Final report for CEBRA project 1608B
Vector-borne Spread of Animal Disease

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1 Executive summary

1. The Australian Government Department of Agriculture and Water Resources has invested in the development of a disease simulation modelling capability, the Australian Animal Disease (AADIS) model, to support disease preparedness and response (Bradhurst et al. 2015). While AADIS was initially developed to simulate outbreaks of foot-and-mouth disease there are a range of other disease threats it could be used for, including vector (insect) borne diseases. The aim of this project is to enhance AADIS to allow it to simulate the spread (and control) of vector-borne diseases of livestock such as bluetongue which is spread by *Culicoides brevitarsis*.

2. This project combines a one-year CEBRA project with a three-year PhD research programme. The first year of the project, including the CEBRA component, focussed on development of: (a) the facility to import data from an external source into AADIS to represent vector abundance; and (b) the facility allowing users to estimate insect vector abundance directly within AADIS. Our intention here was to provide decision makers with flexibility. Simulation of vector distribution dynamics within AADIS will allow deployment of models to assist rapid decision making at the national level. Provision of a facility that permits the importation of spatial grids developed using third party statistical tools allows subject matter experts to develop (and then deploy) their own vector distribution models better suited to support decision making at finer spatial scales. A hypothetical vector with similar characteristics to *C. brevitarsis* was used as a case study for the AADIS vector module development.

3. The *C. brevitarsis* distribution estimates developed external to AADIS were based on the published work of Kelso & Milne (2014) with estimates of long distance dispersal of midges simulated using the Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT) model (Stein et al. 2015).

4. The prototype AADIS vector module used the existing AADIS grid to represent the distribution of the hypothetical culicoides vector and a logistic growth equation to represent within-cell vector population dynamics. Jump and diffusion pathways were defined based on existing pathways in the AADIS agent-based model. The AADIS vector module was calibrated using data from the National Arbovirus Monitoring Programme.

5. The following remaining tasks will be completed during the three year PhD programme: (a) verify and validate the AADIS vector module as a means for estimating insect vector abundance; (b) verify and validate the Kelso & Milne (2014) HYSPLIT *C. brevitarsis* modelling approach described in this report; (c) provide guidelines for those developing vector abundance maps external to AADIS on how to numerically express vector abundance so that it is in a format suitable for use by AADIS; and (d) develop appropriate program logic to allow an infectious agent to spread within the vector population and to allow transfer of infection from the vector population to a livestock population at risk.

2 Abbreviations

AADIS	Australian Animal Disease model
AKAV	Akabane virus
BEFV	Bovine ephemeral fever virus
BT	Bluetongue
BTV	Bluetongue virus
CEBRA	Centre for Excellence in Biosecurity Risk Analysis
EBM	Equation-based model
EAD	Emergency Animal Disease
ELISA	Enzyme-linked immunosorbent assay
FMD	Foot-and-mouth disease
GUI	Graphic user interface
LGA	Local Government Area
NAMP	National Arbovirus Monitoring Program
NDVI	Normalised Difference Vegetation Index
PCR	Polymerase chain reaction
SLA	Statistical Local Area
VNT	Virus neutralisation test

3 Introduction

A key component of managing emergency animal disease (EAD) incursions, and minimising their economic impact, is timely and effective decision making. This requires a good understanding of the potential transmission and control of EADs under local conditions, something which is difficult to achieve for diseases that have not recently occurred in Australia. Foot-and-mouth disease (FMD) is recognised as the single greatest disease threat to Australia's livestock industries (Mathews 2011) and the Australian Government Department of Agriculture and Water Resources has invested in the development of a new modelling capability — the Australian Animal Disease model (AADIS) — to support FMD preparedness and response (Bradhurst et al. 2015). However, there are a range of other disease threats that Australia needs to be prepared for. In particular, vector-borne diseases pose significant challenges due to the involvement of insect vectors which are free-ranging and strongly influenced by weather and landscape factors. Vector-borne pathogens are particularly sensitive to climatic conditions due to their dependence on vector survival and reproduction, biting and feeding patterns, pathogen incubation periods, and the efficiency of pathogen transmission among multiple hosts. Climate change adds complexity and uncertainty to human and animal health issues through modifications in vector, reservoir, and pathogen lifecycles (Patz & Hahn 2013).

A number of vector-borne diseases have been spreading either regionally or globally, or have been recognised for the first time in recent years. These present risks to Australia that could be studied with the aid of an appropriate disease simulation model. For example, in 2006, Europe experienced an outbreak of bluetongue virus serotype 8 (BTV-8) in The Netherlands, Belgium and Germany where the virus had not previously occurred. In subsequent years, larger outbreaks occurred in more countries, suggesting that the virus had overwintered in indigenous palearctic *Culicoides* species that were not thought to be competent vectors. There was also spread across the English Channel into Norfolk and Suffolk in the east of Great Britain (Gloster et al. 2008). Another virus transmitted by culicoides midges is Schmallenberg virus, an orthobunyavirus first isolated in Germany in late 2011 (Wernike et al. 2014) that causes an arthrogryposis-hydrancephaly syndrome in lambs and calves.

African swine fever has been spreading in eastern Europe since 2007 when it was introduced to Georgia, though the tick vector is absent in that region and spread is by direct transmission (Cisek et al. 2016). In recent years lumpy skin disease has been spreading in the Middle East, Turkey and into southern Europe (Tasioudi et al. 2016). The virus is spread by biting insects by mechanical transmission, so it is not strictly speaking a vector-borne disease. However, the role of biting flies in transmission could be represented in a model in a similar way to a true vector-borne disease. Public health examples include chikungunya, which has been spreading in the Caribbean, Americas and Pacific in recent years (Wahid et al. 2017), Zika virus, currently spreading in the Americas and the Caribbean (Song et al. 2017), and yellow fever virus, which re-emerged in Angola in 2015 with cases exported to neighbouring countries and as far afield as China (Ahmed & Memish 2017).

In Australia, bluetongue remains an important disease for trade in animals and animal products, with ongoing active surveillance to support zoning for trade purposes (Animal Health Australia 2016). Changes to the distribution of the vector or introduction of a new, pathogenic, strain of the virus may lead to clinical cases of bluetongue. This threat was the main driver for this project to develop a vector disease modelling capability within AADIS. This capability will inform objective decision making around control and/or eradication efforts in the event of an outbreak. Australia has preparedness

planning documents including a disease strategy manual that outlines agreed policy for managing bluetongue disease (Animal Health Australia 2015). Disease simulation studies can help to refine these policies even without the experience of an actual disease outbreak.

Currently there are no national-scale modelling tools combining vector populations and disease simulation that are parameterised for Australia. However, there is a disease simulation tool, AADIS, parameterised with Australian herd and other data that can simulate the spread of foot-and-mouth disease. AADIS is a spatial stochastic disease simulation model with a hybrid, asynchronous architecture (Bradhurst et al. 2015). It combines an equation-based within-herd disease spread model with an agent-based between-herd disease spread model, with all components operating independently but simultaneously. A grid-based spatial indexing system enables spatial data to be incorporated without the need for a Geographic Information System. This maximises computational efficiency, allowing simulations involving large datasets to be carried out rapidly on a desktop computer. The existing AADIS architecture provides many of the components necessary for simulation of a vector-borne disease of livestock. With some adaptations, the AADIS model could become an integrated tool for simulating vector-borne livestock diseases. The key requirements of the final product are that it is flexible enough to model different types of vectors and infectious agents, it adequately represents the vector population and infection dynamics and can operate at a national scale whilst remaining sufficiently computationally efficient to operate on a desktop computer.

This project combines a one year CEBRA project with a three year PhD research programme. The first year of the project, including the CEBRA component, focussed on representing vector population dynamics through a simulation modelling environment. The PhD programme will build on this work in subsequent years, with additional modules to represent the infection dynamics of vector-borne agents such as bluetongue virus, and spread of these agents from vectors to livestock and between herds in the existing model architecture.

4 Literature review

4.1 Vector-borne diseases of animals

Arthropod vectors and the diseases they transmit negatively impact on the health and productivity of humans, domestic livestock and wildlife in most parts of the world (Gubler 2009). The most common vectors are arthropods which include flies (mosquitoes, midges, black flies, sand flies and tsetse flies), ticks, fleas, and lice. Many of the important pathogens carried by arthropod vectors are viruses (arboviruses) and these are the most important categories of emerging pathogens in human and domestic animals worldwide (Contigiani et al. 2017). The number of arthropod-borne infections occurring each year and the geographical extent of affected areas is increasing due to a number of factors including climatic change, urbanisation and changing patterns of travel and trade (Jones et al. 2008).

Approximately 500 arboviruses have been listed (Karabatsos 1985), however, only 50 are pathogenic in humans and/or animals (Contigiani et al. 2017). These include arboviruses belonging to the families Asfarviridae, Bunyaviridae, Flaviviridae, Orthomyxoviridae, Rhabdoviridae, Reoviridae and Togaviridae, as listed in Table 1 (Contigiani et al. 2017). An overview of the most important arboviruses affecting animals worldwide is provided in Table 2. Arboviruses are passed from a viraemic host when the insect vector feeds on the host. Within the insect vector virus replication occurs (biological transmission) allowing the virus to be passed to an uninfected host the next time feeding occurs (Weaver & Barrett 2004). A number of factors influence the ability of an arthropod to transmit a disease agent. For example, the ability to transmit a pathogen biologically differs greatly among arthropod species, and even among strains within a species (Gubler 2009). As an example, within a single mosquito species, there are species strain differences influencing the susceptibility to infection and how well a virus can replicate within the vector's body. Because these characteristics are genetically controlled, vector competence changes over time as a result of selective pressure (Gubler 2009).

There are many arboviruses endemic in domestic livestock populations in Australia, particularly in the tropical north (Geoghegan et al. 2014). The main arboviruses of concern according to the National Arbovirus Monitoring Program (NAMP) are: Orbiviruses (bluetongue, epizootic haemorrhagic disease); Bunyaviruses (Akabane, Aino) and Rhabdoviruses (bovine ephemeral fever). Ross River, Barmah Forest, Murray Valley encephalitis, Japanese encephalitis and West Nile (Kunjin strain) viruses cause disease in humans (Geoghegan et al. 2014). Sporadically, outbreaks of dengue fever in Australia occur due to the arrival of overseas travellers incubating the disease (Van der Saag et al. 2015). Bluetongue and Akabane viruses are transmitted by culicoides biting midges (Geoghegan et al. 2014, Mellor et al. 2008).

Culicoides are among the world's smallest haematophagous flies (1-3mm). More than 1400 culicoides species have been identified and they are found in most parts of the world except for Antarctica, New Zealand, Patagonia and the Hawaiian Islands (Mellor et al. 2008). The life cycle of *Culicoides* includes four larval stages, a pupa stage and an adult stage. Each of the immature stages of the culicoides life cycle require free water or moisture and they can be found in various habitats including pools, streams, animal dung, saturated soil and rotting fruit (Blanton & Wirth 1979, Wirth & Hubert 1989). Adult females are obligate blood suckers (males are not) and they are crepuscu-

lar with their main period of activity occurring around sunset and sunrise (Mellor et al. 2008). In general, female flight activity is mainly to mate, seek a blood meal or seek oviposition sites (Mellor et al. 2008, Lillie et al. 1981). Culicoides dispersal is short and typically one to two hundred metres (Kettle 1995) although on some occasions it can be up to 2 to 3 kilometres (Lillie et al. 1981). With the assistance of the wind culicoides dispersal can reach up to hundreds of kilometres (Sellers et al. 1977). Climate plays a major role in allowing culicoides to complete their life cycle and the extent of their flight activity. For example, the activity of midges ceases if environmental temperatures are less than 12.5 °C (Bishop et al. 1996).

In Australia approximately 250 *Culicoides* species have been reported (Animal Health Australia 2015) though only a small number have been shown to be capable of transmitting BTV and AKAV. *Culicoides brevitarsis* is the most widespread and is capable of transmitting both BTV and AKAV. Other *Culicoides* species that can transmit BTV (with different efficiencies) include *C. fulvus*, *C. actoni* and *C. wadai* (Bishop et al. 1995, Eagles et al. 2013). *C. fulvus* is the most efficient vector (Standfast et al. 1984), however, this species has little involvement in disease transmission because it is restricted to areas with high summer rainfall and does not occur in the drier sheep rearing areas of Australia. On the other hand, *C. brevitarsis* is an inefficient vector (Standfast et al. 1984) but is widely distributed and more abundant than either *C. fulvus* and *C. wadai*. It also has a distribution similar to that of BTV in cattle, and for these reasons is considered to be the main vector for BTV in Australia (Mellor et al. 2008).

BTV is generally regarded as an emerging disease and 27 serotypes have been reported worldwide (Maan et al. 2012) of which 12 have been isolated in Australia (Johnson & Hoffmann 1992, Animal Health Australia 2015). While some BTV strains are endemic in Australia, they have a limited and well-documented distribution (Animal Health Australia 2017). Exotic strains could be introduced as a result of movement of viraemic animals, inoculation of infected, imported biological products into ruminants, use of attenuated vaccines or wind dispersal of infected midges from neighbouring countries (Animal Health Australia 2015). Of these, all but wind dispersal are very unlikely as importation of live animals, biological products and vaccines into Australia are regulated to reduce the risk of entry of new diseases. An incursion of a new serotype of BTV to Australia could have a severe impacts on animal health if it causes high rates of mortality in sheep or cattle.

4.2 Bluetongue

Bluetongue is an arbovirus disease of ruminants (MacLachlan 2011). Bluetongue primarily causes severe disease in sheep but other ruminants, such as cattle and buffalo, can become infected but do not usually show clinical signs (St George et al. 2001). Spreull (1905) was the first to provide a comprehensive description of the disease, calling it malarial catarrhal fever. Spreull described the condition as one in which there was high fever lasting 5 to 7 days after which time distinctive lesions appeared in the mouth and on the tongue (Spreull 1905). In 1944 du Toit identified *Culicoides* spp. as the insect vector for bluetongue (du Toit 1944). Bluetongue was classified as a disease of cattle up until 1943 when the disease was responsible for the death of 2500 sheep in Cyprus (Gibbs & Greiner 1994, Gambles 1949). In 1952, bluetongue virus (BTV) was isolated for the first time from sheep with ‘sore muzzle’ in California, USA (McKercher et al. 1953). Later the disease was responsible for high rates of mortality in sheep in outbreaks that occurred in Portugal and Spain in

1956 (Manso-Ribeiro et al. 1957). In these outbreaks mortality rates reached up to 75% in affected sheep and caused approximately 179,000 deaths over a period of 4 months. BTV was identified throughout much of the world during the second half of the 20th century and this spread justified its listing by the World Organisation for Animal Health (Gibbs & Greiner 1994).

Aetiology

Bluetongue virus belongs to the Orbivirus genus of the Reoviridae family based on its morphological and physicochemical criteria (Borden et al. 1971). The genome of BTV consists of 10 segments of double-stranded RNA and 27 serotypes are recognised internationally (Maan et al. 2012). BTV strains vary considerably in their virulence, as some can produce disease that remains subclinical whereas others can lead to severe disease with high rates of mortality (MacLachlan 2011). Serotype 8 (BTV-8) which emerged in northern Europe in 2006 (Toussaint et al. 2006) was associated with high rates of mortality and impaired production and resulted in bans on the trade of ruminants between BTV infected and BTV non-infected areas (Zientara & Sanchez-Vizcaino 2013).

In Australia, twelve of the 26 strains of BTV have been isolated (BTV- 1, 2, 3, 5, 7, 9, 12, 15, 16, 20, 21 and 23) (Animal Health Australia 2015), and most of these are distinct from those originating in Africa or the Americas and more related to those originating from Asia (St George et al. 2001).

Geographical distribution

Except Antarctica, BTV has been identified on all continents (Gibbs & Greiner 1994, MacLachlan 2010, MacLachlan & Osburn 2006, Mellor et al. 2008, Tabachnick 2003). The distribution of BTV is within the geographical distribution of various *Culicoides* spp. that are accepted as vectors of the disease (MacLachlan 2011). BTV exists in an extensive band that includes tropical, subtropical and temperate regions of the world between the latitudes of approximately 40° North and 35° South (MacLachlan & Osburn 2006). An exception to this generalisation is western North America, where the disease occurs as far as 50° North (Tabachnick 2003, Clavijo et al. 2000, Lundervold et al. 2003, Shoorijeh et al. 2010). In the outbreak of BTV-8 that commenced in Europe in 2006 the disease extended to a latitude of at least 45° North, expanding into areas of Italy, Greece, Spain, France and the Balkans (Giovannini et al. 2004, Purse et al. 2005).

The geographical distribution of BTV serotypes and their insect vectors differ remarkably throughout the world, supporting the hypothesis that specific vectors exist with specific groups of BTV serotypes and topotypes in relatively distinct global ecosystems (Gibbs & Greiner 1994, MacLachlan & Osburn 2006, Tabachnick 2003, Balasuriya et al. 2008) (Figure 1).

In 2006, BTV-8 was first identified in northern Europe and BTV-8 has now spread widely, from the Mediterranean basin to northern Europe (Saegerman et al. 2008, Conraths et al. 2009, Agren et al. 2010, Kampen & Werner 2010). The BTV serotypes that have been identified in the Mediterranean basin after 1998 (with the exception of BTV-8) have all originated in northern Africa (Purse et al. 2005). Virus incursions into Europe are thought to have occurred as a result of wind-borne spread of virus-infected vector insects, which then spread disease to ruminants (MacLachlan 2010). BTV-2, 10, 11, 13 and 17 have long occurred in areas of North America, but some 10 additional BTV

serotypes (1, 3, 5, 6, 9, 12, 14, 19, 22 and 24) have been identified in the southeast of the USA since 1998 (MacLachlan 2010, Ostlund 2010).

In Australia, most of the endemic serotypes are closely grouped and are distinguishable from those originating in Africa or the Americas (St George et al. 2001). In 1975, BTV-20 was isolated from culicoides midges trapped near Darwin in Australia (Ward 1994). Later, viruses belonging to a further eleven serotypes (1-3, 5, 7, 9, 12, 15, 16, 21 and 23) have been isolated from healthy sentinel cattle, primarily in the Northern Territory (Animal Health Australia 2015).

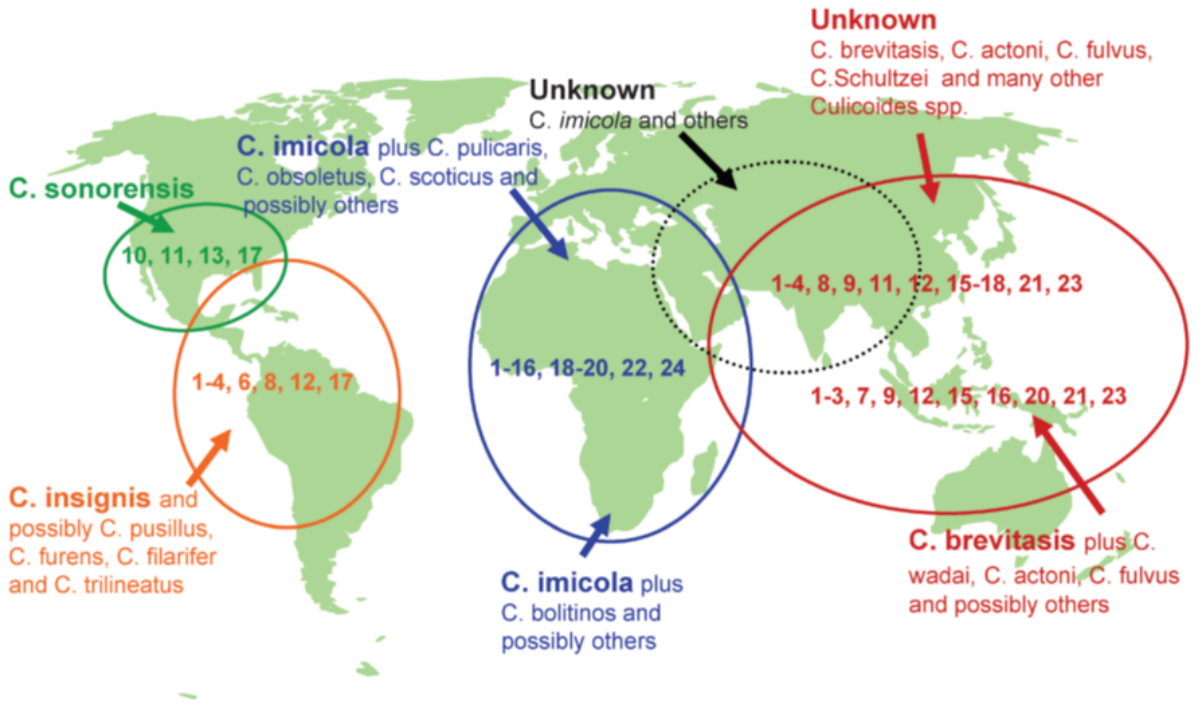


Figure 1: Global distribution of bluetongue virus serotypes and (known) *Culicoides* spp. species in different regions of the world. Reproduced from Tabachnick (2003).

Pathogenesis

The pathogenesis of BTV infection in sheep and cattle is similar (Pini 1976, Mahrt & Osburn 1986, MacLachlan 1994, Darpel et al. 2009). Even though the disease is often subclinical in ruminants, some serotypes are associated with high mortality rates, particularly in sheep (MacLachlan 2011). Infection occurs in a susceptible host after a bite from a BTV-infected culicoides midge, where the virus travels to regional lymph nodes and undergoes replication (Pini 1976, Barratt-Boyes et al. 1995). The virus then circulates to other organs where replication occurs primarily in mononuclear phagocytic and endothelial cells, lymphocytes and other cell types (Mahrt & Osburn 1986, Darpel et al. 2009, MacLachlan et al. 1990, Ellis et al. 1993, Barratt-Boyes & MacLachlan 1994). Viraemia is highly cell associated (red blood cells and platelets) and is prolonged but not persistent in ruminants (Barratt-Boyes et al. 1995, Singer et al. 2001, Bonneau et al. 2002, Melville et al. 2004). The presence of virus in red blood cells facilitates transfer of infection to insect vectors that feed on a viraemic host (Brewer & MacLachlan 1992, Barratt-Boyes & MacLachlan 1995, Bonneau et al. 2002). Most BTV-infected animals, particularly those in BTV-endemic areas develop mild or no obvious clinical signs of disease (Gibbs & Greiner 1994, MacLachlan & Osburn 2006). Outbreaks of BT mainly occur when virus is introduced into areas with naïve ruminant populations (MacLachlan 2010). Infected sheep develop oral erosions and ulceration, lameness and coronitis, weakness and depression, and facial oedema (Spreull 1905, MacLachlan et al. 2008). In acute cases, the lips and tongue become swollen and small red or purple haemorrhagic patches appear in the mouth, nose and the conjunctival linings (Animal Health Australia 2015). Mortality rates are variable in susceptible sheep, reaching up to 70%. Deaths continue to occur up to five weeks after the onset of clinical signs in the index case (Animal Health Australia 2015). It is not clear why virulent strains of BTV produce disease in sheep but not in cattle (Spreull 1905, Barratt-Boyes & MacLachlan 1995, Russell et al. 1996).

Diagnosis

Reliable and rapid confirmation of the presence of BTV infection and serotype differentiation is important at the start of an outbreak. Early laboratory confirmation of BTV serotype is based on the isolation and amplification of virus by inoculation of washed and lysed sheep red blood cells or homogenised tissue into embryonated chicken eggs and/or cell cultures, and the subsequent serotyping of the virus using the virus neutralization test (VNT) (Bréard et al. 2004). Indirect enzyme-linked immunosorbent assay (ELISA) is used for serogroup confirmation of BTV however it should be noted that ELISA is not suitable for the detection of BTV soon after infection because of the relatively low concentration of BTV antigen associated with the red blood cell membrane (Bréard et al. 2004). Real time polymerase chain reaction (PCR) methods have been developed for rapid detection and serotyping of BTV (Bréard et al. 2003). Different techniques have been used to detect antibodies against BTV, such as agar gel immunodiffusion, haemagglutination inhibition, complement fixation and ELISA, which are serogroup-specific. At the time of writing, only agar gel immunodiffusion and competitive-ELISA are recommended tests for BTV by the OIE (Bréard et al. 2004).

Control

A range of measures can be used to limit the spread of BT once an outbreak occurs. Traditional control measures include rapid slaughter of infected animals to prevent them from acting as a source of disease for insect vectors, imposing restrictions on the movement of animals from one location to another, and housing susceptible animals during periods of high insect activity to minimise exposure to biting insects (Spreull 1905, Bréard et al. 2004). The use of protective housing is often impractical for extensive livestock production systems, and the utility of stabling is dependent on the degree of endo/exophilic activity exhibited by the vector species resident in affected areas (Cheah & Rajamanickam 1991, Doherty et al. 2004, Napp et al. 2011). Insecticides applied to susceptible animals may be used to eliminate midges, but they are typically not effective if they require the vector to first feed on the animal, as any feeding midge would have the chance to transmit BTV before succumbing to insecticide (MacLachlan & Mayo 2013).

Animal movement restrictions are important for the control of BT outbreaks, but they are often associated with a range of negative economic impacts (Mellor et al. 2009). For example, during a BTV-8 outbreak in Italy, cessation of movement of livestock from Sardinia to Tuscany led to social unrest and a potential animal welfare crisis that was only resolved by a mass vaccination campaign that allowed animal movements to resume (Giovannini et al. 2004). Arboviral diseases such as BT are not easily resolved by culling because of the high rate of subclinical infections in wild and domestic animals, and infected midges have the ability to disseminate widely (MacLachlan & Mayo 2013).

While vaccination is often the most efficient way of controlling BT outbreaks it is important that the vaccine used for outbreak control matches the circulating BTV serotype (Mellor et al. 2009, Zientara et al. 2010). Currently, only attenuated (modified live virus) vaccines are commercially available and used to prevent BT in sheep.

Vector-based control strategies are used to reduce or eradicate populations of either adult or immature stages of culicoides and could theoretically be used to control the disease and limit BTV spread. Vector control is challenging due to the fact that different species of midges predominate in different areas, and relatively little is known how individual species vary in terms of their host feeding preferences, the frequency with which they enter livestock stabling facilities and the location and type of their preferred breeding sites (MacLachlan & Mayo 2013).

5 Methods

5.1 Workshop

At the initiation of the project a workshop was held to gain advice and expertise from identified experts in bluetongue virus biology in Australia, the entomology of key vector species, disease control policy and computer simulation modelling. The aim of the workshop was to better define the requirements of the final product, and gain insights into how this could best be achieved. A copy of the workshop report is included in Appendix 1.

The key outcomes of the workshop were:

1. The project should initially focus on simulating seasonal distribution of *C. brevitarsis* and a hypothetical Simbu group virus for which this species is moderately to highly competent. This would provide a foundation for further development of vector-borne disease modelling capability within AADIS.
2. *C. brevitarsis* distribution and density would be represented by a 'suitability index' using the spatial grid capacity of AADIS to capture climatic and geographical features that influence vector population dynamics. The grid would also be used to model the spread of the vector by diffusion and wind-assisted dispersal.
3. The study scenario to be used for initial evaluation would involve a novel introduction of a virus that is pathogenic to sheep into the Darling Downs area of Queensland (e.g. BTV-16 introduced from the Northern Territory). The effectiveness of movement restrictions would be investigated by running simulations with and without movement restrictions.

5.2 Approach

Two capabilities for representing vector population dynamics were developed during this project. The first was the ability to import series of raster data (generated externally to AADIS) that define vector activity over space and time. The second capability was the explicit simulation of vector population dynamics within AADIS. Ultimately, the AADIS vector module will be able to represent any vector species for which there is adequate information on ecological requirements and life cycle. For this project, a culicoides midge was used as an example vector. Parameters were based on available information on *C. brevitarsis* in Australia where this information was readily available, or other members of the genus, where necessary. It was agreed that, given the limited time available for this project, the focus would be on the necessary changes to the software architecture rather than pursuing absolute accuracy of the parameter values. These will be refined in the future once the software architecture is in place.

When simulating FMD, the AADIS grid is simply a static store of climate data that informs the airborne spread of FMD. In order to simulate the spatial distribution of a vector population the AADIS grid was extended to operate as a geographic automata. This approach captures dynamic changes in vector populations, with conditions in any given cell potentially influencing conditions in neighbouring cells. There are three aspects of modelling a vector population: (1) distribution, captured by means of cell states representing the presence or absence of the vector; (2) density, captured by means of an equation-based growth model embedded in each populated grid cell; and (3) spread, represented by diffusion and jump pathways (analogous to the direct, indirect, local and airborne pathways used to model the spread of foot-and-mouth disease).

5.3 Vector abundance maps generated by AADIS

Assumptions and exclusions

Some simplifications and assumptions were made in order to represent the vector population biology within the AADIS model. Firstly, the use of the geographic automata simplified the distribution of the population to a gridded representation, rather than continuous variation in the landscape as occurs in the real world. This has the effect of giving the entire land area covered by the grid cell the same state, ignoring any fine-scale variation within the grid cell. It also creates an artificial truncation at the edge of the grid cell when the neighbouring cells have a different state. However, a grid is the most appropriate available representation for continuous spatial variables and experts present at the August 2016 workshop agreed that this was a suitable approach.

Secondly, the population of midges in each raster cell was represented on a relative scale [0,1], rather than as absolute counts. We assumed that the maximum number of midges per cell was proportional to some limiting resource. This approach was taken because of the difficulties in estimating total vector population size, even though trapping data are available (Animal Health Australia 2017). For the example culicoides vector, the limiting resource was cattle density, due to the necessity of cattle dung for the important Australian species *C. brevitarsis* to breed.

A decision was also made not to explicitly model all population lifecycle stages due to the additional computational requirements. The adult vector population was explicitly represented, but the immature stages were represented only implicitly in the behaviour of the cells when conditions become unsuitable for adult survival. For the culicoides example, larvae survive longer than adults when conditions are unsuitable, so population decay under unsuitable conditions reflects the survival of the larvae rather than the adults.

The potential effects of competition with other insect species, and the interactions with other circulating viruses that may modulate vector competence for the pathogen of interest were not considered.

Cell states and starting conditions

The raster cell size of the AADIS grid is user definable. For this project a raster cell size suitable for making inference at the national level of 0.09×0.09 decimal degrees was used.

The cell state dictates how a grid cell can behave, including the ways in which it can influence the state of other cells. Each grid cell can take only one of a number of defined states with regards to the vector population. The state that an individual cell can take is influenced by both fixed and variable characteristics of that cell; these characteristics are stored as raster data and accessed dynamically by AADIS as part of a simulation. Fixed characteristics include data such as elevation, while variable characteristics include data such as temperature. The cell state is also influenced by the state of other grid cells, for example when an infested cell spreads vectors to nearby grid cells.

The three cell states defined for the purposes of simulating vector population biology are active, quiescent and free. An active cell contains adult vectors that are feeding and breeding. A quiescent cell contains adults that are not actively feeding and breeding, or contains larvae but not adults. A

Table 1: Endemic criteria for the prototype vector model.

Variable	Setting
State: active if:	
Cattle density (km^{-2})	$>$0
Annual rainfall (mm)	$>$450
Max annual days with temperature $<$14 °C	0
State: quiescent if:	
Cattle density (km^{-1})	$>$0
Annual rainfall (mm)	$>$450
Max annual days with temperature $<$14 °C	60

free cell contains no vector lifecycle stages. An active cell becomes quiescent when environmental conditions become unsuitable. For the example culicoides vector, this occurs when the mean daily temperature is less than 13.5 °C or greater than 35 °C. A quiescent cell can become active if environmental conditions become suitable before all vectors have died due to age. For the example culicoides vector, this means the mean daily temperature is once again within the range of 13.5 – 35 °C, after less than 60 days below 13.5 °C or less than 5 days above 35 °C.

A cell may be free because vectors have not yet been introduced, because the population has expired due to prolonged unsuitable environmental conditions, or because there are no cattle present. A free cell that contains cattle can become active by introduction of vectors from neighbouring cells, assuming temperature is greater than 13.5 °C.

Each grid cell must have a state attributed at the commencement of a simulation, and at least one grid cell must have a state that signifies the presence of the vector; i.e. either active or quiescent. There are two options available:

1. One or a few cells can be manually selected as a point introduction. This approach can be used to simulate the process of invasion and establishment of maximum range for a novel vector if long simulations (for example, 50 simulation years) are run until the population stabilises.
2. Infested cells can be selected using an algorithm when AADIS initialises. This approach can be used to define endemically infested areas.

The endemic criteria for the prototype model are shown in Table 1. All grid cells not meeting the criteria specified in Table 1 are given a free state.

Population dynamics

Within-cell population growth was modelled with an embedded equation-based model (EBM), analogous to the EBM embedded in the herd structure used to represent within-herd infection dynamics

of FMD. For population growth, a logistic growth equation (Equation 1) was considered appropriate for the prototype. This is a commonly used approach to represent insect population dynamics (Daly et al. 1998) and has the advantage of simplicity. However, the model architecture has the flexibility to replace the logistic equation with another equation without disrupting other model components.

$$x(t) = \frac{1}{1 + (\frac{1}{x_0} - 1)e^{-rt}} \tag{1}$$

Where:

x = population density
x_0 = initial population density
r = population growth rate (population recruitment rate minus population depletion rate)
t = time (in days) since introduction

As a starting point for the prototype, it was assumed that under ideal conditions the vector population would peak at 10,000 times its starting value 6 weeks after initial infestation. The daily population growth rate under ideal conditions can therefore be calculated: r = 0.35. These assumptions were made to allow a functional prototype to be developed, but the validity would need to be evaluated for each specific vector that may ultimately be modelled. In some cases specific research may be required, or the value may need calibration against available datasets.

The logistic expression shown in Equation 1 was modified in the following two ways for this project. Firstly, since a relative scale was used for the vector population density, the output is multiplied by the grid cell value of the population-limiting resource. For the example culicoides vector, this is the normalised cattle density of the cell. Raw cattle density is highly right skewed (due to spatial clustering of feedlots). The normalised cattle density is calculated from the raw cattle density by multiplying by 100 (this ensures no negative values in the transformed data), taking a log base 10 transformation, and then dividing all values by the maximum (transformed) value, producing a final range between zero and one.

Secondly, the r value was modified on the basis of the mean daily temperature in the cell to account for the effects of temperature on rates of vector recruitment and mortality. For the purpose of the prototype, a lookup table was generated with adjusted r values for different mean temperatures, using the assumption that 25 °C represents ideal temperature conditions (Table 2). The derivation of the values provided in Table 2 is described in Appendix 2.

The spread of vectors from one grid cell to another was represented through an agent-based modelling approach, in which grid cells operate as agents and can influence the state of other grid cells by means of a number of pathways. This is analogous to the means by which herds may influence the infection status of other herds in the FMD model via various infection pathways.

The vector spread pathways considered were:

1. Short distance movements associated with local dispersal.
2. Longer distance movements associated with natural (e.g. wind) or man-made (e.g. transport)

Table 2: Lookup table for correcting r under ideal conditions based on ambient temperature.

Temp °C	B	g	$b-g$	Weight	r
10	0	0.205825	-0.20583	-0.33186	-0.20583
11	0	0.205825	-0.20583	-0.33186	-0.20583
12	0	0.205825	-0.20583	-0.33186	-0.20583
13	0.0766	0.21573	-0.13913	-0.22433	-0.07851
14	0.1535	0.226112	-0.07261	-0.11708	-0.04098
15	0.2304	0.236992	-0.00659	-0.01063	-0.00372
16	0.3073	0.248397	0.058903	0.094972	0.03324
17	0.3842	0.26035	0.12385	0.199689	0.069891
18	0.4611	0.272879	0.188221	0.303478	0.106217
19	0.538	0.28601	0.25199	0.406295	0.142203
20	0.6149	0.299774	0.315126	0.508093	0.177833
21	0.6918	0.3142	0.3776	0.608824	0.213088
22	0.7687	0.329319	0.439381	0.708435	0.247952
23	0.8456	0.345167	0.500433	0.806873	0.282405
24	0.9225	0.361777	0.560723	0.904081	0.316428
25	0.9994	0.379187	0.620213	1.000001	0.35
26	1	0.397434	0.602566	0.971547	0.340042
27	1	0.416559	0.583441	0.940711	0.329249
28	1	0.436605	0.563395	0.90839	0.317936
29	1	0.457615	0.542385	0.874514	0.30608
30	1	0.479636	0.520364	0.839008	0.293653
31	1	0.502717	0.497283	0.801793	0.280628
32	1	0.526909	0.473091	0.762788	0.266976
33	1	0.552265	0.447735	0.721905	0.252667
34	1	0.578841	0.421159	0.679055	0.237669
35	1	0.606696	0.393304	0.634143	0.22195
36	0.9	0.606696	0.293304	0.472908	0.165518
37	0.9	0.606696	0.293304	0.472908	0.165518
38	0.9	0.606696	0.293304	0.472908	0.165518
39	0.9	0.606696	0.293304	0.472908	0.165518

phenomena.

Based on European studies, the likelihood of 'long-distance' dispersal of *Culicoides* spp. over land is low (Sedda et al. 2012, Kluiters et al. 2013, Kirkeby et al. 2013). Bishop et al. (2004) reported that it took midges around 17 weeks to travel 100 km. Thus, from a modelling perspective, short distance dispersal is the main mechanism by which the vector spreads, with occasional longer distance dispersal events.

The state of the grid cell (active, quiescent or free) determines whether it can be a source or recipient of a vector spread event. Only an active cell can be a source, and only a free cell can be a recipient. A number of other factors influence the likelihood and nature of spread. These include:

- Vector population density: with dispersal from grid cells with higher density areas to those with lower density.
- Temperature: influences both the survival and activity of vectors, and thus the likelihood of voluntary movement or wind-assisted movements.
- Wind speed: voluntary flight is maximal at lower wind speeds, and vectors cease voluntary flight when winds become too strong. At lower wind speeds vectors can take advantage of winds to disperse over longer distances. For the example culicoides vector, the threshold wind speed used was 8 km.hr^{-1}. When this is exceeded, the vector ceases local flight (Bishop et al. 2000).
- Terrain: influences the speed at which dispersal can occur. Dispersal is fastest on relatively flat terrain and slower with increasing elevation (Bishop et al. 2000).
- Cattle density: vectors will disperse to seek resources such as hosts and breeding sites. For the example culicoides vector, cattle provide both.

Local dispersal

Local dispersal was based on the existing AADIS diffusion pathway, which uses a spatial kernel. The pathway can only operate when weather conditions are suitable, including wind speed of less than 8 km.hr^{-1}.

All free grid cells within a user-specified distance of a source cell are at risk. For example, if the user specifies a distance of 30 km, three layers of cells around the source cell are at risk. These cells are selected and if vectors are not present but they are suitable for vector colonisation then a stochastic process is used to determine which (if any) of the at-risk grid cells become infested from that source cell. This process is described in detail in Appendix 2. Care must be exercised in selecting a local dispersal distance that the processes represented at that scale do not overlap with those represented by the long distance dispersal pathway.

Table 3: Input data for the AADIS vector model.

Data	Format	Source
Cattle density	Number of animals/holdings per LGA	Australian Bureau of Statistics 2011
Temperature	Point locations (weather stations)	Bureau of Meteorology 2014
Wind speed	Point locations (weather stations)	Bureau of Meteorology 2014
Wind direction	Point locations (weather stations)	Bureau of Meteorology 2014
Rainfall	Raster data	Bureau of Meteorology 2014

Long distance dispersal

Long distance spread is represented by means of a jump pathway, which can cover any type of longer distance dispersal event. For an insect vector, this could involve wind-borne spread only, or could include both natural and anthropogenic activities. This is an important consideration as it will influence how the pathway is parameterised. In the prototype, longer distance dispersal was parameterised for a natural phenomenon mimicking wind-borne dispersal events. Long distance spread events have a low probability, so for modelling purposes they were represented as discrete events characterised by:

- Frequency of occurrence: expressed as a daily probability.
- Direction: this could be random or directed, but in the prototype is directed based on wind direction.
- Distance: defined by a beta pert distribution.

The pathway can only operate when weather conditions are suitable, including temperature of at least 18 °C and wind speed of less than 8 km.hr^{-2}. A higher threshold temperature was used for long-distance dispersal than local dispersal because it was considered that a greater degree of activity would be needed for culicoides vectors to move far enough from their hosts to be moved by wind currents. This would not apply if the jump pathway was being used to represent movements of vectors by vehicle, as may occur when cattle are trucked from an infested to a free area.

If conditions are suitable, a stochastic process is used to determine whether a spread event occurs and if so, which grid cells become infested from that source cell. This process is described in detail in Appendix 2.

Data sources and processing

Details of input data for the AADIS vector model are shown in Table 3.

The number of cattle and number of properties with cattle within each statistical local area (SLA) were obtained from the Australian Bureau of Statistics 2010 – 2011 Agricultural Census. A map of

grazing areas within Australia was produced by starting with the Land Use map of Australia. Land parcels of the following land use types were selected and saved as individual digital map files:

- grazing native vegetation
- grazing improved pastures
- irrigated grazing
- dairies
- feedlots
- irrigated sown grasses
- rural residential

These individual files were combined into a single file and this file was assumed to represent all grazing areas within Australia and was further assumed to be the only areas in which cattle could be located. All objects in the layer were combined into one polygon.

The map of SLAs map was trimmed by overlaying the map of grazing areas and using the delete outside function of MapInfo to remove all areas of the SLAs that were not grazing land.

The remaining area of each SLA was calculated automatically in MapInfo and combined with the number of cattle to produce a cattle density for each SLA. The map of SLAs was overlaid with the existing AADIS grid and a column for the cattle density in each grid square added to the AADIS grid.

A raster map of average annual rainfall was downloaded from the Bureau of Meteorology website. The raster was opened in MapInfo Pro Extended (Pitney Bowes, Stamford, Connecticut) and overlaid with a set of points corresponding to the centroids of each grid cell in the AADIS grid. The point interrogate function was used to add a column with the annual average rainfall to the set of centroids. These centroids were then overlain with the AADIS grid and the grid updated to include a column with the average annual rainfall for that grid cell using the MapInfo 'within' function.

Temperature data was processed by calculating the mean weekly temperature as the sum of the weekly mean maximum and weekly mean minimum temperatures divided by two. This information already existed within the AADIS grid from development of the original AADIS FMD model. Each grid cell sourced temperature data from the nearest weather station.

Wind speed was converted to a weekly probability of suitability. This is the proportion of all readings during a week that were suitable for culicoides flight (i.e. wind speed 0 – 8 km.hr^{-1}). Again, wind direction and speed already existed within the AADIS grid from development of the original AADIS FMD model. Each grid cell sourced wind data from the nearest weather station.

Within the AADIS grid, all cells outside of the Australian mainland have a default value of -99 for each parameter.

Software updates

The implementation of this pathway in the AADIS model required a large number of updates to the existing software. These are described in Appendix 3.

Prototype calibration

Vector trapping data from the National Arbovirus Monitoring Program (NAMP) (Animal Health Australia 2017) was sourced from on-line records with permission of Ian Langstaff, Surveillance Manager, Animal Health Australia.

The following validation studies were completed with AADIS version 2.39. The vector spread component of AADIS was installed with a set of default parameters.

All studies were conducted using the graphical user interface (GUI) for ease and so that changes were not permanent. Initially changes were made to one parameter at a time and the model run for 575 days (1 September to 30 March) to allow a short burn-in period followed by a complete cycle of the seasons to observe the impacts of the winter quiescent period.

The aim of this process was to examine whether AADIS could closely parallel historical records of the presence or absence of *C. brevitarsis* in various locations in Australia. To do this, the model parameters were varied to find a parameter set that best mimics the historic NAMP insect trap results. Particular emphasis was placed on the New South Wales (NSW) coastal region where the activity of *C. brevitarsis* is seasonal and is known to vary from year to year.

Other vectors

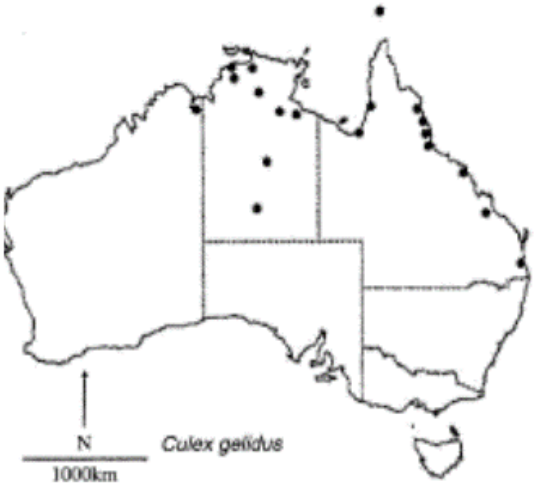
To assess the flexibility of the new AADIS vector module, further analyses were carried out to assess whether other insects could be adequately represented by the model. The two examples selected were *Culex gelidus* and *Haematobia irritans*. In the absence of information about the spread parameters for other species of insects, AADIS cannot predict their speed of spread. However, the model can still be used to visualise the final extent of invasion of an insect species if the climatic requirements of that insect are known.

Culex gelidus

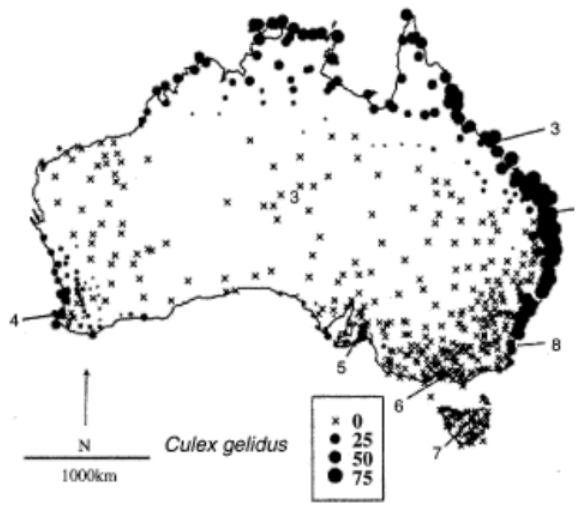
The following information on the mosquito, *Culex gelidus* was gathered from various sources. A minimum annual rainfall requirement of 725 mm per annum was estimated by comparing the known distribution of *C. gelidus* from Williams et al. (2005) with a world total annual rainfall map.[1] The quiescent period was set at 90 days. There is no diapause in *Culex* spp. but females can hibernate over winter for greater than 3 months (Bailey et al. 1982). Williams et al. (2005) reported *C. gelidus* as having a low temperature threshold of 10 °C, a lower optimum temperature of 20 °C, an upper optimum temperature of 35 °C and an upper threshold temperature of 37.5 °C.

[1] www.climate-charts.com/images/world-rainfall-map.png

AADIS was run for 10,000 days starting with point introductions of *C. gelidus* in Cairns and Darwin. Other parameters were varied by trial and error to obtain a final distribution similar to that shown in (Williams et al. 2005) (Figure 2).



(a) Known *Culex gelidus* distribution



(b) Predicted *Culex gelidus* distribution

Figure 2: Map of Australia showing: (a) the known distribution, and (b) the predicted distribution of *Culex gelidus*. Adapted from Williams et al. (2005). Note that in (a) the records at Alice Springs and Katherine are associated with artificial wetlands at water treatment (sewage) plants.

Haematobia irritans

Haematobia irritans (buffalo fly) was originally introduced into the Cobourg Peninsula in the Northern Territory in 1838 (Seddon 1967) and has since spread across the north of Australia and down the east coast as far as Coffs Harbour (Williams et al. 1985). In some mild winters it can overwinter as far south as the Hastings River (Spence 2007). The reported climatic conditions for its survival include a requirement for an annual rainfall of less than 500 mm (Tillyard 1931). In warmer areas of Australia, rainfall is the limiting factor whereas in southern areas temperature is limiting. The flies are only killed by heavy frost (Tillyard 1931). However, when the temperature falls below 21 °C, the flies become sluggish (Seddon 1967) and they cannot survive if the average temperature falls below 20 °C for considerable portions of the year. They can overwinter at an average minimum temperature of 8 °C but not at 5.5 °C (Williams et al. 1985). Wellings (1994) calculated the rate of colonisation of *H. irritans* in Australia as 0.95 km per year.

The parameter settings were the subject of considerable variation through trial and error trying to mimic the endemic area shown in the maps in Seddon (1967) (Figure 3) and Williams et al. (1985) (Figure 4).

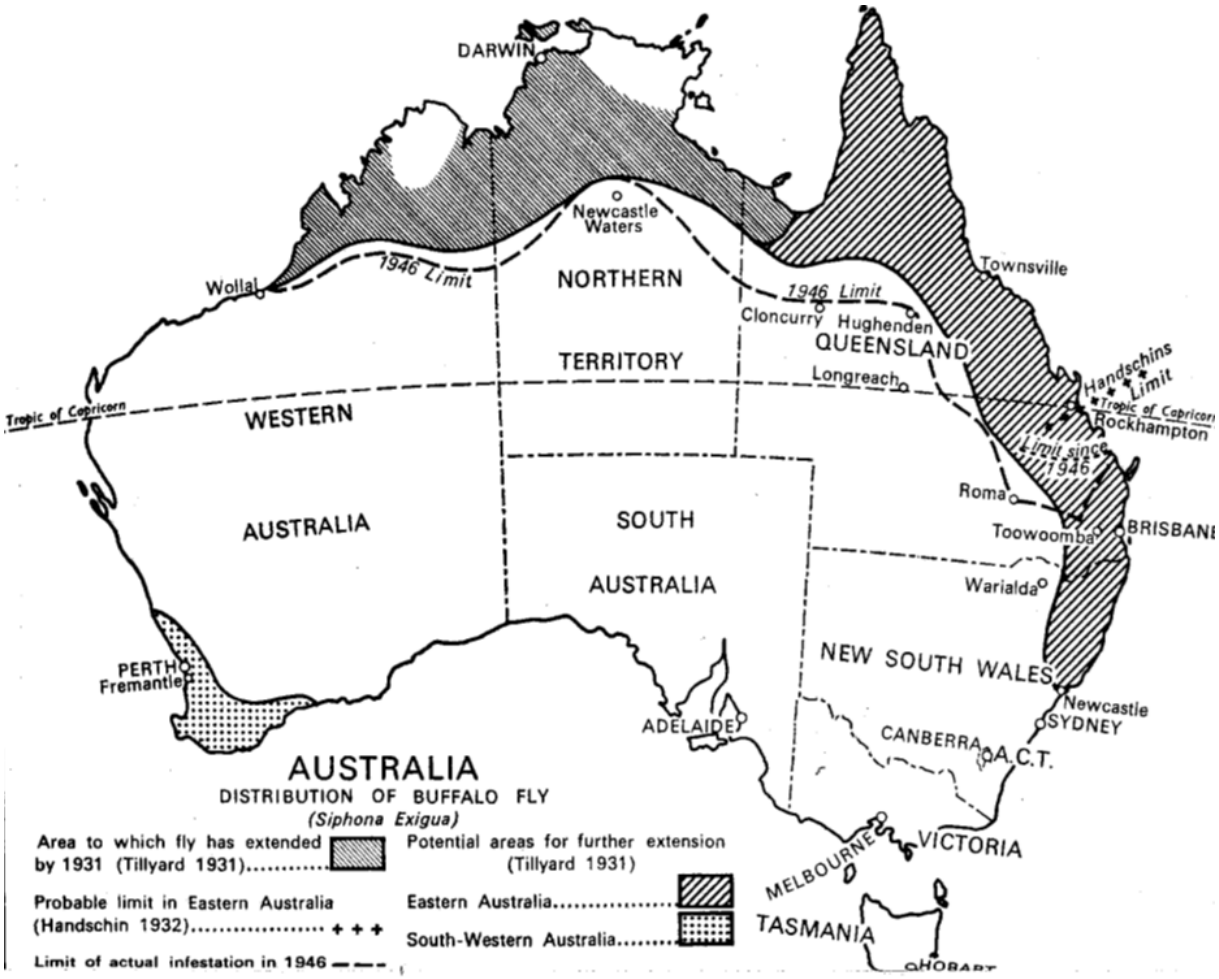


Figure 3: The known distribution, in 1931 and 1946, of buffalo fly and its predicted maximum distribution from Seddon (1967).

Changes in the geographical distribution of buffalo fly in coastal areas of eastern Australia are illustrated in Figure 1. The map shows the steady expansion of its range from Bororen, north of Bundaberg in 1974 to south of Coffs Harbour by 1982. In the three years 1976-1978 the most rapid spread occurred through south eastern Queensland into New South Wales. Flies reached the Brisbane Valley and Nambour in 1977 and were first reported in the Tweed Valley in New South Wales in April 1978.

Figure 1. The change in geographical distribution of buffalo fly in coastal eastern Australia from 1974 to 1982.

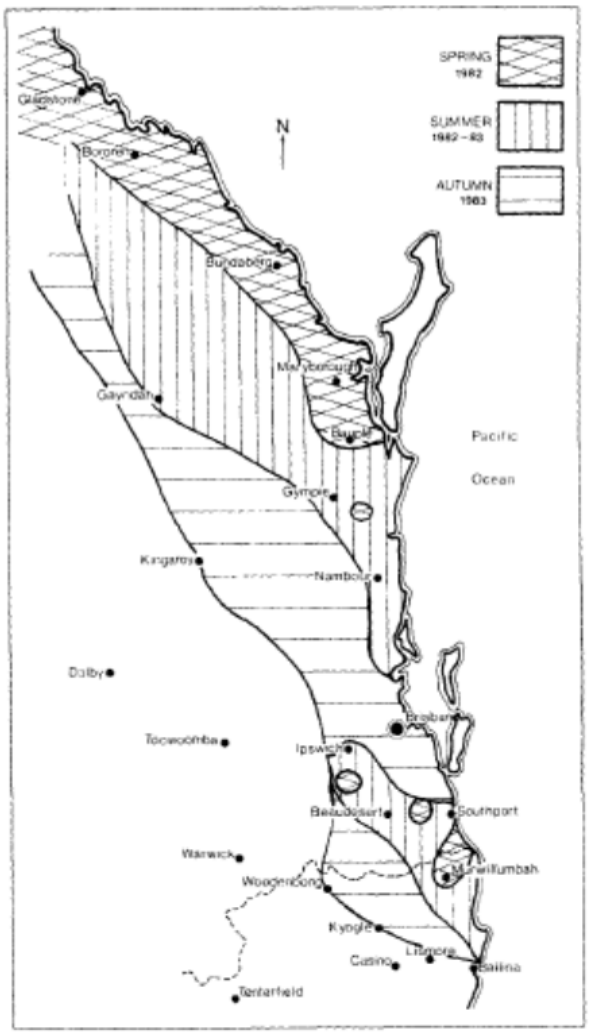


Figure 2. The spread of buffalo fly in coastal eastern Australia from spring 1982 to autumn 1983. Spring refers to the period up to the end of 1982 and summer to the first 2 months of 1983.

Figure 4: The southern extent of buffalo fly distribution in 1974 - 1982 (Williams et al. 1985).

Inter-annual variation of climatic conditions

The actual distribution and abundance of vectors varies not only seasonally but also between years as climatic conditions vary. The current input climate datasets contain only a single value, usually an average, which removes the inter-annual variability of the climatic conditions. One way that the effect of this variation can be investigated is to apply a change to these inputs using a slider bar. This has the effect of applying the change uniformly across the entire Australian continent. It has so far only been implemented for rainfall. Therefore, the distribution of the example culicoides vector under different rainfall scenarios was investigated by varying the annual rainfall using the slider bar.

Firstly, the distribution of the vector assuming no requirement for rainfall was determined (i.e. minimum annual rainfall = 0 mm). This was compared with the distribution assuming the default requirement of 380 mm annual rainfall (Cannon and Raye 1966). Finally, the default requirement was modified by adding or subtracting 200 mm annual rainfall using the slider bar, to see the effect this would have on the distribution of the vector.

5.4 Vector abundance maps generated externally

In this section we describe a data-driven approach to estimate the geographic distribution of *Culicoides spp*. throughout Australia external to AADIS based on the methodology described by Kelso & Milne (2014). A schematic diagram of the sequence of analyses is shown in Figure 5. In brief, for each day of a defined simulation period temperature data was used to update the densities of immature and mature *C. brevitarsis* in each cell of a regular grid covering the land area of Australia. If the average daily temperature was greater than 18 °C adult midges were permitted to move to adjacent grid cells by a process referred to as diffusion spread. Once diffusion spread had occurred an airborne dispersion model (HYSPLIT) was used to disperse adult *C. brevitarsis* subject to daily weather conditions. Updated grid cell estimates of immature and mature midge densities were then passed to the next simulation day and the three-step process repeated. A number of simplifications have been applied to this (first) version of the externally generated vector population model: (a) we have not accounted for the presence or absence of cattle in each cell of the regular grid; and (b) long distance dispersal of midges was set to always occur on each simulation day, using HYSPLIT (ignoring entomologist observations that long distance dispersal of *Culicoides* spp. over land is a relative infrequent event Bishop et al. (2004)).

Meteorological data from the Australian Bureau of Meteorology was provided in raster format as a regular grid of 886 cells of 0.5° in the west to east direction (longitude 111.975° to 156.275°) and 691 cells of 0.5° in the south to north direction (-44.525° latitude to -9.975° latitude), 612,226 cells in total. The raster data sets were derived from automatic weather station and topographic data. An estimate of minimum and maximum temperature in each raster cell was obtained by interpolating the weather station data using the Barnes successive correction technique (Koch et al. 1983). Average daily temperature was calculated as the mean of minimum and maximum temperature for each cell, for each day from 1 January 2015 to 31 December 2015 (inclusive).

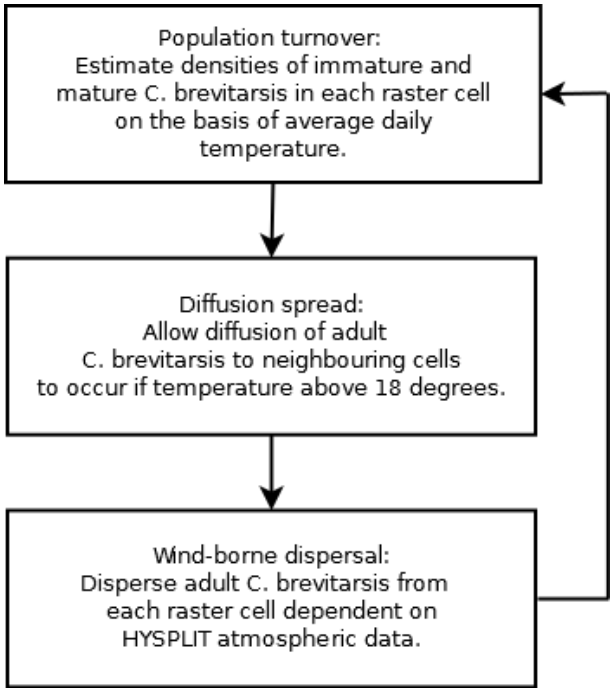


Figure 5: Schematic diagram showing the three-step process used to simulate geographic distribution of *C. brevitarsis* throughout Australia.

Population dynamics

For each cell of our raster surface, two population density estimates were computed to represent the immature and adult stages of the *C. brevitarsis* life cycle (Kelso & Milne 2014). Temperature dependent midge population dynamics (that is, estimation of the density of immature *C. brevitarsis* entering the population each day and estimation of the number of immature *C. brevitarsis* transitioning from the immature state to the mature state) were estimated using the approach described by (Kelso & Milne 2014). As described by Kelso and Milne three ongoing (temperature dependent) processes determine the density of immature and adult *C. brevitarsis* in each raster cell: (a) oviposition of eggs by adult females to produce immature *C. brevitarsis*; (b) the maturation of immature *C. brevitarsis* to adult *C. brevitarsis*; and (c) the death of both immatures and adults. The relationship between each of these processes is shown in Figure 6. A complete description of the *C. brevitarsis* model and the values used for each of the constants are listed in Tables S1.3 and S1.4 of Kelso & Milne (2014).

In Figure 6 and Equation 2, the change in immature *C. brevitarsis* density per day is dependent on the birth rate b (following oviposition by adult females) which reduces to zero when the habitat capacity of a raster cell reaches a maximum, p_{max}. Immature *C. brevitarsis* population density is depleted as a result of the number of immatures that exit the population as deaths, $d_i p_i$, and from maturation of immature *C. brevitarsis* into adults, mp_i. In Equation 2 the constants b, d_i, d_a, and m are temperature dependent.

$$\frac{dp_i}{dt} = b\left(1 - \frac{p_i}{p_{max}}\right)p_a - d_i p_i - mp_i \tag{2}$$

The change in adult *C. brevitarsis* density per day equals the number of immatures transitioning to the adult state, mp_i, and the number of adults which exit the population as deaths, $d_a p_a$:

$$\frac{dp_a}{dt} = mp_i - d_a p_a \tag{3}$$

To develop estimates of immature and adult *C. brevitarsis* densities we populated each cell of our raster surface for 1 January 2015 with 100 immature and 100 adults. The change in immature and adult *C. brevitarsis* densities was calculated using temperature data for 1 January 2015 and the updated density estimates used as the starting point for calculations that were repeated for 2 January 2015. This process was repeated until 31 December 2015. Raster maps showing the geographic distribution of immature and adult *C. brevitarsis* were plotted for each day and presented as a time series. Using this approach, credible estimates of the geographic distribution of *C. brevitarsis* were achieved after 21 simulation days (that is, after 22 January 2015). Future versions of the model will use a substantially longer (e.g. 12-month) time period for initialisation.

Local dispersal

Movement of *C. brevitarsis* occurs by two mechanisms: (a) local dispersal, arising from active flight; and (b) long distance (wind-borne) dispersal.

Culicoides in the absence of wind or other directional stimuli, move according to a random walk process with typical movement distances of up to 100 metres per day (Kirkeby et al. 2013, Lillie et al. 1981). Kelso & Milne (2014) proposed that a small percentage of midges will move up to 5 kilometres per day with the amount of diffusive spread dependent on midge population density and a species-dependent diffusion coefficient. Two studies have reported diffusion coefficients of 60 m^2s^{-1} for *C. impunctatus* (Rudd & Gandour 1985, Kettle 1995) and 13 m^2s^{-1} for *C. variipennis* (Lillie et al. 1981, Backer & Nodelijk 2011). In the absence of reported diffusion coefficients for *C. brevitarsis* we assumed the same values for *C. variipennis*.

Following Kelso & Milne (2014) diffusive spread was assumed to occur only on days when mean temperature was 18 °C or greater. Given the dimensions of each cell of our raster surface were 0.5° × 0.5° (approximately 10 kilometres × 10 kilometres), the proportion of adult *C. brevitarsis* in each cell that undertook diffusive spread was set to a fixed value of 1%.

Long distance dispersal

Long distance dispersal of *C. brevitarsis* can occur over several hundred kilometres when winds are no stronger than 8 $km.h^{-1}$ (if winds are stronger they generally stay on the ground attached to plants) (Murray 1987). Once airborne, *C. brevitarsis* may be lofted above their usual 3 to 4 metre flying height by thermals (upward currents of warm air) or topography-induced wind turbulence, allowing them to reach relatively high altitudes (Eagles et al. 2013, Burgin et al. 2013). In this situation midges can be dispersed several hundreds of kilometres.

As suggested by Kelso & Milne (2014) as an improvement to their model of the spatial and temporal distribution of culicoides across Australia, we used the Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT) model (Stein et al. 2015) to simulate long distance dispersal of *C. brevitarsis* from each raster cell. HYSPLIT has previously been used to model long distance dispersal of culicoides (Kedmi et al. 2010, Garcia-Lastra et al. 2012, Eagles et al. 2013) and other insects (Zhu et al. 2006) as well as foot-and-mouth disease virus (Garner et al. 2006). The model allows for assessment of both trajectories and concentration/dispersion of a particle or pollutant, with the latter based on Eulerian and Langrangian methods. The Lagrangian methodology is used for advection[2] and diffusion calculations, whereas concentrations are calculated on a fixed grid (Draxler & Hess 1998). Both trajectory and dispersion calculations use vertical motion fields directly from input meteorological data.

Calculation of *C. brevitarsis* trajectories were based on time integration of an air parcel's position as it is transported by wind speed estimates that vary at specified heights above the ground (McGowan & Clark 2008). Trajectory calculations do not take into account pollutant or particle (i.e. insect) specific parameters. HYSPLIT allows for clustering of trajectories, by assessing all the trajectories from one location and analysing them to create subsets of trajectories (NOAA 2011). The choice of which trajectories are clustered together is based on total spatial variance (the sum of the spatial variances of all clusters), with trajectories sequentially combined to achieve the lowest increase in total spatial variance.

For atmospheric concentrations and dispersion, HYSPLIT can be run in either puff or particle mode.

[2]The transfer of heat or matter by the flow of a fluid, especially horizontally in the atmosphere or the sea.

For our analyses particle mode, which allows for the release of a fixed number of particles, was used. This mode allows for the transport of particles dependent on wind speed and a random component to account for wind turbulence. The particle source was simulated by the release of a set number of adult midge particles from each raster cell on a given day.

Global HYSPLIT weather data sets for the period 1 January 2015 to 31 December 2015 (inclusive) were retrieved from the Air Resources Laboratory Gridded Meteorological Data Archive.[3] Following estimation of immature and adult *C. brevitarsis* densities in each raster cell and adjustment of adult densities to account for midge dispersal by local spread, adult midges in each raster cell were dispersed using HYSPLIT. HYSPLIT generates particle trajectories at 1 hour time intervals and takes into account upper-atmospheric winds to estimate wind-borne midge dispsersal.

[3] URL: https://www.ready.noaa.gov/archives.php

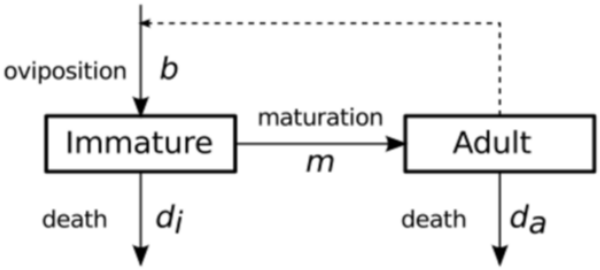


Figure 6: *C. brevitarsis* population sub-model compartments. State transitions of individuals are indicated by solid lines (with the associated rate parameter symbol given in italic type). The influence of adult population on oviposition rate is indicated by the dashed line (Kelso & Milne 2014).

6 Results

6.1 Vector abundance maps generated by AADIS

Importation of grids

For this project, raster data were produced for: elevation, weekly mean temperature, proportion days wind suitable and cattle density. A time series of vector population distribution and densities was produced using the approach described in Section 5.3.

Starting conditions

Figure 7 shows the winter vector distribution map produced by the algorithm programmed into AADIS. This was considered adequate as the starting conditions for simulation of the spread of *C. brevitarsis* in Australia.

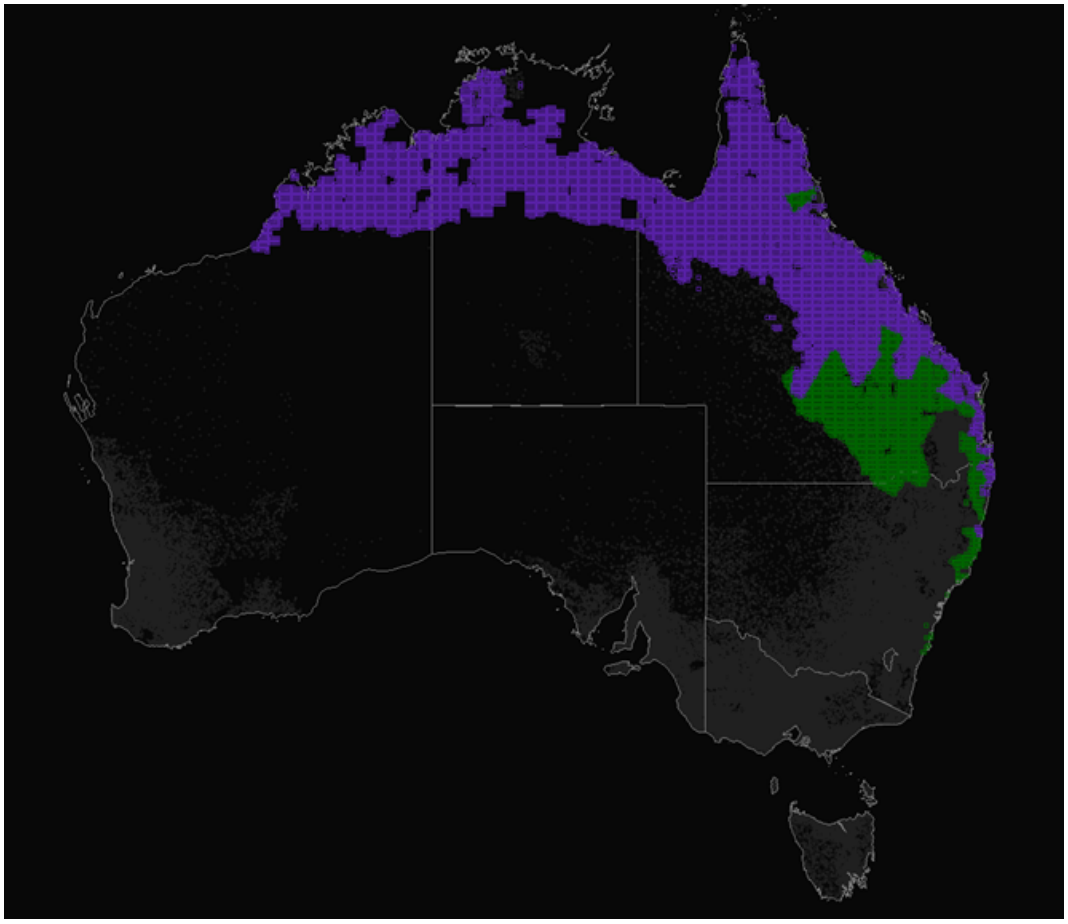
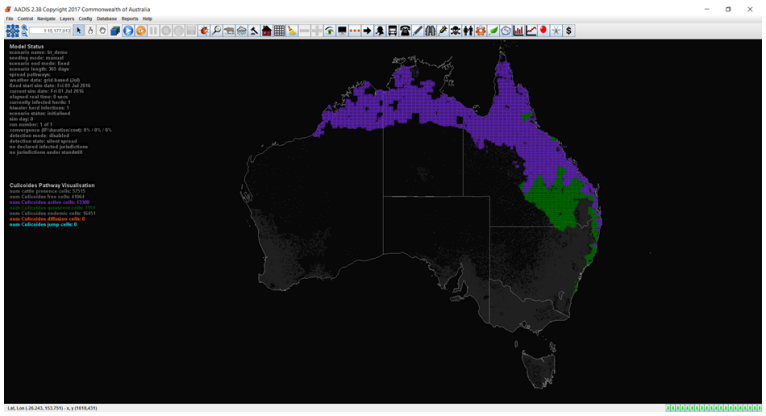


Figure 7: Winter vector distribution in Australia, using the algorithm programmed into AADIS. Purple cells are active and green cells are quiescent.

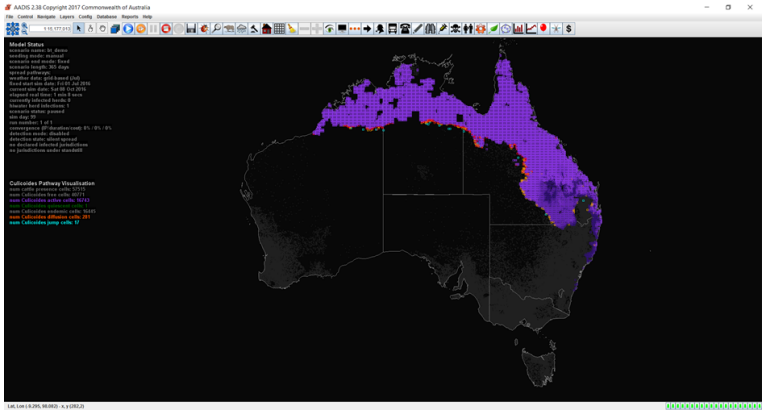
Operation of prototype

The new AADIS vector borne model has a similar look to the original FMD model. There are a number of new features, including a vector dialog and an option to manually seed infestation via the cell popup.

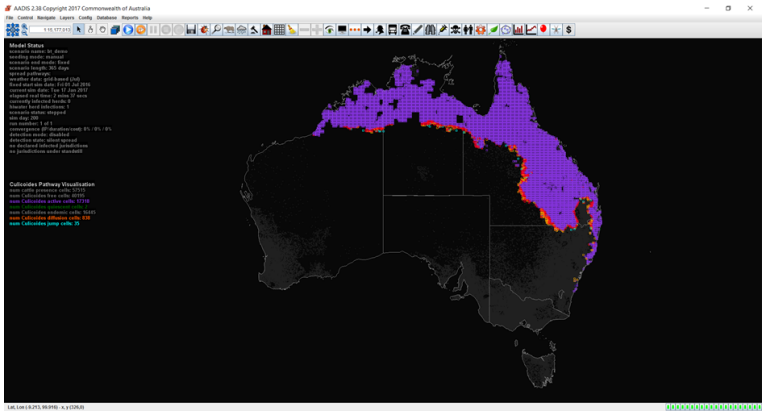
The configurable parameters, and their default settings, are listed in Table 5. If these defaults are accepted, a simulation run can be commenced immediately using the run simulation button. Within-cell vector population biology equation based models, and between-cell (agent-based) pathways then commence, and the spread of infestation can be viewed on the screen. Reports can also be written to file for later analysis. The current report includes the simulation number, number of days in the simulation, number of endemic, active and quiescent cells, number of diffusions, number of jumps and the runtime (in real time). Figures 8 and 9 show the progress of a single simulation run. Purple cells are active year-round (endemic), with a colour ramp from dark purple to light purple as the relative population density increases. Green cells are quiescent. Red and orange cells are active but only seasonally, with a colour ramp from orange to red as relative population density increases. Default parameters in the AADIS vector dialogue menu are shown in Table 4.



(a) Simulation day 0

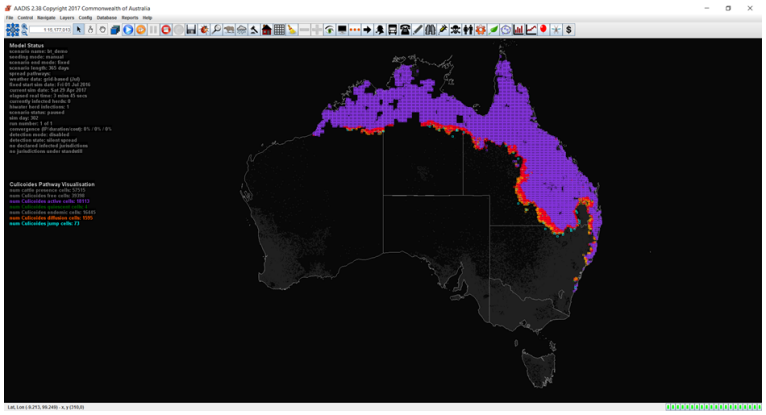


(b) Simulation day 100

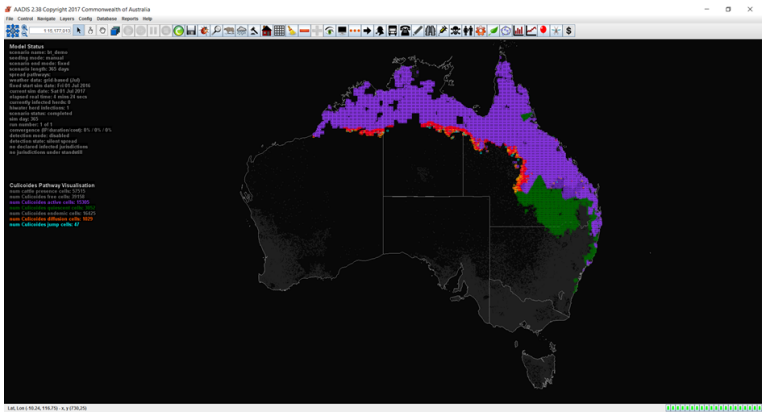


(c) Simulation day 200

Figure 8: AADIS simulations.



(a) Simulation day 300



(b) Simulation day 365

Figure 9: AADIS simulations.

Calibration of the prototype

Initially, the parameters were systematically changed and the maximum spread area was compared with insect trapping records from NAMP to see how well the model could represent the seasonal distribution of *C. brevitarsis*, even though the default parameter values may need further work. With the default values, it was noted that the Pilbara area of Western Australia was never infested with the vector. Manual interrogation of individual cell values in this area suggested that the limiting setting was rainfall. The minimum rainfall requirement was set to zero and the Pilbara became part of the endemically infected area. This setting however, allowed the vector to spread throughout the Northern Territory, well into South Australia and much further into Western Australia than does C. brevitasis in reality. Again, manual interrogation of the values of individual cells suggested that raising the minimum raw cattle density to 1.2 produced limits of spread more in accord with historical records.

Similarly, the original parameters allowed culicoides to spread from its endemic area over the Great Dividing Range, again a situation not recorded in the trapping results. This was resolved by increasing the elevation increase effect to 0.2. Further trial and error variation of vector spread parameters combined with visual observation resulted in a set of parameters that best reflected NAMP trapping records. The default AADIS parameters are shown in Table 5. If parameters are not shown in Table 5, the default value was used.

All sites in the NAMP program that have never recorded the presence of *C. brevitarsis* fall outside area of maximum spread

All Victorian, South Australian and Tasmanian sites have always tested negative for *C. brevitarsis* and all fall outside the area of maximum spread. The maximum spread of the example culicoides vector in AADIS using the optimal parameters is shown in Figure 10. Spread within AADIS did not reach these three states.

The trap sites at Hay, Wentworth, Narrabri, Bourke, Goulburn, Wagga Wagga, Dubbo, Narrabri, Bellata, Menindee, Tenterfield and Armidale in NSW have never recorded *C. brevitarsis*. The maximum extent of spread of the example culicoides vector in the AADIS model did not reach these locations (Figure 11).

In Western Australia, trapping sites below -24 degrees latitude have never recorded the presence of *C. brevitarsis*. This area also falls outside of the maximum spread area predicted by AADIS (Figure 12).

In the Northern Territory, Alice Springs has never recorded trapping of *C. brevitarsis*. It is located outside of the predicted area of maximum spread for *C. brevitarsis* in the AADIS model. However, site T060 which has never recorded *C. brevitarsis* is within a small isolated area that is classified as active by the algorithm used by AADIS at initialisation (Figure 13).

Table 4: Default parameters in the vector dialogue menu of AADIS.

Item	Parameter	Setting
Culicoides presence	Enable culicoides intra-cell population growth/decline	Yes
	Global temperature delta	0
	Manually defined seed cells	Off
	Endemic seed cells	On
	Minimum raw cattle density	0.01
	Minimum weekly mean endemic temperature	13.5
	Maximum weekly mean endemic temperature	38
	Minimum annual endemic rainfall	450
	Maximum annual endemic rainfall	5000
	Minimum endemic elevation	0
	Maximum endemic elevation	10000
	Initial endemic vector cell density	0.5
	Maximum days quiescent	63
	Minimum weekly mean active temperature	13.5
	Maximum weekly mean active temperature	35
	Minimum annual active rainfall	0
	Maximum annual active rainfall	5000
	Minimum active elevation	0
	Maximum active elevation	10000
Culicoides diffusion	Baseline probability	0.3
	Spatial kernel radius	30
	Spatial kernel decay mode	Exponential decay
	Exponential decay exponent	-6
	Elevation increase effect	0.05
	Elevation decrease effect	0.05
	Initial diffused vector cell density	0.0001
Culicoides jumps	Enable vector inter-cell jump spread	On
	Baseline probability	0.003
	Jump mode	Windborne
	Minimum distance	30
	Most likely distance	50
	Maximum distance	100
	Initial jumped vector cell density	0.0001

Table 5: Parameters settings for the vector spread component of AADIS to mimic historical *C. brevitaris* trapping records.

Item	Parameter	Setting
Culicoides presence	Mean raw cattle density	1.2
	Minimum annual endemic rainfall	0
Culicoides diffusion	Spatial kernel decay mode	Linear
	Spatial kernel radius	20 km
	Elevation Increase effect	0.2
	Initial diffusion vector density	0.001
Culicoides jumps	Maximum jump distance	200 km
Settings	Start on	1 Sep 2016
	Fixed end on day	585

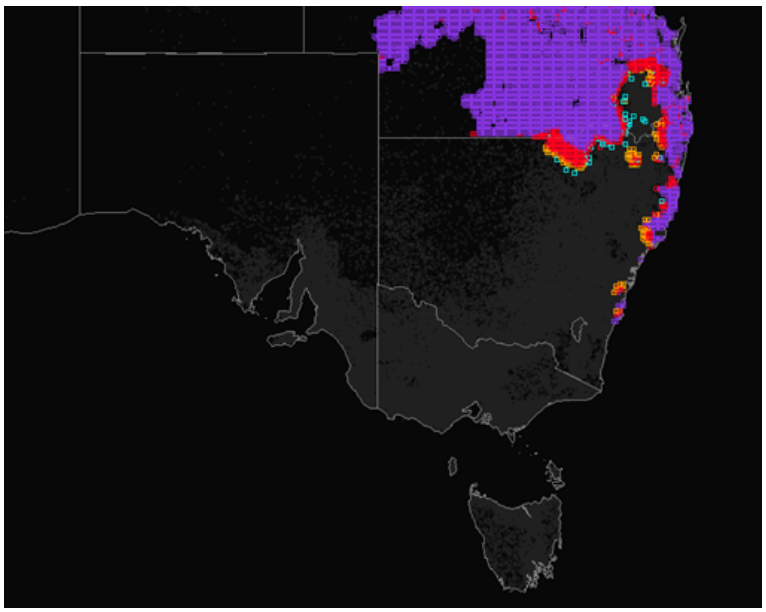


Figure 10: Maximum predicted extent of spread of the example culicoides vector AADIS model in eastern Australia with the optimal set of parameters.

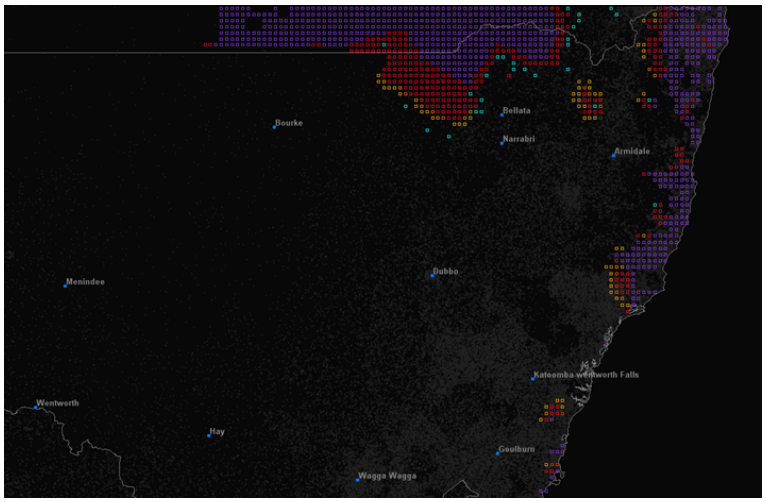


Figure 11: Maximum predicted extent of spread of the example culicoides vector in the AADIS model in eastern Australia with the optimal set of parameters and the location of various NAMP trapping sites.

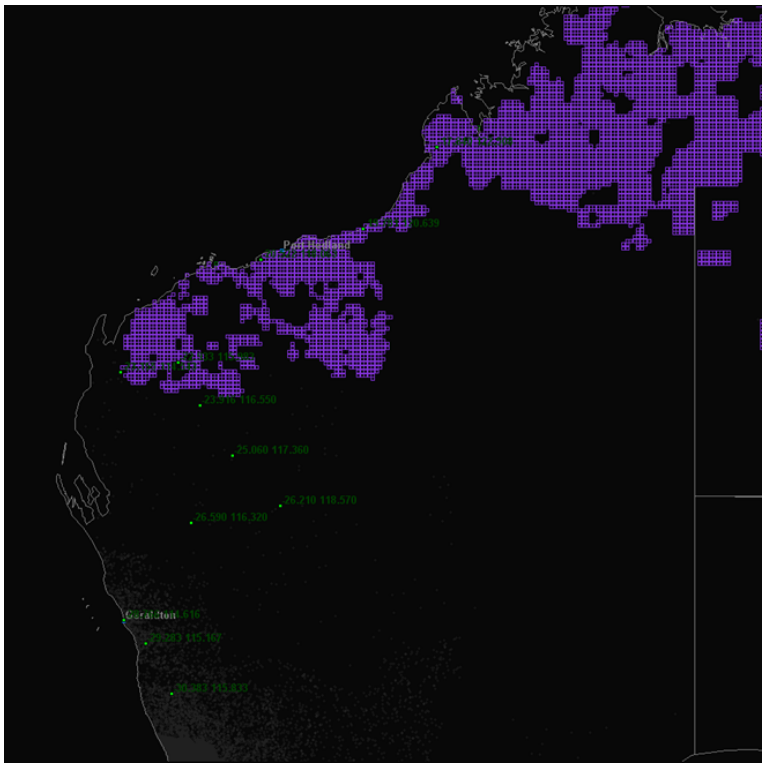


Figure 12: Maximum predicted extent of spread of the example culicoides vector in the AADIS model in Western Australia with the optimal set of parameters and the location of various NAMP trapping sites.

In Queensland, the sites at Prairie, Tambo and Charleville have never recorded the presence of *C. brevitarsis* but occur within areas identified as active at initialisation of the model (Figure 14). These apparent discrepancies can perhaps be explained by the very limited nature of the collections at these sites. Samples were only collected at Tambo in 2005. This was a dry year (316 mm cf average 557 mm) and, in 2005, the next nearest site Q226 was also negative for *C. brevitarsis*. Prairie was only collected in 2005 – 2007 comprising one dry and two average years. Note the very limited western distribution of bluetongue in 2005 – 2006 and 2006 – 2007 (Figure 15). Charleville was only collected in 2009 and this was a relatively dry year (345 mm compared with an average of 492 mm per annum).

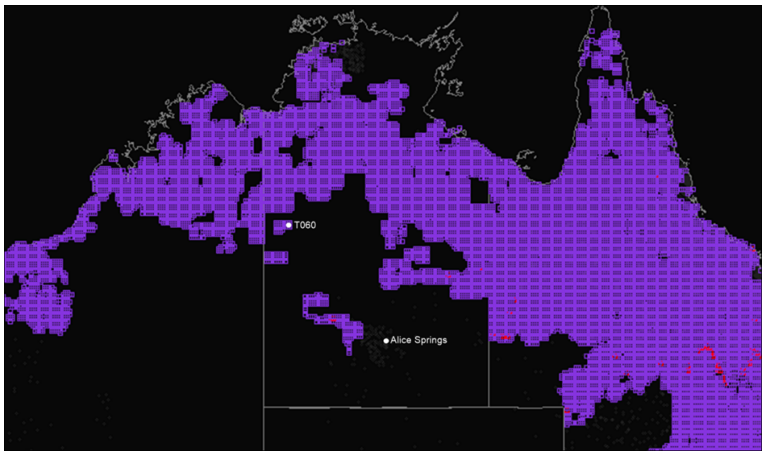


Figure 13: Maximum predicted extent of spread of the example culicoides vector in the AADIS model in the Northern Territory with the optimal set of parameters and the location of various NAMP trapping sites.

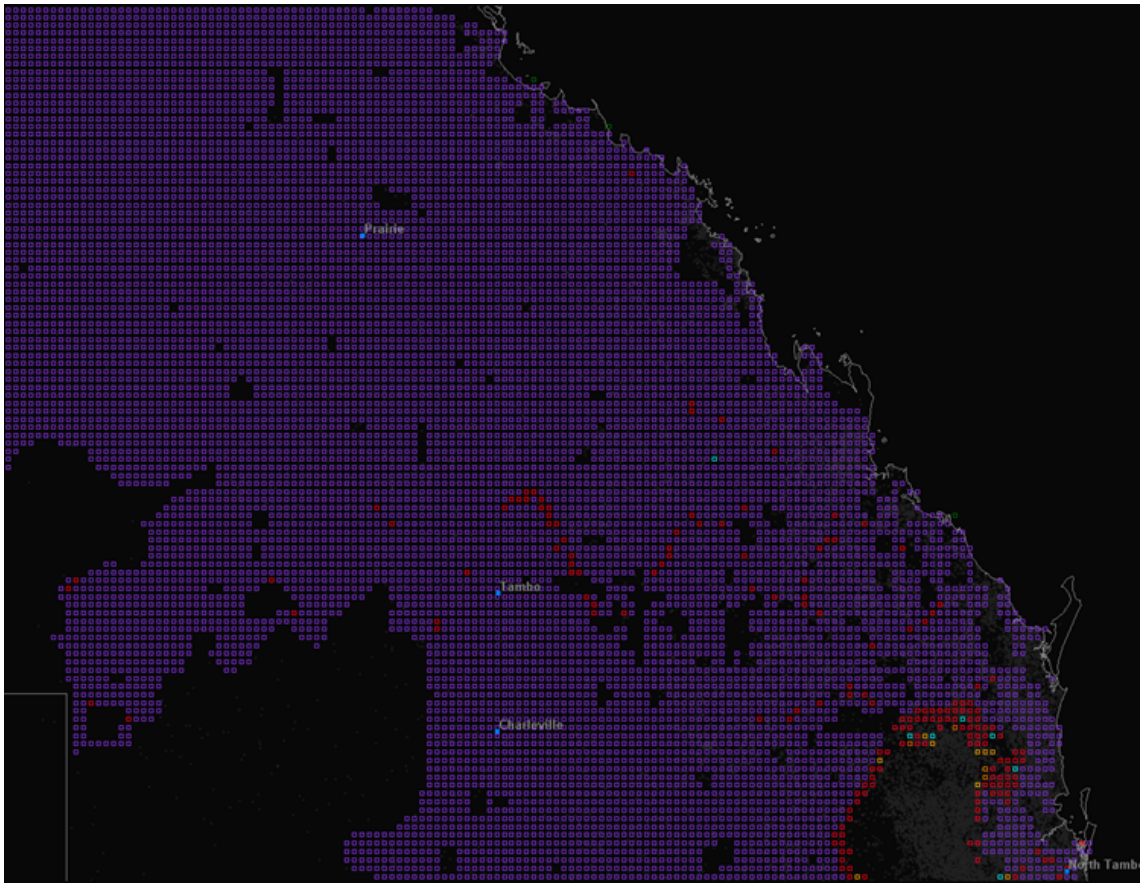


Figure 14: Maximum predicted extent of spread of the example culicoides vector in the AADIS model in Western Queensland with the optimal set of parameters and the location of various NAMP trapping sites.

All sites where *C. brevitarsis* has been trapped each of June, July and August are within the predicted endemic area

The trap sites at Weipa, Daly River, Kalumburu, Cooktown, Kununurra, Victoria River, Normanton, Townsville, Maryborough, Seisia, Berrimah, East Arnhem, Beatrice Hill, Katherine and Broome all have recorded positive findings for *C. brevitarsis* in each of June, July and August for multiple years. All are within the area identified as active by the algorithm at initialisation of AADIS.

Fitzroy River and Innisfail where records are not as complete tested positive in at least two of the three winter months on at least one occasion and are both located in the area identified as endemic by AADIS.

All historically positive sites are within the area of maximum spread

All Northern Territory trapping sites that have recorded the presence of *C. brevitarsis* are located within the endemic area predicted by AADIS (Figure 17).

Most *C. brevitarsis* positive sites in Western Australia are within the maximum limit of spread of the example culicoides vector predicted by the AADIS model. However, two sites at Minilya and Dairy Creek that have tested positive fall outside of the predicted maximum limit of spread of the AADIS model (Figure 18).

***Culicoides* are endemic as far south as Port Macquarie (-31.4° south)**

The Hastings Valley (Port Macquarie, -31.4°) is the approximate southern limit of the *C. brevitarsis*-endemic area (Bishop et al. 2000). There is no winter trapping in this area but *C. brevitarsis* are found in October in Lismore, Casino, Ballina, Grafton and Bellingen (-28° to -30.45° South). These locations are all within either the endemic or the quiescent area of the model (Figure 19). Kempsey (-31.08°), Wauchope (-31.45°) and Taree (-31.95°) show more variability in earliest trapping date but *C. brevitarsis* is recorded in October in at least 50% of years.

Kempsey, Wauchope and Taree always infested by December

Kempsey, Wauchope and Taree were always infested by December, in years when trapping was conducted at these sites. The model shows the example culicoides vector active in these areas by mid-December.

Berry and Camden are always infested by February

C. brevitarsis was always found at Berry and Camden by February in years when trapping was conducted. The AADIS model shows the example culicoides vector active in these areas by mid-February.

Other insect vectors

The final parameter settings that best represented the known and predicted distributions of *C. gelidus* are shown in Table 6.

With the parameters shown in Table 6, the final distribution of *C. gelidus* predicted by AADIS is

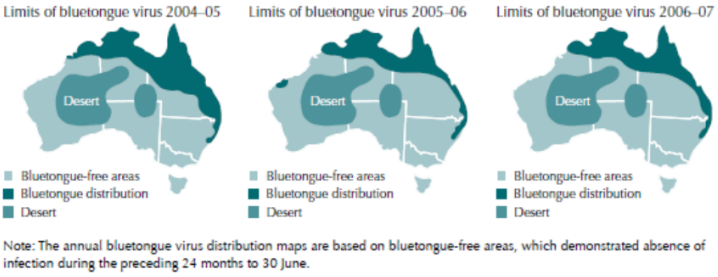


Figure 15: Official NAMP bluetongue distribution maps for the years of 2004 – 2005 to 2006 – 2007.

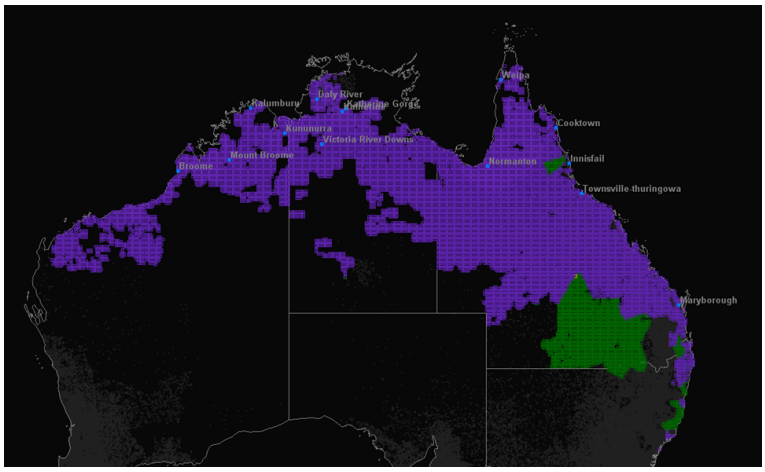


Figure 16: The endemic area for C. brevitarsis predicted by the AADIS startup algorithm and the location of trap sites that record the presence of *C. brevitarsis* in June, July and August.

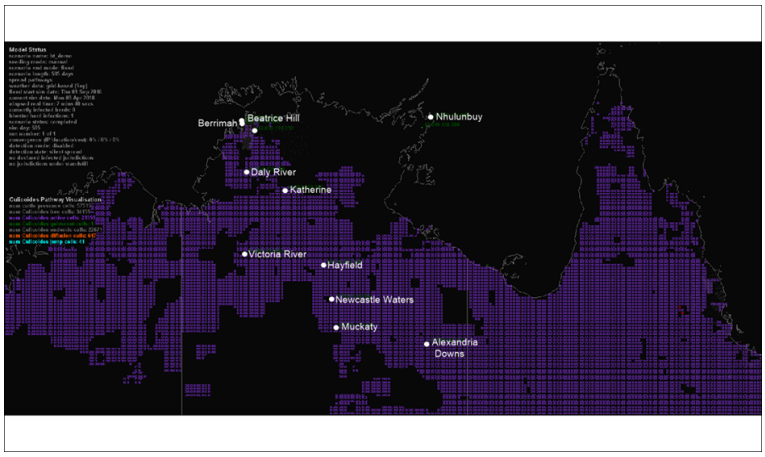


Figure 17: The endemic area for *C. brevitarsis* predicted by AADIS and the location of trap sites that have recorded the presence of *C. brevitarsis*.

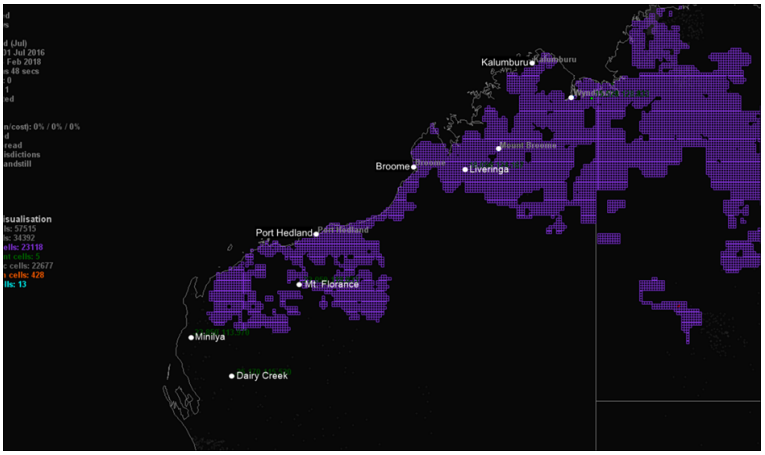


Figure 18: The endemic area for *C. brevitarsis* predicted by AADIS and the location of trap sites that have recorded the presence of *C. brevitarsis*.

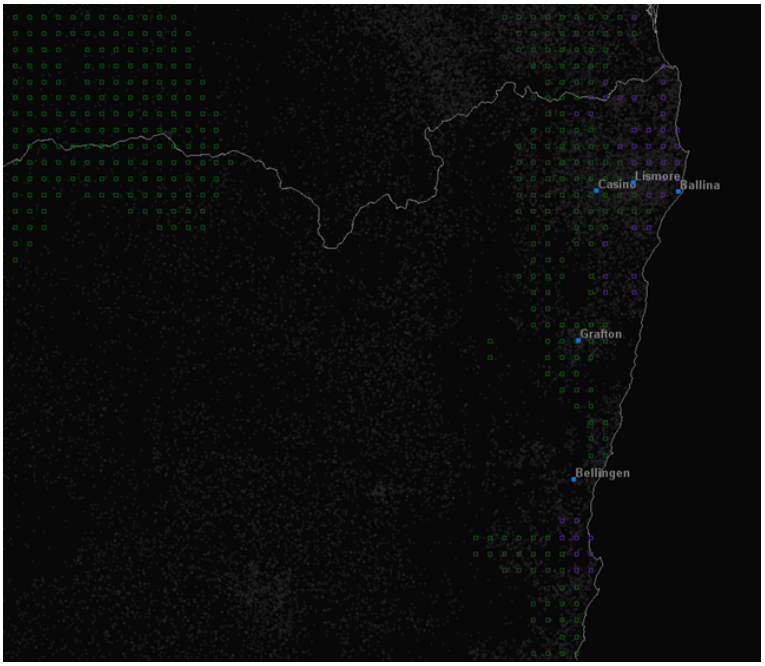


Figure 19: AADIS predicted endemic active and quiescent areas in July and the location of five towns where *C. brevitarsis* is reported to over-winter.

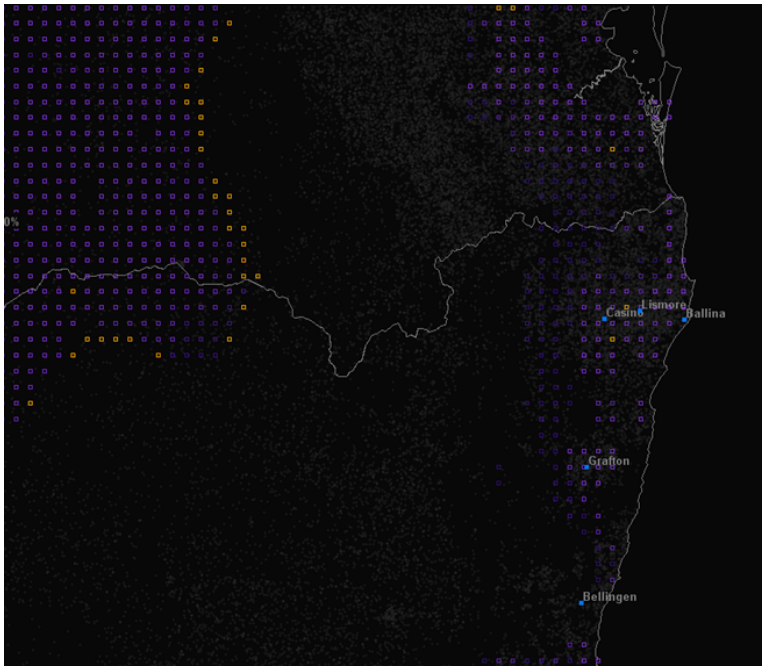


Figure 20: The region in northern NSW predicted by AADIS to be active for the example culicoides vector in October and the location of five trapsites where *C. brevitarsis* is known to be active in October.

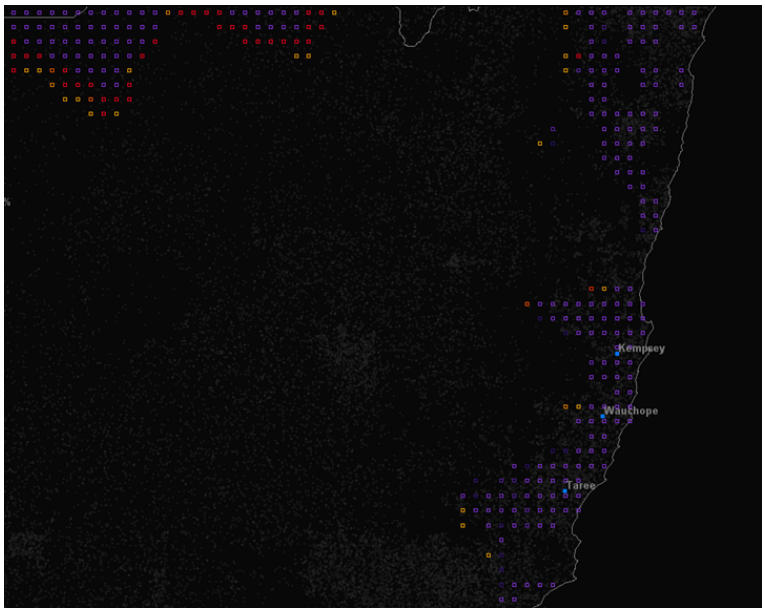


Figure 21: The region in northern NSW predicted by AADIS to be active for the example culicoides vector in December and the location of three trapsites where *C. brevitarsis* is known to be active in December.

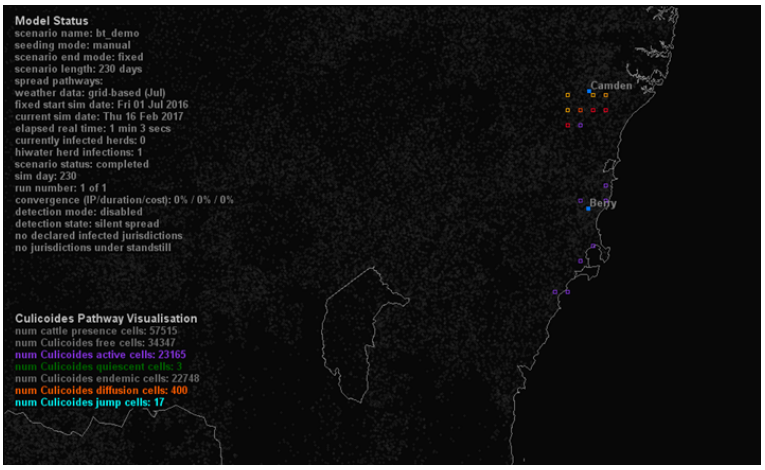


Figure 22: The region in central NSW predicted by AADIS to be active for the example culicoides vector in February and the location of two trapsites where *C. brevitarsis* activity is reported in February.

Table 6: AADIS parameter settings for representing the distribution of *Culex gelidus*.

Item	Parameter	Setting
Culicoides presence	Manually define seed cells	On
	Minimum weekly mean temperature	10
	Maximum weekly mean temperature	37.5
	Mean annual endemic rainfall	725 mm
	Maximum days quiescent	90
	Minimum weekly mean temperature	10
	Maximum weekly mean temperature	37.5
	Minimum annual rainfall	725 mm
Culicoides diffusion	Initial diffusion vector density	0.001
Culicoides jumps	Maximum distance	200 km
Settings	Start date	30 April
	Fixed end day	10000

Table 7: Parameters settings for the vector spread component of AADIS for *Haematobia irritans*.

Item	Parameter	Setting
Culicoides presence	Mean raw cattle density	0.1
	Minimum weekly mean temperature	17.5
	Minimum annual rainfall (mm)	500
	Maximum days quiescent	100
Culicoides diffusion	Spatial kernel decay mode	Linear
	Spatial kernel radius	20 km
	Elevation increase effect	0.2
	Initial diffusion vector density	0.001
Culicoides jumps	Maximum jump distance	200 km
Settings	Start on	30 April 2016
	Fixed end on day	3615 [a]

[a] 10 year simulation period (in days) less one month to avoid the onset of autumnal quiescence.

shown in Figure 23. It closely resembles the distribution from (Williams et al. 2005).

Haematobia irritans

The final set of parameters chosen as best being able to replicate the distribution of buffalo fly are shown in Table 7. Only parameters that differ from the default settings are shown in Table 7.

Using the set of parameters shown in Table 7 predicted distributions of *H. irritans* are shown in Figures 24 and 25.

Inter-annual variation of climatic conditions

The distribution of the example culicoides vector at 1 July, assuming no effect of rainfall, is shown in Figure 26.

The parameter settings for AADIS were then changed so that both endemic areas and the areas to which the vector may spread require a minimum annual rainfall of 380 mm. With these parameters, the distribution of the vector on July 1st changes to that shown in Figure 27.

If the annual rainfall in each grid cell was 200mm less than the stored annual rainfall value (representing a dry year), the distribution of the vector would contract to the area shown in Figure 28.

Figure 29 shows the predicted distribution of the vector if annual rainfall at each location is 200 mm greater than the rainfall value stored in the AADIS database (a wet year).

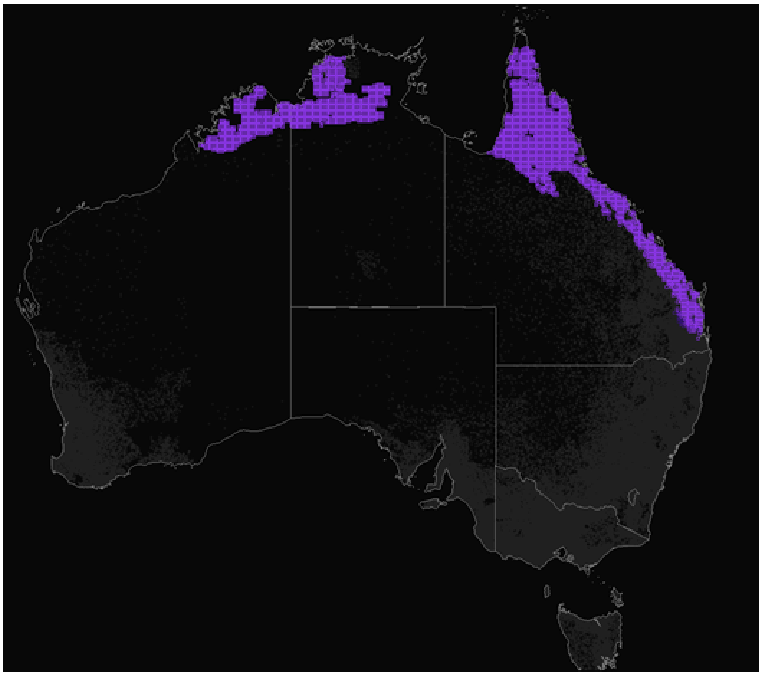


Figure 23: The distribution of *C. gelidus* in Australia predicted by AADIS.

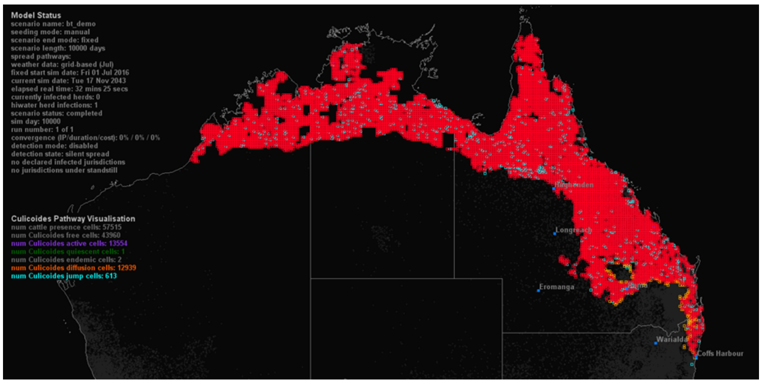


Figure 24: The distribution of *Haematobia irritans* as predicted by the AADIS model and the location of various major towns.

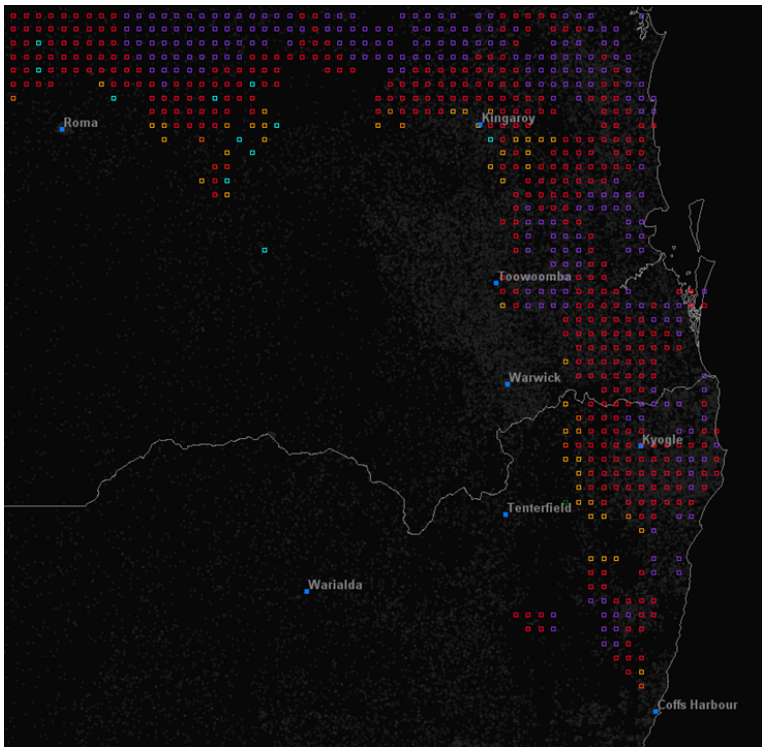


Figure 25: The distribution of *Haematobia irritans* in southern Queensland and northern NSW as predicted by AADIS.

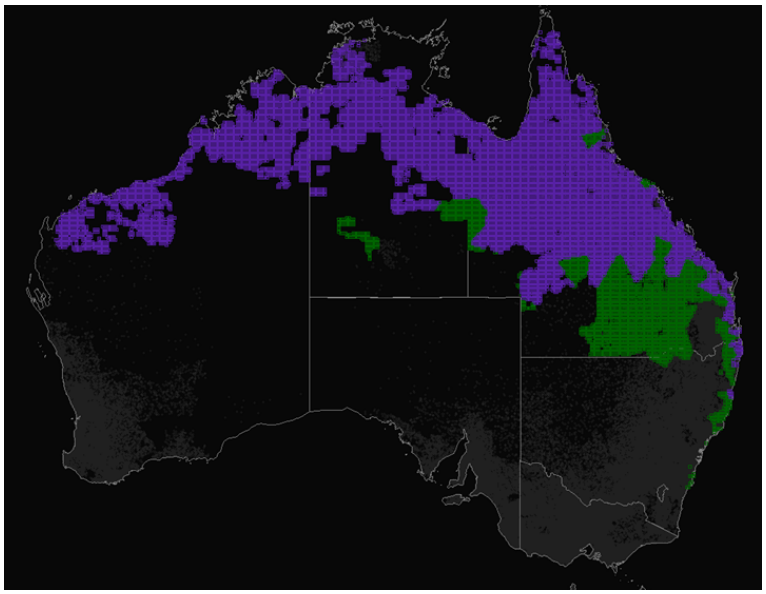


Figure 26: The predicted distribution of the example culicoides vector on July 1st assuming no effect of annual rainfall.

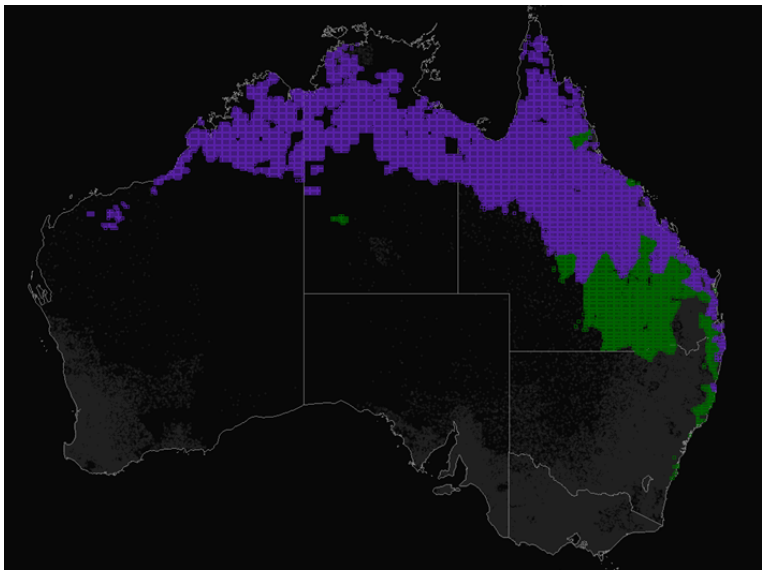


Figure 27: The predicted distribution of the example culicoides vector on 1 July if a minimum requirement of 380 mm annual rainfall is imposed.

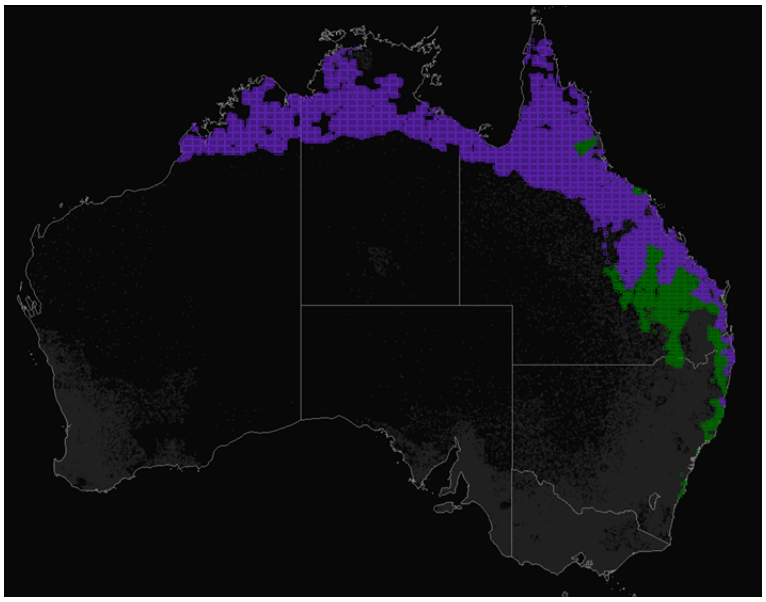


Figure 28: The predicted distribution of the example culicoides vector if the observed rainfall is 200 mm less than the stored rainfall value used in the model.

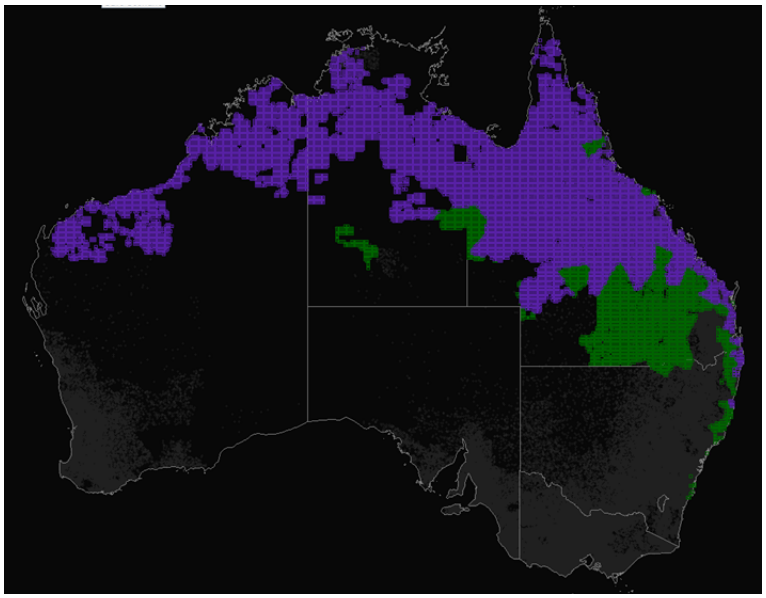


Figure 29: The predicted distribution of the example culicoides vector if the observed rainfall is 200 mm greater than the rainfall value stored in the database.

6.2 Vector abundance maps generated externally

Figure 30 is a line plot showing minimum and maximum daily temperatures for Byron Bay (northern NSW) for the period 1 January 2015 to 31 December 2015. Superimposed on this plot are estimates of adult culicoides densities (expressed in arbitrary population units, minimum 0, maximum 1). For Byron Bay temperatures and culicoides densities are at a maximum from January to April. Culicoides densities then decrease (due to reductions in mean daily temperature), reaching a minimum in July. By the end of August adult culicoides densities start to increase, with a rapid rise from October on.

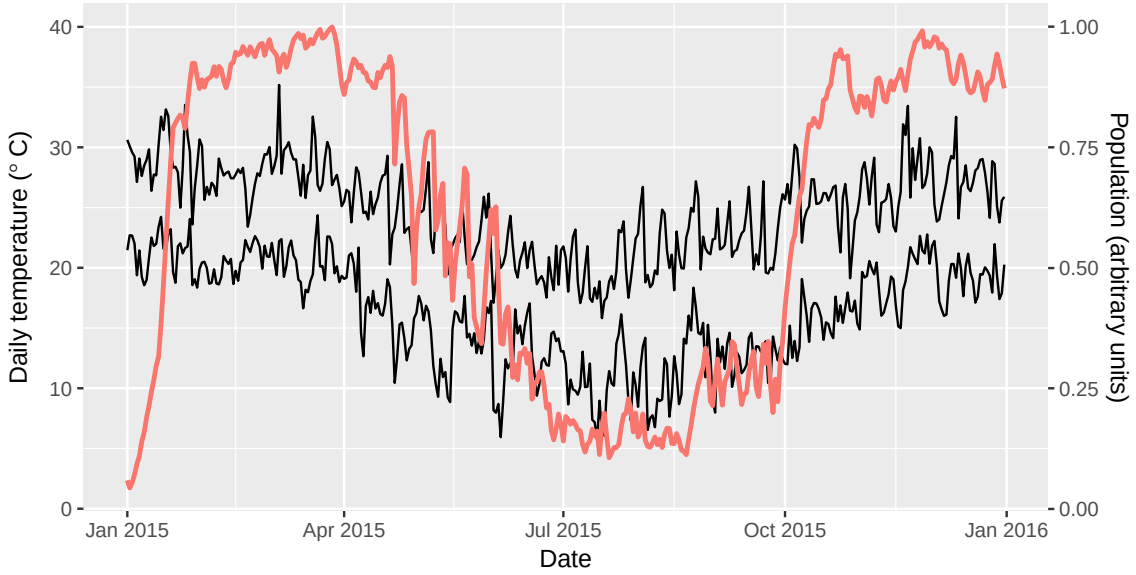


Figure 30: Line plot showing, for Byron Bay (northern NSW), daily minimum and maximum temperature (lower and upper solid black lines, respectively) as a function of calendar date, 1 January 2015 to 31 December 2015. Superimposed on this plot (as a red line) are the simulated adult *Culicoides* densities expressed in relative population units (minimum 0, maximum 1).

Figure 31 is a raster map showing the predicted spatial distribution of culicoides-active sites across Queensland on 1 March 2015, ignoring the effect of local and long distance dispersal. Figure 31 shows the predicted spatial distribution of culicoides-active sites across Queensland on 1 March 2015, accounting for the effect of temperature, local dispersal and long distance dispersal.

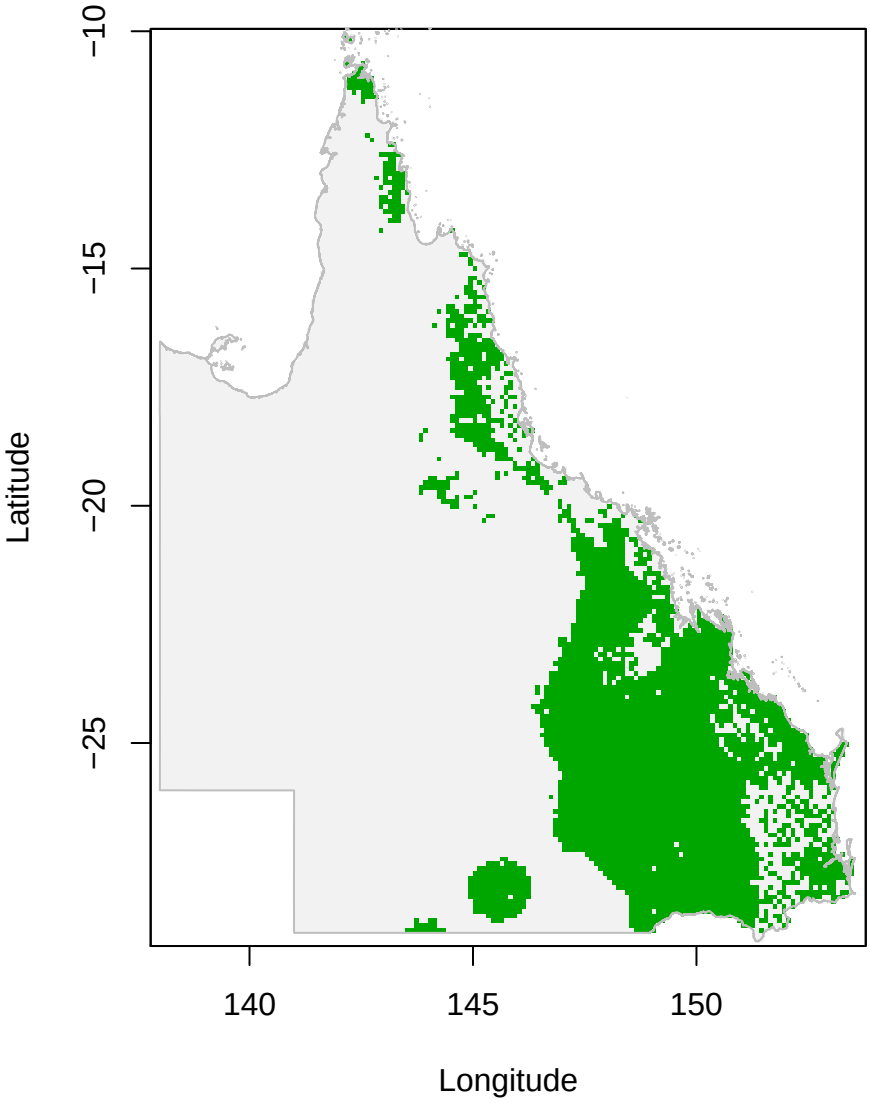


Figure 31: Map of Queensland showing locations of active *Culicoides* growth (dark green) on 1 March 2015, predicted on the basis of temperature, as described in Section 5.4.

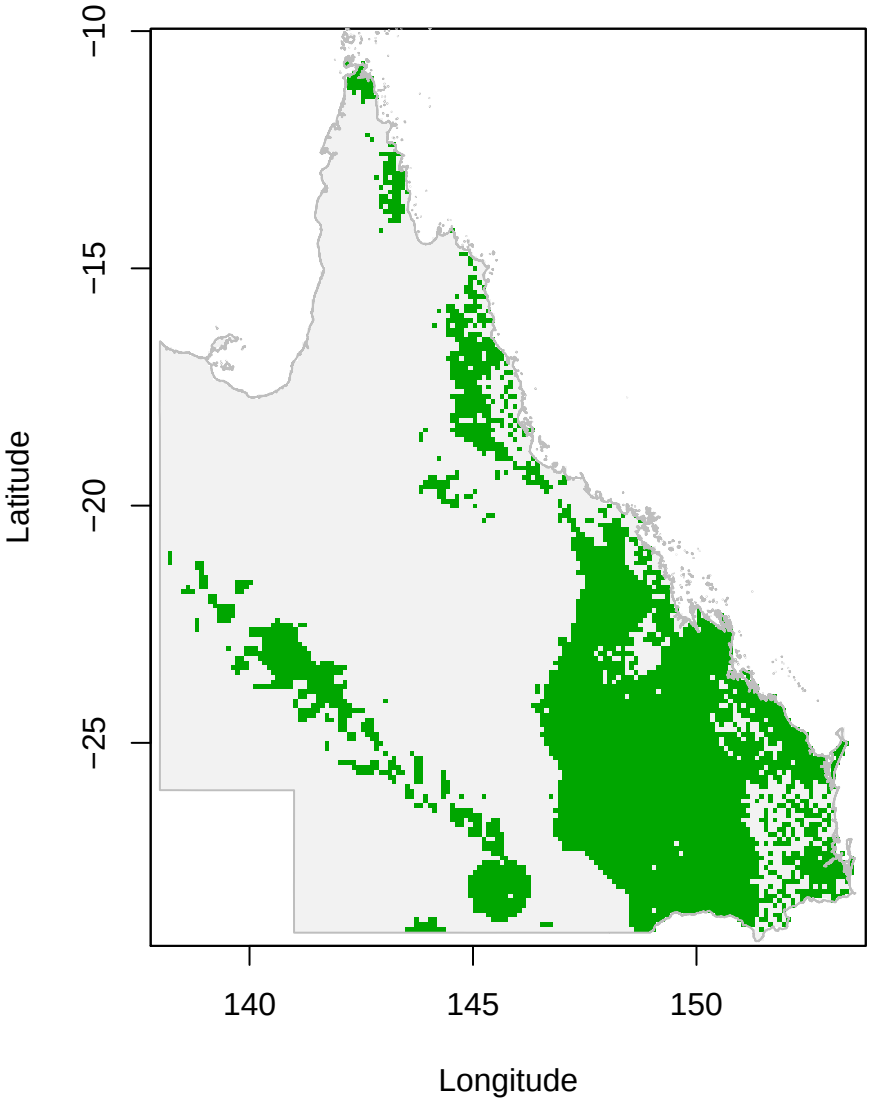


Figure 32: Map of Queensland showing locations of active *Culicoides* growth (dark green) on 1 March 2015, predicted on the basis of temperature, local dispersal and long distance dispersal, as described in Section 5.4.

Our predictions of the spatial distribution of culicoides over time were consistent with that reported by Kelso & Milne (2014) (compare Figure 30 with Figure 6A in Kelso and Milne 2014) and broadly consistent with predictions from the AADIS vector module. The use of HYSPLIT to account for long distance spread produced a large band of culicoides-positive sites in the south west of Queensland which is probably unrealistic (compare Figure 31 with Figure 32). Future versions of the model will use a random draw from a binomial distribution to determine if long distance dispersal of midges occurs on a given day.

Processing times for adult and juvenile culicoides density estimates using temperature were relatively quick. Using a personal computer with a processor speed of 1.60 GHz it took approximately 5 minutes to produce adult and juvenile culicoides density estimates for all of Australia for a single day. Inclusion of local and long distance dispersal into the prediction algorithm increased processing times considerably. Using the same computer it took approximately 8 hours to produce adult and juvenile culicoides density estimates for all of Australia for a single day.

7 Discussion

The first year of this project has produced two capabilities for representing vector populations within AADIS. The first is the facility to import data from an external source to represent vector abundance. The second is the facility allowing users to estimate insect vector abundance directly within AADIS. Our reasoning for implementing these two options was pragmatic. On one hand, in the face of an outbreak requiring rapid decision making at the national level, we acknowledge that there is a need for vector abundance maps to be developed quickly and then seamlessly integrated into models of livestock disease spread. On the other hand, the ability to import data representing vector abundance produced independent of AADIS acknowledges the importance of collaborative approaches to disease modelling. It is our expectation that in the face of an ongoing vector-borne disease outbreak subject-matter experts will provide vector distribution maps for use in AADIS. In this way, modelling teams will be seen to be using the best available information to inform AADIS as a decision support tool.

While good progress has been made during the first year of this project, the following remaining tasks will be completed during the three year PhD programme:

1. Verify and validate the within-AADIS facility to estimation of insect vector abundance. A basic evaluation of the AADIS vector module shows that it represents the spatial distribution of *C. brevitarsis* reasonably well (Section 6.1).
2. Verify and validate the Kelso & Milne (2014) HYSPLIT culicoides modelling approach described in this report.
3. Provide guidelines for those developing vector abundance maps external to AADIS on how to numerically express vector abundance so that it is in a format suitable for use by AADIS.
4. Develop appropriate program logic to allow an infectious agent to spread within the vector population and to allow transfer of infection from the vector population to the livestock population at risk.

By definition, the ability to import externally generated vector abundance maps provides the greatest flexibility: if an entomologist can generate a time series set of vector abundance maps, they can be used by AADIS. This said, it is noted that the AADIS vector module contains all of the necessary components for representing any vector species of interest, including a means to represent vector population increase and decrease, temperature dependence, moisture dependence, a population limiting resource, and the means by which vectors may move from one location to another. While the input data and format required may vary for different vector types, the necessary structures in AADIS are in place to accommodate these data, allowing adaptation if and when this is required. This was demonstrated by the use of different parameter inputs to produce a maximum distribution for two other insects (*Culex gelidus* and *Haematobia irritans*), which aligned well with data from (dated) published sources. Appropriate spread parameters were not available for these species, so AADIS could not be used to assess the rate of spread of these insects following an incursion. If this information became available, appropriate changes could be made.

In Australia there is currently a lack of modelling tools to support national level decision making in the event of an incursion of an exotic, vector-borne disease. Kelso & Milne (2014) described an approach for estimating the spatial and temporal distribution of *C. brevitaris* that performed well at a local and regional scale. It is not known whether this model would perform as well at the national level. 'Scaling up' a local model to the national level could be problematic for a number of reasons. Firstly the required datasets may not be available, or may not be available in the required format. While national level data was available to support scale-up of the Kelso & Milne (2014) model to the national level (including long distance dispersal of culicoides spread using HYSPLIT), this approach carried with it significant computational overhead, with the time required to produce a set of raster maps to represent the spatial distribution of *C. brevitarsis* for each day of a single year is estimated to be around 17 weeks.

AADIS is a computationally efficient model that can run complex simulations on a desktop computer. Long term, further efficiencies may be required to handle the additional computational burden imposed by the need to simulate the spread of vector-borne disease. For the prototype AADIS vector module, the existing 10 $\times$ 10 km grid cell was used as the spatial unit of interest, and the temporal resolution for input datasets (such as temperature) was a weekly average. At the moment there is no capacity to introduce stochastic variation in climatic conditions, something which is likely to have substantial effects on the distribution of the vector between years as demonstrated using the example of varying annual rainfall with the slider bar. Similarly, the current version of AADIS is restricted to allowing vector distribution maps summarised at the weekly level. If increased temporal resolution of vector distributions is required, new strategies for accessing and using input data will be required to minimise the likely negative impacts of these changes on simulation run time.

8 Appendix 1: Workshop report

Decision Support Tools for Vector-Borne Diseases of Animals (CEBRA Project 1608B)

8.1 Overview

A key component of managing emergency animal disease incursions, and minimising their economic impact, is timely and effective decision-making in the face of uncertainty. This requires a good understanding of the potential transmission and control of such diseases under Australian conditions. The Department of Agriculture and Water Resources has invested in the development of a new modelling capability — Australian Animal Disease model (AADIS) — to support foot and mouth disease preparedness and response. This model is readily adaptable to other directly transmitted livestock diseases. However, there is currently no capacity to model vector-borne animal diseases, and there are a number of economically important livestock diseases that are transmitted by vectors for which preparedness and response policies may be better informed by disease simulation modelling. The purpose of this CEBRA Project is to provide AADIS with a capability to simulate vector-borne animal diseases, using bluetongue disease as a case study.

A workshop was held on 30 August 2016 in Canberra to seek expert advice on what processes the AADIS model should be able to represent and how they should be represented in order to adequately simulate a vector-borne disease. Advice was also sought on what scenarios could be used for preliminary study to test the function of the modified AADIS model.

8.2 Workshop outcomes

The project will initially focus on seasonal distribution of *C. brevitarsis* and a hypothetical Simbu group virus for which this species is moderately to highly competent. This will provide a foundation for further development of vector-borne disease modelling capability within AADIS.

The grid capacity of AADIS will be used to capture climatic and geographical features to produce a 'suitability index' for *C. brevitarsis* presence and survival, and will also be used to model the spread of the vector by diffusion and wind-assisted dispersal.

The scenario to be used for initial study is that of a novel introduction of a virus that is pathogenic to sheep into the Darling Downs area (e.g. BTV-16 introduced from the Northern Territory). The effectiveness of movement restrictions will be investigated by running simulations with and without movement restrictions. Depending on timing, another of the proposed scenarios may also be explored, though these were judged less suitable.

Session 1

The participants were thanked for their attendance, and the background and context of the project were outlined by Graeme Garner and Robyn Martin. The participants then introduced themselves

and provided information on their background, and what they hoped to get out of their attendance at the workshop. Participants are listed in Table 8. Most participants indicated that they expected to provide information and advice, and some expressed interest in the model and how it could be used to inform policy decisions. One participant had recent experience with a similar disease simulation modelling project involving bluetongue disease, and indicated a willingness to try to synthesise that model into AADIS.

Richard Bradhurst demonstrated the functionality of the current AADIS model for foot and mouth disease, and described the top-down (population-based) and bottom-up (individual-based) approaches to modelling disease spread, and how both are combined in AADIS.

Session 2

The group discussed the essential elements (vector, livestock and disease control processes) that would need to be incorporated into the model, and how these could be represented. Amongst the workshop participants there was a wealth of expertise on *C. brevitarsis* ecology, and this species was identified as the most important vector species in Australia due to its wide distribution and abundance relative to other species. However, this species is known to be much less competent as a vector of bluetongue virus than other *Culicoides* species present in Australia (approximately 0.5% – 1%). It was therefore suggested that in the first instance, a hypothetical Simbu group virus, for which *C. brevitarsis* is moderately to highly competent, be used to test the model (such that vector and virus distribution are essentially the same). The group agreed generally that the best way to represent a vector distribution was through construction of a 'suitability index' using the grid capacity of AADIS. Critical factors identified for vector survival were temperature (with both minimum and maximum limits), cattle density and altitude, although the Normalised Difference Vegetation Index (NDVI) was suggested as an alternative to temperature as it captures more factors that may influence vector survival. In terms of wind-borne movement of the vector, the important factors were wind speed and direction, temperature and relative humidity. In a new location, the vector would need to build up to a critical population level before onward spread would be expected to occur. A question was raised about whether infected vectors could be transported to new locations with consignments of cattle. While the group believed that this was possible, it was thought to be less important than other mechanisms of spread of the vector, and would probably be adequately captured with movements of infected cattle.

It was agreed that the important livestock populations were already present within the AADIS model, as was the capacity to spread infection with the movements of viraemic animals through existing pathways. The group then discussed the relative attractiveness of sheep and cattle for vector feeding. Cattle are favoured by *C. brevitarsis*, although the reasons for this are unknown, and may be as simple as lack of access to the skin on sheep due to the fleece. A saturation effect was described, whereby vector preference becomes less apparent above a threshold vector population density.

Finally, control options were discussed. The options that would be required in the model were surveillance visits, movement controls, declared areas and vaccination. Culling was discussed as a tool for managing animal welfare, rather than as a disease control measure. The two measures of most interest in terms of current disease control policy discussion were vaccination and movement controls, particularly whether movement controls within the Bluetongue Zone (i.e. where vector

populations are known to be) are effective in disease control. There was some discussion of barrier vaccination ahead of a vector/ disease front, raising questions of how wide it would need to be, and what level of compliance can be expected. In local areas, control measures could include housing high value animals during risk periods (dawn and dusk), using light of a particular colour such that *C. brevitarsis* is not attracted, topical insect repellents and detection of virus in vectors as an early warning for livestock producers. The latter was not thought to be feasible because of the difficulty in detecting virus in vectors, and none of these options were believed to be important to incorporate into AADIS.

Session 3

The workshop participants divided into three groups to discuss scenarios for potential study later in the project. Two groups physically present were each given two potential scenarios for discussion (below), and the group on teleconference discussed a version of one of those. The scenarios proposed for discussion were as follows:

1. A single introduction of a novel serotype resulting in disease in cattle in the far north of the NT. Investigate whether spread to other states is likely, or whether a localised outbreak with spontaneous resolution is more likely.
2. A single introduction of BTV-8 into Victoria (Bendigo area) in spring, with a local *Culicoides* species serving as a sufficiently competent vector.
3. A single introduction of BTV-16 (pathogenic for sheep) in south-east QLD in a region producing both cattle and sheep (Darling Downs). Investigate the impact of movement restrictions in preventing spread by simulating outbreaks with and without the application of movement restrictions.
4. Extension of the range of *C. brevitarsis* that would be expected with a 2 degree increase in minimum temperatures, with introduction of endemic strains of bluetongue into northern NSW (Moree area).

One group was given Scenarios 1 and 2, and selected scenario 2 because scenario 1 was thought to involve too many uncertain factors, including the vector species that may be involved. However, the selection was made with the caveat that they were uncertain about the competence of southern *Culicoides* species, and whether they would actually feed on livestock. The Gippsland area was also considered more likely than the Bendigo area. A member of the other group advised that current research indicates that southern *Culicodes* species do not become infected with bluetongue viruses.

A second group was given Scenarios 3 and 4, and selected scenario 3 because it was considered plausible and allowed investigation of the effects of movement restrictions. Scenario 4 was also thought to be plausible, since a similar situation had arisen in recent years and was detected by the National Arbovirus Monitoring Program, although there was no disease in that case.

Table 8: Workshop participants.

Name	Organisation
Alan Bishop	NSW Department of Primary Industries
Jean-Bernard Duchemin	CSIRO Australian Animal Health Laboratory
Deb Finlaison	Elizabeth Macarthur Agricultural Institute
Ann Hillberg-Seitzinger	USDA Centre for Epidemiology and Animal Health (teleconference)
Angela James	USDA Centre for Epidemiology and Animal Health (teleconference)
Peter Kirkland	Elizabeth Macarthur Agricultural Institute
Ian Langstaff	Animal Health Australia
Lorna Melville	NT Department of Primary Industries and Fisheries
George Milne	University of Western Australia
Kelly Patyk	USDA Centre for Epidemiology and Animal Health (teleconference)
Sally Thomson	Department of Agriculture and Water Resources
Michael Ward	University of Sydney
Belinda Wright	Animal Health Australia
Tom Kompas	CEBRA (Project Lead)
Richard Bradhurst	CEBRA
Mark Stevenson	University of Melbourne
Iain East	Department of Agriculture and Water Resources
Graeme Garner	Department of Agriculture and Water Resources
Rachel Iglesias	Department of Agriculture and Water Resources

Wrap up

The workshop finished with an opportunity for each participant to provide some closing remarks. The key pieces of advice included:

- Focus initially on producing an effective model for *C. brevitarsis*, and novel introduction of a hypothetical Simbu group virus for which this species is moderately to highly competent.
- Keep in mind that what happens in one year affects what happens the following year (the starting conditions of a simulation will have a significant effect on the outcomes observed).
- Look more closely at the existing literature to inform the project.

9 Appendix 2: Vector simulation

9.1 The effect of temperature on population dynamics

Both vector recruitment and vector mortality are influenced by ambient temperature dependent, so an adjusted r must be calculated to allow for the effects of temperature. Available information for *C. brevitarsis* was used to generate these adjusted r values. The prototype model uses the weekly average of the mean daily temperature. We assumed that recruitment (birth plus maturation) is 0 at $\leq$12 °C and maximal at 25 °C. If temperatures (T) are $\leq$12 °C then recruitment = 0; if temperatures are $>$25 °C then recruitment = 1; if temperatures are $>$35 °C then recruitment = 0.9 (larval development is restricted); and if temperatures are between 12 °C and 25 °C then recruitment is defined assuming the linear relationship shown in Equation 4.

$$R = 0.0769T - 0.9231 \tag{4}$$

Adult midges usually live for about 20 days depending on ambient conditions. Survival falls as temperature increases. It was assumed that there is a 99% probability of death by age 21 days at 12 °C in adult vectors, then using the standard formula:

$$P = 1 - exp^{-rate \times time} \tag{5}$$

the average daily probability of death is 0.219. It is assumed that survival is maximum at 12 °C and declines as temperature increases an exponential curve can be fit to these data, as shown in Figure 33.

Combining assumptions around recruitment and mortality rate, r values are adjusted for temperature with a maximum value of r = 0.35 at a mean daily temperature of 25 °C. The population increases if mean daily temp is $>$ 15 °C albeit at varying rate. Below this, the population declines.

The value of r under ideal conditions was multiplied by a correction factor which takes into account the effects of temperature on recruitment and mortality as described. The prototype uses a lookup table to make this correction. Future iterations of AADIS could include the ability for AADIS to dynamically calculate r based on a user defined formula, the ability to import a different lookup table, or the ability to define a constant value for r.

9.2 Local spread

The probability that a free cell is colonised asa result of local spread can be expressed by the expression shown in Equation 6.

$$P = pls \times tw \times vd \times cd \times ew \times dw \tag{6}$$

Where:

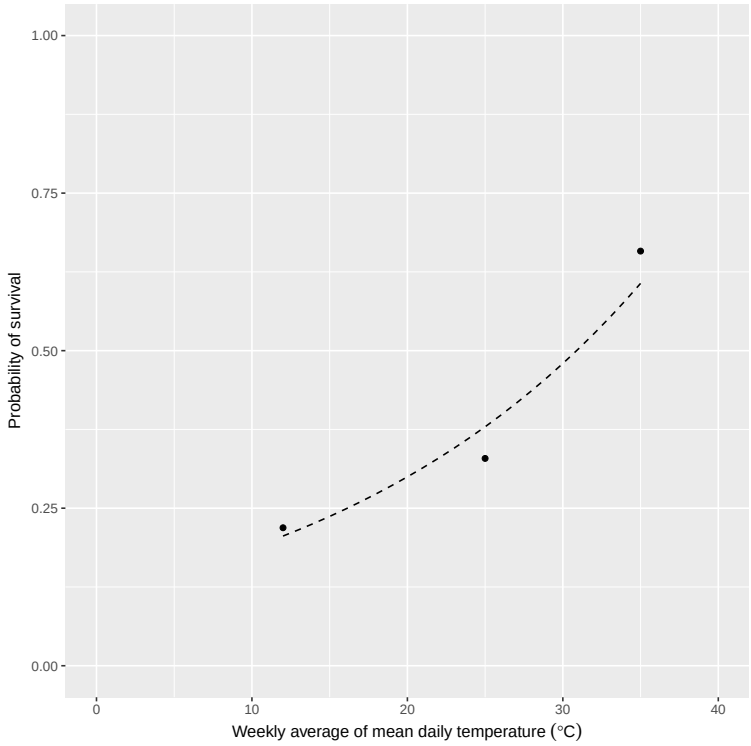


Figure 33: Line plot showing the daily probability of *Culicoides* survival as a function of weekly average of mean daily temperature ambient temperature (°C).

pls = the baseline local dispersal probability.
tw = temperature weighting.
vd = relative vector density in source cell.
cd = relative cattle density of recipient cell.
ew = elevation weighting.
dw = distance weighting.

There is a baseline probability that the vector colonises a free cell under ideal conditions. This probability was modified using weightings that take into account actual conditions on any given day.

The baseline local dispersal probability is a theoretical probability that the vector colonises a free cell under ideal conditions. It must be estimated by calibrating to an existing dataset.

Using what is known of the effects of temperature on culicoides, the following values will be used to modify the baseline local dispersal probability according to temperature. This relationship is shown graphically in Figure 34.

Based on available information (Bishop et al. 2000), increases in elevation will increase dispersal time and reduce the daily probability of spread. There is an approximately 5% increase to dispersal time for 100 metre increases in altitude (Figure 35).

It can be expected that risk of infestation of a given cell decreases as a function of distance from a source cell. The AADIS model diffusion pathway currently provides three possible options: (1) linear; (2) exponential; or (3) power-law.

For any given vector species it would be be necessary to calibrate and fit the most appropriate function using available field data. For simplicity we have initially assumed an exponential function. Assuming a 50% probability that spread is $\leq$3 km and a 90% probability that spread is $\leq$10 km. Sedda et al. (2012) found that 54% of bluetongue outbreaks were $<$ 5 km from a source premises and 92% $<$31 km. Based on these data we fitted the exponential function shown in Figure 36. This is the baseline setting for applying a distance weighting in the model. The user has the option of modifying the size of the kernel (maximum distance) and shape (b value).

Figure 37 shows the AADIS graphic user interface for setting the parameter values for the culicoides diffusion pathway.

9.3 Long distance spread

Assuming conditions are suitable, simulation of long distance dispersal of culicoides follows the following sequence:

- A stochastic process is used to determine whether a long-distance spread event does occur on the day of interest.
- A direction for the event is selected, either randomly or based on likely wind direction.
- The distance of the spread event is selected randomly from a user configurable beta pert distribution. The user specifies the minimum, most likely and maximum distance (in kilometres).

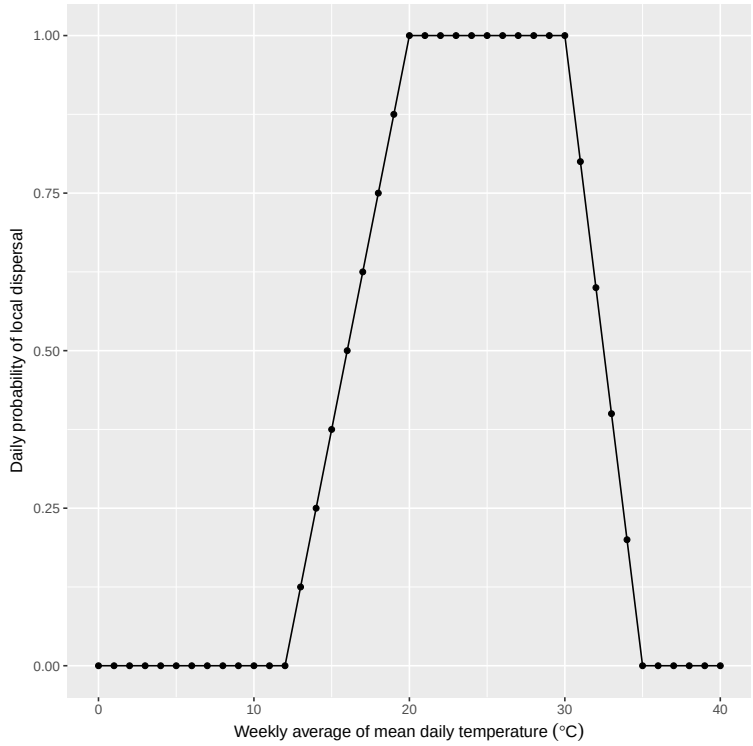


Figure 34: Line plot showing the daily probability of local dispersal as a function of weekly average of mean daily temperature ambient temperature (°C).

- A single cell is selected as the recipient at the appropriate distance and direction.

The probability that a cell will be colonised can be considered as a function of a baseline probability of a long distance jump leading to establishment, the vector density of source cell, and cattle density of recipient cell and is given by the expression shown in Equation 7.

$$p = pd \times vd \times cd \tag{7}$$

Where:

pd = baseline long distance dispersal probability.
vd = relative vector density in source cell.
cd = relative cattle density of recipient cell.

Baseline long distance dispersal probability is a theoretical probability that the vector establishes in a free cell exposed through a long distance 'jump' event under ideal conditions. It must be estimated by calibrating to an existing dataset. The baseline probability is modified to account for the relative vector density of the source cell and the relative cattle density of the recipient cell. As with the local dispersal pathway it will be necessary to adjust the parameters to suit a given vector.

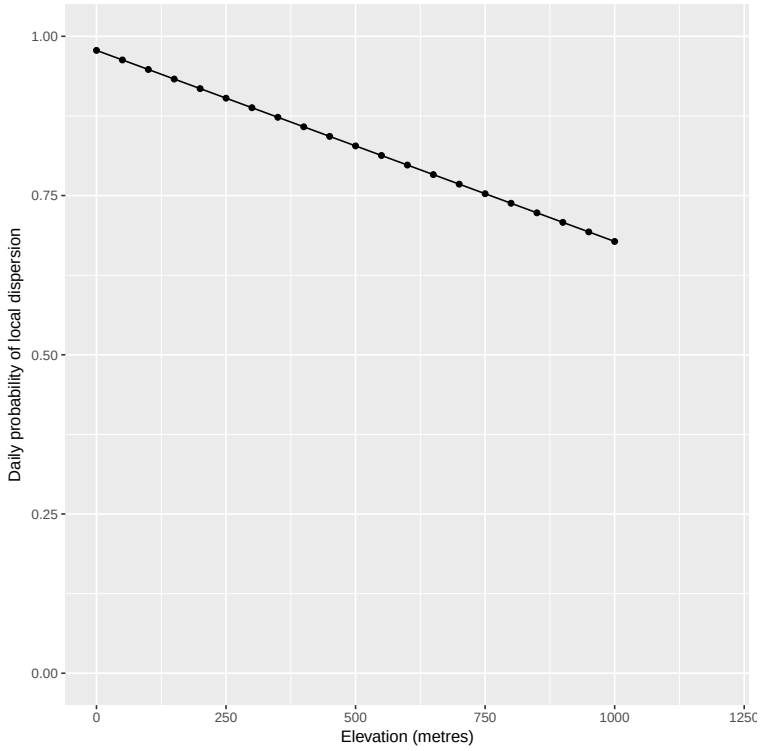


Figure 35: Line plot showing the daily probability of local dispersal as a function of elevation (metres).

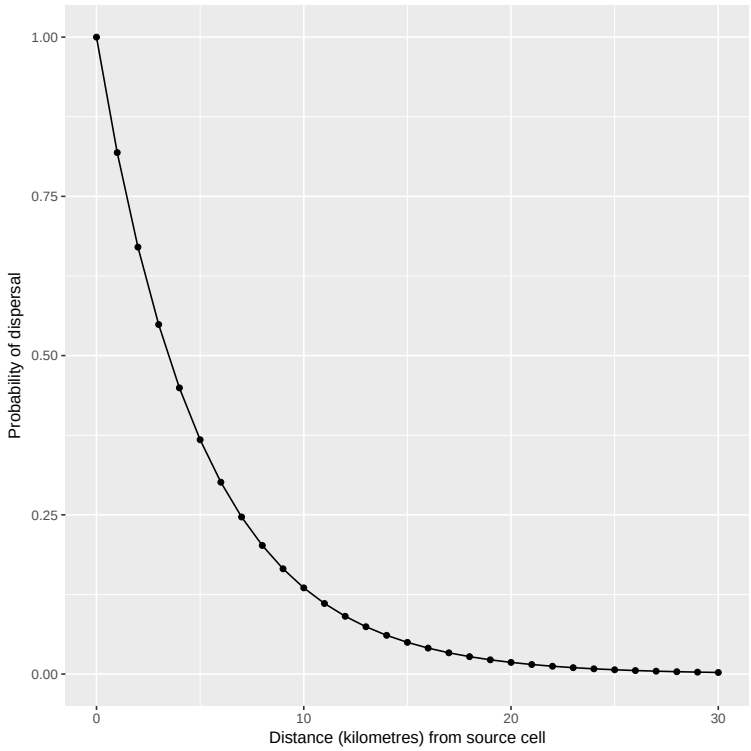


Figure 36: Line plot showing the daily probability of local dispersal as a function of distance (in kilometres) from a source cell.

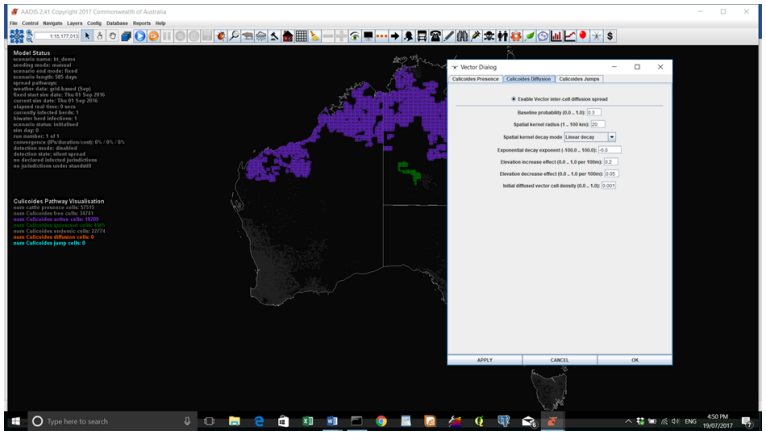


Figure 37: AADIS graphic user interface for setting the parameter values for the *Culicoides* diffusion pathway.

10 Appendix 3: Software updates

10.1 Database

AADIS (Bradhurst et al. 2015) uses a PostgreSQL relational database (PostgreSQL Global Development 2015) to store datasets such as the national herd population, weather data and animal movement patterns. An AADIS database is comprised of approximately 40 tables with each table having a corresponding comma-separated values (CSV) input file. Users update the database by editing the CSV file corresponding to the table of interest and then rebuilding the entire database (to ensure relational integrity between tables). A user may only add/delete/modify rows of an existing table. The creation of a new database table or the addition of new columns to an existing table is a software development activity.

The following tables were added to the AADIS database to support the new vector functionality:

The Weather Grid Data table (Figure 38) was updated with the following new (per grid cell) attributes:

- mean temperature monthly mean temperature for the grid cell (degrees Celsius)
- nearest weather station identifier of the weather station nearest to the grid cell
- annual rainfall average annual rainfall of the grid cell (mm)
- cattle density cattle density of the grid cell (head per square km)
- elevation elevation of the grid cell (metres above sea level)
- region ID identifier of the region containing the grid cell

The Weather Station Weekly Data table (Figure 39) was created with the following (per weather station) attributes:

- weather station ID identifier of the weather station
- month (1 .. 12)
- week of the month (1st, 2nd, 3rd, 4th)
- weekly temperature average weekly temperature (degrees Celsius) for the weather station
- weekly wind speed average weekly wind speed (km per hour) for the weather station

The Weather Station Data table was populated with vector-specific data:

- Climate probabilities monthly probabilities that wind conditions are suitable for vector diffusion

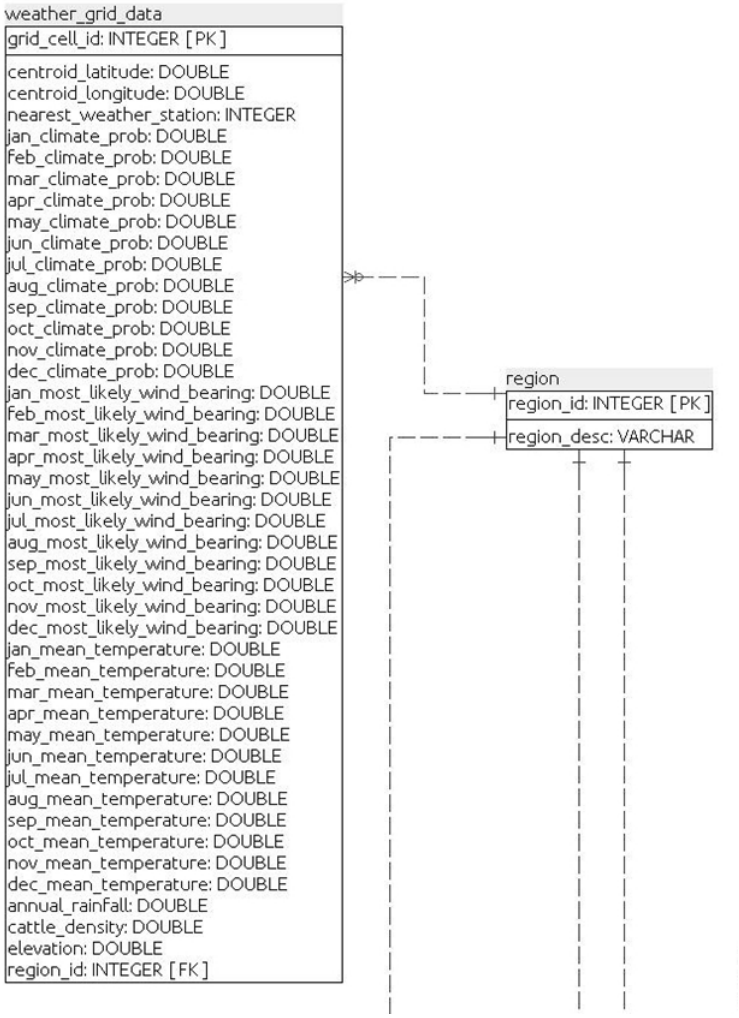


Figure 38: Weather Grid Data database table.

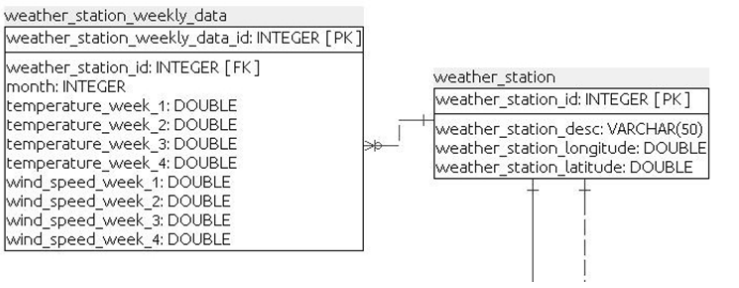


Figure 39: Weather Station Weekly Data database table.

10.2 Configuration files

Scenario configuration

The Scenario Configuration class was updated with the following new parameters:

- temperature delta the amount ($\pm$ fractional degrees Celsius) by which to (optionally) globally increase/decrease temperature data
- minimum temperature delta the largest allowable global temperature decrease (degrees Celsius)
- maximum temperature delta the largest allowable global temperature increase (degrees Celsius)
- rainfall delta the amount ($\pm$ mm) by which to (optionally) increase/decrease rainfall data
- minimum rainfall delta the largest allowable global rainfall decrease (mm)
- maximum rainfall delta the largest allowable global rainfall increase (mm)
- vector report enabled enabling/disabling of the per-run vector report
- vector monthly dump enabled - enabling/disabling of the per-month vector dump
- vector dump day of month the day of the month on which to carry out the monthly dump
- vector seed mode determines how the vector population is established (manual or endemic). Manual seeding is where the initial vector population exists only in specified grid cells. Endemic seeding is where the initial vector population is defined according to endemic criteria in the disease configuration file
- vector num manual seeds - the number of grid cells to be manually seeded with a vector population
- vector seed cell IDs - the identifiers of the grid cells to be manually seeded with a vector population

Disease configuration

The Disease Configuration class was updated with the following new parameters:

- vector presence enabled determines whether the vector presence pathway is enabled
- vector name the name of the vector being modelled
- vector population model the means by which to model growth of the vector population within a grid cell (only 'logistic' is currently supported)

- vector presence min cattle density the minimum cattle density (head per square km) required for a grid cell to support a vector population
- vector endemic min temperature - the minimum mean weekly temperature (degrees Celsius) required for a grid cell to support an endemic vector population
- vector endemic max temperature - the maximum mean weekly temperature (degrees Celsius) allowable for a grid cell to support an endemic vector population
- vector endemic min rainfall - the minimum annual average rainfall (mm) required for a grid cell to support an endemic vector population
- vector endemic max rainfall - the maximum annual average rainfall (mm) allowable for a grid cell to support an endemic vector population
- vector endemic min elevation - the minimum elevation (metres above sea level) required for a grid cell to support an endemic vector population
- vector endemic max elevation - the maximum elevation (metres above sea level) allowable for a grid cell to support an endemic vector population
- vector endemic initial cell density - the initial population density (0.0 to 1.0) of the vector within a grid cell
- vector active min temperature - the minimum mean weekly temperature (degrees Celsius) required for a grid cell to support a non-endemic vector population
- vector active max temperature - the maximum mean weekly temperature (degrees Celsius) allowable for a grid cell to support a non-endemic vector population
- vector active min rainfall - the minimum annual average rainfall (mm) required for a grid cell to support a non-endemic vector population
- vector active max rainfall - the maximum annual average rainfall (mm) allowable for a grid cell to support a non-endemic vector population
- vector active min elevation - the minimum elevation (metres above sea level) required for a grid cell to support a non-endemic vector population
- vector active max elevation - the maximum elevation (metres above sea level) allowable for a grid cell to support a non-endemic vector population
- vector quiescence max days the maximum number of days outside the allowable temperature range that a vector population in a grid cell can survive quiescently
- vector diffusion enabled determines whether the vector diffusion (spatial kernel) pathway is enabled
- vector diffusion baseline probability baseline probability that the vector population in a given grid cell will diffuse out of the cell on any given day

- vector diffusion radius maximum extent (km) of the spatial kernel from the centroid of the source grid cell
- vector diffusion decay mode linear or exponential
- vector diffusion decay exponent (only applicable to exponential decay)
- vector diffusion elevation increase effect the dampening effect (0.0 to 1.0) that an increase in elevation (from source cell to target cell) has on the probability of diffusion
- vector diffusion elevation decrease effect - the amplifying effect (0.0 to 1.0) that a decrease in elevation (from source cell to target cell) has on the probability of diffusion
- vector diffusion max wind speed the maximum average weekly wind speed (kmh^{-1}) at which diffusion can occur
- vector diffusion initial cell density - the initial population density (0.0 to 1.0) of the vector after a diffusion event has occurred
- vector jump enabled determines whether the vector jump pathway is enabled
- vector jump baseline probability baseline probability that the vector population in a given grid cell will jump out of the cell on any given day
- vector jump mode windborne (where the jump bearing is influenced by wind direction) or random
- vector jump min distance 1st parameter for the beta pert distribution governing jump distance (km)
- vector jump most likely distance 2nd parameter for the beta pert distribution governing jump distance (km)
- vector jump max distance 3rd parameter for the beta pert distribution governing jump distance (km)
- vector jump initial cell density - the initial population density (0.0 to 1.0) of the vector in the destination cell after a jump event has occurred

10.3 Grid subsystem

Grid cells are now agents in the AADIS agent-based model alongside herds, farms, and saleyards, and as such, the Cell class now extends the Agent class. A grid cell is now capable of hosting a vector population (Figure 40), the growth characteristics of which is determined by the Logistics class. A population could be represented by any growth model, however, for this project only a Logistic growth model was implemented.

The Grid Manager class was expanded beyond its original purpose of spatial indexing (Bradhurst et al. 2015) to manage dynamic grid cell updates in the same way that the Herd Manager class manages herd updates and the Farm Manager class manages farm updates (Figure 41). The AADIS

agent-based model scheduler synchronously updates the various agent caches at the conclusion of each simulation day's asynchronous processing. The Grid Manager maintains dynamic lists of cells are maintained that correspond to the endemic, active and quiescent vector population.

10.4 Agent-based model

A new Vector abstract class was created that extends the AADIS Agent-Based Model Environment class in a similar fashion to the Spread and Control abstract classes. Three Vector concrete classes were created: Vector Presence, Vector Diffusion and Vector Jump (Figure 42). As with all AADIS Agent-Based Model components the Vector Presence, Diffusion and Jump classes operate concurrently and independently (Bradhurst et al. 2015).

The Vector Presence class is responsible for:

1. Establishing the initial vector population based on the configured seeding mode (manual or endemic). In manual mode the seed cells are user-specified while in endemic mode the seeds cells are determined by the configured cattle density, rainfall, temperature and elevation criteria. A vector population is introduced into each seed cell by creating and attaching a Logistic (Population) object to the Cell agent. The Population object predicts the population density of the vector in the cell over time.
2. Determining whether an active vector population becomes quiescent (based on the weekly mean temperature falling below the configured minimum).
3. Determining whether a quiescent vector population becomes active again (based on the weekly mean temperature rising above the configured minimum within the maximum number of days that a population can remain quiescent).
4. Determining whether a quiescent vector population becomes extinct (based on the weekly mean temperature remaining below the configured minimum beyond the maximum number of days that a population can remain quiescent).

The Vector Diffusion class stochastically determines whether the vector population in a cell spreads into surrounding grid cells. For each active source cell a set of candidate destination cells is derived based on the configured spatial kernel radius. The probability that diffusion will occur on any given day is influenced by the vector population density of the source cell, the cattle density and average weekly temperature of the candidate cell, and the distance and elevation difference between the cells. If a candidate cell is deemed to have been diffused into it is seeded with a new vector population by creating and attaching a Logistic (Population) object to the Cell agent.

The Vector Jump class stochastically determines whether the vector population in a cell jumps into grid cells that lie beyond the diffusion radius. An active cell is only eligible as a jump source if the average wind speed (based on data from the nearest weather station) is less than or equal to the configured maximum value. The jump distance is determined by sampling the configured beta pert distribution. The jump bearing is dictated by the configured jump mode - windborne (governed by wind direction) or random. The probability that a jump will occur on any given day is influenced

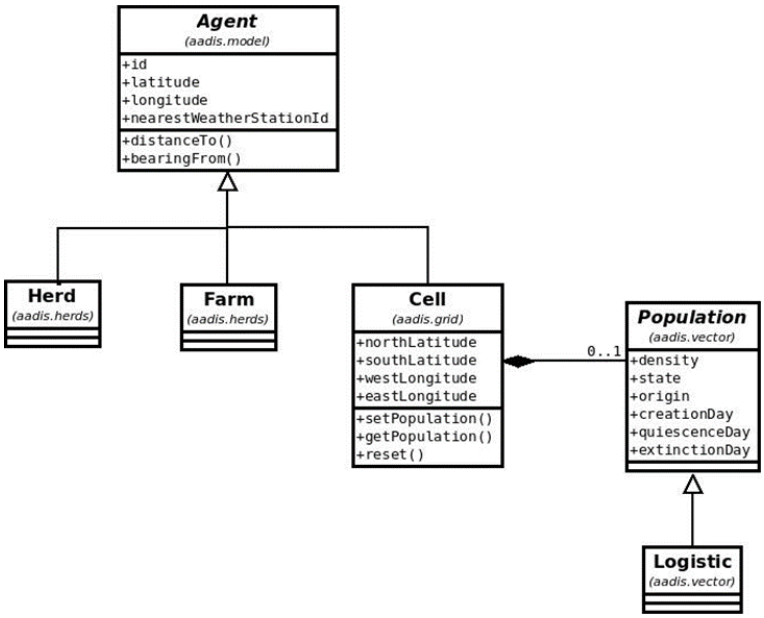


Figure 40: Grid subsystem.

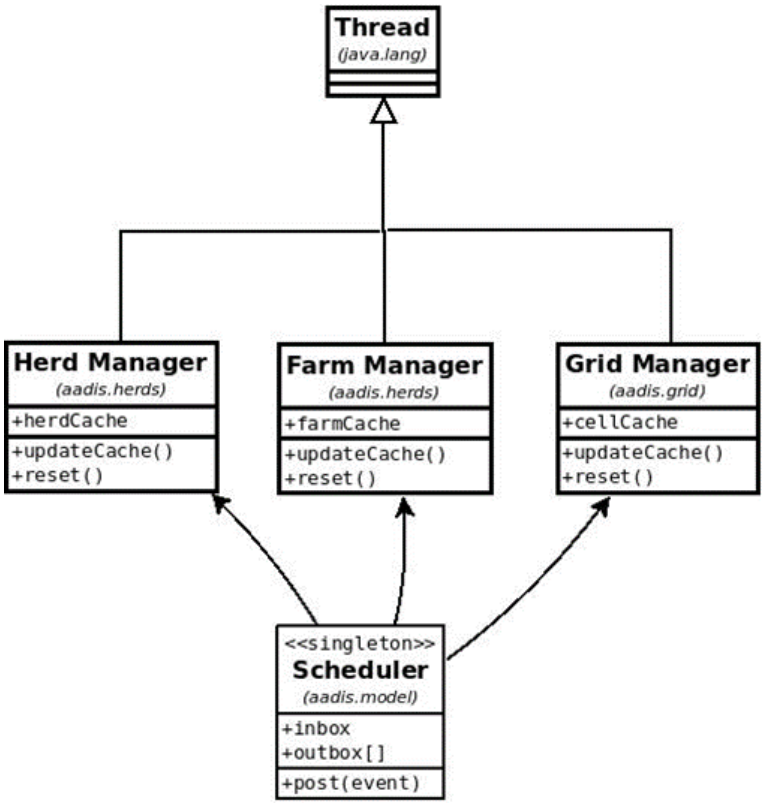


Figure 41: Grid manager.

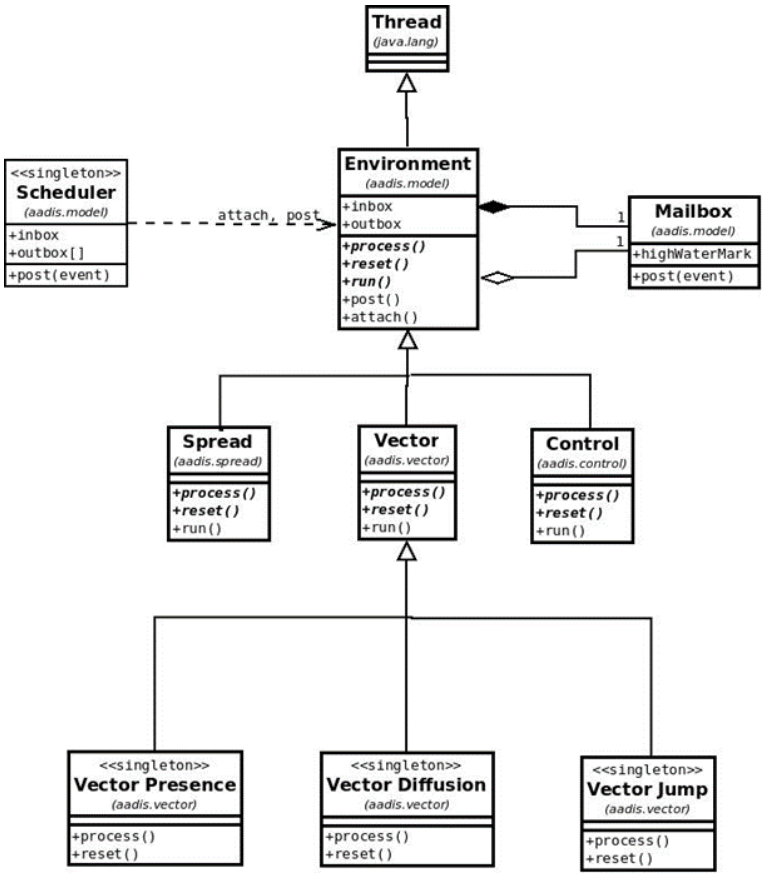


Figure 42: Vector subsystem.

by the vector population density of the source cell and the cattle density of the candidate cell. If a candidate cell is jumped into it is seeded with a new vector population by creating and attaching a Logistic (Population) object to the Cell agent.

10.5 Graphical user interface

- A Cattle Density display layer was created to visualise the cattle density raster data in graduated colours.
- A Rainfall display layer was created to visualise rainfall raster data in graduated colours.
- A Temperature display layer was created to visualise temperature raster data in graduated colours.
- An Elevation display layer was created to visualise elevation raster data in graduated colours.
- A Towns display layer was created to visualise cities and towns on demand (to assist with visual assessment of vector spread). A Town Popup was created to manually inspect data for specific towns.
- A Lat Long display layer was created to visualise points of latitude and longitude on demand (to assist with visual assessment of vector spread).
- A Vector display layer (Figure 43) was created to dynamically visualise the vector population as either graduated colours (depicting densities) or directed arrows (depicting the jump/diffusion spread networks).
- The Visualisation Key (Figure 43) was updated to report the number of cells with cattle, number of cells free of vector, number of cells with an active vector population, number of cells with a quiescent vector population, number of cells with an endemic vector population, number of non-endemic active cells due to diffusion, and number of non-endemic active cells due to jump.

A Grid Popup (Figure 44) was created (akin to the Herd Popup, Farm Popup, Saleyard Popup, Town Popup and Weather Station Popup) to manually display data for individual cells. Static cell data includes the boundary lines of latitude and longitude, elevation, cattle density, and annual average rainfall, and dynamic data includes temperature, wind speed, vector population state, density and source. If the grid cell is hosting a vector population then the vector prevalence curve (Figure 44) can be displayed via the Grid Popup.

A Vector Dialogue (Figure 45) was created that allows the manual setting of a range of parameters pertaining to vector presence, diffusion and jump.

The Grid Dialogue (Figure 46) was updated with display controls for the cattle density, temperature, rainfall and elevation visualisation layers, and the global temperature and rainfall adjusters.

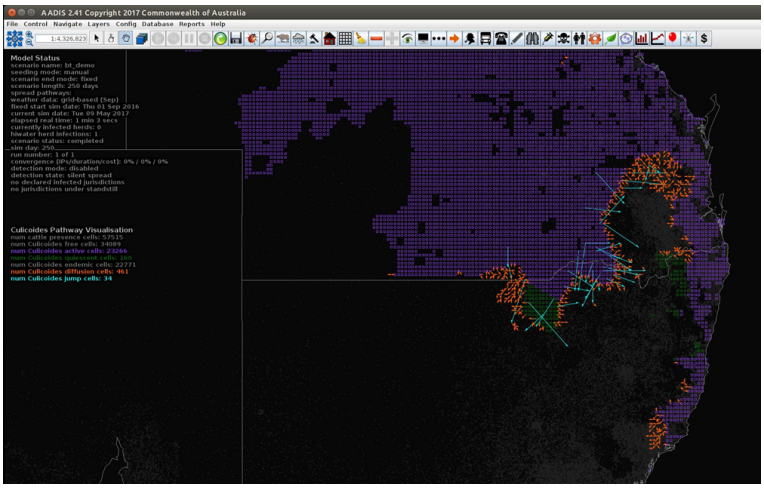


Figure 43: Vector population visualisation.

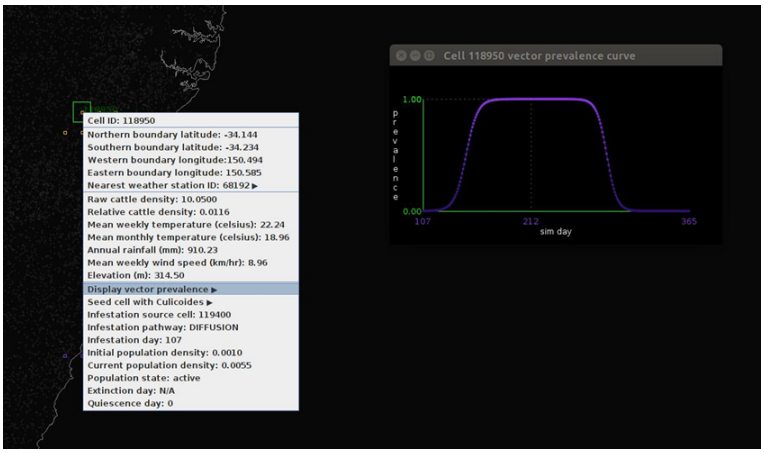


Figure 44: Grid pop-up.

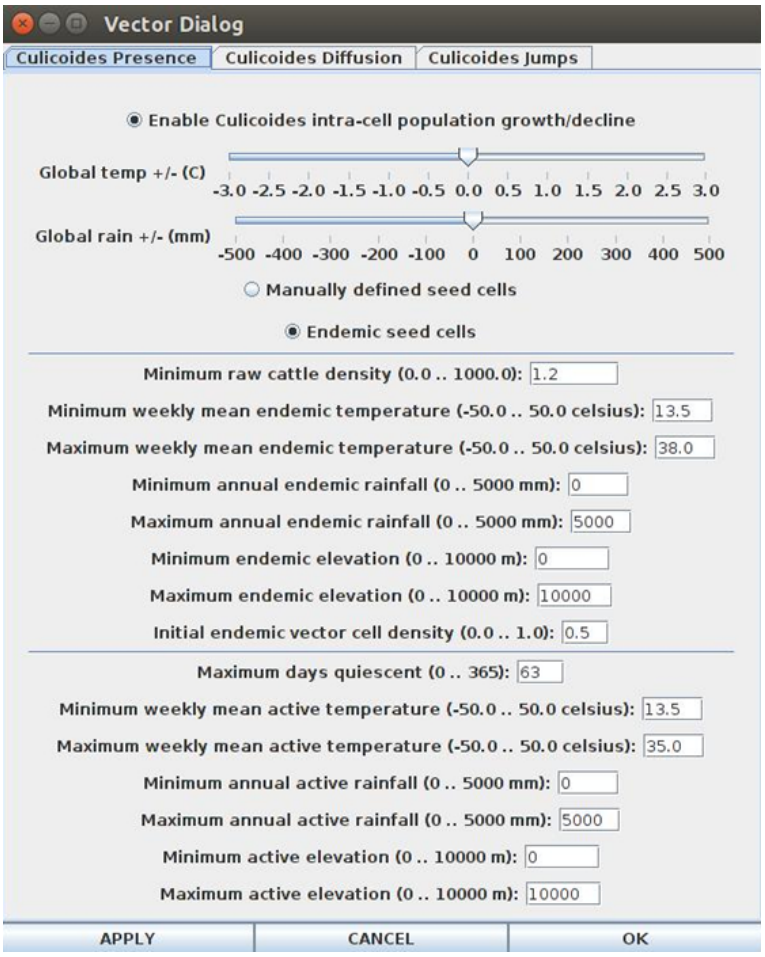


Figure 45: Vector Dialogue.

10.6 Reports

A Vector Report class was created that reports (on a per-run basis):

- number of cells with an endemic vector population
- number of cells with an active vector population
- number of cells with a quiescent vector population
- number of cells with no vector population
- number of non-endemic cells where a vector population arose via the diffusion mechanism
- number of non-endemic cells where a vector population arose via the jump mechanism

A Vector Dump class was created that reports (on a per-day basis):

- the vector population state of each grid cell (free, active or quiescent)
- the population density of each grid cell that has a vector population

10.7 Documentation

The AADIS configuration guide (accessible via the Help menu) was updated with descriptions of all new user configurable parameters.

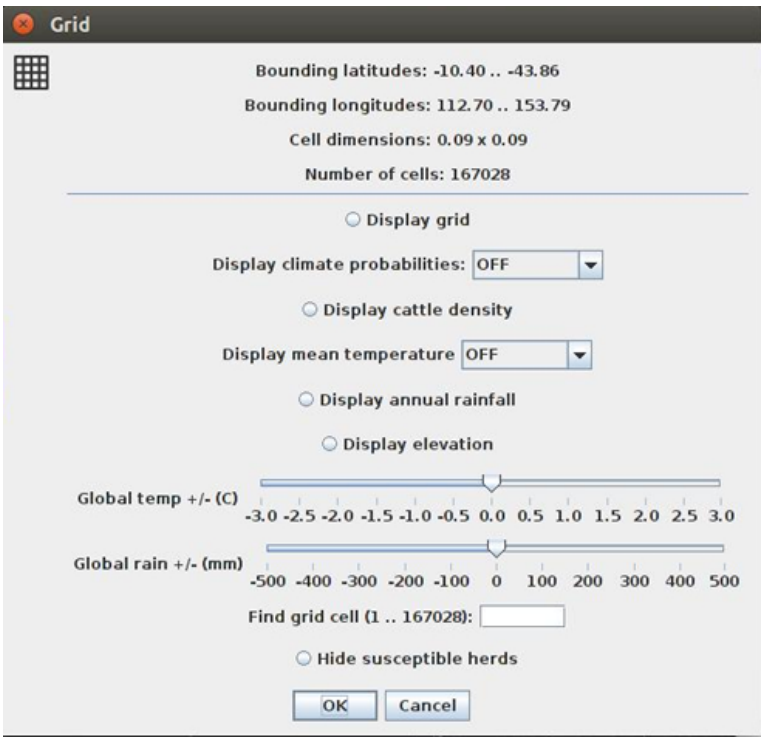


Figure 46: Vector Dialogue.

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