Animal & Plant Health Agency

Early decision indicators to predict the severity of an FMD outbreak

A simulation modelling study by the QUADS epiteam

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Outline

- The QUADS epiteam
- Motivation
- Study design / model seeding
- Early decision indicators investigated
- Preliminary linear regression results
- Discussion
- Next steps

The QUADs Epiteam

Members

- Canada, USA, Australia, New Zealand, UK, Sweden
- All have independently developed models for simulating FMD outbreaks
  - Interspread plus (Canada and NZ)
  - North American Animal Disease Spread Model (USA)
  - Australian Animal Disease model (AADIS)
    - Previous QUADs studies have used AusSpread
  - Exodis-FMD (UK)
  - Davis Animal Disease Spread model (DTU-DADS)

Motivation

- Bring together expertise in modelling and epidemiology
- FMD provides a focus for skills
- All countries are disease free without vaccination

Motivation for study

Early decision indicators (EDIs)

- Can epidemiological features early in outbreak predict severity of epidemic outcome
  - Large numbers of infected premises (IPs)
  - Long duration outbreaks lasting months
  - Large areas of the country under disease restrictions
- Early decisions can start vaccination earlier
  - Vaccine matching options
  - Stand-up vaccination resourcing contracts
  - Decisions on vaccination zones
  - Decisions on vaccine deployment strategies
- Modelling study
  - Create large numbers of outbreak iterations (10,000)
  - Cover a range of starting conditions
  - Investigate a number of different EDIs

Study design & model seeding

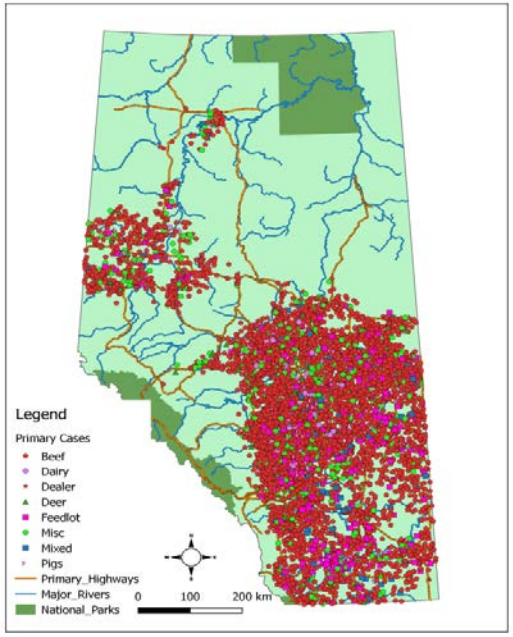
Study design (determined by each country)

- Study area included range of farm density, species and practices
- First detection simulated based on reporting likelihoods for each country
- Control measures based on stamping out policy
  - Dangerous and contiguous culling and vaccination excluded at this stage
- Model iterations continued until eradication or 365 days elapsed

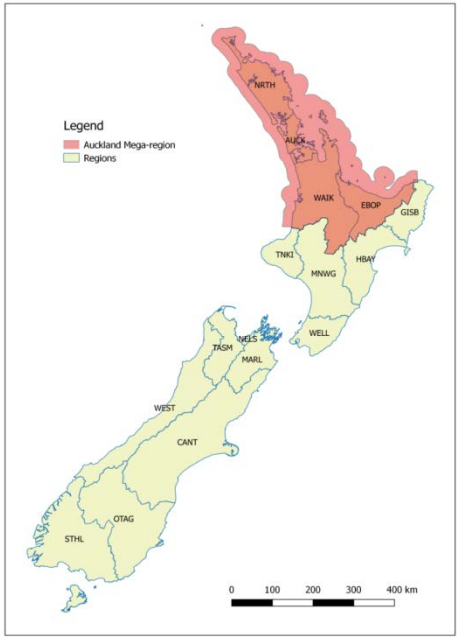
Seeding

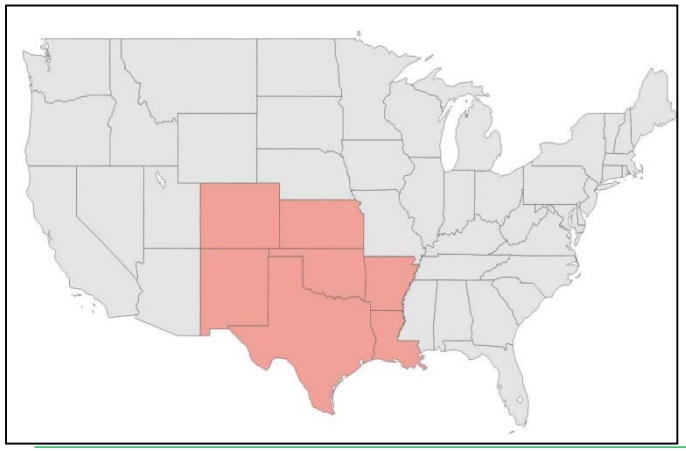
- Iterations seeded infection randomly over the study area
  - Some restrictions applied e.g. minimum number of animals present
- 10,000 iterations with random seeding for each iteration
  - Iterations without detection of infection are excluded

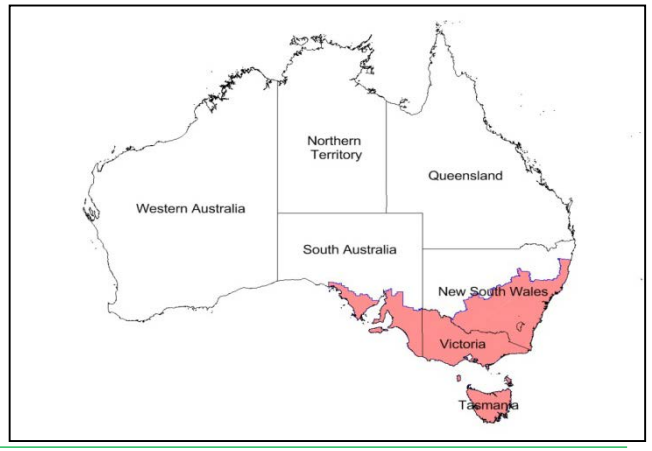
Study design & model seeding



- Canada – Province of Alberta
- New Zealand – Auckland and surrounding regions for seeding
- USA – Texas and surrounding states
- Australia - SE Australia for seeding
- UK – England, Scotland and Wales







Early decision indicators to be investigated

Explanatory variable	Comments
IPs	Cumulative IPs found up to 7, 14 and 21 days
Herd density	Density of herds using a 5 x 5 km cell centred on index farm
Cattle density	Density of cattle using a 5 x 5 km cell centred on index farm
Pig density	Density of pig using a 5 x 5 km cell centred on index farm
Sheep/goat density	Density of sheep/goats using a 5 x 5 km cell centred on index farm
Human population density	Gridded 2015 world population estimate will be used (available online), resolution of 5km^2 centered on index farm

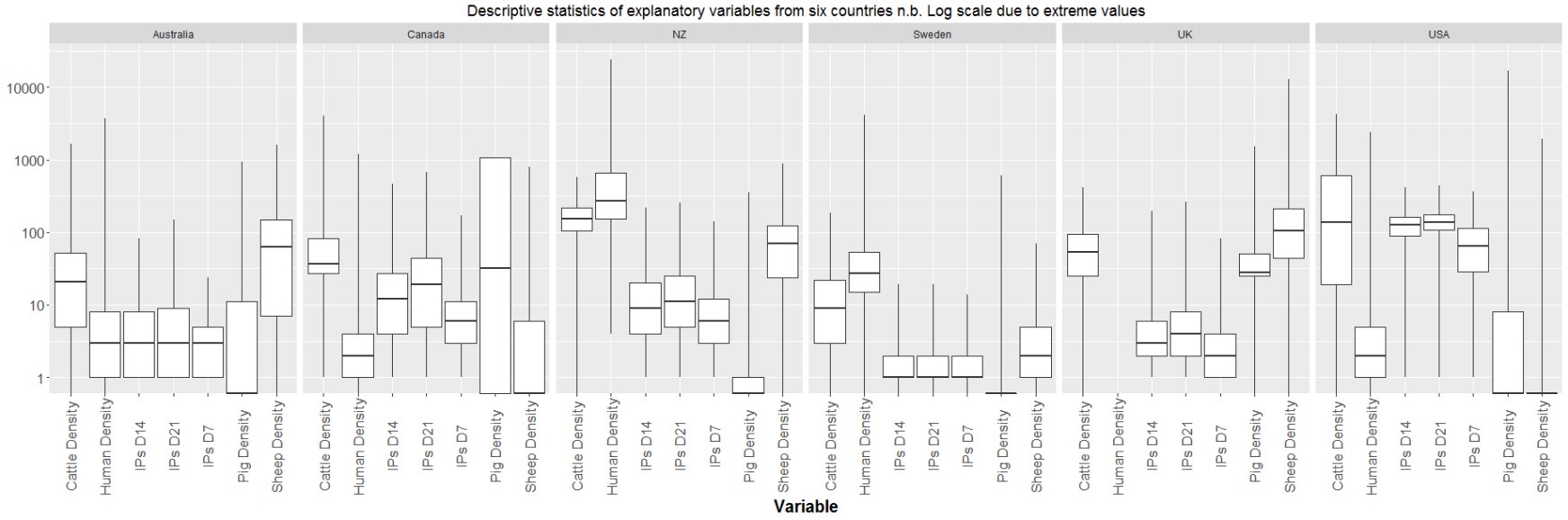
Outbreak metrics

- Total number of Infected Premises (IPs)
- New IPs from a given time point
- Epidemic duration
- Area under control (AUC) – area of the study zone under FMD controls

Descriptive statistics explanatory variables

Country	Australia	Canada	NZ	Sweden	UK	USA
Model	AADIS	ISP	ISP	DTU-DADS	Exodis-FMD	NAADSM
Number of simulations	9113	9879	8784	10000	10000	10000
Value	Median value of number of simulations					
Variable						
IPs day 7	3	6	6	1	2	64
IPs day 14	3	12	9	1	3	125
IPs day 21	3	19	11	1	4	138
Cattle Density (per km²)	21	37	152	9	53	136
Sheep Density (per km²)	62	0	70	2	104	0
Pig Density (per km²)	0	32	0	0	28	0
Human Density (per km²)	3	2	273	27	NA	2

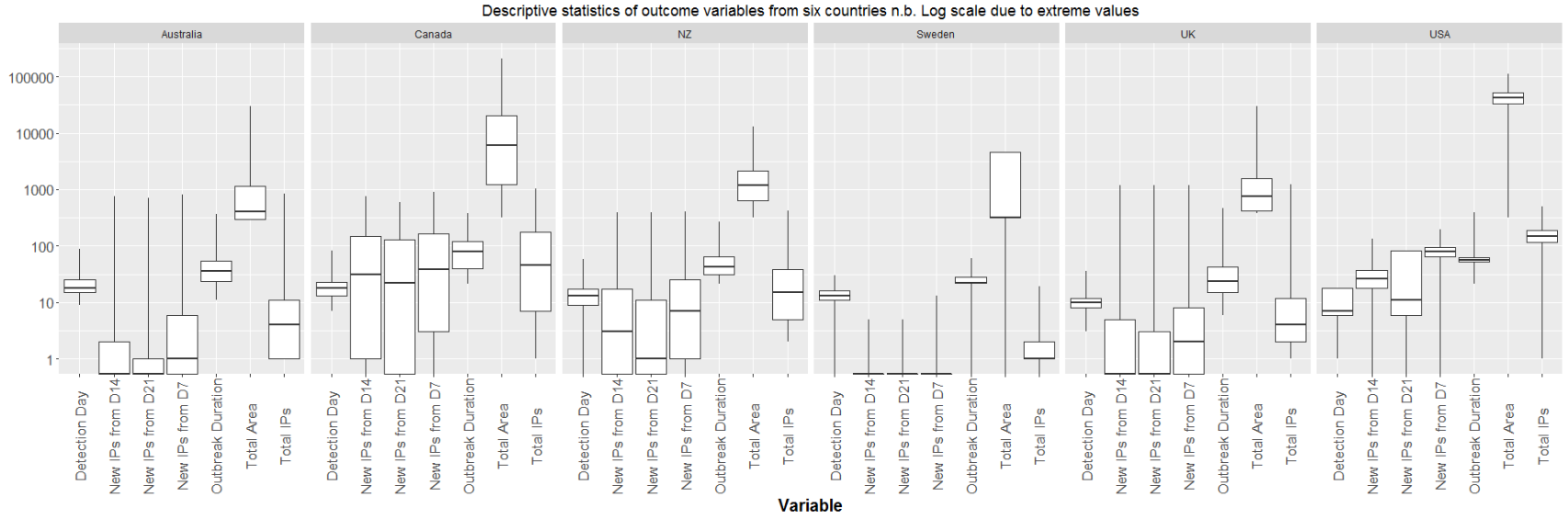
Variables distribution



Descriptive statistics outcome variables

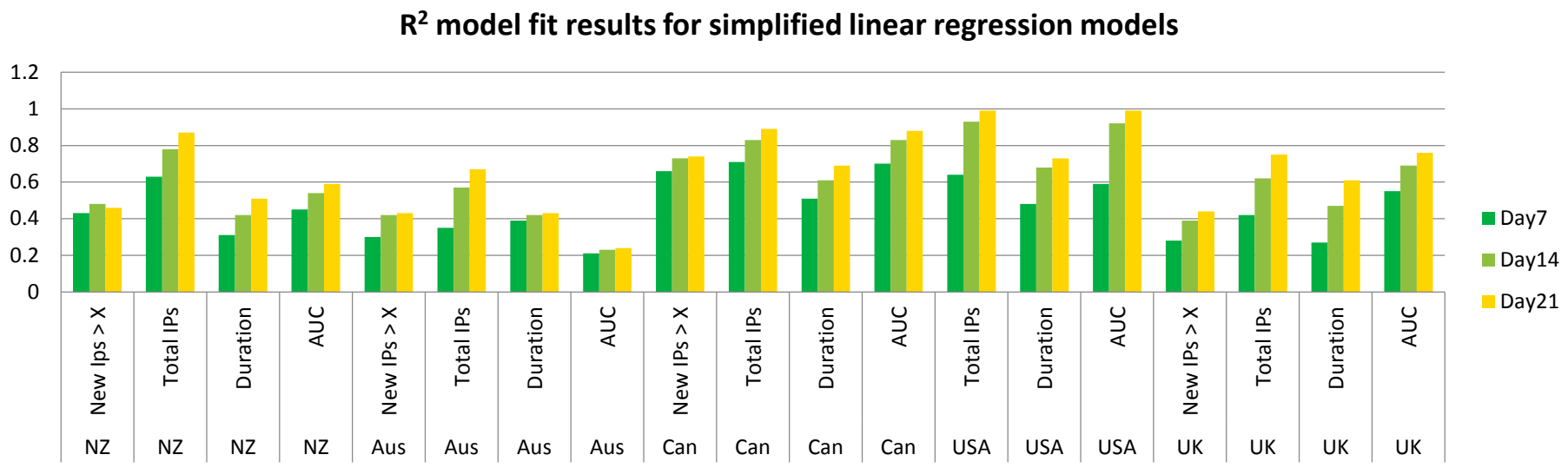
Country	Australia	Canada	NZ	Sweden	UK	USA
Model	AADIS	ISP	ISP	DTU-DADS	Exodis-FMD	NAADSM
Number of simulations	9113	9879	8784	10000	10000	10000
Value	Median value of number of simulations					
Variable						
Detection Day	18	18	13	13	10	7
Total IPs	4	46	15	1	4	148
New IPs after day 7	1	39	7	0	2	80
New IPs after day 14	0	31	3	0	0	26
New IPs after day 21	0	22	1	0	0	11
Outbreak duration (days)	36	79	43	22	24	57
Total area (km²)	409	6020	1176	314	766	41521

Outcome variables distribution



Linear Regression Model Fit

- Outcome variables
  - Duration, Total IPs, AUC, New IPs after day ‘X’ (New IPs > X)
- Simplified linear regression models for each country contained different explanatory variables
  - Most models dropped Human density as an explanatory variable
  - Number of IPs at day ‘X’ retained by all models
- Model fit increases from day 7 to day 21 data



Linear Regression Predictive Results

- Ability for model to predict large or small outbreaks
  - Cut points for large and small outbreaks are arbitrary
  - Definitions of large and small differ between countries
- Individual countries concentrated on the most relevant time point
  - Area under control and total IP outcomes had the most correctly classified iterations
  - Number of IPs up to a given time point had the most predictive power across the countries

Discussion

- Similar studies have focused on early data
  - Halasa et al (2013), Hutber et al (2006)
  - First fortnight spatial spread and first fortnight incidence
- We attempt to investigate other time points
  - Some countries will be able to mount a response before day 14 if required
  - Previous work has highlighted benefits of starting vaccination early
- Some explanatory variables are more useful than others
  - Total number of IPs is very explanatory
  - Relatively easy to access during an outbreak
  - Human density estimates were dropped from all models
  - Calculation of human density may not be ideal
- Incorrect deployment of vaccine has cost implications
  - Extended time under export restrictions
  - Cost of vaccination program
  - Management of vaccinated animals

Next steps

- Other EDIs can be investigated from same model iterations
  - Pending culling, delays to culling from resource constraints
  - Seed farm type, interactions contributing to spread
  - Estimated dissemination rate, frequency of reporting IPs
  - IP density, clustering features of outbreaks
  - Different time points, more frequent intervals
- Original modelling outputs are retained as data library
  - Additional iterations of different control strategies
  - Additional iterations of different FMD virus characteristics

We would like to thank

- Supporting Governments, Departments and Organisations
  - Department for Environment Food and Rural Affairs, Scottish Government and Welsh Government
  - Ministry for Primary Industries
  - Canadian Food Inspection Agency
  - Alberta Agriculture and Forestry
  - U.S. Department of Agriculture
  - National Centre for Food Protection and Defense
  - Department of Agriculture and Water Resources
  - National Veterinary Institute
  - AsureQuality Ltd
  - University of Melbourne
  - University of Minnesota-Twin Cities
- QUADS Epi team members

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