

# DEVELOPMENT OF A TEMPERO-SPATIAL DISEASE DISTRIBUTION MODEL FOR ARBOVIRUSES AND THEIR VECTORS IN AUSTRALIA.

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Unlike many other pathogens, the distribution of arboviruses can vary widely and rapidly due to changes in distribution of the vector population. These changes are due to many factors including geographical and meteorological factors. To undertake risk assessments and avoid the transmission of these viruses through international trade, it is important to clearly understand the distribution of the viruses at any given moment. Approaches to determining the distribution of arboviruses used in the past have relied on estimating the historical maximum actual or potential extent of the virus over a specified time period, varying from 2 to 10 years or more. The problem with this approach is that, due to annual or seasonal variations, large areas of the 'infected' zone will in fact be free for much of the time. In addition, it is possible that unusual weather conditions could cause the incursion of viruses into the 'free' zone.

To address these problems, a model is being developed which aims to determine the risk of arboviral activity (specifically bluetongue virus) in real time.

## **Materials & Methods**

The model is implemented in a geographical information system (ArcView GIS 3.1<sup>1</sup>) which uses a 'software socket'<sup>2</sup> to allow simple and rapid model development, testing and refinement. The model uses a series of grid-based data sources to make predictions for each point in Australia. Input data include livestock population, topography, vegetation, temperature, rainfall and direct vector and virus distribution observations derived from sentinel herds and traps in the National Arbovirus Monitoring Program (NAMP). The NAMP data is collected and managed using a Web-based information system<sup>3</sup>.

The model is divided into two major components, as shown in Figure 1. The first is a model to predict the probability of vector activity, and the second uses these predictions to determine the probability of virus activity, both components using a combination of biological and statistical sub-models. The vector model uses a statistical (logistic) model to determine the suitability of the environment for vector survival, based on historical vector trapping data and weather observations, and includes factors such as average minimum temperature, vegetation, and livestock population (the main *Culicoides* vector can only breed in cattle dung). An elimination model detects extreme conditions under which the vector would be eliminated. A dispersal model determines the probability of the vector spreading to adjacent areas, and uses vector concentrations, distance of spread, speed of spread, and inhibiting geographical factors such as steeply sloping ground,

forested and non-grassed areas. Under certain conditions, the vector is able to over-winter with no apparent activity, and re-emerge when the weather becomes warmer, so a separate component models the probability of this. The final component of the vector model incorporates actual vector distribution observations from NAMP to constantly re-calibrate the predictions.

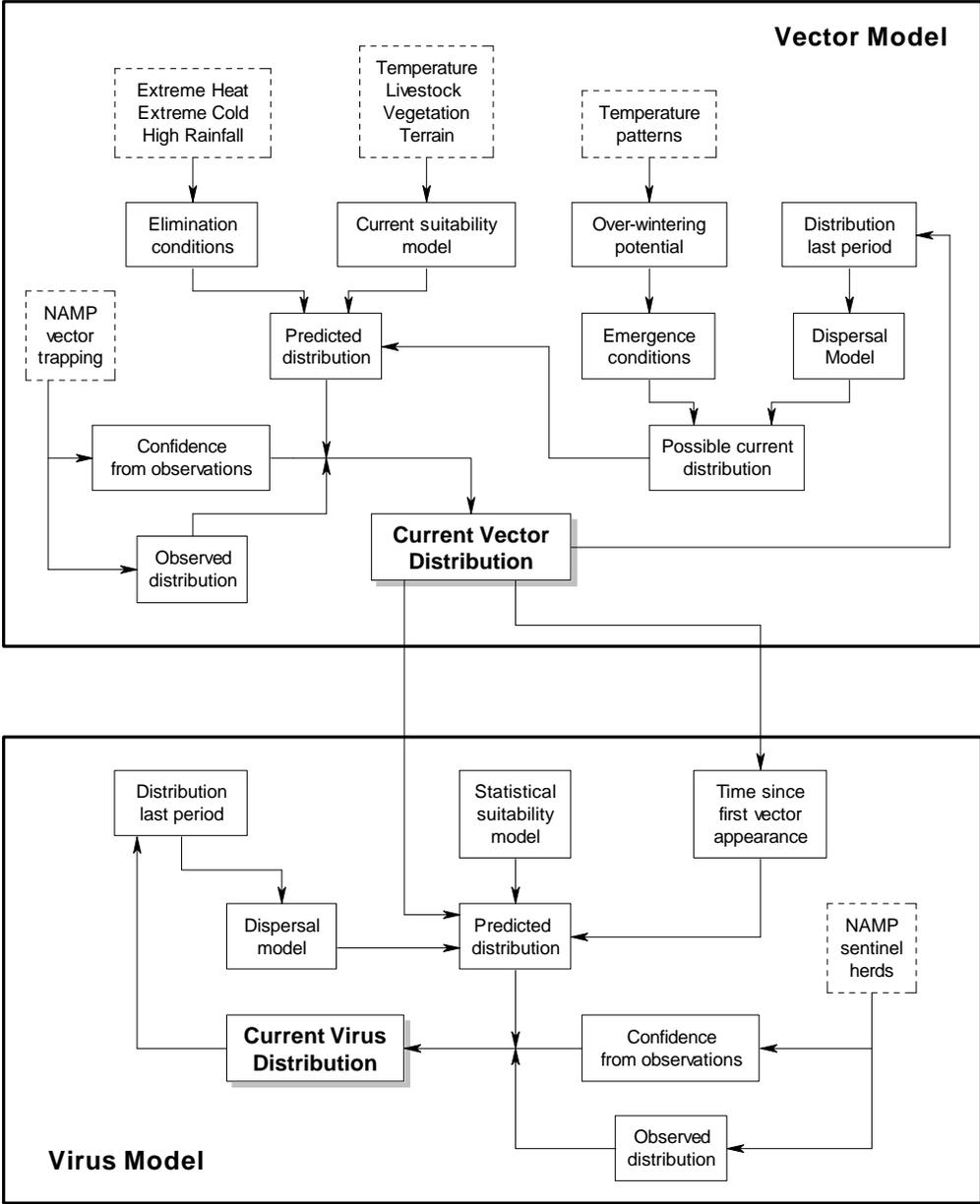


Figure 1: Schematic outline of the model structure.

The virus model uses the outputs of the vector model to determine the maximum possible distribution of the virus. In addition, a statistical model based on long term seroconversion data gathered from NAMP sentinel herds is used to predict the environmental suitability for vector activity. The probability of transmission is related to the density of the vector population, and this is modelled using the

time elapsed since the first appearance of vectors in an area. A dispersal model predicts the spread of the virus amongst the vector population. As with the vector model, real time NAMF sentinel herd seroconversion data is used to constantly recalibrate the model.

### Results

The outputs of all the components of the model are expressed in terms of probability, and are presented as grids with a cell size of approximately 25km by 25km. The final model output is a grid predicting the probability of virus activity and is recalculated on a weekly basis. At the time of writing, the final model predictions were still being validated. Figure 2 shows an example of the summer-time predicted distribution of the vector, with darker areas indicating a higher probability of activity.

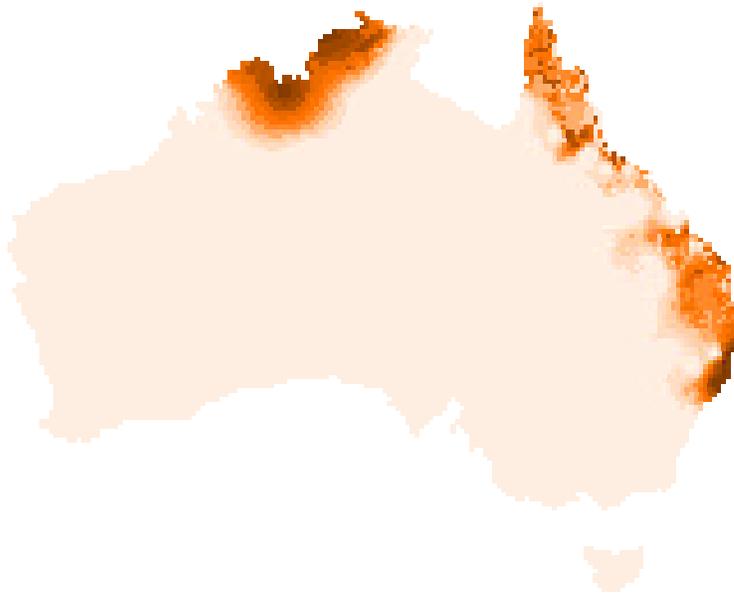


Figure 2: Example map showing the predicted probability of vector activity during summer 1997.

### Discussion

Once validated, it is anticipated that the model will be able to be used as the basis for a new dynamic zoning system. Based on the probability grids, a zone will be defined (eg with greater than 1% probability of viral activity) as a zone of potential viral activity. The remainder of the country will be considered free from the virus for the period of validity of the prediction. The final output will therefore be a simple map divided into the two zones, based on the cut-off probability. This will enhance Australia's capability to meet trading partner health certification requirements and ensure a negligible risk of the international spread of selected arboviruses.

### References

- <sup>1</sup> ESRI (Environmental Systems Research Institute), 1998. ArcView GIS 3.1 (software program).
- <sup>2</sup> Cameron AR, 2000. Increasing the lifespan of predictive disease models: The use of a Software Socket in a tempero-spatial disease distribution model for arboviruses and their vectors. ISVEE 2000 (Paper number 260)
- <sup>3</sup> Cameron AR, 2000. Development of an Internet-based information system for monitoring veterinary arboviruses and their vectors. ISVEE 2000 (Paper number 264)