



CEBRA Report Cover Page				
Title, ID, & Output #	<i>Using decision support tools in emergency animal disease planning and response: Foot and mouth disease. Project 1404D</i>			
Project Type				
Project Sponsor	<i>Tim Chapman, First Assistant Secretary, Biosecurity Animal Division</i>	DAWR Project Leader/s	<i>Dr Graeme Garner</i>	
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Project Objectives	<p><i>The aim of this extension is to evaluate decision tools to improve decision-making for managing an FMD incursion. The specific objectives are:</i></p> <ol style="list-style-type: none"> <i>1. To assess the utility of information that would be available to disease managers in real time early in an FMD outbreak to 'predict' the potential size of the outbreak in order to inform choice of appropriate control measures;</i> <i>2. To evaluate the metrics and outbreak parameters that may indicate the size of an FMD outbreak through a thorough statistical analysis of information that would be known to disease managers, using results from both Australian and New Zealand simulations;</i> <i>3. Evaluate a series of strategies and combination of strategies, including vaccination, given multiple management objectives using dynamic optimisation</i> 			
Outputs	<p><i>A detailed report on the work and the findings to be provided</i></p> <p><i>Papers for publication in the scientific literature</i></p> <p><i>Presentations to key stakeholders</i></p>			
CEBRA Workplan	Year 2015-16			
Budget	<i>\$90,000</i>			
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Research Outcomes				
Recommendations				
Related Documents				
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2 Publications

2.1 Peer-reviewed papers

Garner, M.G., East, I.J., Stevenson, M.A., Sanson, R.L., Rawdon, T.G., Bradhurst, R.A., Roche, S.E., Pham, H. and Kompas, T. (2016) Early decision indicators for foot-and-mouth disease outbreaks in non-endemic countries. *Frontiers in Veterinary Science* (accepted for publication 15 November 2016).

2.2 Conference presentations

Stevenson, M.A. Early decision indicators for foot-and-mouth disease outbreaks in non-endemic countries. Presented at the AAHL Emergency Animal Disease Symposium, Australian Animal Health Laboratory, Geelong, Victoria, October 26 - 27, 2016.

East, I.J. Early decision indicators to predict the severity of an FMD outbreak. Presented at Science Week, Australian and New Zealand College of Veterinary Scientists, Gold Coast, July 7 - 9, 2016.

Rawdon, T.G. Presentation to Centre for Epidemiology Animal Health, USDA – Fort Collins, Colorado, September 2015.

Rawdon, T.G. Presentation to Korea - New Zealand Animal Health and Epidemiology Workshop – Seoul, April 2016.

Presentation to Chief Veterinary Officers of Australia, New Zealand, United States and Canada at Quadrilateral group of countries meeting, 25 October, 2016.

Cook, C. Open Session of the European Commission for the Prevention of Foot and Mouth Disease, Cascais, Portugal, 26 - 28 October, 2016.

3 Glossary

AADIS	Australian Animal Disease Model
ABARES	Australian Bureau of Agriculture and Resource Economics and Sciences
AUC	Area under control
BRT	Boosted regression tree
CART	Classification and regression tree
CCEAD	Consultative Committee on Emergency Animal Diseases
DCP	Dangerous contact premises
EAD	Emergency animal disease
EDR	Estimated dissemination ratio
FFI	First fortnight incidence
FFO	First fortnight outbreaks
FFS	First fortnight spatial spread
FMD	Foot and mouth disease
IP	Infected premises
ISP	Interspread Plus
NPV	Negative predictive value
PPV	Positive predictive value
OIE	World Organisation for Animal Health
ROC	Receiver operating characteristic (curve)
SO	Slaughter out
VEAG	Vaccine Expert Advisory Group

4 Executive summary

Disease managers face many challenges when deciding on the most effective control strategy to manage an outbreak of foot and mouth disease (FMD). Decisions have to be made under conditions of uncertainty and where the situation is continually evolving. In addition, resources for control are often limited. A modelling study was carried out to identify characteristics measurable during the early phase of a FMD outbreak that might be useful as predictors of the total number of infected places, outbreak duration and the total area under control.

The study involved two modelling platforms in two countries (Australia and New Zealand) and encompassed a large number of incursion scenarios. Linear regression, classification and regression tree and boosted regression tree analyses were used to quantify the predictive value of a set of parameters on three outcome variables of interest: the total number of infected places, outbreak duration and the total area under control. The number of infected premises, number of pending culls, area under control, estimated dissemination ratio, and cattle density around the index herd at days 7, 14 and 21 following first detection were associated with each of the outcome variables. Regression models for the size of the area under control had the highest predictive value ($R^2 = 0.51 - 0.9$) followed by the number of infected premises ($R^2 = 0.3 - 0.75$) and outbreak duration ($R^2 = 0.28 - 0.57$). Predictability improved at later time points in the outbreak. Predictive regression models using various cut-points at day 14 to define small and large outbreaks had positive predictive values of 0.85 - 0.98 and negative predictive values of 0.52 - 0.91, with 79% to 97% of outbreaks correctly classified. On the strict assumption that each of the simulation models used in this study provide a realistic indication of the spread of FMD in animal populations we conclude that relatively simple metrics available early in a control program can be used to indicate the likely magnitude of an FMD outbreak under Australian and New Zealand conditions.

5 Introduction

Foot-and-mouth disease (FMD) continues to represent the most serious threat to the Australian and New Zealand livestock industries. Australia's freedom from FMD underpins an annual trade in live animal and meat exports of AUD 6.9 billion and a further AUD 8.0 billion of other livestock products ([Anonymous, 2013b](#)). An outbreak of FMD would seriously impact both Australia's livestock sector and the economy as a whole. A recent study estimated the present value of total direct economic losses over 10 years for a large multi-state outbreak at AUD 52 billion ([Buetre et al., 2013](#)). Animal products constitute a significant proportion of New Zealand exports, and the provisional results of recent modelling of the economic impacts of a large FMD outbreak have put net GDP losses over an eight year period at between NZD 17 and NZD 20 billion dollars ([Forbes & Halderen, 2014](#)).

Both Australia's and New Zealand's preferred approach to control an outbreak of FMD is to eradicate the disease in the shortest possible time while minimising economic impact using stamping out, supported by a combination of strategies that include national livestock standstills, quarantine and movement controls, tracing and surveillance ([Anonymous, 2011](#); [Animal Health Australia, 2014](#)). Additional measures that may be taken if authorities consider that they would be beneficial in containing and managing the outbreak include vaccination, pre-emptive slaughter, zoning/compartimentalisation and risk-based movement controls.

Australia and New Zealand invest considerable resources in preparedness and planning for emergency animal diseases (EADs), including maintaining government/industry funded vaccine banks for FMD. Despite recent changes to both Australian and New Zealand contingency plans to recognise that vaccination could be an important component of an FMD control program, it is unclear how, when or even if vaccination should be used, and if it is used, how vaccinated animals should be managed.

Modelling studies in Australia ([Garner et al., 2014](#); [Roche et al., 2014](#); [Abdalla et al., 2005](#)) and overseas ([Roche et al., 2014](#); [Keeling et al., 2003](#); [Tomassen et al., 2002](#)) have shown that vaccination could be effective in reducing the duration and/or size of outbreaks in situations where disease is widespread, where there is a high rate of spread or resources for stamping out are limited. Reports indicate that early vaccination could have been beneficial in eradicating the disease earlier than was the case with recent FMD outbreaks in Korea ([Sakamoto, 2012](#)) and Japan ([Akashi, 2012](#)). Thus, vaccination is increasingly being recognised as a potential useful tool to assist in containing and eradicating FMD outbreaks. However, while vaccination can contribute to earlier eradication of the disease, it will be associated with additional costs — keeping vaccinated animals in the population will delay the period until FMD-free status is regained under the World Organization for Animal Health guidelines ([OIE, 2015](#)) and add additional complexity to post-outbreak surveillance programs. These issues are of particular concern for countries with significant exports of livestock and livestock products as, under current conditions, the use of vaccination and the presence of FMD vaccinated animals in the population could be expected to cause significant market access difficulties.

Disease managers are faced with a number of challenges when deciding on the most effective disease control strategy to implement in an exotic animal disease outbreak. FMD is particularly challenging given its wide host species, potential for rapid spread and serious socio-economic consequences. During an outbreak, decisions are often made under significant uncertainty and in conditions that are continually evolving. Resources are often limited and will drive the effectiveness

of disease control efforts. Experience overseas suggests that resource and logistical issues are critical considerations when evaluating disease control strategies ([Davies, 2001](#); [Bouma et al., 2003](#); [Nishiura & Omori, 2010](#)).

Decision support tools including disease simulation models can offer valuable insights into the effectiveness of different control limitations ([Garner & Hamilton, 2011](#)). Although there have been a number of modelling studies comparing control strategies for FMD, virtually all of these start with the application of a pre-determined strategy, regardless of the actual disease situation. For example, in the case of vaccination, comparisons are made on the basis of sets of model runs with and without vaccination. This approach can measure the statistical performance of control strategies with and without vaccination but provides limited assistance to the disease manager to know exactly when vaccination should be applied. This is particularly important as vaccination is likely to perform better when used early in an outbreak ([Roche et al., 2014](#)). However, a decision to vaccinate early in the outbreak may result in using vaccination in situations where it is not actually required with consequent implications for post-outbreak surveillance, management of vaccinated animals and regaining FMD-free status and access to markets. Conversely, not using vaccination in some situations may lead to larger and longer outbreaks, increased control costs and greater on-going impacts on industry and local communities.

From a planning and management perspective it would be very useful to have access to decision support tools that take into account the information that would be available to disease managers in 'real time' that could provide an indication of the potential severity of outbreak that could ensue, thus enabling decisions on specific measures like vaccination to be made early when they are likely to be most effective.

[McLaws & Ribble \(2007\)](#) explored the relationship between early detection and epidemic size for a number of FMD outbreaks in non-endemic countries. They did not find a direct relationship between time to detection and total number of infected premises or total animals killed for disease control. They suggest that movement of animals through markets was the most critical factor contributing to very large outbreaks. [Sarandopoulos \(2015\)](#) conducted a review of 125 FMD epidemics in non-endemic temperate countries that were reported to the OIE between 1 January 2005 and 31 December 2013 to look for associations between epidemic size/duration and potential predictor variables. The variables assessed in this study included susceptible animal densities, weather conditions at the time of detection, the number of infected premises (IPs) detected in the first seven days and the size of the infected area at seven days (based on a convex hull calculation). In total, ten candidate predictor variables were tested for their association with epidemic size and duration using a zero inflated negative binomial regression model. Cattle density, pig density and the number of IPs at seven days were all positively associated with epidemic size while increased average temperature in the month of detection was associated with 'smaller' outbreaks.

Using data from the outbreak of FMD that occurred in the United Kingdom in 2001, first fortnight incidence (FFI) i.e. the cumulative number of new FMD-infected premises found in the first two weeks of the response, was found to be a useful predictor of the size and duration of outbreaks at the regional and national scale ([Hutber et al., 2006](#); [Kitching et al., 2005](#)). The larger the number of detected herds within the first two weeks, the greater the probability of a large outbreak. [Halasa et al. \(2013\)](#) extended the approach of [Hutber et al.](#) to incorporate the first fortnight spatial spread (FFS) as well as FFI (which they renamed first fortnight outbreaks — FFO, since a true incidence

rate is not actually calculated) in a simple decision tool using simulated FMD outbreaks. In terms of outcome, in addition to outbreak size (the number of infected herds and outbreak duration) they also considered geographical size and costs. Halasa and colleagues found good correlations between FFO and FFS and all of the outcome variables, indicating that both FFO and FFS have the potential as reasonable predictors of epidemic outcomes. They also found that the type of index herd was a significant predictor of epidemic outcome.

The work of [Hutber et al. \(2006\)](#), [Halasa et al. \(2013\)](#) and [Sarandopoulos \(2015\)](#) indicates that information available to disease managers early in an outbreak can be used to make inferences about the potential severity of the outbreak and could perhaps be incorporated into decision support tools. However, a concern is that FFO and FFS are quite simple parameters that can be expected to be sensitive to outbreak management response, especially the effectiveness of the surveillance/reporting system. For example while a low FFO may be indicative of a limited spread and small number of infections, it could also be indicative of the adequacy of resources to undertake surveillance and tracing. In addition, based on [McLaws & Ribble \(2007\)](#) and [Sarandopoulos \(2015\)](#) other factors such as local animal densities and involvement of animal markets may also be important. It would also be useful to see how robust the findings are across different incursion scenarios and between countries.

Accordingly, this study was undertaken to test the value of a broad range of parameters to predict the severity of the epidemic outcome, concentrating on those that would be known or available to disease managers early in an FMD outbreak. The study included Australia and New Zealand. In the absence of outbreaks of FMD in the two countries, disease modelling has been used to simulate FMD outbreaks.

6 Materials and Methods

6.1 Disease models

The Australian Animal Disease spread model (AADIS) ([Bradhurst et al., 2015a,b](#)) is a hybrid model that simulates the spread and control of FMD in livestock populations at a national scale. AADIS uses the herd as the epidemiological unit of interest and models the spread of disease both within and between herds. Spread of disease within a herd is modelled using a deterministic equation based approach and between-herd spread is modelled with a spatially-explicit stochastic agent-based model. There are five discrete spread pathways in the between-herd model: direct animal movements, local spread (infection of farms within close geographical proximity by unspecified means), indirect contact (via contaminated equipment, people or animal products), animal movements via saleyards and windborne spread.

Ten different herd types are recognised in the model including specialist intensive and extensive beef, dairy and sheep enterprises, large and small piggeries, mixed beef and sheep enterprises, smallholders and feedlot producers. This allows common attributes, such as patterns of livestock turnoff, to be applied based on herd type. The model incorporates the attributes and spatial locations of individual farms, saleyards, weather stations, local government areas and various other features of the regional environment.

For FMD control, AADIS is configured to support the range of mitigation strategies described in Australia's contingency plans for FMD ([Animal Health Australia, 2014](#)) with the effectiveness of these measures dependent on resources.

InterSpread Plus (ISP) ([Stevenson et al., 2013](#)) is a spatial and stochastic simulation model of infectious disease in domestic animal populations. ISP is a state-transition model meaning that the epidemiological units of interest (farm locations) exist in either the susceptible, infected and not-at-risk state at any given time. Similar to AADIS, ISP uses a series of user-defined parameters to define the spread of an infectious agent from one farm location to another through local spread, windborne spread, and direct and indirect contacts. Control measures such as depopulation, vaccination, and movement restrictions in addition to varying disease surveillance intensity can be simulated, with the ability to carry out each of these activities subject to user-defined resource constraints.

6.2 Study design

Table 1 lists potential early indicators (explanatory variables) that were considered for inclusion in the study, taking into account earlier work referred to above. A workshop to discuss and finalise the study design was held at the Department of Agriculture, Canberra, on 12 – 13 August 2015. A copy of the workshop agenda and list of participants is provided in Appendix 1.

While FFO and FFS have been shown to correlate with epidemic size ([Halasa et al., 2013](#)), it was recognised that it would be more useful to consider a broader range of times. Accordingly, it was agreed to look at three time points (day 7, day 14 and day 21 after first detection) and a number of potential explanatory variables in terms of:

- Farm and animal densities around the location of the index farm;
- The number of IPs reported and number of traced premises identified at a given point in time;
- Involvement of markets/saleyards;
- The rate of spread as quantified using the estimated dissemination ratio (EDR);
- The extent of spatial spread; and
- The adequacy of resources for control.

Table 2 lists the agreed explanatory variables to use in an initial screening study, and approaches for defining these variables. The following methodological approach was discussed and agreed. Each country would select a (relatively large) pilot region that would provide some variability in animal densities and production systems. Selection of the pilot region was decided by each country and the source farm would be randomly selected, based on assessed risks, from the population of farms within each pilot region. The FMD models that were developed using AADIS and InterSpread Plus would include: (1) passive detection (i.e. probabilistically determined) time to first report; and (2) a standard stamping out (SO) strategy with no vaccination and no dangerous contact premises (DCP) culling.

The models were run with baseline controls for 10,000 iterations. Two output file structures were identified and discussed with spreadsheet templates defined for reporting results: (1) a summary file by iteration listing each of the early decision indicator measures; and (2) a control farms detail file.

Three outcome variables of interest were agreed: (1) the total number of IPs; (2) outbreak duration, defined as the number of days between detection of the index premises and completion of destruction, disposal and decontamination activities on the last infected premises; and (3) the total area under control.

6.3 Approach to seeding of infection

Australia

The study area for the project comprises the whole of Australia. Australia has been divided into 12 livestock production regions (East et al., 2013) as shown in Figure 1, some of which cross jurisdictional boundaries. This regional classification is based on the Australian Bureau of Agriculture and Resource Economics (ABAREs) farm survey regions, which comprise groups of local government areas or shires, and takes into account topographic, climatic, land use, production and marketing factors. In brief, livestock production in Australia is largely based on extensive grazing and is dominated by wool, sheepmeat, beef and dairy production. Australia also has smaller intensive pig and poultry industries. Extensive beef cattle production is the dominant system in northern Australia, with more intensive production systems being found in the south east and south west of the country.

While the study area was the whole of Australia, initial seeding of infection was confined to south eastern Australia (Figure 2). South eastern Australia comprising the states of Victoria and Tasmania

and parts of New South Wales and South Australia (livestock production regions 8, 9, 10 and 11) was the area for initial introduction of FMD into Australia. This area contains a mix of farming enterprises; is the centre of Australia's dairy production; and is considered a higher risk area for introduction, establishment and spread of FMD ([East et al., 2013](#)).

In AADIS disease spread is modelled using 'herds' as the epidemiological unit of interest. The FMD susceptible livestock population in Australia ([Animal Health Australia, 2014](#)) has been divided in 10 herd types and nine farm types based on the epidemiology of FMD and farm management practices ([Garner & Beckett, 2005](#)). Herds are made up of a single species. A farm can be made up of one or more herds (e.g. an extensive beef farm will typically be comprised of three cattle herds, whereas a beef-sheep farm will be made up of a beef herd and a sheep herd). Table 3 shows the population by herd type for this area ([Anonymous, 2013a](#)). Smallholders comprise the largest herd type by number (44%). Given the relatively low frequency of direct and indirect contacts and low infectivity pressure associated with this herd type, it could be anticipated that most outbreaks involving smallholders will be small and readily controlled ([Garner et al., 2015](#)). The (illegal) feeding of swill to pigs has been identified as the most viable and likely way for FMD virus to establish in Australia ([Mathews, 2011](#)). Pig farms account for <1% of the herd population. As large intensive pig farms tend to operate with high biosecurity, small pig farms would appear to be the highest risk group for FMD introduction. For this study, the intention was to provide a range of scenarios involving different seed herd types and a range of outbreak sizes. However, it is apparent that a simple random selection would result in smallholders being over-represented and small pig producers under-represented. Accordingly, we applied a weighted selection process (see Table 3) that was anticipated to provide a cross-section of outbreak sizes that might be consistent with Australia's expected risk.

New Zealand

The study area for New Zealand comprised the whole of mainland New Zealand, incorporating the North and South Islands. New Zealand is divided up into sixteen regional councils (excluding the Chatham Islands). It was assumed that the most likely introduction scenario for FMD into New Zealand would involve people or contaminated products coming into New Zealand through Auckland, which has the largest air and sea ports. Furthermore, yachts visiting the country are more likely to make landfall in the north. Therefore, the four regions comprising Auckland and its three neighbouring regions were combined into a single mega-region, to represent the area within which an outbreak would most likely start (Figure 3). The numbers and proportions of farm types within the Auckland mega-region are listed in Table 4 ([Sanson & Pearson, 1997](#)). The selection of seed herds for the New Zealand study was unweighted and based on simple random selection (Table 4).

6.4 Model parameter settings

Each country parameterised its model according to what they considered to be realistic and plausible, both in terms of disease transmission and control.

Australia

Values for disease transmission parameters are based on the published literature and expert opinion, drawing on reports on the structure and dynamics of the contemporary livestock industries ([Cutler & Holyoake, 2007](#); [AusVet Animal Health Services, 2006](#); [Hassall & Associates, 2006](#); [Kokic & Mues, 2006](#); [AusVet Animal Health Services, 2005](#)) and on previous FMD modelling studies ([Roche et al., 2013](#); [Garner et al., 2014](#)). These reports, along with analyses of cattle movements sourced from the National Livestock Identification System ([Iglesias & East, 2015](#)), enabled values of parameters like movement rates and contact patterns to be estimated for different regions of Australia. Parameter values used in AADIS have been reported previously ([Bradhurst et al., 2015a](#)).

AADIS is configured to support the range of mitigations described in Australia's veterinary AUSVET-PLAN manual for FMD ([Animal Health Australia, 2014](#)). For this study, passive first detection was used i.e. time to first report was probabilistically determined for each iteration based on a previous study ([Martin et al., 2015](#)). The control strategy was stamping out (SO) with no vaccination and no dangerous contact premises (DCP) culling. Key control settings used in this study included:

- Movement restrictions: Initial 3 day national livestock movement standstill after first report. Control areas: initially whole of the jurisdiction(s) where IPs have been reported reducing to: (a) 25 km radial areas around IPs after 14 days, and (b) 10 km radial areas after a further 28 days. Restricted areas: initially the whole of the local government area(s) where IPs have been reported reducing to: (a) 10 km radial areas around IPs after 14 days, and (b) 3 km radial areas after a further 28 days.
- Suspect premises reporting based on suspect clinical disease cases, including false (i.e. non-FMD) reporting with an average of 2.34 false reports for every true report.
- Tracing of direct and indirect contacts, assuming a 14 day tracing window.

Resources for key operations like surveillance, culling and vaccination are based on the availability of teams. The number of surveillance teams is assumed to increase linearly over a 21 day period and the number of culling teams over 28 days. Vaccination was not used in this simulations. The initial and maximum number of surveillance and culling teams by jurisdiction is shown in Table 5.

Simulations were run until disease eradication was achieved or for 365 days, whichever came first.

New Zealand

- The first infected farm was randomly selected from the population of farms within the Auckland mega-region (see Figure 3).
- Passive detection of the index IP was used rather than setting a pre-configured time to detection. The likelihood of recognition and reporting of FMD clinical signs in their livestock by farmers and their veterinarians was based on a survey of farmers biosecurity practices conducted in 2007 ([Murray, 2006](#)).

- When detection occurred, a stamping out control program (without vaccination) was applied using New Zealand's default approach (i.e. national livestock standstill for 14 days, area movement restrictions, stamping out of IPs, surveillance and tracing) as specified in the New Zealand Standard Model of FMD ([Sanson et al., 2006](#); [Owen et al., 2011](#)).

Similar to Australia, simulations were run until disease eradication was achieved or for 365 days, whichever came first.

6.5 Statistical methods

Linear regression

The Stata/IC statistical package ([StataCorp, 2015](#)) was used for linear and negative binomial regression modelling. Datasets were imported into Stata and the three agreed outcome variables viz. the total number of IPs, outbreak duration and the area under control were checked for normality. Each of the outcome variables were log transformed to minimise problems with non-normality and heteroscedasticity of residuals ([Osborne & Waters, 2012](#)). The linear relationship between the outcome variable and each of the explanatory variables was assessed using Lowess plots. After log transformation, none of the univariate relationships substantially departed from linearity. Subsequent analysis used two modelling techniques: (1) linear regression modelling with robust standard errors to account for non-normally distributed outcome variables ([Acock, 2010](#)) and, (2) negative binomial regression. It was considered appropriate to use linear regression techniques because the methodology is robust to violations of the requirement for normally distributed outcome variables if the number of observations is large ([Xiang et al., 2012](#); [Anonymous, 2015](#)). Analysis using the two different approaches yielded similar results.

The explanatory variables were initially tested for unconditional associations with each of the three outcome variables. Explanatory variables that were associated with the outcome variables with $P < 0.20$ were selected for inclusion in the initial multiple regression model. The initial multiple regression model was then reduced step-wise by removing the explanatory variable with the highest P_{Wald} value. After removal of each variable, the new model was compared to the previous model containing that variable using the likelihood ratio test. The variable was discarded if the $P_{lrtest} > 0.05$. After the most parsimonious model was developed, all excluded variables were reassessed by addition individually back to the model. All first-order interactions were tested, one at a time and retained in the model if the $P_{Wald} < 0.05$ (no interaction terms were retained). The extent of confounding was assessed using the variance inflation factor. No significant confounding was observed in the final models presented.

This process was completed separately for the Australian and New Zealand data sets. Subsequently, the models were examined to determine whether a simpler model that: (1) had fewer explanatory variables and, (2) was applicable to both data sets could be identified. For linear models, the R^2 value is reported as a measure of the goodness of fit of the model.

The explanatory power of the regression models was assessed using Receiver Operating Characteristic (ROC) curves. In a ROC analysis, the outcome variable needs to be dichotomous so, in the

absence of an existing definition of what a large or small outbreak is, a number of arbitrary definitions of large or small were chosen to examine each model's explanatory ability. For each outcome variable, the predict function in Stata was used to generate the regression model predictions based on the day 14 explanatory variables.

For the total number of IPs and outbreak duration the predict function in Stata was used to generate the regression model predictions based on day 14 data. The iterations for each data set were divided using the same arbitrary definitions and tabulated to compare the actual values and the regression model predictions. The optimum cut point for the prediction of large or small (or long or short) outbreaks was determined by calculating the Youden Index from the ROC curve data ([Schisterman et al., 2005](#)). These data were then used to calculate negative and positive predictive values for the day 14 model estimates using standard techniques ([Dohoo et al., 2003](#)).

Regression trees

Classification and regression tree (CART) analysis is a statistical technique that can be used to identify factors important in determining the value of a numeric outcome. CART is mathematically identical to some multivariable regression techniques, but presents the results in a way that is easily interpreted by those not familiar with statistical analysis. In this way, CART provides a summary of the relationship between a set of explanatory variables and a given outcome and can be used as a first step in constructing an informative model or a final visualisation of important associations.

A simplified description of a CART analysis is as follows. Given a set of explanatory variables $x_1, x_2, x_3, \dots, x_n$ in the domain X we want to predict a continuous outcome of interest, Y . In Figure 4 the plot on the right shows the domain of all factors associated with Y in descending order of importance. In traditional regression models (linear or polynomial) an equation is developed wherein regression coefficients quantify the strength of the association between a given explanatory variable and the outcome. CART is an alternative approach to this, where the data space is partitioned into smaller sections where exposure-outcome associations are (visually) clearer. In a CART analysis the outcome of interest occupies the root node. The explanatory variable having the strongest association with the outcome is shown adjacent to the root node. A value is assigned to the explanatory variable to identify 'high' and 'low' values of the outcome variable, selected using a squared residuals minimisation algorithm. The final split or node in the CART is sometimes referred to as a leaf.

Boosted regression trees

In contrast to CART, a boosted regression tree (BRT) analysis generates a large number of regression trees based on random samples of the data ([Elith et al., 2008](#)). A BRT model returns a list of explanatory variables used to create the splits in the different trees. A relative weight is then calculated for each variable by computing the average number of times the variable was chosen for splitting weighted by the squared improvement to the model from each split and scaled to sum to 100. Larger weights indicate a stronger influence between an explanatory variable and the outcome.

Boosted regression trees require the analyst to specify the learning rate and tree complexity. Learning rate controls how much each tree contributes to the model as it develops. In general, smaller

learning rates result in better predictions than larger learning rates. Tree complexity sets the number of interactions fitted in the model: a tree complexity of two allows for two-way interactions, three allows for three-way interactions, and so on. Boosted regression trees require the analyst to specify the learning rate and tree complexity. Learning rate controls how much each tree contributes to the model as it develops. In general, smaller learning rates result in better predictions than larger learning rates. For these analyses a relatively low learning rate of 0.005 was used (after [Elith & Leathwick 2016](#)). For these analyses tree complexity was set to five.

Coefficient of variation statistics were calculated within each fold of each BRT and the mean and the standard error of these fold-based statistics presented as a quantitative measure of model fit.

Whereas the single trees produced by the CART analysis are easily interpreted, they are less able to predict linear relationships, they are sensitive to small variations in data, and tend to provide an oversimplification of the 'real' associations between a set of explanatory variables and a given outcome. In contrast, BRTs are better able to describe linear relationships and are more robust in terms of predictive accuracy, although interpretability suffers as a result. CARTs and BRTs are complementary. CARTs are relatively simple and provide readily interpretable output; BRTs are more complex and robust, but with reduced interpretability.

7 Results

7.1 Descriptive statistics

Prior to analysis, model runs where the outbreak was not detected (IPs = 0) or where disease did not spread from the seeded farm (IPs = 1) were removed from subsequent analyses. This left 6790 model runs in Australia (AADIS) and 8784 model runs in New Zealand (InterSpread Plus). Descriptive statistics of the explanatory variables used for the AADIS and InterSpread Plus linear regression, CART and BRT analyses are shown in Table 6 and Table 7, respectively. Descriptive statistics of the outcome variables for the AADIS and InterSpread Plus models (that is, total number of infected premises, outbreak duration and total area under control) are shown in Table 8. Frequency histograms showing the distribution of the outcome variables are shown in Figure

For the InterSpread Plus simulations, FMD outbreaks were seeded into areas where the density of cattle was substantially higher (median of 152 head per square km) than the areas where FMD was seeded for the AADIS simulations (median of 28 head per square km). Compared with the FMD outbreaks simulated by AADIS, InterSpread Plus simulated relatively high numbers of IPs during the early phase of each epidemic. The median number of IPs by day 7, 14 and 21 for InterSpread Plus was 6, 9, and 11 (respectively) compared with 3, 5, and 5 for AADIS. Similarly, the number of traces generated by InterSpread Plus in the early phase of each epidemic were higher than those generated by AADIS. The median number of traces generated by day 7, 14 and 21 for InterSpread Plus was 8, 11, and 12 (respectively) compared with 2, 3, and 4 for AADIS. There are three possible explanations for these findings: (1) differences in characteristics of the study regions and incursion scenarios used for each model; (2) differences in model parameterisation, resulting in different probabilities of farm-to-farm transmission of virus; and (3) differences in model design (in InterSpread Plus probabilities of transmission vary according to farm type but not farm size whereas in AADIS both farm size and farm type influence probabilities of transmission).

Outbreak durations for the two models were similar: a median of 43 (minimum 16, maximum 365) days for AADIS compared with a median of 43 (minimum 21, maximum 263) for InterSpread Plus. The size of the area under control was substantially lower for the AADIS simulations. The median area under control for the AADIS simulations was 680 (minimum 300, maximum 29,953) square km compared with 1176 (minimum 316, maximum 12,815) square km for InterSpread Plus.

The distribution of each of the three outcome variables was highly skewed (Figure 5) with most model runs resulting in shorter outbreaks with few IPs. Only 14% of AADIS model runs resulted in outbreaks with >20 IPs and only 7% with >50 IPs. Only 21% of outbreaks had a duration of more than 50 days while only 6.5% had a duration of more than 90 days. Similarly, only 26% of outbreaks involved an AUC of >1000 km² and only 9% involved an AUC of >3000 km². The equivalent figures for modelling runs with InterSpread Plus in New Zealand were: 36% of modelling runs >20 IPs and 17% >50 IPs; 34% of runs >50 days duration and 8.5% >90 days; 50% of modelling runs with an AUC >1000 km² and 11% >3000 km².

7.2 Linear regression

After log transformation, the distribution of outcome data sets still did not achieve normality but the skewness and kurtosis of each data set more closely approached the normal distribution values of one and three respectively (Table 9). Frequency histograms of the transformed data sets (Figure 6) indicated that the data were closer to normally distributed than before transformation. Estimated regression coefficients and their standard errors for the day 14 linear regression models for Australia and New Zealand are shown in Tables 10 and 11, respectively.

For both the Australian and New Zealand data, the models were substantially better at explaining the observed variability in AUC (R^2 0.95 and 0.82, respectively) compared with the total number of IPs (R^2 0.88 and 0.80, respectively) and outbreak duration (R^2 0.61 and 0.46, respectively).

The number of explanatory variables in each model does not make the various models easy to explain and the models for the same outcome variables varied between the two countries in the study. An examination of the beta weights for the various explanatory variables within each model (last column, Tables 10 and 11) shows that these explanatory variables make vastly different contributions to the explanatory power in the models. Further, the explanatory variables that contributed the most to the explanatory power of the models were consistent between the two countries. The various regression models were therefore modified to delete various explanatory variables to examine whether 'simple' models that included only the most important explanatory variables and that were consistent across the two countries could be built without sacrificing the explanatory power of the models (Tables 12 and 13).

The power of the simplified models to explain the variation in each outcome variable, compared to the complete models is shown in Table 14. As indicated by the beta weights in Tables 10 and 11, removal of most of the explanatory variables from each model had virtually no effect on the explanatory power of each model. The simplified models also had the advantage of containing the same explanatory variables for both the Australian and the New Zealand data. The summary statistics derived from the ROC curves are presented in Table NN. The predictive power of the regression models was examined using ROC curves (Figures 7 and 8). The area under the ROC curves varied from 0.77 to 0.98. For reference, an area under a ROC curve of 0.9 to 1.0 is considered to be 'outstanding discrimination' and the values for the predictive models for the number of IPs and the AUC fell within this range. The predictive models for the duration of an outbreak fell into the 'acceptable discrimination' range (Hosmer & Lemeshow, 2000).

For each outcome variable (IPs, duration, AUC), a series of values were arbitrarily selected to divide the modelled iterations into large or small (or long or short) outbreaks. These decision points might hypothetically represent a trigger point for an outbreak manager to deploy vaccine. That is, using the models and the day 14 data, the outbreak manager can predict that the final size-duration of an outbreak and decide whether vaccine will be necessary in the control program.

The ability of each of these regression models to correctly predict whether an outbreak would be large or small (or long or short) from data available 14 days after the detection of the outbreak was assessed by calculating the positive (PPV) and negative (NPV) predictive values for each model at each of these arbitrary cut points. The PPVs, NPVs and the percentage of iterations correctly classified as large and small (or long and short) is shown in Table 15.

7.3 Regression trees

For the CART analyses three sets of explanatory variables were used: those at day 7 post detection, day 14 post detection and day 21 post detection. Two models using three sets of explanatory variables and three outcome variables resulted in 18 CART analyses in total.

Explanatory variables associated with each of the outcome variables for Australia and New Zealand are shown in Table 16 and Table 17, respectively. Regression trees summarising day 14 post detection variables predictive of the total number of IPs for Australia and New Zealand are shown in Figure 21 and Figure 22, respectively.

For AADIS, using the day 14 post detection variables, the number of IPs identified at day 14 post-detection had the strongest association with the total number of IPs followed by cattle density. Relatively large outbreaks were those where there were more than 32 IPs identified by day 14 and where the outbreak started in an area where the density of cattle was greater than 82 head per square km. While day 14 IP numbers and cattle density were the best predictors of total number of IPs for the CART analyses, day 14 IP numbers and the number of pending culls at day 14 were the best predictors of the total number of IPs for the 'simple' linear regression models presented in Tables 12 and 13.

For InterSpread Plus the number of IPs identified at day 14 post detection had the strongest association with the total number of IPs. Relatively large outbreaks were those where there were more than 69 IPs identified by day 14. Regression trees for the other CART analyses are provided in Appendix 3.

In regression modelling, the term R^2 is the coefficient of determination, the percentage of the response variable variation that is explained by the model (higher values of R^2 indicate a better model fit). In Tables 16 and 17 the column titled relative error is equivalent to $1 - R^2$ (that is, lower relative error values indicate a better model fit). For each of the three outcomes modelled the relative errors were substantially less for the day 21 explanatory variable set compared with the day 7 explanatory variable set.

For the Australian outbreaks, the size of the area under control at day 7, day 14 and day 21, and the number of IPs detected at day 7, day 14 and day 21 were predictive of the total number of IPs, outbreak duration and the size of the area under control. For the New Zealand outbreaks, the number of IPs at day 7, 14 and 21 were predictive of the total number of IPs and outbreak duration. The number of IPs at day 7, 14, and 21 was predictive of the total area under control.

7.4 Boosted regression trees

Boosted regression tree analyses were carried out for each model for the outcome variables and explanatory variable sets listed in Table 6 (for AADIS) and Table 7 (for InterSpread Plus). The relative weights of the explanatory variables that were associated with each of the three outcomes are listed in Table 18 (AADIS) and Table 19 (InterSpread Plus). Horizontal bar plots showing the day 14 explanatory variable boosted regression tree weights for the total number of infected premises are shown in Figure 11 (AADIS) and Figure 12 (InterSpread Plus). In a BRT analysis, larger weights

represent a stronger association between a given explanatory variable and the outcome.

Coefficient of variation statistics (essentially a measure of model fit) for each the boosted regression models for Australia and New Zealand are presented in Tables 20 and 21. Figure 13 is a scatterplot showing the number of infected premises predicted by the boosted regression tree model as a function of the number of infected premises predicted by AADIS using the first 14 day early decision indicators. Figure 14 shows the equivalent data for New Zealand. As a general trend, the BRT models using the day 21 explanatory variables provided a better fit to the data compared with the BRT models using the day 14 and day 7 explanatory variables. The BRT models using the day 14 explanatory variables provided a better fit to the data compared with the BRT models using the day 7 explanatory variables.

8 Discussion

FMD is recognised as the single greatest disease threat to Australia's livestock industries ([Mathews, 2011](#)). Early detection of an incursion, effective control of an outbreak and rapid return to trade are essential to minimise the economic impact. Australia and New Zealand's response will implement rapid action to contain, control and eradicate the disease in order to re-establish their FMD-free status as quickly as possible, while minimising social and financial disruption ([Anonymous, 2011](#)). Modelling studies, both in Australia and overseas, have shown that vaccination in addition to standard stamping out (SO) measures can be effective in reducing the size and duration of an FMD outbreak (e.g. [Tomassen et al. 2002](#), [Keeling et al. 2003](#), [Abdalla et al. 2005](#), [Roche et al. 2013](#), [Garner et al. 2014](#), [Roche et al. 2014](#)).

Although vaccination is increasingly being recognised as an important tool to assist in containing and eradicating FMD outbreaks ([Roche et al., 2014](#)) it will make achieving recognition of free status more difficult. Keeping vaccinated animals in the population will delay the period until FMD-free status is regained under the World Organisation for Animal Health (OIE) guidelines and add additional complications to the post-outbreak surveillance program. Shifting attitudes to vaccination means it is no longer viewed as a measure of last resort and will be given consideration as a potential additional measure (alongside SO) from day one of any FMD eradication response. However, given the complications and costs associated with implementing a vaccination strategy, it would only be used, if authorities consider that it would be beneficial in managing the outbreak ([Anonymous, 2011](#); [Animal Health Australia, 2014](#); [Anonymous, 2014](#)).

A number of (modelling based) studies have shown that vaccination is more beneficial when used early in an outbreak ([Tildesley et al., 2006](#); [Porphyre et al., 2013](#); [Roche et al., 2014](#)). Vaccination has been shown to be most effective in situations where disease is spreading rapidly or resources are inadequate to maintain effective stamping out ([Roche et al., 2013](#)).

It is recognised that there are a range of factors that could be expected to influence the decision to use vaccination or not to control FMD. Australia's FMD Vaccine Expert Advisory Group (VEAG) provides advice to the Consultative Committee on Emergency Animal Diseases (CCEAD) on the use of emergency vaccination in an FMD outbreak. VEAG has developed a decision support matrix, and New Zealand has a similar decision framework, that provides a rational structure to support its technical decision making ([Anonymous, 2009, 2016a](#)). These frameworks assist in providing a qualitative ranking of a range of technical factors including: (1) the nature of the outbreak, (2) the risk of spread or escalation, and (3) resources for stamping out. However, the framework is quite subjective. It would be useful for disease managers if they could identify early in an outbreak those situations that are likely to develop into 'large' outbreaks and for which additional measures like vaccination are likely to be beneficial. In this context, measurable parameters such as the number of IPs, the numbers of traced premises and/or farms under surveillance and estimated rates of spread might be useful indicators of the potential severity of an outbreak.

The overarching aim of this project was to identify factors that could be used to predict the total number of infected premises, outbreak duration and size of the area under control in the event of a FMD incursion into Australia or New Zealand. Here, 'factors' refers to characteristics of the physical environment in which an FMD incursion is first detected (e.g. farm density, animal density, human population density) or characteristics of the outbreak itself (e.g. the number of infected premises

detected 14 days after the date on which disease is first detected).

This study considered a wide range of FMD incursions in terms of location and seed farm type, and time to first detection (determined probabilistically). This approach generated a large number of plausible FMD outbreaks. Based on the 10,000 simulation runs, median outbreak sizes in Australia and New Zealand were 3 and 11 respectively and, for duration, 35 and 40 days respectively.

It is reassuring for animal health authorities, in both countries, that the simulated FMD outbreaks tended to be small and readily able to be contained and eradicated with available resources. For both countries median outbreak duration was around 6 weeks. This finding assumes that FMD is reported relatively quickly and resources are adequate to implement effective control programs. For Australia, the median time from first introduction to reporting was 17 (range 9 – 89) days and for New Zealand the median time to detection was 13 days. A previous Australian study found considerable regional variability in the probability that an individual infected farm would report suspect FMD ([East et al., 2013](#); [Martin et al., 2015](#)). Recent experience of outbreaks of FMD in previously free countries would suggest that it tends to take about three weeks after introduction of the virus to the index farm before the disease is recognised ([Anderson, 2002](#); [Bouma et al., 2003](#); [Yoon et al., 2013](#); [Wada et al., 2016](#)). However, even with relatively early detection, it does not mean that an outbreak may not be large. For Australia, under the baseline control strategy there was a 3.4% probability that the outbreak would have more than 100 IPs and a 7.2% probability that the outbreak would last longer than 90 days. For New Zealand there was a 7.2% probability of the outbreak involving more than 100 IPs and an 8.6% probability of an outbreak lasting more than 90 days.

The key objective of this study was to test whether information known or available to disease managers early in an FMD outbreak, can be used to predict the severity of the epidemic outcome. Epidemic outcome was defined in terms of epidemic duration, total number of IPs, number of additional IPs after a given time point and the size of the area under control. Three time points were considered: 7, 14 and 21 days into the control program. A wide range of potential predictor variables were assessed using different analytical approaches including linear regression, CART analysis and BRT analysis.

Although there was some variability between the outputs of the different analyses and between countries, across all models, the number of IPs at a given time point was consistently found to be strongly associated with the final number of IPs and the duration of an outbreak. It was possible to build relatively simple linear regression models for predicting the magnitude and duration of simulated FMD outbreaks that fitted both the Australian and New Zealand data (see Tables [12](#) and [13](#)). R^2 values as a measure of goodness of fit ranged from 0.3 – 0.9 depending on time point, outbreak variable and country. A consistent pattern was observed with the fit of the models improving from day 7 to day 14 to day 21 for all explanatory variables and for both Australia and New Zealand. The total area under control had the highest predictability and outbreak duration the lowest. In this study we found that the number of IPs occurring up to the time point provided the most predictive power for both size (total IPs, additional IPs after the decision day) and outbreak duration. This concurs with previous findings by [Hutber et al. \(2006\)](#) and [Halasa et al. \(2013\)](#). For area under control, the area under control at the time point was most informative.

These findings were confirmed in the CART and BRT analyses. Consistency between the different approaches helps build confidence that the criteria identified are relevant to response decision making. CART techniques are a useful alternative as they provide a visual decision tree output that

is intuitive and likely to be well received by those not familiar with statistical analysis (see Figures 21 and 22). Boosted regression trees, while more complex from an analytical perspective have the advantages of being able to handle a range of predictor variable type, not requiring any data transformations and can be used for complex non-linear relationships (Elith et al., 2008). The BRT models for both countries had good predictive ability when the total number of IPs was less than 100. When the predicted number IPs was greater than 100 the BRT analyses tended to under predict. In general, the predictive ability of BRTs with continuous explanatory variables is inferior to that of generalised linear models and, in addition, BRT models tend to be adapted to specific features of the input dataset resulting in loss of generality. It appears that the predominance of continuously distributed explanatory variables in each of the BRT models has limited their predictive ability in this particular case.

Although it is informative to build statistical models to summarise factors influencing outputs from complex simulation models of FMD, for disease managers the key issue is how this information can be used to support decision-making i.e. how and when during an FMD outbreak should decisions on additional measures like using vaccination be made. There are consequences associated with using vaccination when it is not actually required with implications for post-outbreak surveillance, management of vaccinated animals and regaining FMD-free status and access to markets. Conversely, not using vaccination in some situations may lead to larger outbreaks, increased control costs and greater impacts on industry and local communities.

From a disease manager's perspective it is useful to consider how good the models are at predicting small and large outbreaks. To do this it is necessary to make some judgment calls about what constitutes a 'large outbreak'. It is difficult in advance to reach agreement on what are acceptable benchmarks in terms of eradicating FMD, as this will be influenced by the time and location of an outbreak, availability of resources, etc. A response from senior animal health managers 'as soon as possible' is not particularly helpful when evaluating the performance of predictive models. Accordingly we looked at a series of arbitrary 'cut points' for classifying outcomes into small and large (or long and short) outbreaks. Model sensitivity, specificity and positive and negative predictive values were calculated across these cut-points. In general, the models were very good at predicting when an outbreak would be small or short; the positive predictive values varied from 0.85 to 0.98 meaning that we would correctly predict a small outbreak between 85% and 98% of the time. It should also be noted that having predicted a small outbreak at day 14 (leading to a decision that vaccination would not be necessary), this decision can be revisited at a later time in the outbreak when more information is available. The models were less accurate at predicting a large or long outbreak with the negative predictive values for duration exceeding 90 days being as low as 0.52 for New Zealand. The negative predictive values for size of the outbreak and the area under control were substantially better ranging from 0.77 to 0.91. In disease management terms, incorrectly predicting a large outbreak and deciding to use vaccine will have minimal consequences because using the vaccine will only make the outbreak smaller and shorter however, using vaccine when it is not necessary has serious trade implications and reversing a decision to use vaccine later in an outbreak does not remove those trade consequences.

It is also useful to think about potential decision rules that can be applied at a given time point in setting go/no go decision criteria for vaccination during a control program. For this analysis we concentrated on day 14 observations. This was to take into account the likely timely of when vaccine is likely to be available. For Australia and New Zealand, based on information on diagnostic testing and

vaccine matching times provided by CSIRO-AAHL and MPI-AHL, it is expected that an appropriate vaccine would not be available to augment an FMD eradication response until 9 – 12 days (earliest) into the control program, but this could stretch out to 16 – 19 days ([Anonymous, 2016b](#)).

To aid this decision whether to use vaccine or not, we have prepared a simple look-up chart for disease managers. Because the number of IPs existing at any time point that a decision to use vaccine is considered is often the measure of greatest interest to a disease manager and because the various statistical models showed that the number of IPs at that time point was the parameter with the greatest impact on the final size and duration of the outbreak, the chart (Table 22) reports, for each possible value of the number of IPs on day 14 after outbreak detection, the probability that the final number of IPs will exceed 5, 10, 20 or 50 and the probability that the duration of the outbreak will exceed 60, 90 or 180 days.

This information, can guide a disease manager's decision regarding vaccine usage whilst still allowing consideration of other factors. The table also accommodates each disease manager's appetite for risk or uncertainty e.g. when there are 10 IPs on day 14, some managers may be willing to accept a 20% risk that there will be more than 20 IPs and a 13% risk that the outbreak will last longer than 90 days whereas other managers may be more conservative in their approach. The equivalent table for New Zealand is shown in Table 23.

As an alternative presentation, predictive curves for the final number of IPs and the outbreak duration are shown in Figures 15 to 18 and these figures include 95% confidence intervals to provide an estimate of reliability that can be placed on our predictive models.

It should be noted that the modelling studies in both Australia and New Zealand focussed on introduction of FMD into the areas with the highest estimated likelihood of disease entry ([East et al., 2013](#)). The results need further validation with modelling data generated from other areas of these countries. Finally, it should be recognised that in the absence of FMD outbreaks in Australia and New Zealand this study has fitted statistical models to simulated, not real disease data. Although the modelling teams have been careful to parameterise the respective models as realistically as possible, it is inevitable that assumptions and extrapolations from overseas experience have had to have been made. These considerations need to be taken into account when using the findings from this study.

Table 1: Potential metrics for predicting the size of FMD outbreaks.

Metric/Parameter	Descriptor
Location characteristics	Farm density, animal density, animal and farm types.
IP characteristics	Animal density, animal and farm types, traces – saleyard involvement?
Silent spread period	Time to first detection.
Season	Animal movement patterns (traces); airborne spread.
Spatial spread (dispersion)	Max distance between IP centroids; number of clusters; first fortnight spread (FFS).
Temporal spread	First day incidence; first week incidence; first fortnight incidence (FFI).
Estimated dissemination ratio	Estimated over 7 days to smooth curve.
Report cases	Farmer report numbers; report cases vs. surveillance team/tracing detections.
Traces	Numbers of back and forward traced properties associated with IPs.
Resource adequacy	Time from detection-to-destruction; time from farmer report-to-visit; number of premises awaiting destruction/disposal; No. pending surveillance visits.
Virus strain/ airborne ability	Models largely parameterised on Type O pan Asia strain, with limited data available for other strains.
Weather conditions	Temperature, humidity.

Table 2: Explanatory variables tested in the current study.

Metric/Parameter	Details
Location characteristics: densities of cattle, sheep, pigs and humans at first detected farm site.	FAO Gridded Livestock Population of the World data (Robinson et al., 2007), Gridded Population of the World data (Anonymous, 2015).
Markets/saleyards: any IP infection via saleyard pathway?	Record as present or absent for day 7, day 14, day 21.
Spatial spread: size of area under control (AUC) and number of clusters.	AUC: use a dissolved polygon around IPs based on 10 km buffer at day 7, 14 and 21. Clusters: number of non-contiguous polygons using a 10 km radius buffer around IPs at day 7, 14 and 21.
Temporal spread.	Number of IPs reported at day 7, 14 and 21.
Estimated dissemination ratio (EDR).	Four day EDR computed at day 14 and day 21.
Traces: cumulative backwards and forward traced premises.	All traces (including high risk, medium risk and low risk) for day 7, 14 and 21.
Resource adequacy.	Number of premises awaiting destruction at day 7, 14 and 21.

Table 3: Counts of herd types in South-east Australia.

Herd type	<i>n</i> (%)	Weight	Weight selection
Extensive beef	0 (0)	0	0
Beef intensive	25303 (18)	1	8.9
Feedlot	190 (0)	1	9.3
Mixed beef	15221 (11)	1	9.1
Mixed sheep	15221 (11)	1	8.3
Dairy	7187 (5)	1	11.5
Small pig	1032 (1)	4	31.5
Large pig	184 (0)	1	9.2
Sheep	16224 (11)	1	8.4
Smallholder	63723 (44)	0.5	3.8

Table 4: Counts of herd types in the Auckland mega region (Sanson and Pearson 1997).

Herd type	<i>n</i> (%)	Weight	Weight selection
Dairy	6273 (18)	1	1
Dairy – dry	3063 (9)	1	1
Lifestyle	15902 (45)	1	1
Pig – breeder	20 (0.1)	1	1
Pig – fattener	3 (0)	1	1
Pastoral - livestock	10,373 (29)	1	1

Table 5: Initial and maximum number of surveillance and culling teams by jurisdiction, Australia.

Jurisdiction	Surveillance		Culling	
	Initial	Maximum	Initial	Maximum
New South Wales	5	60	2	30
Victoria	3	50	2	25
Queensland	5	40	1	25
South Australia	5	20	1	15
Western Australia	4	30	1	20
Tasmania	4	15	1	10
Northern Territory	2	15	1	10

Table 6: Descriptive statistics of explanatory variables from the AADIS model of foot-and-mouth disease outbreaks in south-eastern Australia using the baseline control strategy.

Variable	<i>n</i>	Mean (SD)	Median (Q1, Q3)	Min, max	Zeros
IPs day 7	6790	4 (3)	3 (2-6)	1, 24	0
AUC day 7 ^a	6790	734 (579)	459 (344-927)	300, 4242	0
Clusters day 7	6790	2 (2)	1 (1-3)	1, 14	0
IPs per km ² day 7	6790	0.007 (0.003)	0.006 (0.005-0.008)	0.003, 0.028	0
Traces day 7	6790	3 (3)	2 (0-4)	0, 30	0
IPs day 14	6790	9 (10)	5 (3-10)	1, 82	0
EDR day 14 ^b	6790	0.55 (0.89)	0 (0-1)	0, 15	3422
AUC day 14 ^a	6790	1168 (1282)	651 (357-1394)	300, 10980	0
Clusters day 14	6790	3 (3)	2 (1-4)	1, 28	0
IPs per km ² day 14	6790	0.008 (0.004)	0.007 (0.006-0.009)	0.003, 0.038	0
Traces day 14	6790	6 (7)	3 (1-8)	0, 97	1001
IPs day 21	6790	12 (16)	5 (3-13)	1, 148	0
EDR day 21	6790	0.42 (0.77)	0 (0-0.78)	0, 9	4350
AUC day 21 ^a	6790	1297 (1564)	667 (364-1543)	300, 16270	0
Clusters day 21	6790	3 (4)	2 (1-4)	1, 34	0
IPs per km ² day 21	6790	0.005 (0.003)	0.005 (0.003-0.006)	0.001, 0.023	0
Traces day 21	6790	8 (12)	4 (1-9)	0, 147	902
Cattle density ^c	6790	49 (83)	28 (9-62)	0, 1644	776
Sheep density ^d	6790	120 (131)	82 (18-176)	0, 1615	1011
Pig density ^e	6790	32 (100)	0 (0-13)	0, 946	3734
Human density ^f	6790	23 (135)	3 (1-8)	0, 3725	23

^a AUC: Area under control (square km).

^b EDR: Estimated dissemination ratio.

^c Cattle density: Number of cattle per square km.

^d Sheep density: Number of sheep per square km.

^e Pig density: Number of pigs per square km.

^f Human density: Number of humans per square km.

Table 7: Descriptive statistics of explanatory variables from the InterSpread Plus model of foot-and-mouth disease outbreaks in the Auckland region of New Zealand using the baseline control strategy.

Variable	<i>n</i>	Mean (SD)	Median (Q1, Q3)	Min, max	Zeros
IPs day 7	8784	9 (10)	6 (3-12)	1, 141	0
AUC day 7 ^a	8784	934 (623)	739 (452-1216)	314, 5856	0
Clusters day 7	8784	2 (1)	1 (1-2)	1, 10	0
IPs per km ² day 7	8784	0.010 (0.008)	0.007 (0.005-0.011)	0.003, 0.110	0
Traces day 7	8784	12 (12)	8 (4-16)	0, 113	358
IPs day 14	8784	15 (18)	9 (4-20)	1, 218	0
EDR day 14 ^b	8784	0.69 (0.93)	0.5 (0-1)	0, 19	3042
AUC day 14 ^a	8784	1169 (830)	928 (576-1553)	314, 7368	0
Clusters day 14	8784	2 (1)	1 (1-2)	1, 10	0
IPs per km ² day 14	8784	0.013 (0.011)	0.009 (0.006-0.015)	0.003, 0.127	0
Traces day 14	8784	16 (16)	11 (5-22)	0, 148	246
IPs day 21	8784	20 (23)	11 (5-25)	1, 255	0
EDR day 21	8784	0.62 (1.05)	0.2 (0-1.0)	0, 20	4308
AUC day 21 ^a	8784	1287 (930)	1021 (617-1716)	314, 8310	0
Clusters day 21	8784	2 (1)	1 (1-2)	1, 9	0
IPs per km ² day 21	8784	0.014 (0.012)	0.010 (0.006-0.018)	0.003, 0.149	0
Traces day 21	8784	18 (18)	12 (5-24)	0, 165	208
Cattle density ^c	8784	166 (84)	152 (104-217)	0, 570	0
Sheep density ^d	8784	86 (79)	70 (24-122)	0, 893	56
Pig density ^e	8784	5 (24)	0 (0-1)	0, 349	1528
Human density ^f	8784	891 (2162)	273 (153-653)	4, 24048	0

^a AUC: Area under control (square km).

^b EDR: Estimated dissemination ratio.

^c Cattle density: Number of cattle per square km.

^d Sheep density: Number of sheep per square km.

^e Pig density: Number of pigs per square km.

^f Human density: Number of humans per square km.

Table 8: Descriptive statistics of the three outcome variables from the AADIS and InterSpread Plus models of foot-and-mouth disease outbreaks in south-eastern Australia and New Zealand (respectively).

Variable	<i>n</i>	Mean (SD)	Median (Q1, Q3)	Min, max	Zeros
AADIS:					
Total IPs	6790	22 (51)	6 (3-16)	2, 844	0
Outbreak duration (days)	6790	53 (38)	43 (30-61)	16, 365	0
AUC (km ²)	6790	1523 (2136)	680 (368-1669)	300, 29953	0
InterSpread Plus:					
Total IPs	8784	32 (46)	15 (5-39)	2, 424	0
Outbreak duration (days)	8784	52 (28)	43 (31-64)	21, 263	0
AUC (km ²)	8784	1542 (1220)	1176 (636-2110)	316, 12815	0

Table 9: Means, variances, skewness and kurtosis of the log transformed outcome variables for the AADIS and InterSpread Plus models of foot-and-mouth disease outbreaks in south-eastern Australia and New Zealand (respectively).

Variable	Mean	Variance	Skew	Kurtosis
AADIS:				
Total IPs	2.06	1.55	0.98	3.34
Outbreak duration (days)	3.81	0.28	0.85	3.72
AUC (km ²)	6.78	0.9	0.85	2.83
InterSpread Plus:				
Total IPs	2.76	1.48	0.23	2.15
Outbreak duration (days)	3.84	0.21	0.58	2.71
AUC (km ²)	7.06	0.58	0.08	2.11

Table 10: Summary of the linear regression models, based on day 14 data, for the magnitude and duration of modelled FMD outbreaks in Australia using AADIS.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI	Beta weight
Total IPs:					
Intercept	0.24 (0.023)	8.66	<0.01	0.19 – 0.29	-
Number of IPs – day 14	1.09 (0.012)	92.75	<0.01	1.07 – 1.12	0.78
EDR – day 14	0.13 (0.012)	11.11	<0.01	0.11 – 0.16	0.16
Forward traces – day 14	0.04 (0.007)	5.46	<0.01	0.02 – 0.05	0.03
Back traces – day 14	0.07 (0.007)	11.38	<0.01	0.06 – 0.09	0.07
Pending culls – day 14	0.18 (0.016)	11.22	<0.01	0.15 – 0.21	0.06
Cattle density	0.02 (0.004)	4.72	<0.01	0.01 – 0.02	0.02
Pig density	-0.03 (0.003)	-9.59	<0.01	-0.03 – -0.02	-0.05
Human density	-0.01 (0.005)	-2.74	<0.01	-0.02 – -0.00	-0.01
Outbreak duration (days):					
Intercept	2.59 (0.115)	22.64	<0.01	2.37 – 2.82	-
Number of IPs – day 14	0.28 (0.014)	20.83	<0.01	0.26 – 0.31	0.48
Cattle density	0.01 (0.003)	4.19	<0.01	0.01 – 0.02	0.05
Pig density	-0.01 (0.004)	-3.1	<0.01	-0.02 – -0.01	-0.05
Human density	-0.01 (0.004)	-2.86	<0.01	-0.02 – 0.00	-0.03
Herd density	0.10 (0.020)	5.08	<0.01	0.06 – 0.14	0.06
EDR – day 14	0.12 (0.008)	14.63	<0.01	0.11 – 0.14	0.14
Forward traces – day 14	0.01 (0.005)	2.65	<0.01	0.00 – 0.02	0.03
Back traces – day 14	0.03 (0.006)	4.69	<0.01	0.02 – 0.04	0.06
Pending culls – day 14	0.06 (0.014)	4.32	<0.01	0.03 – 0.09	0.05
Area under control – day 14	0.14 (0.019)	7.55	<0.01	0.10 – 0.18	0.22
Minimum convex hull – day 14	-0.02 (0.003)	-6.57	<0.01	-0.02 – -0.01	-0.16
Index farm type					
Dairy	-0.11 (0.021)	-5.21	<0.01	-0.15 – -0.07	-0.07
Feedlot	-0.21 (0.020)	-10.49	<0.01	-0.24 – -0.17	-0.12
Mixed beef-sheep	0.12 (0.017)	7.07	<0.01	0.09 – 0.16	0.09
Pigs - big	-0.39 (0.031)	-12.5	<0.01	-0.45 – -0.33	-0.24
Pigs - small	-0.23 (0.021)	-10.68	<0.01	-0.27 – -0.18	-0.19
Sheep	0.29 (0.020)	14.47	<0.01	0.25 – 0.33	0.15
Smallholders	-0.21 (0.049)	-4.21	<0.01	-0.30 – -0.11	-0.02
Area under control (km ²):					
Intercept	2.64 (0.385)	6.85	<0.01	1.88 – 3.39	-
Area under control day 14	1.06 (0.012)	87.25	<0.01	1.04 – 1.08	0.93
Cattle density	0.01 (0.002)	4.13	<0.01	0.00 – 0.01	0.01
Pig density	-0.01 (0.001)	-6.73	<0.01	-0.01 – -0.01	-0.02
Human density	-0.01 (0.002)	-2.54	0.011	-0.01 – 0.00	-0.01
Herd density	0.04 (0.012)	3.11	0.002	0.01 – 0.06	0.01
EDR day 14	0.05 (0.006)	8.38	<0.01	0.04 – 0.07	0.03

Table 10 (continued)

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI	Beta weight
Forward traces – day 14	0.01 (0.004)	3.39	<0.01	0.01 – 0.02	0.01
Back traces – day 14	0.03 (0.004)	7.78	<0.01	0.02 – 0.04	0.03
Pending culls – day 14	0.07 (0.008)	8.25	<0.01	0.05 – 0.09	0.03
IP density – day 14	4.22 (0.597)	7.08	<0.01	3.05 – 5.39	0.03
Minimum convex hull – day 14	-0.01 (0.002)	-3.05	<0.01	-0.01 – 0.00	-0.03

Number of IPs R^2 : 0.88.

Outbreak duration (days) R^2 : 0.61.

Area under control R^2 : 0.95.

Table 11: Summary of the linear regression models, based on day 14 data, for the magnitude and duration of modelled FMD outbreaks in New Zealand using InterSpread Plus.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI	Beta weight
Total IPs:					
Intercept	-0.46 (0.102)	-4.51	<0.01	-0.66 – -0.26	-
Number of IPs – day 14	0.97 (0.013)	74.92	<0.01	0.94 – 0.99	0.75
EDR – day 14	0.20 (0.013)	15.4	<0.01	0.17 – 0.22	0.1
Pending culls – day 14	0.09 (0.010)	9.14	<0.01	0.07 – 0.11	0.06
Area under control – day 14	0.05 (0.014)	3.84	<0.01	0.03 – 0.08	0.03
Cattle density	0.02 (0.009)	2.18	0.03	0.00 – 0.04	0.01
Sheep density	0.02 (0.004)	5.05	<0.01	0.01 – 0.03	0.02
Pig density	0.02 (0.006)	3.31	<0.01	0.01 – 0.03	0.02
Human density	0.08 (0.005)	14.37	<0.01	0.07 – 0.09	0.08
Outbreak duration (days):					
Intercept	3.61 (0.279)	12.93	<0.01	3.06 – 4.15	-
Number of IPs – day 14	0.16 (0.018)	9.28	<0.01	0.13 – 0.20	0.33
EDR – day 14	0.15 (0.007)	20.28	<0.01	0.14 – 0.17	0.2
Pending culls – day 14	0.04 (0.007)	6.54	<0.01	0.03 – 0.06	0.08
Area under control – day 14	0.07 (0.018)	3.95	<0.01	0.04 – 0.11	0.1
IP density – day 14	1.41 (0.512)	2.76	<0.01	0.41 – 2.42	0.06
Cattle density	0.01 (0.006)	2.21	0.027	0.00 – 0.03	0.02
Sheep density	0.01 (0.003)	3.58	<0.01	0.00 – 0.01	0.03
Pig density	0.01 (0.004)	2.17	0.03	0.00 – 0.02	0.02
Human density	0.04 (0.003)	12.69	<0.01	0.04 – 0.48	0.11
Index farm type					
Dairy - dry	-0.01 (0.016)	-0.92	0.36	-0.04 – 0.02	-0.02
Lifestyle	-0.02 (0.016)	-1.1	0.271	-0.05 – 0.01	-0.02
Pig – breeder	-0.06 (0.016)	-3.41	0.001	-0.09 – -0.02	-0.05
Pig – fattener	-0.22 (0.168)	-1.34	0.182	-0.55 – 0.10	-0.01
Pastoral livestock	0.21 (0.250)	0.82	0.411	-0.28 – 0.69	0.01
Area under control (km ²):					
Intercept	2.68 (0.295)	9.06	<0.01	2.09 – 3.25	-
Number of IPs – day 14	-0.07 (0.017)	-3.74	<0.01	-0.07	-0.08
EDR – day 14	0.08 (0.008)	10.59	<0.01	0.07 – 0.09	0.06
Trace premises – day 14	0.03 (0.006)	4.26	<0.01	0.01 – 0.04	0.03
Pending culls – day 14	0.03 (0.006)	5.02	<0.01	0.02 – 0.04	0.03
Area under control – day 14	1.01 (0.019)	54.15	<0.01	0.97 – 1.05	0.88
IP density – day 14	3.82 (0.537)	7.12	<0.01	2.77 – 4.88	0.1
Sheep density	0.01 (0.003)	2.18	<0.01	0.00 – 0.01	0.01
Human density	0.02 (0.003)	5.46	<0.01	0.01 – 0.02	0.03

Number of IPs R² 0.80.

Outbreak duration (days) R² 0.46.

Area under control R² 0.82.

Table 12: Summary of the 'simple' linear regression models, based on day 14 data, for the magnitude and duration of modelled FMD outbreaks in Australia using AADIS.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI
Total IPs:				
Intercept	-0.02 (0.019)	-0.8	0.421	-0.05 – 0.02
Number of IPs - day 14	1.27 (0.008)	164.51	<0.01	1.25 – 1.28
Pending culls - day 14	0.18 (0.017)	10.64	<0.01	0.15 – 0.22
Outbreak duration (days):				
Intercept	13.87 (0.480)	28.88	<0.01	12.92 – 14.81
Area under control day 14	0.39 (0.008)	51.72	<0.01	0.38 – 0.40
EDR day 14 a	0.12 (0.009)	14.31	<0.01	0.11 – 0.14
IP density day 14	18.45 (0.721)	25.6	<0.01	17.04 – 19.86
First detected farm type:				
Beef - intensive	Reference			
Dairy	-0.09 (0.021)	-4.16	<0.01	-0.13 – -0.05
Feedlot	-0.20 (0.020)	-9.98	<0.01	-0.23 – -0.16
Mixed beef/sheep	0.11 (0.018)	6.24	<0.01	0.08 – 0.14
Pig - large	-0.50 (0.020)	-25.28	<0.01	-0.54 – -0.46
Pig - small	-0.27 (0.017)	-15.66	<0.01	-0.30 – -0.24
Sheep	0.25 (0.019)	12.73	<0.01	0.21 – 0.28
Smallholder	-0.26 (0.048)	-5.44	<0.01	-0.35 – -0.17
Area under control (km ²):				
Intercept	-0.57 (0.023)	-25.09	<0.01	-0.62 – -0.52
Area under control day 14	1.10 (0.003)	313.84	<0.01	1.09 – 1.11

Table 13: Summary of the 'simple' linear regression models, based on day 14 data, for the magnitude and duration of modelled FMD outbreaks in New Zealand using InterSpread Plus.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI
Total IPs:				
Intercept	0.19 (0.016)	11.63	<0.01	0.15 – 0.22
Number of IPs - day 14	1.11 (0.006)	174.93	<0.01	1.10 – 1.12
Pending culls - day 14	0.13 (0.010)	13.22	<0.01	0.11 – 0.15
Outbreak duration (days):				
Intercept	7.07 (0.173)	40.76	<0.01	6.73 – 7.41
Area under control day 14	0.29 (0.005)	55.24	<0.01	0.28 – 0.30
EDR day 14 a	0.21 (0.007)	29.62	<0.01	0.19 – 0.22
IP density day 14	7.82 (0.241)	32.36	<0.01	7.34 – 8.29
First detected farm type:				
Dairy - dry	Reference			
Lifestyle	-0.003 (0.015)	-0.25	0.805	-0.03 – 0.03
Beef/sheep/mixed	-0.042 (0.016)	-2.63	0.009	0.03
Dairy – in milk	-0.084 (0.016)	-5.33	<0.01	-0.07
Pig - breeding	-0.138 (0.087)	-1.59	0.111	-0.31 – 0.03
Pig - fattening	0.232 (0.271)	0.86	0.392	-0.30 – 0.76
Area under control (km ²):				
Intercept	-0.28 (0.027)	-10.45	<0.01	-0.33 – -0.23
Area under control day 14	1.07 (0.004)	275.96	<0.01	1.06 – 1.08

Table 14: Comparison of the R² values for each complete linear regression model using information available at day 14 after outbreak detection with simple models built with only explanatory variables that have the largest contribution to the various models explanatory power.

Model	Variable	Complete	Simple
AADIS	Total IPs	0.88	0.87
AADIS	AUC (km ²)	0.95	0.94
AADIS	Outbreak duration (days)	0.61	0.57
InterSpread Plus	Total IPs	0.8	0.79
InterSpread Plus	AUC (km ²)	0.82	0.8
InterSpread Plus	Outbreak duration (days)	0.46	0.44

Table 15: Positive and negative values and the proportion of outbreaks correctly classified as large or small (or short or long) using the day 14 linear regression model for for the AADIS and InterSpread Plus models of foot-and-mouth disease outbreaks in south-eastern Australia and New Zealand (respectively).

Variable	Cutpoint	Optimum cutpoint	Se	Sp	Youden Index	PPV	NPV
AADIS:							
Total IPs	>20	18.1	0.90	0.92	0.82	0.97	0.75
Total IPs	>50	22.4	0.91	0.88	0.79	0.99	0.47
Outbreak duration (days)	>50	49.1	0.81	0.81	0.62	0.9	0.66
Outbreak duration (days)	>90	60.7	0.83	0.83	0.66	0.97	0.33
AUC (km ²)	>1000	1090.1	0.94	0.98	0.92	0.96	0.97
AUC (km ²)	>3000	2365.5	0.93	0.94	0.87	0.99	0.73
InterSpread Plus:							
Total IPs	>20	21.22	0.81	0.92	0.74	0.87	0.89
Total IPs	>50	35.11	0.79	0.89	0.67	0.94	0.63
Outbreak duration (days)	>50	49.52	0.75	0.75	0.5	0.81	0.67
Outbreak duration (days)	>90	53.9	0.71	0.7	0.41	0.96	0.21
AUC (km ²)	>1000	1216.3	0.83	0.99	0.82	0.81	0.99
AUC (km ²)	>3000	2091.9	0.8	0.86	0.66	0.96	0.44

Table 16: Identified explanatory variables and relative error estimates from nine CART analyses of simulated outbreaks of foot-and-mouth disease in Australia using AADIS.

Outcome	Variable set	Explanatory variables	Relative error
Total IPs	Day 7	IPs d7, AUC d7, clusters d7, traces d7, cattle density	0.438
Total IPs	Day 14	IPS d14, AUC d14, traces d14, clusters d14, saleyard d14	0.244
Total IPs	Day 21	IPs d21, AUC d21, traces d21, clusters d21, IPs per km d21	0.199
Outbreak duration (days)	Day 7	IPs d7, AUC d7, clusters d7, cattle density, pig density	0.646
Outbreak duration (days)	Day 14	IPs d14, AUC d14, traces d14, clusters d14, pig density	0.556
Outbreak duration (days)	Day 21	IPs d21, traces d21, AUC d21, clusters d21, EDR d21	0.500
AUC (km ²)	Day 7	IPs d7, AUC d7, clusters d7, traces d7, saleyard d7	0.323
AUC (km ²)	Day 14	Clusters d14, IPs d14, traces d14, saleyard d14, EDR d14	0.158
AUC (km ²)	Day 21	AUC d21, clusters d21, IPs d21, traces d21, IPs per km d21	0.104

Table 17: Identified explanatory variables and relative error estimates from nine CART analyses of simulated outbreaks of foot-and-mouth disease in New Zealand using InterSpread Plus.

Outcome	Variable set	Explanatory variables	Relative error
Total IPs	Day 7	IPs d7, traces d7, AUC d7, IPs per km d7, clusters d7	0.468
Total IPs	Day 14	IPs d14, traces d14, AUC d14, IPs per km d14, clusters d14	0.350
Total IPs	Day 21	IPs d21, traces d21, IPs per km d21, AUC d21, clusters d21	0.267
Outbreak duration (days)	Day 7	IPs d7, AUC d7, traces d7, IPs per km d7, human density	0.735
Outbreak duration (days)	Day 14	IPs d14, EDR d14, AUC d14, traces d14, IPs per km d14	0.646
Outbreak duration (days)	Day 21	EDR d21, IPs d21, IPs per km d21, AUC d21, traces d21	0.525
AUC (km ²)	Day 7	AUC d7, traces d7, IPs d7, clusters d7, saleyard d7	0.422
AUC (km ²)	Day 14	Traces d14, IPs d14, clusters d14, IPs per km d14, saleyard d14	0.440
AUC (km ²)	Day 21	AUC d21, traces d21, IPs d21, clusters d21, EDR d21	0.221

Table 18: Identified explanatory variables and their weights (in brackets) from nine boosted regression tree analyses of simulated outbreaks of foot-and-mouth disease in Australia using AADIS.

Outcome	Variable set	Explanatory variables
Total IPs	Day 7	IPs d7 (31), cattle density (24), AUC d7 (15), traces d7 (10), pig density (6), human pop density (5), sheep density (4)
Total IPs	Day 14	IPs d14 (61), cattle density (10), AUC d14 (9), traces d14 (4), EDR d14 (3), pig density (3), human pop density (3)
Total IPs	Day 21	IPs d21 (64), traces d21 (10), cattle density (6), AUC d21 (6), EDR d21 (5), IPs per sq km d21 (2), pig density (2)
Outbreak duration (days)	Day 7	IPs d7 (25), cattle density (25), AUC d7 (13), human pop density (8), sheep density (7), pig density (7), traces d7 (6)
Outbreak duration (days)	Day 14	IPs d14 (41), cattle density (15), AUC d14 (9), pig density (8), EDR d14 (6), traces d14 (6), sheep density (4)
Outbreak duration (days)	Day 21	IPs d21 (44), traces d21 (12), cattle density (11), EDR d21 (8), pig density (8), IPs per sq km d21 (5), AUC d21 (4)
AUC (km ²)	Day 7	AUC d7 (68), IPs d7 (14), traces d7 (5), saleyard event d7 (5), cattle density (4), IPs per sq km d7 (1), human pop density (1)
AUC (km ²)	Day 14	Number of clusters d14 (90), IPs d14 (10)
AUC (km ²)	Day 21	AUC d21 (96), IPs d21 (2), cattle density (1)

Table 19: Identified explanatory variables and their weights (in brackets) from nine boosted regression tree analyses of simulated outbreaks of foot-and-mouth disease in New Zealand using InterSpread Plus.

Outcome	Variable set	Explanatory variables
Total IPs	Day 7	IPs d7 (67), human pop density (11), IPs per sq km d7 (4), AUC d7 (4), cattle density (4), pig density (3), sheep density (3)
Total IPs	Day 14	IPs d14 (81), human pop density (5), EDR d14 (4), IPs per sq km d14 (2), cattle density (2), pig density (2), AUC d14 (1)
Total IPs	Day 21	IPs d21 (88), EDR d21 (3), human pop density (3), IPs per sq km d21 (2), cattle density (1), AUC d21 (1), traces d21 (1)
Outbreak duration (days)	Day 7	IPs d7 (39), human pop density (22), cattle density (8), sheep density (7), IPs per sq km d7 (7), AUC d7 (6), pig density (6)
Outbreak duration (days)	Day 14	IPs d14 (50), human pop density (14), EDR d14 (12), IPs per sq km d14 (5), cattle density (4), AUC d14 (4), pig density (4)
Outbreak duration (days)	Day 21	EDR d21 (45), IPs d21 (28), human pop density (9), IPs per sq km d21 (5), AUC d21 (4), cattle density (3), pig density (2)
AUC (km ²)	Day 7	AUC d7 (84), IPs d7 (6), human pop density (2), IPs per sq km d7 (2), traces d7 (2)
AUC (km ²)	Day 14	IPs d14 (40), traces d14 (36), IPs per sq km d14 (12), clusters d14 (7), EDR d14 (2), human pop density (1), sheep density (1)
AUC (km ²)	Day 21	AUC d21 (95), EDR d21 (2), IPs d21 (1), IPs per sq km d21 (1)

Table 20: Coefficient of variation statistics for the boosted regression tree analyses of the simulated outbreaks of foot-and-mouth disease in Australia using AADIS.

Outcome	Variable set	Deviance mean	Deviance SE
Total IPs	Day 7	15.515	1.258
Total IPs	Day 14	8.941	0.446
Total IPs	Day 21	6.95	0.517
Outbreak duration (days)	Day 7	10.562	0.308
Outbreak duration (days)	Day 14	8.572	0.361
Outbreak duration (days)	Day 21	7.75	0.271
AUC (km ²)	Day 7	0.219	0.007
AUC (km ²)	Day 14	0.178	0.005
AUC (km ²)	Day 21	0.048	0.003

Table 21: Coefficient of variation statistics for the boosted regression tree analyses of the simulated outbreaks of foot-and-mouth disease in New Zealand using InterSpread Plus.

Outcome	Variable set	Deviance mean	Deviance SE
Total IPs	Day 7	15.948	0.817
Total IPs	Day 14	11.481	0.283
Total IPs	Day 21	8.262	0.284
Outbreak duration (days)	Day 7	8.463	0.169
Outbreak duration (days)	Day 14	7.378	0.143
Outbreak duration (days)	Day 21	6.179	0.173
AUC (km ²)	Day 7	0.24	0.007
AUC (km ²)	Day 14	0.108	0.004
AUC (km ²)	Day 21	0.099	0.002

Table 22: Lookup table showing the probability that an outbreak of FMD introduced in south-east Australia and responded to with the baseline strategy (no vaccination) will exceed a final size of 5, 10, 20 or 50 infected premises and the probability that the duration of the outbreak will exceed 60, 90 or 120 days for each possible number of infected premises existing on day 14 after detection of the outbreak.

Day 14 IPs	Number of IPs				Outbreak duration (days)		
	IPs ≥ 5	IPs ≥ 10	IPs ≥ 20	IPs ≥ 50	Days ≥ 60	Days ≥ 90	Days ≥ 180
1	0	0	0	0	0.01	0	0
2	0.02	0.01	0	0	0.04	0.01	0
3	0.05	0.01	0.01	0	0.07	0.01	0
4	0.16	0.04	0.01	0	0.11	0.02	0
5	0.44	0.04	0.01	0.01	0.13	0.03	0
6	-	0.13	0.03	0.01	0.19	0.04	0
7	-	0.25	0.06	0.02	0.25	0.07	0.01
8	-	0.34	0.07	0.01	0.26	0.05	0
9	-	0.61	0.14	0.05	0.32	0.11	0.01
10	-	0.83	0.2	0.09	0.36	0.13	0.03
11	-	-	0.27	0.05	0.46	0.14	0.03
12	-	-	0.34	0.06	0.45	0.18	0
13	-	-	0.45	0.11	0.51	0.23	0.03
14	-	-	0.54	0.11	0.4	0.11	0.03
15	-	-	0.6	0.17	0.52	0.22	0.03
16	-	-	0.73	0.17	0.52	0.23	0.09
17	-	-	0.79	0.22	0.59	0.26	0.02
18	-	-	0.83	0.15	0.53	0.24	0.07
19	-	-	0.94	0.21	0.65	0.25	0.04
20	-	-	0.98	0.24	0.63	0.3	0.1
21-25	-	-	-	0.42	0.71	0.32	0.05
26-30	-	-	-	0.61	0.71	0.46	0.09
31-35	-	-	-	0.87	0.89	0.49	0.14
>35	-	-	-	1	0.9	0.6	0.19

Table 23: Lookup table showing the probability that an outbreak of FMD in the Auckland region of New Zealand and responded to with the baseline strategy (no vaccination) will exceed a final size of 5, 10, 20 or 50 infected premises and the probability that the duration of the outbreak will exceed 60, 90 or 120 days for each possible number of infected premises existing on day 14 after detection of the outbreak.

Day 14 IPs	Number of IPs				Outbreak duration (days)		
	IPs ≥ 5	IPs ≥ 10	IPs ≥ 20	IPs ≥ 50	Days ≥ 60	Days ≥ 90	Days ≥ 180
1	0.02	0.01	0.01	0	0.01	0.01	0
2	0.07	0.04	0.02	0	0.04	0.01	0
3	0.13	0.09	0.04	0.01	0.07	0.02	0
4	0.28	0.15	0.08	0.02	0.11	0.04	0
5	0.44	0.17	0.08	0.03	0.12	0.03	0
6	-	0.25	0.13	0.03	0.16	0.05	0
7	-	0.3	0.13	0.03	0.14	0.05	0.01
8	-	0.44	0.15	0.04	0.19	0.05	0
9	-	0.6	0.26	0.08	0.25	0.08	0
10	-	0.76	0.24	0.06	0.23	0.05	0
11	-	-	0.32	0.11	0.28	0.12	0
12	-	-	0.38	0.09	0.28	0.09	0
13	-	-	0.35	0.08	0.23	0.08	0
14	-	-	0.41	0.09	0.24	0.09	0.01
15	-	-	0.52	0.14	0.3	0.11	0
16	-	-	0.59	0.16	0.35	0.11	0.01
17	-	-	0.65	0.15	0.35	0.11	0.01
18	-	-	0.84	0.19	0.41	0.13	0
19	-	-	0.87	0.17	0.33	0.14	0.01
20	-	-	0.93	0.2	0.4	0.12	0
21-25	-	-	-	0.28	0.45	0.14	0.01
26-30	-	-	-	0.37	0.48	0.14	0.01
31-35	-	-	-	0.6	0.62	0.62	0.01
>35	-	-	-	0.93	0.75	0.75	0.01

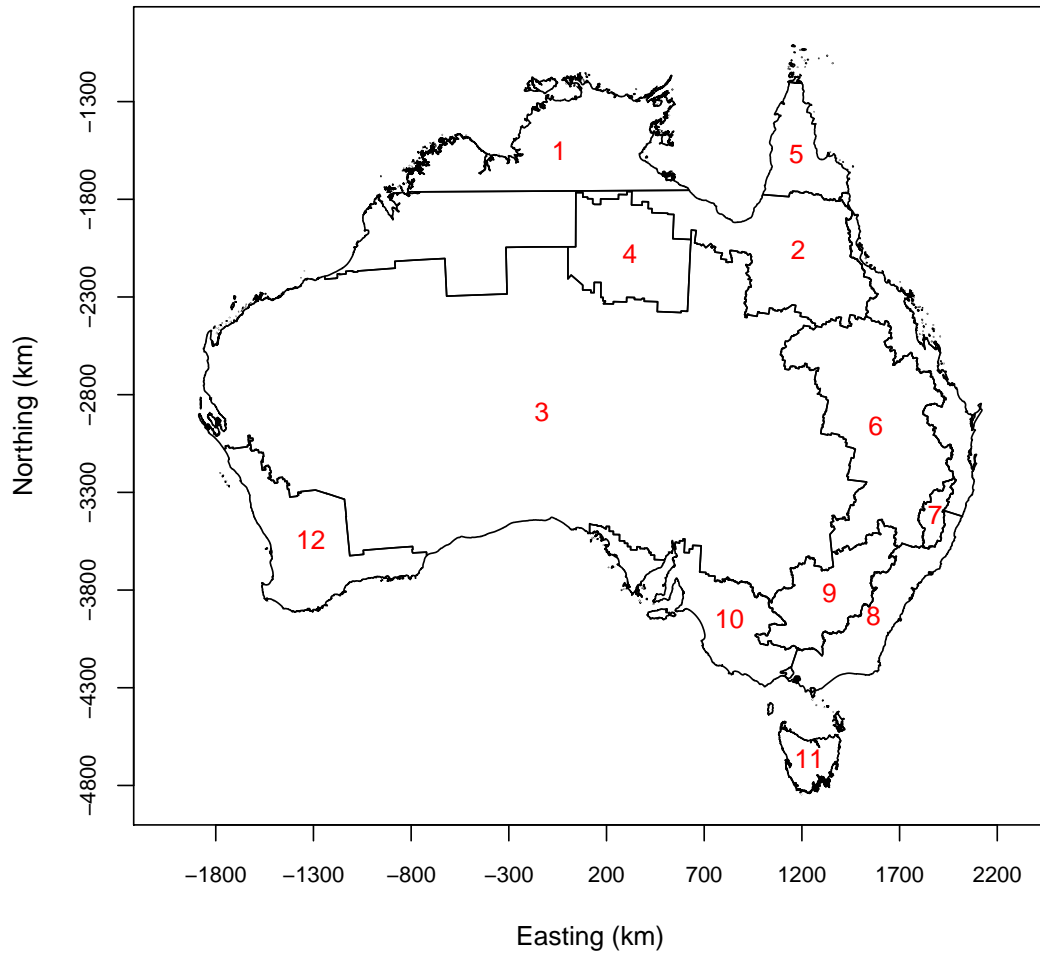


Figure 1: Map of Australia showing the boundaries of the 12 livestock production regions. Key: 1 Far North; 2 Lower North; 3 Arid Zone; 4 Barkley Tableland; 5 Tropical North-East Coast; 6 Central Queensland and North-West New South Wales; 7 New England; 8 Temperate South-East Coast; 9 Temperate Slopes and Plains; 10 Mediterranean; 11 Tasmania; 12 South-West Western Australia.

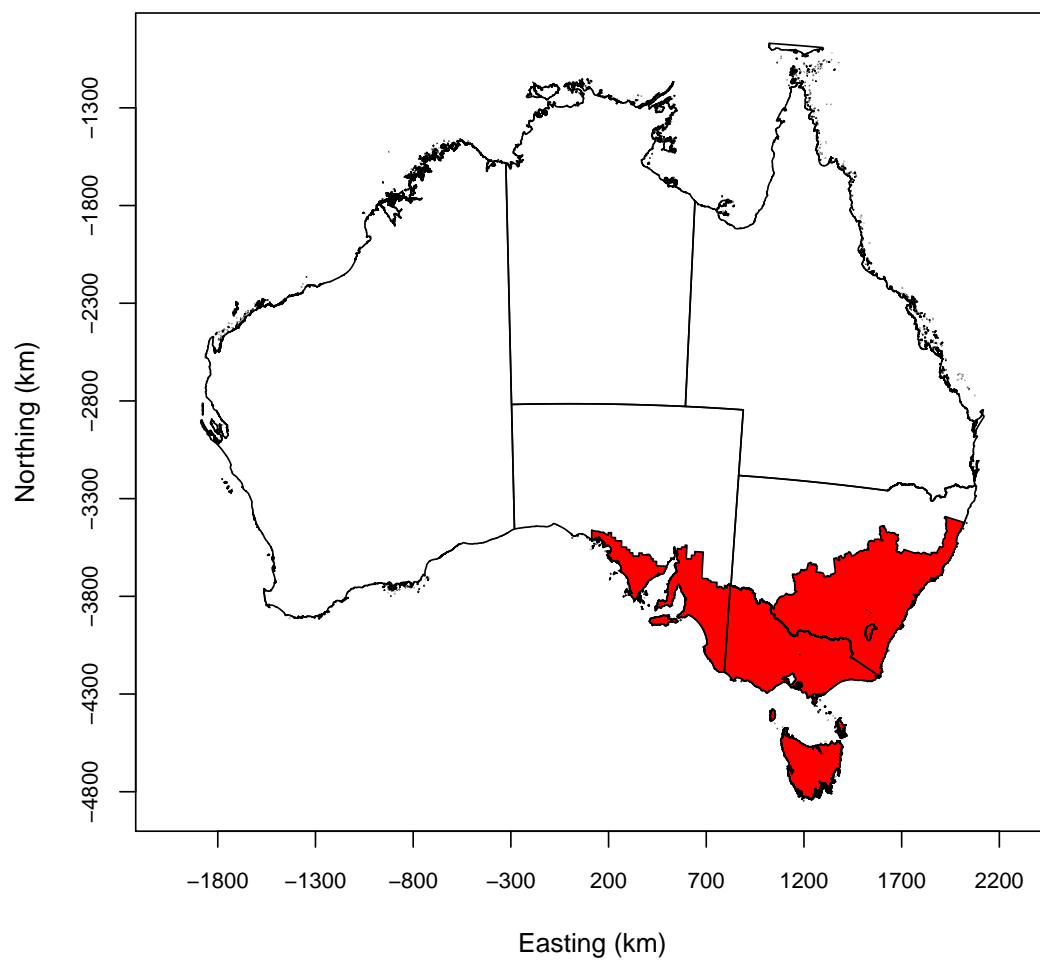


Figure 2: Map of Australia showing jurisdictional boundaries and the south east region (red shaded area) in which FMD outbreaks were initiated using AADIS.

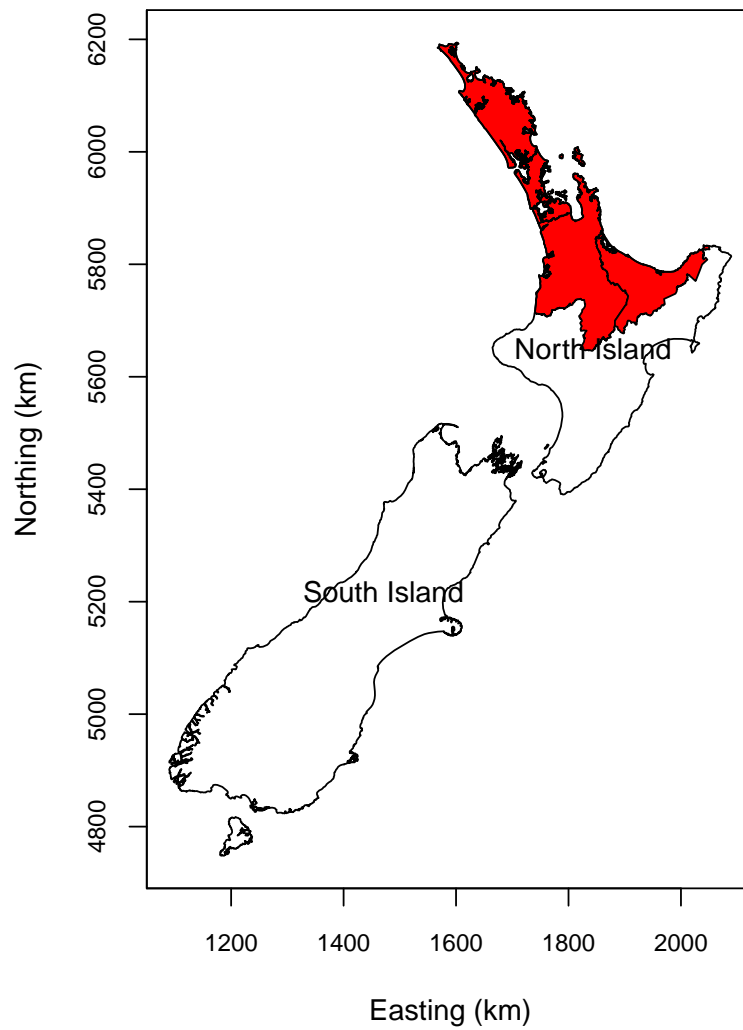


Figure 3: Map of New Zealand showing jurisdictional boundaries and the Auckland mega-region (red shaded area) in which FMD outbreaks were initiated using InterSpread Plus.

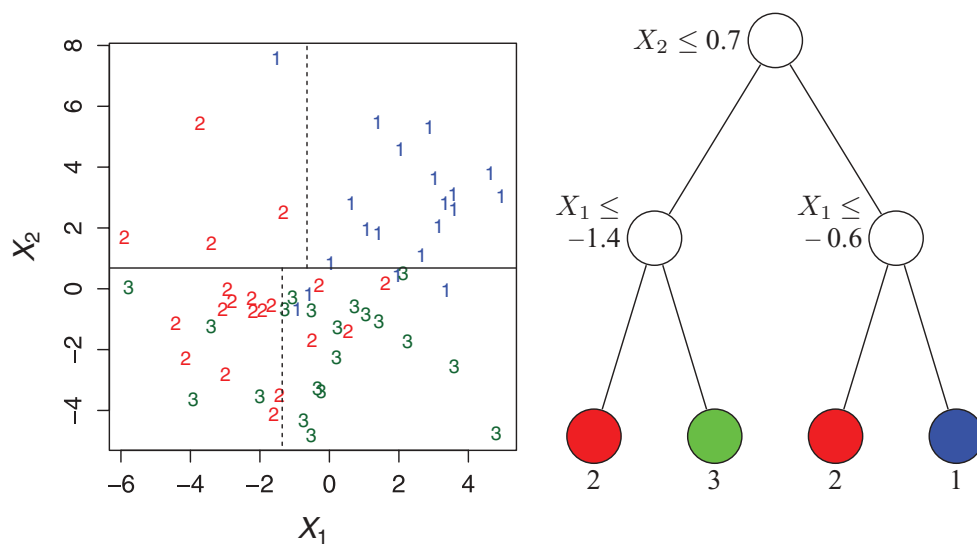


Figure 4: Partitions (left) and decision tree structure (right) for a classification tree model with three outcomes labeled 1, 2, and 3. At each intermediate node, a case goes to the left child node if the condition is satisfied. The predicted class is given beneath each leaf node. Adapted from Loh (2011).

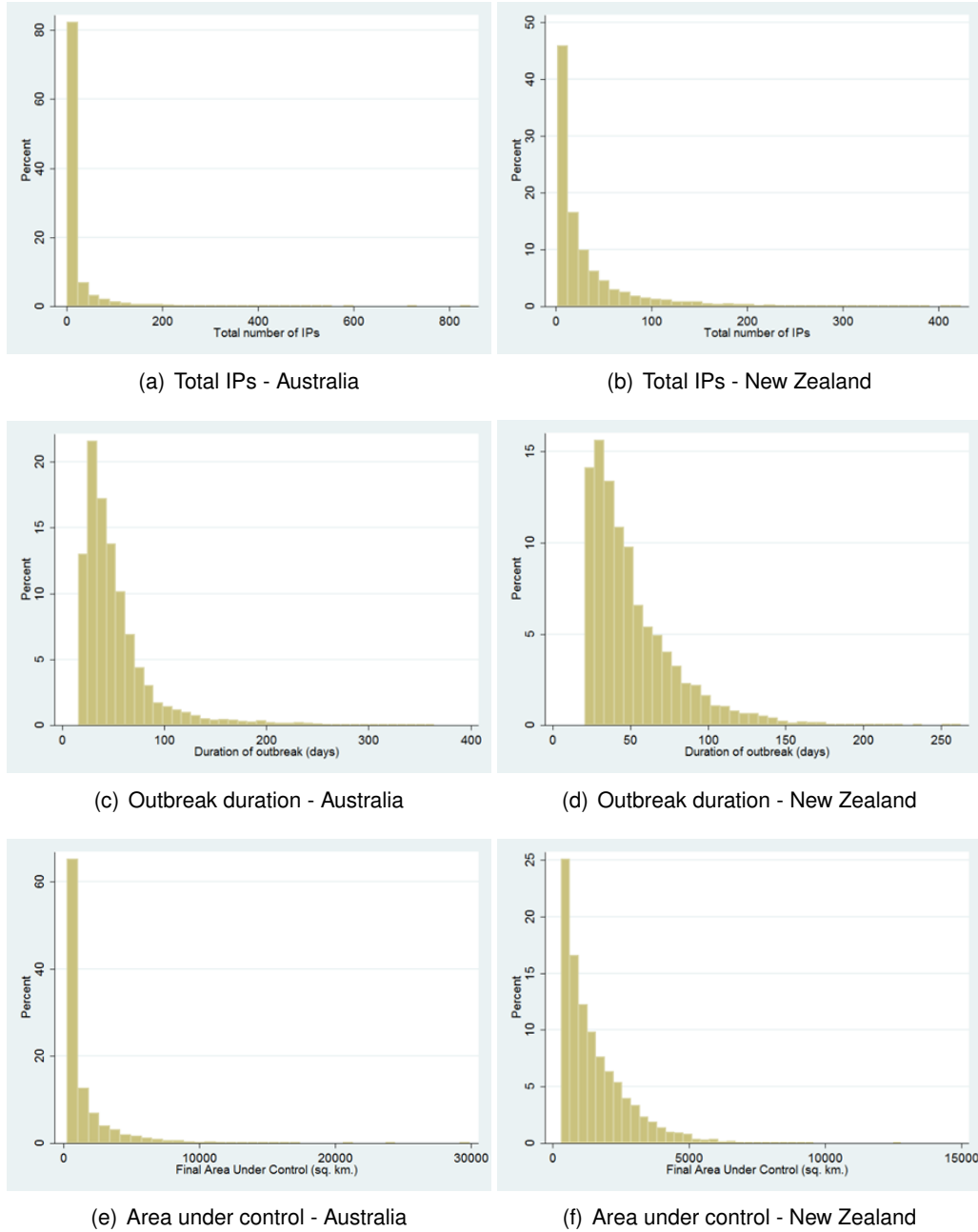


Figure 5: Frequency histograms showing the distribution of values for the total number of IPs, outbreak duration (days) and the area under control (km^2).

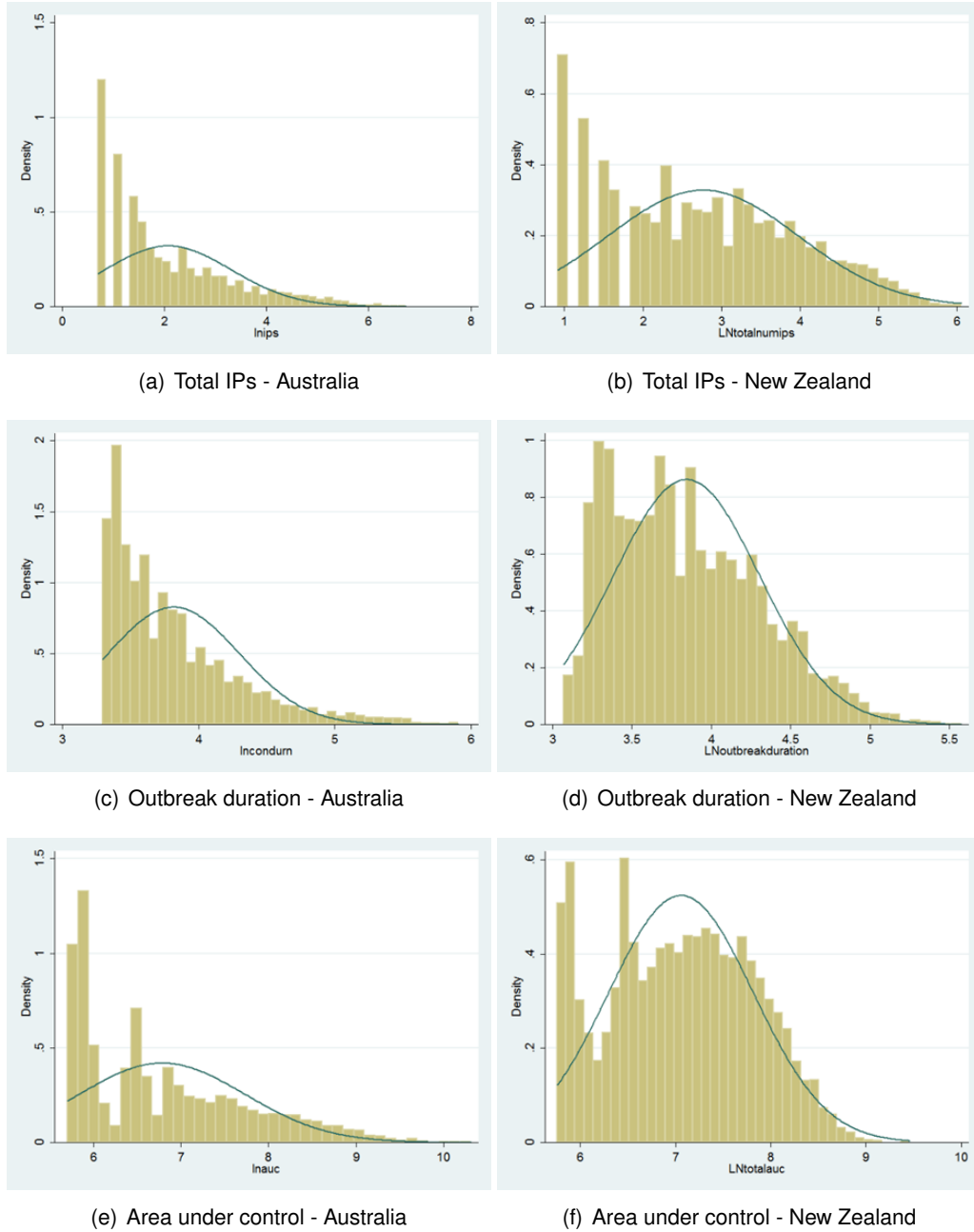
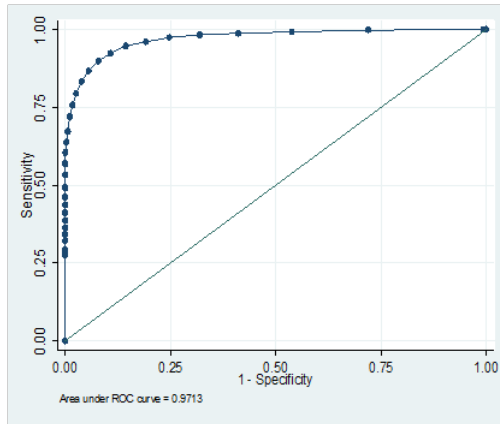
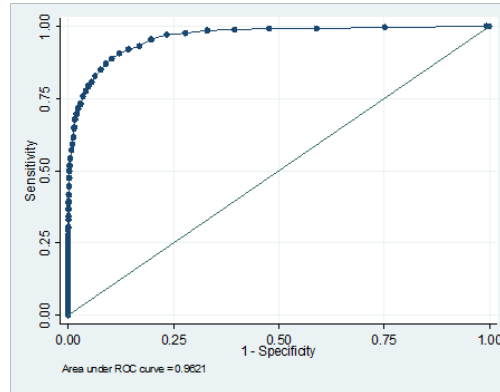


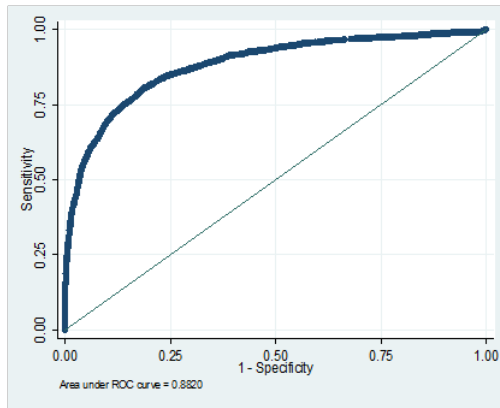
Figure 6: Frequency histograms (with normal distribution curve) of the log transformed data sets for the total number of IPs, outbreak duration (days) and area under control (km^2).



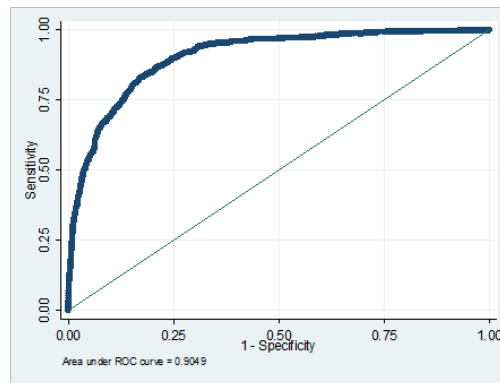
(a) Total IPs (20 IPs)



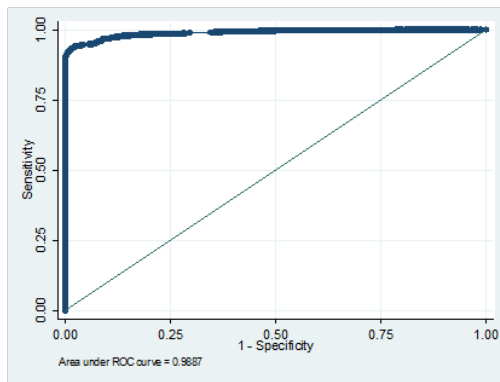
(b) Total IPs (50 IPs)



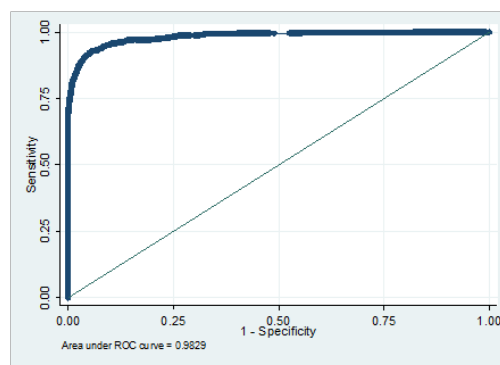
(c) Outbreak duration (50 days)



(d) Outbreak duration (90 days)



(e) Area under control (1000 km²)



(f) Area under control (1000 km²)

Figure 7: Receiver Operating Characteristic (ROC) curves for the total number of IPs, outbreak duration (days) and area under control for modelled FMD outbreaks in south-eastern Australia.

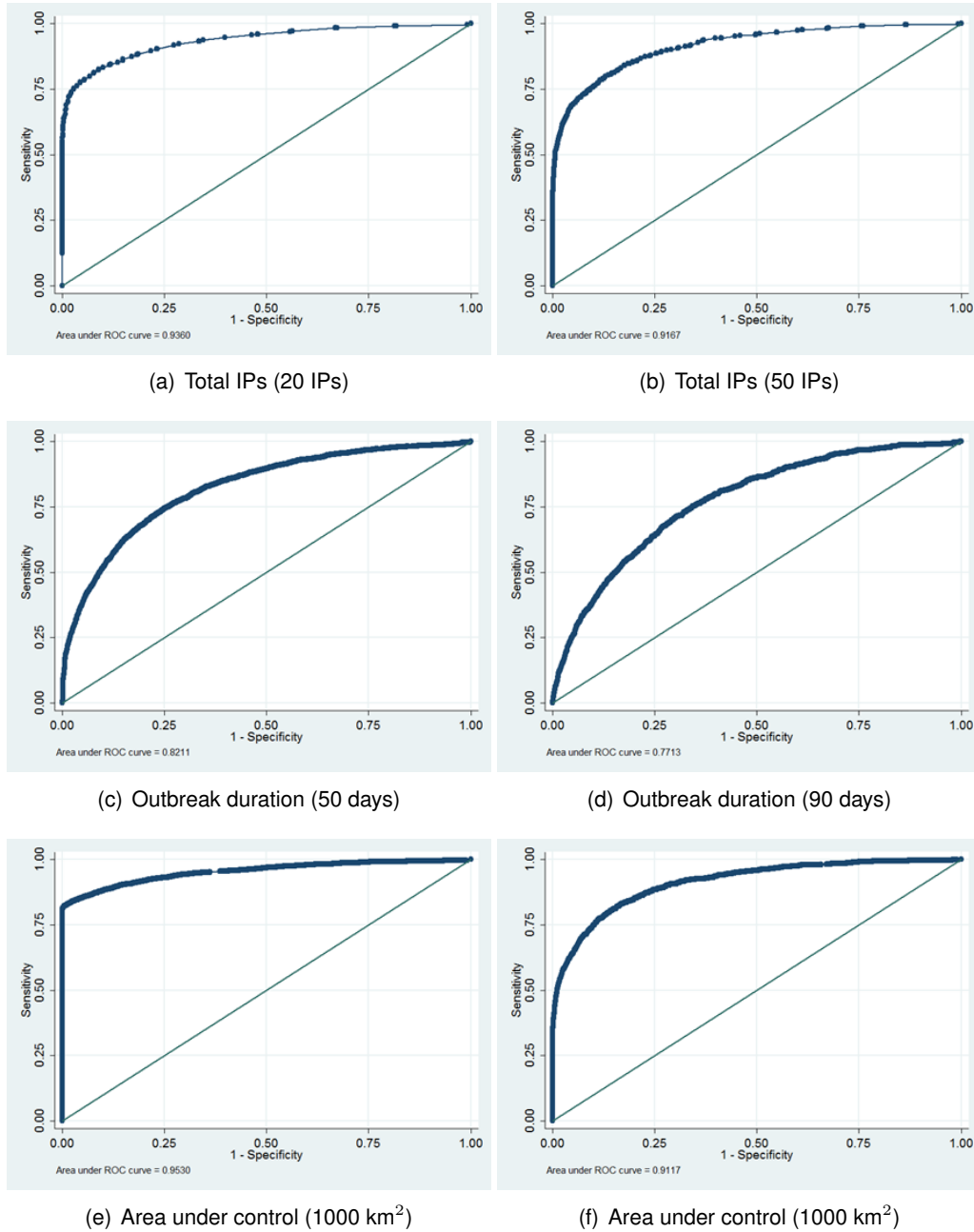


Figure 8: Receiver Operating Characteristic (ROC) curves for the total number of IPs, outbreak duration (days) and area under control for modelled FMD outbreaks in New Zealand.

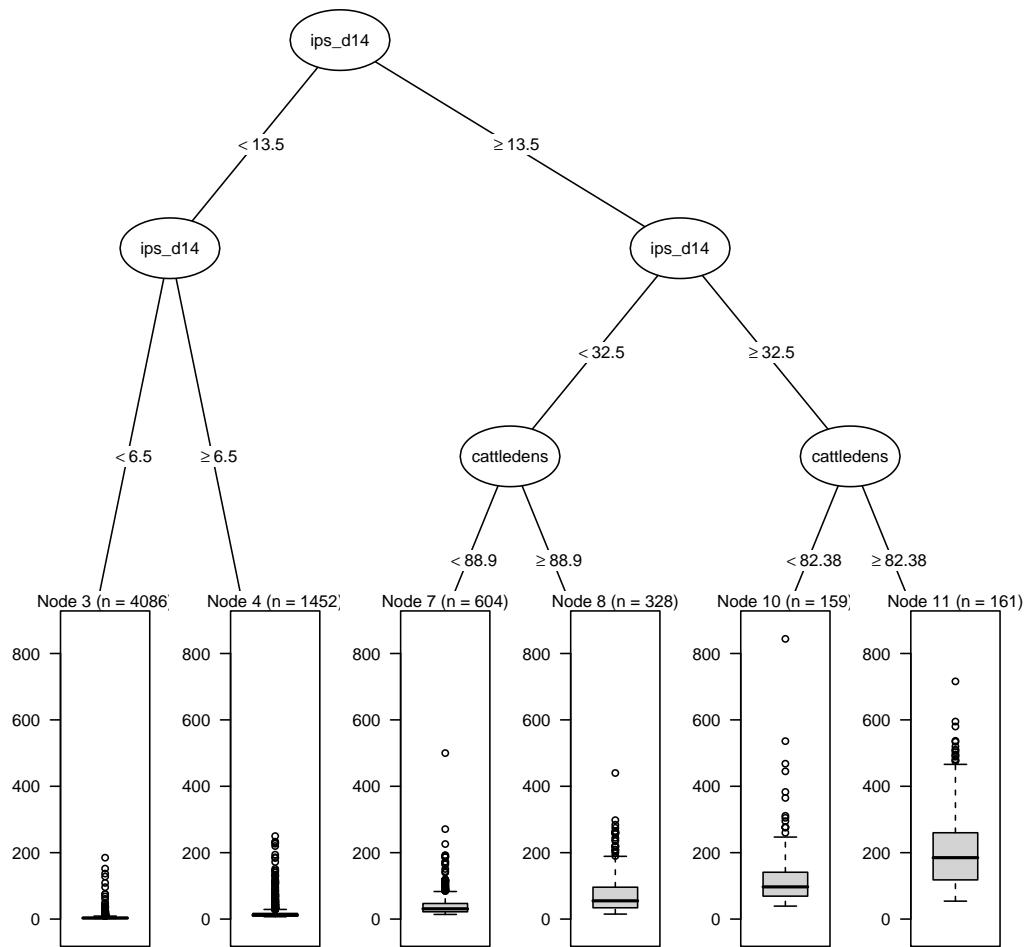


Figure 9: Regression tree summarising day 14 post detection variables predictive of the total number of IPs using AADIS. The number of IPs identified at day 14 post-detection had the strongest association with the total number of IPs followed by cattle density. Relatively large outbreaks were those where there were more than 32 IPs identified by day 14 and where the outbreak started in an area where the density of cattle was greater than 82 head per square km.

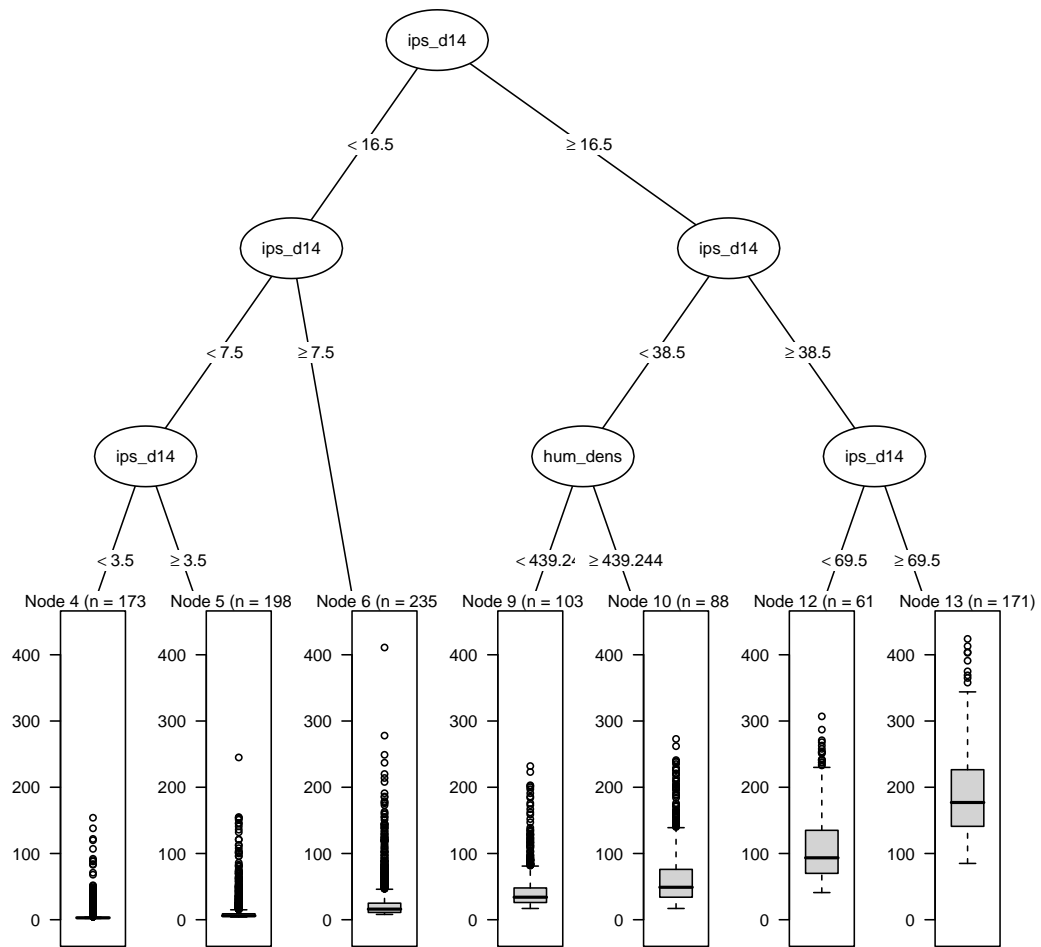


Figure 10: Classification and regression tree summarising day 14 post detection variables predictive of the total number of IPs using InterSpread Plus. The number of IPs identified at day 14 post detection had the strongest association with the total number of IPs followed by human population density. Relatively large outbreaks were those where there were more than 38 IPs identified by day 14.

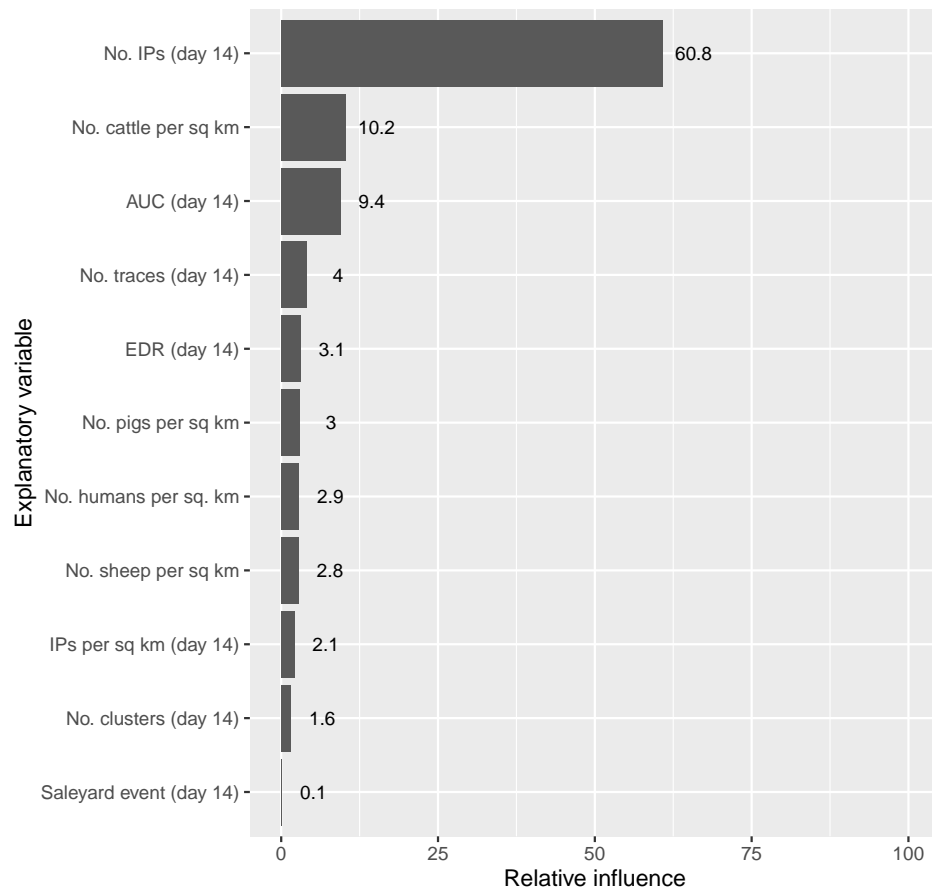


Figure 11: Horizontal bar plot showing the boosted regression tree weights for the day 14 explanatory variables for the total number of infected premises, based on simulated outbreaks of foot-and-mouth disease in Australia using AADIS.

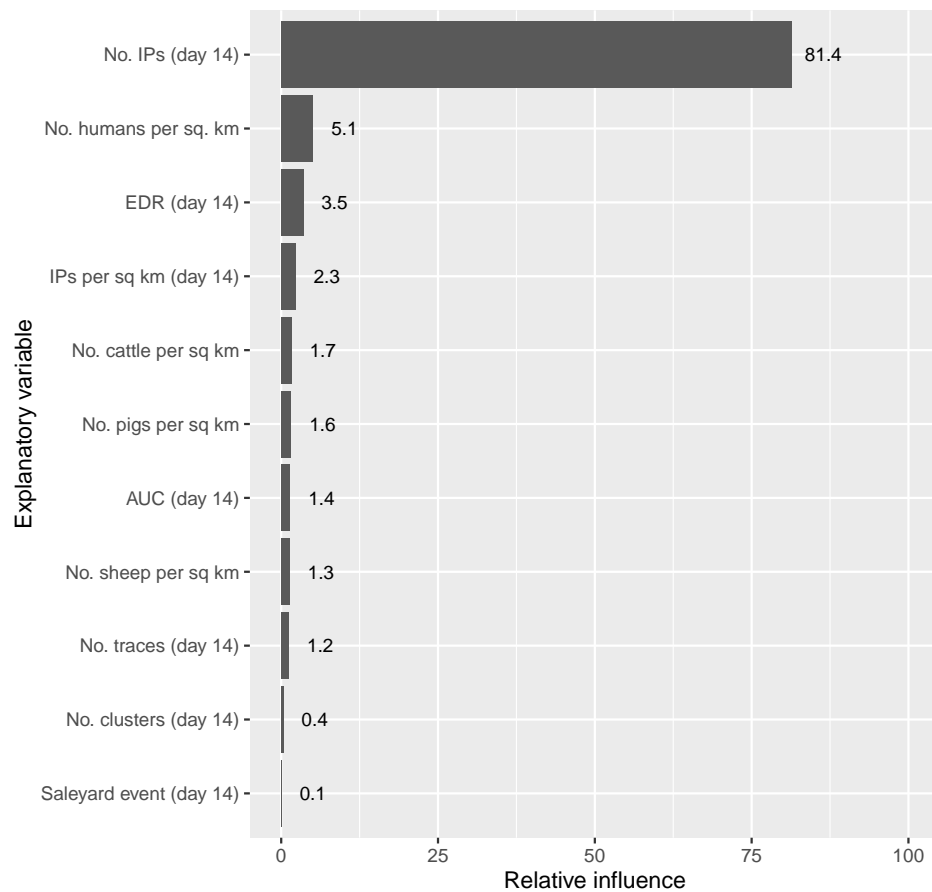


Figure 12: Horizontal bar plot showing the boosted regression tree weights for the day 14 explanatory variables for the total number of infected premises, based on simulated outbreaks of foot-and-mouth disease in New Zealand using InterSpread Plus.

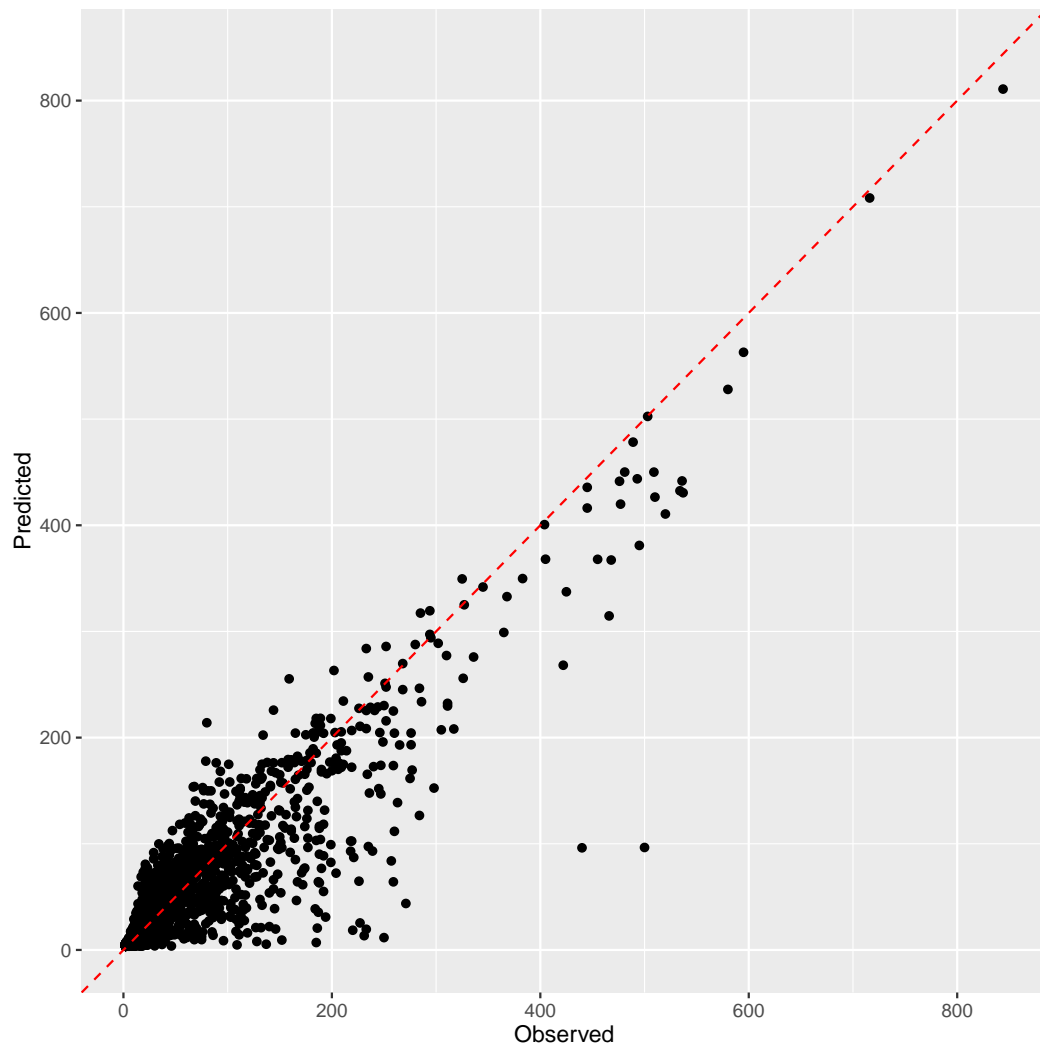


Figure 13: Scatterplot showing the number of infected premises predicted by the boosted regression tree model (vertical axis) as a function of the number of infected premises predicted by AADIS using first 14 day early decision indicators (horizontal axis).

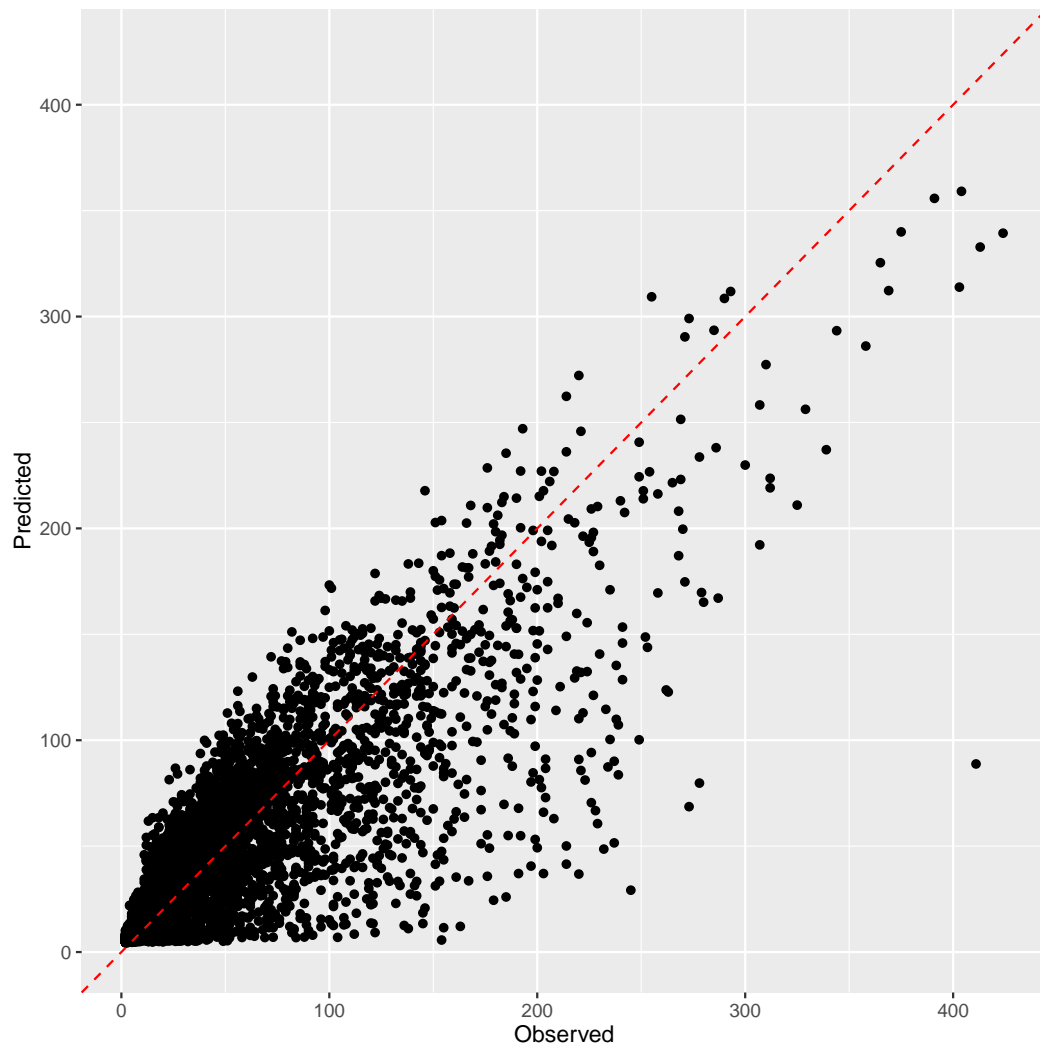


Figure 14: Scatterplot showing the number of infected premises predicted by the boosted regression tree model (vertical axis) as a function of the number of infected premises predicted by InterSpread Plus using first 14 day early decision indicators (horizontal axis).

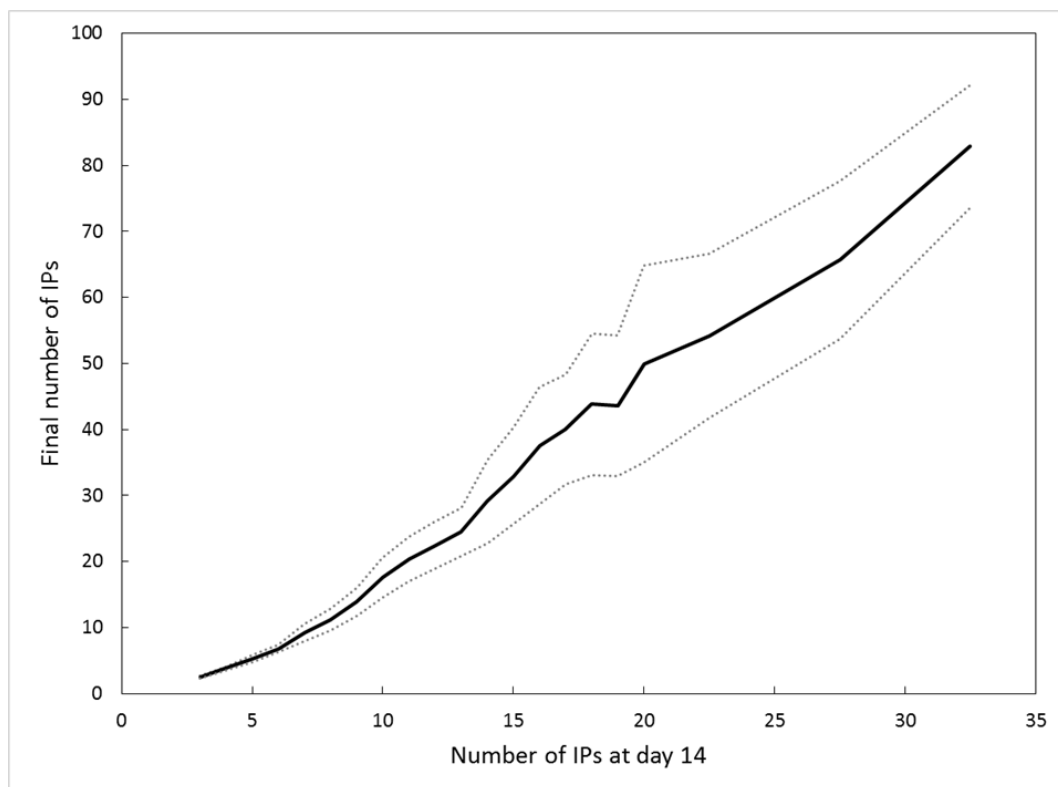


Figure 15: The predicted final number of IPVs (with 95% confidence intervals) during an outbreak of FMD in south-eastern Australia using data available 14 days after the outbreak commenced.

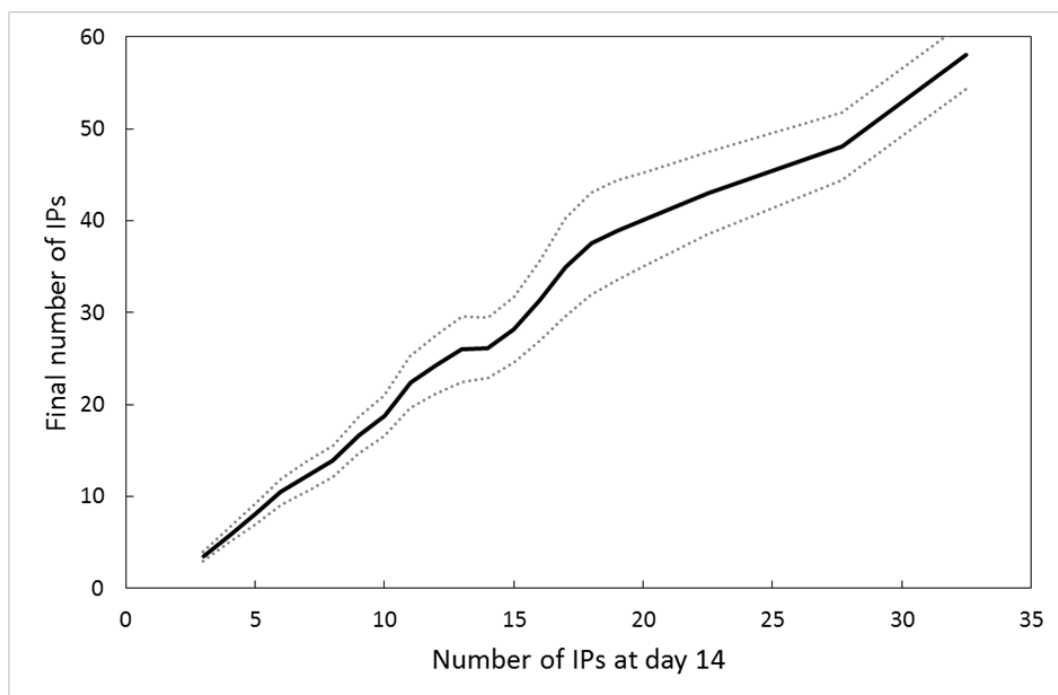


Figure 16: The predicted final number of IPVs (with 95% confidence intervals) during an outbreak of FMD in the Auckland region of New Zealand using data available 14 days after the outbreak commenced.

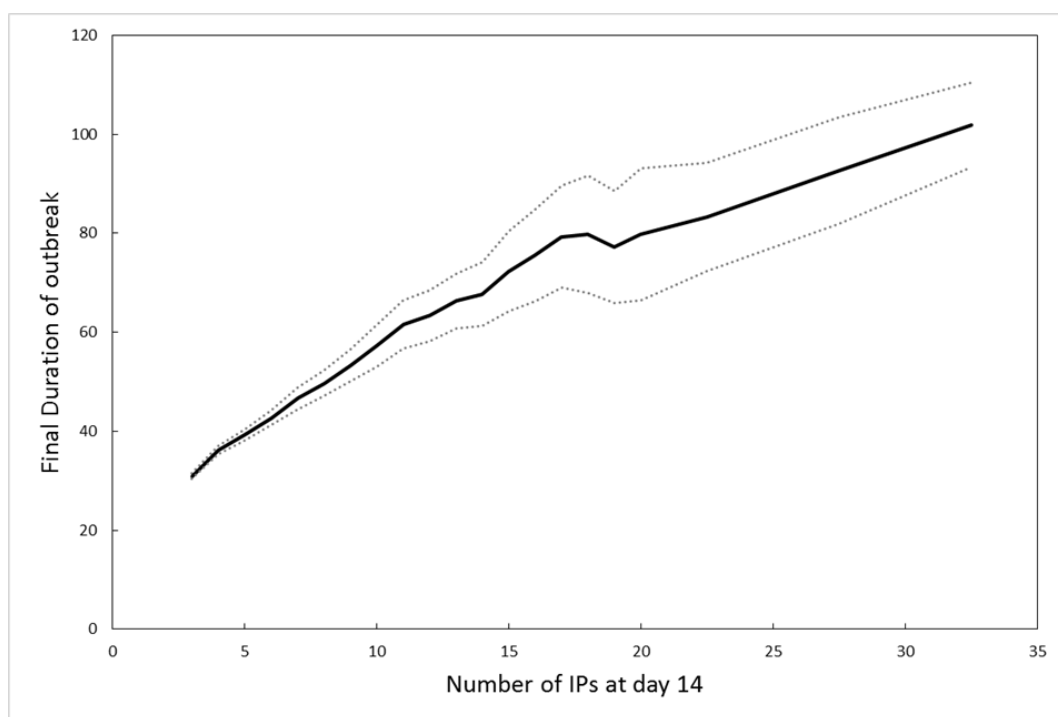


Figure 17: The predicted final number of IPs (with 95% confidence intervals) during an outbreak of FMD in south-eastern Australia using data available 14 days after the outbreak commenced.

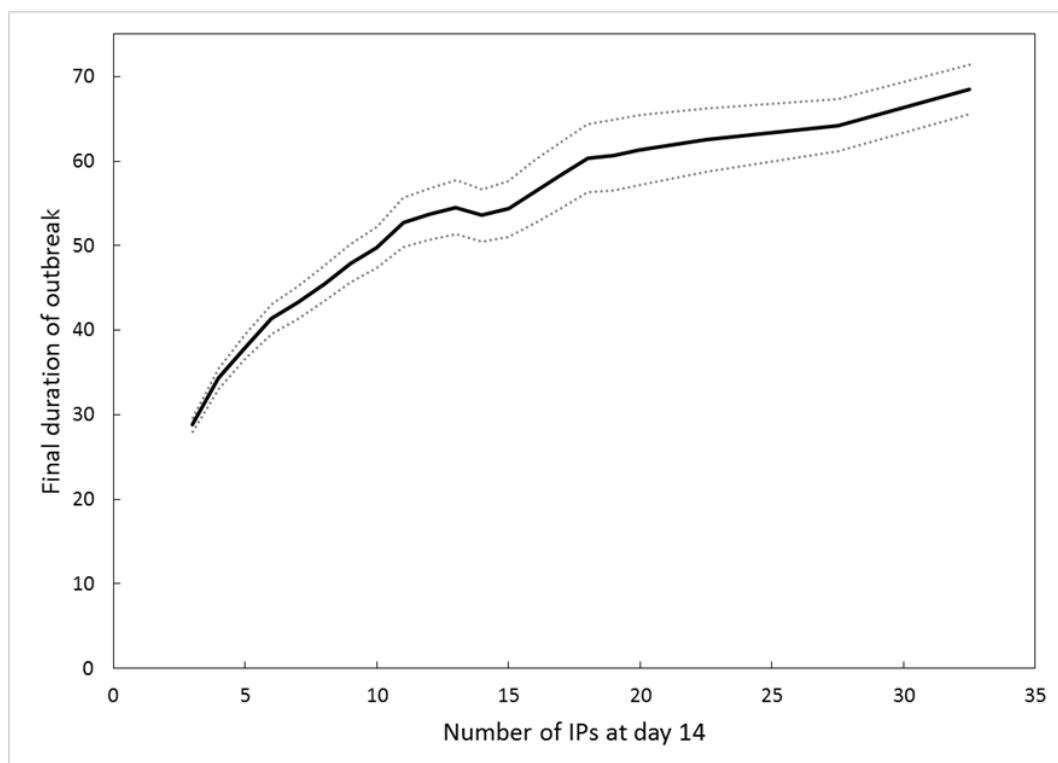


Figure 18: The predicted duration (with 95% confidence intervals) of an outbreak of FMD in the Auckland region of New Zealand using data available 14 days after the outbreak commenced.

Appendix 1

CEBRA Project 1404D (2015-16) Workshop Report

12-13 August 2015

Department of Agriculture, Canberra

Attendees: Richard Bradhurst³, Iain East¹, Graeme Garner¹, Pham Van Ha³, Tom Kompas³, Corissa Miller¹, Tom Rawdon², Robert Sanson⁵, Mark Stevenson⁴,

¹ *Australian Department of Agriculture*

² *New Zealand Ministry of Primary Industries*

³ *Australian National University*

⁴ *University of Melbourne*

⁵ *AsureQuality Limited New Zealand*

Session 1: Workshop Introduction

Graeme Garner stated the objectives of the workshop:

- Clarify project objectives.
- Summarise results of the project thus far.
- Finalise work plan, roles and responsibilities.
- Agree on project deliverables and milestones.

A copy of the workshop agenda is attached. As Iain East was unavailable on day 1 and Tom Kompas was unavailable on day 2, it was agreed to address phase 3 prior to phase 2.

Given the relatively short timeframe to complete the project, the importance of having well-scoped activities, identified deliverables and milestones was emphasised. Further, phases 2 and 3 should be worked in parallel wherever possible.

Graeme provided an overview of the project objectives:

- Phase 1: Relative validation of AADIS and InterSpread Plus.
- Phase 2: Early decision indicators - assess utility of information available to disease managers in real time to 'predict' potential outbreak size.

- Phase 3: Optimising disease control - evaluate control strategies (and combinations), given multiple management objectives.

Graeme provided a brief summary of the work carried out for Phase 1. The AADIS and InterSpread Plus models were both used to model 28 days of uncontrolled spread of FMD in the Australian Goulburn Valley and Darling Downs regions, and the New Zealand Taranaki and Canterbury areas. It was encouraging that the models produced broadly similar outbreaks. Details of the Phase 1 study and results are provided in the CEBRA 2014-15 progress report tabled in July 2015.

Richard Bradhurst provided a demonstration of AADIS version 1.71, and an overview of recent model enhancements and planned work.

Robert Sanson described recent improvements in the way InterSpread Plus handles the resourcing of control measures.

Session 2: Optimising disease control strategies (Phase 3)

Tom Kompas presented the objectives of the proposed economic analysis:

- Minimising the cost of an FMD response (such as control costs and compensation costs).
- Maintaining business continuity of the uninfected producers.
- Rapid eradication of the disease to reduce trade impacts.

Tom described how the Sample Average Approximation method can be used to minimise the cost of a control program by varying specific control parameters such as the radius of the vaccination zone around infected premises. The model seeks to find the point where the extra costs of a control activity are just equal to the extra benefits (or avoided losses).

Control variables that may be of interest in the optimisation process include:

- Start day of the vaccination program (relative to the first day of the control program).
- Radius of the vaccination zone around infected premises.
- Number of IPs as a trigger point for commencing the vaccination program.
- Duration of national standstill. Australia currently enforces a 3 day standstill while New Zealand specifies a 14 day standstill.
- Size of control zones (radii of RAs and CAs).

It was decided that the initial focus of the optimisation study will be the vaccination program start day and the vaccination zone radius. Once the optimisation model is functional the focus may broaden to other control variables.

The AADIS and InterSpread Plus models will initially be used to model a baseline scenario of stamping out only (i.e., no vaccination). The models will subsequently be used to model control

scenarios where the vaccination program start day and vaccination zone radius are randomly varied across a large number of runs.

Model output files (CSV):

1. Population data:

- Farm ID, herd ID²
- Farm type, herd type¹
- Farm (herd¹) location (long, lat)
- State ID, Region ID, local government ID
- Farm (herd¹) population (number of cattle, sheep, pigs, etc.)

2. Simulation data (for each IP and vaccinated farm per iteration):

- Run number
- Farm (herd¹) ID
- Farm (herd¹) source ID
- Transmission route (spread pathway that caused infection)
- Infection day
- Detection day
- Cull day
- Vaccination day

3. Control data (per iteration):

- Run number
- Vaccination program start day
- Vaccination zone radius

Economic parameters of interest:

1. Control and management costs:

- Management (disease control centre costs/day)
- Vaccination
 - vaccine cost per head (cattle, pigs, sheep)
 - labour/management costs
 - coverage (vaccination zone radius)

² Australian (AADIS) output only

- Decontamination, slaughter and disposal costs per farm type (Beef, Dairy, Sheep, Pigs, Mixed beef/sheep, Small holder, Feedlot etc.)
 - labour/management cost (if any)
 - include vaccinated farms if applicable

2. Compensation and other economic (trade) costs

- Average compensation cost per head per farm type (Beef, Dairy, Sheep, Pig, Mixed beef/sheep, Small holder, Feedlot etc.)
 - labour/management cost (if any)
 - include compensation for vaccinated farms if applicable
- National export revenue losses/day
- Other expenses if any

Outbreak scenarios:

A pilot region is to be selected in each country that has a variety of animal densities and production systems. Options for the New Zealand pilot region include Auckland, Northland, Waikato and the Bay of Plenty. Suggested pilot region for Australia is Victoria or the 'mega-region' enclosing Victoria.

2. Baseline scenario:

- Infection to be introduced randomly into a small to medium pig farm in the pilot region. Note that if there are insufficient numbers of pig farms in New Zealand to provide an adequate sample space then the primary case may need to be chosen from several farm types – perhaps with weighting towards pig farms.
- Standard stamping out policy (SO) - culling of IPs only (i.e., no culling on suspicion, no culling of dangerous contact premises, no contiguous culling), and no vaccination.
- 10,000 runs

3. Vaccination scenario:

- Infection to be introduced using the same technique as the baseline scenario.
- Passive or active first IP detection?
- Suppressive ring vaccination:
 - Direction = 'outside-in'
 - All species (priorities)
 - Retrospectivity window = 5 days (i.e., median incubation period)
 - Vaccination zone radius to be randomly varied (per run) in the integer range 1km-10km

- Vaccination program start day to be randomly varied (per run) in the integer range 10 days to 28 days (relative to the start of the control program)
 - Resourcing levels
 - 20,000 runs
4. Silent spread scenario:
- Infection to be introduced using the same technique as the baseline scenario.
 - 90 days of silent spread (i.e., no control program).
 - This scenario will be computationally intensive. It is estimated that AADIS will take approximately 1 minute to complete 1 run and thus take about 16.7 hours to complete 1,000 runs. It is estimated that InterSpread Plus will take approximately 10 minutes to complete 1 run and thus take about 167 hours to complete 1,000 runs. TBD as to the number of runs actually required and whether it is feasible to include both models in this scenario.

Session 3: Early predictors of outbreak size (Phase 2)

Iain East presented an overview of the work undertaken thus far. A zero-truncated negative binomial regression model was successfully fitted for two variables (number of IPs at day 14 and number of trace premises at day 14), from outbreak data generated by AADIS for a fixed source of infection. Future areas for investigation include:

- Other explanatory variables.
- Inclusion of InterSpread Plus data for Australian outbreaks.
- Introduction of infection in random premises.

Mark Stevenson presented an overview of early predictor work undertaken by a postgraduate student of his.

Table of potential predictors:

Metric/Parameter	Comment
Location characteristics - animal density (use FAO data grid (5km cell) at 1 st detected farm: cattle, sheep, pig, total LSU), human density (gridded population of the world), farm density, animal and farm types	<i>Use of FAO data agreed</i>
Silent spread period – time to first detection	<i>Not in first round</i>

IP characteristics – Any IP infection via saleyard pathway? Record as a 0/1 for 7d, 14d, 21d, animal density on farm, animal and farm types, traces	
Season – climate variables (temp in previous month), animal movement patterns (traces), airborne spread (NIWA)	<i>Oz only</i>
Spatial spread – Number of clusters (Robert); Ratio of AUC (10km dissolved around IPs) to IP number, max distance between IP centroids, First Fortnight Spread (FFS)	<i>Robert script</i>
Temporal spread – d7, d14, d21 number IPs, D1 incidence; First 1 week incidence; First Fortnight Incidence (FFI)	<i>D14 initial assessment in linear model</i>
Estimated dissemination rate (EDR) – 4d EDR d14 (IPs at d14-11/IPs at d10-7), d21 (IPs at d21-18/IPs at d17-14); R0	<i>Graeme to look at R0 ref from South America</i>
Traces cumulative TPs for back and forward movements d7, d14, d21 – all traces incl. high, med, low;	
Resource adequacy: number of premises awaiting destruction/disposal; No. surveillance visits; time from detection-to-destruction; time from farmer report-to-visit	
10. Report Cases: farmer report numbers; report cases vs. Patrol Vet/Tracing detections	
11. Virus strain/ airborne ability: molecular unlikely to be useful due to constant mutation, outbreak description will help if direction visible as in UK1967-8. NB models largely parameterised on Type O pan Asia strain, with limited data available for other strains.	

Scenario:

The baseline scenario is to be used for both phases 2 and 3.

Model output files:

The three model output files are to be used for both phases 2 and 3. The control data file contains the following phase 2-only columns:

- Day of first IP detection
- First IP farm ID
- First IP longitude

- First IP latitude
- Saleyard event
- IPs at day 7
- IPs at day 14
- IPs at day 21
- EDR at day 14
- EDR at day 21
- Traces at day 7
- Traces at day 14
- Traces at day 21
- QforDep at day 7
- QforDep at day 14
- QforDep at day 21
- AUC at day 7
- AUC at day 14
- AUC at day 21
- Clusters at day 7
- Clusters at day 14
- Clusters at day 21
- Ipperkm at day 7
- Ipperkm at day 14
- Ipperkm at day 21
- Cattle density
- Sheep density
- Pig density
- Human density
- Total number of IPs
- Outbreak duration
- Total AUC

Definitions:

- Duration: either last cull complete (for SO strategy), or last vaccine applied (for VAC strategies).
- Cluster: Non-contiguous polygons using a 10km radius buffer around IPs.
- Day 1 = first day of potential spread, first day of simulation.

- AUC = Area under control, the total area in 10km buffers around each IP adjusted for overlapping areas
- EDR = estimated dissemination rate (calculated as the ratio of IPs in the last 7 days to those in the previous 7 day period)
- Ipperkm = ratio of number of IPs to area (calculated as merged 10 km radial buffers around all IPs)
- QforDep = premises queued for depopulation

Session 4: Project Management

ID	Action Item Description	Who	Phase	Due
1	Silent spread scenario - determine requirements and whether InterSpread Plus is to be involved. Conduct runs.	RB, RS, Ha	3	31 Aug 2015
2	Baseline scenario – finalise scenario parameterisation (e.g., resourcing). Conduct runs. Provide model outputs to Ha.	GG, RB, RS	3	15 Sep 2015
3	Upgrade AADIS to handle random variation of vaccination radius and vaccination program start date.	RB	3	31 Aug 2015
4	Vaccination scenario – finalise scenario parameterisation (e.g., resourcing). Conduct runs. Provide model outputs to Ha.	GG, RB, RS	3	30 Sep 2015
5	Generate farm output files (AADIS and ISP). Note: some estimation will be required for NZ. Look at farm type and assess species numbers - any zeros will need estimation.	RB, RS	3	15 Sep 2015
6	Provide economic data for New Zealand to Ha.	TR	3	30 Sep 2015
7	Economic analysis update.	Ha, TR	3	31 Oct 2015
8	Economics report write up – Tom K and Ha to lead economics write up. Graeme & Tom to assist Intro and Objectives as required.	TK, Ha, GG, TR	3	TBD
9	Generate scripts to assimilate animal density and human density, AUC for each iteration.	RS	2	TBD
10	Finalise baseline scenario runs with EDI fields calculated using scripts from action item 9.	RS, RB	2	TBD

11	Statistical regression analysis using CEBRA_summ.xlsx for SO runs in R and/or Stata – Mark and Iain. Note: need to consider possible use of CART and random forest approaches.	MS, IE	2	TBD
12	Report write up – Graeme & Tom R introduction and objectives, Robert/Mark/Iain materials and methods, Results and Discussion to come.	GG, TR, RS, MS, IE	2	TBD
13	Workshops to get information out to NZ stakeholders – Tom R, Timeframe: dependent on other workloads.	TR	2, 3	TBD
14	Monthly teleconference. Next telecon: 9am OZ (11am NZ) - Thursday 24 th September 2015.	All	2, 3	24 Sep 2015

CEBRA Workshop Agenda

Decision support tools for animal disease preparedness

Department of Agriculture

12-13 August 2015

Wednesday 12 August

9.00am	Welcome Purpose of the workshop Objectives and desired outcomes of the project Summary of Phase 1	Graeme Garner
9.30am	Current status of AADIS Proposed enhancements	Richard Bradhurst
10.00am	Current status of Interspread Plus Issues (if any) around Interspread Plus	Tom Rawdon/Robert Sanson
10.30am	Morning tea	
10.45	Phase 3 – Effectiveness and cost-effectiveness of models <ul style="list-style-type: none"> • Identification of economic data required • Identification of key variables to be modelled <ul style="list-style-type: none"> ○ Duration of standstill ○ Size of control zone ○ Control strategies ○ Species to be vaccinated ○ Size of vaccination zones ○ other • 	Tom Kompas
12.30pm	Lunch	
1.30pm	Group Discussion around Phase 3	
3.30pm	Afternoon tea	
3.45pm	Recording of objectives, tasks, milestones and responsible person for phase three	
5.00pm	Close	

Thursday 13 August

9.00am	Reiteration of workshop day one – outstanding issues	Graeme Garner
9.30am	Prediction of outcomes (work to date)	Iain East
10.00am	Literature review – predictors of outbreak size	Mark Stevenson
10.30am	Morning tea	
10.45am	<p>Group Discussion one</p> <p>Identification of additional parameters to incorporate into models</p> <p>What is big? When does an outbreak manager start to think of alternative management approaches</p> <p>Assessing robustness of models</p> <ul style="list-style-type: none"> • geographic variation • random premises of introduction • No. and type of outbreak scenarios 	
12.30pm	Lunch	
1.30pm	Recording of objectives, tasks, milestones and responsible person for phase two	
3.00pm	Workshop close	

Appendix 2 – Additional Statistical data

Table 1: Regression coefficients and their standard errors for the linear regression models of first 7 day predictors of area under control, the total number of infected places and outbreak duration for the AADIS and ISP models of FMD.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI
AADIS – AUC:				
Intercept	-1.33 (0.062)	-21.61	0.000	-1.45 – -1.21
Area under control day 7	1.27 (0.010)	131.21	0.000	1.25 – 1.29
AADIS – IPs:				
Intercept	-0.55 (0.036)	-15.21	0.000	-0.62 – -0.48
Number of IPs at day 7	1.83 (0.021)	88.01	0.000	1.79 – 1.87
Pending culls day 7	0.04 (0.021)	2.01	0.045	0.00 – 0.08
AADIS – outbreak duration				
Intercept	16.00 (0.628)	25.48	0.000	14.77 – 17.24
Area under control day 7	0.45 (0.010)	44.76	0.000	0.43 – 0.47
IP density day 7	22.13 (0.943)	23.47	0.000	20.28 – 23.97
First detected farm type				
Beef - intensive	Reference			
Dairy	0.15 (0.024)	6.00	0.000	0.09 – 0.19
Feedlot	0.01 (0.023)	0.24	0.811	-0.04 – 0.05
Mixed beef/sheep	0.00 (0.021)	0.01	0.992	-0.04 – 0.04
Pig - large	-0.14 (0.022)	-6.20	0.000	-0.18 – -0.09
Pig - small	-0.07 (0.020)	-3.65	0.000	-0.11 – -0.03
Sheep	-0.07 (0.022)	-3.07	0.002	-0.11 – -0.02
Smallholder	-0.20 (0.059)	-3.42	0.001	-0.31 – -0.08
ISP – AUC:				
Intercept	0.25 (0.053)	4.73	0.000	0.15 – 0.35
Area under control day 7	1.02 (0.008)	133.86	0.000	1.01 – 1.04
ISP – IPs:				
Intercept	0.72 (0.031)	23.38	0.000	0.66 – 0.78

Number of IPs at day 7	1.04 (0.016)	66.30	0.000	1.01 – 1.08
Pending culls day 7	0.14 (0.013)	10.69	0.000	0.11 – 0.17
ISP – outbreak duration				
Intercept	8.02 (0.231)	34.63	0.000	7.57 – 8.48
Area under control day 7	0.29 (0.007)	43.29	0.000	0.28 – 0.31
IP density day 7	9.04 (0.330)	27.40	0.000	8.40 – 9.69
First detected farm type				
Dairy - dry	Reference			
Lifestyle	0.016 (0.018)	0.91	0.363	-0.02 – 0.05
Beef/sheep/mixed	-0.076 (0.019)	-4.07	0.000	-0.11 - -0.04
Dairy – in milk	-0.135 (0.018)	-7.33	0.000	-0.17 - -0.10
Pig - breeding	-0.104 (0.023)	-4.58	0.000	-0.15 – 0.06
Pig - fattening	0.106 (0.217)	0.49	0.624	-0.32 – 0.53

^a EDR: estimated dissemination ratio.

Table 2: Regression coefficients and their standard errors for the linear regression models of first 14 day predictors of area under control, the total number of infected places and outbreak duration for the AADIS and ISP models of FMD.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI
AADIS – AUC:				
Intercept	-0.57 (0.023)	-25.09	0.000	-0.62 – 10.52
Area under control day 14	1.10 (0.003)	313.84	0.000	1.09 – 1.11
AADIS – IPs:				
Intercept	-0.02 (0.019)	-0.80	0.421	-0.05 – 0.02
Number of IPs at day 14	1.27 (0.008)	164.51	0.000	1.25 – 1.28
Pending culls day 14	0.18 (0.017)	10.64	0.000	0.15 – 0.22
AADIS – outbreak duration				
Intercept	13.87 (0.480)	28.88	0.000	12.92 – 14.81
Area under control day 14	0.39 (0.008)	51.72	0.000	0.38 – 0.40
EDR day 14 ^a	0.12 (0.009)	14.31	0.000	0.11 – 0.14
IP density day 14	18.45 (0.721)	25.60	0.000	17.04 – 19.86
First detected farm type				
Beef - intensive	Reference			
Dairy	-0.09 (0.021)	-4.16	0.000	-0.13 – -0.05
Feedlot	-0.20 (0.020)	-9.98	0.000	-0.23 – -0.16
Mixed beef/sheep	0.11 (0.018)	6.24	0.000	0.08 – 0.14
Pig - large	-0.50 (0.020)	-25.28	0.000	-0.54 – -0.46
Pig - small	-0.27 (0.017)	-15.66	0.000	-0.30 – -0.24
Sheep	0.25 (0.019)	12.73	0.000	0.21 – 0.28
Smallholder	-0.26 (0.048)	-5.44	0.000	-0.35 – -0.17
ISP – AUC:				
Intercept	-0.28 (0.027)	-10.45	0.000	-0.33 – -0.23
Area under control day 14	1.07 (0.004)	275.96	0.000	1.06 – 1.08
ISP – IPs:				
Intercept	0.19 (0.016)	11.63	0.000	0.15 – 0.22
Number of IPs at day 14	1.11 (0.006)	174.93	0.000	1.10 – 1.12

Pending culls day 14	0.13 (0.010)	13.22	0.000	0.11 – 0.15
ISP – outbreak duration				
Intercept	7.07 (0.173)	40.76	0.000	6.73 – 7.41
Area under control day 14	0.29 (0.005)	55.24	0.000	0.28 – 0.30
EDR day 14 ^a	0.21 (0.007)	29.62	0.000	0.19 – 0.22
IP density day 14	7.82 (0.241)	32.36	0.000	7.34 – 8.29
First detected farm type				
Dairy - dry	Reference			
Lifestyle	-0.003 (0.015)	-0.25	0.805	-0.03 – 0.03
Beef/sheep/mixed	-0.042 (0.016)	-2.63	0.009	-0.07 - -0.10
Dairy – in milk	-0.084 (0.016)	-5.33	0.000	-0.12 - -0.05
Pig - breeding	-0.138 (0.087)	-1.59	0.111	-0.31 – 0.03
Pig - fattening	0.232 (0.271)	0.86	0.392	-0.30 – 0.76

^a EDR: estimated dissemination ratio.

Table 3: Regression coefficients and their standard errors for the linear regression models of first 21 day predictors of area under control, the total number of infected places and outbreak duration for the AADIS and ISP models of FMD.

Explanatory variable	Coefficient (SE)	<i>t</i>	P-value	95% CI
AADIS – AUC:				
Intercept	-0.37 (0.016)	-23.09	0.000	-0.41 – -0.34
Area under control day 21	1.07 (0.003)	420.00	0.000	1.06 – 1.07
AADIS – IPs:				
Intercept	-0.41 (0.019)	-22.14	0.000	-0.45 – -0.38
Number of IPs at day 21	1.28 (0.005)	235.78	0.000	1.27 – 1.29
Pending culls day 21	0.08 (0.021)	3.89	0.000	0.04 – 0.12
AADIS – outbreak duration				
Intercept	6.36 (0.543)	11.71	0.000	5.30 – 7.43
Area under control day 21	0.32 (0.008)	41.64	0.000	0.31 – 0.34
EDR day 21 ^a	0.26 (0.009)	27.24	0.000	0.24 – 0.28
IP density day 21	6.75 (0.828)	8.16	0.000	5.13 – 8.37
First detected farm type				

Beef - intensive	Reference			
Dairy	0.05 (0.020)	2.51	0.012	0.01 – 0.09
Feedlot	0.01 (0.018)	0.66	0.509	-0.02 – 0.05
Mixed beef/sheep	0.01 (0.017)	0.77	0.442	-0.02 – 0.05
Pig - large	-0.16 (0.018)	-8.75	0.000	-0.19 – -0.12
Pig - small	-0.05 (0.016)	-3.08	0.002	-0.08 – -0.02
Sheep	-0.03 (0.018)	-1.50	0.133	-0.06 – 0.01
Smallholder	-0.14 (0.035)	-4.09	0.000	-0.21 – -0.07
ISP – AUC:				
Intercept	-0.14 (0.028)	-4.89	0.000	-0.19 – -0.08
Area under control day 21	1.04 (0.004)	267.93	0.000	1.03 – 1.05
ISP – IPs:				
Intercept	0.22 (0.019)	11.89	0.000	0.19 – 0.26
Number of IPs at day 21	1.04 (0.006)	169.55	0.000	1.03 – 1.05
Pending culls day 21	0.18 (0.009)	20.33	0.000	0.16 – 0.20
ISP – outbreak duration				
Intercept	7.07 (0.173)	40.76	0.000	6.73 – 7.41
Area under control day 21	0.24 (0.005)	45.85	0.000	0.23 – 0.25
EDR day 21 ^a	0.23 (0.006)	37.21	0.000	0.22 – 0.24
IP density day 21	6.32 (0.194)	32.58	0.000	5.94 – 6.70
First detected farm type				
Dairy - dry	Reference			
Lifestyle	-0.007 (0.015)	0.47	0.637	-0.02 – 0.04
Beef/sheep/mixed	-0.037 (0.015)	-2.46	0.014	-0.07 – -0.01
Dairy – in milk	-0.070 (0.015)	-4.73	0.000	-0.10 – -0.04
Pig - breeding	-0.091 (0.042)	-2.19	0.029	-0.17 – 0.01
Pig - fattening	0.136 (0.145)	0.94	0.348	-0.15 – 0.42

^a EDR: estimated dissemination ratio.

11 Appendix 3

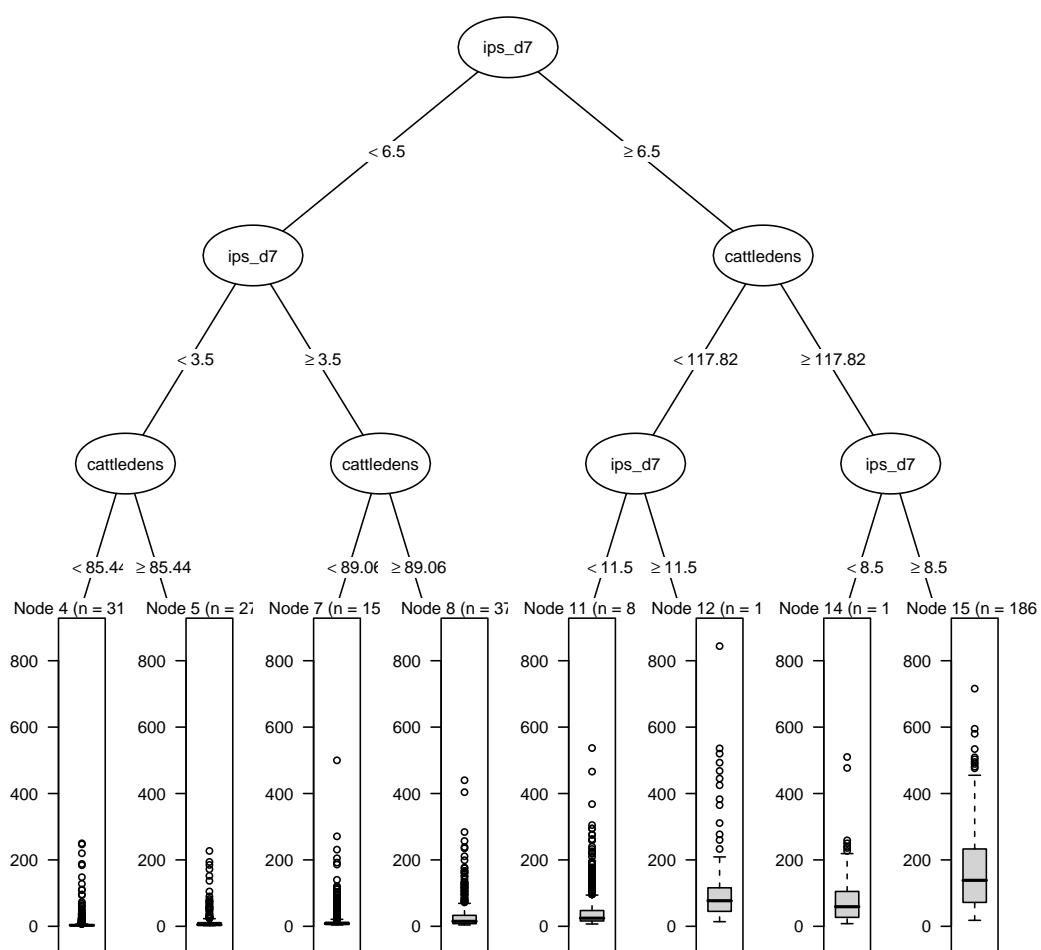


Figure 19: Classification and regression tree summarising day 7 post detection variables predictive of the total number of IPs using AADIS.

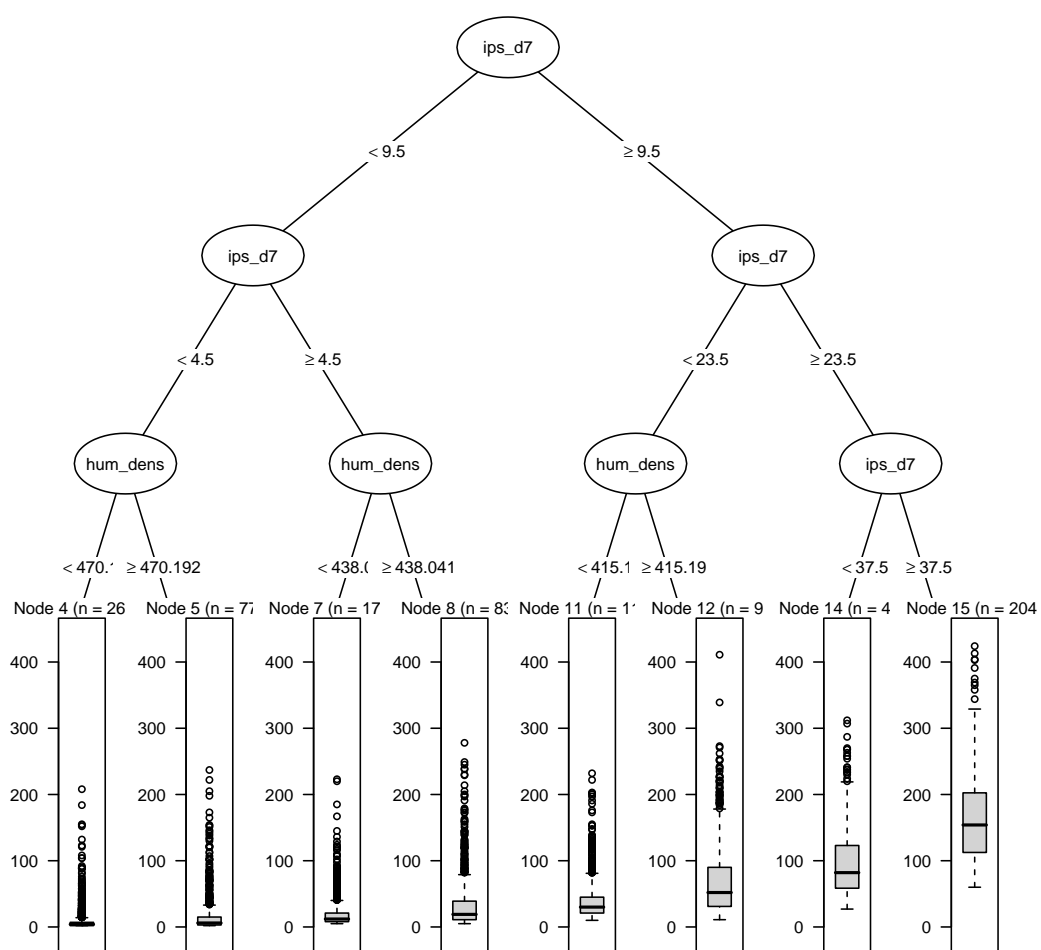


Figure 20: Classification and regression tree summarising day 7 post detection variables predictive of the total number of IPs using InterSpread Plus.

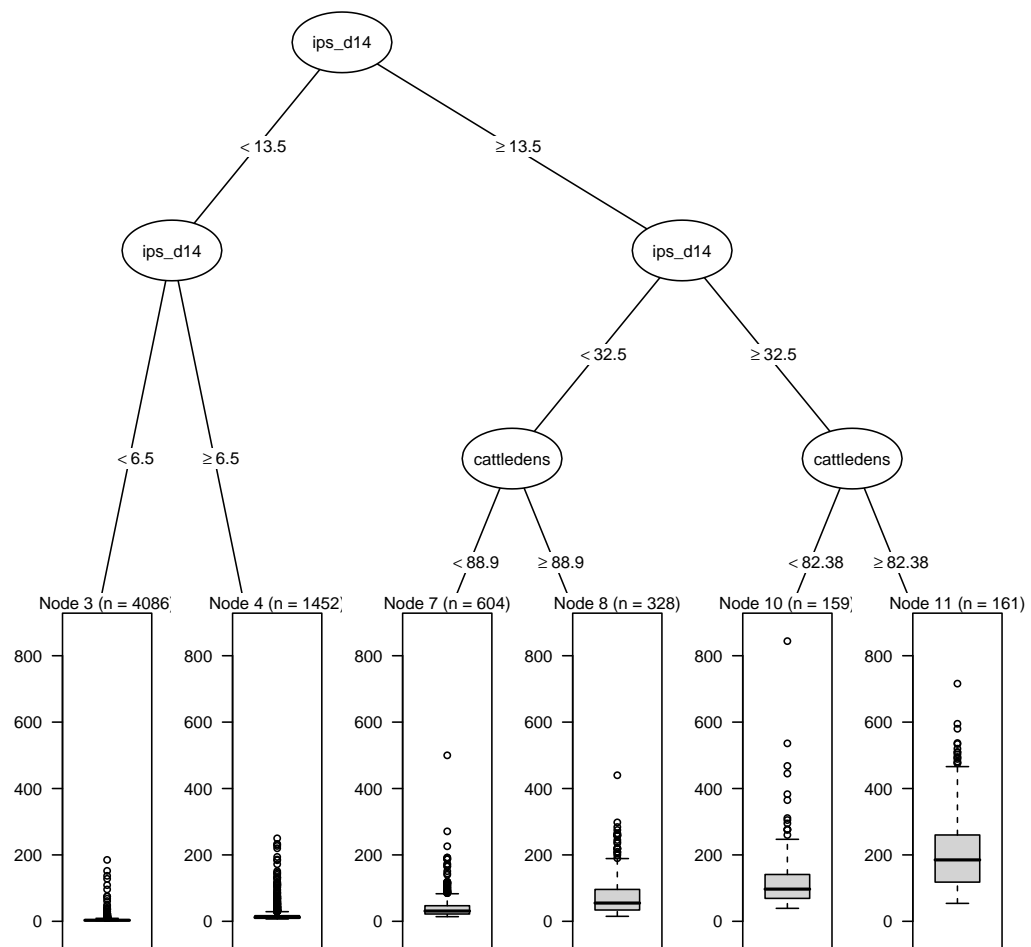


Figure 21: Classification and regression tree summarising day 14 post detection variables predictive of the total number of IPs using AADIS.

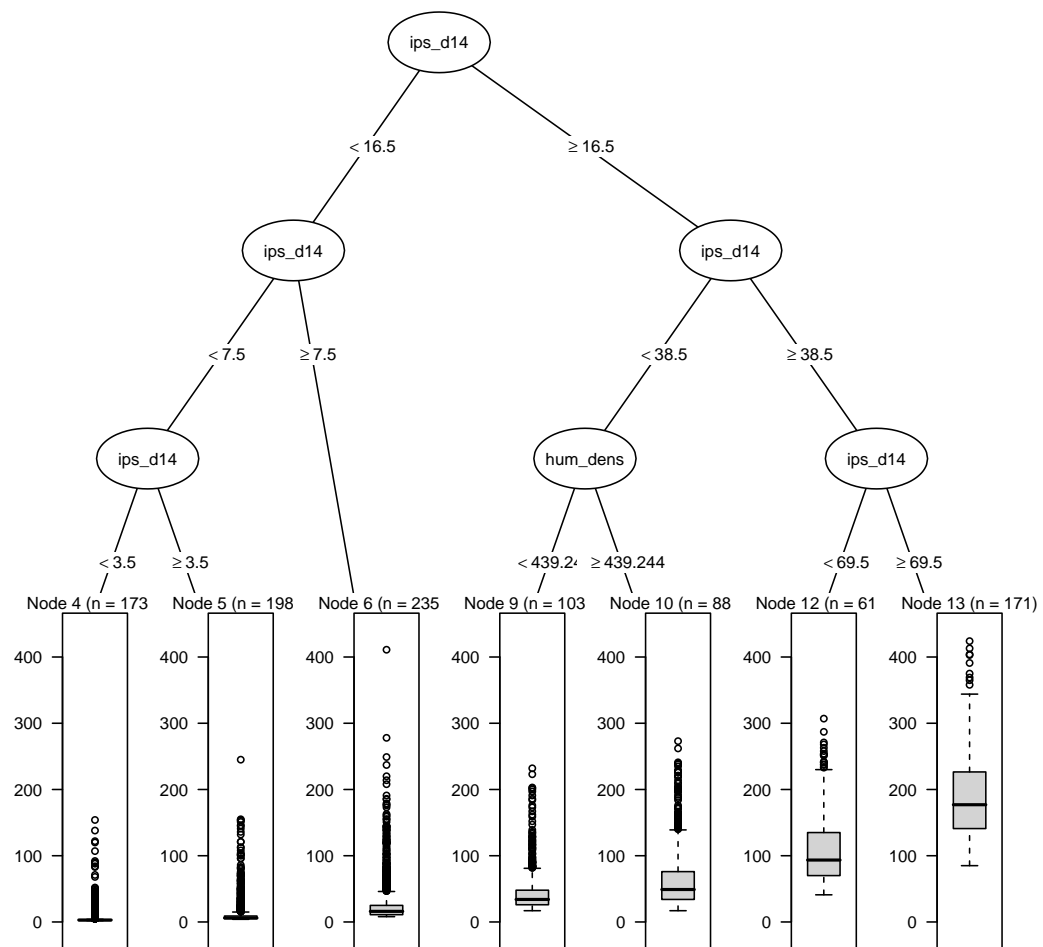


Figure 22: Classification and regression tree summarising day 14 post detection variables predictive of the total number of IPs using InterSpread Plus.

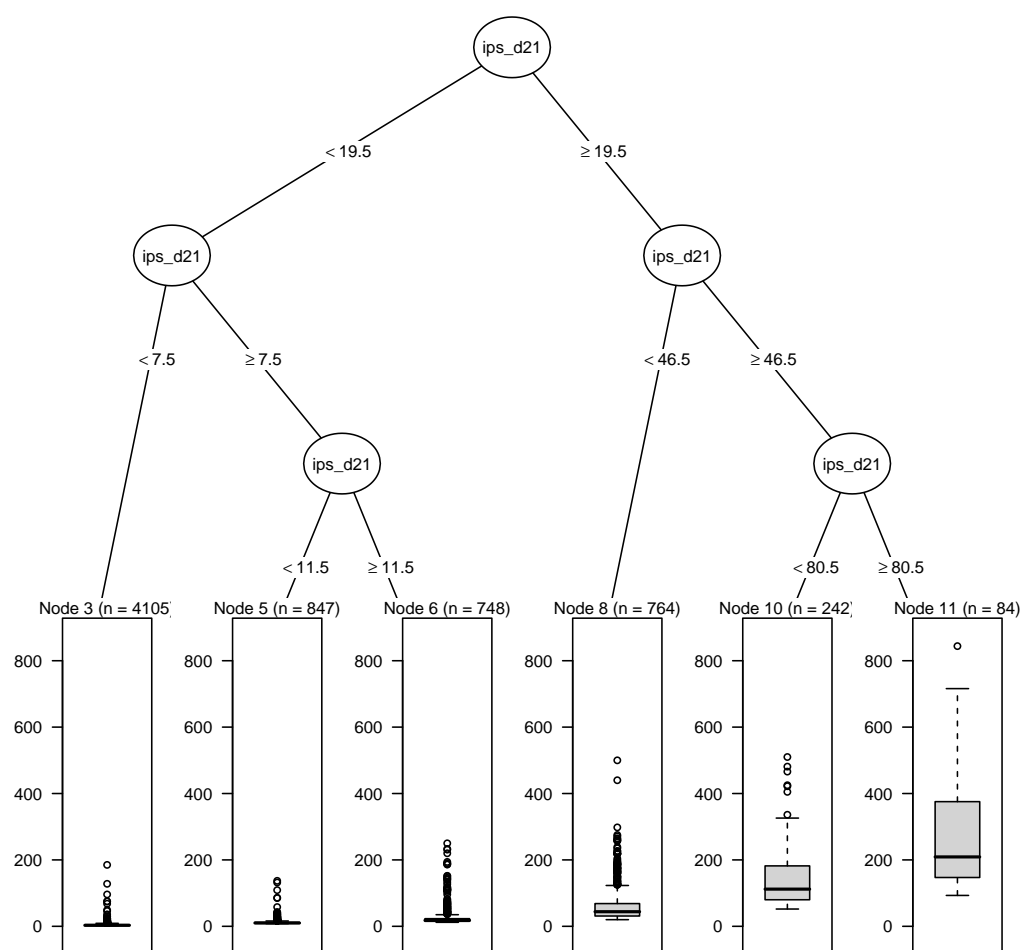


Figure 23: Classification and regression tree summarising day 21 post detection variables predictive of the total number of IPs using AADIS.

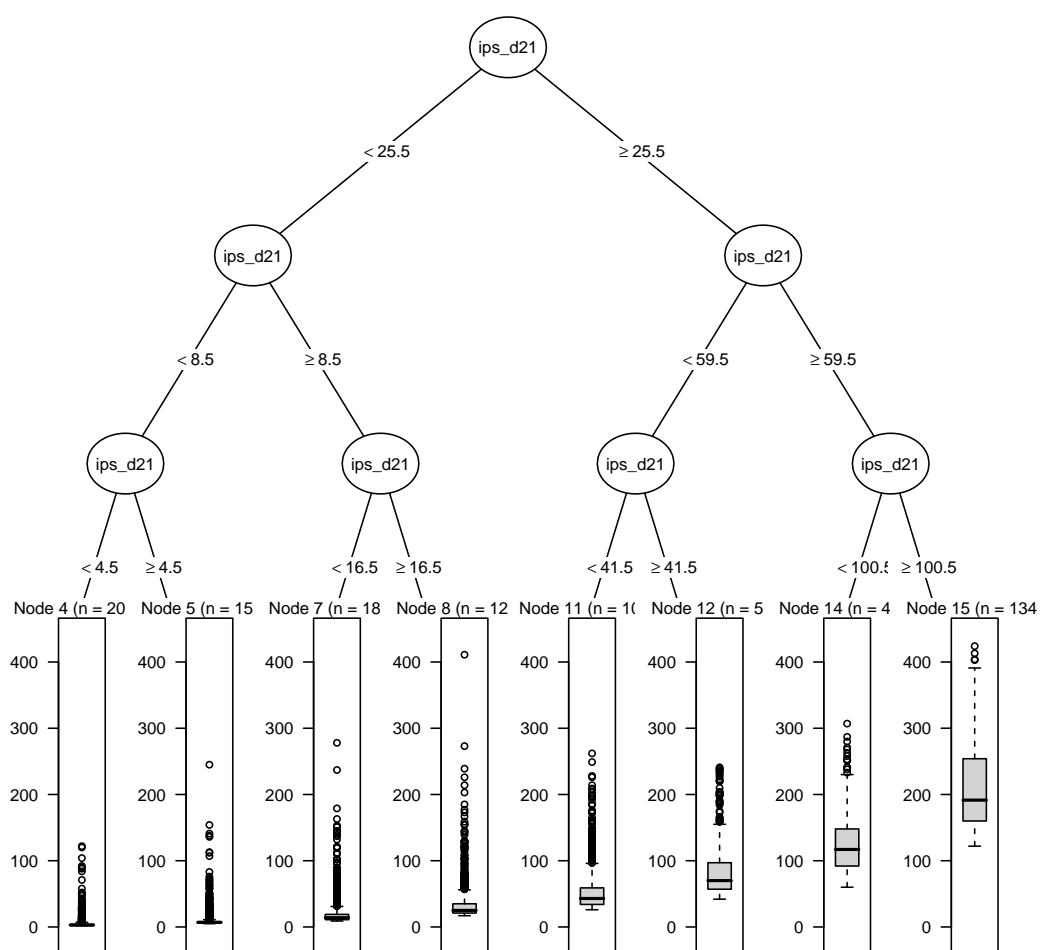


Figure 24: Classification and regression tree summarising day 21 post detection variables predictive of the total number of IPs using InterSpread Plus.

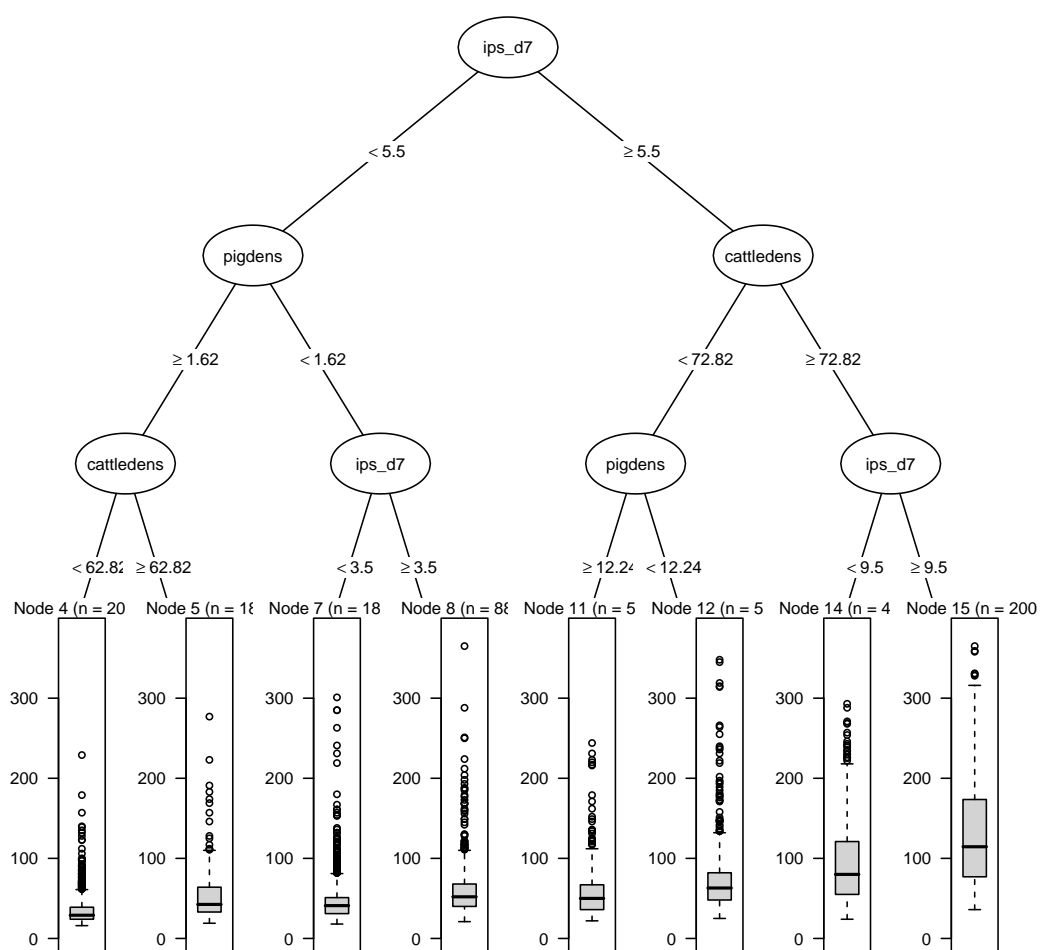


Figure 25: Classification and regression tree summarising day 7 post detection variables predictive of outbreak duration using AADIS.

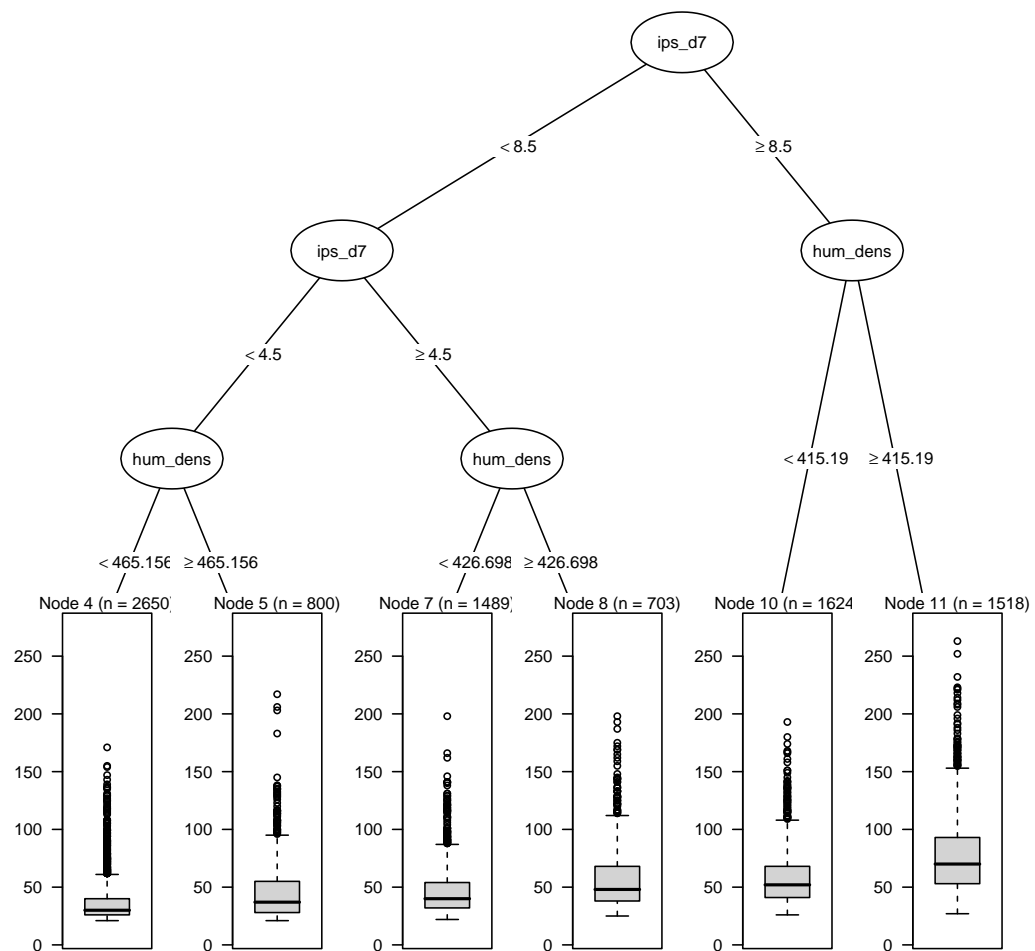


Figure 26: Classification and regression tree summarising day 7 post detection variables predictive of outbreak duration using InterSpread Plus.

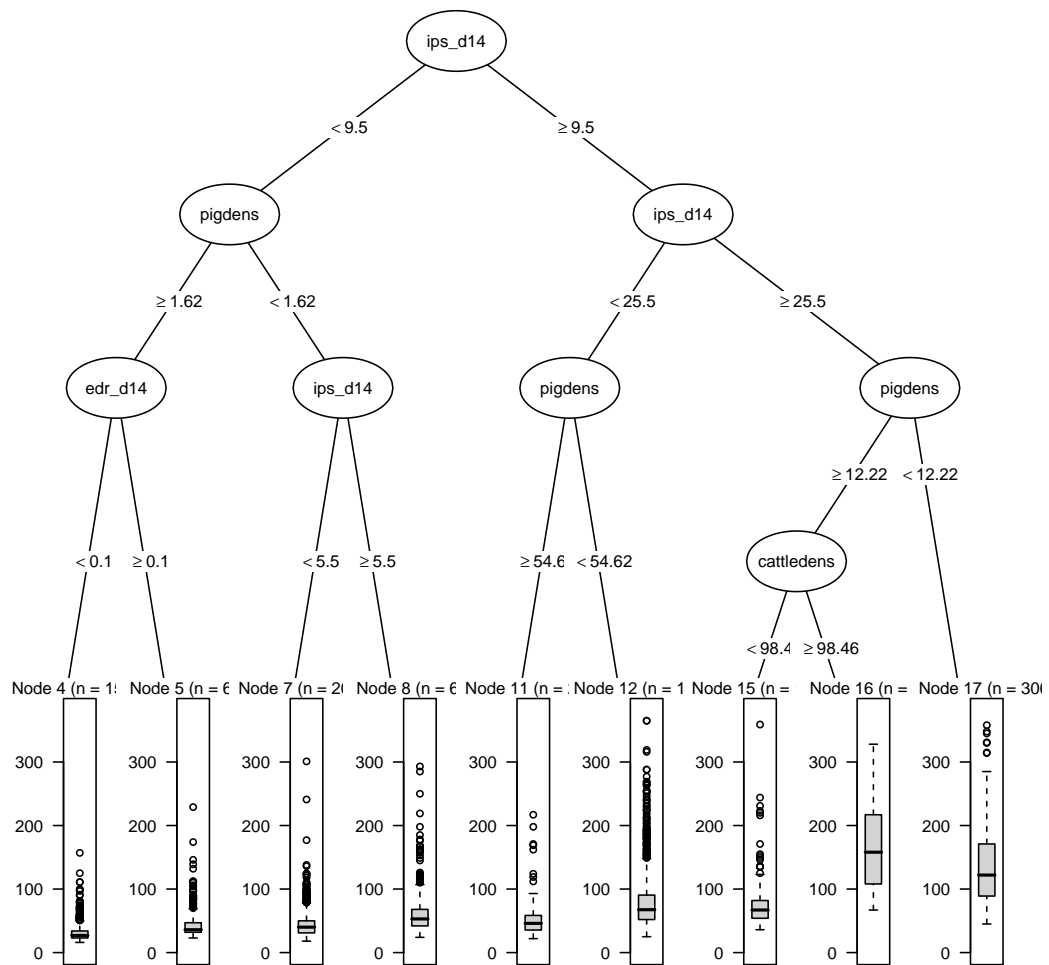


Figure 27: Classification and regression tree summarising day 14 post detection variables predictive of outbreak duration using AADIS.

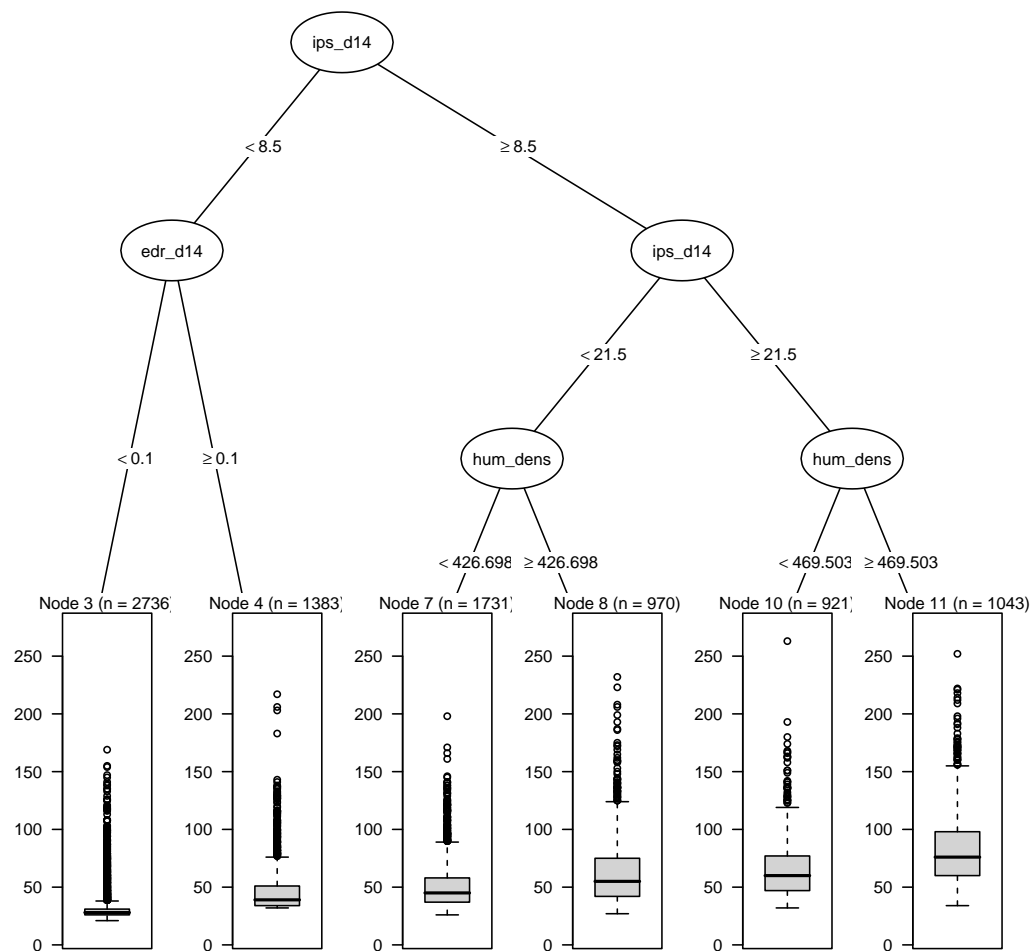


Figure 28: Classification and regression tree summarising day 14 post detection variables predictive of outbreak duration using InterSpread Plus.

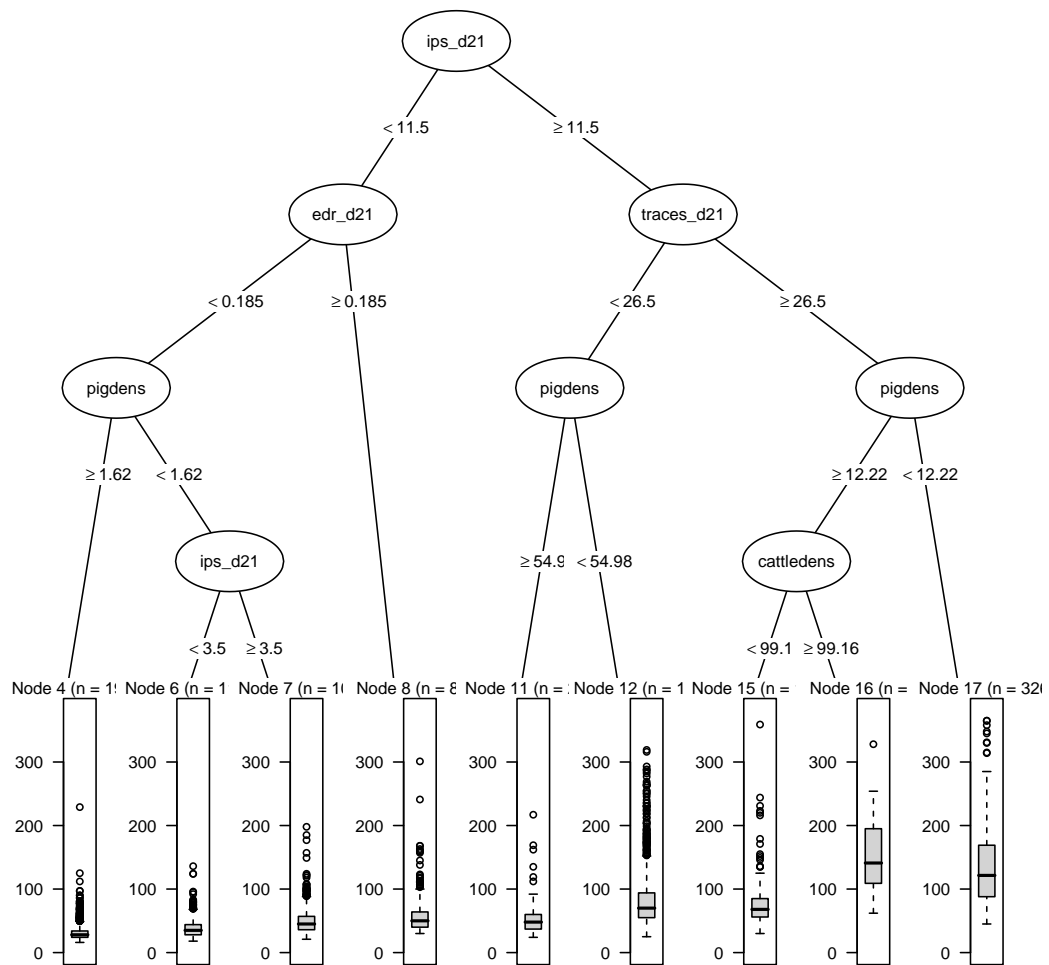


Figure 29: Classification and regression tree summarising day 21 post detection variables predictive of outbreak duration using AADIS.

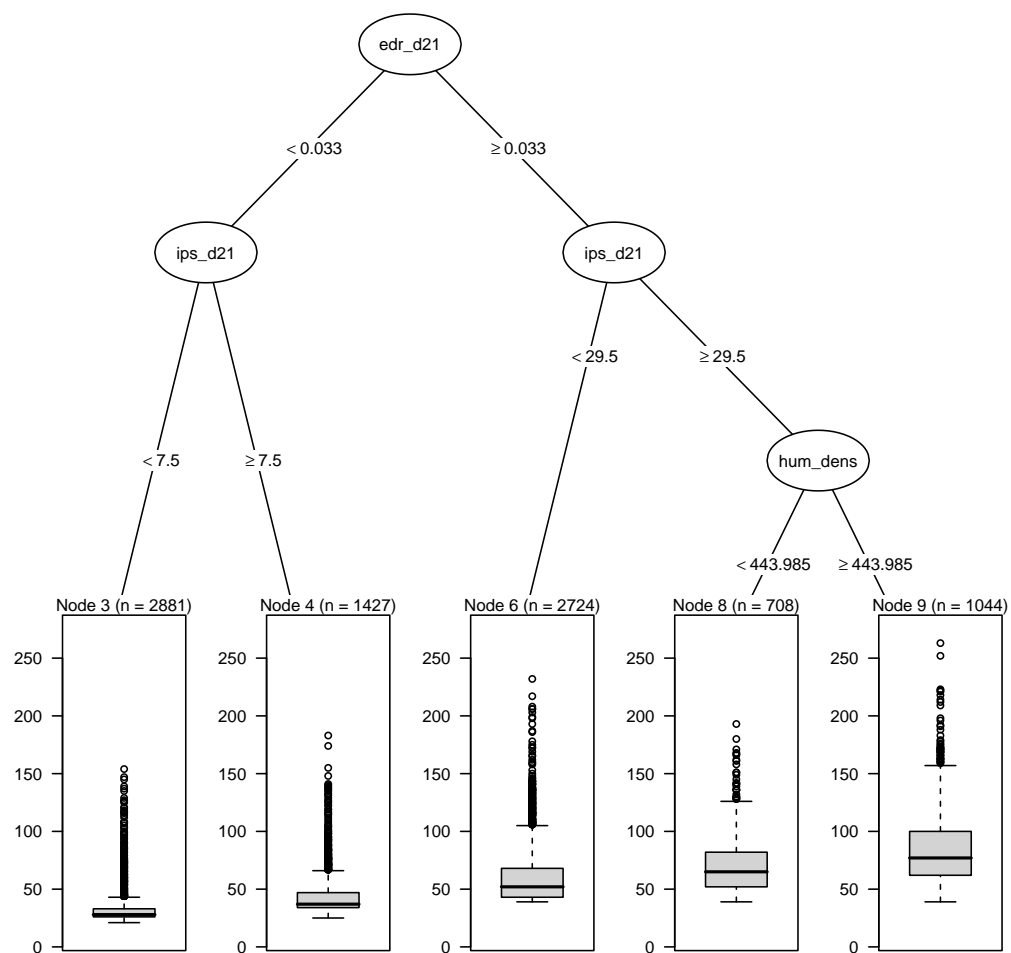


Figure 30: Classification and regression tree summarising day 21 post detection variables predictive of outbreak duration using InterSpread Plus.



Figure 31: Classification and regression tree summarising day 7 post detection variables predictive of total area under control using AADIS.

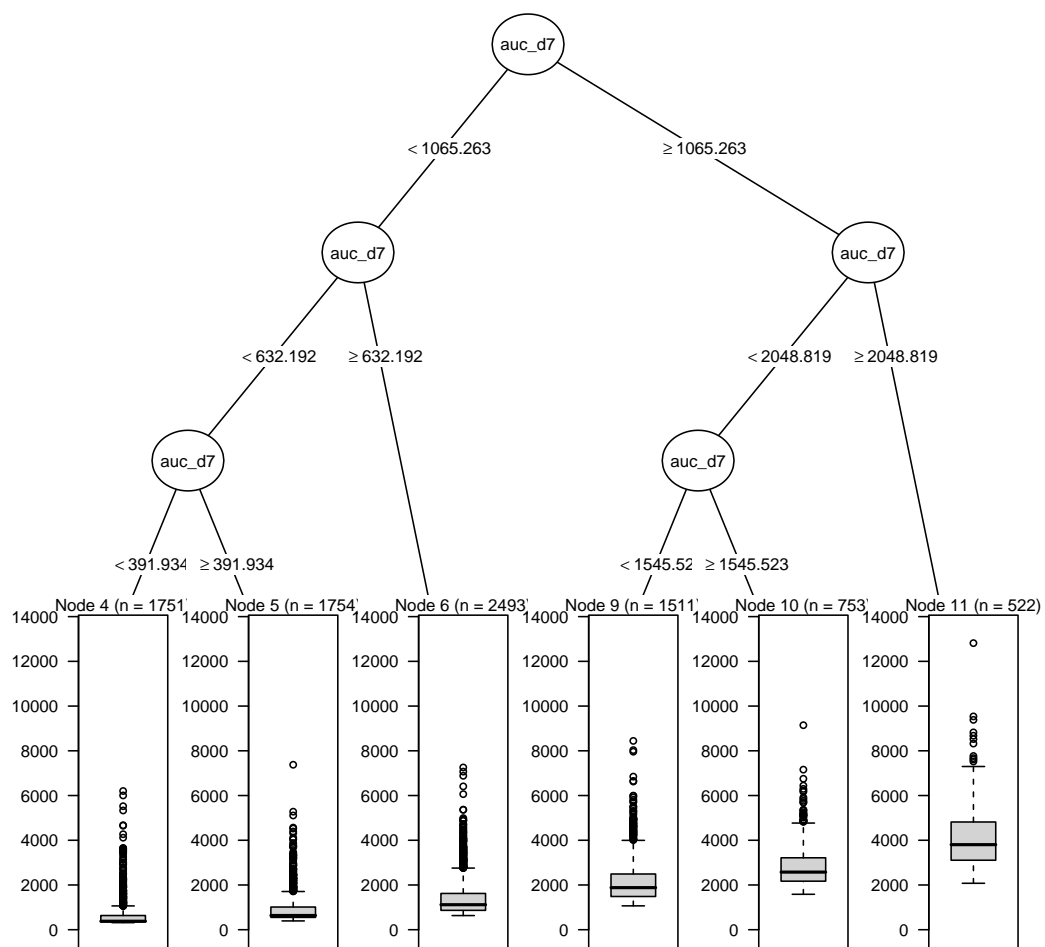


Figure 32: Classification and regression tree summarising day 7 post detection variables predictive of total area under control using InterSpread Plus.

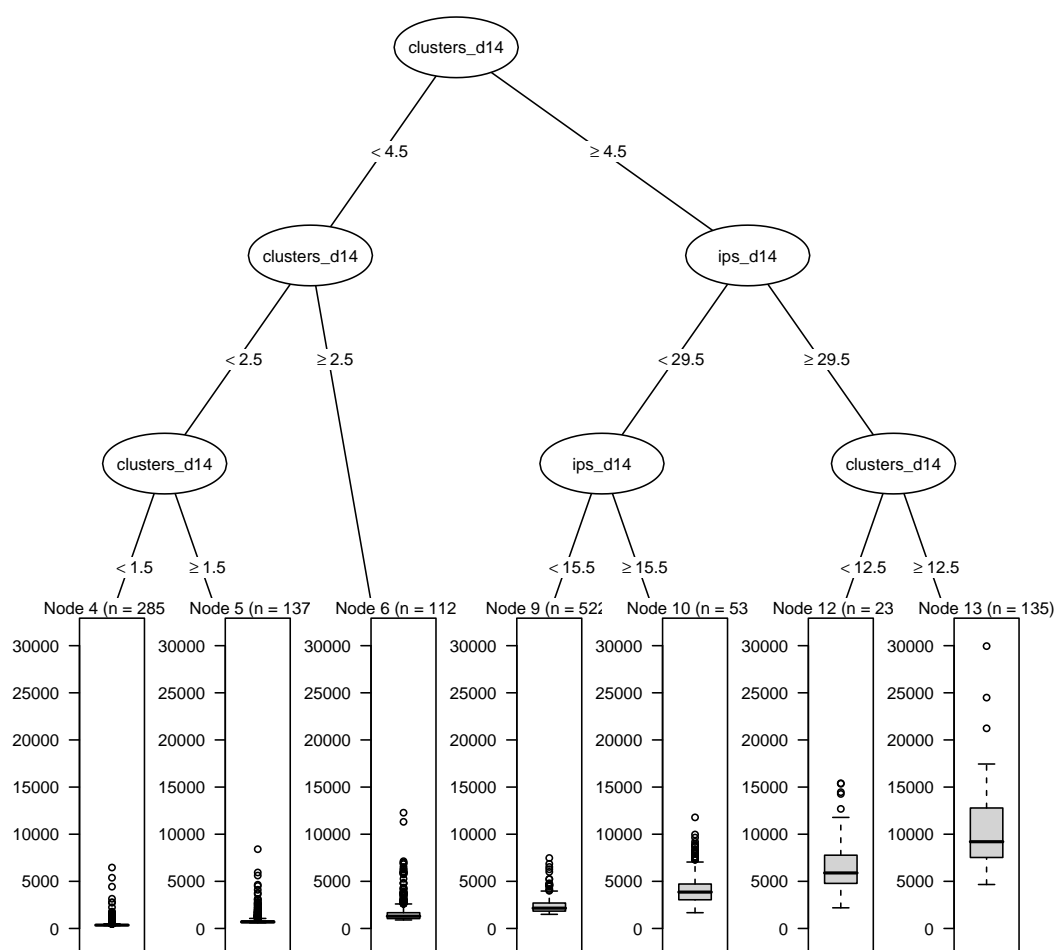


Figure 33: Classification and regression tree summarising day 14 post detection variables predictive of total area under control using AADIS.

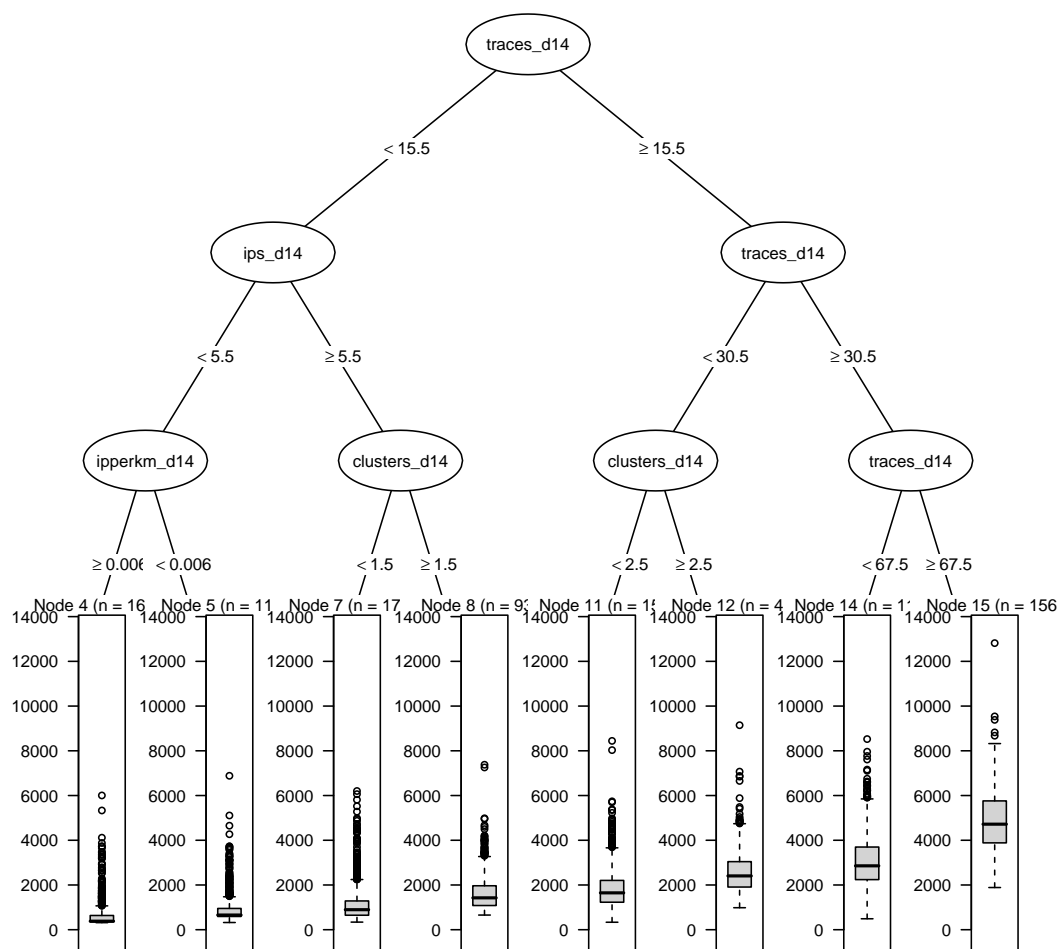


Figure 34: Classification and regression tree summarising day 14 post detection variables predictive of total area under control using InterSpread Plus.

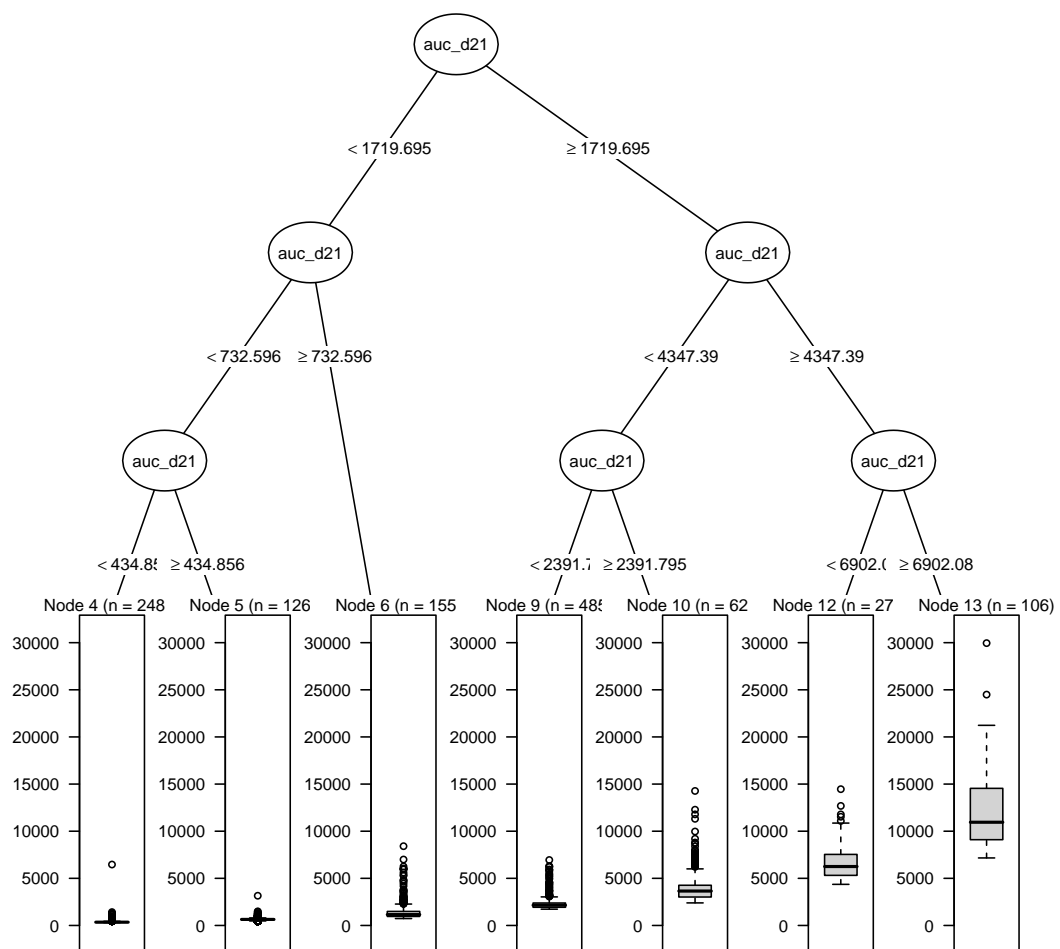


Figure 35: Classification and regression tree summarising day 21 post detection variables predictive of total area under control using AADIS.

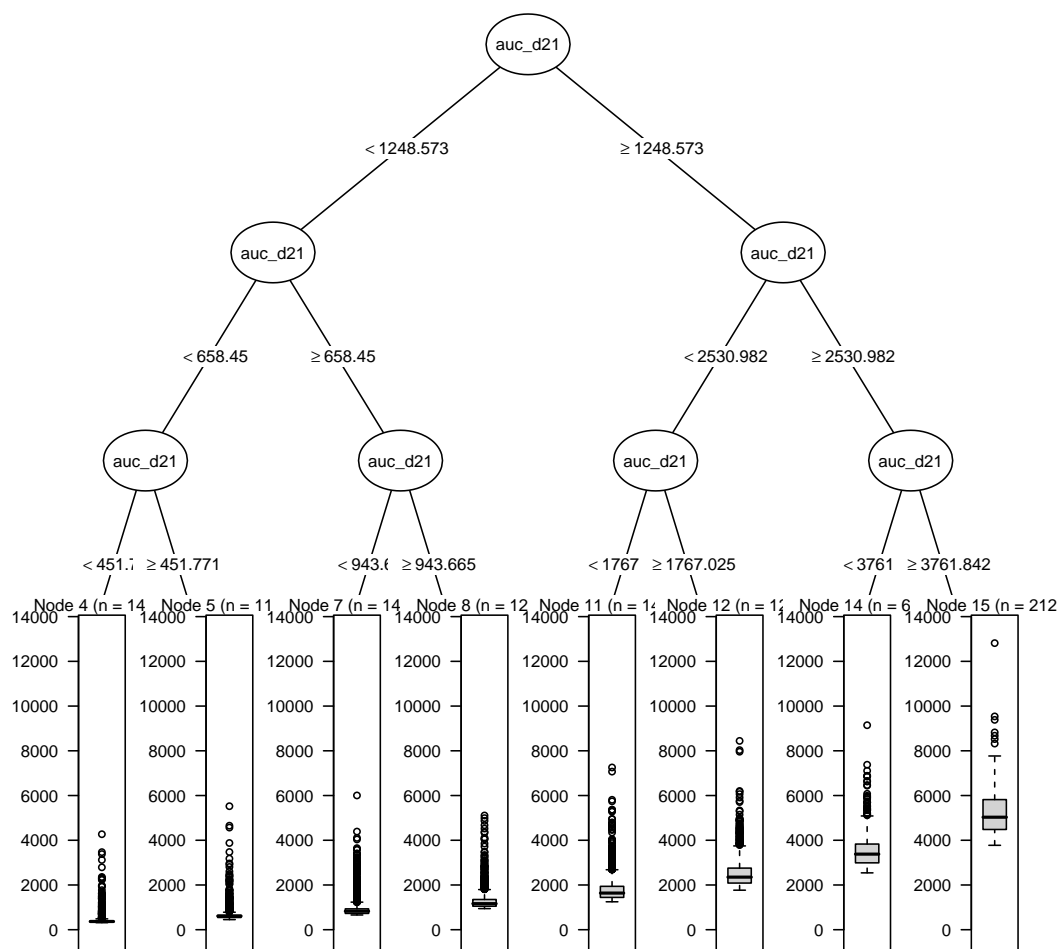


Figure 36: Classification and regression tree summarising day 21 post detection variables predictive of total area under control using InterSpread Plus.

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