations;
    randomly assign the required number of OA-located false SPs;
}
```

Figure 3.21. Daily processing for SP reporting

3.6.6 IP operations

IP Operations is comprised of the valuation, destruction and disposal of animals
(stamping out), and decontamination of premises. Stamping out is Australia's default
initial policy for controlling an outbreak of FMD (Animal Health Australia, 2014a). It
is considered the fastest way to reduce viral excretions on IPs and thus dampen
spread. Stamping out is implemented on all IPs, and potentially on DCPs, subject to
risk assessment.

Premises undergoing IP Operations transition through the following states: cull
pending, cull in progress, disposal pending, disposal in progress, decontamination
pending, decontamination in progress, and resolved. Each jurisdiction has separate
pools of teams for culling, disposal and decontamination. When a pool is exhausted

(i.e., all of the teams are on assignment), pending jobs are held in a queue. Visits to premises are prioritised based on premises classification, herd/species priority, herd size, time in queue, and proximity to an IP. The times required for a premises to undergo culling, disposal and decontamination are defined by herd type in the Herd Type database table (Appendices B and C). The decision on whether to conduct pre-emptive culling of DCPs and/or premises contiguous to IPs is defined per jurisdiction in the IP Operations database table (Appendices B and C).

The pseudo-code for the daily processing of the IP Operations component is provided in Figure 3.22.

```
for (each IP Ops job currently in progress) { // check for completion
    if (the job is due to complete today) {
        if (the job is a cull) {
            add the premises to the pending disposal queue;
        } else if (the job is a disposal) {
            add the premises to the pending disinfection queue;
        } else if (the job is a disinfection) {
            transition the premises classification to RP;
        }
        return the IP Ops team to the resource pool;
    }
}
for (each IP) { // check if IP operations is required
    if (IP Ops is configured for all IPs AND the IP is not already undergoing IP Ops) {
        add the premises to the pending culling queue;
        if (IP Ops is configured for adjacent premises) {
            assemble the set of premises within the configured radius of the IP;
            for (each adjacent premises) {
                if (the premises is not already undergoing IP Ops) {
                    add the premises to the pending culling queue;
                }
            }
        }
        if (IP Ops is configured for local SPs) {
            assemble the set of SPs within the configured radius of the IP;
            for (each local SP) {
                if (the premises is not already undergoing IP Ops) {
                    add the premises to the pending culling queue;
                }
            }
        }
    }
}
if (IP Ops is configured for DCPs) {
    for (each DCP) {
        if (the premises is not already undergoing IP Ops) {
            add the premises to the pending culling queue;
        }
    }

}
while (there are pending jobs queued AND an IP Ops team is available) { // start new jobs
    retrieve the highest priority job from the queue;
    request an IP Ops team from the resource pool;
    calculate the job completion day per configuration data;
    update the premises IP Ops status as 'job in progress';
}
```
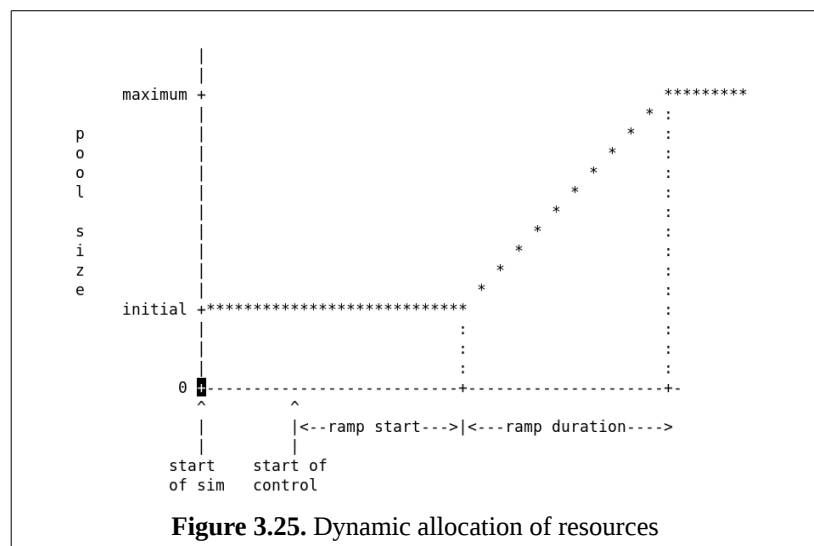
Figure 3.22. Daily processing for IP operations

3.6.7 Vaccination

Vaccination is one of the available options to support stamping out of an FMD outbreak (Bouma et al., 2003; Backer et al., 2012a; Roche et al., 2014; Roche et al., 2015). The decision to vaccinate and the specific role of vaccination in an FMD response varies according to the outbreak scenario (Animal Health Australia, 2014a). Vaccination strategies include:

- Suppressive – vaccination is carried out inside known infected areas (RAs) in order to suppress virus production in at-risk and exposed herds to reduce further spread.

- Protective – vaccination is carried out outside known infected areas in order to protect susceptible animals from infection.

- Mass – vaccination is carried out across a broad area to large numbers of animals. This strategy can be applied if an outbreak is not under control and there is a risk of spread escalating.

AADIS provides two triggers for commencing a vaccination program: on a configurable day into the control program, or once a configurable number of IPs has been declared. AADIS models all vaccination policies with an annulus of configurable inner and outer radii. The inner radius is set to zero for suppressive and mass vaccination. A vaccination annulus is established around each target IP, and eligible premises inside the annulus are scheduled for vaccination. The user can select to only vaccinate around IPs found on or after the day the vaccination program begins, or around all new and previously identified IPs. The vaccination candidates inside each annulus can be prioritised according to herd type, herd size, and proximity to the nearest IP. It is also possible to omit certain herd types from vaccination. The direction of vaccination is configurable from the outside in, or from the inside out.

The effect of vaccination is to increase herd immunity (i.e., reduce a herd's susceptibility to infection) over time. When a partially immune herd is exposed to

infection, the virus production profile generated by the EBM reflects that some of the animals have protective immunity. Figure 3.23 illustrates how a fully susceptible herd's immunity level increases from 0% to 100% over a configurable number of days (default 6), after vaccination is completed.

```
   100% +                                         .*'*'*'*'*
        |                                      .*
  i     |                                   .*
  m     |                                .*
  m     |                             .*
  u     |                          .*
  n     |                       .*
  i     |                    .*
  t     |                 .*
  y     |              .*
        |           .*
    0% *-*-*-*-*-*-*-*-*-*-*--------------------+-------> time
        ^                       ^                   ^
        |                       |                   |
     vaccination            immunity            immunity
      complete                start             complete
      (day v)              (day v + 3)         (day v + 6)
```

Figure 3.23. Herd attaining immunity over time
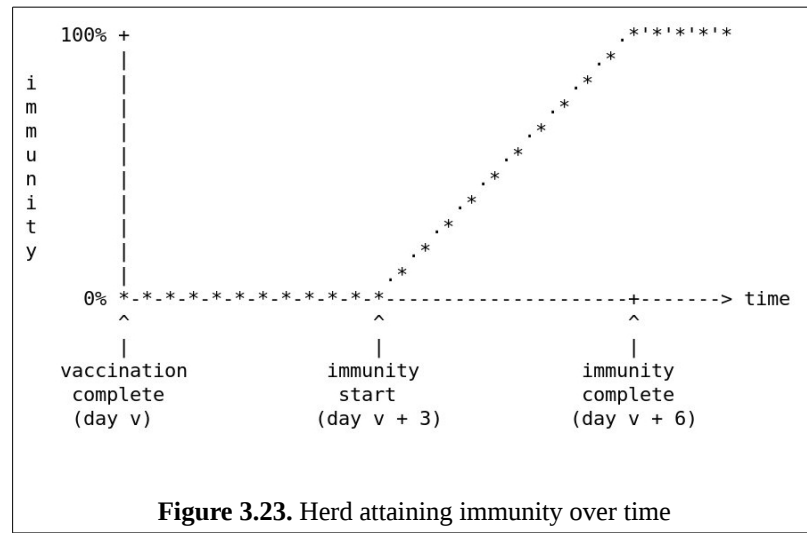
As with surveillance and IP operations, the ability to implement a vaccination program depends on the availability of resources (vaccination teams). Each jurisdiction has a separate pool of vaccination teams. When a pool is exhausted (i.e., all of the teams are on assignment), pending jobs are held in a queue. Visits to premises can be prioritised according to herd type, herd size, time in queue, and proximity to an IP. The time required for a premises to undergo vaccination is defined by herd type in the AADIS configuration data.

The pseudo-code for the daily processing of the Vaccination component is provided in Figure 3.24.

```
if (the control program has commenced and the vaccination program has not yet commenced) {
    if (vaccination is configured to start by control day) {
        if (today is greater than or equal to the first IP detection day +
            the configured vaccination start day) {
            flag the commencement of the vaccination program;
        }
    } else if (vaccination is configured to start by IP count) {
        if (the cumulative number of IPs is greater than or equal to the configured
            vaccination start IP count) {
            flag the commencement of the vaccination program;
        }
    }
}
if (the vaccination program has commenced) {
    for (each vaccination visit currently in progress) { // check for completion
        if (the visit is due to complete today) {
            set the premises vaccination state to vaccinated but not immune;
            return the vaccination team to the resource pool;
        }
    }
    for (each IP) { // check if vaccination is triggered
        if (vaccination is configured for all IPs OR (vaccination is configured for new
            IPs only AND the IP was declared on or after the start of the vaccination
            program) AND the IP has not already triggered a vaccination) {
            determine the vaccination annulus dimensions per database configuration data;
            find all candidate ARPs, PORs and UPs inside the annulus that are in the
                same jurisdiction as the IP AND are not already undergoing
                vaccination AND are not undergoing IP operations;
            schedule vacc visits (by adding candidate premises to pending queue);
        }
    }
    while (there are pending visits queued AND a vacc team is available) { // start visits
        retrieve the highest priority pending visit from the queue;
        request a vaccination team from the resource pool;
        calculate the visit completion date per configuration data;
        update the premises vaccination status as 'visit in progress';
    }
}
```

Figure 3.24. Daily processing for vaccination

3.6.8 Resources

The resources required to manage an emergency animal disease outbreak include: personnel (including veterinarians, animal health officers, control centre staff and security staff); equipment (including vehicles and pen-side diagnostic tests); facilities (including laboratories, rendering plants and landfill/burial sites); and consumables (including vaccine and disinfectant). Some aspects of disease control and eradication

are resource-intensive and shortfalls can severely hamper the response to an outbreak (Bourn, 2002; Anderson, 2002; Matthews, 2011; Garner et al., 2014; Roche et al., 2014). During the UK 2001 FMD control program, the backlog of animals awaiting culling peaked at 622,000 and the backlog of carcasses awaiting disposal peaked at over 230,000 (Anderson, 2002).

AADIS models the personnel resources required for the key operational activities of surveillance, culling, disposal, decontamination and vaccination. As state and territory governments are responsible for their own emergency animal disease management (Animal Health Australia, 2014a), the teams are organised into pools by jurisdiction (i.e., each jurisdiction has five pools). It is anticipated that resource levels ramp up over time, so initially the pools are small and increase in a linear manner up to a maximum size (Figure 3.25). The initial pool size, duration of the ramp-up, and maximum pool size are defined in the Resources database table (Appendices B and C), by resource type and by jurisdiction.

```
               |
               |
     maximum   +                                        ********
               |                                   * :
       p       |                                 *   :
       o       |                               *     :
       o       |                             *       :
       l       |                           *         :
               |                         *           :
       s       |                       *             :
       i       |                     *               :
       z       |                   *                 :
       e       |                 *                   :
     initial   +**************************           :
               |                     :               :
               |                     :               :
               |                     :               :
          0    +-----------------------------+-------+-
               ^         ^
               |         |<---ramp start--->|<---ramp duration---->
               |         |
             start     start of
             of sim    control
```
Figure 3.25. Dynamic allocation of resources

AADIS tracks the availability and allocation of resources to provide immediate feedback as to whether/where the control program is resource constrained. Resource backlogs are recorded (Appendix E), and this allows the resource requirements for a particular scenario to emerge as a modelling outcome (as opposed to a pure top-down

approach that prescribes resourcing levels ahead of time). The pseudo-code for the daily processing of the Resources component is provided in Figure 3.26.

```
while (the current simulation day is in progress) {
        if (a component requests a team) {
                if (a team is available for the requested jurisdiction) {
                        decrement the number of available teams in the applicable pool;
                        advise the component that a team has been dispatched;
                } else
                        advise the component that no teams are available;
                }
        }
        if (a component releases a team) {
                increment the number of available teams in the applicable pool;
        }
}
for (each jurisdiction) {
        update the pool sizes per the ramping algorithm;
}
```

Figure 3.26. Daily processing for resources

3.7 Summary

This chapter first reviewed the three options for the modelling unit of interest for an FMD model of national-scale: the animal, the herd and the farm. AADIS takes the novel approach of modelling the spread of disease on a per-herd basis and the control and eradication of disease on a per-farm basis. The Australian population of over 107 million FMD-susceptible livestock was then characterised into 235,668 herds of ten types, located on 202,775 farms.

The AADIS hybrid architecture was presented whereby each herd agent has an embedded mass-action EBM that deterministically models the spread of disease within the herd. The EBM is specialised for the herd type, herd size and strain of FMD, and generates infected, infectious and clinical prevalence predictions over time. The herd agents participate in an ABM that stochastically models the spread of disease between herds, and the control and eradication of disease on farms. The

epidemiology, algorithms and formulae for each of the ABM spread and control components were described.

This chapter illustrated the complexities involved in modelling the spread and control of FMD in Australia on a national scale. One of the aims of the project is the ability to conduct complex national-scale simulations on a standard desktop computer. Compounding this challenge is the need for a stochastic model to re-run a given scenario hundreds, if not thousands of times to allow outcome distributions to stabilise. The next chapter presents highlights of the software design and implementation that has made this possible.

4 SOFTWARE DESIGN AND IMPLEMENTATION

Chapter 3 described the extensive functionality required for a model to support FMD policy and planning. An Australian national model of livestock disease spread and control must handle a population of over 100 million animals spread across approximately 236,000 herds. It has to capture heterogeneities of species, environment, region, production systems and marketing systems that influence the spread of FMD, and provide highly configurable disease management and control measures, taking into account jurisdictional heterogeneities in both policy implementation and resourcing. Further, the model must be computationally efficient such that it is feasible to run a given scenario perhaps thousands of times on a desktop computer. The NetLogo, Repast and Mason modelling frameworks (Section 2.4.2.5), were reviewed at the commencement of the PhD project. At that point in time they were not capable of supporting a model that potentially had over 100 million discrete agents. It was decided that a high level of control would likely be needed over the model architecture, software architecture and implementation. As such, a custom development was undertaken in lieu of employing an off-the-shelf agent-based modelling framework.

AADIS is written in Java (Oracle, 2015) and runs under either Linux™ or Windows™. AADIS employs open-source products such as SQL Power Architect (SQL Power Group, 2015), PostgreSQL (PostgreSQL, 2015), Log4j (Apache, 2012) and OpenMap (BBN, 2015). Natively compiled languages with low-level memory management such as C and C++ are popular language choices for applications that are computationally intense and/or have real-time processing requirements. Although AADIS is computationally intense, it does not have real-time processing requirements. Java offers platform-independence courtesy of the Java Virtual Machine (JVM) and a rich collection of utility libraries. The delegation of low-level memory management to the JVM results in a development environment that is 'safer' from subtle bugs arising

from memory mismanagement. Parker and Epstein (2011) describe how the Java-based GSAM pandemic model scales up to 6.5 billion agents distributed across a 32-node HPC cluster.

This chapter provides an overview of the static architecture, dynamic architecture and implementation highlights. AADIS is a substantial piece of software, comprising over 28,000 lines of code across 271 classes. As such, only the key design and implementation themes are presented.

4.1 Agent-based model

At the heart of the AADIS architecture is a custom ABM comprising lightweight agents and an active concurrent environment. Each spread pathway and control measure is a component of the ABM environment.

4.1.1 Active ABM environment

An ABM is comprised of autonomous agents that interact with each other, and with the environment. The relative complexity of the agents and the environment depends on the modelling domain. An ABM environment can be as simple as a two-dimensional lattice or as complex as a nation. An agent can be as simple as a cell, or as complex as the resident of a large city. A livestock epidemic exists in a complex, heterogeneous and irregular environment (with respect to climate, geography, biosecurity levels on individual farms, production systems, market systems, and jurisdiction-dependent disease control policies and resourcing). In a similar spirit to Claude Bernard's counter to Louis Pasteur's germ theory, that the 'pathogen is nothing, the terrain is everything' (Longmore et al., 2014), an agent outside the context of an environment is 'effectively useless' (Odell et al., 2003). If you 'remove' the environment from an outbreak you are left with a disconnected meta-population of susceptible herds that will never interact with virus carrying animals, plumes or fomites, and thus never become infected. The importance of the outbreak environment is reflected in the AADIS design priority of a detailed ABM environment that is

spatial, stochastic, active and concurrent, and herd agents that are simplified and lightweight.

At the start of a simulation day the environment components independently and concurrently proceed with their daily processing, making various stochastic decisions on the spread and control of disease amongst the herd population. During the simulation day all data accesses to the cohort of herd agents are read-only. As each component finishes its daily processing a set of herd/farm update requests are sent asynchronously to the ABM 'scheduler' where they are queued. When all updates for the day have been received, they are collated and submitted to the cohort of herd agents. If, for example, a herd agent receives a vaccination message it reacts by resolving its EBM ODE system which yields updated predictions for infected, infectious and clinical prevalence. Once all the queued herd/farm updates have been processed the new herd/farm reality is released back into the environment for the start of the next simulation day.

4.1.2 Component coordination via the blackboard pattern

As the environment components are independent and concurrent it is inevitable that at some stage one or more components will send update messages for the same herd/farm. It is the job of the ABM scheduler to arbitrate in this case and choose a particular update to succeed. The arbitration may be random or rule-based. For example, if the direct and indirect spread pathways both attempt to infect the same herd on the same day then the scheduler randomly selects one pathway to succeed. On the other hand, if for example, the IP Operations component and the Vaccination component both attempt to control the same farm on the same day, then the scheduler always gives priority to IP Operations. There are parallels between the ABM architecture and the blackboard design pattern that is sometimes employed in artificial intelligence applications (Corkhill, 1991; Buschmann et al., 1996; Dong et al., 2005; Bandini et al., 2009). Each ABM component is an independent 'knowledge source' for a specific aspect of an FMD epidemic. The cohort of herds/farms is the 'blackboard' from which the knowledge sources obtain their view of the problem domain. The

knowledge sources work independently and concurrently on their sub-problem with no knowledge of, or assistance from, other knowledge sources, and iteratively contribute partial solutions to the overall problem onto the blackboard. The ABM scheduler is the blackboard 'controller' and arbitrates when knowledge sources submit conflicting partial solutions. Over time, a solution to the greater problem emerges on the blackboard. In the case of an FMD epidemic, the emergent 'solution' is the spatiotemporal spread and control of disease in the population of herds/farms.

The blackboard pattern stems from the analogy of multiple professors (knowledge sources), working on a complex problem and sharing a single chalkboard. Each professor works on the problem purely from the point of view of their individual specialities. Whilst individual professors cannot solve the problem alone, the iterative sharing of partial solutions on the blackboard contributes to the group's overall understanding of the problem (Figure 4.1).
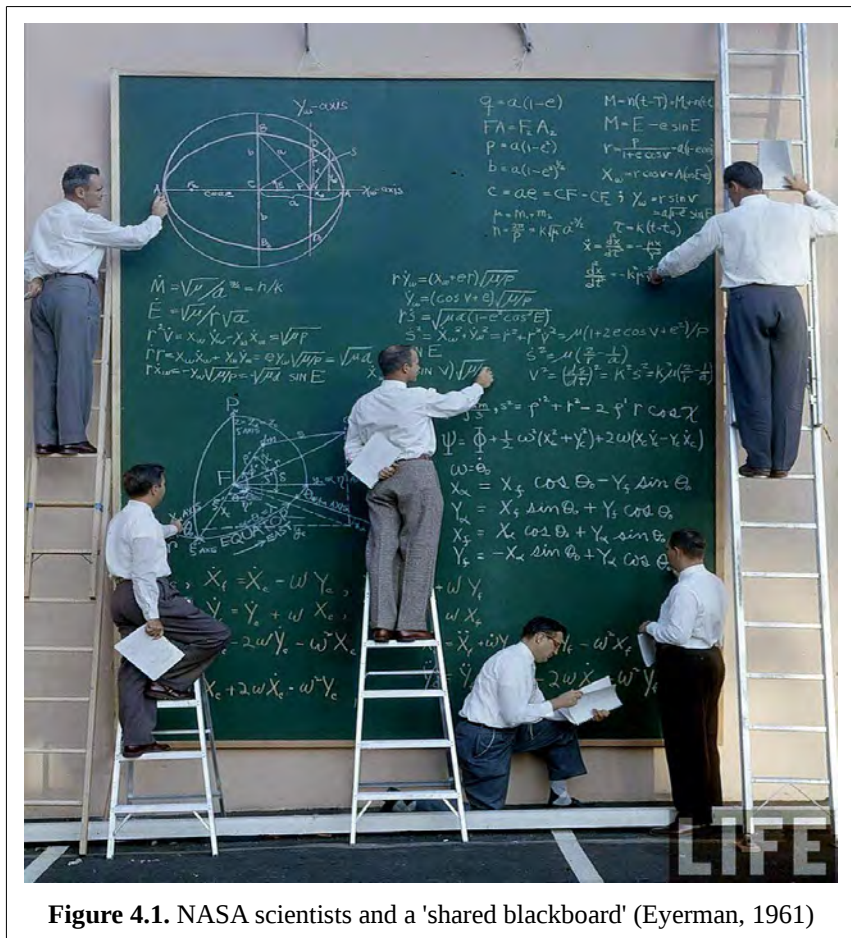
Figure 4.1. NASA scientists and a 'shared blackboard' (Eyerman, 1961)

4.1.3 Lightweight agents

Agents in an ABM are autonomous and in a simple software implementation this usually equates to an agent having its own thread of execution. This approach however does not scale well for large populations as platform thread/process limits are quickly reached (Bellifemine et al., 2001; Shi et al., 2014). In the absence of a specialised parallel hardware platform it is simply not feasible to have large numbers of threads/processes. Large populations can be handled through strategies such as lightweight agents that share pools of threads (Kim et al., 2007), custom memory management (Parker and Epstein, 2011), and aggregated 'super-individuals' (Parry and Evans, 2008). Each AADIS herd agent has autonomous state and logic but is not threaded. All updates to herd agents are carried out on the ABM Scheduler's thread at the end of each simulation day.

4.1.4 Advantages of concurrent processing

The AusSpread microsimulation simulates the spread and control of disease in discrete time steps of a day. The constituent tasks of a simulation day are carried out sequentially, i.e., disease is given the opportunity to spread in turn over the local, direct, indirect, saleyard and airborne pathways, and then the surveillance, stamping out, tracing, vaccination and movement restrictions control measures are conducted. Even though the order of these may be randomised, they still occur sequentially. The execution time of a simulation day is largely the sum of the times needed for each constituent task. AADIS also operates in discrete time steps of a day, but has an asynchronous architecture that supports concurrent processing. All ABM environment components have an independent thread of execution and the constituent tasks of a simulation day occur concurrently. This approach is computationally efficient as it takes advantage of the inexpensive parallelism available on a multi-core desktop computers. The execution time of a simulation day is effectively only limited by the longest time taken by any one component. A benefit of each component executing on its own thread is that it allows computationally intensive components to be easily identified and potentially assigned higher runtime thread priorities.

Components have varying day-to-day computational demands depending on the nature of the scenario and the particular simulation day. Daily runtimes per component are (optionally) written into the AADIS log file. Table 4.1 presents the average daily runtime in milliseconds for each ABM component over the course of 1000 runs. The times are taken from the comparison study of AADIS with AusSpread in Section 5.2. Only the silent spread (SS) and stamping out with suppressive ring vaccination (SORV) scenarios are used – refer to Section 5.2 for definitions. The table shows that on average, the Indirect Spread and Local Spread components are more computationally intense than the Direct Spread and Airborne Spread pathways. (The Saleyard Spread component runtimes are included in the Direct Spread runtimes as the comparison employs the simpler non-sale-based saleyard spread pathway). The table also shows that the Movement Restrictions and Surveillance components are the most computationally intensive control measures. This type of information is useful from a development and test perspective as computational bottlenecks are easily identified. For example, given the concurrent architecture, there is not much value in improving the runtime efficiency of the Direct, Local and Airborne components as the predominant daily computational drain is generally the Indirect component.

A concurrent modelling approach also reflects the epidemiological reality that spread and control proceed independently and in parallel during an outbreak.

Table 4.1. Average daily runtimes of the ABM components

Scenario Name	Direct Spread [1]	Indirect Spread [1]	Saleyard Spread [1,2]	Local Spread [1]	Airborne Spread [1]	First Detection [1]	Movement Restrictions [1]	SP Reporting [1]	Tracing [1]	Surveillance [1]	IP Operations [1]	Vaccination [1]
42189 SS	1.148	4.663	N/A	2.092	0.400	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7779 SS	1.728	5.305	N/A	2.032	0.398	N/A	N/A	N/A	N/A	N/A	N/A	N/A
33812 SS	1.767	4.285	N/A	2.120	0.001	N/A	N/A	N/A	N/A	N/A	N/A	N/A
98 SS	0.021	0.203	N/A	0.058	0.003	N/A	N/A	N/A	N/A	N/A	N/A	N/A
315 SS	0.299	0.752	N/A	0.589	0.000	N/A	N/A	N/A	N/A	N/A	N/A	N/A
42189 SORV	1.251	2.592	N/A	2.589	0.122	0.00	2.831	0.000	0.008	0.281	0.030	0.100
7779 SORV	1.711	2.792	N/A	3.066	0.168	0.000	4.331	0.003	0.013	0.361	0.068	0.171
33812 SORV	1.232	2.012	N/A	2.226	0.003	0.000	2.527	0.002	0.002	0.189	0.008	0.063
98 SORV	0.012	0.019	N/A	0.032	0.000	0.001	0.004	0.001	0.004	0.000	0.001	0.000
315 SORV	0.190	0.306	N/A	0.462	0.002	0.002	0.212	0.001	0.011	0.011	0.000	0.001
Mean	**0.936**	**2.293**	**N/A**	**1.527**	**0.110**	**0.001**	**1.981**	**0.001**	**0.008**	**0.169**	**0.021**	**0.067**

[1] average daily runtime in milliseconds

[2] the Saleyard Spread component runtimes are included in the Direct Spread runtimes as the scenarios employed direct-driven saleyard spread (Section 3.5.5)

4.2 Subsystems

Figure 4.2 depicts the major AADIS subsystems and some important control/data flows between them. The diagram is a high-level summary of the key functional software areas – there is no implied sequencing information. Individual subsystems are described in subsequent sections with UML class diagrams (Fowler and Scott, 2000).

Figure 4.2. Main AADIS subsystems
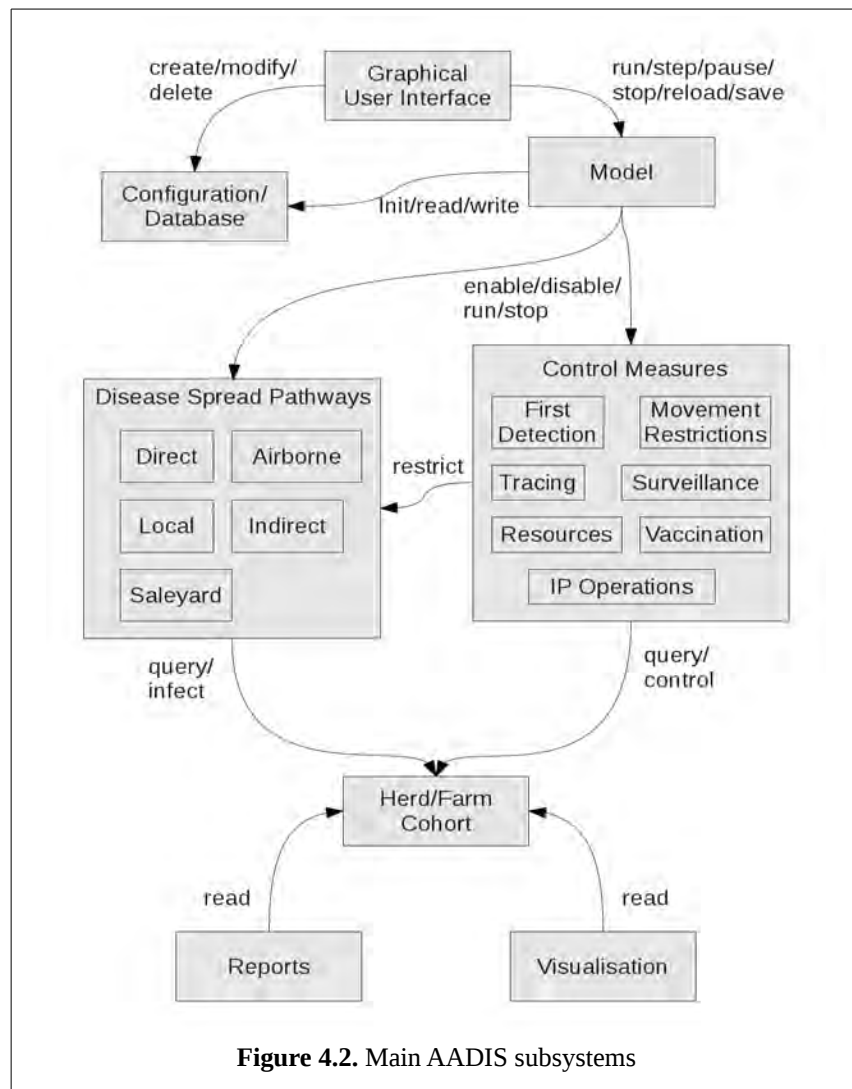
4.2.1 Database subsystem

A relational database (PostgreSQL, 2015) is used to store data that typically does not change often and may be large with cross-dependencies. This includes the herd population, weather data, movement patterns and pathogen specific parameters. An example of a cross-dependency is the Herd table which contains references to several other tables (herd type, farm type, region, weather station and local government area (LGA)). To ensure referential integrity, any change to a table requires a database rebuild. The Database subsystem provides offline database creation and online database access.

4.2.1.1 Database creation

AADIS database creation is comprised of three distinct activities (Figure 4.3).

- Database schema design - The SQL Power Architect data modelling tool (SQL Power Group, 2015) is used to create and maintain the relational database schema (Appendix B), and generate the corresponding data definition language (DDL) script.

- Dataset creation – A Comma-Separated Values (CSV) input data file is created for each relational table defined in the schema (Appendix C).

- Database creation and population – The AADIS database builder uses the DDL script and CSV data files to create and populate the database.
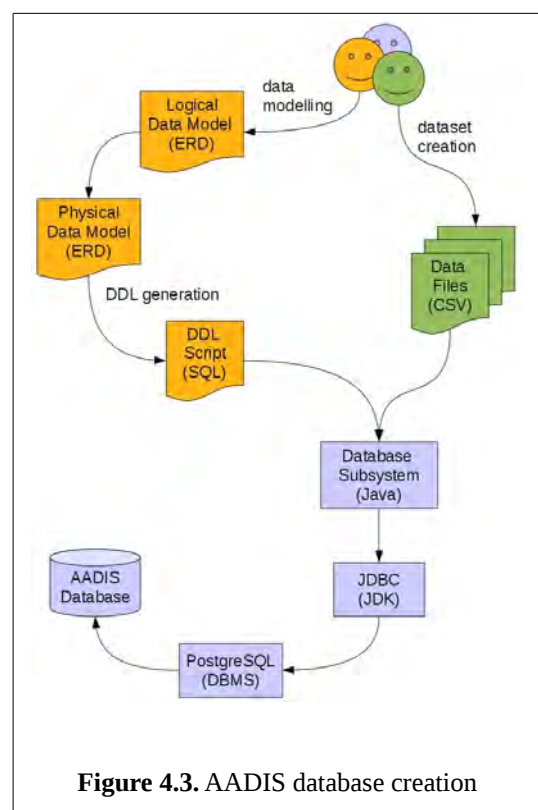
Figure 4.3. AADIS database creation

4.2.1.2 Database classes

The classes in the Database subsystem are presented in Figure 4.4.

Figure 4.4. Classes in the Database subsystem
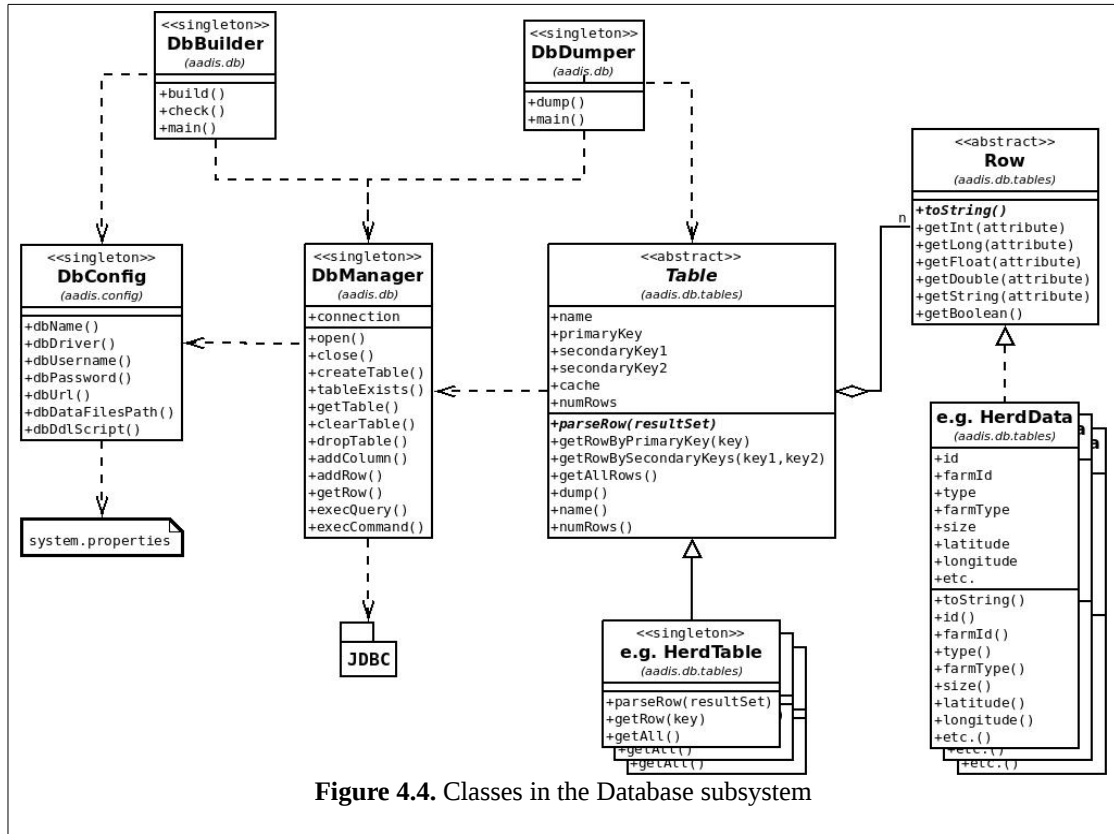
The database builder is a standalone program included in the **DbBuilder** class. It uses the DDL script and CSV data files to create and populate the database from scratch. The builder also provides a simple check as to whether the database is synchronised to the DDL and CSV input files. The check compares the size and modification date of each input file with that recorded at the time of the last database build. The **DbManager** class interfaces to the PostgreSQL database via the Java database connectivity (JDBC) application programming interface. It is responsible for database connections, general table operations (such as create, update, clear, and drop), and execution of arbitrary Structured Query Language (SQL) commends/queries. The database dumper is a standalone test program included in the **DbDumper** class. It accesses and dumps database tables via the **DbManager** class in the same way that

the model accesses the database. The **Table** and **Row** abstract classes provide generic access to any database table. The concrete classes (e.g., **HerdTable** and **HerdData**), capture table and row specifics. The concrete classes are simplified due to inheritance and polymorphism provided by the **Table** and **Row** abstract classes. This means that adding new tables and new table columns is primarily declarative. The cohort of **Table** and **Row** concrete classes form a simple in-memory database.

4.2.1.3   In-memory database

During model initialisation all data is retrieved from the disk-based relational database and cached in a custom in-memory database. The in-memory database provides access based on primary or secondary keys in terms of microseconds (rather than in terms of milliseconds through SQL exchanges with the PostgreSQL server). As AADIS caches all database tables, there are no further accesses to the database after model startup. When a spread pathway requires the distance and/or bearing between two herds, mathematical calculations are performed on points of latitude and longitude (as opposed to issuing geospatial SQL queries into the relational database). There is no requirement to dynamically write AADIS data back into the database. Epidemiological outputs are written to CSV files for external statistical analysis. AADIS uses the database purely as an offline organizational aid for large datasets and to ensure relational consistency between tables.

4.2.2 Configuration subsystem

The classes in the Configuration subsystem are presented in Figure 4.5.

Figure 4.5. Classes in the Configuration subsystem
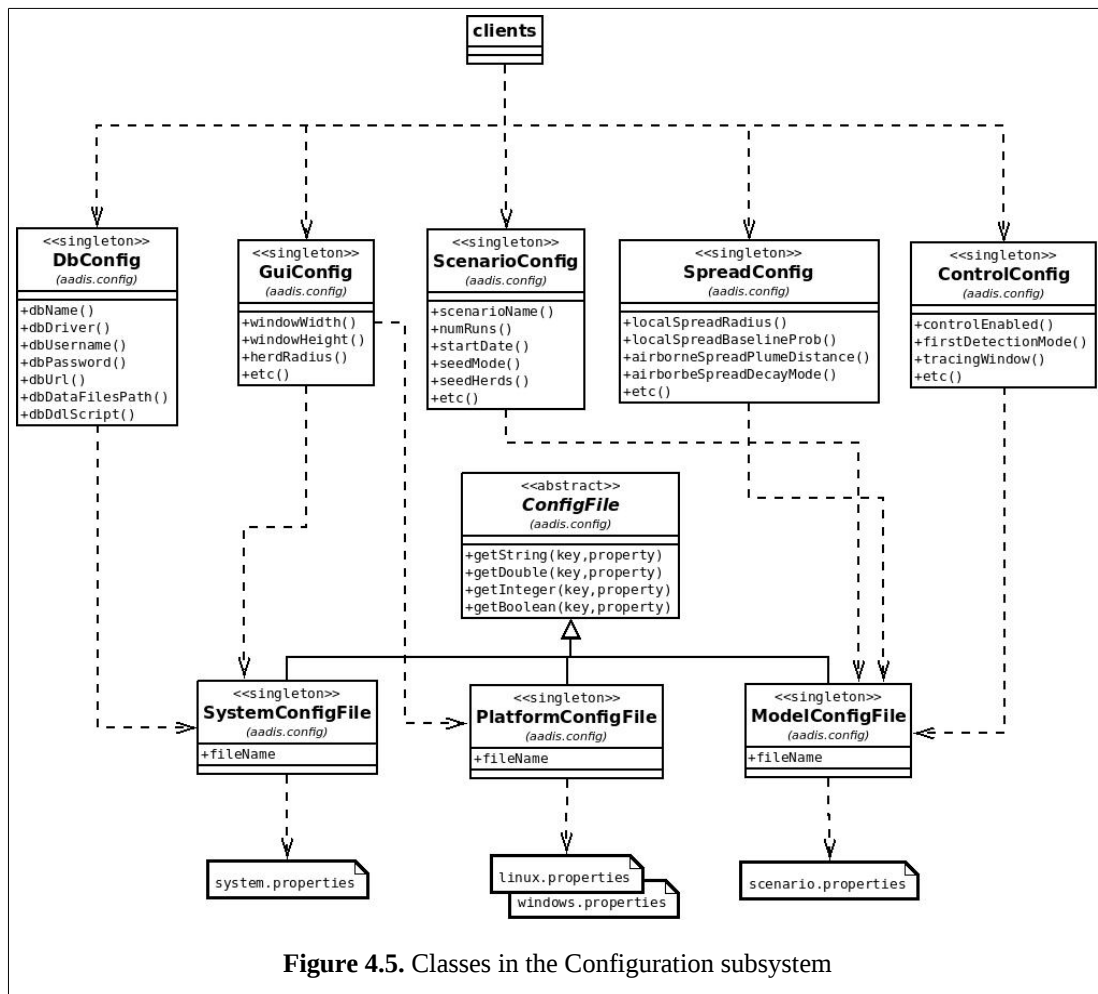
The **ConfigFile** abstract class provides generic access to key/value pairs in a Java properties file (i.e., string, double, integer and Boolean values for a specified key). The **SystemConfigFile**, **PlatformConfigFile** and **ModelConfigFile** concrete classes provide access to the AADIS system, platform and model configuration files respectively. Clients retrieve configuration data on a functional basis from the **ControlConfig**, **DbConfig**, **GuiConfig**, **ScenarioConfig** and **SpreadConfig** classes. Clients are insulated from the specifics of how and where configuration data is stored.

4.2.3 Model subsystem

The classes in the Model subsystem are presented in Figure 4.6.

Figure 4.6. Classes in the Model subsystem
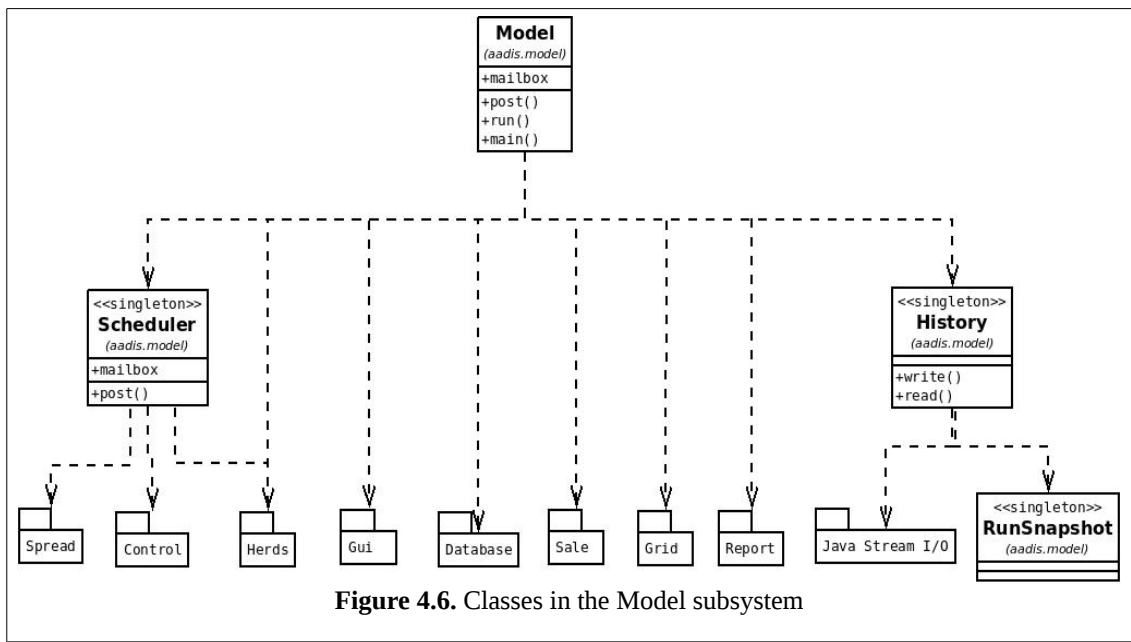
Model is the top-level class (i.e., has a linkable main), and initialises all other subsystems. The **Model** class is the overall coordinator of a simulation. The ABM **Scheduler** class coordinates disease spread and control processing on a per-day basis. The **History** class saves a snapshot of the simulation to disk at the end of each run. This facilitates a visual review of each outcome of a multi-run simulation via the GUI.

4.2.4 Herds subsystem

The classes in the Herds subsystem are presented in Figure 4.7.

Thread
(java.lang)

<<singleton>>
Farm Manager
(aadis.herds)

+mailbox
+cache

+post()
+updateCache()
+reset()
+refresh()
+get(id)
+getAll()
+getFarmsByDistance(farm,radius)
+getIps()
+etc.()

<<singleton>>
Herd Manager
(aadis.herds)

+mailbox
+cache

+post()
+updateCache(herdUpdates)
+reset()
+refresh()
+get(id)
+getAll()
+getHerdsByType(type)
+getHerdsByDistance(herd,radius)
+getHerdsByTypeAndDistance(herd,type,radius)
+getHerdsByTypeAndDistanceRing(herd,type,inner,outer)
+getExposedHerds()
+getInfectiousHerds()
+getInfectedHerds()
+getClinicalHerds()
+getRecoveredHerds()

1

Farm List
(aadis.herds)

+ArrayList

+add()
+append()
+get(id)
+size()
+clear()

Farm
(aadis.herds)

+id
+type
+herds
+etc.

n

EBM
(aadis.herds)

+infectionRatios
+clinicalSigns

1

Herd
(aadis.herds)

+id
+type
+size
+etc.

n

n

Herd List
(aadis.herds)

+ArrayList

+add()
+append()
+get(id)
+size()
+clear()

1

1

SEIR
(aadis.herds)

+mu (birth/death rate)
+beta (tx rate)
+U (incubation period)
+T (infectious period)
+S0
+E0
+I0
+R0

Figure 4.7. Classes in the Herds subsystem

During model initialisation the **HerdManager** creates the cohort of **Herd** agents. Each **Herd** agent has its own **EBM** which in turn is implemented with an **SEIR** ODE system. There is a single cache of **Herd** agents and several lookup tables of Herd IDs, for example, herds per type, herds per grid cell (Figure 4.10), infected herds and clinical herds. Whilst the herd cohort is derived from the database, the farm cohort is derived from the herd cohort during model initialisation. This is possible as each herd database record contains a farm ID and a farm type. A farm object references one or more herd objects.

4.2.5 Grid subsystem

4.2.5.1   The need for spatial-indexing

AADIS is a data-driven computational model that makes constant and intensive use of the underlying data. The disease spread pathways and control measures issue spatial queries concerning herds, farms, weather stations, saleyards, jurisdictions and regions. Examples of spatial queries are: 'locate all susceptible herds inside a specific search area', and 'calculate the distance and bearing between an infected herd and a susceptible herd'. The incorporation of spatially-referenced data enhances the realism of a model, but this comes with increased computational complexity (Kennedy et al., 2009). One dimensional indexing techniques such as primary and secondary keys, do not extend naturally to higher-dimensional geographic data (Guttman, 1984). A spatial query may involve data not explicitly stored in the database, for example, the intersection of spatial objects (Samet, 1995). Spatial queries in the absence of some form of spatial-indexing such as an R-Tree (Guttman, 1984), can result in the sequential scanning of database records. The performance of spatially-based models then becomes heavily dependent on the size of the underlying population.

An alternative approach to spatial-indexing is to satisfy spatial queries through 'neighbour lists' (Dominguez et al., 2010). For example, all neighbouring herds within 3km, 10km, 50km and 100km can be precomputed for every herd. This approach may be appropriate when there is limited variability of distance in spatial queries, and

when populations are moderately sized. However for highly stochastic models with large populations this approach is memory intensive and not particularly granular.

AusSpread is an example of a traditional approach to spatially-explicit modelling whereby the storage and querying of spatial objects is delegated to an underlying GIS platform (in this case MapInfo which employs R-Tree spatial-indexing). In the case of AADIS, the PostGIS (OSGeo, 2015) extension to PostgreSQL provides a R-Tree-over-GiST (R-Tree-based Generalised Search Tree) spatial-indexing system. However, AADIS, employs a novel grid-based spatial-indexing system developed for this project, that provides an eight-fold improvement in spatial query response time over the PostGIS R-Tree-over-GiST spatial-indexing system. This in turn yields a two to three-fold overall improvement in the mean runtime of a scenario (Section 5.1). Moreover, a uniform grid-based spatial-indexing is easily understood and maintained with just a basic knowledge of Java and simple mathematics.

During model initialisation the entire relational database is cached in the in-memory database (Section 4.2.1.3). As there is no need to access the database for non-spatial queries, it is a natural extension to not access the database for spatial queries as well. This is possible through the elimination of all spatial objects from the database. Herds and farms are represented as points rather than polygons. This simplifies spatial queries from polygon intersections to simple distances and bearing calculations. Weather stations, saleyards, LGAs, states and territories are also not represented as spatial objects. Each herd has attributes identifying the IDs of its jurisdictional area, LGA and closest weather station. A spatial query as to whether a herd is in a particular state/LGA is thus simplified from the intersection of a point with an irregular area to a simple herd attribute read. When, for example, the model determines if an infected herd poses an airborne threat to a susceptible herd on a particular day, the prevailing weather conditions at the closest weather station are a simple indexed lookup based on the weather station ID. As part of this ID cross-referencing scheme, the model

maintains various lookup tables that map LGA IDs to lists of herd IDs, and jurisdiction IDs to lists of farm IDs.

All AADIS spatially-referenced data (herds, farms, saleyards and weather stations) pertain to stationary entities. Although consignments of animals may move between herds, abattoirs and saleyards, herds are considered to be of a fixed size at a fixed location. Stationary spatial objects suit the simplicity of a uniform grid-based spatial-indexing scheme, as there is no need to dynamically maintain the grid. When spatial objects are mobile a dynamic indexing scheme is needed that efficiently updates object location mappings without impacting overall database performance (Kwon et al., 2002; Xia and Prabhakar, 2003; Lee et al., 2003). The AADIS approach of eliminating spatial objects is possible as the entire database is easily cached in memory and spatial entities are stationary. Models with larger populations, more complex spatial requirements and/or the need to dynamically update data may be better suited a more database-centric approach to spatial processing.

A criticism of uniform grid-based spatial-indexing is non-efficient handling of skewed population densities (Lettich et al., 2014). The AADIS herd population mapped onto a uniform grid indeed presents highly variable density. The default grid cell dimensions of 10km x 10km result in herd densities ranging from 0 to 264 with a median of four herds per cell. Further, of the 167,028 total cells approximately 86% of the cells are devoid of herds. The desire to efficiently handle variable population densities led to the development of variable grid cell size schemes such as quad trees (Finkel and Bentley, 1974). High density cells are disaggregated into four sub-cells, and so on, until all populated cells are in the desired density range. The downside of variable cell sizes is an increase in the complexity of cell addressing and grid search schemes. A uniform grid with contiguous IDs is accessed via simple arithmetic. It is trivial to calculate the home grid cell for any given latitude and longitude, and also to identify the extended Moore neighbourhood cells of any given cell (Section 4.2.5.2). The

AADIS grid-based spatial-indexing scheme is in effect a generalisation of neighbour lists with granularity determined by the configured cell size.

4.2.5.2 Implementation

The classes in the Grid subsystem are presented in Figure 4.8. During model initialisation the **GridManager** constructs a national grid based on configurable latitude and longitude boundaries, and cell dimensions (default 10km x 10km).

Figure 4.8. Classes in the Grid subsystem
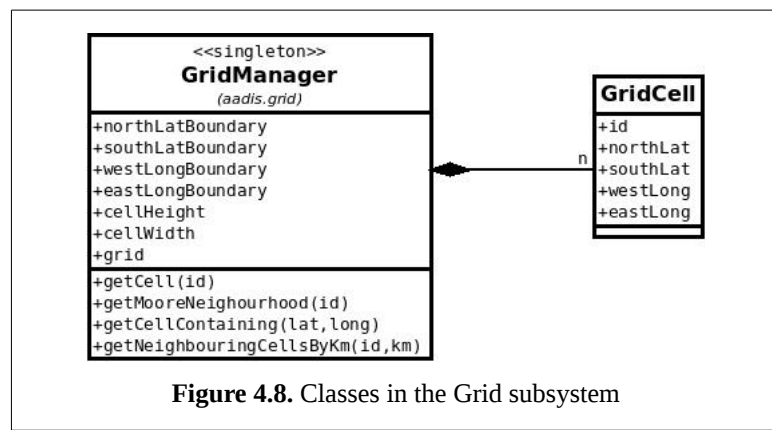
In effect, a cellular automata-style lattice is superimposed over the continuous geographical environment (Figure 4.23). The grid cells are numbered in row-major order and each herd is assigned a home grid cell according to its latitude and longitude. Figure 4.9 depicts the Moore neighbourhood with radius $r = 1$ (Weisstein, 2015) of cell ID 13. The red dots represent herds located in the cells.

Figure 4.9. Visualisation of the Moore neighbourhood for a cell.
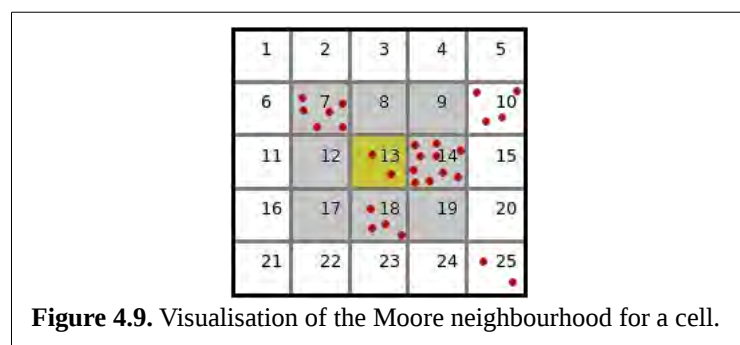
The **HerdManager** constructs a grid lookup table (Figure 4.10) that maps the ID of each populated cell to a list of the constituent herd IDs. The empty cells contain Java

null references and are effectively just place-markers in the addressing scheme described below.

Figure 4.10. The grid lookup table maps grid cell IDs to lists of herd IDs.
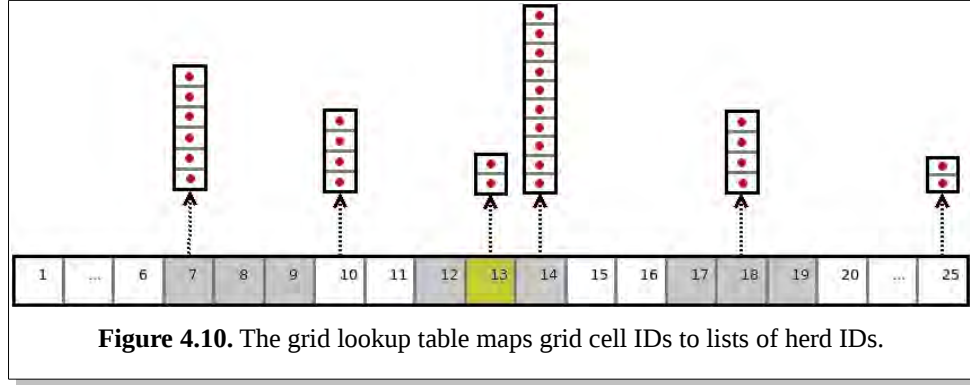
As the cells are uniform and the IDs contiguous, the Moore neighbourhood for any cell is derived through simple arithmetic on the cell ID. For any cell ID i, the cell IDs of the immediate Moore neighbourhood ($r = 1$) are given by:

$$west(i) = i - 1 \qquad (1 < i \leq n, \ i \bmod c \neq 1) \qquad (4.1)$$

$$east(i) = i + 1 \qquad (1 \leq i < n, \ i \bmod c \neq 0) \qquad (4.2)$$

$$north(i) = i - c \qquad (c < i \leq n) \qquad (4.3)$$

$$south(i) = i + c \qquad (1 \leq i \leq n - c) \qquad (4.4)$$

$$northwest(i) = i - c - 1 \qquad (c < i \leq n, \ i \bmod c \neq 1) \qquad (4.5)$$

$$northeast(i) = i - c + 1 \qquad (c < i \leq n, \ i \bmod c \neq 0) \qquad (4.6)$$

$$southwest(i) = i + c - 1 \qquad (1 \leq i \leq n - c, \ i \bmod c \neq 1) \qquad (4.7)$$

$$southeast(i) = i + c + 1 \qquad (1 \leq i \leq n - c, \ i \bmod c \neq 0) \qquad (4.8)$$

where

n = number of cells in the grid

c = number of columns in the grid

Figure 4.11. Primitives for deriving the Moore neighbourhood of a grid cell

Equations 4.1 to 4.8 in Figure 4.11 are used as primitives to obtain the IDs of cells in the extended Moore neighbourhood ($r > 0$). Figure 4.12 illustrates how, for example, the northerly neighbours of cell i within radius r are determined by simply iterating over r in a northerly direction.

111

```
create a list to hold the neighbouring cell IDs;
int neighbour = i;
for (int row = 0; row < r; row++) {
        neighbour = north(neighbour);
        add neighbour to the list;
}
```

Figure 4.12. Deriving the extended Moore neighbourhood of a grid cell
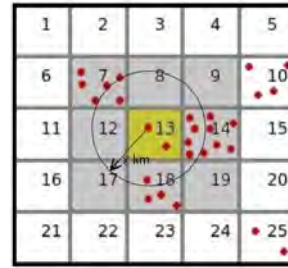
Figure 4.13. Moore neighbourhood enclosing a spatial query search radius.

Consider, for example, the spatial query 'find all herds within x km of a particular infected herd'. The AADIS grid-based spatial-indexing scheme addresses this with a blend of table lookups and simple arithmetic:

1) An extended Moore neighbourhood is defined for the home cell of the infected herd that fully encloses the circular search area (Figure 4.13). The required radius r of the neighbourhood is easily determined as the cells are uniform.

2) The herd IDs corresponding to all cells in the Moore neighbourhood of radius r are retrieved from the grid lookup table.

3) The herds that lie outside the circle but inside the Moore neighbourhood are discarded from the set. Distances between herds are dynamically calculated using the Haversine formula on the points of latitude and longitude (Williams, 2011).

4) The set of candidate herd IDs is returned to the client. The client then uses the herd IDs to retrieve herd data as required from the herd cache.

The performance of the grid-based spatial-indexing system is described in Section 5.1.

It is possible that AADIS will upgrade to raster-based weather data in the future. Interpolated weather conditions could then be directly mapped to cells of the grid-based spatial-indexing scheme. This would provide finer granularity than the current

weather-station-based approach in the determination as to whether conditions are conducive to the airborne spread of FMD (Section 3.5.4).

4.2.6 Spread subsystem

The classes in the Spread subsystem are presented in Figure 4.14.
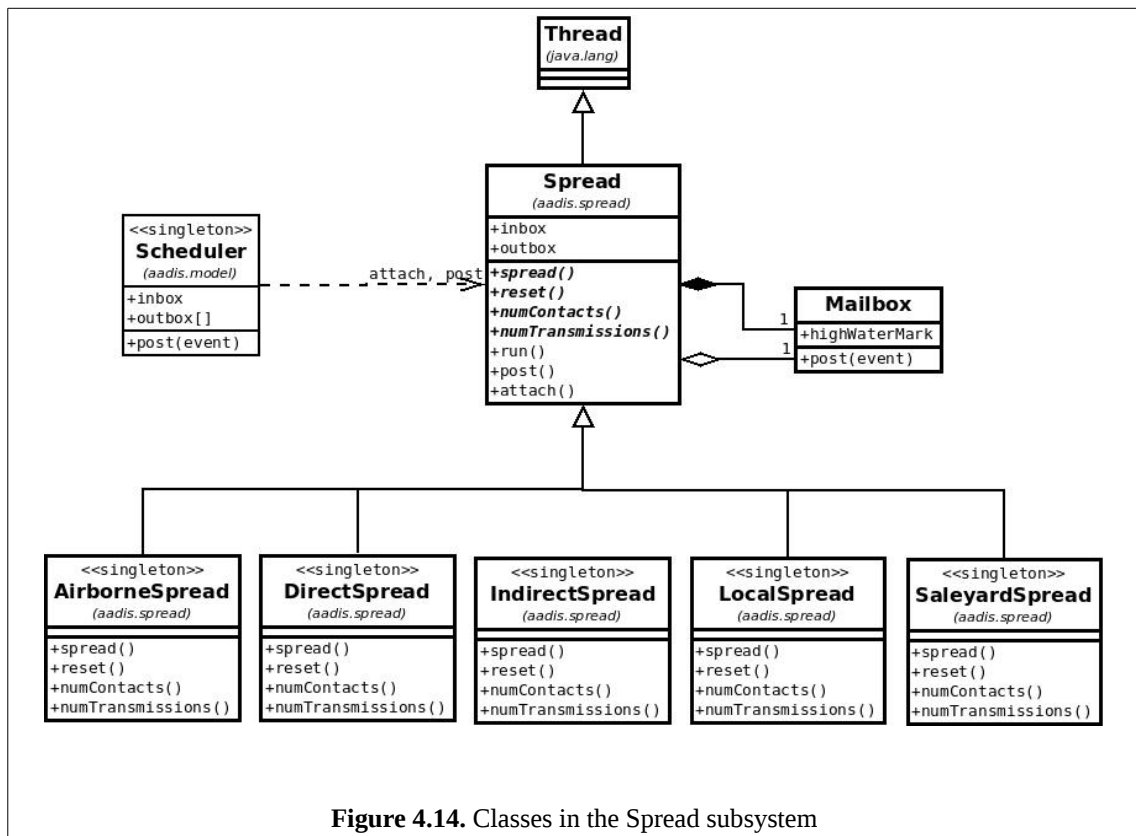
Figure 4.14. Classes in the Spread subsystem

The **Spread** class provides general disease spread pathway functionality. Pathway specifics are implemented in the **AirborneSpread**, **DirectSpread**, **IndirectSpread**, **LocalSpread** and **SaleyardSpread** concrete classes. Each spread concrete class inherits a thread and two mailboxes from the **Spread** superclass. The inbox is for receiving command events from the **Scheduler**. The outbox is for sending result events back to the **Scheduler**. All spread pathways operate independently and concurrently. AADIS is extensible to any number of spread pathways.

4.2.7 Control subsystem

The classes in the Control subsystem are presented in Figure 4.15.
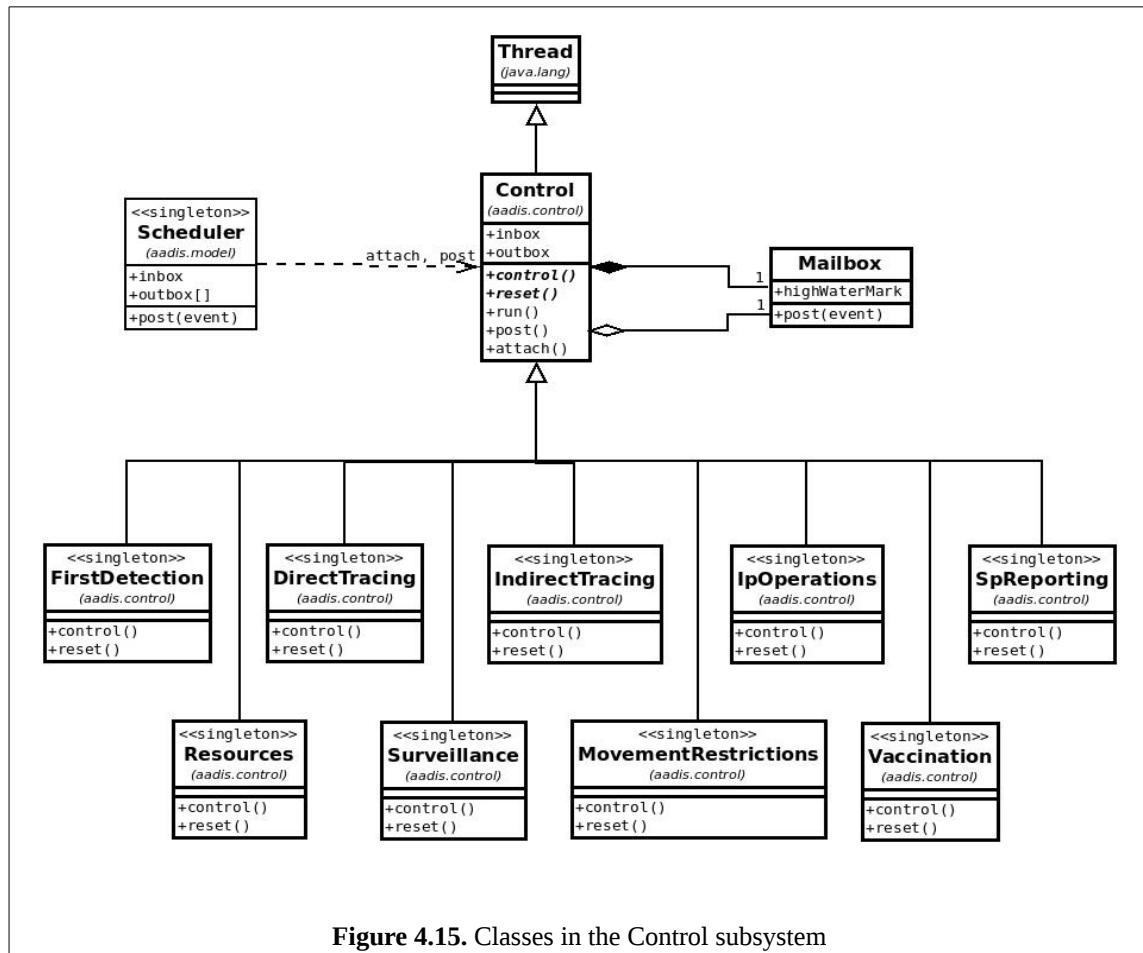
Figure 4.15. Classes in the Control subsystem

The **Control** class provides general control measures functionality. Control specifics are implemented in the **DirectTracing**, **FirstDetection**, **IndirectTracing**, **IpOperations, MovementRestrictions, Resources, SpReporting, Surveillance** and **Vaccination** concrete classes. Each control concrete class inherits a thread and two mailboxes from the **Control** superclass. The inbox is for receiving command events from the **Scheduler**. The outbox is for sending result events back to the **Scheduler**. All control measures except **Resources** operate independently and concurrently. The **Resources** control measure is a special case as other control measures are dependent

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on it to obtain team resources. AADIS is extensible to any number of control measures.

4.2.8 Graphical User Interface / Visualisation subsystem

The GUI subsystem is responsible for all user interaction with the model and visualisation of model outcomes. The classes in the GUI subsystem are presented in Figure 4.16.
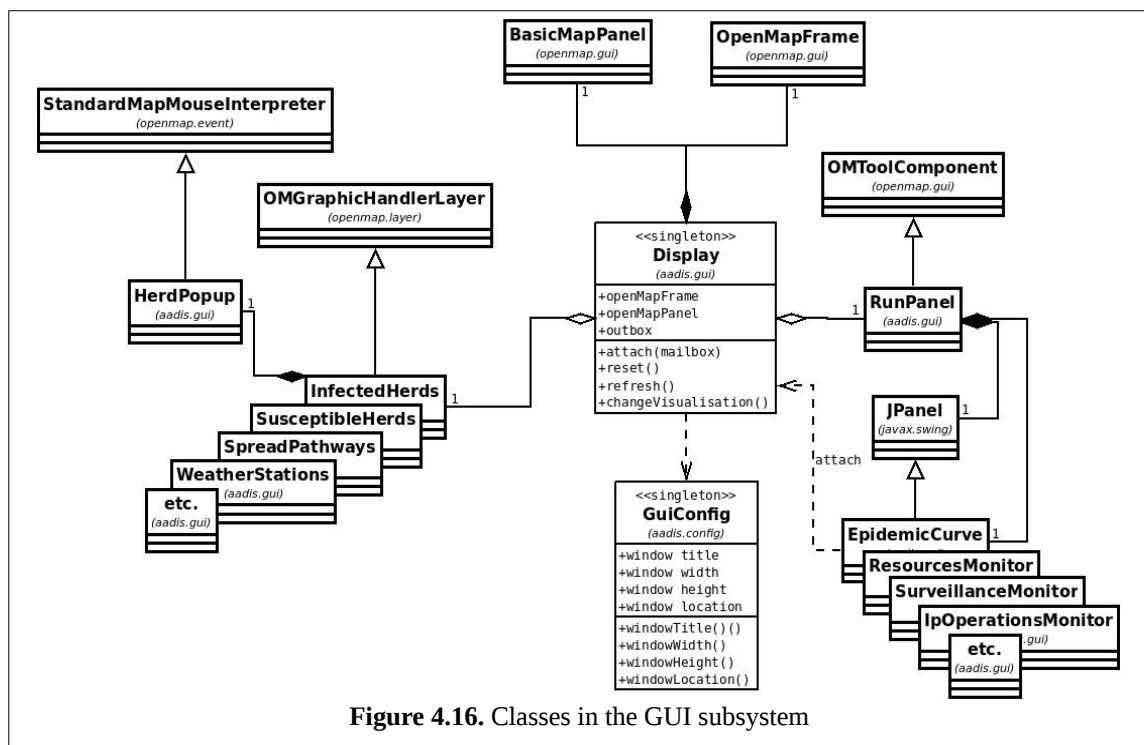
Figure 4.16. Classes in the GUI subsystem

The **Display** class is responsible for initialising OpenMap and creating the model window frame. OpenMap layers are defined in the OpenMap configuration file and implemented as client Java classes (e.g., **SusceptibleHerds**). The **RunPanel** contains the scenario control buttons (run, step, pause, stop, reload and save), and buttons to invoke various popups such as the **EpidemicCurve**. Standard OpenMap graphical tools (including zoom, pan, layer selection and screen capture), are accessed via the OpenMap Tool Menu or the OpenMap Tool Panel. The user can also interact directly with layers (e.g., **InfectedHerds**), via specialised popup menus (e.g., **HerdPopup**).

4.2.9 Reports subsystem

The classes in the Reports subsystem are presented in Figure 4.17.
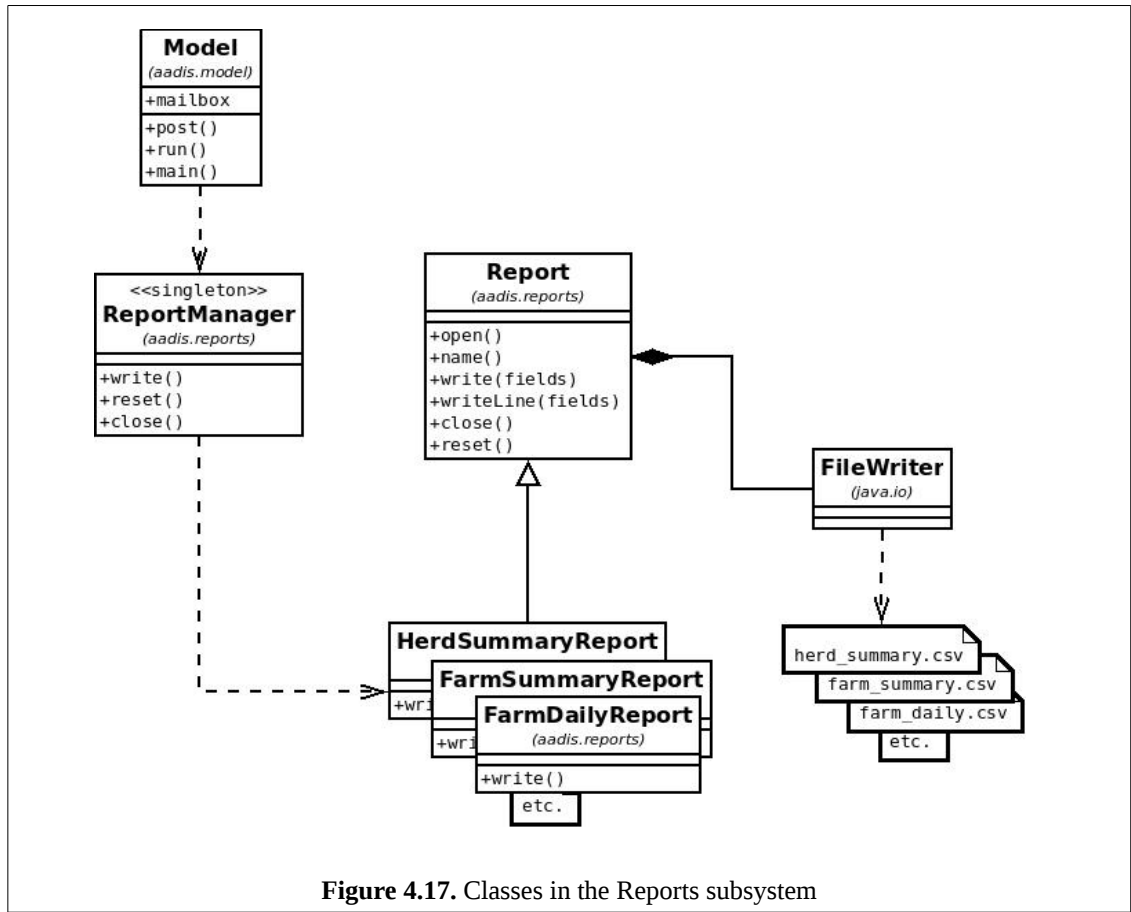
Figure 4.17. Classes in the Reports subsystem

The **ReportManager** class is responsible for writing all report files. The **Report** class provides general functionality for writing a CSV file. Specific report file structures are defined in the concrete classes, for example, **HerdSummaryReport**. AADIS is extensible to any number of report files.

4.2.10   Logging subsystem

AADIS uses the open source Log4j (Apache, 2012) logging system. This provides granular tailoring of logging density via the log4j configuration file (Appendix D).

4.3 Dynamic architecture

4.3.1 Threads, events and mailboxes

The AADIS asynchronous architecture is implemented with threads, events and blocking queues. For a class to participate it must have its own thread and one or more event mailboxes (inbox and/or outboxes). A mailbox has a blocking queue that can hold a number of events simultaneously. The asynchronous means by which two classes can communicate is illustrated in Figure 4.18. Class A sends an event to class B by synchronously calling the *post()* method in class B. This places the event in the inbox of the receiving class under the thread of the sending class A. The event is harvested from the inbox by the thread of the receiving class B. Class A can register interest in return events from class B, by attaching its inbox via the *attach()* method in class B. Class B maintains a list of outboxes (i.e., the inbox of each attached listener). Class B multicasts an event to the attached listeners by invoking the *post()* method of each mailbox in the outbox list.

Figure 4.18. The AADIS mailbox mechanism
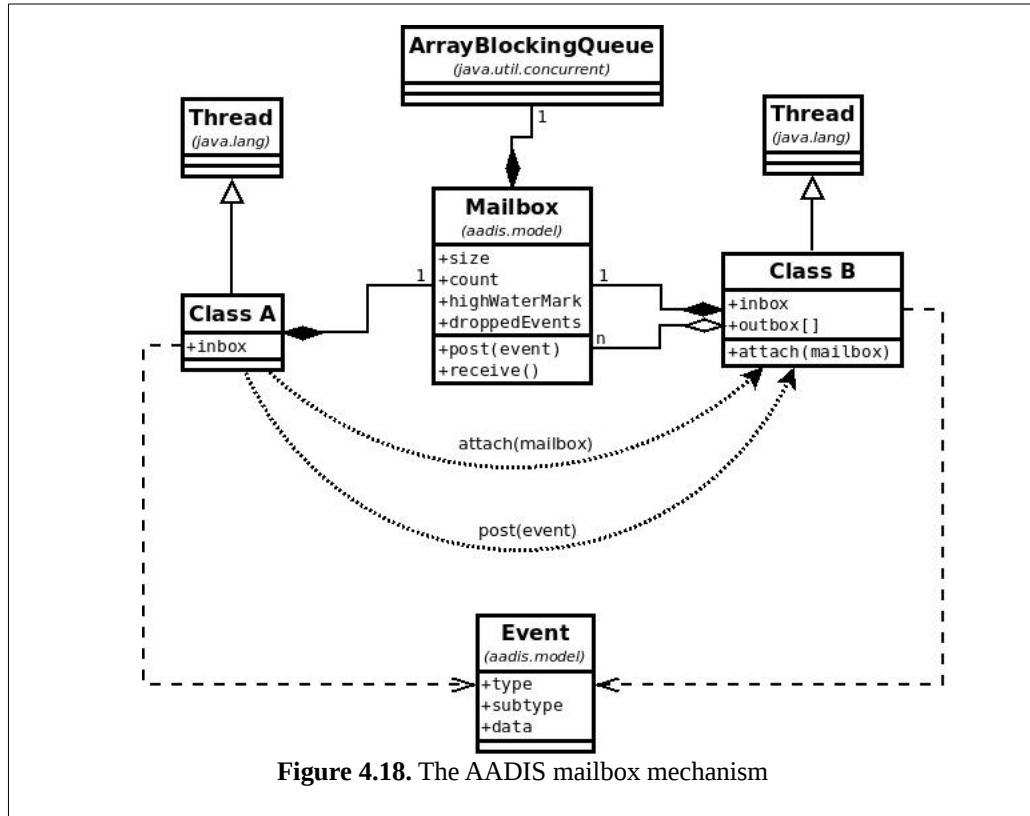
4.3.2 Simulation flow

The overall scenario logic is implemented as a finite-state machine (FSM) (Figure 4.19). The FSM is driven by GUI events (*play*, *step*, *pause*, *stop* and *reload*), and internal model events (e.g. *runSimDay, simDayCompleted, herdsLayerUpdated*). At the start of a simulation day the **Model** sends a *runSimDay* event to the **Scheduler**. The **Scheduler** coordinates all intra-day simulation processing by the spread pathways. When all pathways have completed the current simulation day, the **Scheduler** updates the **Herd** cohort and sends a *simDayCompleted* event back to the **Model** (Figure 4.20). The **Model** then coordinates the updating of the visualisation via the GUI subsystem. When the scenario has completed, the **Model** class writes to the scenario report files.
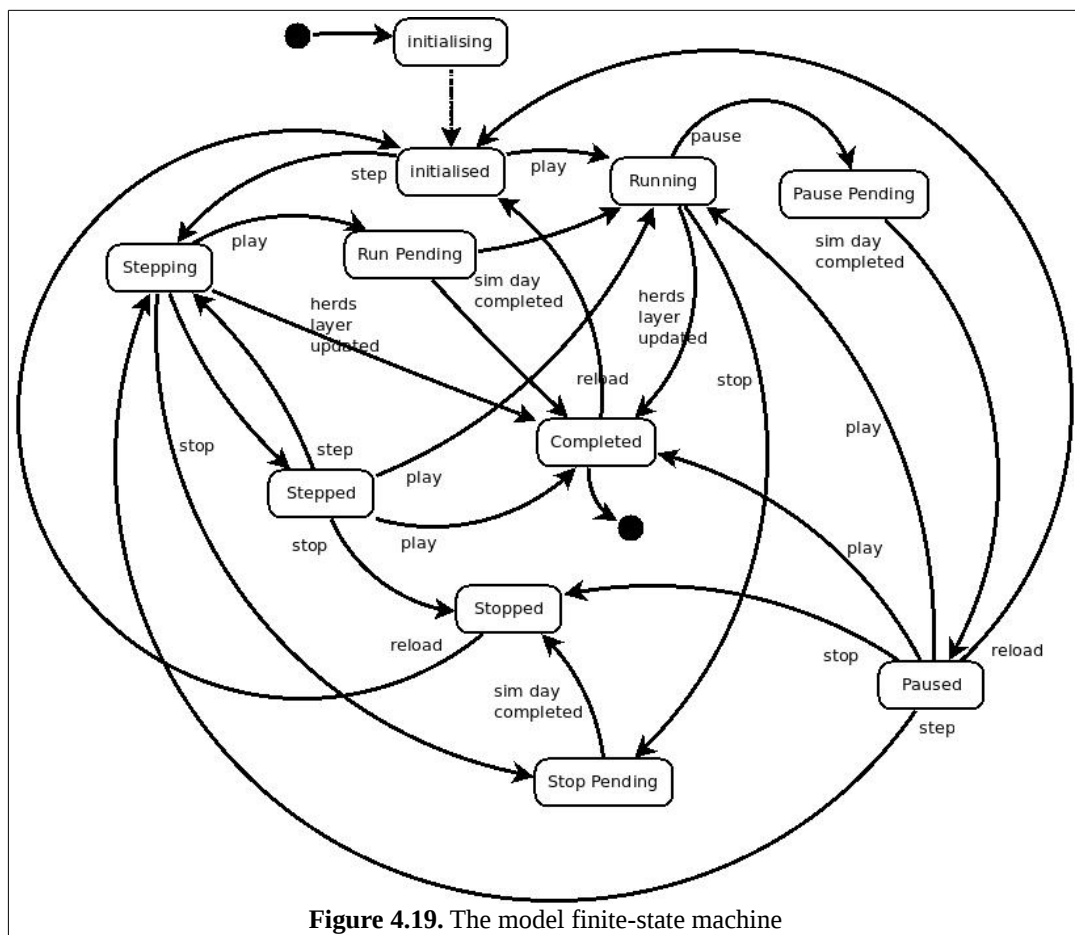
Figure 4.19. The model finite-state machine

The **Scheduler** class is responsible for coordinating all spread and control activities per simulation day (Figure 4.20). Simulating in discrete time steps of a day means that there is no need for herd/farm updates to be applied as they occur. This greatly simplifies the level of synchronisation between competing updaters. All **Herd** agent updates are processed on the **Scheduler**'s thread of execution.
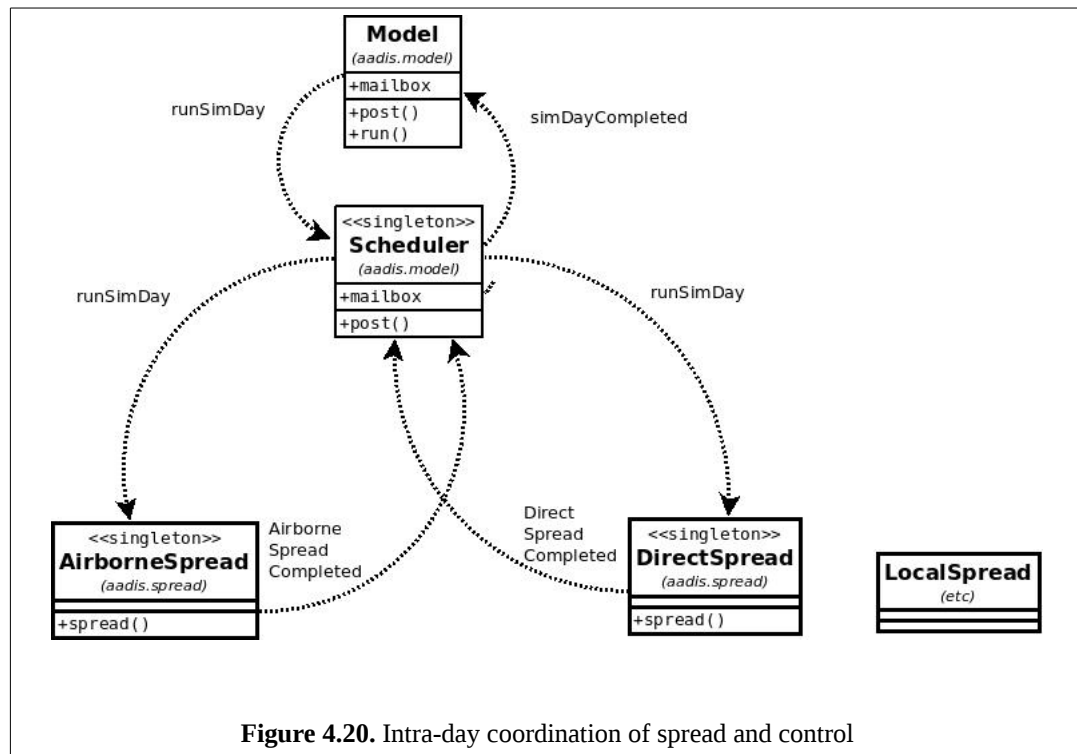
Figure 4.20. Intra-day coordination of spread and control

The **Model** class is responsible for coordinating the refreshing of the GUI after all spread pathways have completed and the herd cache has been updated. This is done by calling the *refresh()* method in the **Display** class (Figure 4.21). GUI updates are carried out under the standard Java event dispatch thread. When all display layers have been updated, the **Display** class notifies the **Model** via a *herdsLayerUpdated* event. This triggers the **Model** to initiate processing for the next simulation day (as per the **Model** FSM).

Figure 4.21. Visualisation refresh
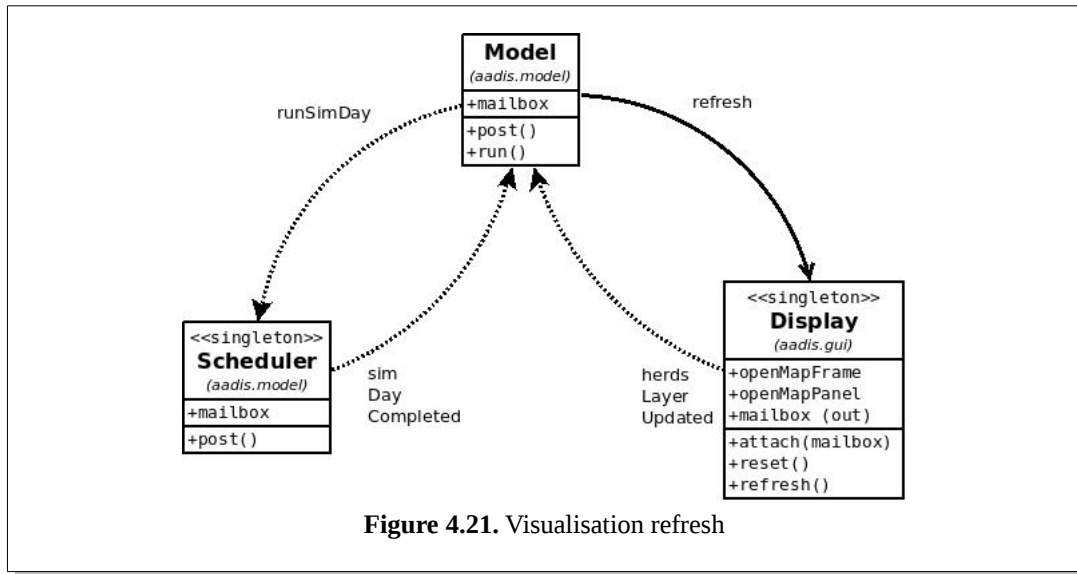
4.4 Configuration

The relational database is used to store project-specific configuration data such as population datasets and contact structures (Appendices B and C). This data may be large and is typically not changed very often.

A Java properties text file is used to store scenario-specific configuration data (Appendix D). Whenever a parameter is changed in the model configuration file the program must be re-invoked at the OS level. There is also a system configuration file and platform configuration file that are typically not modified by the user.

The graphical user interface is used for temporary configuration that is only required during the current program invocation.

4.5 Model Outputs

The formal outputs of an AADIS simulation are CSV files. All model output files are prepended with the scenario name. The files report a range of metrics at the herd, farm and scenario level (Table 4.2). Appendix E contains the field structure of each file.

Table 4.2. AADIS output files

Report name	Primary contents	Writing frequency
Startup	Primary cases (scenario seed herds)	Once at start of scenario
Farm Summary	Cumulative counts of declared premises per farm type	At the end of each run
Farm Daily	Cumulative counts of declared premises per day	At the end of each run
Herd	Infected herds (day and source of infection)	At the end of each run
Saleyard	Infected consignments into and out of saleyards	At the end of each run
Spread	Contacts and infections per spread pathway	At the end of each run
Control	Index case and control measures resource usage summary	At the end of each run
Resources	Detailed control measures resource usage	At the end of each run
Config	Scenario configuration and overrides	Once at start of scenario

4.6 User interface and visualisation

This section presents examples of the user interface to help illustrate the key features of the model.

The Run Panel (Figure 4.22) is located at the top of the main AADIS window (Figure 4.23), and is the primary means of interacting with the model.

Figure 4.22. Run Panel

The dynamic grid used for spatial-indexing (Section 4.2.5), can be temporarily displayed in the AADIS window for development and test purposes (Figure 4.23).
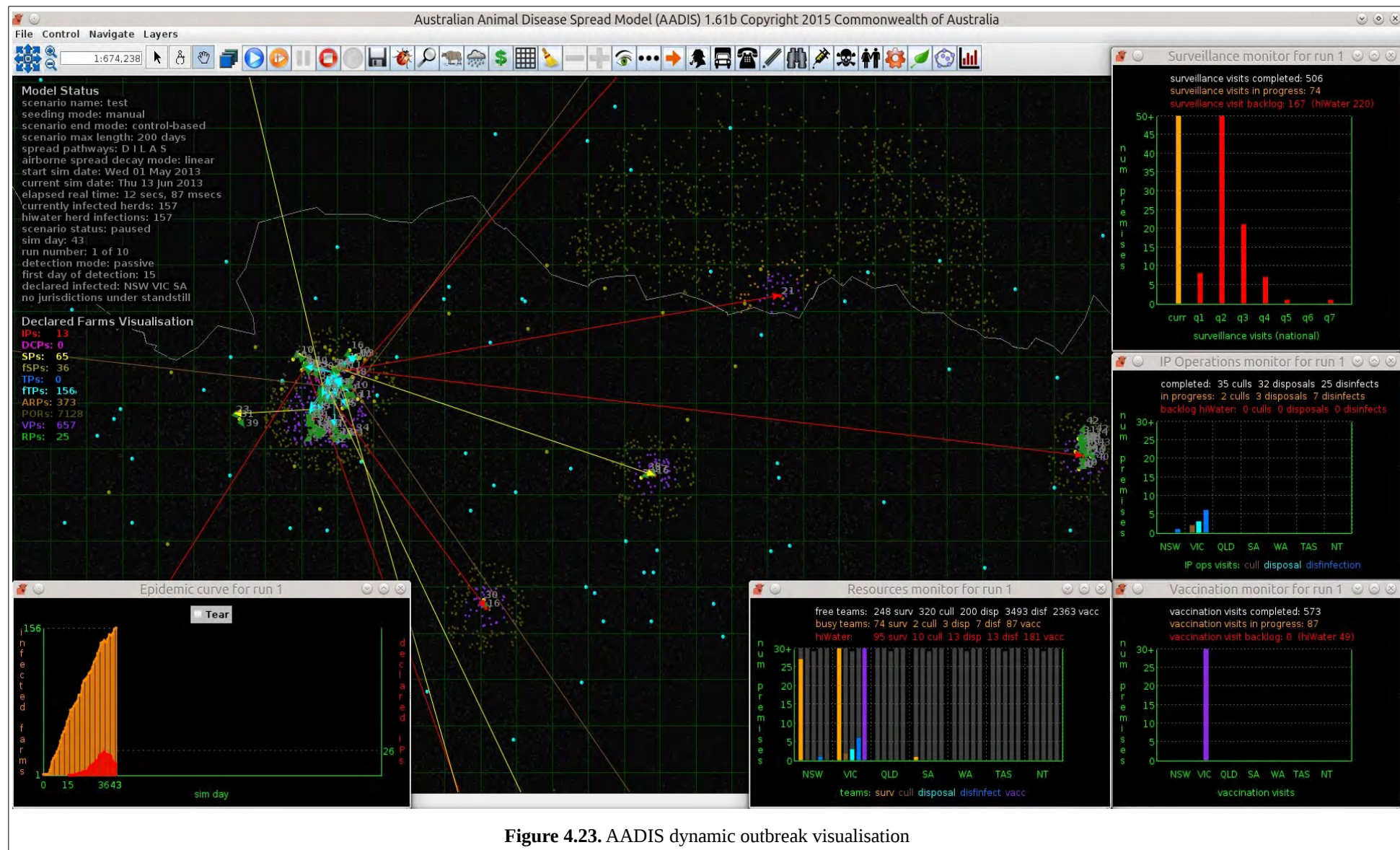
Figure 4.23. AADIS dynamic outbreak visualisation

4.6.1 Browsing the herd population

The Find Dialog (Figure 4.24) is invoked via the Run Panel. Individual herds, farms, weather stations and saleyards can be searched for by ID and highlighted on the display.

Temporary graphical displays such as 'found' objects are dismissed via the Clear button located on the Run Panel.

Figure 4.24. Find Dialog

The Herd Type Locator dialog (Figure 4.25) is invoked via the Run Panel. The 10 herd types can be individually highlighted in contrasting colours against the back drop of susceptible herds (Figure 4.26). This provides insight into the distribution and density of the herd population and is useful for choosing herds to be 'seeds' of infection in what-if scenarios (for example, a medium sized pig herd that is close to a dairy herd).

Figure 4.25. Herd Type Locator Dialog

Figure 4.26. Pig herds located via the Herd Type Locator Dialog
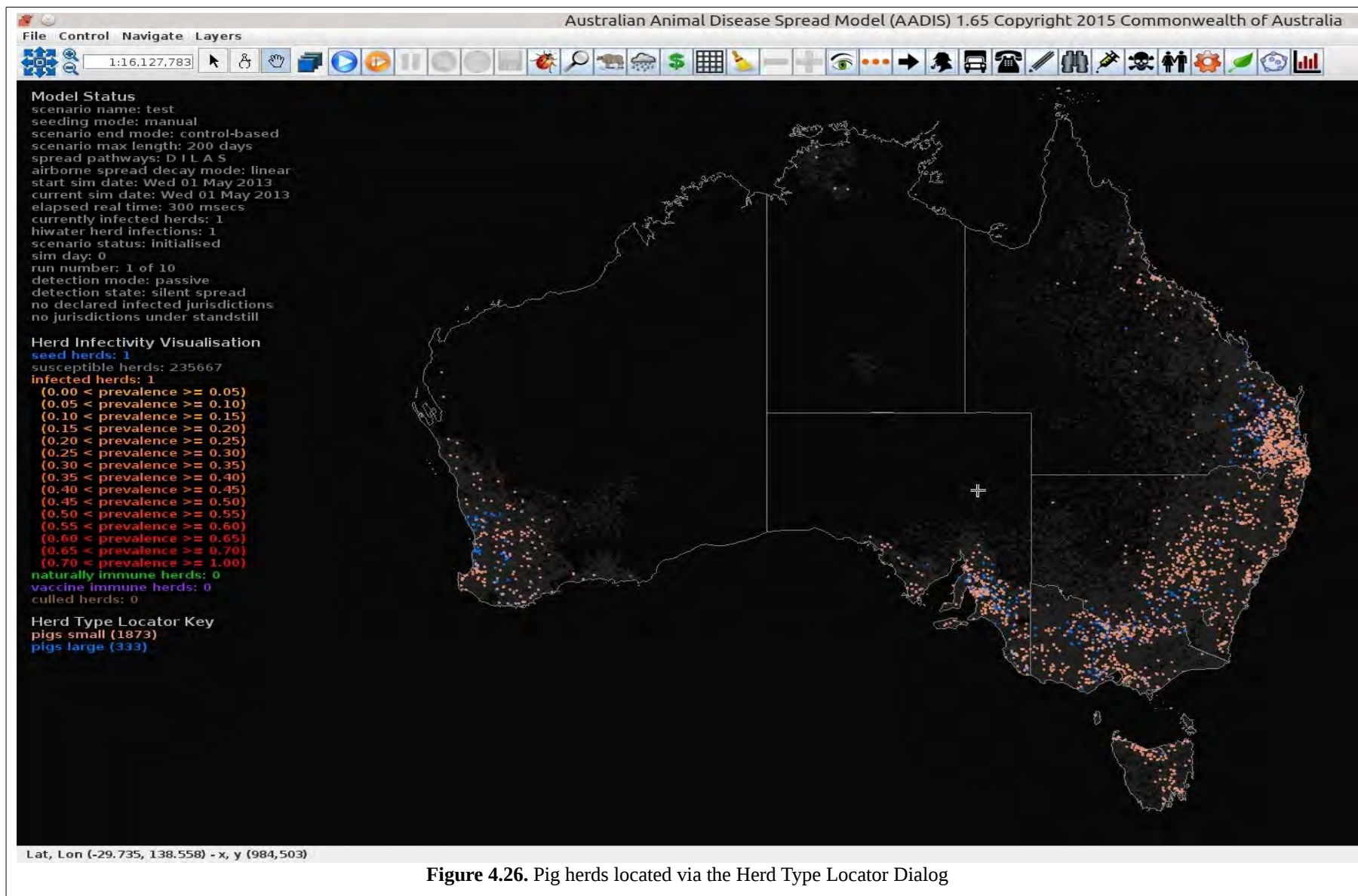
The Herd Popup (Figure 4.27) is invoked via a left mouse click on any herd (Herd Infectivity and Spread Pathway visualisation modes only – refer to Section 4.6.5). It displays a range of static attributes (such as herd size, type, location, region), and dynamic attributes (such as prevalence, and first and last days of infection). Graphical utilities such as the Prevalence Curve, Infection Route, Infection Fan and Infection Network are invoked via the Herd Popup. The Farm Popup (Figure 4.28) is invoked via a left mouse click on any farm (Declared Farms visualisation mode only). It displays a range of static attributes (such as farm size, type, location and region), and dynamic attributes (such as premises classification and declared area).

Figure 4.27. Herd Popup

Figure 4.28. Farm Popup
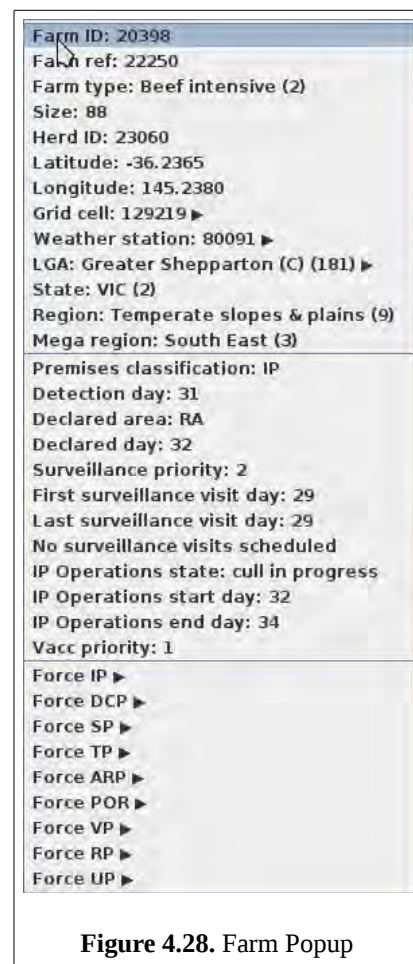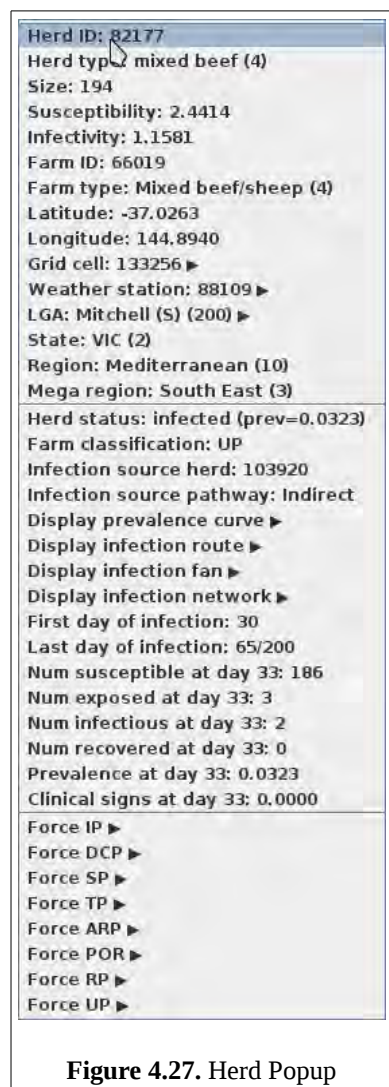
4.6.2 Browsing weather stations

The Weather Station Locator Dialog (Figure 4.29) is invoked via the Run Panel and is used to search for specific weather stations by ID, or to display all weather stations.
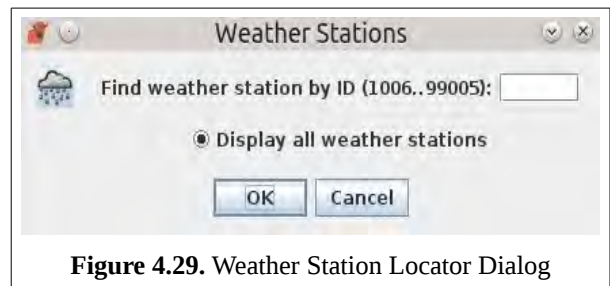
Figure 4.29. Weather Station Locator Dialog

The Weather Station Popup (Figure 4.30) is invoked via a left mouse click on any weather station. It displays static station attributes (ID, name, latitude, longitude) and dynamic attributes pertaining to the likelihood of airborne spread (current probability that relative humidity and wind speed is conducive to the airborne spread of FMD, and the likely range of wind bearings (min, most likely, max)).
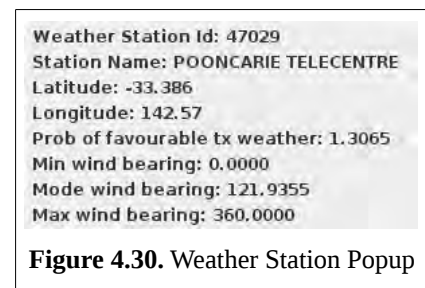
Figure 4.30. Weather Station Popup

4.6.3 Browsing saleyards

The Saleyard Locator Dialog (Figure 4.31) is invoked via the Run Panel and is used to search for specific saleyards by ID, or to display all saleyards. The Saleyard Popup (Figure 4.32) is invoked via a left mouse click on any saleyard. It displays static saleyard attributes: ID, name, location, region, state, IDs of sales that occur at the saleyard, and buyer and seller catchment areas.
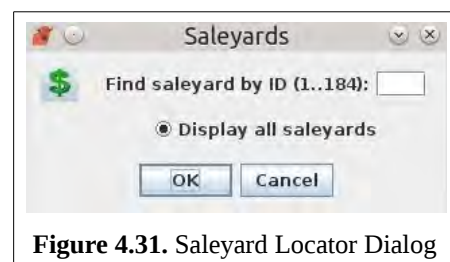
Figure 4.31. Saleyard Locator Dialog

Figure 4.32. Saleyard Popup

4.6.4 Running a scenario

⚙️ The Scenario Dialog (Figure 4.33) is invoked via the Run Panel.

Scenario parameters are defined in the model configuration file but can be temporarily overridden via the Scenario Dialog. This includes: scenario name, number of runs, scenario end mode and the enabling/disabling of specific spread pathways and control measures. The number of days in a scenario runs is dictated by the end mode:

- **Detection** – the scenario ends on the day that the first IP is detected.

- **Fixed** – the scenario ends after a fixed number of days.

- **Control-based** – the scenario ends when the outbreak is under control (no infected premises and no outstanding control actions (e.g. surveillance visits)). To prevent run-away outbreaks a scenario will automatically end once the maximum length has been reached.
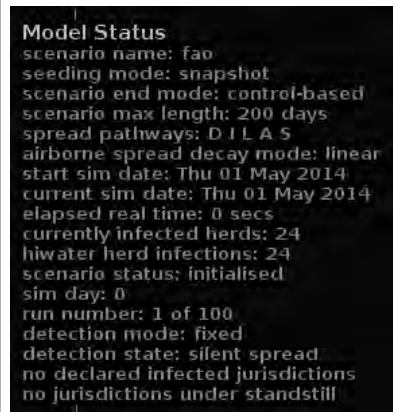
Figure 4.33. Scenario Dialog

- **Earliest** – earliest of the fixed length and control-based modes.

Scenario run controls are located in the Run Panel.

 Run the scenario from start to finish.

 Step through the scenario a day at a time.

 Pause the running scenario.

 Stop the running scenario.

 Reload the scenario.

The run status of the scenario is provided in the Model Status Panel (Figure 4.34).

Figure 4.34. Model Status Panel

When all scenario runs have completed the end-states of each run can be browsed.

 Display the previous run of a completed scenario.

 Display the next run of a completed scenario.

4.6.5 Visualisation

AADIS provides three modes for visualising an outbreak in progress: herd infectivity, spread pathway and declared farms. The Change Visualisation button on the Run Panel cycles through the modes.

Herd Infectivity Visualisation depicts the level of infection within each herd. Herds may be susceptible, infected, naturally immune, vaccine immune or culled. The prevalence within an infected herd is visualised as heat-colours ranging from yellow (low prevalence) to red (high prevalence). This provides insight into the state of within-herd spread of disease (driven by a herd's EBM). The visualisation key is shown in Figure 4.35.

Figure 4.35. Herd infectivity visualisation key

Spread Pathway Visualisation depicts the means by which an infected herd contracted the disease. This provides an insight into the between-herd spread of disease (driven by the ABM). The visualisation key is shown in Figure 4.36.
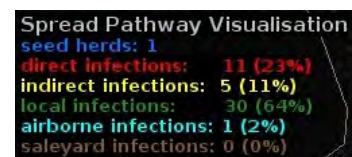
Figure 4.36. Spread pathway visualisation key

Declared Farms Visualisation depicts the current declared classification of a premises. This provides insight into the impact of control measures on the outbreak (driven by the ABM), and represents a disease managers perception of the outbreak. The visualisation key is shown in Figure 4.37.

Figure 4.37. Declared farms visualisation key

The national set of herds can be viewed abstractly as nodes in a network (Dubé et al., 2011a; Nöremark et al., 2011). Over time a network topology forms as the spread

pathways create edges. The topology takes the form of a directed acyclic graph, until such time as recovered herds lose their immunity. Network paths can subsequently be traversed forward to determine the downstream impact of an infected herd, and backward to trace the historical infection route. The network topology thus captures the spatiotemporal history of the outbreak.

➡️ The infection network (Figure 4.38) is displayed via the Vector Mode button on the Run Panel. The vector colour corresponds to the spread pathway that was responsible for the transmission (Figure 4.36).
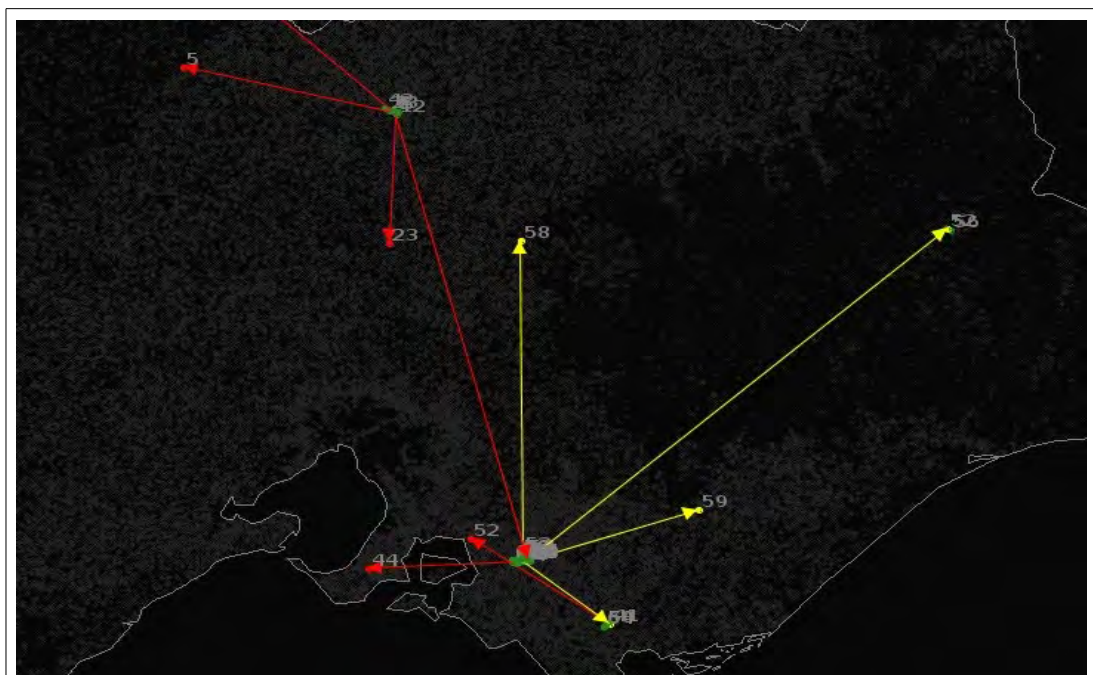
Figure 4.38. Infection network visualisation

📊 The Epidemic Curve popup (Figure 4.39) is invoked via the Run Panel. The Epidemic Curve dynamically depicts the number of infected farms (in orange) and the number of declared infected farms (in red) for each day of the scenario run. This provides real-time visualisation of the progress of the control program. The Tear

button on the Epidemic Curve 'tears off' a copy of the current curve. This allows multiple epidemic curves to be retained on the screen for comparative purposes.

Figure 4.39. Epidemic Curve Popup
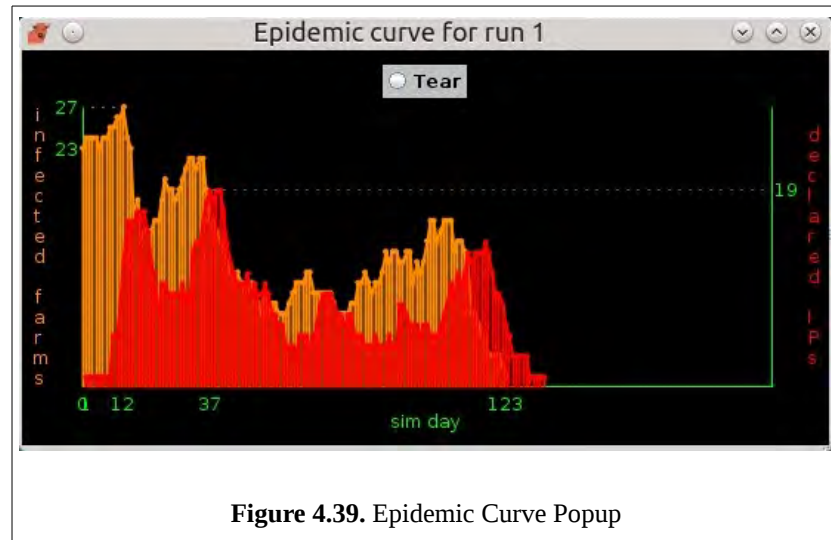
The map is panned by selecting the Pan button on the Run Panel and then dragging and dropping as desired. (This is standard OpenMap functionality.)

Panning mode is exited via the Gestures button on the Run Panel.

The map is zoomed by selecting the Zoom In/Out buttons on the Run Panel or via the mouse scroll wheel (if available). (This is standard OpenMap functionality.)

The distance measuring tool (Figure 4.40) is invoked via the Distance button on the Run Panel. Distances are measured by selecting the starting point (with a left mouse click) and then moving the mouse cursor to the destination point. Distance measuring mode is exited by double clicking anywhere on the map. (This is standard OpenMap functionality.)

Figure 4.40. Distance measuring tool
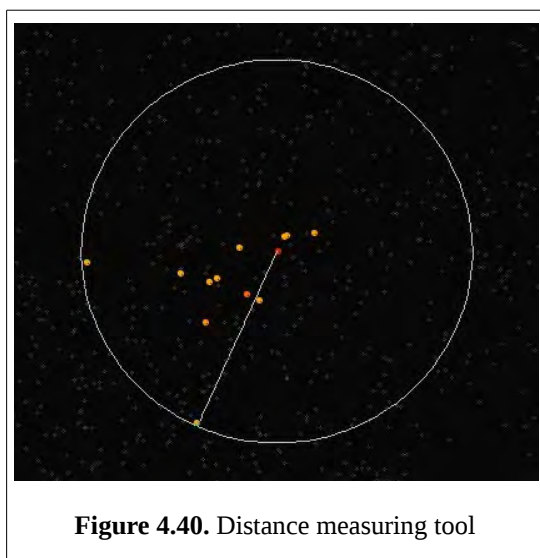
The latitude and longitude of the starting point, and the distance and bearing to the destination point are dynamically displayed at the bottom left hand corner of the model.

Figure 4.41. Location/distance display
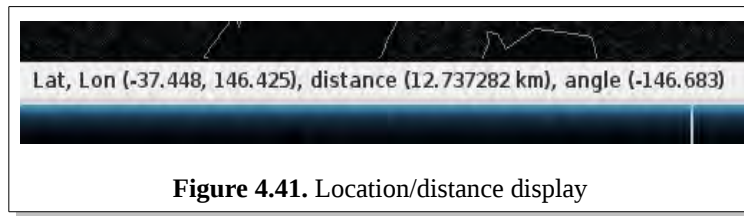
The distance measuring tool is exited via the Gestures button on the Run Panel.

4.6.6 Adjusting control measures

Control measures are configured and resourced on a per-jurisdiction basis (Appendices B and C). For convenience it is possible to override per-jurisdiction configurations with national-level configurations through the GUI.

Fixed first IP detection is configured via the model configuration file (Appendix D), which can be temporarily overridden via the First IP Detection Dialog (Figure 4.42) invoked via the Run Panel.

Figure 4.42. First IP Detection Dialog

Movement restrictions are configured per jurisdiction in the database (Appendices B and C). They can be temporarily overridden with a single national policy via the Movement Restrictions Dialog (Figure 4.43) invoked via the Run Panel.
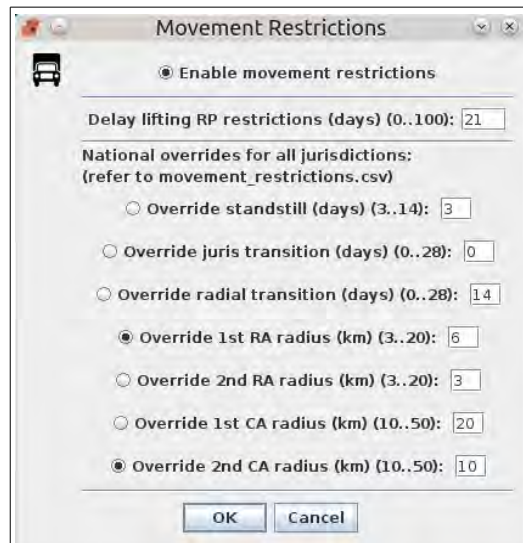
Figure 4.43. Movement Restrictions Dialog

The Surveillance Monitor (Figure 4.44) is invoked from the Resources Dialog (Figure 4.54) via the Run Panel. It depicts the dynamic reprioritisation of surveillance visits over time according to premises classification, declared area type, herd type and the time waiting for a visit. The yellow bar depicts the number of surveillance visits in progress while the red bars represent the dynamic priority queues of visits (q1 is the highest priority). The backlog highwater is the largest number of pending surveillance jobs at any time during a run.

Figure 4.44. Surveillance Monitor

The Surveillance Dialog (Figure 4.45) is invoked from the Run Panel. It provides a means of temporarily overridding the surveillance configuration defined in the model configuration file.
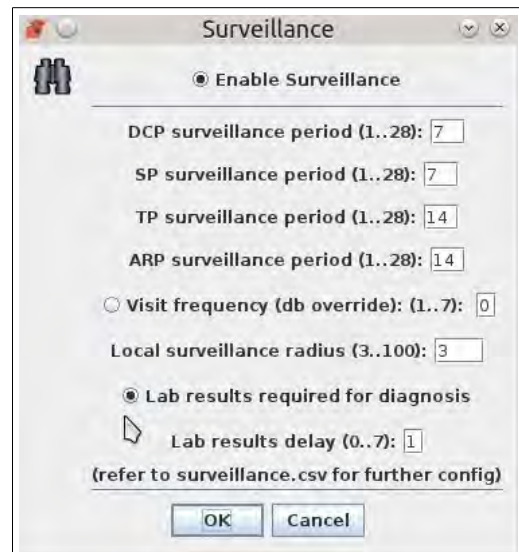
Figure 4.45. Surveillance Dialog

The tracing Dialog (Figure 4.46) is invoked via the Run Panel. All backward and forward trace routes are displayable (Figure 4.47). The colour of the trace vector corresponds to the type of trace (yellow for an indirect trace and red for a direct trace).

Figure 4.46. Tracing Dialog
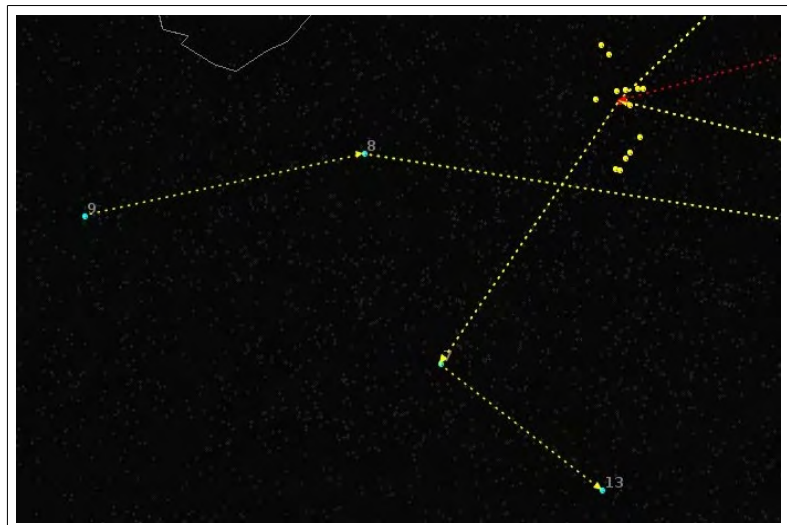
Figure 4.47. Optional display of trace routes

The SP Reporting Dialog (Figure 4.48) is invoked via the Run Panel. The configuration for false reporting is defined in the model configuration file and can be temporarily overridden via the SP Reporting Dialog.

Figure 4.48. SP Reporting Dialog

👫 The IP Operations Monitor (Figure 4.49) is invoked from the Resources Dialog (Figure 4.54) via the Run Panel. It dynamically shows the number of culling, disposal and disinfection jobs in progress and the backlog (in red), per jurisdiction. The backlog highwater is the largest number of pending IP operation jobs at any time during a run.
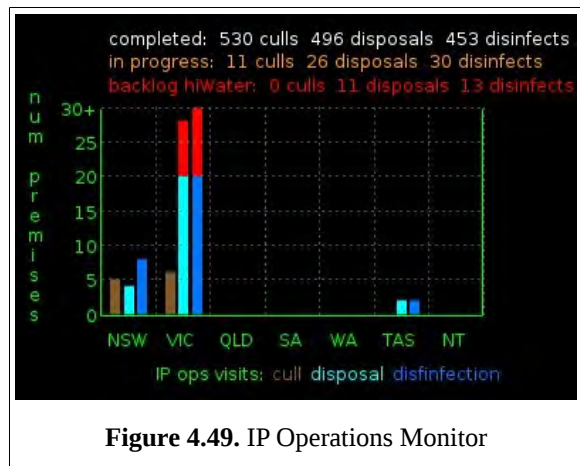
Figure 4.49. IP Operations Monitor

☠ The IP Operations Dialog (Figure 4.50) is invoked from the Run Panel. The default policy is the immediate culling of confirmed infected premises (subject to available resources). Pre-emptive culling is configured per jurisdiction in the database however these values can be temporarily overridden with a national policy via the IP Operations Dialog.
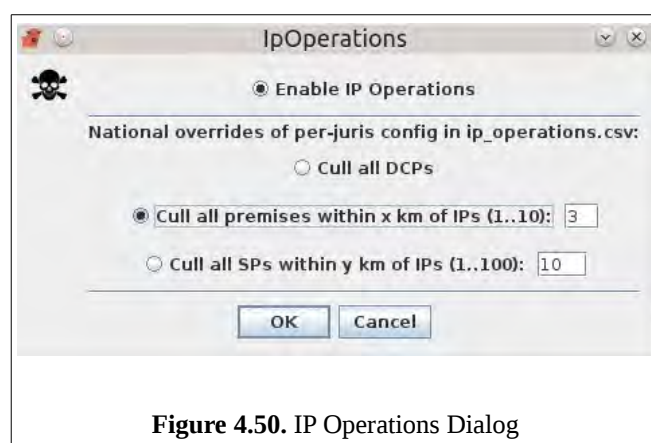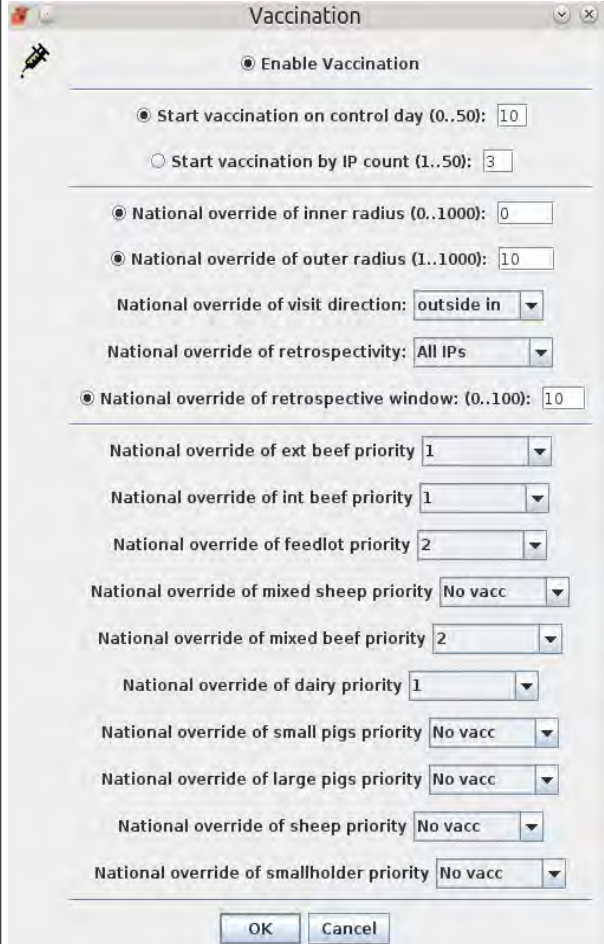

Figure 4.50. IP Operations Dialog

The Vaccination Dialog (Figure 4.51) is invoked from the Run Panel. Vaccination is configured per jurisdiction in the Vaccination database table however these values can be temporarily overridden with a national policy via the Vaccination Dialog.

Figure 4.51. Vaccination Dialog

The Vaccination Monitor (Figure 4.52) is invoked from the Resources Dialog (Figure 4.54) via the Run Panel. It dynamically shows the number of vaccination jobs in progress and the backlog (in red) per jurisdiction. The backlog highwater is the largest number of pending vaccination jobs at any time during a run.
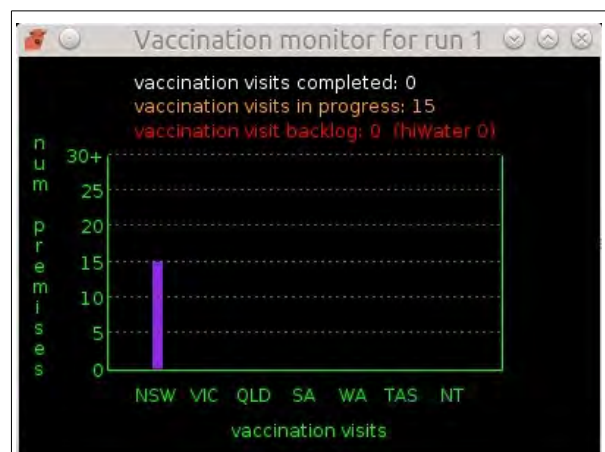
Figure 4.52. Vaccination Monitor

The Resources Monitor (Figure 4.53) is invoked from the Resources Dialog (Figure 4.54) via the Run Panel. It dynamically shows the numbers of free and busy teams, and the busy teams highwater. The grey bars represent pool capacity (per team type per jurisdiction), and the superimposed coloured bars represent current pool usage. The highwater is the largest number of pending jobs at any time during a run.

The Resources Dialog (Figure 4.54) is invoked via the Run Panel. Resources are allocated per-jurisdiction in the Resources database table (Appendices B and C), and can be overridden with national values via the Resources Dialog. This allows quick experiments as to how resource bottlenecks influence the efficacy of the control program. Disabling resources means there are unlimited teams available.

Figure 4.53. Resources Monitor

Figure 4.54. Resources Dialog

5 MODEL VERIFICATION AND VALIDATION

When developing a model, particularly one that will assist with the development of policy, it is essential that the model is verified as constructed correctly and validated as fit for purpose (Taylor, 2003; Garner and Hamilton, 2011).

Verification

Verification is the process of ensuring that a model has been implemented correctly (Dent and Blackie, 1979; Sargent, 2013). It targets the mechanics of the software development process, as to whether 'the product has been built right', as opposed to validation that looks at the bigger operational picture, as to whether 'the right product has been built' (Siviy et al., 2007). Verification can include static testing such as peer reviewing of code, and dynamic testing such as software testing at the unit, module and system level (Booch, 1994; Sargent, 2013). A unit test is a self-contained repeatable means of verifying a piece of software in isolation from the rest of the system. In the context of object-oriented programming, a class is a typical candidate for a unit test (Booch, 1994). A module test verifies a logical group of classes such as a subsystem. The AADIS software is verified through a combination of unit tests and module tests. For example, the **DbManager** class in the Database subsystem has a built-in unit test that verifies atomic database operations such as server connections, table creation/dropping and general SQL queries. Another example is the **HerdManager** class unit test that verifies the accuracy of spatially-based herd queries (Figure 5.1).

```
testing herd query by distance
grid herds 3km from 109051: 23320 23367 23398 81291 81292 104777 104780 104991 162298
164932 165044 166587 167261 172873 174521 175657 176162 178826
db seq herds 3km from 109051: 23320 23367 23398 81291 81292 104777 104780 104991 16229
8 164932 165044 166587 167261 172873 174521 175657 176162 178826
db seq query matches grid query = pass
db idx herds 3km from 109051: 23320 23367 23398 81291 81292 104777 104780 104991 16229
8 164932 165044 166587 167261 172873 174521 175657 176162 178826
db idx query matches grid query = pass

testing herd query by type and distance
grid herds of type 2 3km from 109051: 23320 23367 23398
db seq herds of type 2 3km from 109051: 23320 23367 23398
db seq query matches grid query = pass
db idx herds of type 2 3km from 109051: 23320 23367 23398
db idx query matches grid query = pass

testing herd query by type and distance ring              I
grid herds of type 2 5km to 10km from 109051: 22423 22444 22467 22540 22565 22945 2298
2 22989 23009 23032 23046 23163 23166 23176 23183 23204 23214 23235 23240 23244 23245
23253 23266 23279 23280 23312 23324 23335 23348 23366 23388 23399
db seq herds of type 2 5km to 10km from 109051: 22423 22444 22467 22540 22565 22945 22
982 22989 23009 23032 23046 23163 23166 23176 23183 23204 23214 23235 23240 23244 2324
5 23253 23266 23279 23280 23312 23324 23335 23348 23366 23388 23399
db seq query matches grid query = pass
db idx herds of type 2 5km to 10km from 109051: 22423 22444 22467 22540 22565 22945 22
982 22989 23009 23032 23046 23163 23166 23176 23183 23204 23214 23235 23240 23244 2324
5 23253 23266 23279 23280 23312 23324 23335 23348 23366 23388 23399
db idx query matches grid query = pass
```

Figure 5.1. Output snippet from the HerdManager unit test

The testing of the grid-based spatial-indexing module (which spans the Grid and Database subsystems), is presented in Section 5.1 as an example of verification. The test compares the AADIS grid-based spatial-indexing scheme with an industry standard R-Tree-based spatial-indexing system, both in terms of accuracy and computational performance.

Validation

Validation is the process of ensuring that a model is operationally fit for purpose, i.e., it is functionally appropriate and accurate for the intended domain (Dent and Blackie, 1979; Sargent, 2013). Validation activities may include: comparisons with other models (Dubé et al., 2007b; Connell et al., 2009; Gloster et al., 2010; Sanson et al., 2011; Reeves et al., 2011); independent assessments by a third party (Sargent, 2013); testing against data not used in the construction process (Green and Medley, 2002; Taylor, 2003); adapting the model for a different country (Dubé et al., 2011b); and sensitivity analysis of parameters (Green and Medley, 2002; Bates et al., 2003b; Owen et al., 2011). A model should make biological and epidemiological sense, both statically (formulae and algorithms), and dynamically (model outputs that reflect the

underlying datasets and parameterisation (Miller, 1976; Taylor, 2003; Dubé et al., 2007b).

The validation of AADIS is ongoing. Activities performed thus far are:

- comparison with the well-published Australian regional FMD model AusSpread (Section 5.2),

- comparison with the well-published New Zealand FMD model InterSpread Plus (Section 5.3), thus adapting AADIS for a different country and using data not involved in the model construction,

- a parameter sensitivity analysis (Section 5.4),

- extensive independent use during an international FMD workshop (Section 5.5),

- a formal independent assessment (Section 5.6).

5.1 Verification of grid-based spatial-indexing

5.1.1 Method

The results and response time of spatial queries using grid-based spatial-indexing was compared to that of the R-Tree-over-GiST spatial-indexing provided in the PostGIS extension to PostgreSQL. When AADIS (optionally) employs R-Tree-over-GiST spatial-indexing, PostGIS geometric *point* objects are precomputed for each herd and spatial queries are carried out via SQL exchanges with the PostgreSQL server. When AADIS employs grid-based spatial-indexing the location of a herd is defined by a point of latitude and longitude, and the PostgreSQL database is not involved in spatial queries. R-Tree-over-GiST spatial-indexing was used as a baseline for verifying, and assessing the performance and scalability of the grid-based spatial-indexing system. To illustrate the importance of spatial-indexing, the response time of PostGIS spatial queries with no spatial-indexing was also recorded.

The test scenario was an outbreak of FMD starting in a medium-sized pig herd that spreads undetected for 21 days. The scenario was re-run 100 times for each of the three spatial query approaches (no spatial-indexing, R-Tree-over-GiST and grid-based). This was repeated across 10 herd populations ranging from 21,617 up to 235,668 FMD-susceptible herds. The test hardware platform was a quad-core laptop with 16GB RAM running 64-bit Kubuntu Linux™.

The Stata/IC statistical package (Stata, 2015) was used to check for significant differences between the following key model outputs for each of the three spatial-indexing methods:

- total number of infected premises,

- number of infections by disease spread pathway (direct, indirect, local, saleyard, airborne),

- size of the infected area based on the convex hull of all infected premises.

Data sets were imported into Stata/IC and checked for normality. Non-parametric statistical methods were used throughout this analysis as some data sets were non-normal and could not be transformed to normality by standard transformation techniques. The number of infected premises, convex hull area, spatial query response time, and scenario run time were analysed using the Kruskal-Wallis test for comparison of multiple independent groups of data (UCLA, 2015a). Post hoc analysis to identify differences between strategies was conducted using the Kruskal-Wallis test with the significance level adjusted per the Bonferroni correction for multiple pairwise comparisons. Data for the proportion of disease spread events occurring by each of the five spread pathways were compared using Pearson's chi-squared test (UCLA, 2015b).

5.1.2 Results

Figure 5.2 illustrates that the mean response time of spatial queries in the absence of spatial-indexing was O(n), i.e., linearly dependent on the size n of the population. This is because each spatial query triggered a sequential scan over all herd records. Figure 5.2 also shows how R-Tree-over-GiST spatial-indexing improved the mean response time of spatial queries to O(log n).
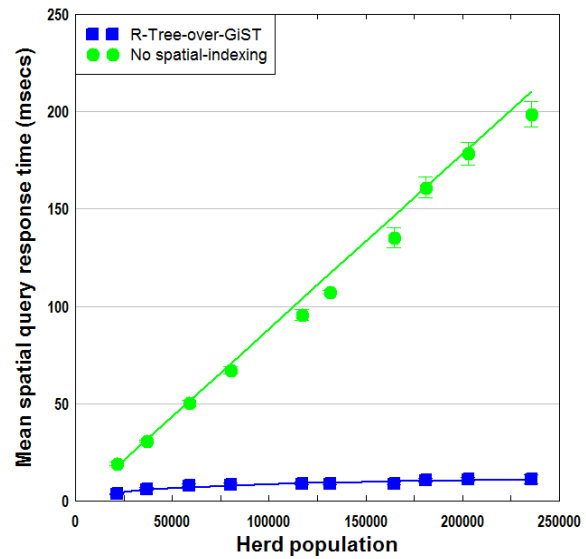
Figure 5.2. Spatial-indexing vs. no spatial-indexing.

Figure 5.3 illustrates how the AADIS grid-based spatial-indexing scheme provided approximately an eight-fold improvement in mean spatial query response time over the PostGIS R-Tree-over-GiST spatial-indexing scheme, and was less sensitive to changes in the size of the herd population.
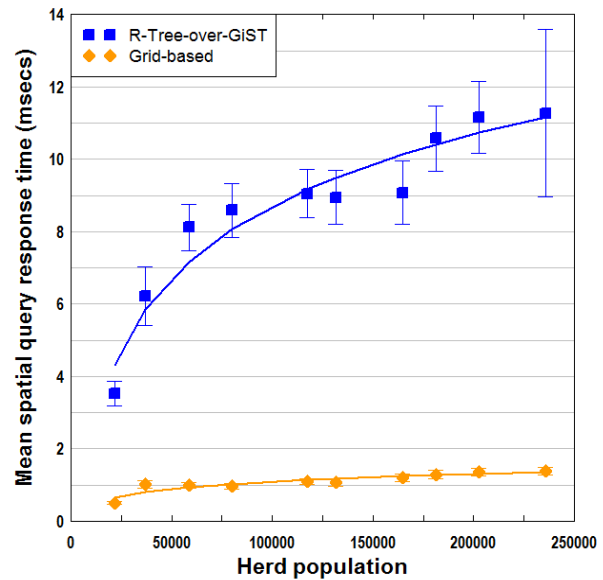
Figure 5.3. R-Tree vs. grid-based spatial-indexing.

Figure 5.4 illustrates how grid-based spatial-indexing provided a three-fold improvement in the mean runtime of a 21-day outbreak across all population sizes. Over the course of 100 runs of a 21-day outbreak across the national herd population, approximately 80,000 spatial queries were made. The runtime performance of AADIS is dependent on the response time of spatial queries. AADIS took three hours to complete the entire simulation when spatial-indexing was not employed. The same task took 10 minutes when R-Tree-over-GiST spatial-indexing was used, and only three minutes when grid-based spatial-indexing was used. A more complex scenario (not shown), that included control measures, made approximately 2,000,000 spatial queries over the course of 1000 runs. In this case, AADIS took approximately six hours to complete the simulation using R-Tree-over-GiST spatial-indexing, and approximately three hours using grid-based spatial-indexing.

Figure 5.4. Scenario run times for R-Tree-over-GiST vs. grid-based spatial-indexing
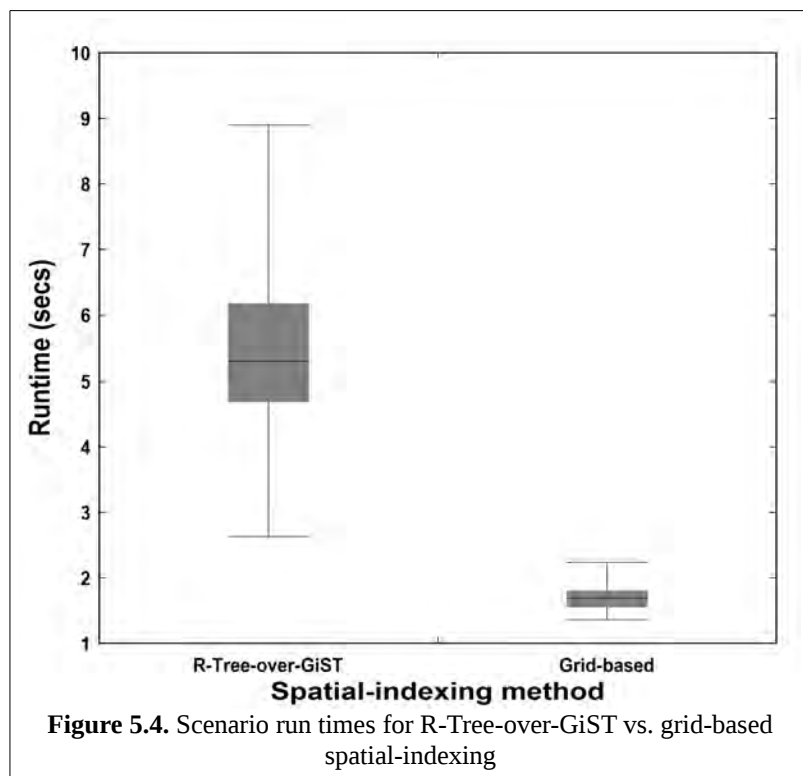
The effects of spatial-indexing method on outbreak metrics are shown in Figures 5.5 to 5.7. There were no significant differences ($p > 0.05$), in total number of infected premises, spread pathway mix, and size of the infected area.

Figure 5.5. Effect of spatial-indexing method on disease spread mechanism

Figure 5.6. Effect of spatial-indexing method on the number of infected premises.

Figure 5.7. Effect of spatial-indexing method on the area of infection
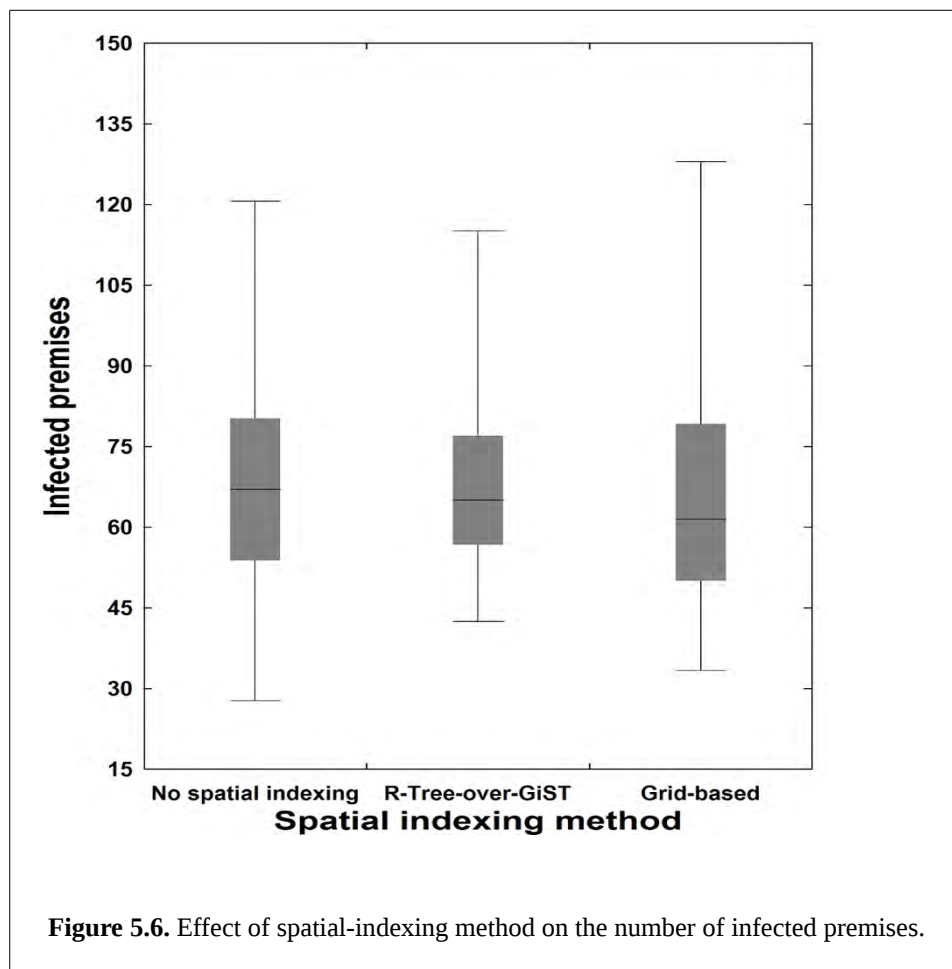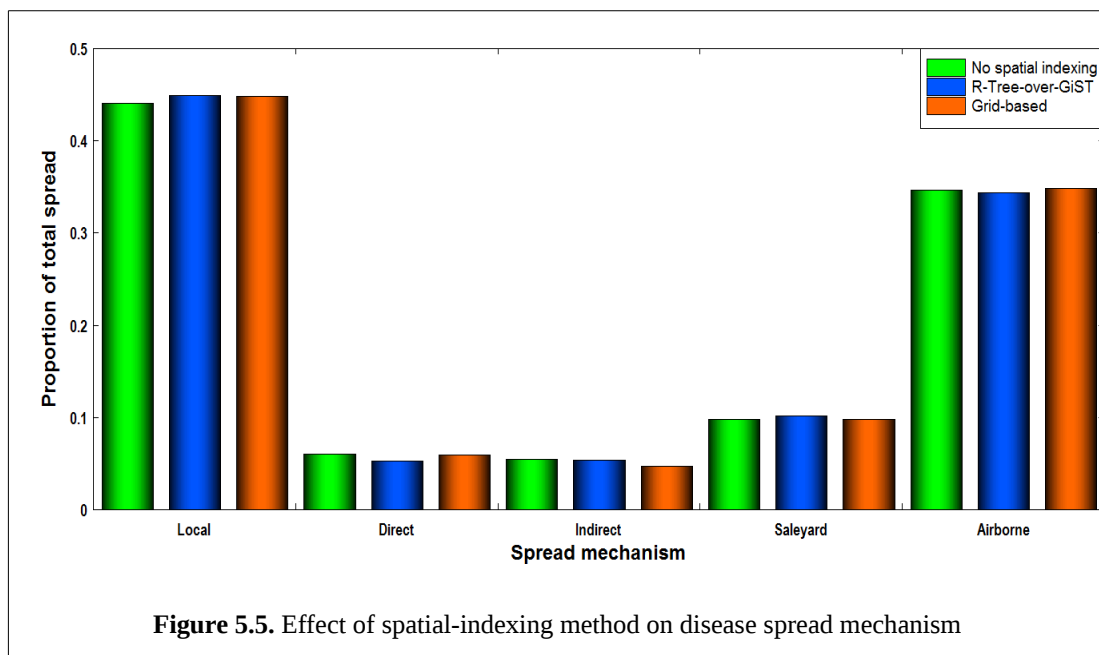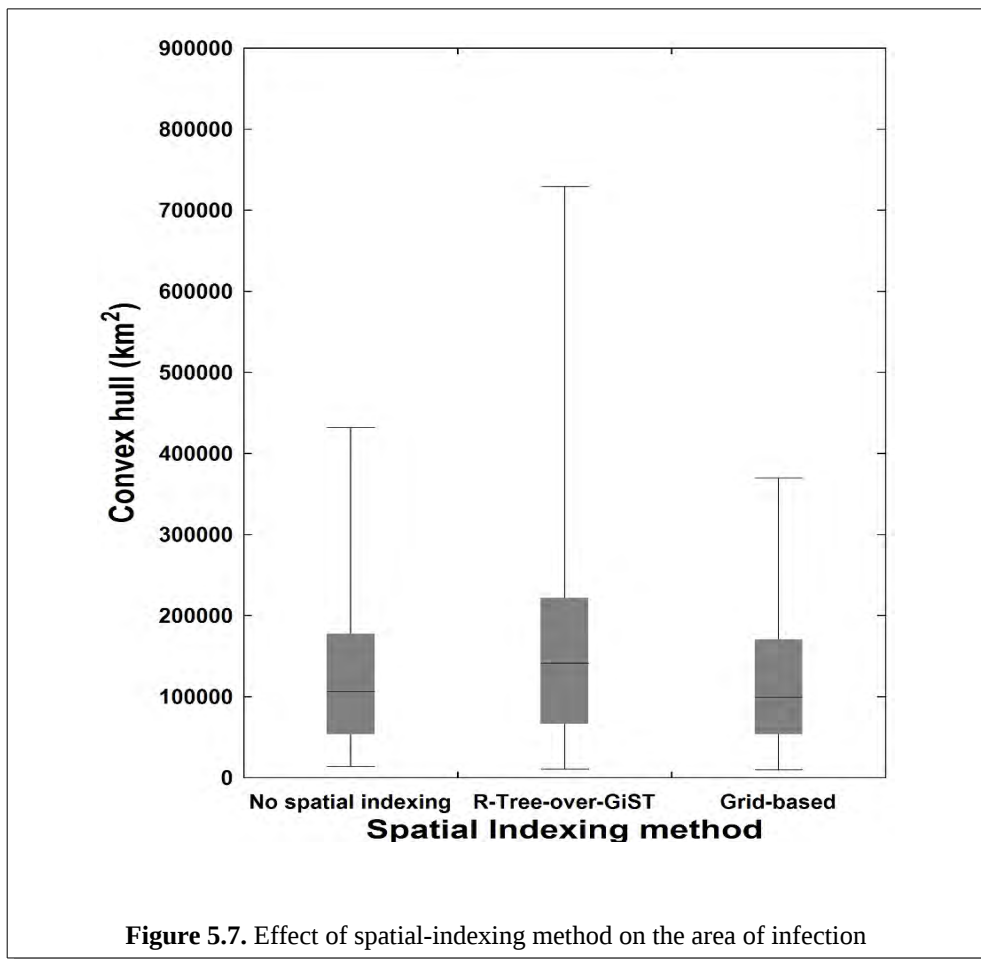
5.1.3 Discussion

The AADIS grid-based spatial-indexing scheme provided approximately an eight-fold improvement in mean spatial query response time over the R-Tree-over-GiST spatial-indexing scheme, with no impact on scenario outcomes. This in turn yielded a two to three-fold improvement in the overall time taken to run the test disease spread and control simulation.

The spatial query response time of PostgreSQL/PostGIS could likely be improved through techniques such as server optimisation and server prepared SQL statements. However, the optimisation of relational databases, servers and SQL for geospatial efficiency is quite a specialised area. The AADIS uniform grid-based spatial-indexing

scheme is simple to implement, test and maintain, and requires no specialised knowledge of mathematics, PostgreSQL and PostGIS. Although AADIS is overall a complex piece of software, keeping components as simple as possible contributes to software longevity and low ongoing maintenance costs (Banker et al., 1993).

5.2 Comparative study with AusSpread

In addition to underpinning many FMD studies (Section 2.4.2.2), AusSpread has taken part in model comparison and relative validation studies with the NAADSM, InterSpread Plus, Exodis and the Netherlands models (Dubé et al., 2007b; Garner et al., 2007; Sanson et al., 2011; Roche et al., 2015). Participants in these studies have included veterinary epidemiologists from the 'Quadrilateral' group of countries (Australia, Canada, New Zealand and the United States), as well as Ireland, the United Kingdom and the Netherlands. As AusSpread is a well published and validated model it was used in a structured model comparison to see whether AADIS produces broadly similar results.

As AusSpread is a regional model it was necessary to tailor AADIS to accommodate the comparison. This was achieved with a reduced population of 42,217 herds, representing the livestock population of the state of Victoria. As the AusSpread modelling unit of interest for disease spread is the farm, in this study AADIS treated a herd as equivalent to a farm. The model comparison initially involved disease spread only, i.e., the pre-detection silent spread phase with no control measures. The models were subsequently compared with control measures enabled.

5.2.1 Silent spread

5.2.1.1   Method

FMD was introduced into five different herd types (small pig, medium pig, dairy, sheep and beef), and allowed to spread without detection for 21 days. The five scenarios were run 1000 times under AADIS and 100 times under AusSpread. AADIS is inherently more stochastic than AusSpread (Section 4.1.4), and more runs were

necessary to adequately represent outcome distributions (see Section 6.2). The following outputs were compared:

- cumulative number of infected herds,

- proportion of spread attributable to each pathway.

The test hardware platform was a quad-core desktop with 16GB RAM running 64-bit Microsoft Windows 7™. Model outcomes are expressed as medians with 90% probability intervals and represented with standard box plots (Tukey, 1977).

5.2.1.2 Results

AADIS and AusSpread produced quite similar numbers of infected herds for each of the five silent spread scenarios (Table 5.1 and Figure 5.8). The proportions of infected herds attributable to the various disease spread pathways were also broadly similar. Local spread was generally the predominant pathway in both models, followed by direct contact spread (including saleyards), indirect spread and airborne. The contribution of airborne spread increased when the outbreak commenced on a pig farm. AusSpread tended to generate less direct and saleyard spread than AADIS.

There was greater statistical error in the AusSpread results, with the sampled mean number of IPs within 8%, 20%, 8%, 48% and 13% respectively of the theoretical population means (with 95% confidence). AADIS on the other hand generated sample means that were within 7%, 6%, 6%, 24% and 9% respectively of the theoretical population means. This can be explained in terms of the number of runs completed per scenario for each of the models – 100 for AusSpread and 1000 for AADIS. The convergence of the AusSpread sample means would be improved with increased runs; however, the slow runtime effectively precluded this. AADIS completed 1000 stamping out scenario runs in under six minutes whereas AusSpread would have taken up to 30 hours to complete 1000 runs.

Table 5.1. AADIS vs AusSpread: silent spread

Model	Small pig herd (ID=42189, size=110)		Medium pig herd (ID=7779, size=1945)		Dairy herd (ID=33812, size=256)		Sheep herd (ID=98, size=3065)		Beef herd (ID=315, size=532)	
	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread
Number of runs	1000	100	1000	100	1000	100	1000	100	1000	100
Mean infections	16.69	18.88	23.73	20.04	14.93	10.99	0.28	0.18	4.57	3.8
Std error of mean[1]	0.64	0.77	0.77	2.06	0.43	0.45	0.03	0.04	0.20	0.25
Convergence[2]	7%	8%	6%	20%	6%	8%	24%	48%	9%	13%
Median infections[3]	8(0-65)	18(4-37)	13(4-80)	13(6-56)	8(0-53)	10(3-24)	0(0-1)	0(0-1)	2(0-16)	3(1-11)
Local spread	50%	78%	45%	43%	43%	69%	53%	33%	68%	73%
Direct spread	12%	5%	11%	5%	15%	7%	6%	17%	8%	7%
Indirect spread	4%	4%	6%	13%	3%	6%	20%	39%	3%	5%
Saleyard spread	24%	9%	24%	9%	39%	18%	21%	11%	21%	15%
Airborne spread	10%	4%	14%	30%	0%	0%	0%	0%	0%	0%
Total runtime	5.7 mins	179 mins	5.8 mins	176 mins	5.7 mins	178 mins	3.2 mins	167 mins	3.3 mins	168 mins
Av. time per run	0.3 secs	1.8 mins	0.4 secs	1.8 mins	0.3 secs	1.8 mins	0.2 secs	1.7 mins	0.2 secs	1.7 mins

[1] standard deviation of the sample mean / square root of the number of runs

[2] sample mean convergence with 95% confidence (z_c = 1.96). See Section 6.2 for definition.

[3] median with 90% probability interval

Figure 5.8. AADIS vs. AusSpread: number of infected herds after silent spread
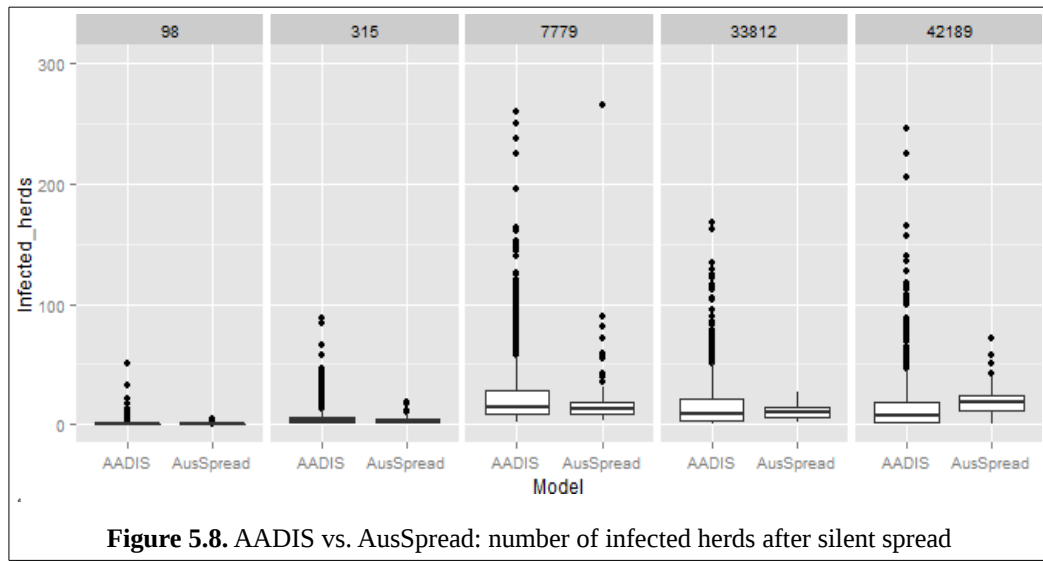
The spatial distributions of the outbreak for the medium pig herd scenario are provided in Figure 5.9 for illustrative purposes only. The AADIS spatial distribution is broadly similar to the AusSpread distribution (for comparative purposes, 100 runs are shown for both models). It would be possible to conduct a more quantitative analysis by superimposing a lattice and comparing cell counts of IPs, however this was not pursued due to the inherent differences between the two models (Section 5.2.3).

Figure 5.9. AADIS (left) vs AusSpread (right): spatial distribution comparison

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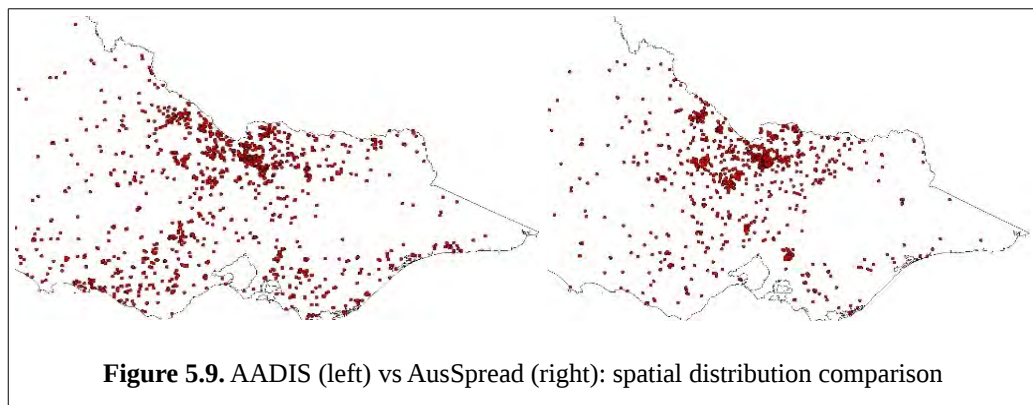
5.2.2 Control measures

5.2.2.1 Method

FMD was introduced into five different herd types (small pig, medium pig, dairy, sheep and beef), and allowed to spread up until fixed detection on the 21st day. The following control measures were trialed for each of the five outbreak scenarios:

- stamping out of infected premises (SO),

- stamping out of infected premises plus suppressive ring vaccination (SORV),

- stamping out of infected premises plus pre-emptive contiguous culling (SOCC).

The control scenarios were run 1000 times under AADIS and 100 times under AusSpread, and the following outputs compared:

- duration of the outbreak (defined as the simulation day when the last infected premises was declared),

- cumulative number of infected premises,

- cumulative number of culled premises,

- cumulative number of vaccinated premises.

Selected parameter settings for the control strategies are provided in Table 5.2.

The test hardware platform was a quad-core desktop with 16GB RAM running 64-bit Microsoft Windows 7™. Model outcomes are expressed as medians with 90% probability intervals and represented with standard box plots (Tukey, 1977).

Table 5.2. AADIS vs AusSpread: selected control parameter settings

Control Parameter	Value
Day that the first infected premises is detected	21
National livestock standstill length	3 days
Controlled area radii	RA = 3km, CA = 10km (around each IP)
Reduction of direct movements during control	95% inside RAs, 85% inside CAs, 80% in OA
Reduction of indirect movements during control	90% inside RAs, 75% inside CAs, 70% in OA
Tracing window	14 days backwards, 14 days forwards
Time needed for a direct trace	0 to 4 days (species-dependent)
Time needed for an indirect trace	1 to 5 days (species-dependent)
Effectiveness of direct tracing	70% to 100% (species-dependent)
Effectiveness of indirect tracing	70% to 90% (species-dependent)
Surveillance visit duration	0.5 to 1 day (herd type-dependent)
Probability of reporting suspect premises	70% to 100% (herd type-dependent)
Time to report SPs after clinical signs	0 to 19 days (herd type-dependent)
Ratio of false SP reports to true reports	2.34:1
Number of surveillance teams (per jurisdiction)	1 on control day 1, ramping up to 60 by day 30
Number of culling teams (per jurisdiction)	1 on control day 3, ramping up to 30 by day 30
Number of disposal teams (per jurisdiction)	10 on control day 10, ramping up to 500 by day 31
Number decontamination teams (per jurisdiction)	Not limited
Number of vaccination teams (per jurisdiction)	10 on control day 10, ramping up to 500 by day 31
Contiguous culling radius	1 km
Days to cull a herd	1 to 3 (herd type-dependent)
Days to dispose a herd	0 (not limited)
Days to decontaminate a premises	0 (not limited)
Start of vaccination program	10th day of the control program
Days to vaccinate a herd	0.2 to 1 (herd type-dependent)
Vaccination annulus radii (km)	inner=0, outer=3
Vaccination retrospectivity and direction	New IPs only, outside-in

5.2.2.2 Results

AADIS and AusSpread produced broadly similar outbreaks for each of the five stamping out scenarios (Table 5.3, Figure 5.10 and Figure 5.11). There was greater statistical error in the AusSpread results, with the sampled mean number of IPs within 18%, 126%, 15%, 12% and 34% respectively of the theoretical population means (with 95% confidence). AADIS on the other hand generated sample means that were within 12%, 9%, 9%, 14% and 12% respectively of the theoretical population means. This can be explained in terms of the number of runs completed per scenario for each of the models – 100 for AusSpread and 1000 for AADIS. The convergence of the AusSpread results would have improved with increased runs; however, the slow runtime effectively precluded this. AADIS completed 1000 stamping out scenario runs in under 23 minutes whereas AusSpread would have taken up to five days to complete 1000 runs.

Table 5.3. AADIS vs AusSpread: stamping out

	Small pig herd (ID=42189, size=110)		Medium pig herd (ID=7779, size=1945)		Dairy herd (ID=33812, size=256)		Sheep herd (ID=98, size=3065)		Beef herd (ID=315, size=532)	
Model	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread
Number of runs	1000	100	1000	100	1000	100	1000	100	1000	100
Outbreak length[1,2]	51(21-100)	54(39-97)	52(27-109)	47(31-88)	47(21-104)	51(31-101)	21(21-29)	22(22-28)	29(21-68)	36(22-64)
Median IPs[2]	15(1-127)	31(14-118)	19(4-124)	18(8-126)	12(1-98)	20(5-65)	1(1-2)	1(1-2)	3(1-21)	4(2-23)
Mean IPs[3]	33 +/- 2	40 +/- 4	36 +/- 2	90 +/- 58	25 +/- 1	24 +/- 2	1 +/- 0	1 +/- 0	6 +/- 1	8 +/- 1
Convergence[4]	12%	18%	9%	126%	9%	15%	14%	12%	12%	34%
Num culled farms[2]	15(1-127)	31(14-118)	19(4-124)	18(8-126)	12(1-98)	20(5-65)	1(1-2)	1(1-2)	3(1-21)	4(2-23)
Elapsed runtime	23 mins	755 mins	21 mins	683 mins	19 mins	718 mins	5 mins	376 mins	8 mins	526 mins
Av. time per run	1.4 secs	7.55 mins	1.3 secs	6.83 mins	1.2 secs	7.18 mins	0.3 secs	3.76 mins	0.5 secs	5.26 mins

[1] day that last IP is declared

[2] median with 90% probability interval

[3] sample mean +/- standard error of the mean

[4] sample mean convergence with 95% confidence ($z_c = 1.96$). See Section 6.2 for definition.

Figure 5.10. AADIS vs. AusSpread: outbreak duration with stamping out

Figure 5.11. AADIS vs. AusSpread: number of IPs with stamping out

AADIS and AusSpread produced broadly similar outbreaks for each of the five suppressive ring vaccination scenarios (Table 5.4, Figure 5.12 and Figure 5.13). AusSpread tended to produce longer outbreaks with higher numbers of IPs and culled premises. There was greater statistical error in the AusSpread results due to the smaller number of runs completed compared to AADIS. The convergence of the AusSpread results would have improved with increased runs.

Table 5.4. AADIS vs AusSpread: stamping out plus suppressive ring vaccination
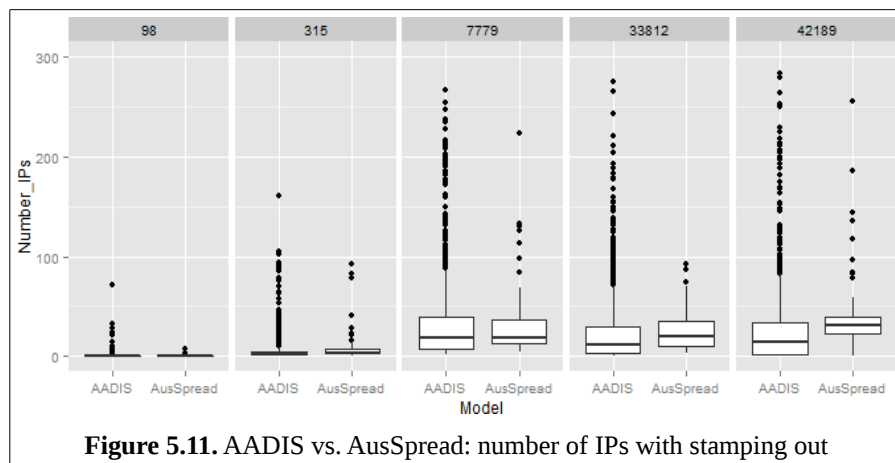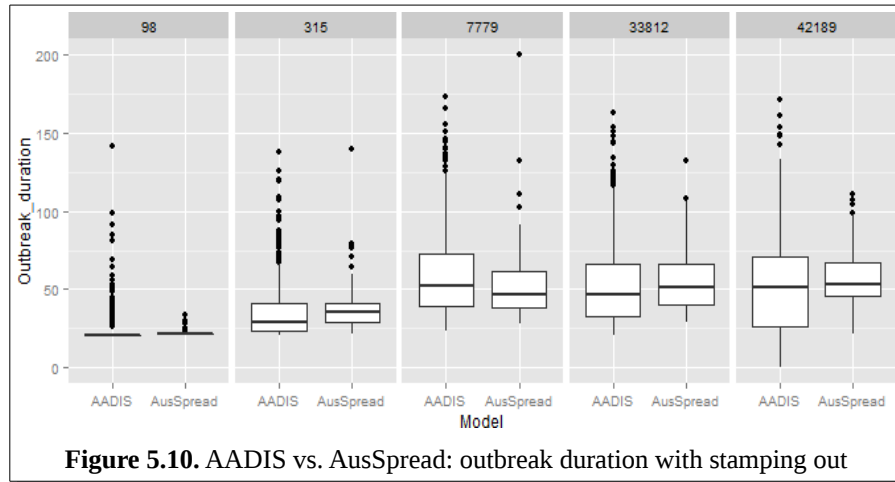
Model	Small pig herd (ID=42189, size=110)		Medium pig herd (ID=7779,size=1945)		Dairy herd (ID=33812,size=256)		Sheep herd (ID=98, size=3065)		Beef herd (ID=315, size=532)	
	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread
Number of runs	1000	100	1000	100	1000	100	1000	100	1000	100
Outbreak length[1,2]	38(21-77)	50(39-85)	42(28-79)	47(31-90)	38(21-72)	48(31-83)	21(21-27)	22(22-28)	29(21-52)	36(22-60)
Median IPs[2]	10(1-78)	28(14-85)	15(4-93)	19(8-116)	9(1-63)	18(5-47)	1(1-2)	1(1-2)	3(1-16)	4(2-20)
Mean IPs[3]	21 +/- 1	35 +/- 3	29 +/- 1	36 +/- 6	18 +/- 1	20 +/- 1	1 +/- 0	1 +/- 0	5 +/- 0	7 +/- 1
Convergence[4]	10%	15%	9%	33%	8%	12%	6%	12%	9%	26%
Culled farms[2]	10(1-78)	28(14-85)	15(4-93)	19(8-116)	9(1-63)	18(5-47)	1(1-2)	1(1-2)	3(1-16)	4(2-20)
Vaccinated farms[2]	27(0-241)	55(14-240)	36(0-293)	29(0-224)	29(0-253)	52(0-154)	0(0-0)	0(0-0)	0(0-51)	2(0-49)
Total runtime	18 mins	696 mins	21 mins	655 mins	18 mins	667 mins	5 mins	400 mins	8 mins	600
Av. time per run	1.1 secs	6.96 mins	1.2 secs	6.55 mins	1.1 secs	6.67 mins	0.3 secs	4.0 mins	0.5 secs	6.0 mins

[1] day that last IP is declared

[2] median with 90% probability interval

[3] sample mean +/- standard error of the mean

[4] sample mean convergence with 95% confidence ($z_c = 1.96$). See Section 6.2 for definition.

Figure 5.12. AADIS vs. AusSpread: outbreak duration with vaccination

Figure 5.13. AADIS vs. AusSpread: number of IPs with vaccination
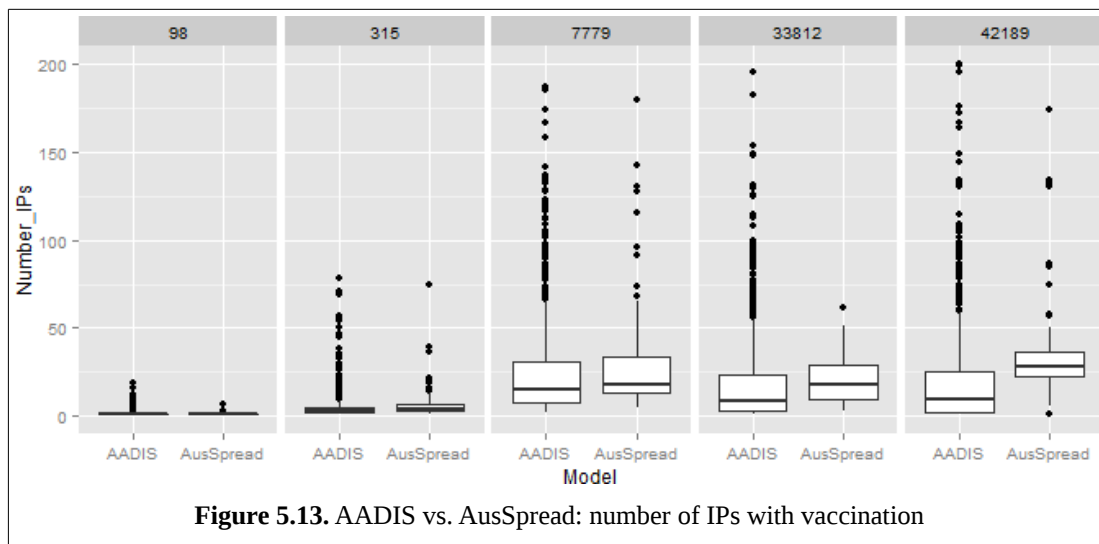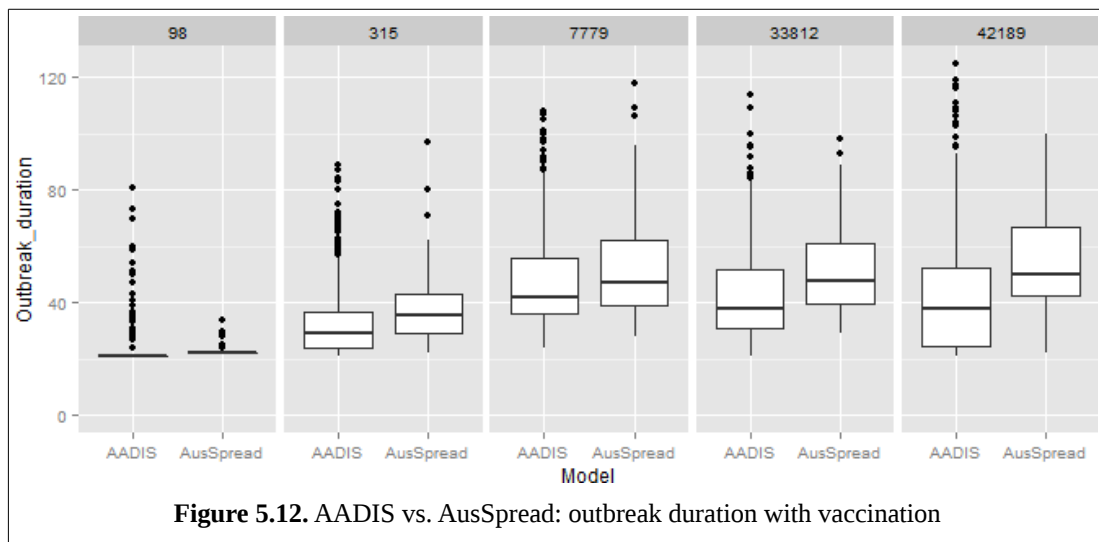
AADIS and AusSpread produced broadly similar outbreaks for each of the three contiguous culling scenarios (Table 5.5, Figure 5.14 and Figure 5.15). AusSpread tended to produce longer outbreaks with higher numbers of IPs and culled premises.

Table 5.5. AADIS vs AusSpread: stamping out plus contiguous culling

	Small pig herd (ID=42189, size=110)		Medium pig herd (ID=7779, size=1945)		Dairy herd (ID=33812, size=256)	
Model	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread
Number of runs	1000	100	1000	100	1000	100
Outbreak duration[1,2]	38(21-70)	54(38-99)	43(26-75)	55(33-97)	38(21-74)	56(34-88)
Median number of IPs[2]	9(1-81)	19(6-91)	14(3-95)	18(6-108)	10(1-61)	16(4-50)
Mean number of IPs[3]	21 +/- 1	33 +/- 5	29 +/- 1	53 +/- 24	18 +/- 1	20 +/- 1
Convergence of mean[4]	13%	31%	9%	88%	8%	14%
Num culled farms[2]	21(5-166)	111(35-373)	27(5-179)	89(19-388)	21(1-134)	91(25-241)
Total elapsed runtime[6]	47 mins	735 mins	49 mins	635 mins	42 mins	575 mins
Average time per run[6]	2.8 secs	7.35 mins	2.9 secs	6.35 mins	2.5 secs	5.75 mins

[1] day that the last IP is declared

[2] median with 90% probability interval

[3] mean +/- standard error of the mean

[4] with 95% confidence ($z_c = 1.96$). See Section 6.2 for definition
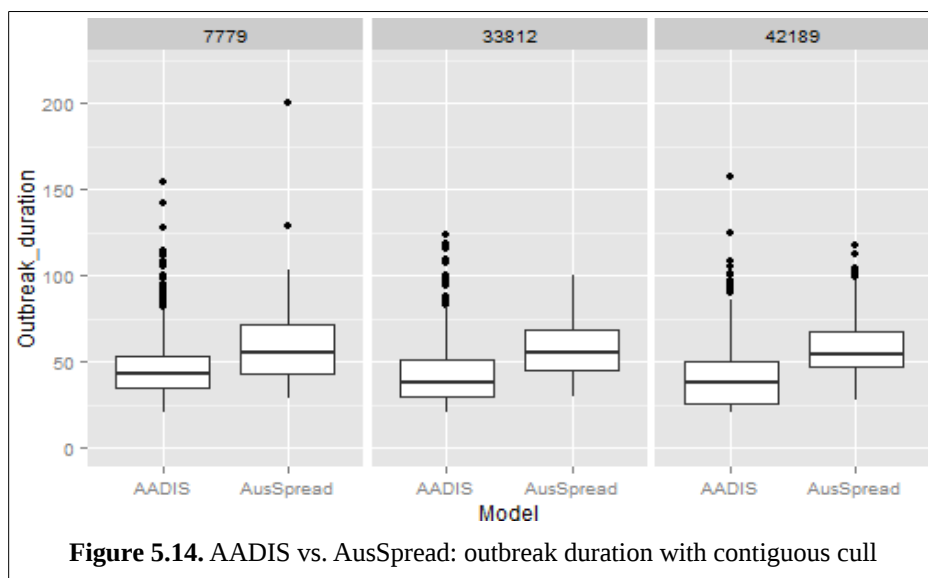
Figure 5.14. AADIS vs. AusSpread: outbreak duration with contiguous cull

Figure 5.15. AADIS vs. AusSpread: number of IPs with contiguous cull
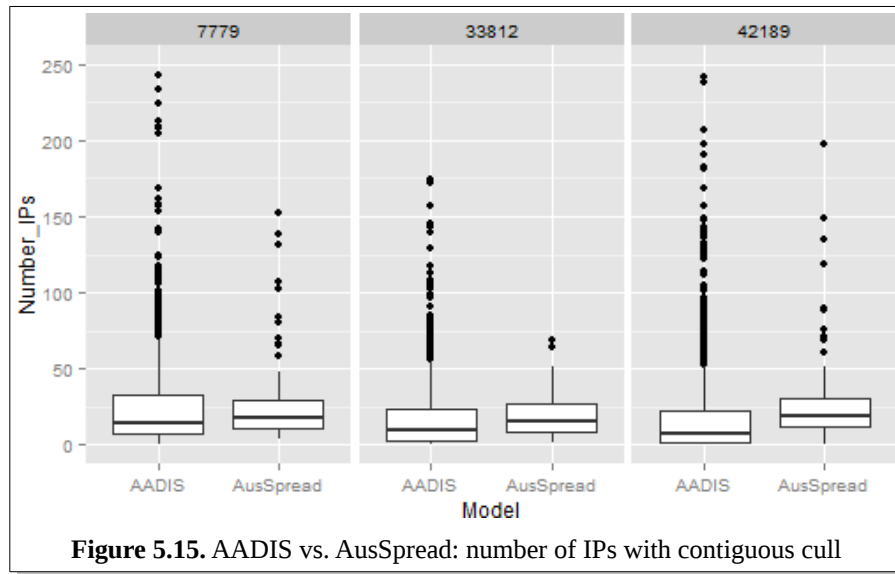
5.2.3 Discussion

It was reassuring that AADIS and AusSpread produced broadly similar outbreaks for both silent spread and control scenarios. Minor outcome variations between the two models are to be expected given the differences in the way the spread of disease within a herd/farm is handled. AADIS explicitly models within-herd spread with an SEIR mass-action EBM that takes into account herd type and size (Section 3.3). The probability of transmission for an infectious consignment depends on the prevalence of the source herd and the consignment size (Equation 3.5 in Section 3.5.1). AusSpread on the other hand does not explicitly model the spread of disease within a farm. An infected farm transitions through atomic infection states according to durations sampled from probability distributions. Relative infectivity varies over time according to a simple step function that applies to all farm types, and does not take outgoing consignment size into account. The different approaches are depicted in Figure 5.16 where the probability of transmission curves for the AADIS intensive beef, sheep and small pig herd types (derived using Equation 3.5 in Section 3.5.1 for average herd size n), contrast with the AusSpread stepped relative infectivity function. The AADIS probabilities incorporate herd prevalence, herd type and consignment size, and are thus more granular than the AusSpread generalised stepped probabilities.

Figure 5.16. AADIS vs. AusSpread: probability of transmission over time
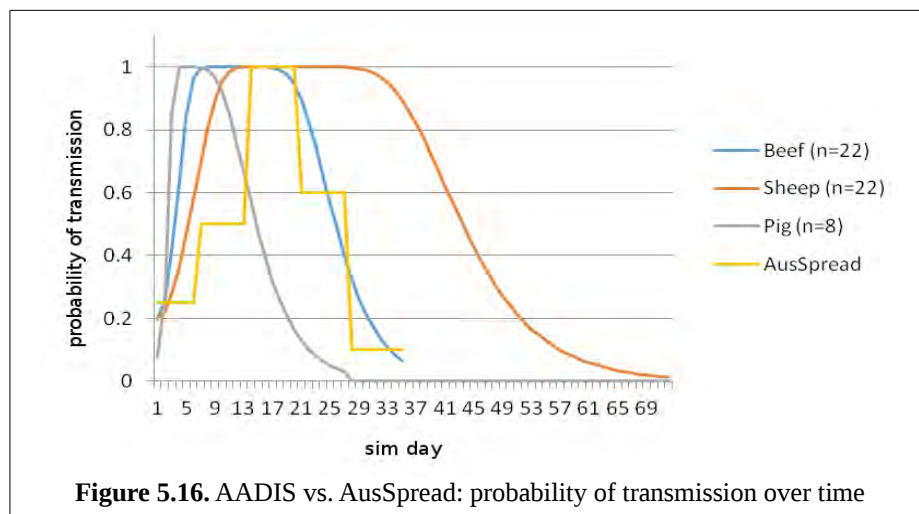
The AusSpread probabilities of infection are generally lower than those of AADIS, which will influence the direct contact and saleyard pathways. This is consistent with the results in Table 5.1 where AADIS generally produced higher levels of direct and saleyard spread than AusSpread.

Figure 5.17 compares the normalised infectious prevalence for the AADIS intensive beef, sheep and small pig herds (generated by the EBM for average herd sizes), with the AusSpread relative infectivity step function. This suggests that AusSpread is underestimating prevalence early in the infectious cycle for cattle and pigs relative to AADIS, which may introduce differences in the levels of indirect and local spread between the two models (Table 5.1).

Figure 5.17. AADIS vs. AusSpread: normalised infectious prevalence

161
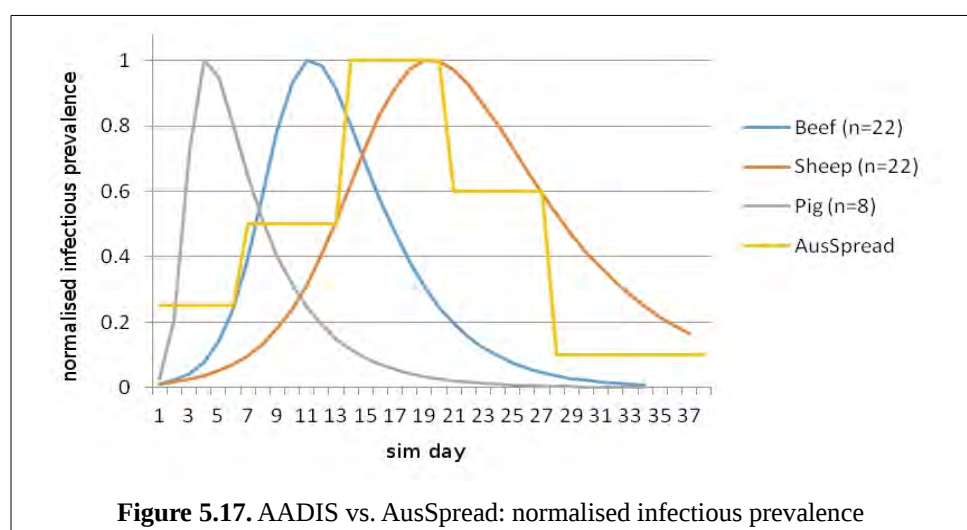
Figure 5.18 compares the infectious prevalence for AADIS small and large pig herds (based on average herd sizes), with the AusSpread prevalence step function. The AADIS prevalence curves peak earlier and slightly higher than AusSpread which may have contributed to variation in the levels of airborne spread between the two models (Table 5.1).

Figure 5.18. AADIS vs. AusSpread: infectious prevalence of pig herds
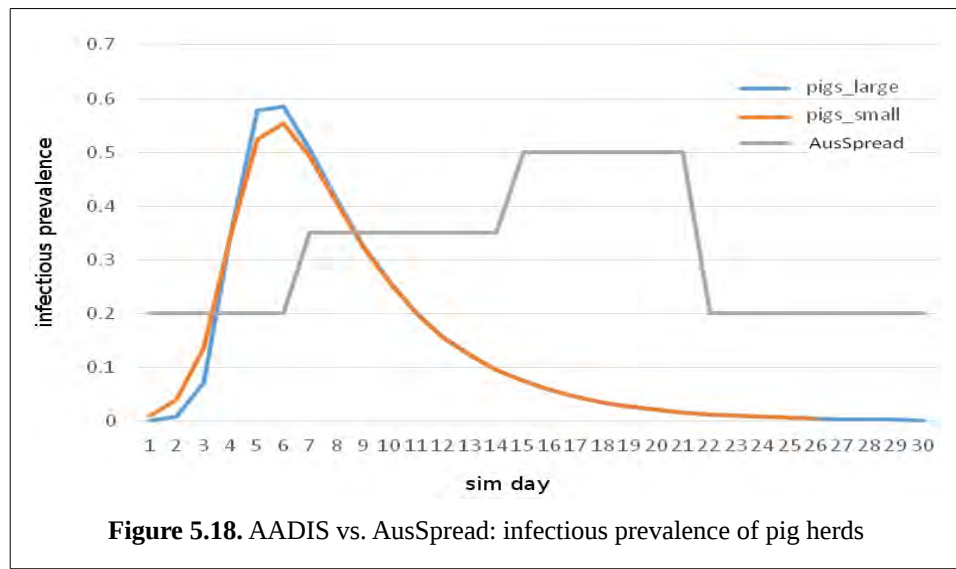
Variation in scenario outcomes between AADIS and AusSpread may also be due to the substantial differences in software architecture. The AADIS concurrent architecture is radically different to, and inherently more stochastic than, the AusSpread sequential architecture (Section 4.1.4). As the epidemiological principles underpinning AADIS and AusSpread are similar, the fact that scenario outcomes are comparable provides confidence in the AADIS concurrent approach.

This model comparison study also highlights the performance advantage that AADIS provided over AusSpread. AADIS completed the 18 Victorian test scenarios between 130 and 800 times faster than AusSpread, and was on average 412 times faster.

5.3 Comparative study with InterSpread Plus

In addition to underpinning many FMD studies (Section 2.4.2.2), the New Zealand model InterSpread Plus has also featured in several multi-model comparison studies with the NAADSM, AusSpread, Exodis, DTU-DADS and the Netherlands FMD models (Dubé et al., 2007b; Garner et al., 2007; Gloster et al., 2010; Sanson et al., 2011; Halasa et al., 2014; Roche et al., 2015).

A model comparison involving AADIS and InterSpread Plus was undertaken as part of a Centre of Excellence for Biosecurity Risk Analysis (CEBRA) funded research project. CEBRA is a research agreement between the University of Melbourne, the Australian Department of Agriculture and Water Resources and the New Zealand Ministry for Primary Industries. Project 1404D ('Using decision support tools in emergency animal disease planning and response: foot-and-mouth disease'), aims to assess the utility of epidemiological information available early in an FMD outbreak as a predictor of eventual outbreak size, and to evaluate the effectiveness of disease management approaches taking into account multiple management objectives (CEBRA, 2014). The project includes configuring AADIS to simulate the spread and control of FMD in New Zealand, and configuring InterSpread Plus to simulate the spread and control of FMD in Australia. This provides an opportunity for a model comparison and relative validation study. Using AADIS to model FMD outbreaks in New Zealand (Figure 5.20), satisfies the recommendation by Taylor (2003) that a model's validation should include data that was not part of its construction. Dubé and colleagues (2011b) note that adapting a model to operate in the context of an alternative region/country can also be beneficial for validation purposes. At the time of writing, the project is still in progress and only interim results are available for simulating outbreaks without control (i.e., silent spread).

The New Zealand simulations were carried out using the national population of 81,912 FMD-susceptible herds. The Australian simulations were carried out with a

reduced national herd population of 199,956 that took into account the farm-based approach of InterSpread Plus.

5.3.1 Method

FMD was introduced into selected herds and allowed to spread without detection for 28 days:

- Pastoral livestock herd of 1400 animals in Canterbury, New Zealand,

- Lifestyle herd of 16 animals in Taranaki, New Zealand,

- Small pig herd of 210 animals in the Goulburn Valley, Victoria, Australia,

- Small pig herd of 132 animals in Toowoomba, Queensland, Australia.

The four scenarios were run 1000 times for AADIS and 100 times for InterSpread Plus and the following outputs compared:

- cumulative number of infected herds,

- proportion of spread attributable to each pathway.

The AADIS simulations were conducted on a quad-core laptop with 16GB RAM running 64-bit Kubuntu Linux™. The InterSpread simulations were conducted on a quad-core machine with 8GB RAM running 64-bit Microsoft Windows 7™. Model outcomes are expressed as medians with 90% probability intervals and represented with standard box plots (Tukey, 1977).

5.3.2 Results

AADIS and InterSpread Plus produced similar outbreaks for the Taranaki, Goulburn Valley and Toowoomba scenarios (Table 5.6 and Figure 5.19). AADIS produced larger outbreaks with more variation than InterSpread Plus for the Canterbury scenario. The proportions of infected herds attributable to the various disease spread pathways were comparable, although AADIS had a tendency to produce more local spread and less indirect spread than InterSpread Plus.

Table 5.6. AADIS vs. InterSpread Plus: silent spread

Model	Pastoral livestock herd Canterbury, NZ (ID=58600, size=1400)		Lifestyle herd in Taranaki, NZ (ID=36369, size=16)		Small pig herd in Goulburn Valley, AUS (ID=108284, size=210)		Small pig herd in Toowoomba, AUS (ID=107717, size=132)	
	AADIS	InterSpread	AADIS	InterSpread	AADIS	InterSpread	AADIS	InterSpread
Num herds in population	81,912	81,912	81,912	81,912	199,956	199,956	199,956	199,956
Number of runs	1000	100	1000	100	1000	100	1000	100
Mean infections/run[1]	100 +/- 3	57 +/- 5	107 +/- 3	97 +/- 7	23 +/- 1	20 +/- 2	15 +/- 1	21+/- 1
Convergence of mean[2]	6%	17%	6%	13%	11%	19%	10%	12%
Median infections/run[3]	71(16-299)	42(12-145)	80(3-309)	81(15-229)	8(1-105)	13(2-64)	8(1-48)	19(4-42)
Local spread	41%	27%	52%	50%	51%	13%	49%	19%
Direct spread	6%	15%	10%	12%	10%	42%	11%	38%
Indirect spread	51%	53%	37%	35%	12%	13%	13%	9%
Saleyard spread	1%	3%	1%	2%	12%	27%	13%	28%
Airborne spread	0%	0%	0%	0%	11%	5%	8%	0%
Total elapsed runtime	8.3 mins	9.4 mins	12.0 mins	8.0 mins	14.3 mins	3.7 mins	14.2 mins	3.6 mins
Average time per run	0.50 secs	5.66 secs	0.72 secs	4.82 secs	0.86 secs	2.20 secs	0.85 secs	2.13 secs

[1] sample mean +/- standard error of the mean

[2] sample mean convergence with 95% confidence ($z_c = 1.96$). See Section 6.2 for definition.

[3] with 90% probability interval

Figure 5.19. AADIS vs. InterSpread Plus: number of infected herds after silent spread
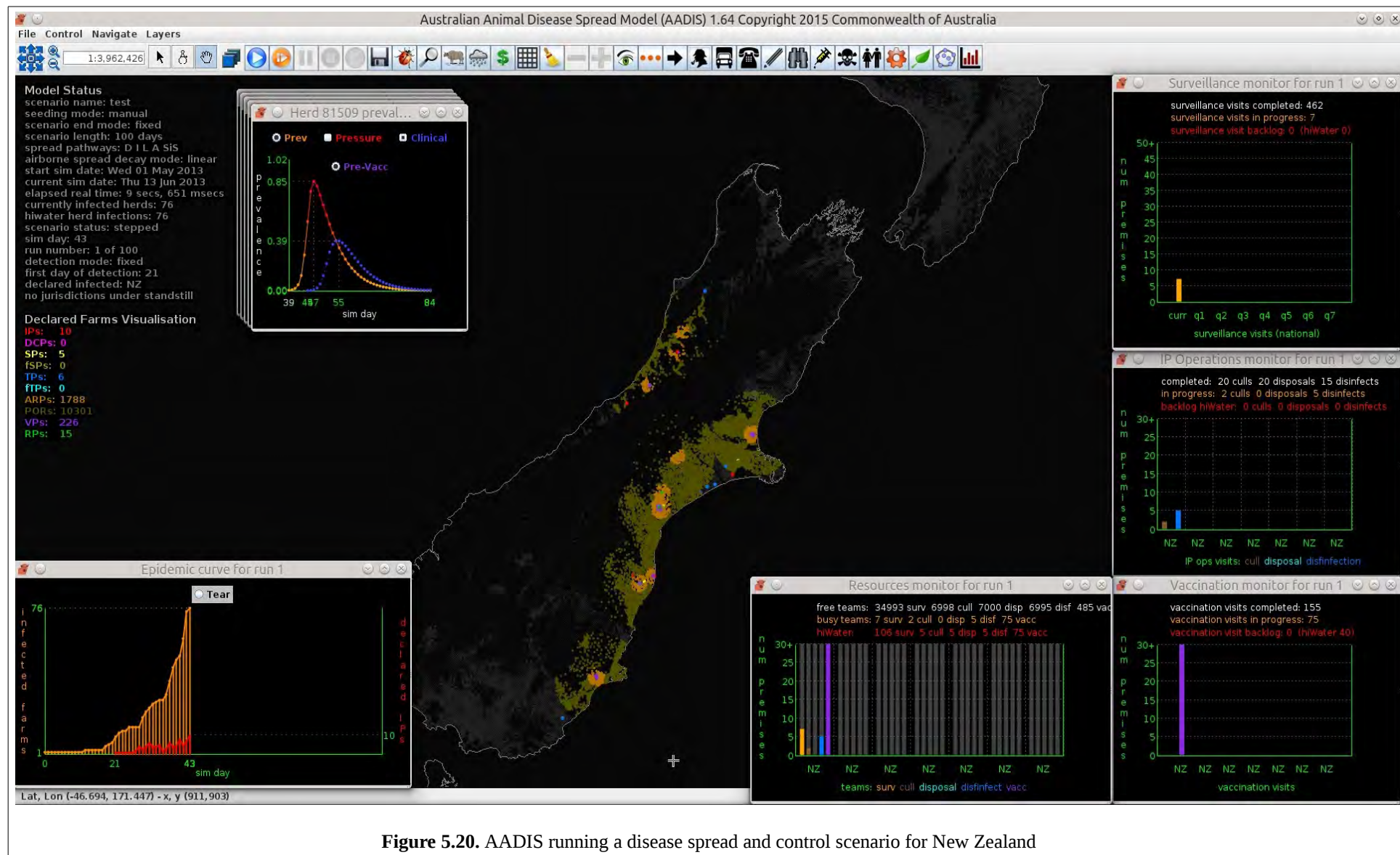
Figure 5.20. AADIS running a disease spread and control scenario for New Zealand

5.3.3 Discussion

It was reassuring that AADIS and InterSpread Plus produced quite similar outbreaks for three of the four test scenarios. Outcome variations between the two models are to be expected given the differences in the way the spread of disease within a herd/farm is handled. Whereas AADIS explicitly models within-herd spread with an SEIR mass-action EBM that takes into account herd type and size (Section 3.3), InterSpread Plus is closer to AusSpread in this regard and does not explicitly model within-herd spread. InterSpread Plus uses a prevalence profile per farm class which does not take into account the number of animals on the farm. This means that AADIS is less likely to generate significant spread from an infected herd with few animals. InterSpread Plus applies averaged prevalence profiles across a farm class, which means a farm with few animals has the same likelihood of generating spread as a large farm.

AADIS accounts for herd size in local and indirect spread such that farms with more animals are more likely to spread infection. This tends to produce greater variation in the outcomes. In contrast, InterSpread Plus does not assume a relationship between herd size and local/indirect spread.

A possible explanation for AADIS generally producing more local spread than InterSpread Plus is differences in the implementation of the local spread pathways between the two models. The AADIS local spread pathway is a catch-all in that all types of spread within the 3km local spread radius around each infected herd are classified as local. The InterSpread Plus local spread pathway, on the other hand, does not include indirect spread within the local spread radius.

The AADIS and InterSpread Plus comparison is still in progress and model configuration, results and discussion will be reported in a later paper.

5.4 Sensitivity Analysis

Sensitivity analysis is a technique of systematically varying model parameters in order to gauge their relative influence on scenario outcomes. It is particularly useful for assessing the influence of parameters that are naturally variable, subject to chance, or uncertain due to inadequate data (Taylor, 2003). It is important that modellers and the users of models know how the quality of specific data influence model outcomes. This helps funnel effort into improving the quality of important data, in lieu of data that does not materially impact the key model outputs (Green and Medley, 2002; Taylor, 2003). The identification of parameters that strongly influence scenario outcomes is also useful from an epidemiological perspective, for example, a delay in the initial detection of FMD can lead to significantly longer outbreaks (Bates et al., 2003b; Owen et al., 2011). This information can then inform planning and preparedness activities, such as a cost benefit analysis of proactive surveillance.

This section provides a high-level sensitivity analysis of parameters pertaining to three functional areas:

- The transmission of FMD. Control measures are disabled for this analysis in order to isolate the effects of spread mechanisms.

- The control and eradication of FMD. Resourcing is disabled for this analysis in order to better isolate the effects of control mechanisms. The disabling of resources has the effect of providing control measures with unlimited team resources. This means that the impact of control parameters is not influenced by the adequacy of resources to implement control.

- The impact of resource constraints on the control and eradication of FMD.

Owing to the breadth of AADIS parameterisation (Appendices B, C and D), the sensitivity analyses are of selected parameters only. As such, it is only a first-pass analysis and a precursor to more focused studies. The test hardware platform for each

of the studies was a quad-core laptop with 16GB RAM running 64-bit Kubuntu Linux™.

5.4.1 FMD transmission

5.4.1.1 Method

FMD was introduced into a medium-sized pig farm and allowed to spread undetected for 21 days. Baseline EBM parameter settings are provided in Table 3.2. Selected parameters pertaining to the spread of FMD were varied one at a time by first halving and then doubling the default value. The exception to this was the relative infectivity and relative susceptibility parameters. As these parameters are defined relative to the sheep species (see Section 3.5.2), only the non-sheep values were varied. The simulation was run 500 times for each parameter variation. The median number of infected herds (with 90% probability interval), was recorded for each run. The parameters and values used (with default values underlined), were:

- baseline probability of local spread: {0.024, <u>0.048</u>, 0.096},

- baseline probability of spread between co-resident herds: {0.25, <u>0.5</u>, 1.0},

- baseline probability of indirect spread: {0.025, <u>0.05</u>, 0.1},

- airborne spread maximum plume distance (km): {10, <u>20</u>, 40},

- airborne spread wind bearing tolerance (degrees): {7, <u>15</u>, 30},

- infectivity powers[1]: {0.5, <u>1.0</u>, 2.0},

- susceptibility powers[2]: {0.5, <u>1.0</u>, 2.0},

- relative infectivity[3]: {(0.91, 1, 0.65, 1), (<u>1.82, 1, 1.3, 1</u>), (3.64, 1, 2.6, 1)},

- relative susceptibility[3]: {(7.6, 1, 0.25, 1), (<u>15.2, 1, 0.5, 1</u>), (30.4, 1, 1, 1)},

- EBM beta parameters: {Table 3.2 values halved, <u>Table 3.2</u>, Table 3.2 values doubled}.

[1]the infectivity powers are used in the calculation of the per-species infectivity weights, and allow tailoring of the effect of herd size on infectivity (Section 3.5.2).

[2]the susceptibility powers are used in the calculation of the per-species susceptibility weights, and allow tailoring of the effect of herd size on susceptibility (Section 3.5.2).

[3]per species (cattle, sheep, pigs, smallholders) relative to sheep – refer to Section 3.5.2.

5.4.1.2   Results

Table 5.7 shows the median number of infected herds for each parameter of interest.

Table 5.7. Sensitivity analysis of selected spread parameters

Parameter	Num infected herds for low parameter values[1]	Num infected herds for default parameter values[1]	Num infected herds for high parameter values[1]
Local spread baseline probability	24(10-53)	35(17-68)	55(30-104)
Coresident herd local spread probability	32(16-62)	35(17-68)	34(16-66)
Indirect spread baseline probability	31(15-61)	35(17-68)	40(19-75)
Airborne spread maximum plume distance	34(16-65)	35(17-68)	34(16-73)
Airborne spread wind bearing tolerance	24(12-53)	35(17-68)	48(24-88)
Infectivity powers	42(17-80)	35(17-68)	22(11-50)
Susceptibility powers	44(23-84)	35(17-68)	18(7-57)
Relative infectivity	27(13-57)	35(17-68)	42(21-85)
Relative susceptibility	34(17-66)	35(17-68)	34(17-68)
EBM beta parameters	28(15-56)	35(17-68)	43(19-86)

[1] median with 90% probability interval

Figure 5.21 is a tornado diagram showing the sensitivity of the median number of infected herds to variations of each of the parameters of interest (in terms of the percentage deviation from the default value). The diagram illustrates how, for example, in this particular scenario, the model outcome was very sensitive to changes in the value of the local spread baseline probability, and was not very sensitive to changes in the value of the airborne spread plume maximum distance.

Figure 5.21. Scenario outcome sensitivity to FMD spread parameters
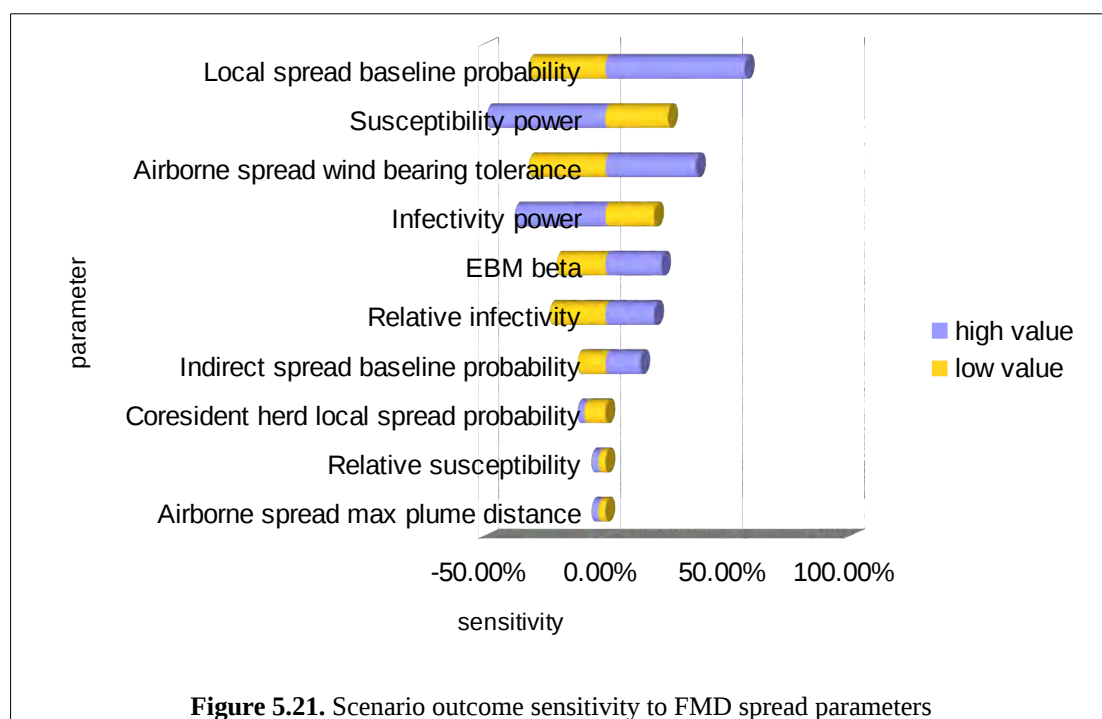
5.4.1.3 Discussion

The number of infected herds was very sensitive to the baseline probability of local spread occurring (Table 5.7 and Figure 5.21). The local spread pathway accounted on average for 43%, 59% and 71% of infected herds in the low, default and high value scenarios respectively (not shown). Given the typical predominance of the local spread pathway it is consistent that the local spread baseline probability strongly influences model outcomes. The number of infected herds was, however, less sensitive to the baseline probability of indirect spread occurring. The indirect spread pathway accounted on average for 4%, 7% and 12% of infected herds in the low, default and high value scenarios respectively (not shown). Given the typical weak contribution of the indirect spread pathway it is consistent that the baseline probability does not strongly influence outcomes.

The number of infected herds was very sensitive to the wind bearing tolerance of airborne spread but not the maximum plume distance (Table 5.7 and Figure 5.21).

This is intuitive as when the plume angle increases, some of the additional susceptible herds at risk are potentially close to the virus-shedding pig herd where the plume strength is higher and risk of infection increases (Figure 3.11). In contrast, as the plume distance increases, the additional susceptible herds at risk are all further away from the virus shedding pig herd where the plume strength is lower and the risk of infection decreases. As the outbreak started in a medium-sized pig herd there were likely higher levels of airborne spread than if the outbreak had started in a non-pig or small-pig herd. This in turn may have influenced the sensitivity of parameters used by the airborne spread pathway. To investigate this further a secondary sensitivity analysis could be conducted over a range of outbreak scenarios with varying seed herd types and sizes.

The number of infected herds was very sensitive to the susceptibility and infectivity powers (Table 5.7 and Figure 5.21). This implies that care needs to be taken when configuring the relationship between herd size and susceptibility/infectivity (Section 3.5.2). A secondary sensitivity analysis could investigate this further by varying susceptibility and infectivity powers on a per-species basis. The ability to tailor the effect of herd size on susceptibility/infectivity is useful when modelling a livestock population such as Australia's that has herds ranging in size from under 50 animals on a smallholding up to tens of thousands of animals on an extensive cattle farm or cattle feedlot.

The number of infected herds was moderately sensitive to variations of the EBM beta values (Table 5.7 and Figure 5.21). This supports the AADIS design decision to explicitly model the within-herd spread of disease. A secondary sensitivity analysis could investigate this further by varying beta values on a per-herd type basis, and perhaps other EBM parameters as well such as the latent periods and infectious periods (Table 3.2).

5.4.2 FMD control and eradication

5.4.2.1   Method

FMD was introduced into a medium-sized pig farm with detection of the index case occurring 21 days after the primary infection. The baseline EBM configuration is provided in Table 3.2. A single control strategy was employed: stamping out of infected premises plus suppressive ring vaccination. Baseline parameter settings for the control strategy are provided in Table 6.1. Resourcing was disabled which equates to the control program being implemented with an unlimited number of disease control operational teams. The simulation was run 500 times for each parameter variation. The median number of infected herds and outbreak duration (with 90% probability interval), was recorded for each run. The parameters and values used (with default values underlined), were:

- time to detection (days): {10, 21, 42},

- movement control areas (CA, RA) radii (km): {(3, 1), (10, 3), (20, 6)},

- vaccination outer radius (km): {1, 3, 6},

- direct tracing effectiveness[1]: {(0.5, 0.35, 0.42, 0.35), (1, 0.7, 0.85, 0.7), (1, 1, 1, 1)},

- indirect tracing effectiveness[1]: {(0.45, 0.35, 0.42, 0.35), (0.9, 0.7, 0.85, 0.7), (1, 1, 1, 1)}.

[1]per species (cattle, sheep, pigs, smallholders), where a value of 1 indicates 100% tracing effectiveness – refer to Section 3.6.4.

5.4.2.2   Results

Table 5.8 shows the median outbreak duration and median number of IPs for each parameter of interest.

Table 5.8. Sensitivity analysis of selected control parameters

Parameter	Low parameter values		Default parameter values		High parameter values	
	Num IPs[2]	Duration[1,2]	Num IPs[2]	Duration[1,2]	Num IPs[2]	Duration[1,2]
Time to detection	16(9-30)	33(21-64)	34(15-79)	50(33-87)	94(34-221)	83(60-130)
CA/RA radii	32(14-82)	58(35-102)	34(15-79)	50(33-87)	33(16-83)	49(32-82)
Vaccination outer radius	43(17-108)	57(38-105)	34(15-79)	50(33-87)	31(15-66)	42(32-69)
Direct tracing effectiveness	33(13-77)	51(34-83)	34(15-79)	50(33-87)	33(13-72)	50(32-82)
Indirect tracing effectiveness	34(14-71)	49(33-92)	34(15-79)	50(33-87)	32(14,81)	50(33-89)

[1] day that last IP is declared
[2] median with 90% probability interval

Figure 5.22 is a tornado diagram showing the sensitivity of the median number of IPs to variations of each of the parameters of interest (in terms of the percentage deviation from the default value).

Figure 5.22. Sensitivity of number of IPs to control parameters
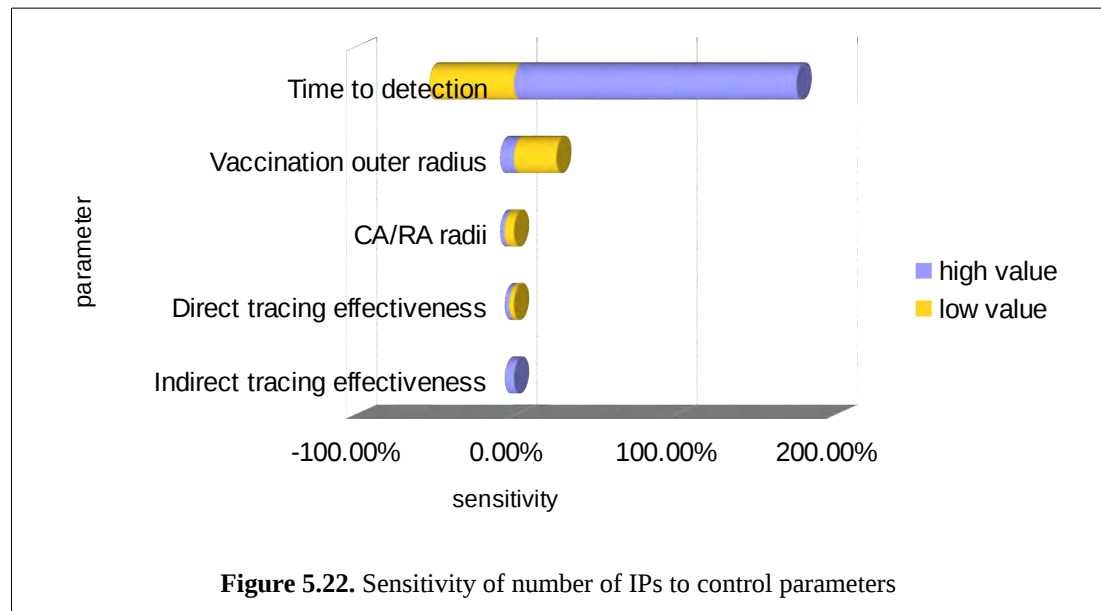
Figure 5.23 is a tornado diagram showing the sensitivity of the median outbreak duration to variations of each of the parameters of interest (in terms of the percentage deviation from the default value).

Figure 5.23. Sensitivity of outbreak duration to control parameters
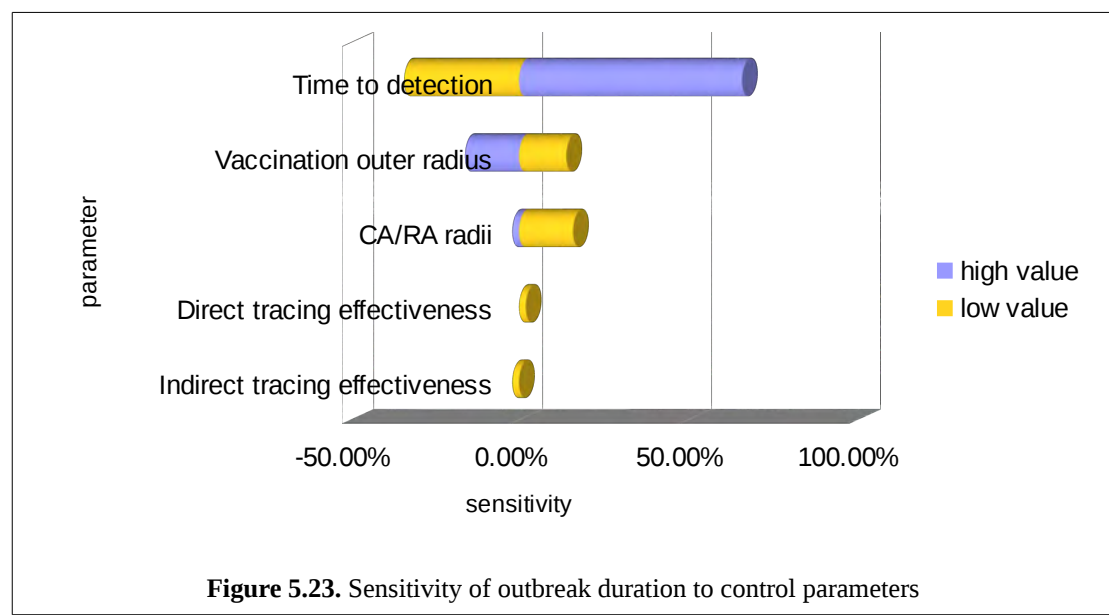
5.4.2.3   Discussion

The size and duration of an outbreak were very sensitive to when infection is first detected. This is intuitive and consistent with previous studies (Carpenter et al., 2011). The case study in Section 6.1 looks at this phenomena in more detail.

The size and duration of an outbreak were somewhat sensitive to the size of the outer vaccination radius. This is intuitive given that resources were not constrained, and is broadly consistent with previous studies (Roche et al., 2014). A follow-up study could look at the sensitivity of model outcomes to the individual parameters that govern vaccination. This includes the starting day of a vaccination program, vaccination inner radius, vaccination direction (inside-out or outside-in), vaccination priorities (by herd type) and vaccination retrospectivity (all IPs or new IPs only) (Section 3.6.7, Appendices B, C and D).

The size and duration of an outbreak were somewhat sensitive to the size of movement control areas, but were relatively insensitive to the effectiveness of tracing. Although not shown in the results, the median number of TPs in an outbreak

correlated with the effectiveness of tracing. This implies that the tracing mechanism in the model was reacting appropriately to the effectiveness parameter. The lack of impact on outbreak size and duration perhaps implies that other control measures such as routine surveillance and SP reporting compensated for the variation in tracing effectiveness. Another potential reason for the lack of sensitivity to tracing effectiveness is that tracing is based on direct and indirect contacts, and in this scenario the dominant spread mechanism was local spread.

5.4.3 The impact of resource constraints on FMD control and eradication

5.4.3.1 Method

FMD was introduced into a medium-sized pig farm with detection of the index case occurring 21 days after the primary infection. The baseline EBM configuration is provided in Table 3.2. A single control strategy was employed: stamping out of infected premises plus suppressive ring vaccination. Baseline parameter settings for the control strategy are provided in Table 6.1. Resourcing profiles (Section 3.6.8), were standardised to 1 on the first day of control, increasing linearly up to the maximum numbers specified below (baseline values are underlined). The simulation was run 200 times for each of the parameter variations. All scenarios were configured to end at the earliest of either a controlled outbreak or 1000 elapsed simulation days.

- maximum number of surveillance teams: {5, 20, 100},

- maximum number of culling teams: {5, 20, 100},

- maximum number of disposal teams: {5, 20, 100},

- maximum number of decontamination teams: {5, 20, 100},

- maximum number of vaccination teams: {5, 20, 100}.

5.4.3.2 Results

Table 5.9 shows the median outbreak duration and median number of IPs for each parameter of interest.

Table 5.9. Sensitivity analysis of selected resourcing parameters

Parameter	Low parameter values			Default parameter values			High parameter values		
	Num IPs[1]	Last IP[1,2]	Last control[1,3]	Num IPs[1]	Last IP[1,2]	Last control[1,3]	Num IPs[1]	Last IP[1,2]	Last control[1,3]
Max surveillance teams	60(16-862)	291(84-1000)	330(127-1000)	42(12-266)	86(51-242)	121(86-345)	36(16-80)	55(37-96)	94(76-131)
Max culling teams	44(15-236)	88(55-327)	122(90-353)	42(12-266)	86(51-242)	121(86-345)	39(11-182)	83(50-230)	117(87-279)
Max disposal teams	44(14-157)	86(57-216)	120(88-255)	42(12-266)	86(51-242)	121(86-345)	42(14-212)	84(55-254)	118(89-348)
Max decontamination teams	43(14-137)	87(55-204)	123(89-241)	42(12-266)	86(51-242)	121(86-345)	41(14-156)	84(54-198)	117(88-254)
Max vaccination teams	47(16-238)	92(56-305)	126(92-347)	42(12-266)	86(51-242)	121(86-345)	41(17-157)	86(58-222)	121(94-249)

[1] median with 90% probability interval
[2] day that the last IP is declared
[3] day that the last IP/DCP/SP/TP/ARP/POR is resolved

Figure 5.24 is a tornado diagram showing the sensitivity of the median number of IPs to variations in resourcing levels (in terms of the percentage deviation from the default value).

Figure 5.24. Sensitivity of number of IPs to resourcing levels
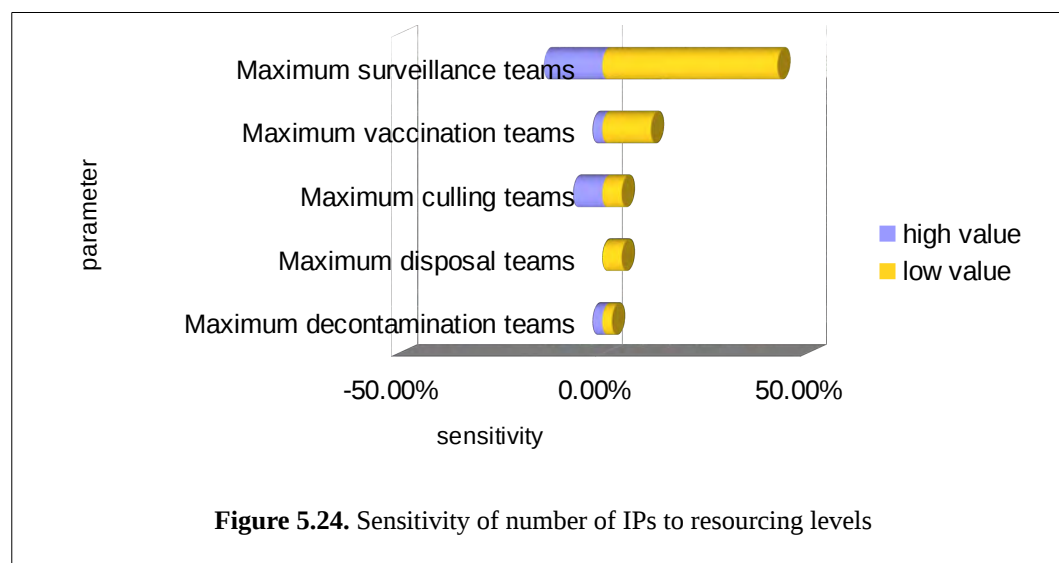
Figure 5.25 is a tornado diagram showing the sensitivity of the median outbreak duration (based on the day that the last IP is declared), to variations in resourcing levels (in terms of the percentage deviation from the default value).

Figure 5.25. Sensitivity of outbreak duration to resourcing levels
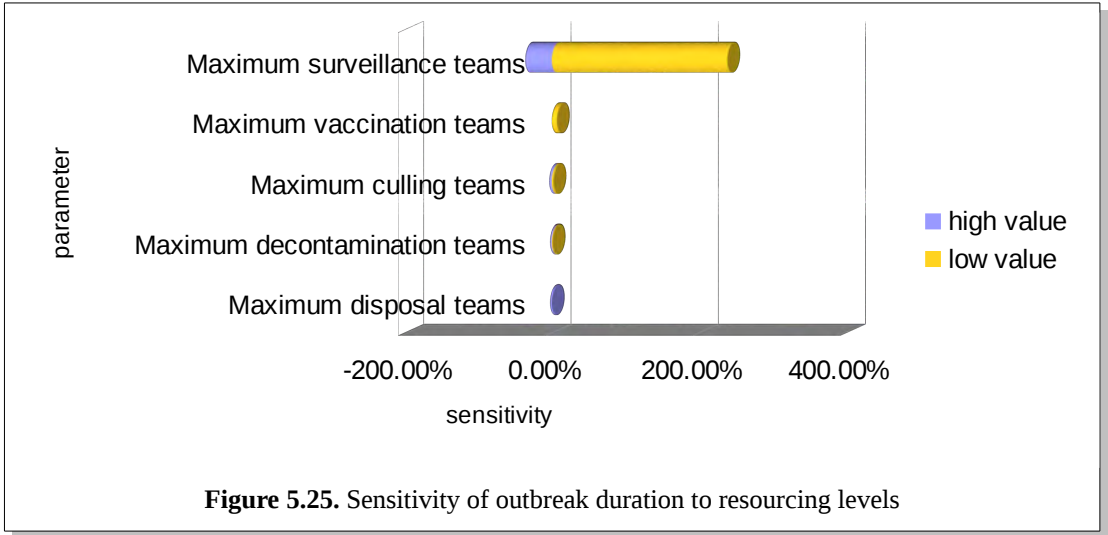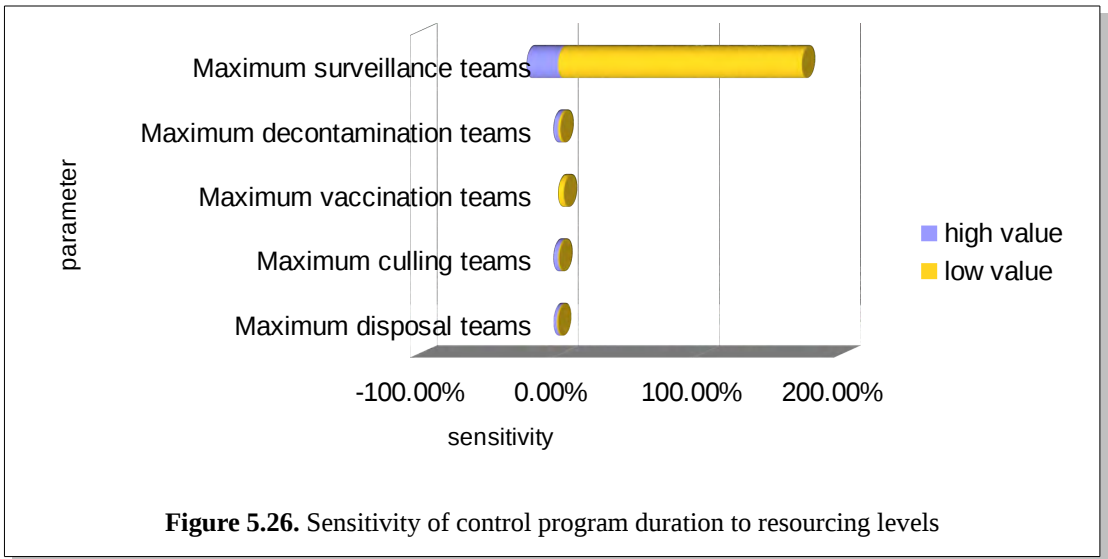
Figure 5.26 is a tornado diagram showing the sensitivity of the median control program duration (based on the day that the last IP/DCP/TP/SP/ARP/POR is resolved), to variations in resourcing levels (in terms of the percentage deviation from the default value).

Figure 5.26. Sensitivity of control program duration to resourcing levels

5.4.3.3 Discussion

The sensitivity analysis in Section 5.4.2 did not constrain the resourcing of control measures, i.e., each jurisdiction had unlimited teams at their disposal. The introduction of default resource levels in this study resulted in a 24% increase in the median number of IPs and a 72% increase in the median outbreak duration. This variation illustrates the usefulness of being able to conduct what-if scenarios on resource constraints that may well hamper the efficacy of the response to an outbreak (Roche et al., 2014).

The size and duration of an outbreak were very sensitive to the number of surveillance teams available per jurisdiction. Reducing the number of teams from the default level to a minimal level resulted in a 48% increase in the median number of IPs, a 338% increase in the median outbreak duration, and a 2700% increase in the number of uncontrolled (after 1000 days) outbreaks. In the default model set-up, IPs are confirmed by a surveillance team visit. This means that while a suspect infection may be reported or a high risk farm identified through tracing, subsequent IP operations (valuation, destruction, disposal and decontamination), won't occur until infection has been confirmed. It is thus consistent that the effectiveness of the control program is sensitive to the availability of surveillance teams. In an actual outbreak, one approach to managing a surveillance resource shortage might be to change the policy for declaring IPs. Another factor contributing to the model sensitivity to surveillance resourcing is that AADIS generates false SPs and false TPs (Sections 3.6.5 and 3.6.4), which also require surveillance visits. A follow-up study could look at the sensitivity of model outcomes to the individual parameters that influence surveillance. This includes: surveillance visit priorities, frequencies, periods and durations, the need for laboratory confirmation of disease, delays in laboratory results affect the timeliness of assessing premises, and the ratio of false SP reports to true SP reports (Appendices B, C and D).

The size and duration of an outbreak were mildly sensitive to the number of culling and vaccination teams available per jurisdiction. As the model was very sensitive to surveillance resourcing, a follow-up study could isolate the sensitivity to culling and vaccination resourcing by setting unlimited surveillance resourcing.

The size and duration of an outbreak were not sensitive to the number of disposal and decontamination teams available per jurisdiction. This is an intuitive outcome as once the animals on an IP are destroyed, the risk of disease transmission is negated. As the model was very sensitive to surveillance resourcing, a follow-up study could isolate the sensitivity to disposal and decontamination resourcing by setting unlimited surveillance resourcing.

5.4.4 Conclusions

AADIS has extensive parameterisation (Appendices B, C and D), and it is important for users of the model to know which parameters strongly influence model outcomes and thus need to be set with care. Examples of this are the herd infectivity and susceptibility power parameters that allow a user to tailor whether the size of a herd has a strong or weak influence on herd infectivity and susceptibility (Section 5.4.1).

Sensitivity analyses are also an important part of model testing. For example, as part of testing the local spread pathway, all parameters that influence local spread can be systematically varied and model outcomes assessed. The AADIS ABM architecture allows individual components to be easily enabled and disabled. This means that there is also the option of conducting targeted sensitivity analysis on components in isolation from the rest of the model.

Further sensitivity analyses will be conducted as part of the ongoing validation of AADIS.

5.5 EuFMD modelling workshop

Another important part of validating a model is to ensure that the outcomes make biological sense (Taylor, 2003). An opportunity arose for AADIS to feature in an FMD modelling workshop sponsored by the European Commission for the Control of Foot-and-mouth Disease (EuFMD), within the Food and Agriculture Organisation of the United Nations. The workshop was designed to expose participants to the use of epidemiological models for FMD contingency planning and response, and ran from 29th September to 3rd October 2014 in Frascati Italy. The workshop was attended by veterinary epidemiologists, animal health policy specialists and researchers from Albania, Austria, Bosnia and Herzegovina, Canada, Denmark, Greece, Estonia, Hungary, Italy, the Netherlands, Norway, Slovenia, Spain, Sweden and the United Kingdom. AADIS was used intensively by participants over the course of the workshop to model a variety of FMD outbreak and control scenarios (Figure 5.27).

EuFMD @Eufmd · Sep 30
#eufmd: the Frascati modelling workshop at work! Thank you to all our trainers who have made this possible! pic.twitter.com/C8F8J9xeuT

Figure **5.27.** AADIS in use at a UN FMD modelling workshop (EuFMD, 2014)

The EuFMD workshop served as a useful informal validation of AADIS. The model performed well over a variety of outbreak scenarios and control strategies, and feedback was positive. Participants considered the model to be user friendly, flexible and intuitive, with outputs valuable for supporting disease management and decision-making. A number of the participants commented that the dynamic visualisation provided useful insights into outbreak dynamics. An interesting comment was made on the potential applicability of the AADIS per-jurisdictional modelling approach in a European context. In the same way that Australian states are responsible for administering their own control program under national policy, European countries are independent, yet guided by OIE policies (OIE, 2012; OIE, 2013). Further, the AADIS ABM has the potential to model the spread of disease on a per-jurisdiction basis. For example, individual spread pathways could be employed for a country with detailed livestock movement data, while a simpler aggregated spatial-kernel approach could be employed for a country with poor livestock movement data.

5.6 Independent review by the University of Melbourne

An independent assessment of a model is an important aspect of verification and validation (Taylor, 2003). This helps to ensure that an epidemiological model is performing as intended and fit for purpose to be used by animal health authorities, and also to build end-user confidence in the model. The Australian Department of Agriculture and Water Resources commissioned the Faculty of Veterinary Science within the University of Melbourne to conduct an independent review of AADIS including:

- a review of the model structure and functionality,

- simulations to assess whether the model is fit for purpose,

- sensitivity and/or statistical analyses to assess the influence and suitability of input parameters on the outputs,

- statistical analysis to assess the appropriate number of simulations to run for convergence.

The assessment is still in progress and at this stage only an interim report is available containing a review of the model structure, and a basic validation of the spread pathway mechanisms (refer to Appendix F).

The report concluded that:

- The frequency of simulated direct movement events and the distance range of simulated direct movement events are consistent with the input values for each of these settings configured by the user.

- The frequency of simulated indirect movement events and the distance range of simulated indirect movement events are consistent with the input values for each of these settings configured by the user.

- The density of local spread infected herds is relatively high at short distances from the seed herd and declines with distance from the seed herd.

- The density of windborne spread infected herds as a function of distance from the seed herds is biologically plausible (the density of infected herds is negligible 0 to 4 km from the source herd, reaching a maximum at 4 to 5 km and then tapering off to zero by 10 km).

The preliminary findings of the external assessment were encouraging. The observed direct movement frequencies and distances (Section 3.5.1), strongly correlated with the model configuration. The observed indirect movement frequencies and distances (Section 3.5.2), also strongly correlated with the model configuration. The observed linear decay in the spatial distribution of infections arising from local spread was consistent with the spatial-kernel-based local spread pathway (Section 3.5.3). The spatial distribution of infections from airborne spread was consistent with the airborne spread pathway operating in linear decay mode (Section 3.5.4). The observed absence of airborne spread close to source herds was consistent with the design of the airborne spread pathway to not operate inside the (3km radius) local spread area.

6 CASE STUDIES

In this Chapter the application of AADIS from a user perspective is explored through three case studies. The first case study is taken from Bradhurst and colleagues (2015a). It compares a control strategy of stamping out with a strategy of stamping out plus suppressive ring vaccination. It provides an example of how AADIS can be used to address policy issues, in this case, whether the adoption of vaccination will improve the management of an FMD outbreak. This case study also illustrates the three AADIS dynamic visualisation modes.

The second case study addresses the question of how many runs are required to provide a reliable estimate of the number of infected herds in a scenario simulation. This is done by performing a large number of simulations and testing for convergence of the sample mean within a desired statistical tolerance.

The third case study looks at the runtime performance of AADIS conducting a national-scale simulation compared to a regional-scale simulation.

6.1 Control strategy comparison

6.1.1 Outbreak scenario

The south-east of Australia is an agriculturally intensive area that has previously been identified as vulnerable to an FMD outbreak (East et al., 2013). The Goulburn Valley is a 14,287 km^2 sub-region of Victoria with significant cattle and horticultural sectors (Regional Development Victoria, 2010). The dairy industry in this region comprises around 3000 farms and accounts for approximately 13% of Australia's milk production (Department of Environment and Primary Industries, 2015). Other livestock-based sectors in the region include beef, wool, sheepmeat and pigs.

The case study scenario is an outbreak of FMD in a medium-sized Goulburn Valley pig farm. The farm has a population of 3209 pigs and there are 20 neighbouring farms within a 3km radius. The outbreak occurs in May when the usual cool weather favours the survival of FMDV outside a host. Detection of the index case occurs 21 days after the primary infection. Table 3.2 lists some of the key EBM parameter values. Two strategies for controlling the outbreak were assessed:

- stamping out of infected premises (SO),

- stamping out of infected premises plus suppressive ring vaccination (SORV).

Selected parameter settings for the control strategies are provided in Table 6.1.

Table 6.1. Selected control program parameter settings

Control Parameter	Value
National livestock standstill	3 days
Restricted area (RA)	Circle of 3km radius enclosing each IP
Controlled area (CA)	Circle of 10km radius enclosing each IP
Num days to report suspect premises after clinical signs	0 to 19 days (herd type-dependent)
Probability of reporting suspect premises	70% to 100% (herd type-dependent)
Ratio of false suspect premises reports to true reports	2.34:1
Tracing window	14 days backwards, 14 days forward
Time needed for a direct trace	0 to 4 days (species-dependent)
Time needed for an indirect trace	1 to 5 days (species-dependent)
Effectiveness of direct tracing	70% to 100% (species-dependent)
Effectiveness of indirect tracing	70% to 90% (species-dependent)
Non-compliance with direct movement controls	2% inside RAs, 2% inside CAs
Reduction of indirect movements	15% inside RAs, 50% inside CAs
Surveillance visit duration	0.5 day (herd type-dependent)
Max number of surveillance teams	20 per jurisdiction
Max number of culling teams	20 per jurisdiction
Max number of disposal teams	20 per jurisdiction
Max number of decontamination teams	20 per jurisdiction

Control Parameter	Value
Max number of vaccination teams	200 per jurisdiction
Days to cull a herd	0.5 to 14 (herd type-dependent)
Days to dispose a herd	0.5 to 18 (herd type-dependent)
Days to decontaminate a premises	1 to 28 (herd type-dependent)
Start of vaccination program	7th day of the control program
Days to vaccinate a herd	0.5 to 7 (herd type-dependent)
Vaccination annulus radii (km)	1, 3
Vaccination direction	Outside-in

6.1.2 Method

The simulation was run 500 times for each control strategy and the following outputs compared:

- duration of the outbreak (defined as the number of days from when the index case was declared to when the last infected premises was resolved),

- cumulative number of infected premises,

- cumulative number of culled premises,

- cumulative number of culled animals,

- cumulative number of vaccinated premises,

- cumulative number of vaccinated animals.

In addition, a simple sensitivity analysis was carried out on selected parameters under strategy SO. The following parameters were varied (the baseline values are underlined):

- time to first detection (7, 14, 21 and 28 days),

- duration of the national standstill (0, 3, 7, 10 days).

The test hardware platform was a quad-core laptop with 16GB RAM running 64-bit Kubuntu Linux™. The Stata/IC statistical package (Stata, 2015) was used to analyse

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the distributions of the key model outputs. Data sets were imported into Stata and checked for normality. Non-parametric statistical methods were used throughout this analysis as some data sets were non-normal and could not be transformed to normality by standard transformation techniques. The number of infected premises, outbreak duration, number of culled animals, number of vaccinated premises and number of vaccinated animals were analysed using the Kruskal-Wallis test for comparison of multiple independent groups of data (UCLA, 2015a). Post hoc analysis to identify differences between strategies was conducted using the Kruskal-Wallis test with the significance level adjusted per the Bonferroni correction for multiple pairwise comparisons. Model outcomes are expressed as medians with 90% probability intervals.

6.1.3 Results

Figures 6.1 to 6.3 illustrate the three AADIS visualisation modes on day 21 of run number 1 of 500, of the baseline stamping out scenario.

Figure 6.1 illustrates how within-herd spread is represented as heat-colours reflecting infected prevalence levels generated by the EBM of each infected herd. The primary case (seed herd) is blue and susceptible herds are light grey. Figure 6.1 also illustrates the optional display of the convex hull area of infection, in this case 33 km^2.
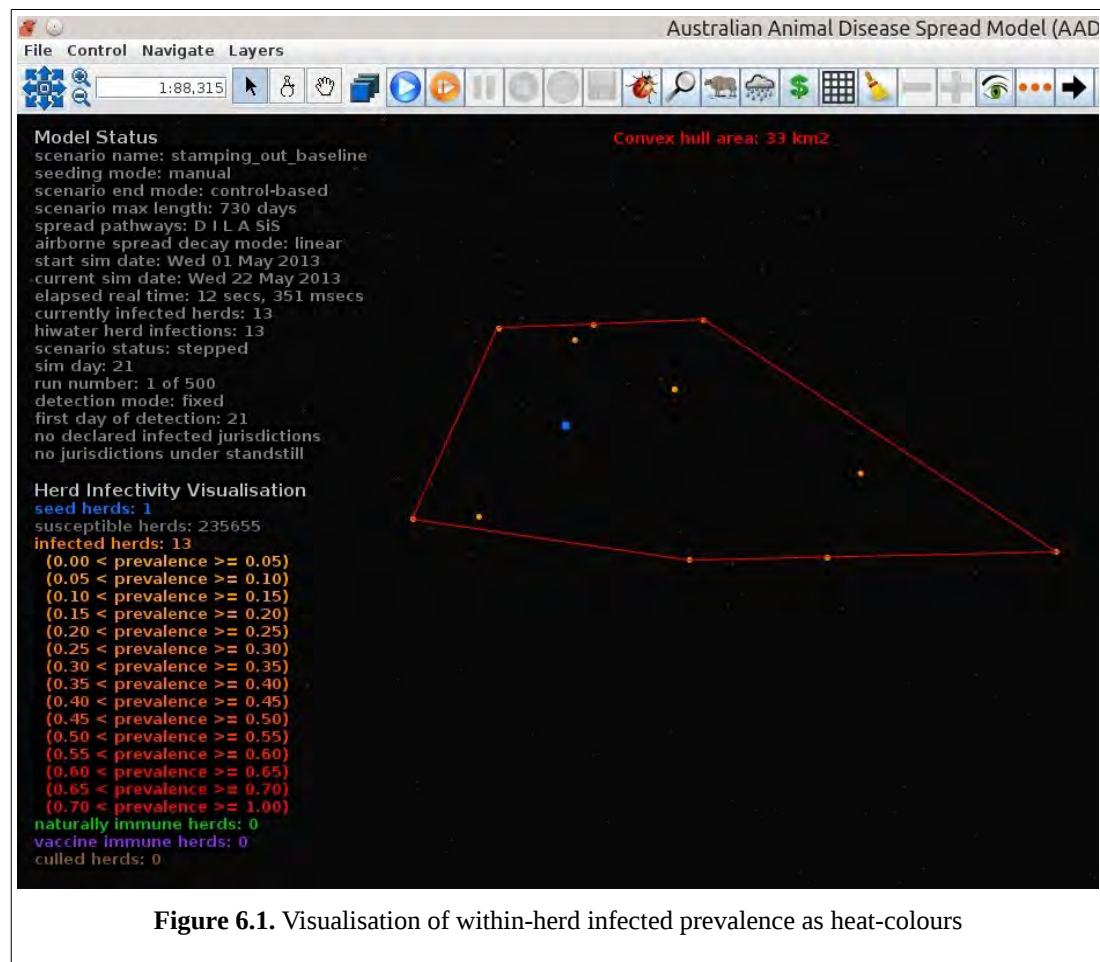
Figure 6.1. Visualisation of within-herd infected prevalence as heat-colours

Figure 6.2 shows the infection network generated by the ABM, with colour-coded vectors reflecting the particular spread pathway that was triggered. Each herd is labelled with the simulation day on which infection occurred. At this stage in the outbreak there was only local (green) and airborne (cyan) spread emanating from the primary case pig herd.
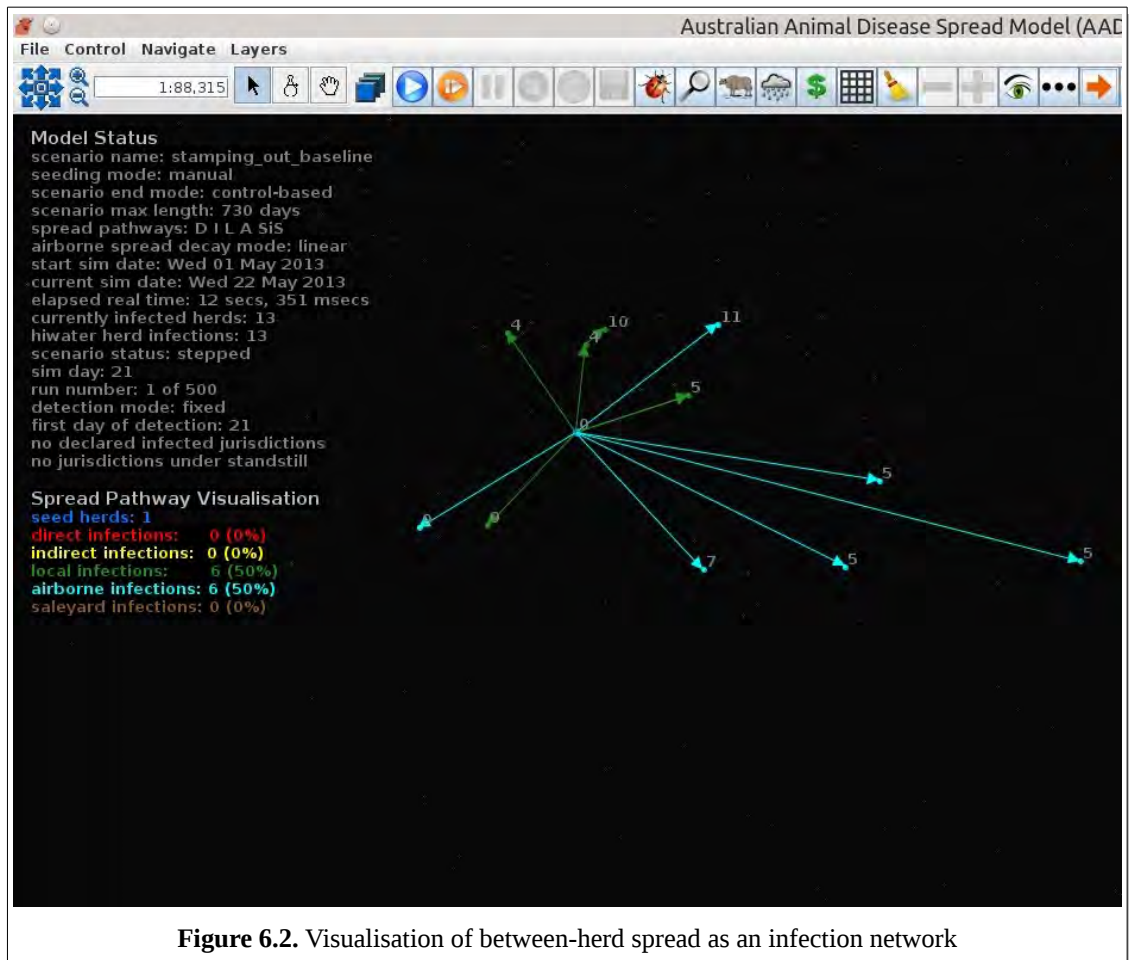
Figure 6.2. Visualisation of between-herd spread as an infection network

Figure 6.3 shows the outbreak on day 21 from a disease management point of view. Despite there being 13 infected herds, there was only one known infected premises (red). Figure 6.3 also shows two optional popup windows: the prevalence curves for a herd (in this case the index case), and the epidemic curve depicting declared infected premises versus actual infected premises.
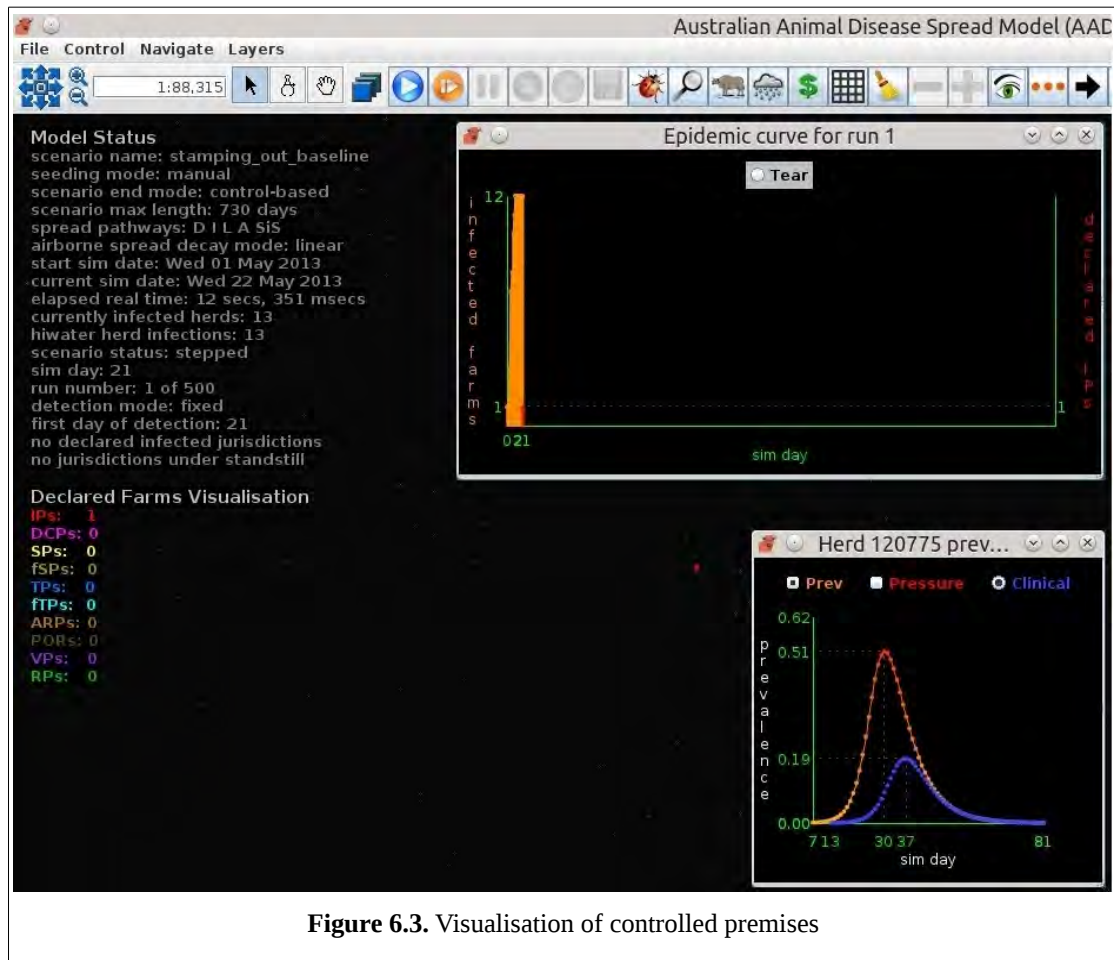
Figure 6.3. Visualisation of controlled premises

Strategy SORV was effective in reducing both the size and duration of an outbreak when compared to the baseline SO strategy. There were significantly less IPs, significantly shorter outbreaks, and significantly less culled animals than stamping out alone ($p < 0.05$) (Figure 6.4 and Table 6.2). SORV was particularly effective in reducing the likelihood of a very large outbreak, which could be an important consideration for a disease manager.

Figure 6.4. Effect of control strategy on outbreak duration, outbreak size, and number of culled animals
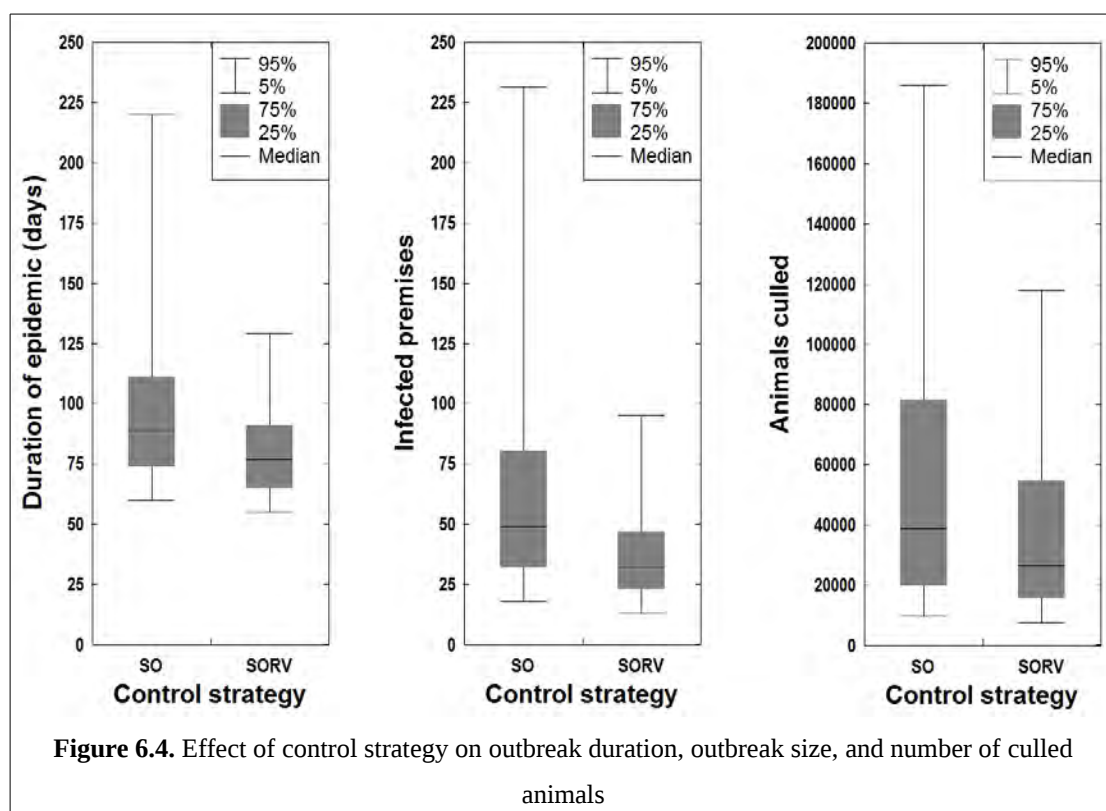
The sensitivity analyses showed that findings were significantly influenced by the time to first detection. Varying the time to detection for strategy SO produced strongly correlated changes to the number of IPs, outbreak duration, and number of culled animals ($p < 0.05$) (Table 6.2). The findings were less sensitive to the duration of the national livestock standstill with only a 0-day standstill and a 10-day standstill producing significantly different outcomes ($p < 0.05$). This suggests that for the outbreak scenario, there is perhaps not a significant advantage in extending the default three-day standstill.

Table 6.2. Control strategy comparison case study results

Control Strategy	Detection Day	Standstill duration (days)	Outbreak duration (days) [3,4,5]	Number of IPs [4,5]	Number of culled animals [4,5]	Number of vaccinated farms [4]	Number of vaccinated animals [4]	Scenario runtime (seconds) [4]
SO [1]	21	3	89(60-220) [a]	49(18-231) [a]	38875(9838-185996) [a]	0	0	5.5(3.3-16.1)
SORV [2]	21	3	77(55-129) [b]	32(13-95) [b]	26388(7688-118036) [b,c]	192(70-561)	51102(15442-153972)	4.8(3.1-9.6)
Sensitivity analysis of the time to detection								
SO	7	3	73(51-107) [b]	20(9-48) [b]	13385(7201-61081) [b]	0	0	3.0(2.0-4.8)
SO	14	3	78(57-146) [b]	32(14-98) [b]	19323(7448-92393) [b]	0	0	4.3(2.9-8.6)
SO [1]	21	3	89(60-220) [a]	49(18-231) [a]	38875(9838-185996) [a]	0	0	5.5(3.3-16.1)
SO	28	3	103(63-380) [c]	78(23-732) [c]	72275(13314-738018) [d]	0	0	7.5(4.0-46.6)
Sensitivity analysis of the duration of the national livestock standstill								
SO	21	0	90(61-215) [a]	53(19-241) [a]	45683(10163-208485) [a]	0	0	5.6(3.3-17.0)
SO [1]	21	3	89(60-220) [a]	49(18-231) [a]	38875(9838-185996) [a]	0	0	5.5(3.3-16.1)
SO	21	7	86(59-184) [a]	48(17-184) [a]	37111(9919-165532) [a]	0	0	6.1(3.9-15.1)
SO	21	10	85(60-189) [a]	46(19-176) [a]	39130(10754-148028) [a]	0	0	5.2(3.4-13.7)

[1] Baseline stamping out policy

[2] Baseline vaccination policy (stamping out plus suppressive ring vaccination)

[3] Time from detection of index case to resolution of final IP

[4] Median (90% probability interval)

[5] Within each column, numbers with a different superscript are significantly different

6.1.4 Discussion

This case study illustrated how AADIS can be used to support FMD contingency planning and response. The study strongly suggests that augmenting stamping out with suppressive ring vaccination reduces the size and duration of an outbreak. The study did not include a cost-benefit analysis, so although vaccination resulted in less culled animals, the cost of the vaccination program, and the return-to-market implications of adopting vaccination were not taken into account (Animal Health Australia, 2014a).

The case study also illustrated the three AADIS dynamic visualisation modes. A disease manager's limited view of an outbreak (Figure 6.3) was contrasted with the physical reality of infected herds in the population (Figures 6.1 and 6.2). Dynamic visualisation is generally not required when conducting epidemiological scenarios, as outcomes are written to CSV files for subsequent statistical analysis. However, dynamic visualisation is very useful for conveying what the model is doing, and illustrates the potential of AADIS as a training tool for disease managers.

6.2 Convergence

Stochastic models that employ Monte Carlo methods generate distributions of outcome variables (Hamra et al., 2013). An important question for model users is how many runs are needed to provide a reasonable representation of a scenario outcome (Byrne, 2013). The central limit theorem implies that for a sufficiently large number of samples of a random variable, the cumulative sample mean of the variable will tend towards the population mean (Vose, 2008). A model thus requires a certain number of runs for the sample mean of a given outcome variable to converge within a desired range of the theoretical population mean. The variability of the outcome variable distribution (as measured by the coefficient of variation), influences the rate at which convergence of the sample mean occurs. This study investigates how many runs of an AADIS scenario are required to achieve a desired convergence.

6.2.1 Method

The runs from the AADIS and AusSpread silent spread comparison (Section 5.2.1), were analysed for convergence of the sampled mean number of infected herds. The technique (Driels and Shin, 2004), estimates the percentage standard error E of the sample mean attained for a given number of runs (Equation 6.1), and the number of runs needed for the sample mean to converge within E% of the theoretical population mean (Equation 6.2). Both equations allow a desired confidence level to be specified.

$$E = \frac{100\,z_c\,S_x}{\bar{x}\sqrt{n}} \quad (6.1)$$

$$n = \left\{\frac{100\,z_c\,S_x}{E\,\bar{x}}\right\}^2 \quad (6.2)$$

$$
\begin{aligned}
\textit{where}\ \ E &= \text{percentage standard error of the sample mean} \\
z_c &= \text{confidence coefficient} \\
S_x &= \text{sample standard deviation} \\
\bar{x} &= \text{sample mean} \\
n &= \text{number of runs}
\end{aligned}
$$

6.2.2 Results

Table 6.3 provides the percentage standard error of the sample mean (with 95% confidence), for the given number of runs. This indicates how close the sample mean has converged to the theoretical population mean. The table also shows the number of runs needed to be 95% confident that the sample mean is within 5%, 8%, 10%, 12%, 15% and 20% of the theoretical population mean.

Table 6.3. AADIS vs. AusSpread: convergence analysis

Model	Small pig herd (ID=42189, size=110)		Medium pig herd (ID=7779, size=1945)		Dairy herd (ID=33812, size=256)		Sheep herd (ID=98, size=3065)		Beef herd (ID=315, size=532)	
	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread	AADIS	AusSpread
Number of runs	1000	100	1000	100	1000	100	1000	100	1000	100
Sample mean (infected herds)	16.69	18.88	23.73	20.04	14.93	10.99	0.28	0.18	4.57	3.8
Sample standard deviation	20.11	7.73	24.48	20.64	13.50	4.52	1.09	0.44	6.30	2.5
Coefficient of variation[1]	1.20	0.41	1.03	1.03	0.90	0.41	3.83	2.46	1.38	0.66
Standard error of sample mean[2]	0.64	0.77	0.77	2.06	0.43	0.45	0.03	0.04	0.20	0.25
Convergence of sample mean[3]	7.5%	8.0%	6.4%	20.2%	5.6%	8.1%	23.7%	48.3%	8.6%	12.9%
Num runs for 5% convergence[4]	2231	258	1635	1631	1257	260	22490	9319	2924	666
Num runs for 8% convergence[4]	871	101	639	637	641	102	11475	3640	1492	260
Num runs for 10% convergence[4]	558	64	409	408	314	65	5623	2330	731	167
Num runs for 12% convergence[4]	387	45	284	283	218	45	3905	1618	508	116
Num runs for 15% convergence[4]	248	29	182	181	140	29	2499	1035	325	74
Num runs for 20% convergence[4]	139	16	102	102	79	16	1406	582	183	42

[1] sample standard deviation / sample mean

[2] sample standard deviation / square root of the number of samples

[3] Equation 6.1 with 95% confidence ($z_c = 1.96$)

[4] Equation 6.2 with 95% confidence ($z_c = 1.96$)

6.2.3 Discussion

Figure 6.5 illustrates how the cumulative sample mean number of infected herds stabilised over time. For the medium pig herd scenario (herd ID 7779), the cumulative mean stabilised after approximately 284 runs, at which point it was accurate to 12%, with 95% confidence (Table 6.3). To achieve 5% convergence the scenario would have needed to be run 1635 times.

Figure **6.5.** Convergence of the cumulative sample mean number of infected herds over time
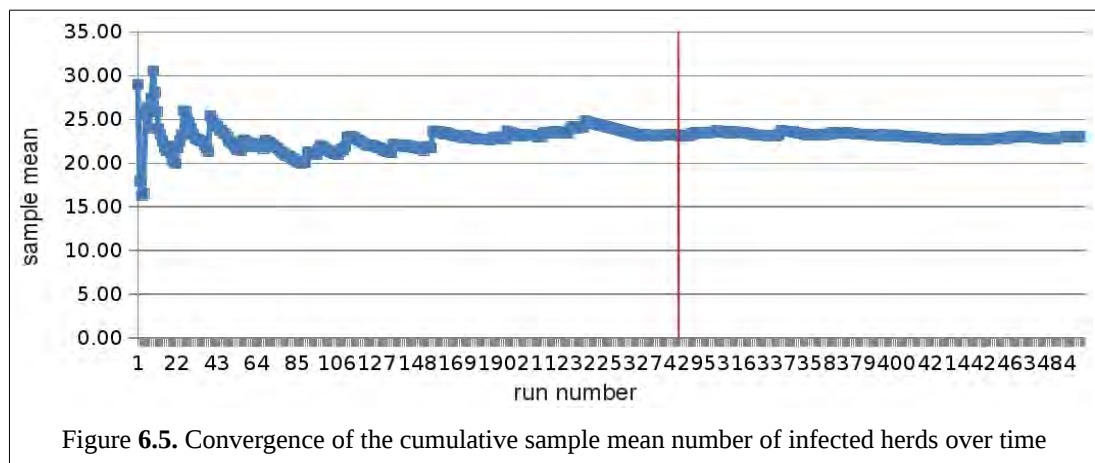
Table 6.3 illustrates how some scenarios are inherently more stochastic than others. For example, outcomes of the sheep scenario (herd ID 98), have much larger coefficients of variation than those of the other scenarios. This means that higher number of runs are required for convergence. AADIS would require 22,490 runs to attain 5% convergence in the sheep scenario but would only need 1257 runs to achieve 5% convergence in the dairy scenario.

AADIS generally produced outcomes with higher coefficients of variation than AusSpread and required more runs to converge than AusSpread (Table 6.3). Likely reasons for the variability between the two models are:

- AADIS explicitly models within-herd spread whereas AusSpread does not (Section 5.2.3),

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- the AADIS concurrent software architecture is inherently more stochastic than the AusSpread sequential software architecture (Section 4.1.4).

Although AADIS required more runs than AusSpread to achieve convergence, the runtime performance advantage that AADIS offered more than compensated for this. For example, AADIS took 11 minutes to achieve 5% convergence in the small pig herd scenario (herd ID 42189), with 2231 runs. AusSpread would have required over 7 hours to achieve 5% convergence in the same scenario with 258 runs.

This case study demonstrates the value of a user knowing the level of convergence for a given scenario outcome, and whether sufficient runs have been conducted in order to achieve the desired statistical confidence in the outcome distribution.

6.3 National and regional scenario runtime performance

This case study looks at the performance of AADIS when conducting a national-scale simulation compared to one at a regional scale. No new scenarios are run – the case study simply contrasts previous results from Chapter 5 and Chapter 6. The goal of the case study is to ascertain whether AADIS is computationally tractable on a national scale.

6.3.1 Method

The regional-scale scenario in Section 5.2.2 involved an FMD outbreak in a medium-sized pig farm in the Goulburn Valley region of Victoria. The livestock population comprised 42,217 herds. The outbreak was allowed to spread for 21 days at which point a control policy of stamping out plus suppressive ring vaccination was employed. The national-scale scenario in Section 6.1 also involved an FMD outbreak in a medium-sized pig farm in the Goulburn Valley region of Victoria. The livestock population was however the full national population of 235,668 herds. The outbreak was allowed to spread for 21 days at which point a control policy of stamping out plus suppressive ring vaccination was employed.

6.3.2 Results

One thousand runs of the regional-scale scenario took 21 minutes and achieved 9% statistical convergence. Five hundred runs of the national-scale scenario took 45 minutes and achieved 7% convergence. On average, the regional-scale scenario took 1.2 secs per run while the national-scale scenario took 5.4 seconds per run. Table 6.4 compares the two scenarios.

Table 6.4. Regional-scale vs national-scale scenario comparison

	Regional-scale scenario	**National-scale scenario**
Primary case herd	Pig (ID=7779)	Pig (ID=109047)
Primary case herd size	1945	3209
Primary case location	Goulburn Valley, Victoria	Goulburn Valley, Victoria
Number of herds in population	42,217	235,668
Number of runs	1000	500
Day of first IP detection	21	21
Control Strategy	SORV	SORV
Outbreak duration[1,2]	42(28-79)	57(40-107)
Median number of IPs[2]	15(4-93)	32(13-95)
Mean number of IPs[3]	29 +/- 1	40 +/- 1
Convergence of mean[4]	9%	7%
Num culled farms[2]	15(4-93)	32(13-95)
Num vaccinated farms[2]	36(0-293)	192(70-561)
Total elapsed runtime	21 mins	45 mins
Average time per run	1.2 secs	5.4 secs

[1] day that the last IP is declared

[2] median with 90% probability interval

[3] sample mean +/- standard error of the mean

[4] sample mean convergence with 95% confidence ($z_c = 1.96$). See Section 6.2 for definition.

6.3.3 Discussion

The national-scale scenario generally produced larger and longer outbreaks than the regional-scale scenario. As the national-scale scenario took into account inter-region disease spread it is suggestive that an outbreak in the Goulburn Valley may well impact jurisdictions other than Victoria. The comparison illustrates the usefulness of a national-scale model that incorporates inter-region livestock movements which have the potential to spread disease quickly and expansively (Sections 2.2 and 3.5.1).

The study illustrates that AADIS is computationally tractable on a national scale. The increase in runtime for the national-scale scenario was very reasonable given the considerably larger population, larger and longer outbreaks with considerably more culled and vaccinated farms, and the inclusion of multi-jurisdictional control and eradication.

7 DISCUSSION

The goal of this PhD project was to develop a next-generation, national-scale epidemiological model to support Australian animal health authorities in the planning and preparedness for EADs. Ten aims for the project were identified in Section 1.4. Chapters 2 to 6 presented the background, design, implementation and testing of the Australian Animal DISease (AADIS) model. This chapter reviews the work that has been carried out in the light of each of the ten project aims.

Model users and policy makers should have a good understanding of the limitations of modelling in general, and specific models in particular (Taylor, 2003; Keeling, 2005; Schley, 2007). Thus, as well as highlighting the strengths of AADIS, this chapter also includes its limitations, and caveats on the use of epidemiological models for disease management.

Finally, potential directions for the future development of AADIS are considered.

7.1 Epidemiological unit of interest

> ___Aim 1___: _Determine the most appropriate modelling unit of interest for an FMD model of national scale._ ☑

It is possible to derive realistic individual-based livestock contact networks from identification and tracing systems such as the NLIS (Section 3.1). However, modelling the spread of disease on a per-animal basis is overkill for a model of national-scale. Apart from the computational burden of representing over 100,000,000 animals, livestock are typically managed as single species herds that effectively share a single contact network whilst on a farm (Section 3.1). Once a highly contagious disease such as FMD is introduced into a susceptible herd it is likely to rapidly progress unchecked (Section 3.4).

Approximately 10% of farms in Australia are mixed beef/sheep (Table 3.1). These farms typically adopt distinct management practices per species which influences the spread of disease between species on the same farm. The choice of the herd as the modelling unit of interest captures heterogeneity in the disease dynamics between herds on a multi-herd farm. The AADIS local spread pathway captures the higher probability of cross-infection between herds managed on the same premises (Section 3.5.3). AADIS thus offers more granular modelling of disease spread than models such as AusSpread and InterSpread Plus that use the farm as the basic modelling unit.

Once a herd is declared infected with FMD, all other herds on the farm are subject to the same control and eradication procedures (Animal Health Australia, 2014a). Thus, from a disease control perspective, the key unit of interest is a farm. AADIS takes the innovative approach of using dual modelling units of interest: the herd for disease spread and the farm for disease control.

7.2 FMD spread

> ***Aim 2**: Model the transmission of disease between herds/farms across spread pathways appropriate to FMD.* ☑

Section 2.4 described a variety of approaches that have been used to model the transmission of disease between units (herds or farms). The simplest approach is to spread disease based on an aggregated transmission rate (Kostova-Vassilevska, 2004); however, this provides no information on how new infections arise. For a disease such as FMD that can spread by multiple mechanisms, understanding how and why infection occurs can assist disease managers determine the type and scale of control measures to apply. The most complex approach to modelling the transmission of disease is to explicitly represent many, perhaps dozens, of individual pathways by which disease might spread. For example, indirect spread can potentially arise from a wide variety of movements of people and equipment, including veterinarians, shearers, feed delivery vehicles, milk tankers, artificial insemination technicians,

friends and relatives. To explicitly model every pathway would introduce a great deal of complexity, and it would be very difficult to parameterise many of these movements with credible data.

AADIS has adopted a middle ground approach in which five discrete pathways of infection are modelled: local spread, direct contact spread, indirect contact spread, spread through markets/saleyards and airborne spread. This approach is sufficiently granular to support the evaluation of targeted control measures such as livestock movement standstills, movement restrictions on animals and animal products, and increases in farm biosecurity. The approach is consistent with that taken by a number of other FMD models (Garner and Beckett, 2005; Risk Solutions 2005a; Harvey et al., 2007; Stevenson et al., 2013).

> ***Aim 3**: Capture the multi-scale nature of the spread of FMD by considering both within-herd/farm and between-herd/farm spread mechanisms.* ☑

The transmission of FMD is a multi-scale process in that the mechanisms and rates of within-herd spread are distinct from those of between-herd spread (Carpenter et al., 2003). The AADIS hybrid approach captures this phenomena by decoupling the two spread mechanisms (Section 3.3). Each infected herd has an EBM that deterministically predicts within-herd infected, infectious and clinical prevalence over time based on the herd type, herd size and pathogen strain (Section 3.4). EBM outputs feed into stochastic ABM decisions on the spread of disease between herds across the direct, indirect, saleyard, local and airborne pathways (Section 3.5). The ABM also uses EBM outputs to predict the probability of detection, and in the control of disease (Section 3.6).

State-transition microsimulations such as NAADSM, AusSpread and InterSpread Plus simplify intra-farm transmission as transitions through atomic infection states

according to durations sampled from probability distributions. A state-transition approach to within-herd spread does not naturally capture the dynamics of intra-herd transmission. A simple herd state of 'infected' does not distinguish between the infectiousness of a herd with 1% of the animals shedding virus and that of a herd with 80% of the animals shedding virus. This leads to a loss of infected and infectious prevalence information that is relevant to between-herd spread, and a loss of clinical prevalence information that influences the detection and control of disease (Carpenter et al., 2003; Chis Ster et al., 2012). Some models allow infectiousness to vary over time using fixed look-up values (Garner and Beckett, 2005), while others augment infection states with transmission probabilities that vary over time (Stevenson et al., 2013), or allow custom within-herd prevalence curves to be pre-loaded (Reeves, 2012). A distinction of the AADIS EBM is that it is dynamic and adaptive. The EBM reacts to ABM events such as vaccination by resolving the ODE-system and generating updated infected, infectious and clinical prevalence profiles (Section 3.4).

> ___Aim 4___: ___Capture heterogeneities of species, environment, region, production systems and marketing systems that influence the spread of FMD.___ ☑

Section 2.2 looked at the expansive and diverse nature of Australia, with respect to both climate and livestock production systems. Farming operations range from, for example, small intensive piggeries, up to extensive outback cattle farms the size of a small country (Kidman, 2015). FMD has a complex epidemiology whereby the virus is multi-strain and can infect multiple species across multiple spread mechanisms (Section 2.1). The task of modelling the spread of FMD on a national-scale in Australia is a complex task owing to the considerable heterogeneities in the susceptible species, production systems and environment.

Section 2.4 reviewed various modelling approaches and noted the advantages of individual-based models (Keeling et al., 2001; Garner and Beckett, 2005; Risk Solutions 2005a; Harvey et al., 2007; Stevenson et al., 2013), and hybrid embedded

models (Bates et al., 2003; Speck, 2008; Backer et al., 2012a; Boklund et al., 2013), in capturing the complexities and heterogeneities that influence the spread of FMD. The AADIS embedded hybrid approach is a continuation in this modelling direction. It provides a flexible and extensible means of capturing population, spatial and environmental heterogeneities (Sections 3.3 and 4.1).

It is important to take population heterogeneities into account when modelling the spread of FMD, as the degree and nature of susceptibility and infectivity varies considerably between species. The Australian population of FMD-susceptible livestock is characterised as comprising 10 distinct herd types (Section 3.2). Herds are further characterised by region, climate data based on the nearest weather station, and direct and indirect movement patterns. The EBM embedded in each AADIS herd agent generates infected, infectious and clinical prevalence curves that take into account the strain of virus, host species, herd type and herd size. The infectivity and susceptibility of a herd is species dependent and scales with the size of the herd (Section 3.5.2).

7.3 FMD control and eradication

> _Aim 5_: **Model all key control measures used in the control and eradication of FMD in Australia, taking into account jurisdictional heterogeneities in both policy implementation and resourcing.** ☑

Section 2.3 described how Australia is a federation and while there are national policies for the handling of EADs such as FMD, the individual states and territories implement control programs under their own legislation. The implication for a national-scale model of FMD is that control measures need to be configurable and resourced on a per-jurisdiction basis.

AADIS provides a highly configurable suite of control measures based on the AUSVETPLAN national guidelines (Animal Health Australia, 2014a). A model user has ready access to a range of control parameters in order to conduct what-if scenarios on existing policies and to trial new policies. Movement restrictions, surveillance, IP operations and vaccination are configured and resourced on a per-jurisdiction basis (Section 3.6.8). Tracing is configured on a per-species basis and SP reporting on a per-herd type basis.

The modelling of false SP reports and false traces provides a more realistic representation of surveillance as it reflects how team resources are consumed regardless of the result of a surveillance visit. The ABM approach allows the required resourcing levels for a scenario to *emerge* rather than be prescribed (Section 3.6.8 and Appendix E).

7.4 Flexibility

> ***Aim 7***: ***The model has a high level of configurability so that a range of what-if scenarios can be conducted on the spread and control of FMD.*** ☑

The AADIS hybrid model architecture and object-oriented software design provide independence between the EBM, the spread pathways and the control measures. The decoupled approach allows the EBM and any spread pathway or control measure to be quickly isolated for tuning or experimentation. This is much harder to accomplish when a model aggregates ecological components, for example, by representing all means of inter-herd spread with a spatial kernel. AADIS provides three types of configuration: project-specific in a relational database, scenario-specific in a text configuration file, and temporary overrides via the GUI. Although control measures are configured on a per-jurisdiction basis, the GUI provides a convenient means of quickly employing national-level overrides (Section 4.6.6). For example, the annulus for suppressive ring vaccination can be quickly set for all jurisdictions to temporary radii via the Vaccination Dialog. Control measures are resource constrained based on

configured per-jurisdiction pools. A user can easily disable resourcing all together which equates to an unlimited supply of teams.

7.5 Extensibility

> ***Aim 8**: **The model has an extensible model architecture and software architecture.** ☑*

The decoupled nature of the AADIS ABM environment allows individual components to be enabled and disabled with no impact on other components. New components are readily added and existing components easily removed. For example, the five spread pathways can be replaced with a simple spatial-kernel with no impact on the rest of the model. This would be useful if AADIS was required to model the spread of a disease where there was insufficient data to parameterise individual spread pathways.

The hybrid model architecture decouples the spread of disease within a herd from the spread of disease between herds. The ABM operates independently of how a herd agent EBM is implemented. The ABM simply requires that an EBM meet the contracted interface of supplying infected, infectious and clinical prevalence profiles over time, and reacting to culling and vaccination events. This means that alternative EBMs can be readily employed as required for the specific pathogen under study, without impacting the ABM. This is awkward to accomplish when intra-herd spread and inter-herd spread are tightly coupled in a pure individual-based model such as a state-transition microsimulation.

It is anticipated that in the future AADIS will incorporate raster-based data layers such as weather, vegetation, feral animal ranges and insect vector distributions. The lattice used in the AADIS grid-based spatial-indexing scheme is a natural fit for raster-based data (Doran and Laffan, 2005).

The ABM architecture of lightweight agents in an active environment scales well with population size. Increasing the number of herds does not increase the number of threads in the system. Section 5.1.2 illustrates how the AADIS spatial query response increases smoothly and mildly for herd population sizes of 21,617 up to 235,668. Although not explored, it is likely that AADIS can comfortably extend beyond the Australian population of 235,668 herds.

The AADIS hybrid model architecture, object-oriented software design and grid-based spatial-indexing scheme provide a solid base for modelling endeavours beyond FMD.

7.6 Target platform and performance

> *<u>Aim 6</u>: The model is computationally efficient such that national-scale simulations of FMD spread and control can be conducted on a standard desktop computer.* ☑

A key requirement of this study was to produce a national scale model that could efficiently operate on standard PC/laptop equipment. Careful attention to model design and the use of some novel implementation tactics has enabled this requirement to be met. The multi-threaded asynchronous AADIS architecture offers significant performance improvements over the sequential approach typical of microsimulations. As all AADIS spread and control tasks proceed concurrently the length of a simulation day is effectively limited by the longest individual task (Section 4.1.4). Computational efficiency is an important consideration for a stochastic model of national-scale as complex scenarios are re-run hundreds if not thousands of times to allow trends to emerge (Driels and Shin, 2004).

AADIS completed national-scale test simulations 3 to 11 times faster than InterSpread Plus (Section 5.3). For example, InterSpread Plus completed 100 runs of a 28-day silent spread scenario in Canterbury, New Zealand in 9.4 minutes. AADIS completed

100 runs of the same scenario in 50 seconds. AADIS completed regional-scale test simulations 130 to 800 faster than AusSpread (Section 5.2). The ease with which AADIS handles large numbers of runs brings with it decreased statistical error. Section 5.2 shows that on average, AADIS completed 1000 runs of a regional-scale scenario 41 times faster than AusSpread completed 100 runs, with the higher number of AADIS runs resulting in outcome distributions that had on average 47% better statistical convergence than the fewer AusSpread runs. Section 6.3 compared AADIS running a regional-scale scenario with a national-scale scenario, and showed how AADIS is computationally tractable on a national scale.

7.7 Fitness for purpose

> ***Aim 9****: Users have confidence that the model is fit for the purpose of supporting the development of animal health policy.* ☑

The control and eradication of FMD is challenging due to the complexities of a highly contagious and multi-host pathogen operating in a heterogeneous environment across multiple jurisdictions. Models of disease spread and control are increasingly recognised as valuable tools for informing policy, provided that modellers and policy makers have confidence that the model is fit for purpose. It is unreasonable to expect important policy decisions to be based on blind trust in a complex piece of software. The first step in creating confidence in a model is to ensure that the underlying data, assumptions and logic are transparent to both users and customers of the model (Macpherson, 2013). Effort has thus been made to make the AADIS architecture, design and implementation as accessible as possible to both modellers and non-modellers alike:

- The disaggregated and decoupled nature of the AADIS hybrid architecture assists with transparency as each spread pathway and control measure is defined as a distinct algorithm (Sections 3.5 and 3.6). In contrast, when ecological components are aggregated mathematically they can become black boxes, for example, a spatial-kernel that condenses the various and diverse

FMD spread mechanisms into distance-dependent probabilities (Kitching et al., 2006).

- The novel AADIS visualisation and GUI provide detailed visibility into the daily progression of a scenario (Section 4.6). An outbreak can be stepped through a day at a time and all the spread and control decisions viewed both graphically and via detailed log files. The AADIS visualisation is a useful mechanism for conveying how the model works to non-modellers. This is not possible with non-visual models such as AusSpread and InterSpread Plus that only output tabular data for subsequent graphical analysis.

- The AADIS data is organised in a standard relational database (Appendices B and C) and accessible either via the CSV data files or via a graphical database viewing utility such as pgAdmin (PostgreSQL, 2015). AADIS is coded in Java which is a very readable programming language and reasonably accessible to non-specialists.

A model can only be used with confidence if it has undergone sufficient verification and validation. This is particularly important when a model may influence policy (Green and Medley, 2002; Garner and Hamilton, 2011). Considerable effort was made in this project to ensure that AADIS was robust, reliable, adequately tested, and fit to be used to support animal health policy. As such, the study included detailed comparisons and 'relative validation' (Dubé et al., 2006; Sanson et al., 2011) with well-tested models (AusSpread and InterSpread plus); independent testing by the University of Melbourne; and a sensitivity analysis. The AADIS validation activities undertaken thus far have yielded encouraging results (Chapter 5). The validation of a complex model is an ongoing process that extends well beyond the period of development and verification. Validation of AADIS will continue through studies such as the CEBRA-funded project on early indicators of outbreak severity (CEBRA, 2014).

Epidemiological authenticity and animal health policy have been a priority during the entire AADIS design and implementation process. This has involved working closely with Australian Government Department of Agriculture and Water Resources staff involved in EAD preparedness and response, and trialing the model with national and international technical and policy experts at workshops, including an international disease modelling workshop organised by the EuFMD (Section 5.5).

7.8 Innovation

> ***Aim 10****: **The project produces an epidemiological model that advances the field of computational science in the context of veterinary epidemiology.** ☑*

Population-based models concisely and efficiently capture the spread of disease in a closed homogeneous population. Individual-based models have a natural affinity for incorporating stochasticity, population heterogeneity, spatial effects, social factors and jurisdictional differences. The AADIS embedded hybrid approach has the granular modelling advantages of an individual-based approach and efficient population-based representation of within-herd spread. Over time, an infection network that captures the spatiotemporal history of an outbreak emerges from the AADIS ABM (Sections 3.3 and 4.6.5). For any given node (i.e., an infected herd), the network can be traced backwards to the source of infection and forwards to subsequent infections (Section 4.6.6). The network can also be mathematically analysed to identify topological features of interest such as sinks and spreaders (Bigras-Poulin et al., 2006; Dubé et al., 2011a; Nöremark et al., 2011).

AADIS provides novel dynamic visualisation of an outbreak unfolding in 'real' time. The herd infectivity visualisation mode depicts the infected prevalence of all infected herds as heat-colours. The infected and clinical prevalence of any infected herd can be viewed as pop-up curves. The spread pathway visualisation mode shows the entire infection network, showing what herds were infected on what day, via what means. The declared premises visualisation mode depicts premises involved in the control program and thus presents a disease manager's limited view of the outbreak that

contrasts with the physical reality of infected herds in the population. The graphical user interface allows a user to interact with an epidemic, for example to pause a scenario and view details of any herd/farm in the model. It is also possible to manually adjust the declared state of any farm. AADIS thus has potential as not only a predictive tool that informs emergency livestock disease preparedness and planning, but also as a vivid training tool for disease managers.

Specific functional advantages of one model over another can be short-lived. Models such as AusSpread, InterSpread Plus, NAADSM, DADS, DTU-DADS and the Netherlands model are active and continue to evolve. The principle innovation of AADIS is perhaps architectural, i.e., the movement away from the state-transition microsimulation approach of AusSpread, InterSpread Plus, Exodis and NAADSM to a hybrid EBM/ABM model. The AADIS model architecture is a more generalised form of the embedded hybrid approach already adopted by the DADS, DTU-DADS and the Netherlands models (Section 2.4.3.2). Not only does AADIS embed explicit modelling of within-herd spread, the active ABM environment is flexible and can implement a contact network, a spatial-kernel, or explicitly model any number of data-driven spread pathways in as much detail as required, and also provide any number of control measures. AADIS also borrows from the lattice approach of cellular automata for the purposes of efficient grid-based spatial-indexing (Section 4.2.5).

The combination of dual modelling units of interest, hybrid model architecture, asynchronous software architecture, an ABM with lightweight agents and an active concurrent environment, grid-based spatial-indexing, and dynamic visualisation has resulted in a flexible, extensible, computationally efficient, national-scale, multi-jurisdictional model of disease spread and control, not seen before in the field of livestock epidemiology.

7.9 Limitations

AADIS is a sophisticated epidemiological model and decision-support tool. The realism of data-driven models such as AADIS hinges on the quality of the underlying data with which it is parameterised (Section 2.4.2.2). Australia is fortunate in that good quality livestock data is available from regular agricultural censuses by the Australian Bureau of Statistics, state-based farm registers, NLIS databases and a series of industry reports commissioned by the Department of Agriculture and Water Resources. There are also good quality production and marketing data from the Australian Bureau of Agricultural and Resource Economics and weather data from the Bureau of Meteorology. For AADIS to be adapted for a jurisdiction with a paucity of data, setting up the model would be problematic. In this situation it would be preferable to use simplified spread and control components, for example, individual data-driven spread pathways could be replaced with a simple spatial-kernel-based spread pathway.

Models with large numbers of parameters provide realism and flexibility but can also introduce difficulties with parameter estimation and model validation (Section 2.4.2.2). AADIS has extensive configuration data spread across 40 tables in a relational database and a text configuration file. This allows for detailed configuration of the heterogeneous environment and population, and pathogen under study. However, a result of this complexity is that a knowledge of epidemiology and a good understanding of the system being studied is required to set up the model correctly.

An artefact of the concurrent architecture adopted by AADIS is that thread scheduling arbitrarily influences the order in which components request random numbers (Section 4.1.4). This means that it is not possible to replay scenarios by specifying the pseudo-random number generator seed (and thus control the stream of random numbers used to sample from probability distributions). The ability to control the random number stream makes a stochastic model temporarily deterministic, and allows specific aspects of a scenario to be isolated. For example, a control measure

such as vaccination can be varied and the impact on the scenario outcome directly observed (in the absence of variability introduced through stochasticity). The implication of this for AADIS is that it is permanently stochastic and a greater number of scenario runs are required for results to converge.

The AADIS user interface while functional, is still only a prototype. This is a result of the project priority of epidemiological authenticity and computational efficiency over ease-of-use. The visualisation relies heavily on colour which is a disadvantage for users with colour vision deficiencies. Modifying the model configuration file with a text editor is functional but unwieldy and it would be desirable to adopt some form of configuration tool.

7.10 Caveats on the use of epidemiological models

Disease models are increasingly being used to study disease dynamics, assess the impact of outbreaks in different settings and to evaluate control measures (Garner et al., 2007). This is evidenced by the large growth in scientific publications on disease modelling in recent years as well as government investment in and support for modelling studies in many countries. There is also growing interest in international collaboration in this area, including model comparison studies and multi-model studies to address important policy issues such as the use of vaccination in FMD control (Roche et al., 2014). It is important to recognise that while models can provide insights and assist in managing disease outbreaks, used inappropriately, or in the face of incomplete or inaccurate data, they can be unreliable and have the potential to mislead rather than inform. This section reviews some experiences and lessons learned from previous use of models in FMD management.

The 2001 outbreak of FMD in the UK was a significant event, both in terms of its economic and social impact (Section 1.1), and also as it was the first time that FMD models were used during the 'heat' of an outbreak to guide policy (Green and Medley, 2002; Taylor, 2003). The models involved were the population-based 'Imperial' model

(Ferguson et al., 2001), the spatial-kernel-based Cambridge-Edinburgh model (Keeling et al., 2001), and the InterSpread microsimulation (Morris et al., 2001). The policy of pre-emptive contiguous culling was supported by modelling studies that predicted it to be crucial to controlling the outbreak (Kao, 2002; Keeling, 2005; Kitching et al., 2006). Of the 10,846 UK premises that were depopulated, more than 80% were done so without confirmation of the presence of disease. The destruction and disposal of vast numbers of uninfected animals raised many social, ethical and environmental concerns (Section 1.1).

While some subsequent studies backed the appropriateness of the model predictions (Keeling, 2005; Tildesley et al., 2008), there have also been criticisms that the models were based on poor quality data, had poor epidemiological assumptions and lacked validation (Kitching et al., 2006; Nerlich 2007; Mansley et al., 2011). Doubt was raised as to whether the quality of modelling, at least initially, was sufficient to underpin such drastic measures as the pre-emptive contiguous culling of millions of otherwise healthy animals. Phrases such as 'carnage by computer' (Campbell and Lee, 2003), and 'armchair epidemiology' (Kitching et al., 2006), describe a perceived disconnect between theoretical model predictions and the grim reality faced by those at the front-line of the outbreak. Despite consensus that veterinary judgement on a farm-by-farm basis is a far more reliable predictor of infection risk than a model (as premises-specific biosecurity, topography and management practices can be taken into account (Scott et al., 2004; Keeling, 2005; Kitching et al., 2006)), premises adjacent to infected premises were automatically classified as dangerous contact premises and culled without formal confirmation of infection (Haydon et al., 2004; Kitching et al., 2006; Mansley et al., 2011). Regardless of the accuracy of the modelling and the justification or not of 'slaughtering on suspicion', the control and eradication of FMD can have enormous economic, environmental, ethical and social consequences, and it is vital that both modellers and those using model outputs are aware of both the strengths and limitations of the models being used.

Parameterising a model with data from a past epidemic (i.e., fitting data to a model), can be useful for retrospective analysis, for example, to assess alternate control strategies (Howard and Donnelly, 2000), but may be of limited value in understanding what might happen in a different setting and different time. A fitted model may become 'self-fulfilling' in that outcomes align well with the outbreak under study primarily because it has been parameterised with data from that outbreak (Taylor, 2003). A fitted model may not necessarily generalise well to other outbreak scenarios (Schley, 2007; Mansley et al., 2011). San Miguel and colleagues (2012) describe the tension between biasing a model by overfitting data, and oversimplifying a model by underfitting data.

An epidemiological model may suffer silently from incomplete data, poor quality assumptions, implementation flaws and inadequate validation, yet the outputs still be detailed and appear definitive (Dent and Blackie, 1979; Taylor, 2003; Kitching et al., 2006). Ecological systems such as epidemics are by nature non-deterministic (Medley, 2001). The propagation of disease is influenced by heterogeneities in species, production systems, marketing systems, climate, environment, and biosecurity, as well as biological variability in the mechanics of transmission. The control and eradication of disease is influenced by heterogeneities in jurisdiction, resources and environment, competing economic, trade, political pressures, and psychosocial variability in such things as self-reporting of disease (Garner and Hamilton, 2011). It is important for modellers and the customers of models not to be seduced by the illusion of certainty (Gupta, 2001; Taylor, 2003). Models are simplifications of complex systems and can only produce theoretical projections of reality. The strength of epidemiological models lies in their ability to aggregate complex population, pathogen and environment variables on a large-scale and, in the case of stochastic models, produce probability distributions of epidemic outcomes (Green and Medley, 2002; Taylor, 2003; Woolhouse, 2004).

The use of epidemiological models as real-time predictors as to how a 'live' epidemic may unfold is controversial (Green and Medley, 2002; Kitching et al., 2006; Dubé et al., 2007a; Garner and Hamilton, 2011). Models can however be usefully employed in a 'war-time' setting to monitor the progress of an outbreak, and compare observed behaviour with expected behaviour in order to alert epidemiologists to potential areas of concern (Taylor, 2003; Kitching et al., 2006). Probably the safest and least contentious view of models is to recognise that they are just one of several tools available for inter-epidemic EAD contingency planning and preparedness (Green and Medley, 2002; Taylor, 2003; Kitching et al., 2006; Dubé et al., 2007a; Garner et al., 2007).

7.11 Future work

Potential functional enhancements to AADIS include: a configurable financial module that allows costs to be attributed to control strategies; a disease manager expert system that dynamically adjusts a control program according to the current state of the outbreak; the simulation of risk-based surveillance whereby high-risk premises are proactively inspected for indications of disease; the incorporation of raster data sets such as weather, feral animal ranges, vegetation, insect vector distributions; the refinement of the user interface; and the development of a configuration tool.

In the short term, as part of a CEBRA-funded study (CEBRA, 2014), there will be an investigation as to whether epidemiological cues exist early in an outbreak that signify eventual outbreak size, for example, are there early indicators as to low-probability but high impact 'black swan' (Taleb, 2010) outbreaks?

Potential strategic directions for AADIS include: modelling of diseases other than FMD; modelling of endemic disease; modelling of diseases in countries other than Australia and New Zealand; and modelling disease in herd populations larger than 235,668.

8 CONCLUSIONS

Disease managers have to take into account technical, socio-political, economic and logistical factors when developing policies for disease control. Often there are conflicting objectives to balance: for example, to eradicate the disease as soon as possible and regain export markets, while minimising the costs of control and compensation, and minimising impacts on other industries and society in general. Draconian measures of control such as contiguous culling and expansive movement restrictions contain FMD, but at what economic and social cost? How is the business continuity of non-infected premises impacted? Suppressive ring vaccination may help to dampen an outbreak but may bring additional costs to regaining FMD-free status. Epidemiological modelling is emerging as an important contributor to the complex task of EAD planning and policy development.

AADIS expands the livestock disease modelling capabilities of the Australian Government Department of Agriculture and Water Resources from regional to national-scale. Complex simulations of disease spread and control on a national-scale can be conducted on a standard desktop computer. Computational efficiencies stem from the hybrid model architecture that fuses population-based and individual-based modelling approaches, an asynchronous software architecture, and a custom grid-based spatial-indexing system.

A pure individual-based approach to modelling the spread and control of livestock disease in Australia implies an ABM with over 100 million animal agents. This would only be plausible with a specialised highly parallel hardware platform. The choice of the herd as the epidemiological unit of interest reduces the size of the model population to a far more manageable 236,000. The tactic of embedding EBMs in herd agents provides dynamic predictions of within-herd infected, infectious and clinical prevalence, based on the herd type, herd size and pathogen strain. The EBM outputs

dynamically inform ABM decisions on the spread of disease between herds, the probability of disease detection, and the control of disease. Threadless EBM-driven agents in an active and concurrent ABM environment may have utility in other modelling domains that deal with large populations. Further, if a spatially-explicit ABM has simple stationary spatial objects, then uniform grid-based spatial indexing may offer computational advantages over R-Tree-over-GiST spatial indexing.

AADIS has been developed to be adaptable and flexible, both in terms of being able to implement and trial different approaches to FMD detection and control, and also future adaptation for other diseases of concern. Recognising the importance of models being fit for purpose, considerable verification and validations activities have been undertaken to give confidence in AADIS's ability to support animal health policy development in Australia.

The AADIS project typifies the multi-disciplinary nature of modern epidemiology. The model utilises veterinary epidemiology, mathematics, statistics and computer science (including concurrent programming, disk-based and in-memory relational databases, grid-based spatial-indexing, artificial intelligence techniques, and multi-view dynamic visualisation). The end result is an innovative and computationally efficient model that prioritises the need for epidemiological authenticity.

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Appendix A **Glossary of acronyms**

Table A.1. Glossary of Acronyms

Name	Description
AADIS	Australian Animal DISease model
ABARES	Australian Bureau of Agricultural and Resource Economics and Sciences
ABM	Agent-based model
ARP	At-risk premises – a premises inside an RA that contains susceptible animals and is not currently designated an IP, DCP, SP or TP
ASF	African swine fever
AUD	Australian dollar
AUSVETPLAN	Australian Veterinary Emergency Plan (Animal Health Australia, 2014a).
CA	Cellular automaton
CA	Control Area - a controlled area enclosing an RA and subject to lower levels of movement restrictions than those applied in RAs
CEBRA	Centre of Excellence for Biosecurity Risk Analysis
CSF	Classical swine fever
CSV	Comma-Separated Values
CVO	Chief Veterinary Officer
DADS	Davis Animal Disease Simulation model (Bates et al., 2003a)
DCP	Dangerous Contact Premises - a premises that, based on a risk assessment, is considered highly likely to contain an FMD-infected animal(s) or contaminated animal products, equipment or other material
DDL	Data definition language
DTU-DADS	Technical University of Denmark - Davis Animal Disease Simulation model (Boklund et al., 2013)
EAD	Emergency animal disease
EADRA	Emergency Animal Disease Response Agreement
EBM	Equation-based model
EuFMD	European Commission for the Control of Foot-and-mouth Disease
FAO	Food and Agriculture Organisation of the United Nations

Name	Description
FIPA	Foundation for Intelligent Physical Agents
FMD	Foot-and-mouth disease
FMDV	Foot-and-mouth disease virus
FSM	Finite-state machine
GA	Geographic automaton
GIS	Geographic information system
GSAM	Global-Scale Agent Model (Parker and Epstein, 2011)
HPAI	Highly pathogenic avian influenza
HPC	High-performance computing
IATA	International Air Transport Association
IP	Infected premises - a premises where infection has been confirmed
JVM	Java Virtual Machine
LGA	Local government area
MABM	Massive agent-based model
MCMC	Markov chain Monte-Carlo
MESA	Multiscale Epidemiologic/Economic Simulation and Analysis model (Speck, 2008).
MSM	Microsimulation model
NAADSM	North American Animal Disease Spread Model (Harvey et al., 2007)
NLIS	National Livestock Identification System
OAG	Official Airline Guide
ODE	Ordinary differential equation
OIE	Office International des Epizooties (World Organisation for Animal Health)
POR	Premises of relevance - a premises inside a CA that contains susceptible animals and is not currently designated an IP, DCP, SP or TP.
PDF	Probability density function
RA	Restricted area - a controlled area surrounding an IP and subject to the highest level of movement restrictions.
RAM	Random access memory
RP	Resolved premises – a former IP or DCP on which IP operations have been completed.

Name	Description
RVF	Rift Valley fever
SAT	South African Territories
SEIR	Susceptible Exposed Infectious Recovered
SEIRS	Susceptible Exposed Infectious Recovered Susceptible
SIR	Susceptible Infected Recovered
SO	Stamping out of infected premises
SORV	Stamping out of infected premises plus suppressive ring vaccination
SOCC	Stamping out of infected premises plus pre-emptive contiguous culling
SP	Suspect Premises – a premises that contains susceptible animals and has been reported as exhibiting clinical signs.
SQL	Structured Query Language
TP	Trace Premises – a premises that contains susceptible animals and has been traced as having been potentially exposed to infection.
USD	United States Dollar
VP	Vaccinated Premises – a premises on which vaccination has completed.

Appendix B   Database schema

Figure B.1. Relational database schema (north-west quadrant)

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weather_data
weather_station_id: INTEGER [PFK]

jan_climate_prob: DOUBLE
feb_climate_prob: DOUBLE
mar_climate_prob: DOUBLE
apr_climate_prob: DOUBLE
may_climate_prob: DOUBLE
jun_climate_prob: DOUBLE
jul_climate_prob: DOUBLE
aug_climate_prob: DOUBLE
sep_climate_prob: DOUBLE
oct_climate_prob: DOUBLE
nov_climate_prob: DOUBLE
dec_climate_prob: DOUBLE
jan_wind_bearing_min: DOUBLE
jan_wind_bearing_mode: DOUBLE
jan_wind_bearing_max: DOUBLE
feb_wind_bearing_min: DOUBLE
feb_wind_bearing_mode: DOUBLE
feb_wind_bearing_max: DOUBLE
mar_wind_bearing_min: DOUBLE
mar_wind_bearing_mode: DOUBLE
mar_wind_bearing_max: DOUBLE
apr_wind_bearing_min: DOUBLE
apr_wind_bearing_mode: DOUBLE
apr_wind_bearing_max: DOUBLE
may_wind_bearing_min: DOUBLE
may_wind_bearing_mode: DOUBLE
may_wind_bearing_max: DOUBLE
jun_wind_bearing_min: DOUBLE
jun_wind_bearing_mode: DOUBLE
jun_wind_bearing_max: DOUBLE
jul_wind_bearing_min: DOUBLE
jul_wind_bearing_mode: DOUBLE
jul_wind_bearing_max: DOUBLE
aug_wind_bearing_min: DOUBLE
aug_wind_bearing_mode: DOUBLE
aug_wind_bearing_max: DOUBLE
sep_wind_bearing_min: DOUBLE
sep_wind_bearing_mode: DOUBLE
sep_wind_bearing_max: DOUBLE
oct_wind_bearing_min: DOUBLE
oct_wind_bearing_mode: DOUBLE
oct_wind_bearing_max: DOUBLE
nov_wind_bearing_min: DOUBLE
nov_wind_bearing_mode: DOUBLE
nov_wind_bearing_max: DOUBLE
dec_wind_bearing_min: DOUBLE
dec_wind_bearing_mode: DOUBLE
dec_wind_bearing_max: DOUBLE

surveillance
surveillance_id: INTEGER [PK]

premises_classification_id: INTEGER [FK]
declared_area_id: INTEGER [FK]
priority: INTEGER
frequency: INTEGER

premises_classification
premises_classification_id: INTEGER [PK]

premises_classification_desc: VARCHAR

declared_area
declared_area_id: INTEGER [PK]

declared_area_desc: VARCHAR

resources
resources_id: INTEGER [PK]

state_id: INTEGER [FK]
surv_min: INTEGER
surv_max: INTEGER
surv_ramp_start: INTEGER
surv_ramp_length: INTEGER
cull_min: INTEGER
cull_max: INTEGER
cull_ramp_start: INTEGER
cull_ramp_length: INTEGER
disposal_min: INTEGER
disposal_max: INTEGER
disposal_ramp_start: INTEGER
disposal_ramp_length: INTEGER
disinfect_min: INTEGER
disinfect_max: INTEGER
disinfect_ramp_start: INTEGER
disinfect_ramp_length: INTEGER
vacc_min: INTEGER
vacc_max: INTEGER
vacc_ramp_start: INTEGER
vacc_ramp_length: INTEGER

...vements
...vements_id: INTEGER [PK]
...id: INTEGER [PFK]

...OUBLE
...OUBLE
...UBLE
...UBLE

herd_type
herd_type_id: INTEGER [PK]
... INTEGER [PFK]

...herd_type_prob_1: DOUBLE
...herd_type_prob_2: DOUBLE
...herd_type_prob_3: DOUBLE
...herd_type_prob_4: DOUBLE
...herd_type_prob_5: DOUBLE
...herd_type_prob_6: DOUBLE
...herd_type_prob_7: DOUBLE
...herd_type_prob_8: DOUBLE
...herd_type_prob_9: DOUBLE
...herd_type_prob_10: DOUBLE

herd
herd_id: INTEGER [PK]

farm_id: INTEGER
herd_type_id: INTEGER [FK]
farm_type_id: INTEGER [FK]
herd_size: INTEGER
farm_longitude: DOUBLE
farm_latitude: DOUBLE
state_id: INTEGER [FK]
region_id: INTEGER [FK]
weather_station_id: INTEGER [FK]
lga_id: INTEGER [FK]
mega_region_id: INTEGER [FK]

weather_station
weather_station_id: INTEGER [PK]

weather_station_desc: VARCHAR(50)
weather_station_longitude: DOUBLE
weather_station_latitude: DOUBLE

region

... GER [PK]
...ARCHAR

Figure B.2. Relational database schema (north-east quadrant)

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consignment_dest_farm_prob: DOUBLE
consignment_dest_abattoir_prob: DOUBLE

consignment_dest_premises3_type
consignment_dest_premises3_type_id: INTEGER [PK]
herd_type_id: INTEGER [PFK]

consignment_dest_farm_prob: DOUBLE
consignment_dest_saleyard_prob: DOUBLE
consignment_dest_abattoir_prob: DOUBLE

consignment_dest_herd_type
consignment_dest_herd_type_id: INTEGER [PK]
herd_type_id: INTEGER [PFK]

consignment_dest_herd_type_prob_1: DOUBLE
consignment_dest_herd_type_prob_2: DOUBLE
consignment_dest_herd_type_prob_3: DOUBLE
consignment_dest_herd_type_prob_4: DOUBLE
consignment_dest_herd_type_prob_5: DOUBLE
consignment_dest_herd_type_prob_6: DOUBLE
consignment_dest_herd_type_prob_7: DOUBLE
consignment_dest_herd_type_prob_8: DOUBLE
consignment_dest_herd_type_prob_9: DOUBLE
consignment_dest_herd_type_prob_10: DOUBLE

consignment_dest_inter_region
consignment_dest_inter_region_id: INTEGER [PK]

herd_type_id: INTEGER [FK]
mega_region_id: INTEGER [FK]
consignment_dest_inter_region_prob_1: DOUBLE
consignment_dest_inter_region_prob_2: DOUBLE
consignment_dest_inter_region_prob_3: DOUBLE
consignment_dest_inter_region_prob_4: DOUBLE

consignment_distance
consignment_distance_id: INTEGER [PK]

herd_type_id: INTEGER [FK]
mega_region_id: INTEGER [FK]
min_distance: INTEGER
most_likely_distance: INTEGER
max_distance: INTEGER

vaccination
vaccination_id: INTEGER [PK]
state_id: INTEGER [PFK]

ext_beef_pri: INTEGER
int_beef_pri: INTEGER
feedlot_pri: INTEGER
mixed_beef_pri: INTEGER
mixed_sheep_pri: INTEGER
dairy_pri: INTEGER
small_pigs_pri: INTEGER
large_pigs_pri: INTEGER
sheep_pri: INTEGER
smallholder_pri: INTEGER
inner_radius: INTEGER
outer_radius: INTEGER
outside_in: VARCHAR
new_ips_only: VARCHAR
retrospective_window: INTEGER

herd_type_id: INTEGER [FK]
ebm_beta: DOUBLE
ebm_beta_pdf_id: INTEGER [FK]
ebm_beta_pdf_p1: DOUBLE
ebm_beta_pdf_p2: DOUBLE
ebm_beta_pdf_p3: DOUBLE
ebm_latent_period: DOUBLE
ebm_infectious_period: DOUBLE
ebm_clinical_period: DOUBLE
ebm_days_b4_clinical: INTEGER
ebm_proportion_clinical: DOUBLE
ebm_immunity_period: INTEGER

farm_type
farm_type_id:

farm_type_de
ip_ops_priorit

ip_operations
ip_operations_id: INTEGER [PK]

state_id: INTEGER [FK]
cull_ips: VARCHAR
cull_dcps: VARCHAR
cull_adjacent: VARCHAR
adjacent_radius: INTEGER
cull_sps: VARCHAR
sp_radius: INTEGER

mega_region
mega_region_id: INTEGER [PI
mega_region_desc: VARCHAR(

moveme
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state_id:
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saleyard_consignment_distance
saleyard_consignment_distance_id: INTEGER [PK]
mega_region_id: INTEGER [PFK]

min_distance: INTEGER
most_likely_distance: INTEGER
max_distance: INTEGER

Figure B.3. Relational database schema (south-west quadrant)

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Figure B.4. Relational database schema (south-east quadrant)

Appendix C   Database files

Table C.1. Summary of database input files

CSV file name	Contents	Clients
consignment_dest_herd_type	Cumulative PDFs of direct movement destination herd types.	Direct Spread, Direct Tracing
consignment_dest_inter_region	Cumulative PDFs of direct movement destination regions.	Direct Spread, Direct Tracing
consignment_dest_premises3_type	Cumulative PDFs of direct movement dest herd/saleyard/abattoir.	Direct Spread
consignment_dest_premises_type	Cumulative PDFs of direct movement destination herd/abattoir.	Direct Spread
consignment_distance	Beta-PERT PDFs of direct movement distances per herd type per region.	Direct Spread, Direct Tracing
consignment_size	Beta-PERT PDFs of direct movement consignment sizes per herd type.	Direct Spread
declared_area	Declared area type enumeration (OA, CA, RA).	Surveillance
direct_movements	Mean num daily outgoing direct movements per month per herd type.	Direct Spread, Direct Tracing
direct_movements_on	Mean num daily incoming direct movements per month per herd type.	Direct Tracing
ebm	EBM ODE system parameterisation (per herd type).	Herd agents
farm_type	Farm type-dependent parameters (e.g., IP operations priority).	Herd agents
herd	National set of herds (e.g., type, size, lat/long, weather station)	Herd agents
herd_type	Herd type-dependent parameters (e.g., surveillance priorities).	Herd agents
indirect_dest_herd_type	Cumulative PDFs of indirect movement destinations.	Indirect Spread, Indirect Tracing

CSV file name	Contents	Clients
indirect_distance	Beta-PERT PDFs of indirect movement distances per herd type.	Indirect Spread, Indirect Tracing
indirect_movements	Mean daily outgoing indirect movements per season per herd type.	Indirect Spread, Indirect Tracing
ip_operations	IP operations configuration (e.g., pre-emptive culling radius), per jurisdiction.	IP Operations
lga	National set of LGAs (name, region and jurisdiction).	Herd agents
mega_region	Mega region enumeration (Pastoral, North East, South East, South West).	Herd agents, Saleyard Spread
movement_restrictions	Movement restrictions parameters (e.g., RA radius), per jurisdiction.	Movement Restrictions
passive_detection	Passive detection configuration (e.g., detection probabilities), per herd type.	First Detection
premises_classification	Declared premises types (UP, IP, DCP, SP, TP, ARP, POR, VP, RP).	Herd agents
region	Region enumeration (Far North, Lower North, Arid Zone, Barkley Tableland, Tropical North-East Coast, Central QLD and North-West NSW, New England, Temperate South-East Coast, Temperate Slopes and Plains, Mediterranean, Tasmania, South-West WA)	Herd agents
resources	Resources parameters (e.g., num surveillance teams), per jurisdiction.	Resources
sale	Scheduled sales per saleyard	Saleyard Spread
sale_directions	Sale bearing types (enumeration only, e.g., north east).	Saleyard Spread
sale_frequency	Sale frequency enumeration (e.g., bi-weekly, weekly, fortnightly, monthly).	Saleyard Spread
sale_type	Sale type enumeration (beef, sheep, calf, pig, dairy).	Saleyard Spread

CSV file name	Contents	Clients
saleyard_consignment_distance	Beta-PERT PDFs of saleyard consignment distances per region.	Saleyard Spread
saleyard_consignments_out	Beta-PERT PDFs of num consignments from saleyard per herd type.	Saleyard Spread
saleyard	National set of saleyards (name, lat/long and jurisdiction).	Saleyard Spread
species	Species-dependent parameters (e.g., Beta-PERT PDF of trace duration).	Herd agents
sp_reporting	SP reporting configuration (e.g. Beta-PERT PDF of report lag), per herd type.	SP Reporting
state	State/territory jurisdictions (enumeration only, e.g. NSW).	Herd agents
surveillance	Surveillance parameters (e.g., visit prioritisation, visit frequency).	Surveillance
vaccination	Vaccination parameters (e.g., ring radii), per jurisdiction.	Vaccination
weather_data	Weather data for each weather station per month.	Airborne Spread
weather_station	National set of weather stations (name and lat/long).	Airborne Spread

Appendix D   Configuration files

Table D.1. Summary of configuration files

File name	Contents
system.properties	System-level configuration parameters, for example: spatial-indexing mode (grid-based, R-Tree-over-GiST, off), cell dimensions of spatial-indexing grid, GUI definitions, PostgreSQL database configuration. These parameters don't change very often and so the file is generally not changed by users.
linux.properties windows.properties	Operating system-dependent configuration parameters, for example directory/folder locations. These parameters don't change very often and so these files are generally not changed by users.
log4j.properties	Configuration of the Apache Software Foundation (Apache, 2012) logging services. These parameters include control of the level of logging output (off, info, debug, trace) for each subsystem. These parameters are for development and test purposes, and so this file is generally not changed by users.
openmap.properties	Configuration of the Openmap (BBN, 2015) GIS platform. These parameters don't change very often and so this file is generally not changed by users.
model.properties (where *model* is a user-defined name specified when building and running the model)	General model and scenario configuration parameters, for example, database name, bounding latitude/longitudes of study area, scenario configuration, spread pathway configuration, control measures configuration. All parameters in this file are user-changeable. An example model configuration file is provided in Figure D.1.

```
############################################################
# AADIS user-changeable configuration parameters.
############################################################

############################################################
# Database configuration.
############################################################
db.name=AADIS_PHASE1

############################################################
# Grid boundaries for Australia.
############################################################
grid.north_lat_bound=-10.40
grid.south_lat_bound=-43.90
grid.west_long_bound=112.70
grid.east_long_bound=153.80

############################################################
# Scenario configuration.
############################################################
# Scenario identification.
scenario.name=test

# Scenario start date (dd/mm/yyyy).
scenario.start_date=1/05/2013

# Scenario end mode (valid modes are: fixed, control-based, earliest, detection).
# fixed - scenario ends on a fixed day.
# control-based - scenario ends when no E/I farms and no pending control actions
# earliest - scenario ends upon the earliest of the fixed and control-based endings
# detection - scenario ends after the detection of the first IP
scenario.end_mode=control-based

# Scenario end day (only relevant to fixed mode and earliest mode).
scenario.fixed_end_day=80

# Maximum scenario length (days). This is only relevant to
# control-based end mode.
scenario.max_length=200

# Optional delay (in days) after scenario ends in controlled mode.
scenario.end_delay=0

# Number of runs.
scenario.num_runs=10

# Seeding mode (manual, random, snapshot).
scenario.seed_mode=manual

# Name of input file for snapshot seeding.
scenario.seed_file=test_snapshot_1

# A snapshot comprises a binary file (.ser) that fully describes a
# run, and an ascii file (.csv) that just has summary data.
# Currently only the binary file can be loaded back into the model
# for seeding purposes. Options for taking snapshots:
```

```
# Manual - via the Save button on the Run Panel.
# Detection - automatically when the first IP is declared.
# Scenario end - automatically at the end of a run.
scenario.manual_snapshot_enabled=true
scenario.detection_snapshot_enabled=false
scenario.scenario_end_snapshot_enabled=false

# Number of manually defined seed herds.
# Note that eventually seed herds will also be definable via
# the Seed Dialog.
scenario.num_manual_seeds=1

# Manual seed herd definitions.
# Starting level of infection can be specified via initial SEIR
# values or initial number of latent and/or infectious animals.
# If either num latent or num infectious animals are specified
# then the initial SEIR values are derived from them (based on
# herd size and assuming R0 is 0), otherwise the specified SEIR
# initial values are used.
scenario.seed_1_herd_id=109051
scenario.seed_1_day=0
scenario.seed_1_s0=0.9
scenario.seed_1_e0=0.1
scenario.seed_1_i0=0.0
scenario.seed_1_r0=0.0
scenario.seed_1_num_latent=2
scenario.seed_1_num_infectious=0

# Random seeding configuration (use 0 for wildcard).
# See note above re initial SEIR values.
scenario.num_random_seeds=3
scenario.random_seed_herd_type=7
scenario.random_seed_megaregion=0
scenario.random_seed_state=2
scenario.random_seed_region=0
scenario.random_seed_min_herd_size=300
scenario.random_seed_max_herd_size=800
scenario.random_seed_day=0
scenario.random_seed_s0=0.9
scenario.random_seed_e0=0.1
scenario.random_seed_i0=0.0
scenario.random_seed_r0=0.0
scenario.random_seed_num_latent=2
scenario.random_seed_num_infectious=0
scenario.random_seed_reuse_between_runs=false

############################################################
# Spread pathway configuration.
############################################################
# Direct spread pathway.
spread.direct.enabled=true
spread.direct.search_distance_tolerance=5
```

```
spread.direct.second_pass_search_distance_tolerance=500
spread.direct.max_herd_type_search_retries=10

# Indirect spread pathway.
spread.indirect.enabled=true
spread.indirect.baseline_prob=0.03
spread.indirect.min_new_infections=1
spread.indirect.mode_new_infections=2
spread.indirect.max_new_infections=5
spread.indirect.search_distance_tolerance=100
spread.indirect.second_pass_search_distance_tolerance=500
spread.indirect.max_herd_type_search_retries=10

# Local spread pathway.
spread.local.enabled=true
spread.local.baseline_prob=0.048
spread.local.multiherd_baseline_prob=0.096
spread.local.detection_weight=0.5
spread.local.radius=3
spread.local.min_new_infections=1
spread.local.mode_new_infections=2
spread.local.max_new_infections=5

# Airborne spread pathway.
spread.airborne.enabled=true
#
# Coefficients for the plume distance (pd) formula:
# pd = base * e ^ (exponent * log10 * n)
# where n is the num infections animals in the shedding herd
#
spread.airborne.plume_distance_base=0.113
spread.airborne.plume_distance_exponent=1.367
spread.airborne.max_plume_distance=20
#
# The potency of a plume diminishes over distance through either
# linear or exponential decay. Valid values for decay mode are:
# linear, exp1, exp2.
#
spread.airborne.decay_mode=linear
#
# Coefficient for the exponential decay functions.
# dw = e ^ (exponent * hd / pd)
# where dw = distance weight
# hd = distance between shedding herd and susceptible herd
# pd = plume distance
#
spread.airborne.exp1_decay_exponent=-6.90776
spread.airborne.exp2_decay_exponent=-3.45388
#
spread.airborne.wind_bearing_tolerance=15
#
```

```
# Probabilities that a single animal will succumb to airborne virus.
spread.airborne.prob_cow_infection=0.03
spread.airborne.prob_sheep_infection=0.003
spread.airborne.prob_smallholder_infection=0.003
spread.airborne.prob_pig_infection=0.00012
#
spread.airborne.min_new_infections=1
spread.airborne.mode_new_infections=2
spread.airborne.max_new_infections=5

# Saleyard spread pathway (enable regular OR simple)
spread.saleyard.enabled=true
spread.simple_saleyard.enabled=false
spread.simple_saleyard.search_distance_tolerance=20
spread.simple_saleyard.second_pass_search_distance_tolerance=500
spread.simple_saleyard.max_herd_type_search_retries=10
# Amplification factor to direct spread average daily movements
# when simple saleyard spread is enabled. This stems from
# direct movements driving saleyard spread (as opposed to
# regular saleyard spread which is sale-based and self-driven).
spread.simple_saleyard.direct_movements_amplifier=1.05

# When the weight overrides are true than all herd infectivity and
# susceptibility weights are set to 1 (i.e., unweighted).
# When the weight overrides are false then the weights are
# calculated using the species-dependent exponents below.
# e.g. cattleSuscWeight = cattleRelativeSusc * (herdSize ^ cattleSuscPower)
# and is then normalised across all herds
#
spread.herd_infectivity_weight_override=false
spread.herd_susceptibility_weight_override=false
spread.cattle_infectivity_power=0.42
spread.cattle_susceptibility_power=0.41
spread.sheep_infectivity_power=0.49
spread.sheep_susceptibility_power=0.2
spread.pig_infectivity_power=0.42
spread.pig_susceptibility_power=0.41
spread.smallholder_infectivity_power=0.49
spread.smallholder_susceptibility_power=0.2

#######################################################
# Control measures configuration.
#######################################################
# Global enabling/disabling of control measures.
control.enabled=true

# First IP detection mode (disabled, fixed, passive)
first_detection.mode=passive

# Fixed detection configuration.|
first_detection.fixed.day=3
# Fixed detection mode (any, herd, species)
```

```
first_detection.fixed.mode=herd
first_detection.fixed.herd_id=109051
# Species priorities 1,2,3 dictate the herd type order when
# searching for and selecting the index IP.
first_detection.fixed.cattle_priority=0
first_detection.fixed.sheep_priority=0
first_detection.fixed.pigs_priority=0
first_detection.fixed.smallholder_priority=0

# Passive detection configuration.
first_detection.passive.abattoir_confirmation_lag=3
first_detection.passive.saleyard_confirmation_lag=4
first_detection.passive.farm_confirmation_lag=5

# Artificial injection of declared premises states.
injection.enabled=true

# Movement restrictions configuration. Note that these are just
# range definitions. The actual values are defined in the database
# per jurisdiction.
movement_restrictions.enabled=true
movement_restrictions.standstill.minimum=3
movement_restrictions.standstill.maximum=14
movement_restrictions.transition.minimum=0
movement_restrictions.transition.maximum=28
movement_restrictions.ra_radius.minimum=3
movement_restrictions.ra_radius.maximum=20
movement_restrictions.ca_radius.minimum=10
movement_restrictions.ca_radius.maximum=50
movement_restrictions.ca_radius.maximum=50

# Number of days that an RP remains enclosed by a controlled area
# after IP Operations have completed.
movement_restrictions.lifting_delay=21

# SP reporting
sp_reporting.enabled=true
sp_reporting.false_report_to_true_ratio=2.34
sp_reporting.moving_average_days=3
sp_reporting.false_report_ra_ratio=0.6
sp_reporting.false_report_ca_ratio=0.3
sp_reporting.false_report_oa_ratio=0.1

# Tracing
tracing.direct.enabled=true
tracing.indirect.enabled=true
tracing.false_traces.enabled=true
tracing.num_days_backward=14
tracing.num_days_forward=14

# Surveillance
surveillance.enabled=true
surveillance.dcp_period=7
surveillance.sp_period=7
```

```
surveillance.tp_period=14
surveillance.arp_period=14
surveillance.local_radius=3
surveillance.min_clinical_signs=0.05
surveillance.min_days_infected=10
surveillance.lab_results_required=yes
surveillance.lab_results_delay=1
surveillance.dcp_sp_tp_overdue_threshold=7
surveillance.arp_overdue_threshold=14

# IP Operations
ip_operations.enabled=true

# Vaccination
vaccination.enabled=false
vaccination.start_by_control_day=false
vaccination.start_day=3
vaccination.start_by_ip_count=true
vaccination.start_ip_count=3
vaccination.immunity_lag=6

# Resource-constraining of control measures.
resources.enabled=true
```

Figure D.1. Example model configuration file

Appendix E   **Output files**

Table E.1. Structure of the Startup report file

Column	Description
Run	Run number
Seed herd ID	Seed herd ID (i.e., initial source of infection in outbreak)
Start offset	Scenario start offset in days (snapshot seeding mode only)
Infection day	Simulation day that the herd was infected
Herd type ID	Herd type ID
Days until detection	Number of simulation days from infection to declaration as an IP

Table E.2. Structure of the Herd report file

Field	Description
Run	Run number
Herd ID	Infected herd ID
Latitude	Latitude of the infected herd
Longitude	Longitude of the infected herd
State ID	ID of the infected herd's jurisdiction
Day infected	Simulation day that the herd was infected
Infection path	Means that the herd was infected
Source herd ID	The ID of the source herd that infected the subject herd
Day diagnosed	Simulation day that the herd's farm was declared an IP*
Day culled	Simulation day that the herd's farm was culled*
Day vaccinated	Simulation day that the herd's farm was vaccinated*

- a value of -1 indicates that the herd was not diagnosed/culled/vaccinated

Table E.3. Structure of the Farm Summary report file

Column	Description
Run	Run number
Num simulation days	Run duration in days
Current latent	Number of latent farms (at least 1 exposed herd and no infectious herds)
Current infectious	Number of farms that are infectious (at least 1 infectious herd)
Current recovered	Number of farms that are recovered (all herds are recovered)
Cum infected farms	Cumulative number of infected farms (latent or infectious)
Cum IPs	Cumulative number of IPs
Cum TPs	Cumulative number of TPs
Cum SPs	Cumulative number of SPs
Cum RPs	Cumulative number of RPs
Cum ARPs	Cumulative number of ARPs
Cum PORs	Cumulative number of PORs
Cum ext beef IPs	Cumulative number of IPs of type Extensive Beef
Cum int beef IPs	Cumulative number of IPs of type Intensive Beef
Cum feedlot IPs	Cumulative number of IPs of type Feedlot
Cum mixed IPs	Cumulative number of IPs of type Mixed Beef Sheep
Cum dairy IPs	Cumulative number of IPs of type Dairy
Cum small pigs IPs	Cumulative number of IPs of type Small Piggeries
Cum large pigs IPs	Cumulative number of IPs of type Large Piggeries
Cum sheep IPs	Cumulative number of IPs of type Sheep
Cum smallholder IPs	Cumulative number of IPs of type Small-holders
Last IP declared	Simulation day that the last IP was declared
Last day of infection	Last simulation day that there was one or more infected farms
Cum VPs	Cumulative number of VPs
Cum ext beef VPs	Cumulative number of VPs of type Extensive Beef
Cum int beef VPs	Cumulative number of VPs of type Intensive Beef
Cum feedlot VPs	Cumulative number of VPs of type Feedlot
Cum mixed VPs	Cumulative number of VPs of type Mixed Beef Sheep
Cum dairy VPs	Cumulative number of VPs of type Dairy
Cum small pigs VPs	Cumulative number of VPs of type Small Piggeries

Column	Description
Cum large pigs VPs	Cumulative number of VPs of type Large Piggeries
Cum sheep VPs	Cumulative number of VPs of type Sheep
Cum smallholder VPs	Cumulative number of VPs of type Small-holders
Cum vacc animals	Cumulative number of vaccinated animals
Cum vacc cattle	Cumulative number of vaccinated cows
Cum vacc sheep	Cumulative number of vaccinated sheep
Cum vacc pigs	Cumulative number of vaccinated pigs
Cum vacc other	Cumulative number of vaccinated smallholder animals
Cum ext beef inf	Cumulative number of infected farms of type Extensive Beef
Cum int beef inf	Cumulative number of infected farms of type Intensive Beef
Cum feedlot inf	Cumulative number of infected farms of type Feedlot
Cum mixed inf	Cumulative number of infected farms of type Mixed Beef Sheep
Cum dairy inf	Cumulative number of infected farms of type Dairy
Cum small pigs inf	Cumulative number of infected farms of type Small Piggeries
Cum large pigs inf	Cumulative number of infected farms of type Large Piggeries
Cum sheep inf	Cumulative number of infected farms of type Sheep
Cum smallholder inf	Cumulative number of infected farms of type Small-holders
Cum cull animals	Cumulative number of culled animals
Cum cull cattle	Cumulative number of culled cows
Cum cull sheep	Cumulative number of culled sheep
Cum cull pigs	Cumulative number of culled pigs
Cum cull other	Cumulative number of culled smallholder animals

Table E.4. Structure of the Farm Daily report file

Column	Description
Run	Run number
Day	Simulation day
Cum inf farms	Cumulative number of infected farms (exposed or latent farms)
Cum inf herds	Cumulative number of infected herds (exposed or latent farms)
Cum IPs	Herd type ID
Cum IPs	Cumulative number of IPs
Cum TPs	Cumulative number of TPs
Cum SPs	Cumulative number of SPs
Cum VPs	Cumulative number of VPs
Cum RPs	Cumulative number of RPs
Cum ARPs	Cumulative number of ARPs
New inf farms	Number of newly infected farms on the current day
New IPs	Number of newly declared IPs on the current day
Cum surv done	Cumulative number of completed surveillance visits
Cum surv deficit	Cumulative number of pending surveillance visits
Cum culls done	Cumulative number of completed culling visits
Cum culls deficit	Cumulative number of pending culling visits
Cum disp done	Cumulative number of completed disposal visits
Cum disp deficit	Cumulative number of pending disposal visits
Cum vacc done	Cumulative number of completed vaccination visits
Cum vacc deficit	Cumulative number of pending vaccination visits

Table E.5. Structure of the Saleyard report file

Field	Description
Run	Run number
Sale ID	Sale ID
Saleyard ID	Saleyard ID
Latitude	Latitude of the saleyard
Longitude	Longitude of the saleyard
Sale Type	Sale type ID
Day infected	Sim day that an outgoing consignment infected a recipient herd
Infected consigns in	Number of infected consignments in for the subject sale
Infected consigns out	Number of infected consignments out for the subject sale
Infected consigns to abattoir	Number of infected consignments sent to abattoirs
Infected consigns to farm	Number of infected consignments sent to farms
Infected consigns to feedlot	Number of infected consignments sent to feedlots

Table E.6. Structure of the Control report file

Field	Description
Run	Run number
First IP detection day	Simulation day that the first IP was declared
First IP detection type	Index case premises type (farm, abattoir, saleyard)
Index case farm ID	Index case farm ID
Index case herd type	Index case herd type
Surveillance resources utilisation	Max[(visits in progress + visits pending)/pool size][1]
Culling resources utilisation	Max[(visits in progress + visits pending)/pool size][1]
Disposal resources utilisation	Max[(visits in progress + visits pending)/pool size][1]
Disinfection resources utilisation	Max[(visits in progress + visits pending)/pool size][1]
Vaccination resources utilisation	Max[(visits in progress + visits pending)/pool size][1]

[1] per-jurisdiction

Table E.7. Structure of the Spread report file

Field	Description
Run	Run number
Local contacts	Number of contacts from the Local spread pathway
Local infections	Number of infections from the Local spread pathway
Direct contacts	Number of contacts from the Direct spread pathway
Direct infections	Number of infections from the Direct spread pathway
Indirect contacts	Number of contacts from the Indirect spread pathway
Indirect infections	Number of infections from the Indirect spread pathway
Saleyard contacts	Number of contacts from the Saleyard spread pathway
Saleyard infections	Number of infections from the Saleyard spread pathway
Airborne contacts	Number of contacts from the Airborne spread pathway
Airborne infections	Number of infections from the Airborne spread pathway
Direct inf to farm	Number of direct infections at farms
Direct inf to abattoir	Number of direct infections at abattoirs

Table E.8. Structure of the Resources report file

Field	Description
Run	Run number
Day	Simulation day
Num surveillance visits in progress	Per jurisdiction
Num surveillance visits pending	Per jurisdiction
Surveillance pool size	Per jurisdiction
Num culling visits in progress	Per jurisdiction
Num culling visits pending	Per jurisdiction
Culling pool size	Per jurisdiction
Num vaccination visits in progress	Per jurisdiction
Num vaccination visits pending	Per jurisdiction
Vaccination pool size	Per jurisdiction

Appendix F   **University of Melbourne report**

Technical advice for national decision support tools for foot-and-mouth disease preparedness

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This document addresses two of the listed activities in the Grant Agreement between The Department of Agriculture and The University of Melbourne titled 'Independent Technical Advice for National Decision Support Tools for Foot and Mouth Disease Preparedness': (a) a review of the structure and functionality of the Australian Animal Disease Simulation Model (AADIS), and (b) a description of simulations and analyses carried out to ensure the model is fit for purpose.

For this report the focus has been on development of analytical approaches and techniques to assess the key features of each of the model's major infection spread mechanisms. For the final report for this Grant Agreement assessment of fitness-for-purpose will be extended to the five disease control measures (surveillance, depopulation, vaccination, tracing and movement restrictions) available within the model.

Review of AADIS model structure and functionality

AADIS is a disease simulation model where the epidemiological units of interest (a group of animals managed as a single unit, called a 'herd') exist in one of several disease classification states at any time. In contrast to other animal disease simulation models such as AusSpread (Garner and Beckett, 2005) and InterSpread Plus (Stevenson et al., 2013) AADIS additionally uses the concept of a 'farm' defined as a location where one or more herds are managed as a single unit. For the most part, where farms are comprised of single herds (for example, in intensive dairying areas of the country), the term 'herd' and 'farm' are synonymous.

To estimate the spread of infectious disease in domestic livestock populations AADIS uses a hybrid approach, incorporating equation-based and agent-based modelling techniques. Equation-based techniques are used to simulate the spread of disease within a herd; agent-based techniques are used to simulate the spread of disease between herds.

A four-compartment SEIR model is used to simulate the spread of infection within individual herd units. The four states of the SEIR model are *susceptible* (individuals in a herd are susceptible to infection), *exposed* (individuals in a herd have been exposed to infective agent; they are incubating disease but are not yet infectious), *infectious* (individuals in a herd are capable of spreading disease to others), and *recovered* (sanitary measures such as depopulation or vaccination have been applied to render the herd [location] incapable of becoming infected). In AADIS transition from S to E, E to I, and I to R compartments is simulated using ordinary differential equations.

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Between-herd spread of disease is addressed using agent-based techniques. Here, the sequence of events that determine transfer of infection from one herd to another by given route are explicitly simulated by the model.

In the situation where an incursion of FMD has occurred it is possible for infection to spread by any one of a number of mechanisms between herds prior to detection (often referred to as the 'silent spread' phase of an epidemic). Once disease has been detected, the focus of control efforts (both in real-life and in the model) are to limit spread of virus by each of these mechanisms. The between-herd spread mechanisms in AADIS include: (a) direct and indirect movements; (b) local spread; and (c) windborne spread. Movement of susceptible livestock to and from saleyards are a specific (and important) subclass of direct movement events.

Spread mechanisms

Direct and indirect spread

AADIS simulates movements from infected herds only. For each infected herd a lookup table of movement frequencies is used to determine whether or not an off-farm shipment of animals will occur on a given simulation day (the probability of a movement event occurring each day will depend on herd type and month of the year).

If a movement event occurs, a consignment size will be selected. Whether or not the consignment is infected will depend on the prevalence of infection in the herd at the time of the movement event. A destination herd type, destination region and movement distance is selected, again from lookup tables. Two concentric circles are drawn around the herd initiating the movement (creating a ring) where the width of the ring is set to a user-defined tolerance of 10 km. Destination herds are then selected from within the ring. If no herd of the selected destination type is present within the ring the width of the ring is increased to (again, a user defined) tolerance of 100 km. If the consignment of animals moved is infected, infection will be transferred from the source herd to the destination herd at the time the movement event takes place.

AADIS uses a similar approach for indirect movements. The only major difference being that the frequency of indirect movement events are often greater than that of direct movements, movement distances tend to be less and the probability of infection transfer once a movement event has occurred is less than that of direct movements.

Saleyards

Saleyards are a well-known 'amplifier' of infection, particularly in the silent spread phase of an epidemic (Gibbens et al. 2001). Spread of infection via saleyards in AADIS can occur using one of two independent approaches: (a) sale-driven saleyard spread; and (b) simplified direct spread-driven saleyard spread.

Sale-driven saleyard spread

A series of saleyards throughout the country are defined (spatially, and in terms of how often sales are run and the species of animals traded). For each simulation day AADIS:

(a) Identifies those saleyards that are operating that day;

(b) Identifies herds within the saleyard catchment area;

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(c) Determines if the herd contributes animals to a sale (a vendor) by sampling from a binomial distribution based on the total number of vendor herds in the catchment area;

(d) Determines the destination of sale animals by sampling from a cumulative probability distribution of the likely destination type (abattoir, farm or feedlot). If the destination premises type is a farm or feedlot the number of outgoing consignments for sale is determined by sampling from a Beta pert probability distribution;

(e) Identifies destination (i.e. buyer) [farms] within the saleyard catchment area;

(f) Transmits infection from each consignment to the destination herds using initial SEIR ratios from the vendor herd.

(g) Within-saleyard spread is then estimated using an equation based model (EBM) similar to that used for modelling within-herd disease spread run for a single day. Compared with the within-herd EBM model, the transmission parameters for the saleyard EBM model are greater due to the substantially higher level of mixing of animals that occurs in a given saleyard.

Simplified direct spread-driven saleyard spread

Sale-driven saleyard spread represents a simplified means for simulating saleyard spread when there is insufficient information to represent individual sales. On any given simulation day the probability that an infected herd sends animals to a saleyard is determined stochastically. Each infected consignment of animals to a saleyard generate infected outgoing consignments to destination herds using a Beta pert distribution.

Note that it is possible for an abattoir to be the destination location for an off-saleyard movement event. For movements of infected animals to an abattoir no further infection transmission occurs.

Local spread

Local spread refers to the spread of infection locally from an infected herd to other, nearby susceptible herds where it is difficult to differentiate the exact mechanism of spread (Sanson et al., 2006). Local spread is a combination of: (a) localised short range aerosol transmission; (b) boundary contact; and (c) fomite transfer. These separate transfer mechanisms are modelled as one single mechanism in AADIS because there is currently insufficient data or understanding to separate the individual mechanisms. AADIS assumes that local spread occurs within a user defined radius of 3 km around an infected herd.

The probability of local spread between two herds on separate farms depends on the prevalence of infection on the source herd, the source herd infectivity weight (e.g. pig herds are more infectious than cattle or sheep herds and large herds are more infectious than small herds), the destination herd susceptibility weight (e.g. cattle herds are more susceptible to infection than sheep flocks which are more susceptible than pig herds), the destination herd biosecurity weight, the destination herd seasonal weight, the distance between the source and destination herds and whether or not a control program is in place. The daily probability of local spread occurring from a

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source herd decays over time as the prevalence of infectious animals on the source herd declines.

Extensive beef herds do not use a local spread pathway as they are presumed to be located more than 3 km from each other. The local spread pathway for multi-herd farms (i.e. farms where one or more herds are kept at a single geographical location) is modified to allow local spread to be more likely to occur to herds on the same farm (as opposed to different farms).

Windborne spread

Input data for AADIS includes weather station location details and, for each location, weather summary information. Key assumptions for windborne spread include: (a) infected pig farms are considered capable of spreading infection via the wind beyond 3 km; (b) most wind-borne spread occurs over distances of up to 10 km; and (c) only ruminants are susceptible to infection via the wind at greater than 3 km distances.

The following conditions need to be met for FMD to spread via the wind. These are: (a) relative humidity greater than 65%; (b) overcast conditions without heavy rain; (c) a stable wind speed of 5 to 10 km per hour in the same direction for a number of hours.

For each weather station a suitability index is calculated, based on the number of days per month where meteorological conditions are suitable for windborne spread. For each simulation day AADIS: (a) finds all infected pig herds; (b) finds the nearest weather station to each pig herd; (c) determines if weather conditions are suitable for windborne spread on the simulation day; (d) selects an appropriate wind direction from a lookup table; (e) identifies susceptible destination cattle and sheep herds within a user configurable radius of 20 km of the source herd; and (f) spreads infection to the destination herds. The probability of windborne spread transmission is fixed and depends on species, herd size, and distance from the source herd.

Control measures

With respect to parameters that define how disease is controlled in AADIS two items require definition. The first is a description of the nature of each control activity. The second requirement is a description of the resources available to implement each activity. Without resource constraints, infectious disease epidemics can be rapidly controlled once effective control measures are implemented. In reality, unlimited resources are seldom available and one of the skills of a disease response manager is to select the mix of control activities that provide the greatest probability of extinguishing an epidemic while working within a prescribed set of resource constraints.

Four general classes of control measure can be applied in AADIS: (a) surveillance; (b) depopulation; (c) vaccination; (d) tracing; and (e) movement restrictions. Control measures in AADIS are applied at the farm (as opposed to herd) level. Control measures and the resources for control measures are configured at the jurisdiction (e.g. state) level.

Surveillance

Surveillance parameters define the likelihood of herds in either the infected or clinical state becoming detected, with the implication that detection results in application of sanitary measures (for example, depopulation or vaccination).

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Depopulation

Depopulation parameters define the nature of stamping out strategies that may be applied to control and eradicate infectious disease outbreaks in animal populations. The first requirement when parameterising a depopulation strategy is to define the conditions that trigger a depopulation event. This may be when a herd is detected with disease, at a specified point in time, or when tracing identifies that a particular movement event has occurred onto a herd. The second requirement is to define which farms will be depopulated following the trigger event. This may be done on the basis of zone or herd infection status. When simulating the management of an epidemic of FMD, those farms in the detected state will usually be listed for depopulation. In some circumstances farms surrounding detected farms may also be depopulated.

Vaccination

Ring and blanket vaccination strategies can be modelled using AADIS. The first requirement is to define the herd state that will trigger a vaccination event. Options in this case are: when a herd is detected as diseased, at a specified point in time, or when a certain threshold number of infected herds have been detected. The second requirement is to define which farms will be vaccinated following the trigger event. If ring vaccination is to be used a radial zone is constructed around each detected farm and all farms within the defined radial zone are listed to receive a vaccination event. Ring vaccination can be used to represent protective or suppressive strategies, and can be defined with an inner radius so that a plot of vaccinated farm locations has a doughnut shape. With blanket vaccination, all farms of a specified type within a prescribed region are vaccinated.

The time taken to complete vaccination on a farm depends on the constituent herd types present. Time to achieve immunity following vaccination depends on a configured immunity lag.

Tracing

An important component of control and eradication programs for epidemics such as FMD and CSF are backward and forward tracing activities (Schnurrenberger et al., 1987; Elbers et al., 2001). Following detection of disease on a farm, backward tracing involves an interview of the farm manager and staff to identify contacts that occurred between the estimated date of infection and (usually) the start of the epidemic. This process identifies those farms that could have introduced disease onto the detected farm. Forward tracing involves identifying contacts made by the detected farm during the infectious period. This identifies farms potentially exposed to infection, and therefore those that are likely to develop disease.

AADIS provides the facility for both backward and forward tracing. The time frame for backward and forward tracing can be specified by the user.

Movement restrictions

Movement restrictions can be imposed on each of the defined direct and indirect movement types, as part of disease control measures. Movement restrictions are quantified in terms of compliance. A setting of 0.98 for direct movements indicates that all direct movements in the model are reduced by a factor of 0.98.

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The resource file defines resources for surveillance, depopulation, disposal, disinfection and cleaning, and vaccination. Resources are defined in terms of the initial number of farms able to be processed per day, the maximum number of farms processed per day and how quickly resources are able to be 'ramped' up during the course of an epidemic response.

Initiation of a simulation

Several options are available to initiate an epidemic: (a) using a user-defined set of one or more seed herds; (b) with randomly selected seed herds that meet criteria relating to herd size and/or herd type; or (c) 'snapshot' seeding, where the user reads in a set of seed herds from a file. Snapshot seeding would be the approach used if AADIS were to be used for modelling during an FMD outbreak. Here, details of identified infected herds up to a given point in time would be read into the model to provide the starting point for simulations.

The general approach to developing a model in AADIS is to populate the required (n = 44) input data tables, build the AADIS database then use the graphic user interface to specify simulation-run specific details such as the number of days to simulate and the number of model iterations to be run.

When a the model is run, herd details are loaded into memory, the simulation time clock is incremented by one, herd states are set, an herd farm is chosen at random, spread of disease is simulated using parameters defined for each of the three spread mechanisms (direct, indirect and saleyard movements, local, and windborne spread) and control measures are applied. This process is then repeated for all infected herds. When this is complete simulation time clock is incremented by one, herd states are updated, and the process is repeated until the last simulation time period has been reached. In contrast to AusSpread and InterSpread Plus, AADIS is not procedural: simulation tasks are not carried out sequentially, that is one after the other. Spread and control algorithms run concurrently on independent execution threads.

Simulations to assess application use and ensure the model is 'fit for purpose'

A series of AADIS models were run to determine if the model outputs were consistent with input parameters defining direct, indirect, local and windborne spread.

Direct spread

Two aspects of direct spread pathways were assessed: (a) the frequency of off-herd direct movement events, and (b) the distance over which direct movement events occurred.

Methodology

One hundred iterations of the AADIS_PHASE1 scenario were run for 31 simulation days starting on 1 May 2015. All spread mechanisms except for those occurring by direct movements were disabled. A single seed herd (109051) initiated the epidemic.

The AADIS log file was then queried to retrieve all successful direct movement events from the seed herd. Movement frequency was then calculated as the number of successful off-herd direct movement events over the 31 simulation days across all

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100 iterations (numerator) divided by the number of herd days at risk (denominator). The calculated direct movement probability was then compared with the direct movement probability value for a herd of type 8 in May (listed in file direct_movements.csv).

For direct movement distances, all successful direct movements from the seed herd were selected from the AADIS log file. Movement distances were retrieved and plotted as a frequency histogram.

Results

For herd 109051 there were a total of 489 direct movement events over (31 simulation days × 1 herd × 100 iterations) 3100 herd direct movement days at risk. The daily probability of making a successful direct movement was (489 ÷ 3100) = 0.158, consistent with the daily movement probability of 0.159 quoted for type 8 herds in May in direct_movements.csv.

Figure 1 is a histogram of direct movement distance frequencies for herd 109051. The median direct movement distance was 100 km (minimum 35 km, maximum 313 km). This compares favourably with direct movement distances for a herd of type 8 in consignment_distance.csv, mode 100 km (minimum 5 km, maximum 580 km).

Conclusions

The frequency of simulated direct movement events and the distance range of simulated direct movement events are consistent with the input values for each of these settings configured by the user.
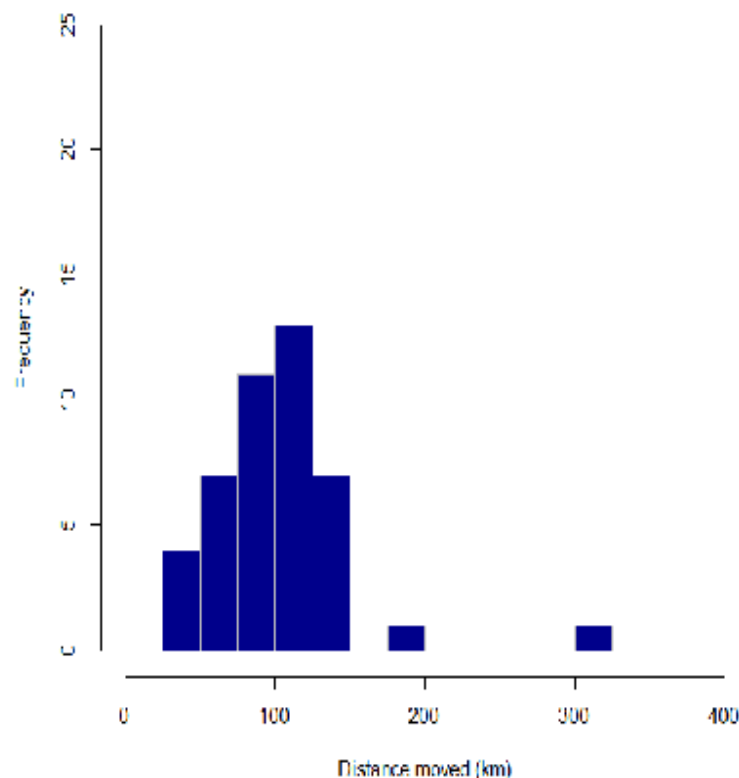
7

Figure 1: Frequency histogram showing direct movement consignment distances for herd 109051. AADIS was run for 31 simulation days for a total of 100 iterations.

Indirect spread

Two aspects of indirect spread pathways were assessed: (a) the frequency of off-herd indirect movement events, and (b) the distance over which indirect movement events occurred.

Methodology

One thousand iterations of the AADIS_PHASE1 scenario were run for 31 simulation days starting on 1 May 2015. All spread mechanisms except for those occurring by indirect movements were disabled. A single seed herd (109051) initiated the epidemic. The AADIS log file was then queried to retrieve all successful indirect movement events from the seed herd. Movement frequency was then calculated as the number of successful off-herd indirect movement events over the 31 simulation days across all 1000 iterations (numerator) divided by the number of herd days at risk (denominator). The calculated indirect movement probability was then compared with the indirect movement probability value for a herd of type 8 in autumn (listed in file indirect_movements.csv).

For indirect movement distances, all successful indirect movements from the seed herd were selected from the AADIS log file. Movement distances were retrieved and plotted as a frequency histogram.

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Results

For herd 109051 there were a total of 14,165 indirect movement events over (31 simulation days × 1 herd × 1000 iterations) 31,000 herd indirect movement days at risk. The daily probability of making a successful indirect movement was (14,165 ÷ 31,000) = 0.457, consistent with the daily indirect movement probability of 0.46 listed for type 8 herds in autumn in indirect_movements.csv.

Figure 2 is a histogram of indirect movement distance frequencies for herd 109051. The median indirect movement distance was 48 km (minimum 4 km, maximum 251 km). The median indirect movement distance from the model compares favourably with that of a herd of type 8 in indirect_distance.csv (mode 50 km, minimum 5 km, maximum 290 km).
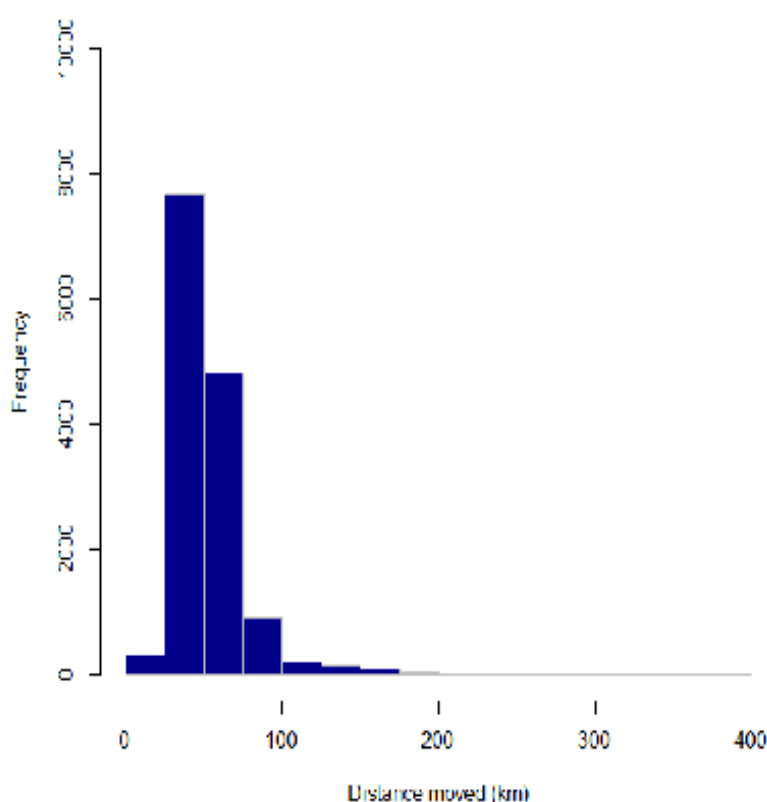

Figure 2: Frequency histogram showing indirect movement consignment distances for herd 109051. AADIS was run for 31 simulation days for a total of 1000 iterations.

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Conclusions

The frequency of simulated indirect movement events and the distance range of simulated indirect movement events are consistent with the input values for each of these settings configured by the user.

Local spread

Methodology

To verify local spread a regular grid of 3780 susceptible herds was generated, separated by a distance of 50 metres. Herd type and herd size details for the 3780 generated herds were populated from the first 3780 herds that appear in the herd file of the AADIS_PHASE1 data set. For this study it was necessary to use a fine grid of herds so local spread probabilities at given scales of distance from a source herd could be quantified with relative certainty.

A single herd in the centre of the grid was selected as the seed herd and AADIS run for 3 simulation days for a single iteration. All spread mechanisms except for local spread were disabled. The following local spread settings were used: local spread baseline probability 0.048, multiherd baseline probability 0.096, detection weight 0.5, local spread radius 3 km. The minimum, mode and maximum number of new infections in animals in herds that were the recipient of local spread infection was 1, 2, and 5, respectively.

A raster surface was then generated to represent the distance of any given point in the study area from the location of the source herd. The point locations of infected herds were then superimposed on this raster surface and the rhohat procedure (Baddeley et al., 2012) implemented in the contributed R package spatstat (Baddeley and Turner 2005) used to quantify the density of (local spread) infected places as a function of distance from the seed herd.

Results

Figure 3 is a point map showing the location of the herd population at risk, the seed herd and herds infected by local spread after three simulation days.

Figure 4 is a rhohat plot showing the density of herds infected by local spread from the source herd as a function of distance from the seed herd.
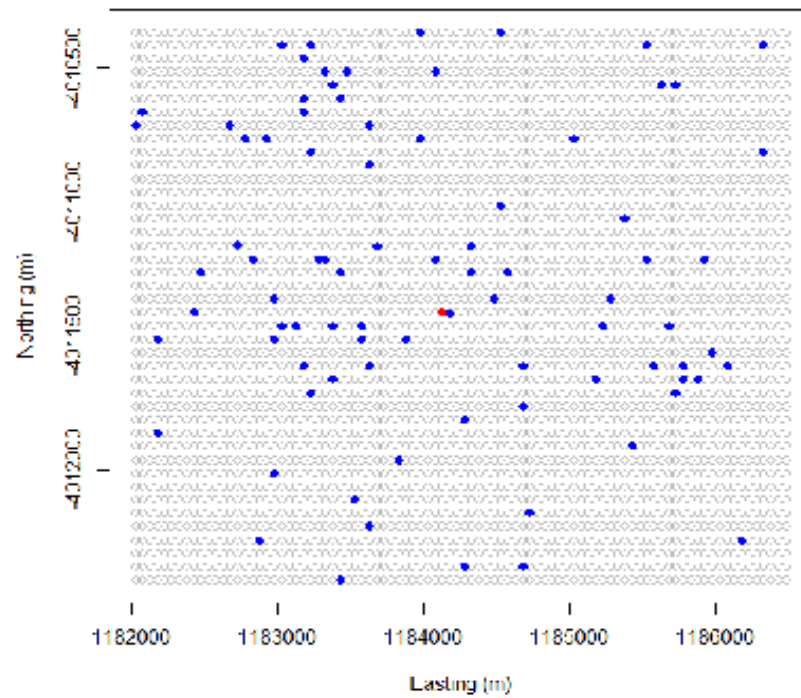
10

Figure 3: AADIS simulations to verify local spread of infection. Key: ○ uninfected herds; ● the seed herd; ● herds infected by local spread after three simulation days.
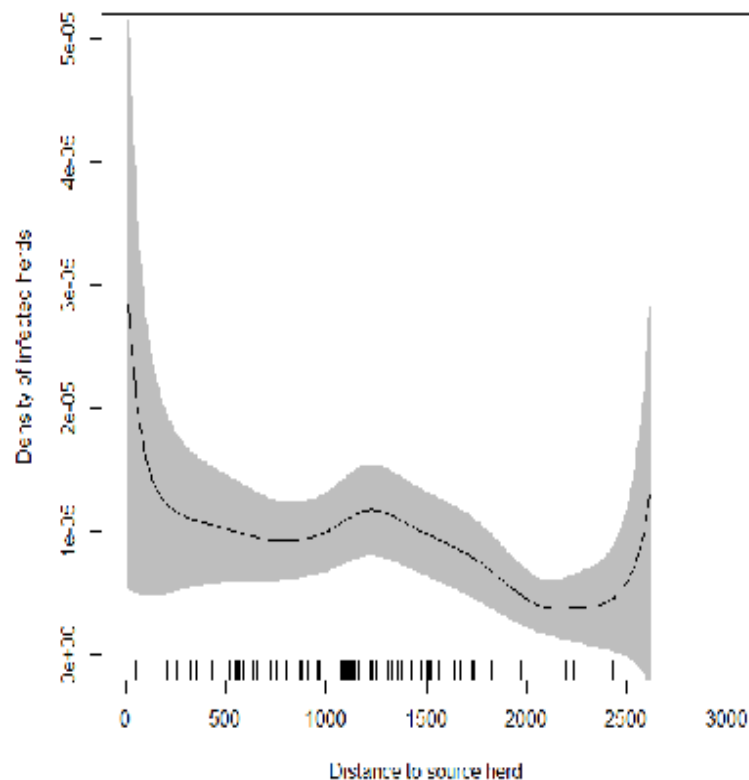
11

Figure 4: AADIS simulations to verify local spread of infection. rhohat plot showing the density of local spread infected herds (expressed as the number of infected herds per square metre) as a function of distance (in metres) from the seed herd. The shaded area shows the uncertainty around the point estimate of infected herd density as a function of distance from the seed herd.

Conclusions

Figure 4 shows a relatively high density of local spread infected herds at relatively short distances from the seed herd, with a decline in local spread infected herds as the distance from the seed herd increases. Further analyses are required to determine how closely Figure 4 matches the probability of local spread transmission function implemented within AADIS.

Windborne spread
Methodology

One hundred iterations of the AADIS_PHASE1 scenario were run for 200 simulation days starting on 1 May 2015. All spread mechanisms except windborne were disabled. A single seed herd (109051) initiated the epidemic.

The AADIS log file was then queried to retrieve all windborne spread infections arising from the seed herd. A raster surface was then generated to represent the distance of any given point in the study area from the location of the source herd. The point locations of windborne spread infected herds were then superimposed on this raster

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surface and the rhohat procedure (Baddeley et al., 2012) implemented in the contributed R package spatstat (Baddeley and Turner 2005) used to quantify the density of (windborne spread) infected places as a function of distance from the seed herd. This analytical approach was used for each of the three windborne spread mechanisms implemented in AADIS (linear, exponential 1, and exponential 2).

Results

Rhohat plots showing the density of windborne spread infected herds as a function of distance from the seed herd are shown in Figure 5. For each of the three spread mechanisms implemented in AADIS peak density of windborne spread infected herds occurred 4 to 5 km from the source herd. The density of infected herds was greatest for the linear windborne spread mechanism, followed by exponential 2, then exponential 1.
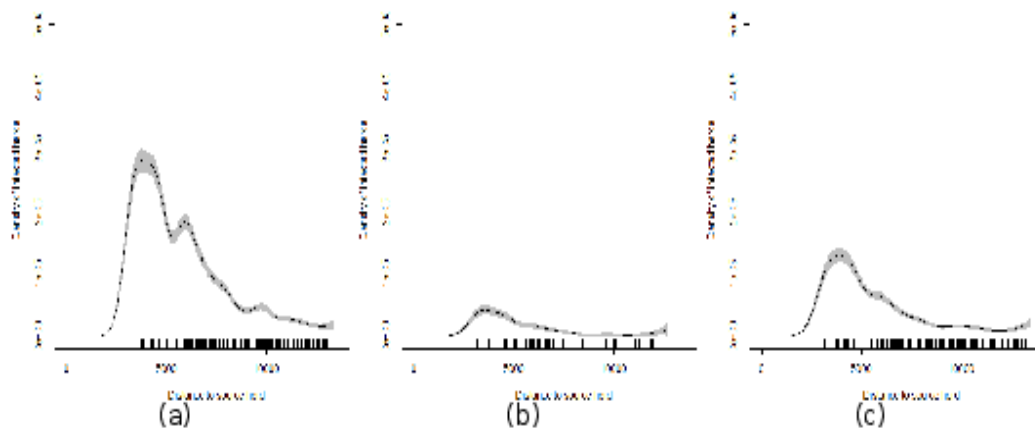

Figure 5: AADIS simulations to verify windborne spread of infection. Rhohat plots showing the density of windborne spread infected herds (expressed as the number of infected herds per square metre) as a function of distance (in metres) from the seed herd: (a) linear; (b) exponential 1; and (c) exponential 2.

Conclusions

The densities of windborne spread infected herds as a function of distance from the seed herds are biologically plausible (the density of infected herds is negligible 0 to 4 km from the source herd, reaching a maximum at 4 to 5 km and then tapering off to zero by 10 km). Further analyses are required to determine how closely the plots shown in Figure 5 match the probability of windborne transmission function implemented within AADIS.

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