

# Decision Support Methodologies for a Foot-and-Mouth Disease Response

(2006 – CO141)

MAF Biosecurity New Zealand Technical Paper No: 2009/12

Prepared for MAFBNZ Operational Research  
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ISBN 978-0-478-35108-8 (Print)  
ISBN 978-0-478-35109-5 (Online)

ISSN 1176-838X (Print)  
ISSN 1177-6412 (Online)

January 2008



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# 1. Introduction

MAF Biosecurity New Zealand's (MAFBNZ's) Incursion Response System (IRS) is a comprehensive information system designed to assist with and record operational activities conducted during an exotic disease or pest response. It utilises a central spatial database, built using an enterprise SQL database (Informix) coupled to a spatial database engine (SDE); and a series of thin client screens accessible via a browser (Internet Explorer). Client screens are configured according to response roles, such that each role only has write access to particular data items for which that particular role has responsibility.

Whilst the system is fairly comprehensive in terms of operational activities that it supports, it has not previously been critically evaluated in terms of its ability to support epidemiological analyses required for decision support during a foot-and-mouth disease (FMD) epidemic. It is clear that at this point in time, the database schema has been designed as a transactional system, to facilitate data entry by "place" (a generic term for spatial location), hence is in a very normalised form. This project was designed to evaluate the database in terms of whether all relevant data required for epidemiological analyses, efficiency and effectiveness measures during a FMD epidemic are collected, and to recommend ways in which the data should be presented to the Intelligence Group to facilitate these analyses.

## 2. Reports and Measures Required by Intelligence Group

### 2.1. TYPES OF REPORTS

#### 2.1.1 Epidemiological

These reports and analyses provide insights into the particular epidemiological features of the particular strain of FMD virus present in the country and its interactions with the host populations and farm management practices in the particular geographical and environmental settings found within the outbreak region(s).

#### 2.1.2 Efficiency

Efficiency measures indicate the operational capacity of the response organisation. They can indicate where resources are lacking. They include such measures as time intervals from report to diagnosis, diagnosis to depopulation, depopulation to cleaning and disinfection (C&D) complete, time delays to process tracing information, times to visit all farms within the protection zone of each IP etc.

#### 2.1.3 Effectiveness

These reports attempt to measure the impact of the control strategies and resource inputs on the epidemic itself. A classic analysis that was used extensively during the UK 2001 FMD epidemic was the estimated dissemination rate (EDR). When this value is below 1, it indicates the control measures are having a positive effect and the epidemic should die out. Conversely, whenever it is consistently above 1, it means the epidemic is outstripping the control effort.

Some of these measures will be of value in terms of establishing parameters for the InterSpread Plus (IS+) simulation model, which should improve model validity as the epidemic progresses.

## 2.2. DESCRIPTION OF REPORTS

### 2.2.1 Description of the distribution of incubation periods for all species combined and by livestock species

Analysis should permit the visualisation of a histogram (binning by days), as well as summary statistics (mean, median, range, variance), and curve fitting to find an appropriate distribution to describe the variation. Potential distributions include the log-normal and gamma.

### 2.2.2 Probability of infection associated with different exposure/transmission mechanisms

In order to properly evaluate the probability of transmission associated with different events, it is important that a standardised set of at-risk event types be established and recorded in the IRS database against each exposure event that places a farm at-risk, and as the most likely explanation for the infection on each infected premises (IP). A suggested set of event types are listed in Table 3.1.2.

Provided the number of farms exposed to each of these risk events is known, it then becomes possible to evaluate the probability of infection associated with exposure to any of these mechanisms. These probabilities can then be utilised within IS+, but also changes in probabilities over time provide valuable insight into the effectiveness of different control measures applied.

### 2.2.3 First day incidence

First day incidence (FDI) is a term coined by Hutber and Kitching (1996) to denote the number of animals showing clinical signs on the first day of a herd outbreak. It provides an estimate of the number of animals initially infected by the particular exposure pathway that brought infection to the farm, and indicates the infectiousness of the farm in terms of forward risk potential during the period from infection to diagnosis. Further, it can assist with parameterisation of the infectivity settings in IS+ and the probability of transmission (PoT) associated with movements.

A report that illustrates and describes the distribution of FDI by farm type, by infection mechanism and through time would provide insights into the transmission dynamics of the epidemic.

### 2.2.4 First fortnight incidence

First fortnight incidence (FFI) is another measure used by Hutber and co-workers (2006) as a predictor for regional (or foci) prevalence and zonal disease duration. The numerator is the number of IPs identified during the period from the initial diagnosis of the first IP within a focus, to the end of the second week following that initial diagnosis. The denominator is the total number of susceptible animal holdings within the region.

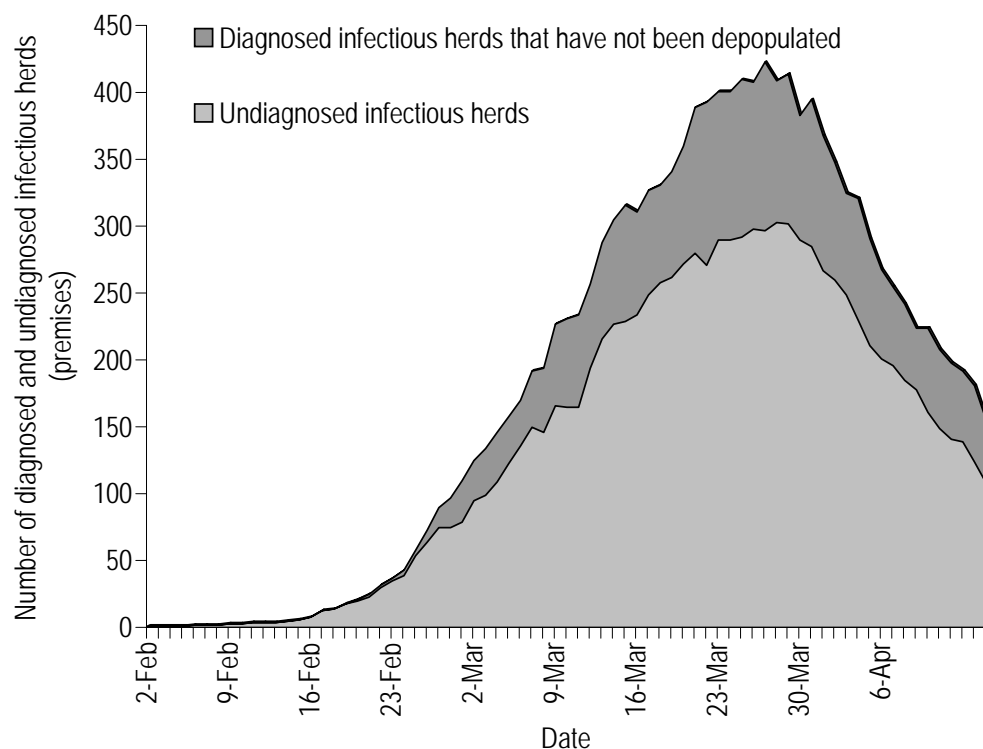
### 2.2.5 Epidemic curves

It is possible to create a number of curves that provide slightly different insights into the rate of propagation of the epidemic over time:

- Number of farms diagnosed per day or per week.
- Number of farms infected per day or per week, based on known or estimated infection date.

- Summation of number of infectious farms present on each day throughout the epidemic.
- Diagnosed infectious places (reported but not yet depopulated) as well as undiagnosed infectious places. The latter can only be included retrospectively, indicating what was happening up until about 2-3 weeks previously.

Figure 2.2.5: Number of infectious places on any day of the Great Britain 2001 outbreak. Infectious places are presented as diagnosed infectious places (reported but not yet slaughtered) and un-diagnosed infectious places (figure courtesy Graham Mackereth).



The above graphs can also be presented as cumulative curves.

## 2.2.6 Generation interval

The concept of generation interval tries to establish the typical time between generations in the network of spread. It is important in the context of understanding how quickly spread is occurring from each IP, and assists with evaluating the appropriate time unit to use when calculating estimated dissemination rates (EDR). The generation interval for FMD would be described as a distribution of days.

- **Earliest generation interval**  
The distribution of earliest generation intervals is assessed by calculating the number of days from the infection date of each source IP to the date of infection of the first secondary IP directly attributed to that source IP. It can also be evaluated by using onset of appearance of clinical signs (i.e. Interval from the date of appearance of the first clinical signs on each source IP to the date of appearance of symptoms on that IP's first secondary farm).
- **"Typical" generation interval**

This report permits the inclusion of multiple secondary IPs per source IP. However, because an IP that avoids detection for a longer time than normal could contribute an inordinate number of IPs and skew the distribution towards the right, secondary IPs whose infection date is after the third quartile of the distribution of times from onset of clinical signs to diagnosis are excluded.

Needless to say, the reports above are contingent on the Place\_ID of the source IP for each secondary IP being recorded in IRS.

### 2.2.7 Estimated dissemination rates (EDR)

The probability of a susceptible property becoming infected in a particular time period is considered as a function of the number of infectious farms (which indicates the number of point sources of agent) in the previous time period, and the dissemination rate (its propensity to spread to other farms). The Dissemination Rate (DR) represents the average number of herds (or premises) to which agent is delivered by each infected herd, irrespective of that herd's status. The DR is estimated by the ratio of the cumulative incidence in one time period to cumulative incidence in the previous time period (Miller, 1979).

The time period is based on the generation interval for the disease in question, which for FMD is typically 4-7 days. Hence, one can evaluate weekly EDR, or 4-daily EDR. The measure is a ratio. Values above 1 indicate an expanding epidemic; values below 1 indicate a contracting epidemic.

The method should also estimate 95 percent confidence intervals (CI) for ratios. In a large epidemic, the CIs are likely to be smaller near the peak of the epidemic, whereas it is expected that the CIs would be wider towards the tail of the epidemic when EDR can swing wildly.

EDR plots can also be smoothed by using rolling averages to get a better appreciation of the secular trends.

EDR plots can be calculated for the whole epidemic, or by any spatial zone.

Calculation of EDR has the benefit that the effect of disease control measures can be appreciated well before there is any observable reduction in the weekly incidence. Conversely, an increase in EDR from one week to the next indicates a failure in disease control, and the possibility of a run-away epidemic.

### 2.2.8 At-Risk/IP ratio per week

When the epidemic first begins, there are no controls in place. The disease has the potential to spread extensively by the time the initial diagnosis is made. The number of farms with direct or indirect contacts with the index farm(s) will have a direct bearing on the number of newly infected premises (IPs), and hence the dissemination rate (see discussion above). This will be influenced by the amount of time between arrival of infection on the index farm(s) and the initial diagnosis.

The denominator for this report is the total number of IPs diagnosed during the week. The numerator is the number of farms exposed to direct or indirect movements off those diagnosed IPs. It is a dimensionless ratio. The plot of these weekly values from the start of the epidemic will indicate how effective movement controls and surveillance are.

As controls are activated, the opportunities for contact between IPs and new properties should be severely curtailed. This is because of general control measures applied within the IA as well as specific measures applied to known at-risk farms. In addition, infected farms should be diagnosed much quicker due to the patrol endeavours and the greater public awareness of the disease. This should mean that the ratio of at-risk farms to IPs should start high and then diminish rapidly.

#### 2.2.9 Ratio of farmer self-reported diagnoses to surveillance activity diagnoses (ratio of unknown farms to known at-risk farms breaking down)

If the IRS information system and associated field surveillance procedures are sufficiently comprehensive, there should be relatively few “surprise” infected farms. Most farms that are diagnosed should already be recorded as “At-Risk”. If this is not the case, then it implies that the epidemic is potentially out-of-control, or IRS is not sufficiently comprehensive in terms of the transmission mechanisms that it records and tracks. In this sense, the ratio of “unknown” farms breaking down to “known at-risk” farms breaking down provides a quality assurance check on the system.

The ratio of “unknown” to “known” is the number of farmer self-reported positive diagnoses of farms previously not recorded as at-risk divided by the number of IPs breaking down where there are pre-recorded episodes and scheduled for visitation by a surveillance team. This ratio should be close to 0 in the ideal case.

#### 2.2.10 Survival analysis of local spread

Local spread is the term coined to cover short distance (generally 10 km or less) spread between livestock units when there is no clear linkage other than geographical proximity (Sanson, 1994).

This analysis attempts to quantify the amount of local spread that is occurring, and then adapt the results to represent local spread transmission within IS+.

Survival analysis is a useful technique to calculate the daily hazard of infection for all susceptible farms in the vicinity of infected premises (IPs) in an infectious state. To do this, it is necessary to establish the most probable source-recipient pairings for all local spread IPs. Candidate source farms are those IPs within 10 km of each recipient farm that were infectious during the likely date(s) of infection. The period of infectiousness for each farm is taken to be from 1 day prior to the onset of clinical signs, when airborne excretion of virus typically commences (Sellers and Parker, 1969), up until the date of depopulation.

To establish likely dates of infection for the recipient farms where infection date are not known, one can sample from the distribution of incubation periods for those farms that have a confirmed infection date (based on a known transmission event) recorded in IRS.

The most probable source farm for each recipient local spread IP can be selected from the set of closest potential source farms, or from the set of source farms that have been infectious the longest (assuming an increasing within-herd prevalence leading to increased transmission potential), or a weighted combination of distance and length of time in an infectious state.

All neighbouring farms within 10 km of each source IP are then selected and grouped into radial distance bands. The risk of local spread to these farms can be evaluated in the following manner:

- Farms that have been depopulated or have a known infection date before the source farm's viral excretion period are excluded from the set of recipient farms, that is, they are considered non-exposed places.
- IPs that have a recorded or estimated infection date after the infectious period of the source IP are treated as exposed but not infected during the time period under consideration (i.e. the event of interest did not occur).
- IPs that have a recorded or estimated infection date during the source farm's infectious period but have a cause of infection coded as other than local spread or whose source of infection is a different farm are right-censored on the date of infection.
- All local spread recipient IPs that are attributed to the source IP in question represent the actual events of interest in terms of the survival analysis.
- Neighboring farms subjected to a contiguous or dangerous contact cull (pre-emptive slaughter) during the source farm's infectious period are right-censored on the date of cull.

Once all spatially proximal farms to each source IP have been evaluated, survival analyses can be conducted to derive the daily probabilities of transmission by distance band.

#### 2.2.11 Other measures of spatial risk (adapted from Mackereth, 2005)

- New infections within specified distance bands of infections occurring in the previous 3 weeks.  
Counts by distance band.
- Risk of new infections by distance from infections occurring in the previous 3 weeks  
This is the above counts divided by the population at-risk i.e. susceptible places within each distance band e.g. contiguous premises; non-contiguous but < 3 km; 3-5 km etc.
- Relative risk of new infections by distance and week.  
Ratio of risk in one distance band to risk in another distance band e.g. risk of new infections in farms contiguous to an IP divided by the risk for farms non-contiguous but within 3 km of IPs detected during the previous 3 weeks.
- Percentage of new infections greater than 10 km from infections in the previous 3 weeks that were self-reported.  
Farmer self-reported farms outside of 10 km surveillance zone – potentially indicating failure of movement controls.
- Risk of new infections by region and week.  
Region could be regional council area, district council area, or user-defined.

#### 2.2.12 Other measures of efficiency and effectiveness (adapted from Mackereth, 2005)

- Distributions of time (days) from onset of clinical signs to diagnosis by species.
- Based on age of oldest lesions reported at time of diagnosis.
- Indicates effectiveness of surveillance.
- Distribution of time (hours or days) from reporting to diagnosis.
- Distributions of times (days) from diagnosis to depopulation, disposal and decontamination.
- Distribution of time (days) from infection to depopulation.
- Indicates how advanced virus excretion is likely to be by the time of slaughter.
- Relationships between various time measures and the likelihood of transmission by IPs.

Generalised linear modelling (GLM) techniques to investigate the influence of delays on diagnosis (age of oldest lesions), slaughter (time from diagnosis to slaughter), disposal (time from slaughter to disposal) and disinfection (time from disposal to C&D completed) on the numbers (or likelihood) of secondary farms being infected by IPs.

The dependent variable could either be the count of attributed secondary IPs to each source IP analysed by Poisson regression, or whether each IP was responsible for any secondary IPs or not (dichotomous variable) analysed using logistic regression.

- Interval from diagnosis date to casing complete within the 10 km surveillance zone.
- Distribution of time (hours or days) from diagnosis to traces completed.
- Interval (days) from diagnosis date to completing first round of patrol visits within 3 km protection zone.
- Laboratory tests per week conducted for zone freedom surveillance.

### 2.2.13 Other reports and measures required for IS+

- Creation of farm file for country or region.  
Space delimited ASCII text file.  
Each line holds: place\_id, farm\_type, livestock number by species, co-ordinates for all places within selected region.
- Creation of markets file for country or selected region.  
ASCII text file containing coordinates of each market in the country or selected region.
- Preparation of epidemic history file.  
Space delimited ASCII text file with a separate row for each farm event.  
Each row contains place\_id, day from start of epidemic, status event name and whether ON or OFF.  
Key events include: INFECTED, CLINICAL\_SIGNS, DETECTED.
- Frequency of movements by conveyor type.  
Mean of counts of all off farm movements recorded per IP, before and after imposition of movement controls.
- Distribution of movement distances by conveyor type.  
Euclidean direct line distances in metres, calculated by the formula:

$$\sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}$$

- Survival analysis for farms at-risk of airborne spread.  
This should be conducted if there is evidence of airborne spread.
- Mean number of animals by species able to be slaughtered per day per depopulation team.
- Mean number of animals by species able to be vaccinated per day per vaccination team.

### 3. Key Recommendations for Database and Template Developments

It appears that IRS collects most of the data required for epidemiological analysis, albeit in a very “normalised” database form, and there would be merit in combining the data in multiple tables into a small number of de-normalised tables in a type of data warehouse.

The only significant “gaps” in data collection include: the species-specific data captured on the Exotic Disease Investigation Report (EDIR), particularly relating to onset of clinical signs, size of initial infection group and number of managements groups; somewhere to specifically record exposure details for farms under FMD virus plumes; a table of reference dates and days, weeks and months relative to the start of the epidemic; and a table holding dates of major events, such as imposition of nationwide movement controls, start of vaccination etc.

There are a number of tables in IRS that act as look-up tables with veterinary descriptors that seek to describe or explain the way in which a farm has been exposed or infected. There is a need to harmonise the look-up values in these tables with standard text strings to permit epidemiological comparisons to be made, so that, for example, the risk or probability of infection following exposure can be calculated. This may be just a matter of ensuring the template for the particular disease is set up properly with this in mind.

#### 3.1. NEED TO HARMONISE CONVEYOR, CAUSE AND VISITPLANREASON TABLES

There are a number of tables in IRS that act as look-up tables with veterinary descriptors that seek to describe or explain the way in which a farm has been exposed or infected. These include the **conveyor**, **cause** and **visitplan** reason tables. There is a need to harmonise the look-up values in these tables with standard text strings to permit epidemiological comparisons to be made, such that the risk or probability of infection following exposure can be calculated.

The **conveyor** table is used by the tracers to record what type of item/product/person/vehicle has been moved onto or off infected premises (IPs). The list needs to be expanded to allow more precision in recording what has moved, so that this level of detail can be transferred to the list of episodes placing susceptible farms at-risk. This information will also be invaluable to the intelligence team trying to identify the source and date of infection for new IPs. If a tracing encounter is the cause of infection, then the information should be recorded in the **ipsdeclaration** table, and ultimately should facilitate analysis of the probability of transmission associated with various exposure mechanisms. The list should therefore include the items listed in Table 3.1.1.

Table 3.1.1: Suggested list of conveyors for the conveyor table.

Conveyordesc	Risk Rating	Type (Host, Person, Product/Thing, Vehicle)	Orgmgtqualifier
Pig	4	Host	y
Cattle	4	Host	y
Deer	4	Host	y
Sheep	4	Host	y
Goat	4	Host	y
Other host animal	4	Host	y
Host product (e.g. meat)	2	Product	
Host animal waste	2	Product	
Host genetic material	2	Product	
Host vehicle (truck)	2	Vehicle	
Dairy tanker	1	Vehicle	
Other vehicles	1	Vehicle	
Non-host animals	1	Product/Thing	
Non-host products	1	Product/Thing	
Animal feed	1	Product/Thing	
Fomites	1	Product/Thing	
People – host contact	2	Person	
People – other	1	Person	
Clothing/footwear used with susceptible animals	2	Product/Thing	

The expanded **cause** table, used by **atrisk/ipspdeclaration/ips** should include the values shown in Table 3.1.2.

Table 3.1.2: Suggested list of causes required for FMD.

Causeid	Description
1	Associated Place
2	Contiguous Place
3	Tracing Encounter – Pig
4	Tracing Encounter -
5	Tracing Encounter – Deer
6	Tracing Encounter – Sheep
7	Tracing Encounter – Goat
8	Tracing Encounter – Other host animal
9	Tracing Encounter – Host product (e.g. meat)
10	Tracing Encounter – Host animal waste
11	Tracing Encounter – Host genetic material
12	Tracing Encounter – Host vehicle (truck)
13	Tracing Encounter – Dairy tanker
14	Tracing Encounter – Other vehicles
15	Tracing Encounter – Non-host animals
16	Tracing Encounter – Non-host products
17	Tracing Encounter – Animal feed
18	Tracing Encounter – Fomites
19	Tracing Encounter – People – host contact
20	Tracing Encounter – People – other
21	Tracing Encounter – Clothing/footwear used with susceptible animals
22	Local Spread – Within Protection Zone
23	Local Spread – Within Surveillance Zone
24	Under Plume
25	Feral animal involvement
26	Deliberate – Agri-Bio-terrorism

### 3.2. CLINICAL FINDINGS DATA CAPTURED ON EXOTIC DISEASE INVESTIGATION REPORT (EDIR) FORM

As far as I can ascertain, although total stock numbers by species/type are updated in the **hostplace** table, only age of oldest signs is transferred into the **ipspdeclaration.signsage** field. It is a pity that the other details on the EDIR (*Part 2: Clinical findings*) are not captured in a simple manner.

At the moment, it seems you have to create a multi-table chain of links:

**place – visit – task – placeresults – hostresults**

or

**place – visit – task – hostresults**

and even then not all details are captured. Furthermore, it appears that **hostresults.prid** and **hostresults.taskid** can be null, as well as **indresults.hrid** resulting in inaccessible “islands” of data. Indeed **hostresults.prid** is empty for all example records in hostresults in fmd0307.

To me, it would be logical to add the extra fields required to the **hostplace** table to record the final findings from an IP required for epidemiological analyses. An “**enttype**” table would act as a look-up of codes for the type of enterprises. It should be initially populated from the **enterprise\_type** table in AgriBase.

Additional fields that would need to be added to the **hostplace** table are shown in Table 3.2.1.

Table 3.2.1 Additional fields required to hold clinical findings from the EDIR form.

Field	Data type	Description
enttype	char(6)	look-up to a short list of acceptable values e.g. Beef breeding, beef dry etc.
mgmntgps	longint	number of management groups
int_ext	char(1)	I = intensive; E = extensive
observed	longint	Number observed
affected	longint	number affected
examined	longint	number examined individually (temp, mouths etc.)
signsage	longint	age of oldest lesions (days since onset of clinical signs)
initaffected	longint	number initially infected
milking	longint	number in milk (applicable for dairy animals)

Table 3.2.2: Look-up codes for enterprise type held in enttype table.

enttype	entdescription
LVBF	Beef Cattle Farming (undifferentiated)
LVBFB	Beef Cattle Farming – Beef Breeding Herd (Suckler)
LVBFBDB	Beef Cattle Farming – Dry Stock Herd (Fattener)
LVDA	Dairy Cattle Farming (undifferentiated)
LVDAADR	Dairy Drystock Rearing and Grazing
LVDAAMI	Dairy Milk Production
LVDE	Deer Farming (undifferentiated)
LVDEBR	Deer – Breeding Herd
LVDEFA	Deer – Fattening Unit
LVDESA	Deer – Safari Park
LVDEVE	Deer – Velvet Production
LVGO	Goat Farming
LVSH	Sheep Farming (undifferentiated)
LVSHCB	Sheep Farming – Commercial Breeding Flock
LVSHFA	Sheep Farming – Fattening flock
LVSHST	Sheep Farming – Stud Flock
OLPG	Piggery (undifferentiated)
OLPGBR	Piggery – Breeding
OLPGFA	Piggery – Fattening

### 3.3. NEED FOR A MASTER LIST OF ALL EXPOSURE/RISK EVENTS FOR PLACES

If we are going to be able to select a valid cause and source IP for a given IP, we need a definitive list of all known exposure/risk events. Furthermore, the ability to track which of many exposure/risk types produce infection, and calculate probabilities of infection associated with each mechanism, will be important in understanding the epidemiology of FMD and being able to parameterise InterSpread Plus (IS+) with valid values.

Currently, these risks/events are scattered in various tables, or not explicitly recorded.

#### 3.3.1 Tracing encounters are recorded in the trace table

The important fields are:

- Placeid – exposed farm where direction = “fwd”
- Originplaceid – source of risk where direction = “fwd”
- Encounterdate
- Conveyor (based on the full list suggested above)
- Risk
- Confirmed

#### 3.3.2 Surveillance reasons recorded in the visitplan table

Specifically, where targettype = “place” and visitplan.plantype = “s” (?)

Relevant reasons are given in reasonid which links to the look-up table **visitplanreason**

Relevant reasonid records contain links via:

- vehicleid
- pzoneid – ProtectionZone spatial table
- czoneid – ContiguousZone spatial table
- szoneid – SurveillanceZone spatial table

### 3.3.3 Under plume

Not sure where/how this information is recorded at present. Perhaps should be a new record in **visitplanreason** for “Under Plume”. However, we need a way to identify the potential source of the plume, and relevant dates. This is not provided for easily via the **PlumeFCyyyymmdd\_nnnnn** table(s).

The key items of information required for all of the above types of exposures are:

- sourceIP
- episodestartdate
- episodenddate

In the case of a “Tracing Encounter” reason, the start and end dates are the same and available from the **trace** table.

In the case of a “Contiguous Place” reason, the **czoneid** will provide a link to the particular **ContiguousZone** record which will contain the **placeid** of the IP that created the zone. The relevant dates of exposure are then the date of earliest clinical signs of the source IP to the date of slaughter completed for that source IP. The links would therefore involve:

**visitplan.czoneid = ContiguousZone.OBJECTID**

**ContiguousZone.placeid = ipsdeclaration.placeid**

**ipsdeclaration.visitid = visit.visitdateon – ipsdeclaration.signsage** – this should provide episodestartdate

Date slaughter completed is also complicated and involves various task related tables:

**visitplan.czoneid = ContiguousZone.OBJECTID**

**ContiguousZone.placeid = visitplan.placeid** (link to all visitplans relating to sourceIP)

**visitplan.requestid = taskreq.requestid**

**taskreq.taskend where tasktype = ‘SLA’** – this would provide date slaughter completed

Similar links would need to be queried for “Protection Zone” and “Surveillance Zone”.

To wrap up, what we need is a master log that combines data from **trace** and **visitplan** and associated tables into a new table of at-risk episodes that is easy to analyse. The table could be called “**atrisk**” (see Table 3.3). Some example SQL code for populating the table is shown in Listing 3.3 below.

Table 3.3: Fields required for atrisk table

Field name	Data type	Description
placeid	longint	Placeid of exposed place
originplaceid	longint	Placeid of source IP
causeid	Int	Look-up to <b>cause</b> table expanded to include all conveyors (refer above) and risk types such as Contiguous Zone etc.
episodestartdate	Date	Equivalent to Encounterdate in <b>trace</b> table, otherwise start of infectious period for other mechanisms – generally date of appearance of earliest clinical signs
episodeenddate	Date	For traces, this is identical to episodeenddate; for other mechanisms is it is the end of the infectious period – generally slaughter date
risk	Int	Risk rating associated with episode/exposure
comment	Text	Comments (e.g. copy reason from <b>trace</b> table)

### Listing 3.3: Some example SQL code for populating atrisk.

```
--Stage 1 - bring in tracing encounters from trace table
insert into atrisk (
    placeid,
    originplaceid,
    causeid,
    episodestartdate,
    episodeenddate,
    risk,
    comment)
select placeid,
    originplaceid,
    conveyer as causeid,
    encounterdate as episodestartdate,
    encounterdate as episodeenddate,
    risk,
    reason as comment
from trace
where placeid is not null
    and direction = "fwd"
    and orgdest = "FRM"
    and confirmed = "y";

--Stage 2 - bring in Contiguous Zone exposures from visitplan
insert into atrisk (
    placeid,
    originplaceid,
    causeid,
    episodestartdate,
    risk,
    comment)
select visitplan.placeid,
    ContiguousZone.placeid as originplaceid,
    1 as causeid, --based on current cause table in fmd0307
    (visit.visitdateon - signsage) as episodestartdate,
    4 as risk,
    "Contiguous Zone" as comment
from visitplan,
    ContiguousZone,
    ipsdeclaration,
    visit
where visitplan.czoneid = ContiguousZone.OBJECTID
    and ContiguousZone.placeid = ipsdeclaration.placeid
    and ipsdeclaration.visitid = visit.visitid;

--Stage 3 - bring in Protection Zone exposures from visitplan
insert into atrisk (
    placeid,
    originplaceid,
    causeid,
    episodestartdate,
    risk,
    comment)
select visitplan.placeid,
    ProtectionZone.placeid as originplaceid,
    4 as causeid, --based on current cause table in fmd0307
    (visit.visitdateon - signsage) as episodestartdate,
    1 as risk,
    "Protection Zone" as comment
```

```

from visitplan,
    ProtectionZone,
    ipsdeclaration,
    visit
where visitplan.pzoneid = ProtectionZone.OBJECTID
    and ProtectionZone.placeid = ipsdeclaration.placeid
    and ipsdeclaration.visitid = visit.visitid;

--Stage 4 - Now update enddate for IPs where slaughter is complete
UPDATE atrisk INNER JOIN (visitplan INNER JOIN taskreq
    ON visitplan.requestid = taskreq.requestid)
    ON atrisk.originplaceid = visitplan.placeid
SET atrisk.episodeenddate = taskreq.taskend
where tasktype = "SLA"
    and atrisk.causeid in (1,4) --Contiguous and Protection Zones
;

```

## 3.4. KEY DATES AND TIMES FOR THE EPIDEMIC

We need a couple of master tables that hold the key dates and times for the epidemic:

### 3.4.1 Master time

This table should be populated with actual date, day relative to time 0, week relative to time 0 and month relative to time 0 to facilitate linking dates in other tables and being able to report the results by day, week or month relative to time 0.

Time 0 may be set as the date of discovery of the first case (index case), or set to the date that infection began in the first farm infected.

Graham Mackereth set such a table up in the FMD DB used during the UK2001 epidemic, as well as during the Korean epidemic. He named his table “**T\_sys\_Date**” (see Table 3.4.1).

Table 3.4.1: Fields required for master date table T\_sys\_Date

Field name	Data type	Description
OBJECTID	longint	Autoincrement
Date	Date	Actual calendar date
day	int	Day relative to Day 0 (can be negative)
week	int	Week relative to Day 0 (can be negative)
month	int	Month relative to Day 0 (can be negative)

There should be a utility/script to populate this table and allow the Intelligence Manager to change the date of Day 0. For instance, at the start of the epidemic, one may not know whether the Index case discovered is the true first farm infected or not. Also, the date of infection of the first farm may never be known, but estimates may be revised during the course of the response. Some Python code capable of populating this table for a given Day 0 and length of the epidemic in months is shown in Listing 3.4.1.

### Listing 3.4.1: Python script for populating T\_sys\_Date

```
import win32com.client, sys, os, string, datetime
from mx.DateTime import *

conn = win32com.client.Dispatch(r'ADODB.Connection')
DSN = 'PROVIDER=Microsoft.Jet.OLEDB.4.0;DATA
SOURCE=N:/giswork/irs2/ds/FMD0307 copy.mdb;'
conn.Open(DSN)
print 'Connection open'
#truncate existing table
trunc_sql = 'delete from T_sys_Date;'
conn.Execute(trunc_sql)

#Process dates
date0 = Date(2007,4,17)
epi_length = 3 #months
day = -21      #go back 21 days
wk = -3
mth = -1
enddate = date0 + RelativeDate(months+=epi_length)
startdate = date0 + RelativeDate(days+=day)
daten = startdate

while daten <= enddate:
    ins_sql = "insert into T_sys_Date ([date],[day],[week],[month]) values
('" + str(daten.date) + "','" + str(day) + "','" + str(wk) + "','" + str(mth) +
");"
    #print ins_sql + "\n"
    conn.Execute(ins_sql)
    daten = daten + RelativeDate(days+=1)
    day = day + 1
    if daten == date0:
        wk = 0
        mth = 1
    if day % 7 == 0:
        wk = wk + 1
    if daten == date0 + RelativeDate(months+=mth):
        mth = mth + 1
conn.Close()
```

### 3.4.2 Key Events

This table should hold the key events relating to the response, including the implementation of major controls e.g. Date of discovery of first IP; Date of imposition of nationwide movement controls etc. Suggested table name is “**keyevents**” (see Table 3.4.2.1). An “**eventtype**” table (Table 4.2.2) would act as a look-up table and be pre-populated with major event types.

Table 3.4.2.1: Keyevents table structure

Field name	Data type	Description
OBJECTID	longint	Autoincrement
Date	Date	Actual calendar date of event or control implemented
eventid	Int or char	Look-up to key event table to avoid “free text”
notes	Text	Notes associated with event
entrydate	date	Date event entered in table
entryby	longint	Id of person entering the record
editdate	date	Date record updated
editby	longint	Id of person editing the record

Table 3.4.2.2: Look-up eventtype table

OBJECTID	eventid	evdescription
1	1	Index case found
2	2	First farm infected
3	3	Nationwide movement controls implemented

### 3.5. MASTER LOG OF KEY EVENTS RELATING TO EACH IP

To facilitate epidemiological analyses, an expanded **ipsdeclaration** or **place** table or view based on either of these tables would be extremely valuable. Table or viewname could be “**ips**” (see Table 3.5). Some example SQL code for populating the ips table is shown in Listing 3.5.

Table 3.5: Required fields for ips table.

Field name	Data type	Description
placeid	longint	Primary key
foreigndbid	Char(20)	AgiBase farm_id (or system generated id)
placetype	Char(3)	From <b>placetype.shortdescription</b>
x	float	From <b>PlaceFC.x</b>
y	float	From <b>PlaceFC.y</b>
ipnumber	int	<b>place.ipnumber</b>
rpnumber	int	<b>place.rpnumber</b>
visitdate	date	<b>visit.visitdateon</b> (linked via <b>ipsdeclaration.visitid</b> )
tasktype	Char(3)	<b>task.tasktype</b> (linked via <b>ipsdeclaration.visitid</b> ) NB this may not be unique
publicreport	int	1=Yes; 0=No
visitplanreason	Char(20)	<b>visitplanreason.description</b> (source of information) belonging to <b>visitplan.reasonid</b> with highest <b>visitplan.riskrating</b> where <b>visitplan.reqtype = 's'</b>
diagnosisdate	date	Date confirmed ( <b>ipsdeclaration.decldatestamp</b> )
ipspreason	Char(20)	from <b>ipspreason.description</b> (how diagnosed, linked via reasonid)
sourceip	int	<b>ipsdeclaration.sourceip</b>
cause	varchar(100)	<b>Cause.description</b> linked via <b>ipsdeclaration.causeid</b>
signsage	int	Age of oldest lesions on IP ( <b>ipsdeclaration.signsage</b> ) – highest of all the individual species values (see below)
signsdate	date	Date of appearance of first clinical signs on farm (computed from datevisited – signsage)
infectiondate	date	<b>ipsdeclaration.estinfdate</b>
confident	Char(1)	Y = yes; N = no
Pig_no	longint	Number of pigs (via join to expanded <b>hostplace</b> – see Note 2 above – could be achieved by views for each species, then linked to <b>ipsdeclaration</b> via an outer join)
Pig_enttype	char(6)	Type of pig farm enterprise – Breeding/Fattening – lookup to <b>enttype</b>
Pig_mgmntgps	int	number of management groups
Pig_int_ext	char(1)	I = intensive; E = extensive
Pig_observed	longint	Number observed
Pig_affected	longint	number affected
Pig_examined	longint	number examined individually (temp, mouths etc.)
Pig_signsage	int	age of oldest lesions (days since onset of clinical signs)
Pig_initaffected	longint	number initially infected
Dai_no	longint	Number of dairy animals (via join to expanded <b>hostplace</b> )
Dai_enttype	char(6)	Type of dairy farm enterprise – Milking/rearing/grazing – lookup <b>enttype</b>
Dai_mgmntgps	int	number of management groups
Dai_int_ext	char(1)	I = intensive; E = extensive
Dai_observed	longint	Number observed
Dai_affected	longint	number affected
Dai_examined	longint	number examined individually (temp, mouths etc.)
Dai_signsage	int	age of oldest lesions (days since onset of clinical signs)
Dai_initaffected	longint	number initially infected
Dai_milking	longint	number in milk
Bef_no	longint	Number of beef animals (via join to expanded <b>hostplace</b> )
Bef_enttype	char(6)	Type of beef farm enterprise – Breeding/Fattening – lookup to <b>enttype</b>
Bef_mgmntgps	int	number of management groups
Bef_int_ext	char(1)	I = intensive; E = extensive
Bef_observed	longint	Number observed
Bef_affected	longint	number affected

Field name	Data type	Description
Bef_examined	longint	number examined individually (temp, mouths etc.)
Bef_signsage	int	age of oldest lesions (days since onset of clinical signs)
Bef_initaffected	longint	number initially infected
Shp_no	longint	Number of sheep (via join to expanded <b>hostplace</b> )
Shp_enttype	char(6)	Type of sheep enterprise – Breeding/fattening/wool – lookup to <b>enttype</b>
Shp_mgmtgps	int	number of management groups
Shp_int_ext	char(1)	I = intensive; E = extensive
Shp_observed	longint	Number observed
Shp_affected	longint	number affected
Shp_examined	longint	number examined individually (temp, mouths etc.)
Shp_signsage	int	age of oldest lesions (days since onset of clinical signs)
Shp_initaffected	longint	number initially infected
Dee_no	longint	Number of deer (via join to expanded <b>hostplace</b> )
Dee_enttype	char(6)	Type of deer enterprise – Breeding/fattening/velvet/safari etc. – lookup to <b>enttype</b>
Dee_mgmtgps	int	number of management groups
Dee_int_ext	char(1)	I = intensive; E = extensive
Dee_observed	longint	Number observed
Dee_affected	longint	number affected
Dee_examined	longint	number examined individually (temp, mouths etc.)
Dee_signsage	int	age of oldest lesions (days since onset of clinical signs)
Dee_initaffected	longint	number initially infected
Goa_no	longint	Number of goats (via join to expanded <b>hostplace</b> )
Goa_enttype	char(6)	Type of goat enterprise – Breeding/dairying etc. – lookup to <b>enttype</b>
Goa_mgmtgps	int	number of management groups
Goa_int_ext	char(1)	I = intensive; E = extensive
Goa_observed	longint	Number observed
Goa_affected	longint	number affected
Goa_examined	longint	number examined individually (temp, mouths etc.)
Goa_signsage	int	age of oldest lesions (days since onset of clinical signs)
Goa_initaffected	longint	number initially infected
goa_milking	longint	number in milk
Slaughter_fin	date	Date slaughter completed (link through to <b>taskreq.taskend</b> where <b>tasktype</b> = 'SLA')
Disposal_fin	date	Date disposal completed (link through to <b>taskreq.taskend</b> where <b>tasktype</b> = 'DIS')
CnD_fin	date	Date cleaning & disinfection completed (link through to <b>taskreq.taskend</b> where <b>tasktype</b> = 'FPI')?

### Listing 3.5: SQL code for populating the ips table.

```
--Stage 1 - initial set of IPs from ipdeclaration
insert into ips (placeid,
  foreigndbid,
  placetype,
  x,
  y,
  ipnumber,
  rpnumber,
  diagnosisdate,
  sourceip,
  signsage,
  infectiondate)
SELECT place.placeid,
  place.foreigndbid,
  placetype.shortdescription as placetype,
  PlaceFC.x,
  PlaceFC.y,
  place.ipnumber,
  place.rpnumber,
  ipspdeclaration.decldatestamp as diagnosisdate,
  ipspdeclaration.sourceip,
  ipspdeclaration.signsage,
  ipspdeclaration.estinfdate as infectiondate
FROM ((place LEFT JOIN PlaceFC ON place.foreigndbid = PlaceFC.foreigndbid)
  LEFT JOIN placetype ON place.placetype = placetype.placetype)
  INNER JOIN ipspdeclaration ON place.placeid = ipspdeclaration.placeid;

--Stage 2 - update ips with cause
UPDATE ips INNER JOIN (ipspdeclaration
  INNER JOIN cause ON ipspdeclaration.causeid = cause.causeid)
  ON ips.placeid = ipspdeclaration.placeid
SET ips.cause = cause.description;

--Stage 3 - update ips with reason
UPDATE ips INNER JOIN (ipspdeclaration
  INNER JOIN ipspreason ON ipspdeclaration.reasonid = ipspreason.reasonid)
  ON ips.placeid = ipspdeclaration.placeid
SET ips.ipspreason = ipspreason.description;

--Stage 4 - update ips with visit.visitdateon
UPDATE (ips INNER JOIN ipspdeclaration ON ips.placeid =
  ipspdeclaration.placeid)
  INNER JOIN visit ON ipspdeclaration.visitid = visit.visitid
SET ips.visitdate = visit.visitdateon;

--Stage 5 - update ips with one of the associated surveillance tasktypes
UPDATE ((ips INNER JOIN ipspdeclaration ON ips.placeid =
  ipspdeclaration.placeid)
  INNER JOIN task ON ipspdeclaration.visitid = task.visitid)
  INNER JOIN tasktype ON task.tasktype = tasktype.tasktype
SET ips.tasktype = task.tasktype
where taskclass = "s";
```

```

--Stage 6 - update ips with publicreport=1 where reasonid=3
UPDATE ips
SET publicreport = 1
where placeid in (select placeid from visitplan where reasonid = 3);

--Stage 7 - update ips with the visitplan reason with the highest risk
update ips set ips.visitplanreason = (
select top 1 visitplanreason.description
from visitplan, visitplanreason
where visitplan.reasonid = visitplanreason.reasonid
and visitplan.placeid = ips.placeid
and visitplan.targettype = "place"
and visitplan.reqtype = "s" and visitplan.reasonid <= 20
order by riskrating desc);

--Stage 8 - hostplace details
UPDATE ips INNER JOIN hostplace ON ips.placeid = hostplace.placeid
SET ips.pig_no = hostplace.hostnumber
where hosttypeid = 1;
UPDATE ips INNER JOIN hostplace ON ips.placeid = hostplace.placeid
SET ips.dai_no = hostplace.hostnumber
where hosttypeid = 5;
UPDATE ips INNER JOIN hostplace ON ips.placeid = hostplace.placeid
SET ips.bef_no = hostplace.hostnumber
where hosttypeid = 4;
UPDATE ips INNER JOIN hostplace ON ips.placeid = hostplace.placeid
SET ips.shp_no = hostplace.hostnumber
where hosttypeid = 7;
UPDATE ips INNER JOIN hostplace ON ips.placeid = hostplace.placeid
SET ips.dee_no = hostplace.hostnumber
where hosttypeid = 6;
UPDATE ips INNER JOIN hostplace ON ips.placeid = hostplace.placeid
SET ips.goa_no = hostplace.hostnumber
where hosttypeid = 8;

--Stage 9 - update with slaughter date
UPDATE ips INNER JOIN (visitplan INNER JOIN taskreq
ON visitplan.requestid = taskreq.requestid)
ON ips.placeid = visitplan.placeid
SET ips.slaughter_fin = taskreq.taskend
where visitplan.reqtype = "m"
and taskreq.tasktype = "SLA";

--Stage 10 - update with disposal date
UPDATE ips INNER JOIN (visitplan INNER JOIN taskreq
ON visitplan.requestid = taskreq.requestid)
ON ips.placeid = visitplan.placeid
SET ips.disposal_fin = taskreq.taskend
where visitplan.reqtype = "m"
and taskreq.tasktype = "DIS";

--Stage 11 - update with C&D completed date
UPDATE ips INNER JOIN (visitplan INNER JOIN taskreq
ON visitplan.requestid = taskreq.requestid)
ON ips.placeid = visitplan.placeid
SET ips.cnd_fin = taskreq.taskend
where visitplan.reqtype = "m"
and taskreq.tasktype = "FPI";

```

## 4. R Incursion Library

An R library “incursion” has been created that contains some sample data and a set of functions for conducting the various epidemiological analyses described in section 1 above.

In the absence of a usable New Zealand FMD epidemic dataset in IRS, an extract of the UK2001 FMD outbreak dataset has been included in the library to permit the functions to be trialled. This data has been manipulated to mimic the table structure recommended in section 3.

Documentation for the incursion library is included as Appendix 1.

The other major issue is how access to data extracted from IRS will be enabled. In the longer term, it is envisaged that there will be an official data warehouse containing the de-normalised data recommended in section 3. In the short term, in the absence of this data warehouse, it is anticipated that the data required for the analyses will be assembled and processed in a Microsoft Access environment prior to loading into R.

## 5. Targets for Measures Identified by InterSpread Plus Modelling

The New Zealand Standard FMD Model (NZSFM) was originally developed in 2005. It comprises a comprehensive set of spatial data and parameters for modelling the spread of the FMD virus (with characteristics similar to the UK2001 strain) within New Zealand, using the InterSpread Plus (IS+) software developed by the EpiCentre, Massey University. There have been some known deficiencies with the model, particularly with respect to how farmer self-reporting is represented. Some of this relates to uncertainty about some of the parameters themselves, such as how frequently do “typical” farmers observe their stock, and what proportion would contact a veterinarian if they suspected something unusual. Improved certainty will hopefully be achieved via a companion research project utilising a farmer questionnaire (BNZ753 – Contact Rates for Livestock). However, there are some deficiencies in the IS+ code itself, with some sections of the underlying computer code not actually carrying out what the modeller would expect. In order to evaluate targets for various efficiency and effectiveness measures, it was necessary to first fix or “workaround” the known or newly discovered deficiencies before any modelling of efficiency and effectiveness targets could be conducted.

### 5.1. UPDATING AND IMPROVING THE NZ STANDARD MODEL

#### 5.1.1 Farm file

The farm file holding data on the location and animal numbers of New Zealand livestock farms was completed updated based on a July 2007 AgriBase extract. The underlying coordinate system is now based on the New Zealand Transverse Mercator (NZTM) projection.

#### 5.1.2 Farmer self-reporting

To better represent farmer self-reporting, both prior to and after initial detection, an @Risk model was constructed in Excel. The parameters included are shown in Table 5.1.2. The

parameter values were mostly based on expert elicitation conducted during the creation of the NZSFM in 2005.

**Table 5.1.2: Parameters modelled to represent background surveillance (passive farmer/vet self-reporting) prior to initial detection and farmer self-reporting after initial detection.**

Parameter	Values	
	Background surveillance	Post-detection self-reporting
Proportion of farmers who know what FMD looks like	RiskTriang(0.5,0.68,0.8)	RiskTriang(0.85,0.9,0.95)
Days per year farmers away from their farms	RiskTriang(7,19,25)	RiskTriang(1,5,2,10)
Likelihood of being present on any given day	Random variate based on days away	Random variate based on days away
Typical stock observation frequency for different farm classes (once every n days)	Dairy = 1 (during milking season) Pig farms = 1 Other farms = 3	Dairy = 1 (during milking season) Pig farms = 1 Other farms = 3
Proportion of animals displaying clinical signs by day since onset of c/s	Linear function from 0.042 (First day incidence) to 1 over a 16 day period	Linear function from 0.042 (First day incidence) to 1 over a 16 day period
Probability of a mob displaying clinical signs	Increasing from 0.525 to 1 over a 16 day period	Increasing from 0.525 to 1 over a 16 day period
Likelihood of farmer being present and recognising FMD	Based on combination of above variables	Based on combination of above variables
Time from recognition of signs to MAF visit	1 day	0 days
Time from visit to when diagnosis is confirmed	RiskBetaSubj(0,0,1,7)	RiskBetaSubj(0,0,1,3)
Time taken by MAF for diagnosis	Sum of Time from recognition of signs to MAF visit and Time taken to reach diagnosis	Sum of Time from recognition of signs to MAF visit and Time taken to reach diagnosis
Time from onset of clinical signs	@Risk output based on all of above, expressed as a distribution	@Risk output based on all of above, expressed as a distribution

The results of the @Risk modelling of farmer self-reporting are shown in Figures 5.1.2.1 and 5.1.2.2 for the periods prior to and post initial detection respectively.

Figure 5.1.2.1: Distribution of times to diagnosis from onset of clinical signs of FMD when reported by farmers or private veterinarians in the period prior to initial detection

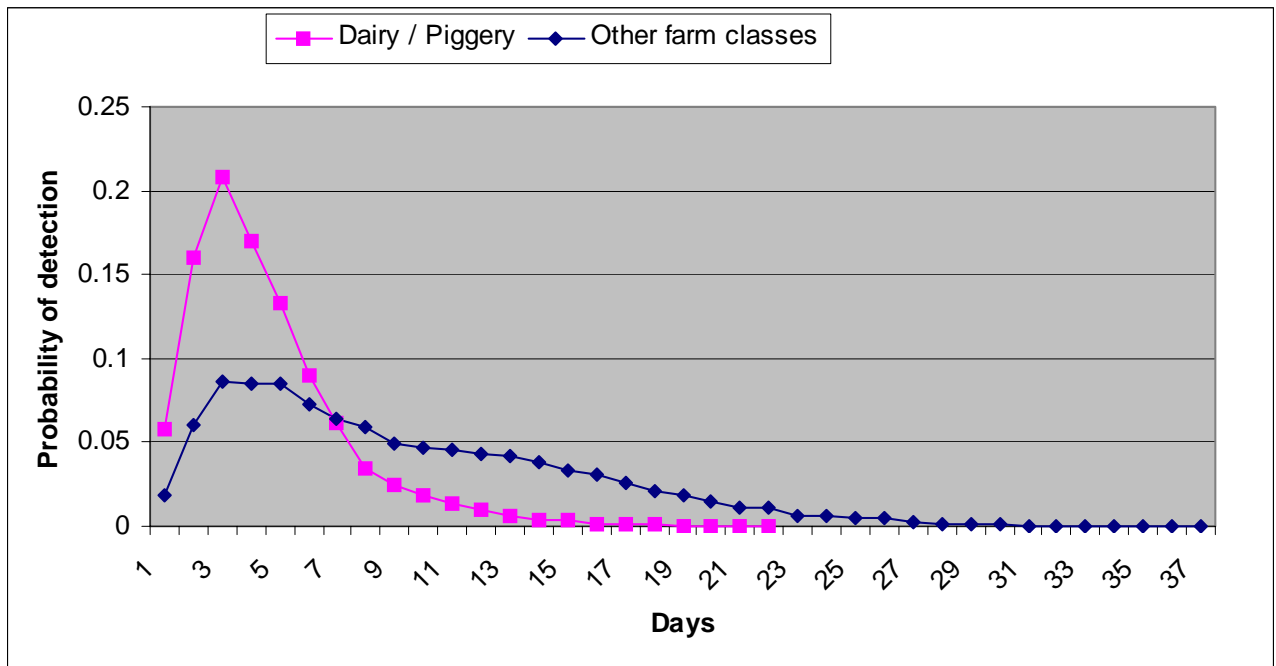
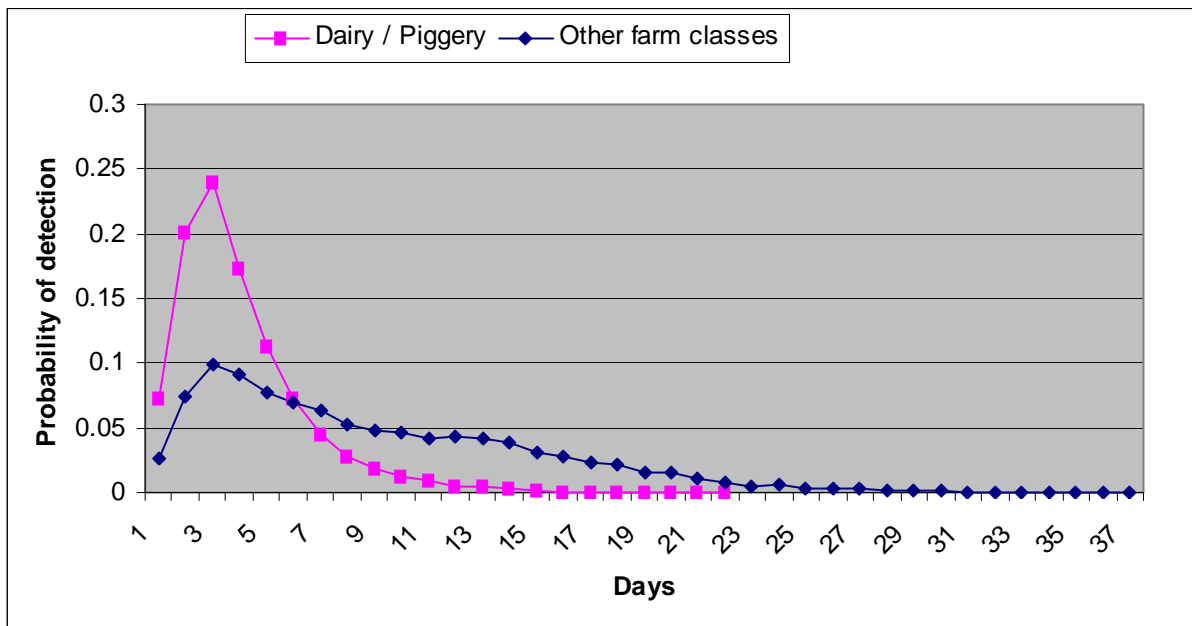


Figure 5.1.2.2 Distribution of times to diagnosis from onset of clinical signs of FMD when reported by farmers or private veterinarians after initial detection



### 5.1.3 Improvement to other surveillance controls

In order to differentiate likely response times in terms of dispatching a patrol veterinarian to investigate high, medium and low risk contacts identified via tracing, separate surveillance sections were defined and linked to the relevant Tracing sections. Detection probabilities were revised. The parameters are documented in Table 5.1.3.

**Table 5.1.3: Surveillance control parameters for at-risk visits resulting from high, medium and low risk traces**

Parameter	High risk	Medium Risk	Low Risk
ActivationOption	tracing	tracing	tracing
SelectionProbability	1	0.9	0.5
VisitDelay	Lookup 0d=0.9; 1d=0.1	Triangular 0 1 2	Triangular 1 2 3
VisitFrequency	Constant 1 (daily)	Constant 2	Constant 3
VisitDuration	Constant 17	Constant 17	Constant 17
DelayToDetection	Lookup 0d=0.9; 1d=0.1	Triangular 0 1 2	Triangular 0 1 2
DetectionRelativeTo	Clinical_signs	Clinical_signs	Clinical_signs
DetectionProbability[beef]	Constant 1	Constant 1	Constant 1
DetectionProbability[dairy]	Constant 1	Constant 1	Constant 1
DetectionProbability[deer]	Constant 1	Constant 1	Constant 1
DetectionProbability[goats]	Constant 1	Logistic 0.25 0.8 0.74 1.7	Logistic 0.25 0.8 0.74 1.7
DetectionProbability[pigs]	Constant 1	Constant 1	Constant 1
DetectionProbability[sheep]	Constant 1	Logistic 0.25 0.8 0.74 1.7	Logistic 0.25 0.8 0.74 1.7

#### 5.1.4 Saleyard movement parameters

Movement frequencies and distance distributions were updated by incorporating the results from Andrea Murray’s saleyard study (Murray 2006).

#### 5.1.5 Resource constraints

These were completely revised from the original NZSFM. Updated estimates of the numbers of animals of different types that could be processed by a slaughter team per day were obtained from Richard Calvert. These are as follows:

- Sheep: 800
- Beef cattle: 350-400
- Dairy cattle: 350-400
- Pigs: 640
- Deer: 480
- Goats: 400

Note, these figures indicate how many of a single type could be slaughtered by a single team if they were only slaughtering that type. The reality is that many farms have a mix of animal types on them (e.g. Sheep and beef properties). An issue with IS+ is that it currently doesn’t permit you to create virtual teams. You have to specify the total resource in terms of numbers of farms or numbers of animals (by type) that can be processed per time period at various stages throughout the epidemic. One cannot directly represent the situation where teams can process so many of one type OR so many of another type.

The solution was to take a random sample of 20,000 farms from the farm file, and load the numbers of animals by type into an Excel spreadsheet and then estimate the time it would take a single team to depopulate the farm, given an estimate of the number of minutes it would take to slaughter a single animal given the time estimates above. It was assumed that slaughter teams would work for no more than 9 hours per day, with some allowance made for driving time, setting-up and personal disinfection at each farm. For extremely large farms, it was assumed that additional personnel would be made available, effectively establishing an upper limit to the time allowable for depopulation under emergency management.

The times were then summarised by farm class. Four resource pools were then defined representing the different farm classes. The IS+ resource parameters are shown in Table 5.1.5.

Table 5.1.5: Resource parameters used for different farm classes

Parameter	Farm class			
	Pastoral livestock	Dairy	Grazing/drystock	Piggeries
ActionOption	depopulation	depopulation	depopulation	depopulation
FarmListOption	multiple_list	multiple_list	multiple_list	multiple_list
FarmProcessingOption	time_period_by_farms	time_period_by_farms	time_period_by_farms	time_period_by_farms
TimePeriodByFarms1	Triangular 0 0 5	Triangular 0 1 3	Triangular 0 0 3	Triangular 0 0 3

This allowed more realistic resource constraints to be modelled.

## 5.2. MODELLING EFFICIENCY AND EFFECTIVENESS TARGETS

Investigating potential targets for efficiency and effectiveness via modelling requires that we have epidemiological knowledge that link the particular operational tasks being evaluated to outputs that can be measured. For instance, if local spread continues off infected farms up until the time of depopulation of livestock, even though the farm may have been detected and placed under quarantine, then delays to depopulation can be measure in terms of impacts on secondary spread. In contrast, if further spread is unlikely off farms once all the FMD-susceptible livestock have been slaughtered, then it is very difficult to quantify the benefits of delays to cleaning and disinfection (C&D) being completed.

### 5.2.1 North Island model

To investigate a selection of targets, a North Island (NI) version of the NZSFM was established, comprising a spatial population of all farms with FMD-susceptible animals in the NI. The epidemic history file specified an infected piggery in the Manawatu District as the source farm. The NI model utilised a 14-day National Standstill following initial detection, followed by the implementation of a reasonably large lower NI Controlled Area (CA), extending from New Plymouth in the north-west to Wairoa in the north-east. Realistic times to depopulation were defined, and it was anticipated that it would take patrol veterinarians two days to visit all farms within each new 3-km Protection Zone, with revisit times also specified at intervals of 2 days. Parameters were then varied from this base model to allow various targets to be evaluated. Each model was configured to run for 300 days, with 100 iterations of each configuration, to allow a distribution of outputs to be analysed.

Likely temporal patterns of spread were described for the NI model, including:

- Estimated dissemination rates.
- Distribution of time to first detection.
- Correlation between length of silent spread phase and size and duration of epidemic.

In addition, the following targets were evaluated:

- Times to visit all farms within 3 km Protection Zones and revisit times.
- Times from detection to slaughter (due to resource constraints).
- The value of improved biosecurity on detected farms awaiting depopulation.
- Duration of national movement standstills.

Output measures included:

- Summary measures of size of epidemic (number of infected farms by the end of the 300-day period).
- Summary measures of epidemic duration (day of last detected farm).
- Number of uncontrolled epidemics (still spreading after 300 days).
- Proportion of infected farms that were responsible for secondary spread.
- Proportion of diagnoses that were farmer self-reports (excluding the index farm).

Figure 5.2.1.1 shows the distribution of times from the date of infection of the first farm to the date of diagnosis of the index infected premises (IP) expected for the NZSFM. This represents the “silent phase” of the epidemic. The mean, median and range were 12, 10.5 and 4-31 days respectively. Figure 5.2.1.2 shows the correlation between the length of the silent phase and the likely duration of the epidemic. Spearman’s rank coefficient rho had a value of 0.69 for this correlation. Figure 5.2.1.3 shows the correlation between the length of the silent phase and the likely number of infected premises (IPs) (Spearman’s rho = 0.59).

Figure 5.2.1.1: Distribution of time that FMD virus was present in the country prior to detection of the index farm

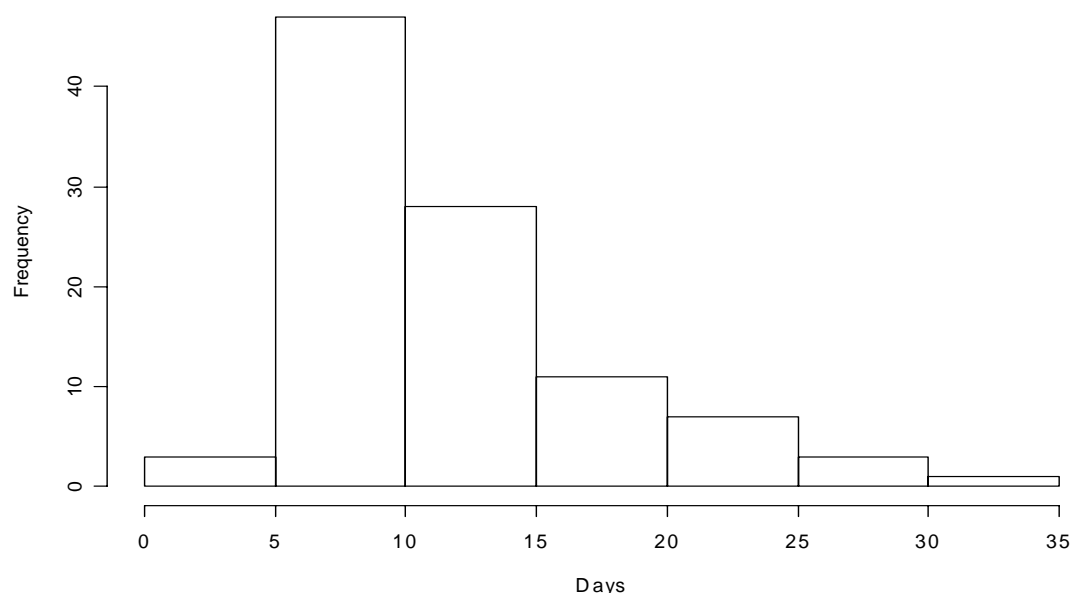


Figure 5.2.1.2: Correlation between the length of the silent phase and likely duration of the epidemic

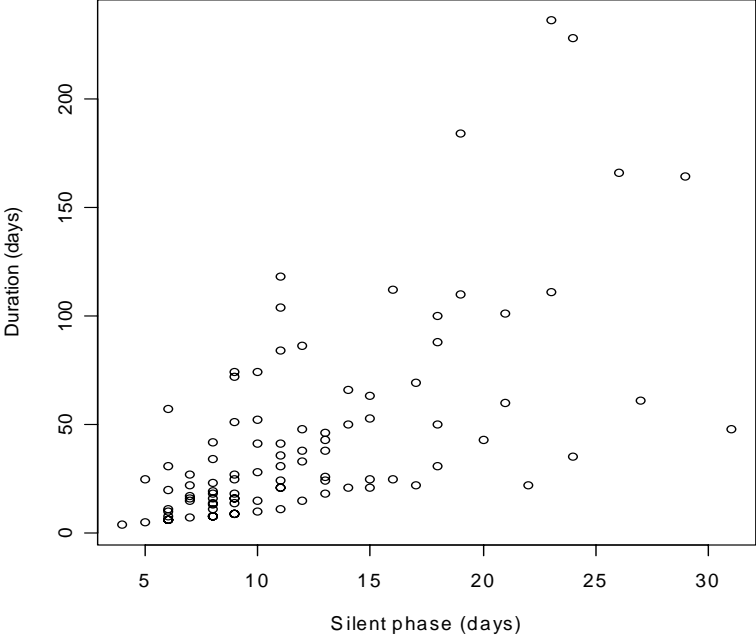


Figure 5.2.1.3: Correlation between the length of the silent phase and likely size of the epidemic

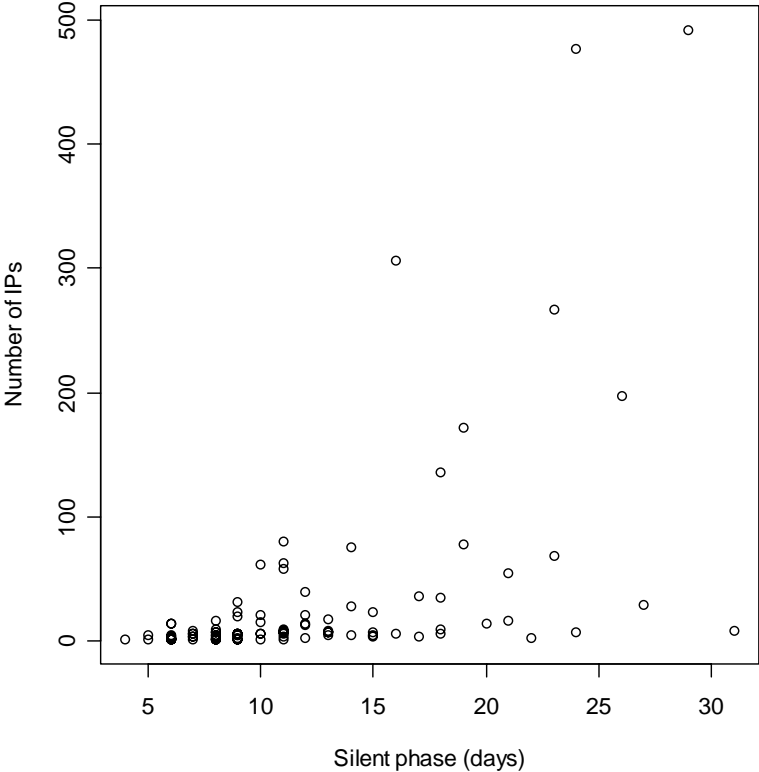


Figure 5.2.1.4 shows the expected weekly dissemination rates (DR) based on actual infection dates derived from 100 iterations of the NZSFM, illustrated as a series of boxplots. The width of the boxes is proportional to the number of iterations contributing to each weekly value. The estimated dissemination rates (EDR) based on diagnosis dates from the same simulations are shown in Figure 5.2.1.5.

Figure 5.2.1.4: Expected weekly dissemination rates for the New Zealand Standard Model of FMD, based on simulated infection dates (horizontal line indicates an EDR = 1)

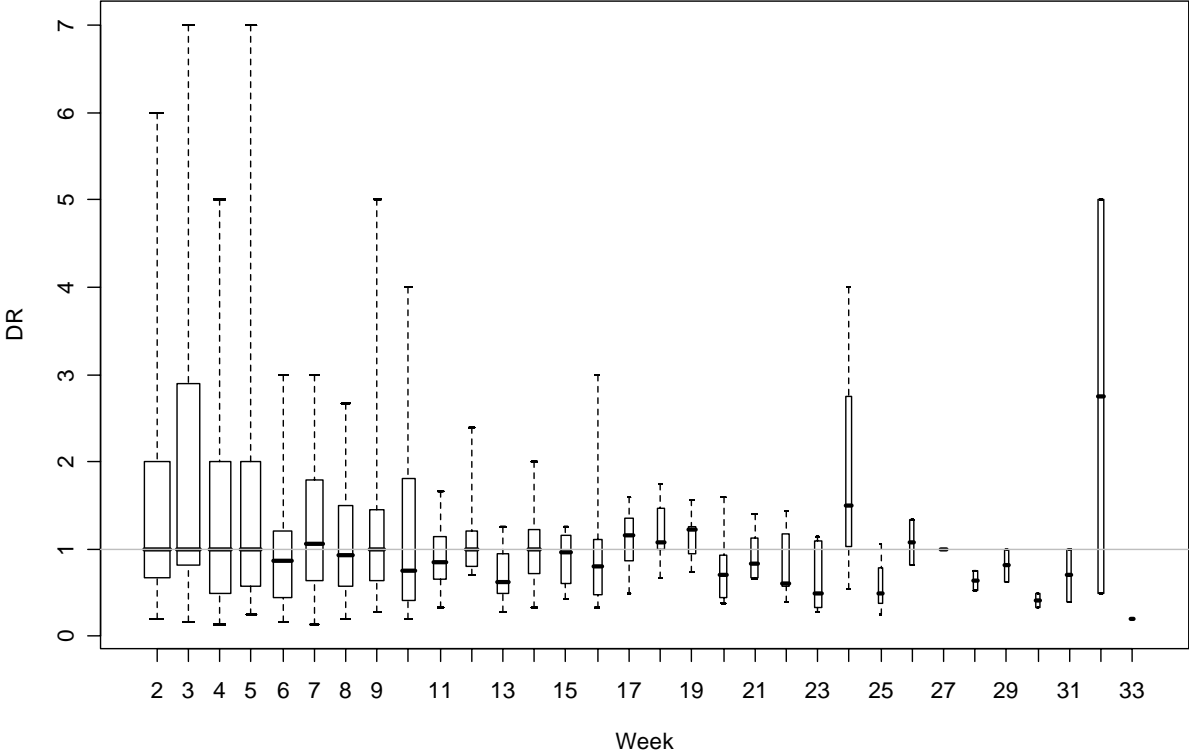


Figure 5.2.1.5: Weekly estimated dissemination rates for the New Zealand Standard FMD Model, based on simulated diagnosis dates (horizontal line indicates an EDR = 1)

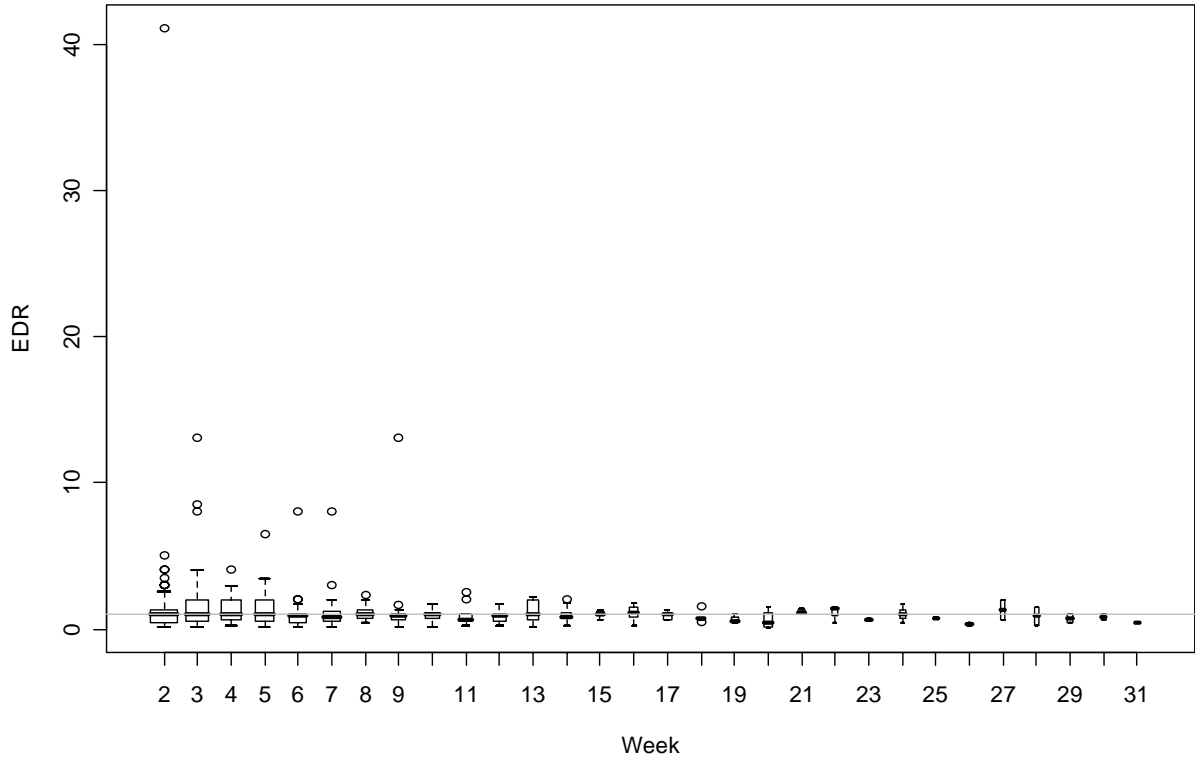


Table 5.2.1.1 provides a synopsis of the effects of the time taken to visit all farms within the 3 km Protection Zone (PZ) following the discovery of a new IP, given unlimited depopulation resources and the majority of farms being slaughtered on the day of discovery.

Table 5.2.1.1: Effects of time taken to visit and re-visit all farms within the 3-km Protection Zone of an IP, given unlimited depopulation resources.

Measure	Visit time within Protection Zone		
	1 day	2 days	3 days
Number of IPs (mean, median, range)	11.35, 7, 1-123	14.46, 7, 1-200	68.15, 8, 1-4925
Duration (mean, median, range)	34.33, 33.5, 4-120	36.72, 33, 4-142	44.18, 35, 4-300
Number of "out of control" epidemics	0/100	0/100	1/100
Proportion secondary spreaders (mean, median, range)	0.398, 0.43, 0-0.67	0.407, 0.43, 0-0.67	0.414, 0.44, 0-0.67
Proportion farmer self-reports (mean, median, range)	0.225, 0.2, 0-1	0.221, 0.2, 0-1	0.224, 0.19, 0-1

Table 5.2.1.2 shows a summary of the effects of the time taken to visit all farms within the PZ following the discovery of a new IP, given more realistic depopulation resources, with farms taking up to 5 days to depopulate, dependent on type of farm and number of animals.

**Table 5.2.1.2: Effects of time taken to visit and re-visit all farms within the 3-km Protection Zone of an IP, when depopulation resources are constrained more realistically**

Measure	Visit time within Protection Zone		
	1 day	2 days	3 days
Number of IPs (mean, median, range)	30.6, 5, 1-1139	33.5, 5, 1-1473	305.3, 6, 1-11050
Duration (mean, median, range)	38.5, 24, 4-300	39.9, 25, 4-300	50.2, 25.5, 4-300
Number of "out of control" epidemics	2/100	1/100	5/100
Proportion secondary spreaders (mean, median, range)	0.395, 0.46, 0-0.75	0.401, 0.48, 0-0.75	0.407, 0.5, 0-0.75
Proportion farmer self-reports (mean, median, range)	0.268, 0.17, 0-1	0.285, 0.25, 0-1	0.298, 0.25, 0-1

Table 5.2.1.3 shows a summary of the effects of improving biosecurity on detected farms awaiting depopulation, given different times to visit and revisit at-risk farms within the PZ. Local spread was reduced to 2/3 of that prior to detection.

**Table 5.2.1.3: Effects of reducing opportunities for local spread off detected farms awaiting depopulation**

Measure	Visit time within Protection Zone		
	1 day	2 days	3 days
Number of IPs (mean, median, range)	8.25, 5, 1-69	9.86, 5, 1-59	12.62, 5, 1-263
Duration (mean, median, range)	27.9, 26, 5-116	30.5, 26, 5-96	34.5, 28, 5-240
Number of "out of control" epidemics	0/100	0/100	0/100
Proportion secondary spreaders (mean, median, range)	0.392, 0.44, 0-0.75	0.404, 0.47, 0-0.8	0.405, 0.46, 0-0.8
Proportion farmer self-reports (mean, median, range)	0.326, 0.25, 0-1	0.322, 0.25, 0-1	0.342, 0.27, 0-1

Table 5.2.1.4 summarises the effects of the duration of national movement standstills and size of the Controlled Area (CA), given 2-day PZ surveillance and "standard" biosecurity on detected farms awaiting depopulation.

**Table 5.2.1.4: Effects of duration of national movement standstills and size of Controlled Area (CA)**

Measure	14 days – large CA	7 days – small CA	7 days – large CA
Number of IPs (mean, median, range)	32.7, 6, 1-492	65.5, 5, 1-4499	62.1, 5, 1-4209
Duration (mean, median, range)	43.5, 25.5, 4-236	41.6, 25, 4-300	42.1, 25, 4-300
Number of "out of control" epidemics	0/100	1/100	1/100
Proportion secondary spreaders (mean, median, range)	0.417, 0.5, 0-0.75	0.41, 0.5, 0-0.75	0.41, 0.5, 0-0.75
Proportion farmer self-reports (mean, median, range)	0.27, 0.21, 0-1	0.27, 0.17, 0-1	0.27, 0.19, 0-1

## 5.2.2 New Zealand models

To further characterize some of the key features of epidemics of "small" (up to 20 IPs), "medium" (approximately 100 IPs) and "large" (UK2001) size, the NI standard model settings (described above) were transferred to a New Zealand-wide model, using the full set of livestock farms and markets. In addition, minimal and maximal versions were configured, utilising the updated parameters described in Section 5.1 above, but adjusted using the

minimal and maximal movement frequencies obtained from the movement study conducted by Sanson (2005). The key differences between the minimal, standard and maximal models are shown in Table 5.2.2.1.

**Table 5.2.2.1: Key differences between the minimal, standard and maximal versions of the New Zealand ‘standard’ FMD model**

Parameter	Minimal model	Standard model	Maximal model
Farm-to-farm movements	Based on Quiet period movements	Mid-point of Quiet and Busy period movements	Based on Busy period movements
Saleyard movements	Based on Quiet period movements	Mid-point of Quiet and Busy period movements	Based on Busy period movements
Airborne spread	None	None	Based on UK67-68
Dairy-tanker spread	None	Based on Denmark 1982	Based on Denmark 1982
Local spread	Based on UK2001, but reduced local spread probabilities (0.5x) once farm detected and awaiting depopulation	Based on UK2001	Based on UK2001
Standstill period	21 days	14 days	14 days
Size of control area	Large	Large	Small

As with the NI model, 100 iterations were repeated for each model, and simulations were set to run for 300 days.

The minimal model produced a mean epidemic size of 9 IPs (median = 3, range = 1-91). The mean length of epidemic (time to last infection) of 20.3 days (median = 14, range 1-100). Thirty of the 100 epidemics only involved a single IP (no secondary spread), and of these, 2 went undetected.

The standard model produced a mean epidemic size of 80.9 IPs (median = 6, range = 1-3033). The mean length of epidemic (time to last infection) of 30.5 days (median = 23, range 1-300). Thirteen of the 100 epidemics only involved a single IP (no secondary spread), however, all were detected. One epidemic produced a ‘run-away’ epidemic i.e. was still spreading by Day 300 of the simulation.

The maximal model produced a mean epidemic size of 131 IPs (median = 12, range = 1-4983). The mean length of epidemic (time to last infection) of 47.5 days (median = 27, range 1-300). Only 1 of the 100 epidemics died out without causing secondary spread. All were detected. Three iterations produced ‘run-away’ epidemics i.e. were still spreading by Day 300 of the simulation.

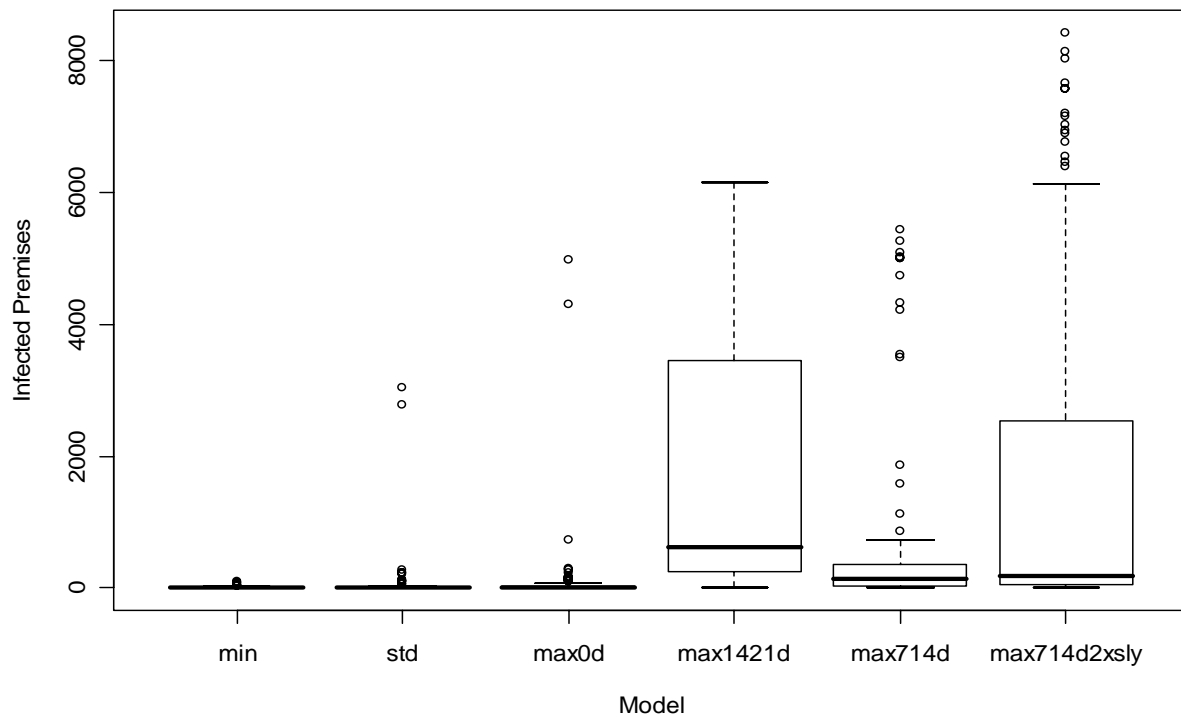
In order to produce more UK2001-sized epidemics, delays to first detection (based on passive surveillance) were progressively forced into the maximal model. Adding a delay of 7-14 days to the expected time to first detection produced a mean epidemic size of 701.8 IPs (median = 142.5, range 3-5430), with mean length of 123 days (median = 106, range 13-300). Twelve epidemics were still spreading by Day 300. Adding a delay of 14-21 days to the expected time to first detection produced a mean epidemic size of 1748 IPs (median = 627, range 5-6161), with mean length of 196.6 days (median = 179, range 29-300). Twenty-six epidemics were still spreading by Day 300.

The size of the epidemics produced by the maximal models was significantly correlated with the length of time from the onset of clinical signs of the first farm to detection of the index farm (Kendall’s rank correlation tau = 0.51,  $p < 0.0001$ ).

Doubling the number of farms exposed for each saleyard consignment from 1.957 to 3.914, and forcing a 7-14 delay to initial detection produced a mean epidemic size of 1769 IPs (median = 184, range 3-8423). Mean length of epidemic was 146.3 (median = 115.5, range 13 – 300). Twenty-three of the 100 epidemics were classed as ‘run-away’.

Figure 5.2.2.1 shows the expected distributions of epidemic sizes for the different model configurations.

Figure 5.2.2.1: Boxplots showing distributions of simulated epidemic sizes for the different configurations of the New Zealand ‘standard’ model of FMD. [Key: min = minimal model; std = standard model; max0d = maximal model; max1421d = maximal model with an extra 14-21 days delay to first detection forced into the model; max7-14d = maximal model with an extra 7-14 days delay to first detection forced into the model; max714d2xsly = maximal model with an extra 7-14 days delay to first detection forced into the model as well as a doubling of the splitting rate for livestock sales through saleyards.]



The distributions of times to first diagnosis from the onset of clinical signs on the first infected farm for small ( $\leq 20$  IPs), medium (50-150 IPs) and large ( $\geq 1000$  IPs) epidemics are shown in Figure 5.2.2.2. The distributions of expected duration of epidemics (days to last infection) for small, medium and large epidemics are shown in Figure 5.2.2.3.

Figure 5.2.2.2: Boxplots of times to first diagnosis from onset of clinical signs associated with large, medium and small epidemics

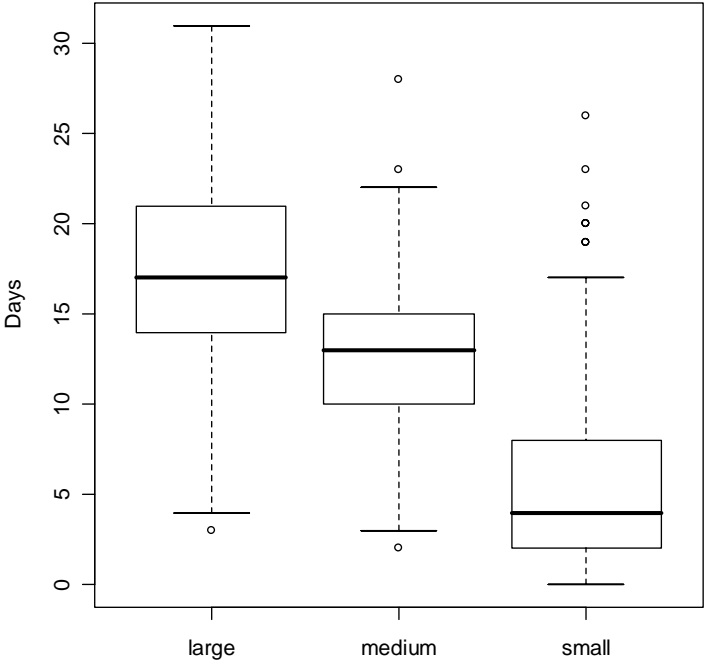


Figure 5.2.2.3: Boxplots of expected duration of large, medium and small epidemics

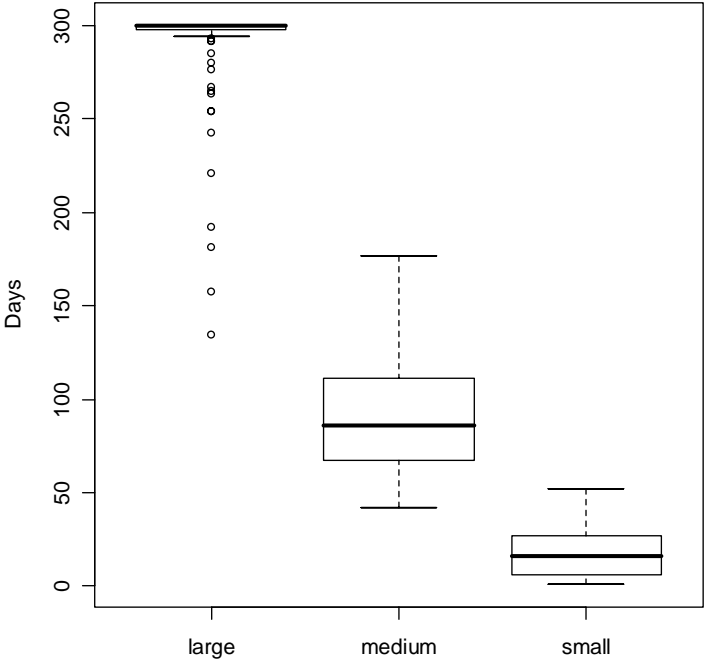
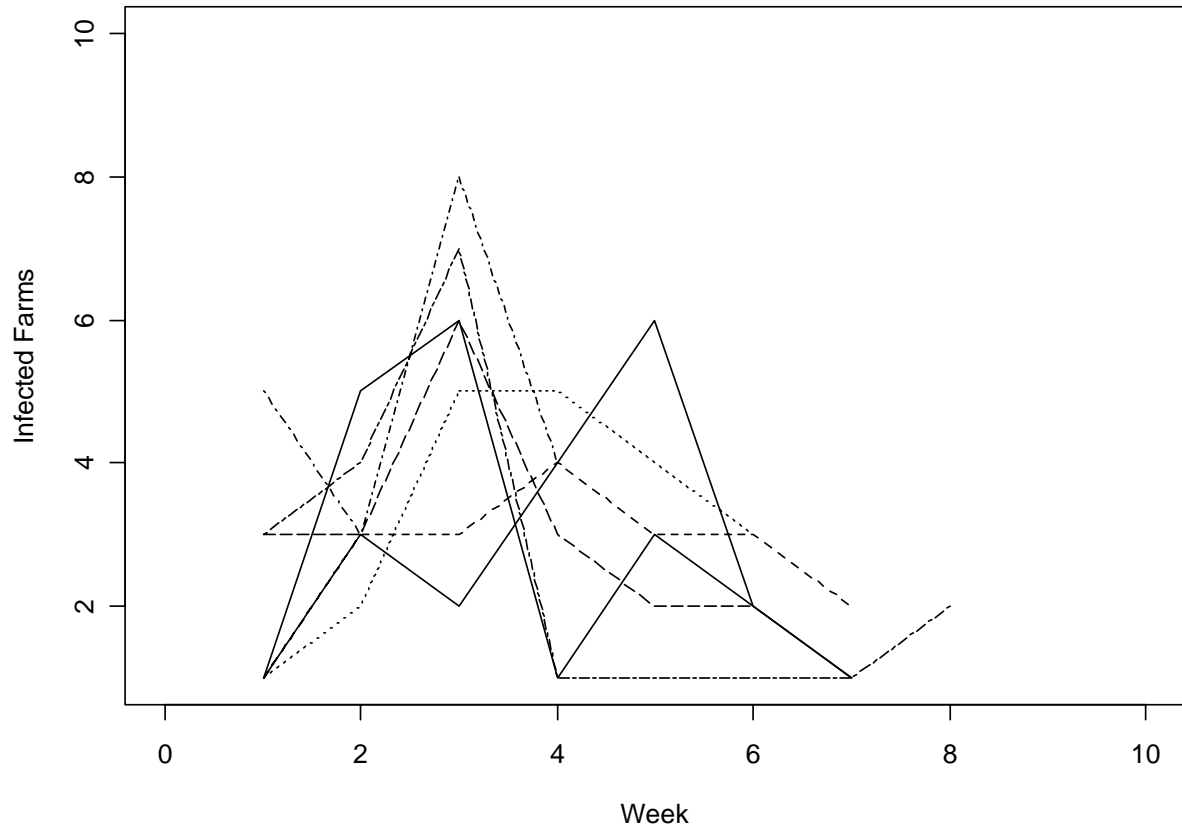


Figure 5.2.2.4 shows the epidemic curves of the model runs that produced epidemic sizes of 19-20 infected farms.

Figure 5.2.2.4: Weekly epidemic curves of the model runs that produced epidemic sizes of 19-20 infected farms



It can be seen that the maximum number of farms infected in a week was 8, and all of the epidemics were over by Week 8. Most epidemics peaked in Week 3, but occasionally, there was a secondary peak. Figure 5.2.2.5 shows the weekly EDR plots for these epidemics. The maximum EDR value was 5 in Week 2, although most had EDR values of 3 or less. Most epidemics had their EDR values drop below 1 by Week 3 or 4. Due to the small numbers of farms involved at the tail of the epidemics, occasionally EDR values would rise above 1.

Figure 5.2.2.5: Weekly EDR plots of the model runs that produced epidemic sizes of 19-20 infected farms. Horizontal grey line indicates EDR=1

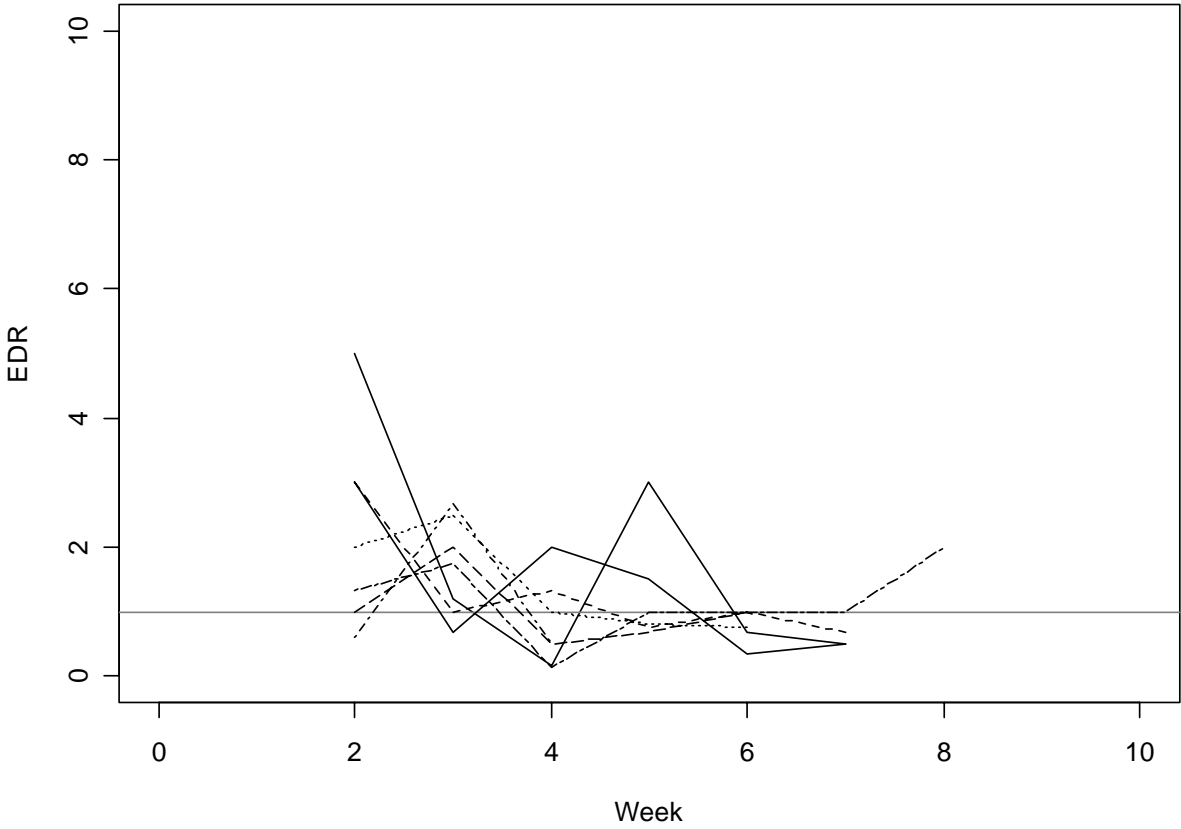
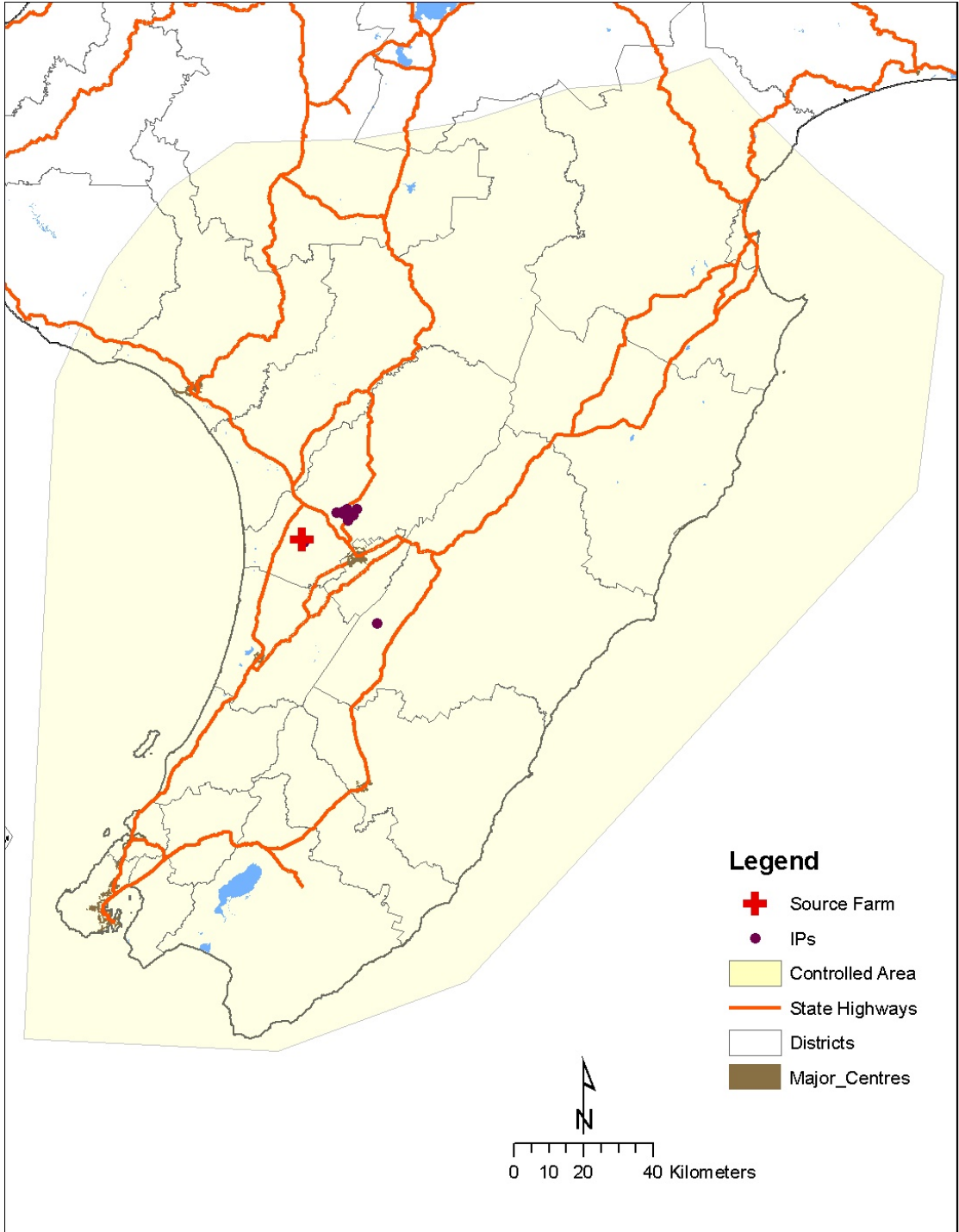


Figure 5.2.2.6 is a map showing the location of IPs for one of the small epidemics. Only 2 of the 9 (22 percent) model runs involved IPs outside of the Controlled Area (CA).

Figure 5.2.2.6: Outbreak map for one of the of the model runs that produced a small epidemic (19-20 infected farms)



The weekly epidemic curves associated with medium sized epidemics with 90-110 infected farms are shown in Figure 5.2.2.7. The EDR plots for the same epidemics are shown in Figure 5.2.2.8. A map showing the locations of IPs for one of the model runs is shown in Figure 5.2.2.9.

Figure 5.2.2.7: Weekly epidemic curves of the model runs that produced medium epidemic sizes of 90-110 infected farms

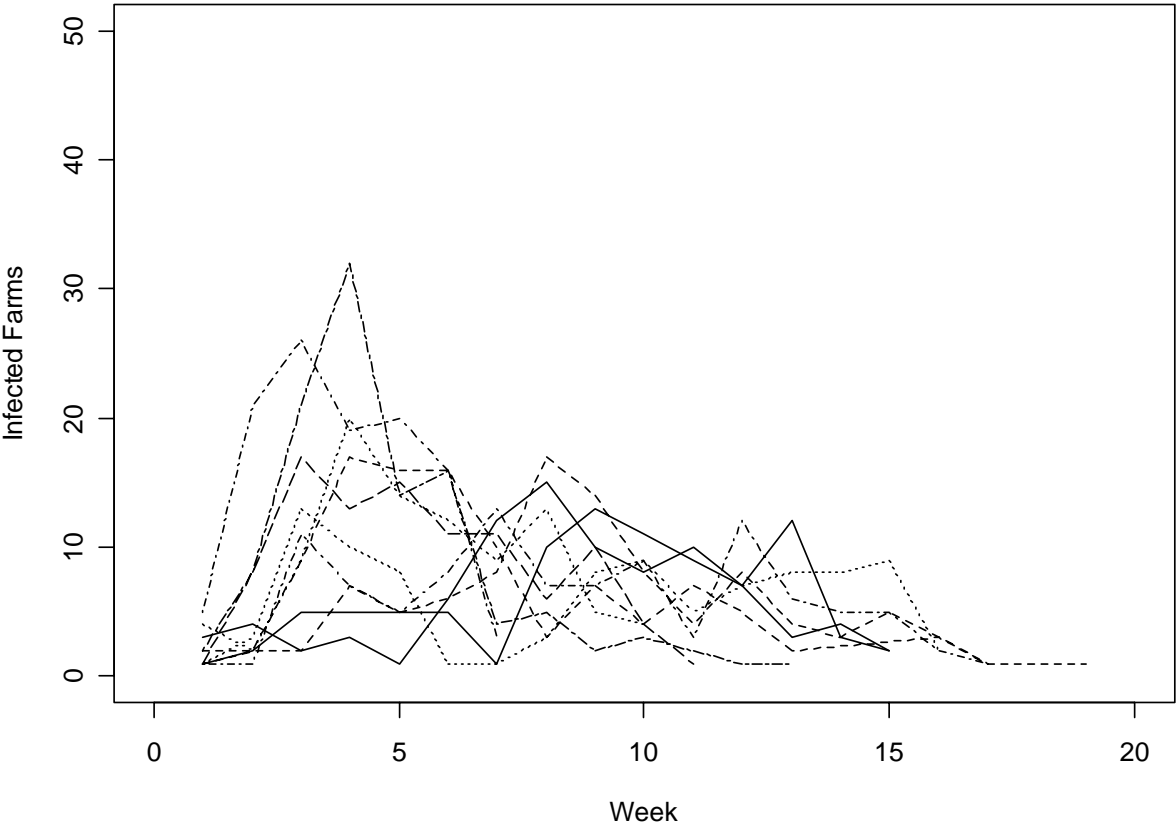


Figure 5.2.2.8: Weekly EDR plots of the model runs that produced medium epidemic sizes (90-110 infected farms). Horizontal grey line indicates EDR=1

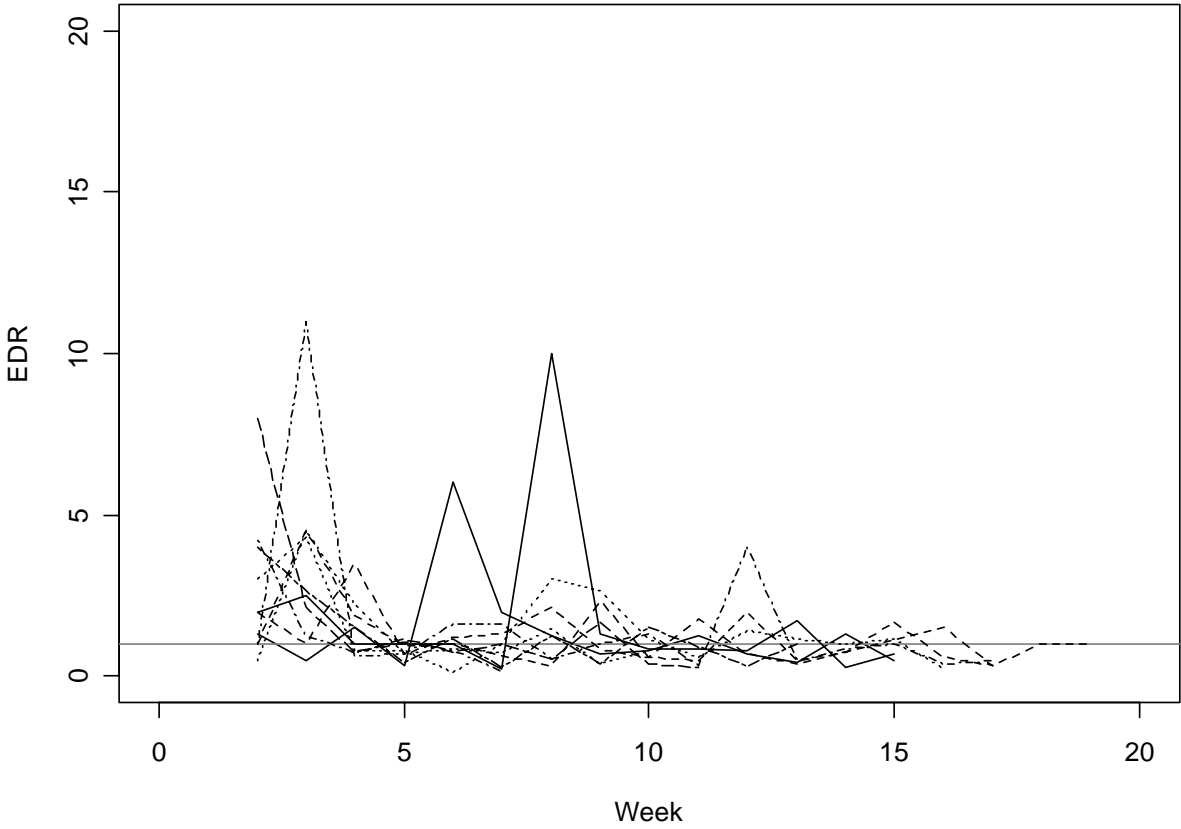
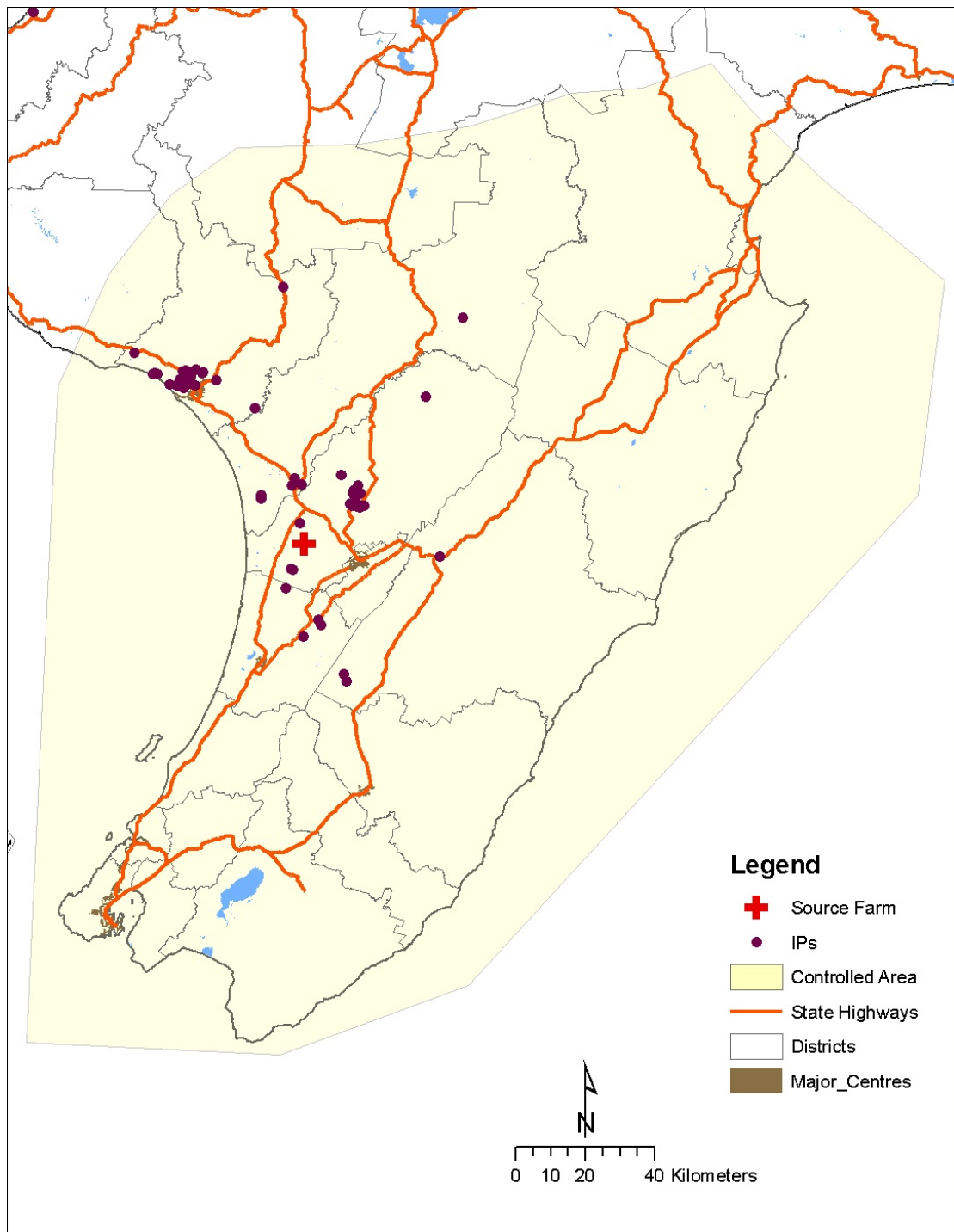


Figure 5.2.2.9: Outbreak map for one of the of the model runs that produced a medium sized epidemic (90-110 IPs)



All of the medium-sized epidemics peaked in terms of numbers of new infections by Week 3 or 4. The maximum number of farms infected in a single week was 32. The duration of these epidemics was up to 19 weeks. EDR values dropped to  $\leq 1$  by Week 4 or 5, although there were occasions when EDR jumped above 1, due to secondary smaller peaks. EDR is sensitive to fluctuations when numbers of infected farms are small. Five of the 10 ‘medium-sized’ epidemics (50 percent) involved IPs outside the CA.

Figures 5.2.2.10 and 5.2.2.11 display the epidemics curves and EDR plots respectively for 11 large epidemics ( $\geq 1000$  cases but eradicated by Day 275). There was one large propagating

epidemic that was eventually brought under control. The locations of the IPs for this epidemic are shown in Figure 5.2.2.12. All (100 percent) of these large epidemics involved IPs outside of the CA.

Figure 5.2.2.10: Weekly epidemic curves of the model runs that produced large epidemics of  $\geq 1000$  infected farms, but which were successfully eradicated by Day 275

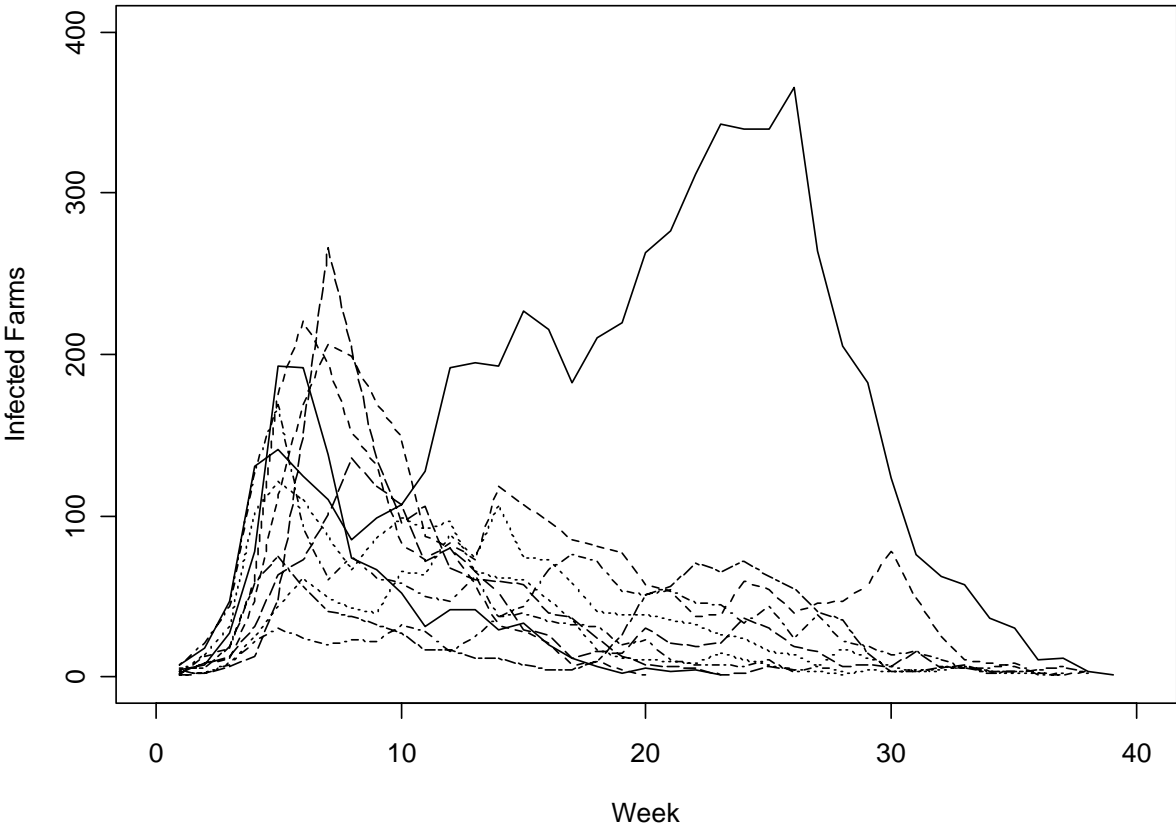


Figure 5.2.2.11: Weekly EDR plots of the model runs that produced large epidemics of  $\geq 1000$  infected farms, but which were successfully eradicated by Day 275. Horizontal grey line indicates EDR=1

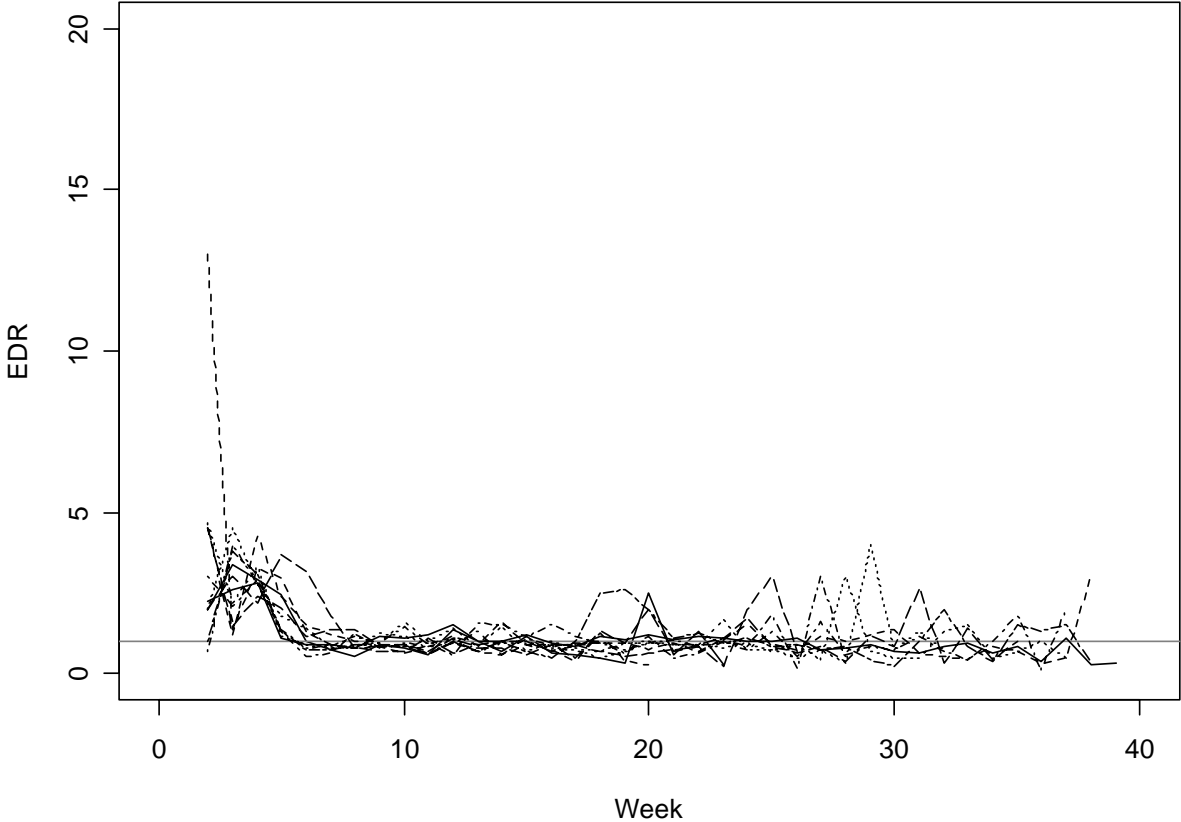
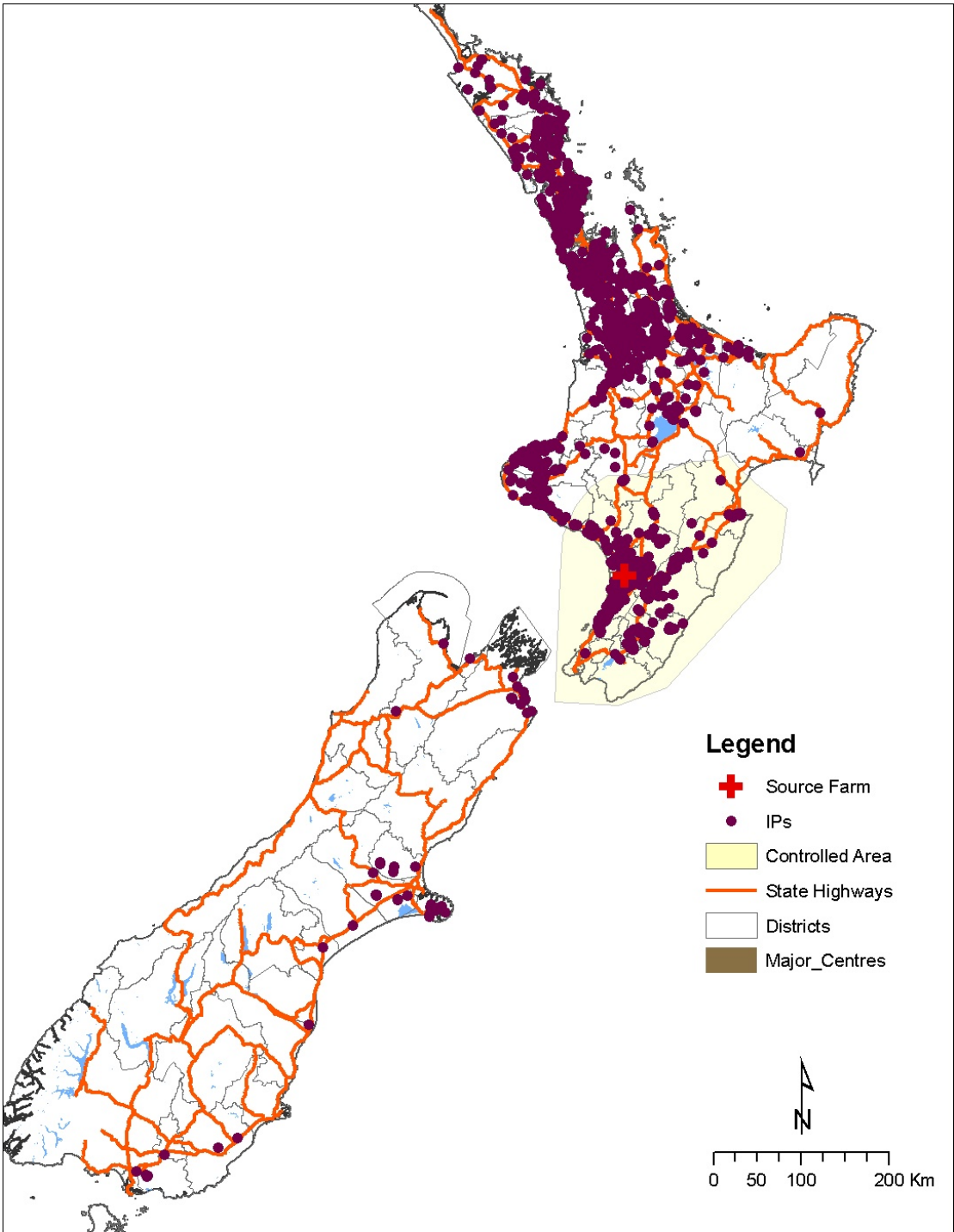


Figure 5.2.2.12: Outbreak map for one of the of the model runs that produced a large epidemic (>= 1000 IPs but eradicated by Day 275)



## 6. Discussion

InterSpread Plus is a complex simulation program, and it takes some time, effort, knowledge and experience to get it configured properly such that you can really start investigating the likely differences in outcomes resulting from changes to biosecurity policy, operational efficiency or resource inputs. The New Zealand Standard FMD Model comprises a very comprehensive set of parameters that utilises most of the capabilities of IS+. The parameters were initially established in 2005, but had not really been comprehensively tested in terms of being applied to a range of policy questions. This study required that certain sections be reviewed, and where necessary, revise or redevelop them to enable the modelling work to proceed.

It soon became obvious that the IS+ code, in sections such as Surveillance, Resource and Depopulation, did not always behave in the manner that the epidemiologist would expect; or presented significant challenges in terms of transferring existing epidemiological knowledge into the particular variables requiring to be specified under each section. Not surprisingly, some software bugs were uncovered, which had to be dealt with by the EpiCentre developers before simulation could continue. Arising from this study are a number of recommendations for improvements or additions to IS+ to enable it to continue as the preferred modelling platform for New Zealand infectious disease and pest spread investigations. These are listed in Appendix 2.

All simulations were initiated from a piggery in the Manawatu District. Using the base model on a North Island farm dataset, the mean length of the silent phase of the epidemic was 12 days (median = 10.5 days) (see Figure 5.2.1.1). The size and duration of the epidemics were correlated with the length of the silent phase (Figures 5.2.1.2 & 5.2.1.3). Actual dissemination rates based on simulated infection dates could be as high as 7 for the first few weeks, but then tended to decline (Figure 5.2.1.4). However, weekly estimated dissemination rates (EDR) based on diagnosis dates could present a far more serious picture (Figure 5.2.1.5), with an extreme outlier at 41 for one of the iterations!

Targets for efficiency and effectiveness were evaluated by varying some of the parameters in the base version of the NZSFM. Targets that could be addressed during this study included the time taken to visit and revisit all farms within each PZ surrounding each diagnosed IP, time taken to depopulate detected farms (specified in terms of resource inputs), impacts of duration of national movement standstills and size of the CA.

Patrol veterinarians should be required to visit all farms within each new PZ within 1-2 days, with revisit times no longer than every second day. If visit and revisit times are allowed to extend to 3 days, the likelihood of an uncontrolled epidemic is increased (Tables 5.2.1.1 & 5.2.1.2).

Time from diagnosis to slaughter of IPs should be as short as possible, as infectious animals excrete huge quantities of FMD virus through all excretions and secretions, and the risk of local spread is high whilst these animals remain alive unless biosecurity on IPs can be guaranteed.

Surprisingly, duration of National Standstills and size of CA did not have a huge impact on epidemic size and duration unless there were movements that spread infection from inside the CA to the outside, or there were undetected infected farms outside the CA, in which case there was an increased risk of a “run-away” epidemic (see Table 5.2.1.4 and Figure 5.2.2.12).

Applying the revised minimal, standard and maximal models to the national farm datasets, and using expected passive surveillance/self-reporting rates only produced small to moderate sized epidemics. It was only when initial diagnosis was significantly delayed, or coupled with doubled saleyard splitting rates, that large epidemics approaching the UK2001 size were produced. All these large epidemics involved extensive spread outside of the CA. This reinforces the need for on-going extension programmes to the livestock industries and diligence by farmers and their veterinarians, in order to ensure that any incursion of FMD is quickly identified and dealt with.

A number of other points concerning FMD eradication were reinforced by the modelling work. These include the importance of movement controls. A reduction in movement controls (or increased non-compliance rates by farmers) increased the risk of uncontrolled epidemics (data not shown). Another finding was that official trace-back and surveillance activities would not be able to keep up with the disease in the absence of farmer self-reporting. Farmer and private veterinary practitioner vigilance provide an important “back-stop” to the official disease investigations, especially where crucial movements are not reported by farmers or unable to be traced.

## 7. References

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## 8. Appendices

### 8.1. APPENDIX 1 – THE PACKAGE ‘INCURSION’

September 27, 2007

**Version:** 0.1-3

**Date:** 2007-9-27

**Title:** Functions for the analysis of infectious disease outbreaks in animal populations

**Authors:**

- Mark Stevenson [M.Stevenson@massey.ac.nz](mailto:M.Stevenson@massey.ac.nz) and
- Robert Sanson [sansonr@agriquality.com](mailto:sansonr@agriquality.com)

**Description:** A collection of functions to assist in the analysis of infectious disease outbreaks in animal populations.

**Maintainer:** Mark Stevenson [M.Stevenson@massey.ac.nz](mailto:M.Stevenson@massey.ac.nz)

**Depends:** R ( $\geq$  2.0.0), survival

**License:** GPL version 2 or later

**URL:** <http://epicentre.massey.ac.nz>

**R Topics Documented:**

- `inc.about` The library incursion: summary information
- `inc.edr` Compute estimated dissemination ratio
- `inc.fdi` First day incidence
- `inc.ffi` First fortnight incidence
- `inc.genint` Estimated generation intervals
- `inc.incubation` Estimated infection dates and incubation periods
- `inc.local` Local spread probabilities
- `inc.nzmap` Map of New Zealand
- `inc.outbreak` Data from a hypothetical outbreak of foot-and-mouth disease
- `inc.ripratio` At-risk infected place ratio
- `inc.selfsurv` Ratio of public reported diagnoses to surveillance activity diagnoses

## inc.about The library incursion: summary information

### **Description**

Functions for the analysis of infectious disease outbreaks in animal populations.

### **Usage**

inc.about()

### **Details**

The most recent version of the library can be obtained from: <http://epicentre.massey.ac.nz/>

### **Value**

### **Note**

### **Author(s)**

- Mark Stevenson, EpiCentre, IVABS, Massey University, Palmerston North New Zealand.
- Robert Sanson, AgriQuality New Zealand, PO Box 1654, Palmerston North New Zealand.

### **References**

### **See Also**

### **Examples**

## inc.edr      Compute estimated dissemination ratio

### Description

Computes the estimated dissemination ratio (EDR) on the basis of a vector of numbers (usually counts of incident cases identified on each day of an epidemic).

### Usage

```
inc.edr(dat, n = 4, na.zero = TRUE, alpha = 0.05)
```

### Arguments

dat	a numeric vector representing the count of incident cases for each day of an epidemic.
n	scalar, defining the number of days to be used when computing the estimated dissemination ratio.
na.zero	logical, replace NaN or Inf values with zeros?
alpha	scalar, defining the magnitude of the confidence intervals to be computed.

### Details

In infectious disease epidemics the n-day EDR at day i equals the total number of incident cases between day i and day [i -(n -1)] (inclusive) divided by the total number of incident cases between day (i -n) and day (i -2n) + 1 (inclusive). EDR values are often calculated for each day of an epidemic and presented as a time series analysis. If the EDR is consistently less than unity, the epidemic is said to be “under control”.

### Value

Returns the point estimate of the EDR and the lower and upper bounds of the confidence interval of the EDR.

### Note

### Author(s)

### References

### See Also Examples

```
data(inc.outbreak)
dat <-inc.outbreak$ips

# Counts of infected premises:dat$sgndate <-as.Date(dat$sgndate, format = "%Y-
%m-%d")range(dat$sgndate)dat$days <-as.numeric(dat$sgndate -min(dat$sgndate))

rval <-hist(dat$days, breaks = seq(from = 0, to = 40, by = 1), plot = FALSE)rval
<-rval$counts

## The vector rval represents the total number of infected premises showing##
clinical signs on a given day. Four-day EDR:edr.04 <-inc.edr(rval, n = 4,
na.zero = TRUE, alpha = 0.05)

# Plot:plot(1:40, edr.04[,1], xlim = c(0,25), ylim = c(0, 10), xlab = "Days",
ylab = "Estimated dissemination ratio", type = "l", lwd = 2, col =
"blue")lines(1:40, edr.04[,2], type = "l", lwd = 1, lty = 2)lines(1:40,
edr.04[,3], type = "l", lwd = 1, lty = 2)
```

## inc.fdi First day incidence

### Description

Returns a data frame of the within-place frequency of disease, expressed as first day incidence.

### Usage

```
inc.fdi(ips, use = "species", alpha = 0.05)
```

### Arguments

---

ips	a 21 column data frame listing listing details of infected places. Columns (in order): unique place identifier, place type, infected place number, and: (1) number of animals present, (2) number of animals initially affected, and (3) estimated age of clinical signs at time of examination for pigs, dairy cattle, beef cattle, sheep, deer, and goats (respectively). There should be one row for each infected place.
use	a character string specifying which group to use as the denominator for the incidence risk calculations. Options are species: select the species with the oldest lesions and express first day incidence was the number of that species with signs divided by the total number of that species present on the infected place, all: select the species with the oldest lesions and express first day incidence was the number of that species with signs divided by the total number of susceptible species present on the infected place
alpha	scalar, defining the width of the confidence intervals to be computed.

---

### Details

First day incidence is a term coined by Hutber and Kitching (1996) to denote the number of animals showing clinical signs on the first day of a herd outbreak. It provides an indication of the number of animals initially infected by each particular exposure pathway that introduced infection onto the farm and indicates the infectiousness of the farm in terms of forward risk potential during the period from infection to diagnosis.

Confidence intervals on the incidence risk estimates are calculated using Wilson's approximation (see Rothman 2002, page 132).

The function takes each infected place in turn and chooses the species with the oldest clinical signs at the time of examination. First day incidence equals the number of that species with signs divided by the total number of that species present on the infected place. Where there are two or more animal species with the oldest clinical signs the function chooses one of them at random.

### Value

A data frame containing the following:

---

placeid	the unique place identifier (taken directly from the input data frame).
ipnumber	the infected premises number (taken directly from the input data frame).
est	the point estimate of first day incidence risk.
lower	the lower bound of first day incidence risk.
upper	the upper bound of first day incidence risk.

---

### Note

### Author(s)

## References

Hutber AM, Kitching RP (1996). The use of vector transition in modelling of intra-herd foot-and-mouth disease. *Environmental and Ecological Statistics* 3: 245 -255.

Rothman KJ (2002). *Epidemiology An Introduction*. Oxford University Press, London, pp. 130 – 143.

## See Also

## Examples

```
data(inc.outbreak)
ips <-inc.outbreak$ips[,c(1:3,11:28)]

res <-inc.fdi(ips, alpha = 0.05)rank <-rank(res$est)

library(Hmisc)
errbar(x = rank, y = res$est, yplus = res$upper.95, yminus = res$lower.95,

                                             inc.ffi
xlab = "Rank", ylab = "First day incidence",pch = 16, lty= 1,lwd = 1, cap=
0.015)
```

## inc.ffi      First fortnight incidence

### Description

Returns a data frame of first fortnight incidence (risk) for farm premises within a defined area.

### Usage

inc.ffi(ips, par, start, period = 14, alpha = 0.05)

### Arguments

---

ips	an 8 column data frame listing details of infected places. Columns (in order): unique place identifier, place type, infected place number, easting coordinate of the place centroid, northing coordinate of the place centroid, infection date, date of onset of clinical signs, and visit date. There should be one row for each infected place.
par	a 5 column data frame listing: unique place identifier, place type, easting coordinate of the place centroid, northing coordinate of the place centroid, date of slaughter, date cleaning and disinfection completed
start	the start date for the analysis.
period	the length of time (in days) to be analysed.
alpha	scalar, defining the width of the confidence intervals to be computed.

---

### Details

First fortnight incidence is a term coined by Hutber et al. (2006) as a predictor for regional prevalence zonal disease duration. The numerator is the number of infected places where the onset of clinical signs is from start to start + period. If start equals 22 Feb 2001 and period equals 14 days then selected interval is from 22 Feb 2001 to 7 Mar 2001 (inclusive). The denominator is the total number of susceptible places in the area of interest. Although “fortnight” is used as the name for this function it should be noted that incidence risk can be calculated for any time interval following start date.

Confidence intervals on the incidence risk estimates are calculated using Wilson’s approximation (see Rothman 2002, page 132).

### Value

A data frame containing the following:

---

est	the point estimate of incidence risk for the prescribed interval
lower	the lower bound of incidence risk for the prescribed interval
upper	the upper bound of incidence risk for the prescribed interval

---

### Note

### Author(s)

### References

Hutber AM, Kitching RP, Pilipcinec E (2006). Predictions for the timing and use of culling or vaccination during a foot-and-mouth disease epidemic. *Research in Veterinary Science* 81: 31-36.

Rothman KJ (2002). *Epidemiology An Introduction*. Oxford University Press, London, pp. 130 – 143.

## See Also

## Examples

```
data(inc.outbreak) ips <- inc.outbreak$ips[,c(1:5,8:10)] par <-  
inc.outbreak$par[,c(1:5)]
```

```
## Incidence risk for the 14 days following 10 Mar 2001:
```

```
res <- inc.ffi(ips = ips, par = par, start = as.Date("2001-03-10", format = "%Y-  
%m-%d"), period = 14, alpha = 0.05)  
round(res * 100, digits = 2)
```

```
## The incidence risk of disease for the 14 days following 10 Mar 2001 was## 29  
cases (95% CI 23 to 36) cases per 100 places at risk.
```

## inc.genint Estimated generation intervals

### Description

This function returns the generation interval, the number of days from the onset of clinical signs on a source place to the onset of clinical signs on one or more identified destination place(s).

### Usage

```
inc.genint(tra, use = "all")
```

### Arguments

---

tra	a 7 column data frame listing details of tracing events. Columns (in order): source place unique identifier, date of onset of signs on the source place, destination place unique identifier, date of onset of signs on the destination place, episode start date (the date that contact between the two places commenced), and episode end date (the date that contact between the two places ceased).
use	a character string, indicating the method to be used. Options are all: calculate all generation interval, or first calculate the first generation interval for each source place (if there are more than one). Option first should be used if you want to calculate the earliest generation interval.

---

### Details

This function uses the unique numeric identifiers for places (as opposed to infected place number). It is assumed that the input data for this function is a complete record of contact events between infected places. That is, both source and destination places are both infected (and therefore have an onset of clinical signs date). Generation intervals that are negative (i.e. cases where the onset of clinical signs date on the destination place occurs before the onset of clinical signs on the source place) are ignored.

### Value

A data frame containing the following:

---

src	the source place identifier (taken directly from the input data frame).
des	the destination place identifier (taken directly from the input data frame).
gen	the generation interval.

---

### Note

#### Author(s)

#### References

#### See Also

### Examples

```
data(inc.outbreak)
tra <- inc.outbreak$tra

gen01 <- inc.genint(tra, use = "first")
hist(gen01$gen)
summary(gen01$gen)

## When all generation intervals are included, there may be some##
outliers:gen02 <- inc.genint(tra, use = "all")
hist(gen02$gen)
summary(gen02$gen)
```

## inc.incubation      Estimated infection dates and incubation periods

### Description

Returns a data frame of infection dates and incubation periods. Where data is missing or unavailable an incubation period is estimated by drawing a random number from a log normal distribution (the parameters of which may be specified by the user).

### Usage

```
inc.incubation(ips, meanlog = log(7), sdlog = log(1.5))
```

### Arguments

---

ips	a 12 column data frame listing details of infected places. Columns (in order): unique place identifier, place type, infected place number, infection date, date of onset of clinical signs, visit date, estimated age of clinical signs at time of examination for pigs, dairy cattle, beef cattle, sheep, deer, and goats. There should be one row for each infected premises.
meanlog	mean of the log normal distribution on the log scale.
sdlog	standard deviation of the log normal distribution on the log scale.

---

### Details

In the input data frame the variables defining infection date and date of onset of signs are recorded at the place level. These values are used in preference to the species age of signs variables for the incubation period calculations.

The arguments meanlog and sdlog are used to define a log normal distribution which is used to estimate incubation period.

If (infection date present, signs date present, species age of signs absent) a random number is drawn from the log normal distribution to estimate incubation period.

If (infection date absent, signs date present, species age of signs absent) a random number is drawn from the log normal distribution to estimate incubation period. Infection date is estimated as signs date minus the estimated incubation period.

If (infection date absent, signs date absent, species age of signs present) a random number is drawn from the log normal distribution to estimate incubation period. Infection date is estimated as visit date minus the largest value of age of signs (across all species) minus the estimated incubation period.

If (infection date present, signs date present, species age of signs absent) incubation period equals signs date minus infection date.

If (infection date absent, signs date present, species age of signs present) a random number is drawn from the log normal distribution to estimate incubation period. Infection date is estimated as signs date minus the estimated incubation period.

If (infection date present, signs date present, species age of signs present) incubation period equals signs date minus infection date.

## Value

A data frame containing the following:

---

ip	the infected place number (taken directly from the input data frame).
inf.date	actual or estimated infection date
inf.est	indicator for status of infection date: 0 = actual, 1 = estimated
inc	actual or estimated incubation period
inc.est	indicator for status of incubation period: 0 = actual, 1 = estimated

---

## Note

Incubation period refers to the period from infection to the development of symptomatic disease. Latent period refers to the period between disease initiation and development of symptomatic disease. The term incubation period is equivalent to latent period: incubation period is the term specifically used for infectious diseases.

The antilog of one standard deviation from the mean log incubation period has been called the dispersion factor (Sartwell 1950). The dispersion factor multiplied by the mean log of the incubation period will define an interval above which 16 percent of the intervals will fall, and the mean divided by the dispersion factor will define the period below which 16 percent will occur.

## Author(s)

## References

Sartwell PE (1950). The distribution of incubation of disease. American Journal of Epidemiology 51: 310 -318.

## See Also

## Examples

```
data(inc.outbreak)
ips <-inc.outbreak$ips[,c(1:3,8:10,13,16,19,22,25,28)]

fmd.inc <-inc.incubation(ips, meanlog = log(7), sdlog = log(1.5))

## Frequency histogram of incubation periods:hist(fmd.inc$inc, xlab =
"Incubation period (days)", main = "")

## Compare the distribution of actual incubation periods with those that## have
been estimated:par(pty = "s", mfrow = c(1,2))hist(fmd.inc$inc[fmd.inc$inc.est ==
0], breaks = seq(from = 0, to = 50, by = 1),
  xlim = c(0, 30), ylim = c(0,50), xlab = "Days", main =
  "Actual")hist(fmd.inc$inc[fmd.inc$inc.est == 1], breaks = seq(from = 0,
to = 50, by = 1),xlim = c(0, 30), ylim = c(0,50), xlab = "Days", main =
  "Estimated")

## Alternative method, using a stacked bar graph:obs <-
hist(fmd.inc$inc[fmd.inc$inc.est == 0],
  breaks = seq(from = 0, to = 50, by = 2), plot =
  FALSE)est <-hist(fmd.inc$inc[fmd.inc$inc.est == 1],breaks
= seq(from = 0, to = 50, by = 2), plot = FALSE)

rval <-matrix(rbind(obs$counts, est$counts), nrow = 2)colnames(rval) <-
obs$midrownames(rval) <-c("Observed", "Estimated")

barplot(rval, ylim = c(0, 100),xlab = "Incubation period (days)", ylab =
```

```

    "Frequency", col = c("red", "dark blue"), border = "gray")
legend("topright", legend = c("Observed", "Estimated"), fill = c("red", "dark
blue"), c("gray", "gray"), bty = "n")

## Epidemic curve computed using the augmented data:fmd.inc <-
inc.incubation(ips, meanlog = log(7), sdlog = log(1.5))inf.date <-
fmd.inc$inf.date
date.bins <- seq(from = as.Date("2001-02-01", format = "%Y-
%m-%d"),
    to = as.Date("2001-03-31", format = "%Y-%m-%d"), by = "1 day")
hist(inf.date,
breaks = date.bins, freq = TRUE)

```

## inc.local      Local spread probabilities

### Description

This function returns data that can be used to estimate the probability of local spread as a function of time and distance from an infected source.

### Usage

```
inf.local(ips, par, src.des, neighbours, relative.to = "signs", offset = -3)
```

### Arguments

---

ips	a 7 column data frame listing details of infected places. Columns (in order): unique place identifier, place type, infected place number, easting coordinate of place centroid, northing coordinate of place centroid, infection date, onset of clinical signs date. There should be one row for each infected place.
par	a 6 column data frame listing details of the place population at risk. Columns (in order): unique place identifier, place type, easting coordinate of the place centroid, northing coordinate of the place centroid, date of slaughter, date cleaning and disinfection completed.
src.des	a 5 column data frame listing details where transmission of infection has occurred from a source place to a destination place by local spread. Columns (in order): unique identifier of source place, date of onset of signs on the source place, unique identifier of destination place, cause identifier, date of onset of signs on the destination place. See details for further information.
neighbours	a list of neighbours within a defined distance band of each place listed in par.
relative.to	a character string, indicating when infectivity starts on the source place. Options are signs: infectivity starts from the date of onset of clinical signs, infection: infectivity starts from the date of infection.
offset	scalar, indicating the offset to be used for defining the risk period for each place acting as an infected source. See details for further information.

---

### Details

In the src.des data frame there is a one to many relationship between source and destination places. An infected source can have many destinations. A destination can receive infection from only one source.

Use the dnearneigh function in the spdep package to generate data for the neighbours list. Setting relative.to to signs and offset to -3 sets the start of the risk period at three days before the date of onset of clinical signs on the source place. Infectivity of a source place ends on the date that animals on the source place were slaughtered.

### Value

A data frame containing the following:

---

time	the number of time periods from the date of onset of infectivity of the source place.
n.risk	the number of places at risk of infection
n.event	the number of places infected

---

### Note

### Author(s)

## References

Sanson R, Stevenson M, Moles-Benfell N (2006). Quantifying local spread probabilities for foot-and-mouth disease. In: Proceedings of the 11th International Symposium on Veterinary Epidemiology and Economics. Cairns Convention Centre, Cairns, Australia.

## See Also

inc.incubation

## Examples

```
data(inc.outbreak) ips <-inc.outbreak$ips[,c(1:5,8,9)]par <-
inc.outbreak$parsrc.des <-inc.outbreak$stran0001 <-inc.outbreak$n0001

## Estimate missing infection dates:

tmp <-inc.incubation(inc.outbreak$ips[,c(1:3,8:10,13,16,19,22,25,28)],meanlog
  = log(7), sdlog = log(1.5))
ips$infdate <-tmp$inf.date

inf.local(ips = ips, par = par, src.des = src.des, neighbours =
  n0001,relative.to = "signs", offset = -3)
```

## inc.nzmap Map of New Zealand

### Description

Map of New Zealand regions and coastal boundary. Two projections are provided: NZMG (based on the New Zealand geodetic datum 1949) and NZTM (based on the New Zealand geodetic datum 2000).

### Usage

```
data(inc.nzmap)
```

### Format

A list with the following objects: `coast.nzmg`, `region.nzmg`, `coast.nztm`, and `region.nztm`. Each object has the following variables:

**xcoord** the easting coordinate of the vertices that comprise each polygonal area.

**ycoord** the northing coordinate of the vertices that comprise each polygonal area.

### Details

NZMG is based on the New Zealand geodetic datum 1949 which uses the 1924 international ellipsoid. NZTM is based on the New Zealand geodetic datum 2000 which uses the GRS80 ellipsoid (as used by WGS84). NZTM is the current standard for defining point locations by Biosecurity New Zealand.

### Source

### References

### Examples

```
## Plot of New Zealand and infected place locations (NZTM):data(inc.nzmap)region
<-inc.nzmap$region.nztmcoast <-inc.nzmap$coast.nztmxlim <-
range(inc.nzmap$coast.nztm[,1], na.rm = TRUE)ylim <-
range(inc.nzmap$coast.nztm[,2], na.rm = TRUE)ratio <-(ylim[2] -ylim[1])/(xlim[2]
-xlim[1])

data(inc.outbreak)
ips <-inc.outbreak$ips[,1:5]

x.lab <-seq(from = 1000000/1000, to = 2000000/1000, by = 2e05/1000)x.points <-
seq(from = 1000000, to = 2000000, by = 2e05)y.lab <-seq(from = 4000000/1000, to
= 7000000/1000, by = 2e05/1000)y.points <-seq(from = 4000000, to = 7000000, by =
2e05)

par(pin = c(3.5, ratio * 3.5), omi = c(0,0,0,0))

plot(x = xlim, y = ylim, xlab = "Easting (km)", type = "n",ylab = "Northing
(km)", xaxt = "n", yaxt = "n", xlim = xlim,ylim = ylim, cex.lab = 1.00)
points(inc.nzmap$region.nztm, lwd = 1, col = "gray", type =
"l")points(inc.nzmap$coast.nztm, lwd = 1, col = "black", type =
"l")points(ips$x, ips$y, type = "p", pch = 16, col = "red")axis(side = 1, at =
x.points, labels = x.lab, tick = TRUE, cex.axis = 0.80)axis(side = 2, at =
y.points, labels = y.lab, tick = TRUE, cex.axis = 0.80)

## Detail of infected place locations (NZTM):

plot(x = xlim, y = ylim, xlab = "Easting (m)", type = "n",ylab = "Northing (m)",
xlim = c(1700000, 1900000),ylim = c(5800000, 6000000), cex.lab = 1.00)
```

```

points(inc.nzmap$region.nztm, lwd = 1, col = "gray", type =
"l")points(inc.nzmap$coast.nztm, lwd = 1, col = "black", type =
"l")points(ips$x, ips$y, type = "p", pch = 16, col = "red")

## Plot of New Zealand (NZMG):data(inc.nzmap)region <-inc.nzmap$region.nzmgcoast
<-inc.nzmap$coast.nzmgxlim <-range(inc.nzmap$coast.nzmg[,1], na.rm = TRUE)ylim
<-range(inc.nzmap$coast.nzmg[,2], na.rm = TRUE)ratio <-(ylim[2] -
ylim[1])/(xlim[2] -xlim[1])

x.lab <-seq(from = 2000000/1000, to = 3000000/1000, by = 1e05/1000)x.points <-
seq(from = 2000000, to = 3000000, by = 1e05)y.lab <-seq(from = 5500000/1000, to
= 7500000/1000, by = 1e05/1000)y.points <-seq(from = 5500000, to = 7500000, by =
1e05)

par(pin = c(3.5, ratio * 3.5), omi = c(0,0,0,0))

plot(x = xlim, y = ylim, xlab = "Easting (km)", type = "n",ylab = "Northing
(km)", xaxt = "n", yaxt = "n", xlim = xlim,ylim = ylim, cex.lab = 1.00)
points(inc.nzmap$region.nzmg, lwd = 1, col = "gray", type =
"l")points(inc.nzmap$coast.nzmg, lwd = 1, col = "black", type = "l")axis(side =
1, at = x.points, labels = x.lab, tick = TRUE, cex.axis = 0.80)axis(side = 2, at
= y.points, labels = y.lab, tick = TRUE, cex.axis = 0.80)

```

**Description**

Data from a hypothetical outbreak of foot-and-mouth disease in New Zealand.

**Usage**

`data(inc.outbreak)`

**Format**

A list comprised of objects *ips*, *par*, *tra*, and *n0001*. These data provide details of 122 farms infected with foot-and-mouth from a population of 28291 farms.

Object *ips* provides summary information for the 122 infected places. Variables are `placeid`: unique place identifier, `placetype`: place type, `ipnumber`: infected place number, `x`: easting coordinate of the place centroid, `y`: northing coordinate of the place centroid, `pubrept`: identifies whether or not the infected place was reported by a member of the public (1 = public report, 0 = other), `cause`: estimated cause of infection, `infdate`: date of infection, `sgndate`: date of onset of clinical signs, and `visdate`: visit date. The next 18 variables provide the following details for pigs, dairy cattle, beef cattle, sheep, deer, and goats present on each infected place: the number of animals present (e.g. `nopig`), the number of animals initially infected (e.g. `inipig`), and the estimated age of lesions at time of examination (e.g. `agepig`).

Object *par* provides details of the premises at risk. Variables are `placeid`: unique place identifier, `placetype`: place type, `x`: easting coordinate of the place centroid, `y`: northing coordinate of the place centroid, `slgtdate` date of slaughter, `disdate` date cleaning and disinfection completed.

Object *tra* provides details of tracing events. Variables are `srplaceid` unique place identifier of the source, `srcsgndate` date of onset of clinical signs on the source place, `desplaceid` unique place identifier of the destination, `causeid` cause identifier, `dessgndate` date of onset of clinical signs on the destination place, `startdate` date event started, and `enddate` date event ended.

Object *n0001* lists places that lie within 0 -1000 metres of each of the 28291 farms included in *par*. This object was produced using the `dnearneigh` in the `spdep` package.

**Details**

Dates are in `Date` format. Easting and northing coordinates are in NZTM format.

**Source****References****See Also**

`inc.incubation`, `inc.incubation`, `inc.incubation`, `inc.incubation`

**Examples**

```
data(inc.outbreak)
dat <-inc.outbreak$ips[,1:9]

## Breakdown of infection explanations for identified infected
places:round(table(dat$cause)/sum(table(dat$cause)), digits = 2)

## Local spread accounted for 74% of all infections.
```

**Description**

Ratio of the number of places exposed to movements off identified infected places to the number of identified infected places for a given time frame.

**Usage**

```
inc.ripratio(ips, tra, start, period = 14, alpha = 0.05)
```

**Arguments**


---

ips	a 4 column data frame listing details of infected places. Columns (in order): unique place identifier, place type, infected place number, and onset of clinical signs date. There should be one row for each infected place.
tra	a 7 column data frame listing details of tracing events. Columns (in order): source place unique identifier, date of onset of signs on the source place, destination place unique identifier, date of onset of signs on the destination place, episode start date (the date that contact between the two places commenced), and episode end date (the date that contact between the two places ceased).
start	the start date for the analysis.
period	the length of time (in days) to be analysed.
alpha	scalar, defining the magnitude of the confidence intervals to be computed.

---

**Details**

When an epidemic commences there are no controls in place and the disease has the potential to spread extensively by the time the index premises is identified. The number of premises with direct or indirect contact with the index premise(s) will have direct bearing on the number of newly infected premises and hence the estimated dissemination ratio.

In this function the numerator is the total number of premises exposed to direct or indirect movements off these identified infected premises. The denominator is the total number of infected premises identified in the specified time frame. If start equals 22 Feb 2001 and period equals 14 days then the time frame is from 22 Feb 2001 to 7 Mar 2001 (inclusive).

Confidence intervals are calculated using the method of Dobson et al. (1991).

**Value**

Returns the point estimate and confidence interval of the at-risk infected place ratio.

**Note****Author(s)****References**

Dobson AJ, Kuulasmaa K, Eberle E, Scherer J (1991). Confidence intervals for weighted sums of Poisson parameters. *Statistics in Medicine* 10: 457 -462.

**See Also****Examples**

```
data(inc.outbreak) ips <-inc.outbreak$ips[,c(1:3,9)] tra <-inc.outbreak$tra

start <-as.Date("2001-02-22", format = "%Y-%m-%d") inc.ripratio(ips, tra, start,
period = 14, alpha = 0.05)

## The at-risk infected place ratio for the period 22 February 2001 to## 7
March 2001 (inclusive) was 0.16 (95% CI 0.09 --0.27).
```

## inc.selfsurv Ratio of public reported diagnoses to surveillance activity diagnoses

### Description

Ratio of public reported diagnoses to surveillance activity diagnoses for a given time frame.

### Usage

```
inc.selfsurv(ips, start, period = 14, alpha = 0.05)
```

### Arguments

---

ips	a 5 column data frame listing details of infected places. Columns (in order): unique place identifier, place type, infected place number, public report flag (0 or 1), onset of clinical signs date. There should be one row for each infected place.
start	the start date for the analysis.
period	the length of time (in days) to be analysed.
alpha	scalar, defining the magnitude of the confidence intervals to be computed.

---

### Details

In a well managed outbreak most infected places will be identified by surveillance activities conducted by the state veterinary service. The ratio of infected places brought to the attention of authorities by members of the public (i.e. 'surprise' infections) to those known to be at risk provides a measure of the effectiveness of epidemic control and eradication measures. Ideally, this ratio should be close to zero at all times.

If start equals 22 Feb 2001 and period equals 14 days then the time frame is from 22 Feb 2001 to 7 Mar 2001 (inclusive).

Confidence intervals are calculated using the method of Dobson et al. (1991).

### Value

Returns the point estimate and confidence interval of ratio of public reported diagnoses to surveillance activity diagnoses.

### Note

### Author(s)

### References

Dobson AJ, Kuulasmaa K, Eberle E, Scherer J (1991). Confidence intervals for weighted sums of Poisson parameters. *Statistics in Medicine* 10: 457 -462.

### See Also

### Examples

```
data(inc.outbreak)
ips <-inc.outbreak$ips[,c(1:3,6,9)]

start <-as.Date("2001-02-22", format = "%Y-%m-%d")inc.selfsurv(ips, start,
period = 14, alpha = 0.05)

## For the period 22 February 2001 to 7 March 2001 (inclusive) the ratio of##
public reported diagnoses to surveillance activity diagnoses was 0.14## (95% CI
0.07 --0.24).
```

## 8.2. APPENDIX 2 – IMPROVEMENTS RECOMMENDED FOR INTERSPREAD PLUS

1. At the moment there are inconsistencies in the way control sections are started and stopped during a simulation. Facilities to start and stop controls should be consistent across all sections of the program.
  - By time period relative to key events in the simulation e.g. start of simulation, first detection.
  - By individual farm state and with the ability to specify a certain number of time periods as an offset to state (positive or negative).
  - By zone, farm state, farm class, animal type.
  - When a certain number of premises have reached a pre-defined threshold state e.g. when 50 farms detected.
  - All controls should be able to be specified as applying to subsets of farms by zone (within or outside of specified zones), farm class, farm state, and animal type. Combinations of selection criteria should be allowed (using AND/OR/NOT etc).
2. Combining all parameters required for the following movement types into single controls:
  - Saleyards/Markets
  - Route
  - FixedRoute
3. Creating a new spread mechanism representing shows/rodeos/other animal congregation events where animals attend the site from their home farms and then return. The site could be a new type of site represented in the same way as markets are (i.e. A file of coordinates), or could be other farms of a certain class. A certain frequency of event would be specified, such that animals from a variable number of farms (sampled from a distribution) would attend on the same day. Suggested parameters include:

Parameter	Description	Possible values
EventName	Unique name of event	
TimePeriodStartReference		Simulation_start/First_d etection
TimePeriodStart		
TimePeriodStopReference		Simulation_start/First_d etection
TimePeriodStop		
SourceFarm[Zone][FarmClass][FarmState][AnimalType]		
DestinationType	Type of destination	Event/Farm
Events	Path to file of Event locations (similar to markets) where 'Event' selected in DestinationType	
DestinationFarm[Zone][FarmClass][FarmState][AnimalType]	Type of farm where event held when 'Farm' selected in DestinationType	
FrequencyOfEvent	Distribution describing the frequency of Events in terms of "an event every so many time periods"	
SizeOfEvent	Distribution describing typical number of farms that attend	
CatchmentSize	Maximum distance (m) that participating farms will travel to attend	
LengthOfEvent	Distribution describing number of time periods that each Event lasts	E.g. Triangular 1 2 3
MixingRate	Distribution representing contact rate per day in terms of number of other farms that are likely to	E.g. BetaPert 4 7 9

ProbabilityOfTransmission	be exposed per day by each infected farm Probability of transmission for each contact
DelayToInfection	A probability distribution indicating the number of days between the contact and when the destination will be determined to be infected. This allows a delay to be introduced for the movement of incubating animals. This item is optional, if not specified 0 days is assumed and the destination farm is immediately infected.

4. Creating a new spread mechanism representing Social Network Spread, whereby infection spreads to other farms on a “social network” that are close in terms of connectedness rather than geographical distance per se.

One way to define the network membership which would work for the situation where there were several mutually distinct networks, and each premises belonged to only one network, would be to add two columns to the farm file – one column would hold the unique name of the particular network that the farm belonged to, and the second column would indicate direction of links, with -1 = sender only, 0 = sender and receiver, 1 = receiver only.

This type of network could have been used to represent the spread of Varroa bee mite amongst apiaries belonging to the same apiarist.

Multiple Social Network sections could be defined for different types of networks.

Parameters required would be:

Parameter	Description	Possible values
SocialNetworkName	Unique name for each Network modelled	
TimePeriodStartReference		Simulation_start/First_detection
TimePeriodStart		
TimePeriodStopReference		Simulation_start/First_detection
TimePeriodStop		
NetworkFarmColumn	Defines the column in the farm file that holds the categorical identifier that places each farm into a particular network	
DirectionFarmColumn	Ddefines the column in the farm file that indicates direction	-1 = sender only 0 = sender & receiver 1 = receiver only
POTOffsetRelativeTo	Specifies which state Probability of Transmission is relative to	Infection/ClinicalSigns
ProportionOfSetMembers	A value between 0 and 1; randomly selects a proportion of the farms belonging to the particular Social Network set to be at-risk of being infected; default = 1)	
ProbabilityOfTransmission	Would allow a function to be defined, including tables, that allow the probability of transmission be modelled by time period relative to POTOffsetRelativeTo	

5. A new type of route representing conveyors such as transport vehicles where the conveyor remains a conveyor for longer than one time period. This would have been useful in modelling the spread of invasive sea squirt (*Styela clava*) representing ships with fouled hulls. What we need to be able to do is specify “states” for the conveyor itself, e.g. latent period – distribution of time periods before the conveyor becomes capable of transmission; infectious period – distribution of time periods indicating how

long the conveyor is infectious for. We also need to specify the number of premises visited per time period, and the distance within which the conveyor operates. Potential parameters include:

Parameter	Description	Possible values
ConveyorName	Unique name for each conveyor type modelled	
TimePeriodStartReference		Simulation_start/First_detection
TimePeriodStart		
TimePeriodStopReference		Simulation_start/First_detection
TimePeriodStop		
SourceFarm[Zone][FarmClass][FarmState][AnimalType]	Type of farm(s) that the conveyor gets "infected" from	
LatentPeriod	Distribution of time periods before the conveyor becomes capable of transmission	Default = 0
InfectiousPeriod	Distribution of time periods indicating how long the conveyor is infectious for	
DestinationFarm[Zone][FarmClass][FarmState][AnimalType]	Type of farm(s) that gets infected from the conveyor	
MovementDistance	Distribution of distances within which the conveyor moves	
NumberPerTimePeriod	Distribution of number of premises visited by an "infectious" conveyor per time period	
ProbabilityOfTransmission	Would allow a function to be defined, including tables, that allow the probability of transmission be modelled by time period relative to POTOffsetRelativeTo	

6. Randomised order of movements and controls each day, rather than movements always being modelled each day before controls. This would make IS+ much more realistic with respect to simulating the different times in a day when events may occur (movements may happen in the morning and detection in the evening so movements should occur first, but equally detection may occur first thing in the morning depending on when the surveillance team might visit).
7. The ability to add a positive or negative shift to any defined distribution. This would add some extra capability in terms of adapting curve fitting results from @Risk.
8. Spatial indexing to improve spatial search routines, which would allow the model to run faster.
9. Improve the code for representation of resources for depopulation and vaccination. Specifically, when using the FarmListOption = multiple\_list parameter and FarmProcessingOption = time\_period\_by\_farm or time\_period\_by\_animals options, the user should be able to create a defined number of teams (with the ability to specify different numbers at different stages of the epidemic). The system should then simulate resource constraints by consuming these resources at different rates dependent on the total number of farms or animals requiring depopulation or vaccination at any given time. It should also be possible to stipulate a time delay from when each farm is completed before processing of the next begins, to allow for setting-up and cleaning stages, and driving time between farms.

10. Allow markets to operate on specific days, rather than on any day, as at present. The Australian model, AusSpread, models sales from specific sale yards on specific days. Enabling this feature in IS+ is expected to introduce more realistic variability in epidemic sizes, as a consequence of sales occurring or not occurring during the silent phase. In the current configuration, sale yard movements off farms are highly averaged. To achieve this, it will be necessary to permit a frequency of sale (once every n days) to be specified for each market represented in the market file.