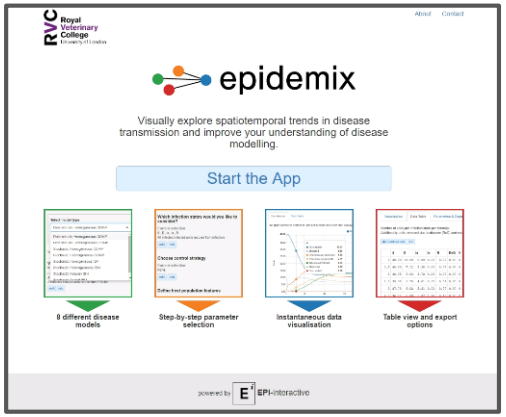
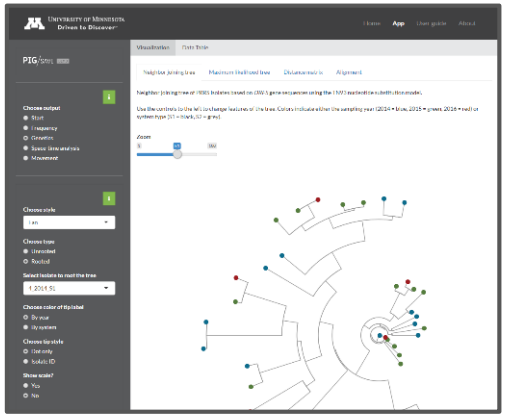
# Connecting data (and epidemiology) with people







**Uli Muellner**

14 December 2017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Received: 1 November 2016
DOI: 10.1111/zph.12351

ORIGINAL ARTICLE

WILEY

# Inferring source attribution from a multiyear multisource data set of *Salmonella* in Minnesota

[1]Epi-interactive, Wellington, New Zealand
[2]University of Warwick, Coventry, UK
[3]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, Saint Paul, MN, USA
[4]Minnesota Department of Health, Saint Paul, MN, USA
[5]Veterinary Diagnostic Laboratory, College of Veterinary Medicine, University of Minnesota, Saint Paul, MN, USA
[6]Division of Environmental Health Sciences, School of Public Health, University of Minnesota, Minneapolis, MN, USA

**Correspondence**
Petra Muellner. Epi-interactive, Wellington, New Zealand.
Email: petra@epi-interactive.com

**Funding information**
Global Food Venture MnDrive Initiative

**Summary**

*Salmonella enterica* is a global health concern because of its widespread association with foodborne illness. Bayesian models have been developed to attribute the burden of human salmonellosis to specific sources with the ultimate objective of prioritizing intervention strategies. Important considerations of source attribution models include the evaluation of the quality of input data, assessment of whether attribution results logically reflect the data trends and identification of patterns within the data that might explain the detailed contribution of different sources to the disease burden. Here, more than 12,000 non-typhoidal *Salmonella* isolates from human, bovine, porcine, chicken and turkey sources that originated in Minnesota were analysed. A modified Bayesian source attribution model (available in a dedicated R package), accounting for non-sampled sources of infection, attributed 4,672 human cases to sources assessed here. Most (60%) cases were attributed to chicken, although there was a spike in cases attributed to a non-sampled source in the second half of the study period. Molecular epidemiological analysis methods were used to supplement risk modelling, and a visual attribution application was developed to facilitate data exploration and comprehension of the large multiyear data set assessed here. A large amount of within-source diversity and low similarity between sources was observed, and visual exploration of data provided clues into variations driving the attribution modelling

ORIGINAL RESEARCH ARTICLE
Front. Vet. Sci., 23 December 2016 | https://doi.org/10.3389/fvets.2016.00116

# Evidence in Practice – A Pilot Study Leveraging Companion Animal and Equine Health Data from Primary Care Veterinary Clinics in New Zealand

Petra Muellner[1]*, Ulrich Muellner[1], M. Carolyn Gates[2], Trish Pearce[3], Christina Ahlstrom[1], Dan O'Neill[4], Dave Brodbelt[4] and Nick John Cave[2]

[1]Epi-interactive Ltd., Wellington, New Zealand
[2]Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand
[3]Equine Health Association, Wellington, New Zealand
[4]The Royal Veterinary College, Hatfield, UK

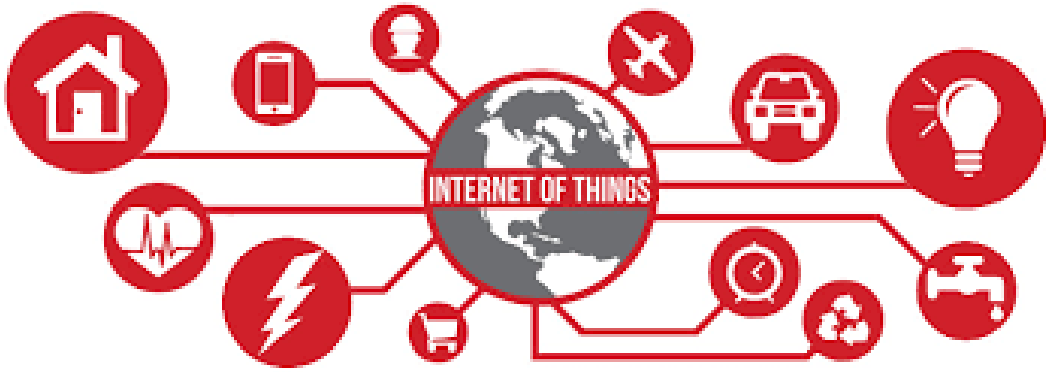
Veterinary practitioners have extensive knowledge of animal health from their day-to-day observations of clinical patients. There have been several recent initiatives to capture these data from electronic medical records for use in national surveillance systems and clinical research. In response, an approach to surveillance has been evolving that leverages existing computerized veterinary practice management systems to capture animal health data recorded by veterinarians. Work in the United Kingdom within the VetCompass program utilizes routinely recorded clinical data with the addition of further standardized fields. The current study describes a prototype system that was developed based on this approach. In a 4-week pilot study in New Zealand, clinical data on presentation reasons and diagnoses from a total of 344 patient consults were extracted from two veterinary clinics into a dedicated database and analyzed at the population level. New Zealand companion animal and equine veterinary practitioners were engaged to test the feasibility of this national practice-based health information and data system. Strategies to ensure continued engagement and submission of quality data by participating veterinarians were identified, as were important considerations for transitioning the pilot program to a sustainable large-scale and multi-species surveillance system that has the capacity to securely manage big data. The results further emphasized the need for a high degree of usability and smart interface design to make such a

# Connecting data and epidemiology with people

User interfaces: information dashboards, infographics …

New data sources

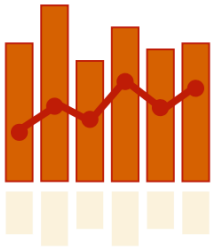
Real-time



# Case studies from our work

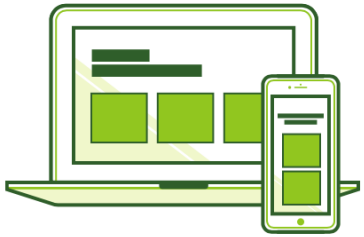
## APPLIED OUTPUTS THAT WORK IN THE REAL WORLD

Our multi-disciplinary expertise allows us to create a variety of outputs that are not only accurate, but also tailored to the audience. Converting abstract data or information into accessible and well-presented media is a passion of ours.



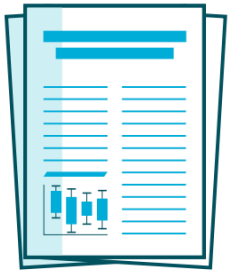
### Data Visualisation

We use our team of developers, designers, and scientists to visualise data in new ways.



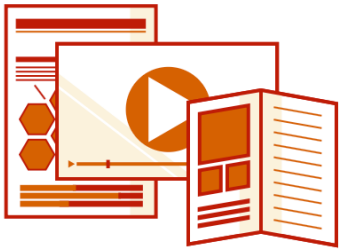
### Online Applications

We design and develop web and mobile applications to make your projects accessible to a wide and varied audience.



### Scientific Reports

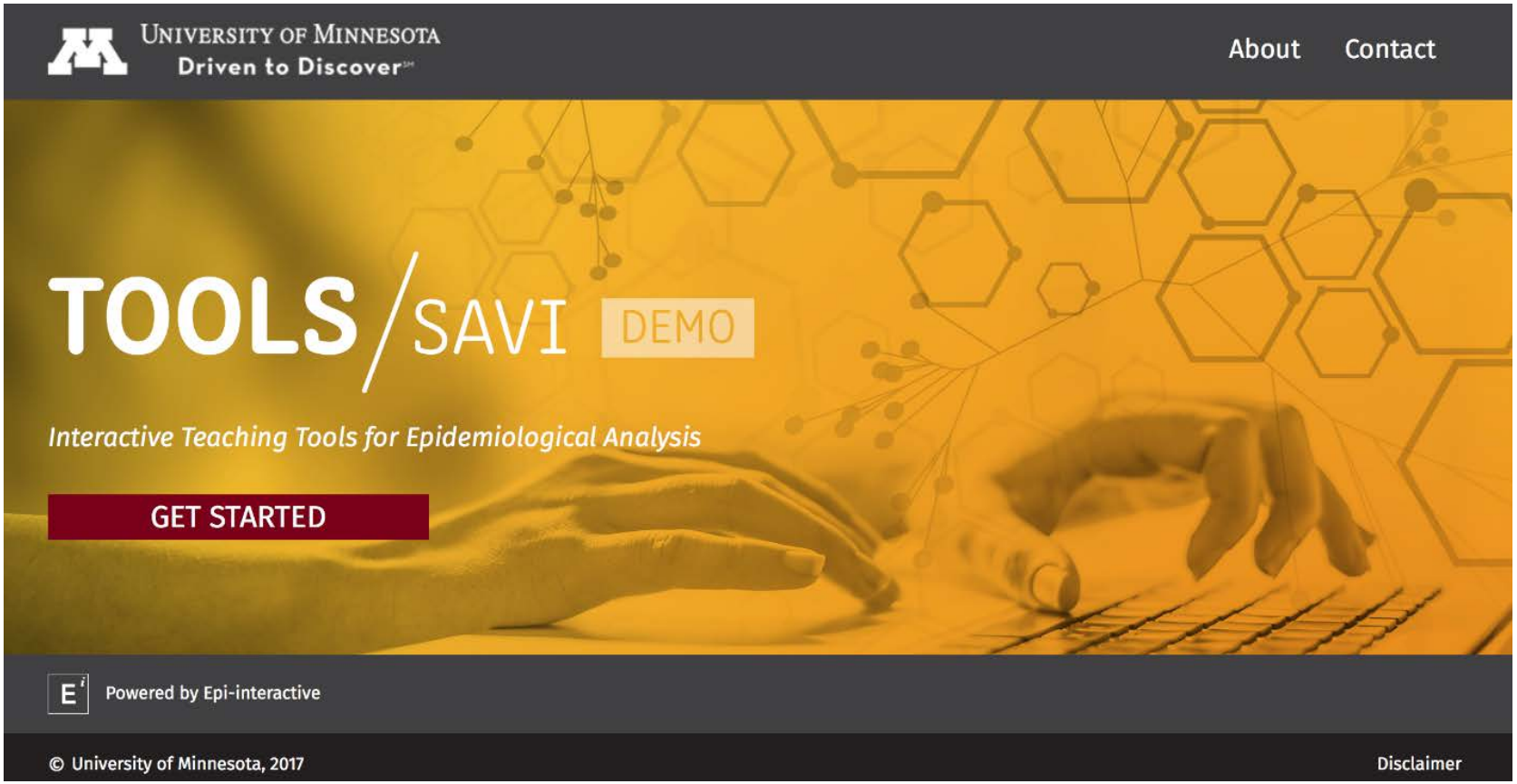
We write, review and assess scientific reports.



### Supporting Media

We design and develop media to support your projects including booklets, posters, motion graphics, infographics, and video tutorials.

# TOOLS / Savi


University of Minnesota
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Contact
TOOLS/SAVI DEMO
Interactive Teaching Tools for Epidemiological Analysis
GET STARTED
Powered by Epi-interactive
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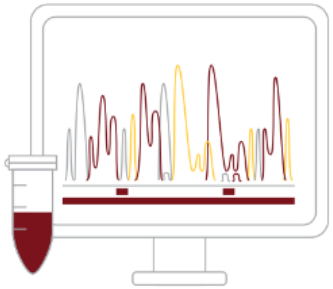
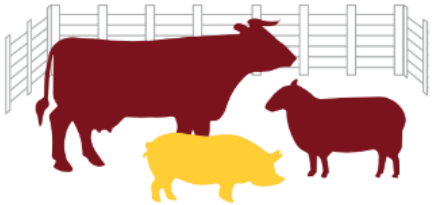


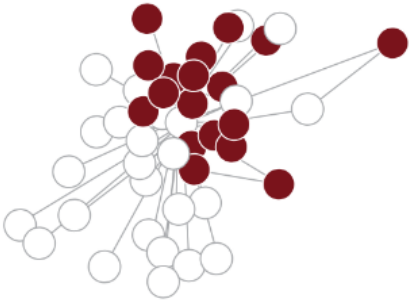
## Genetic Analysis

Explore distance matrices, phylogenetic trees and nucleotide substitution models.



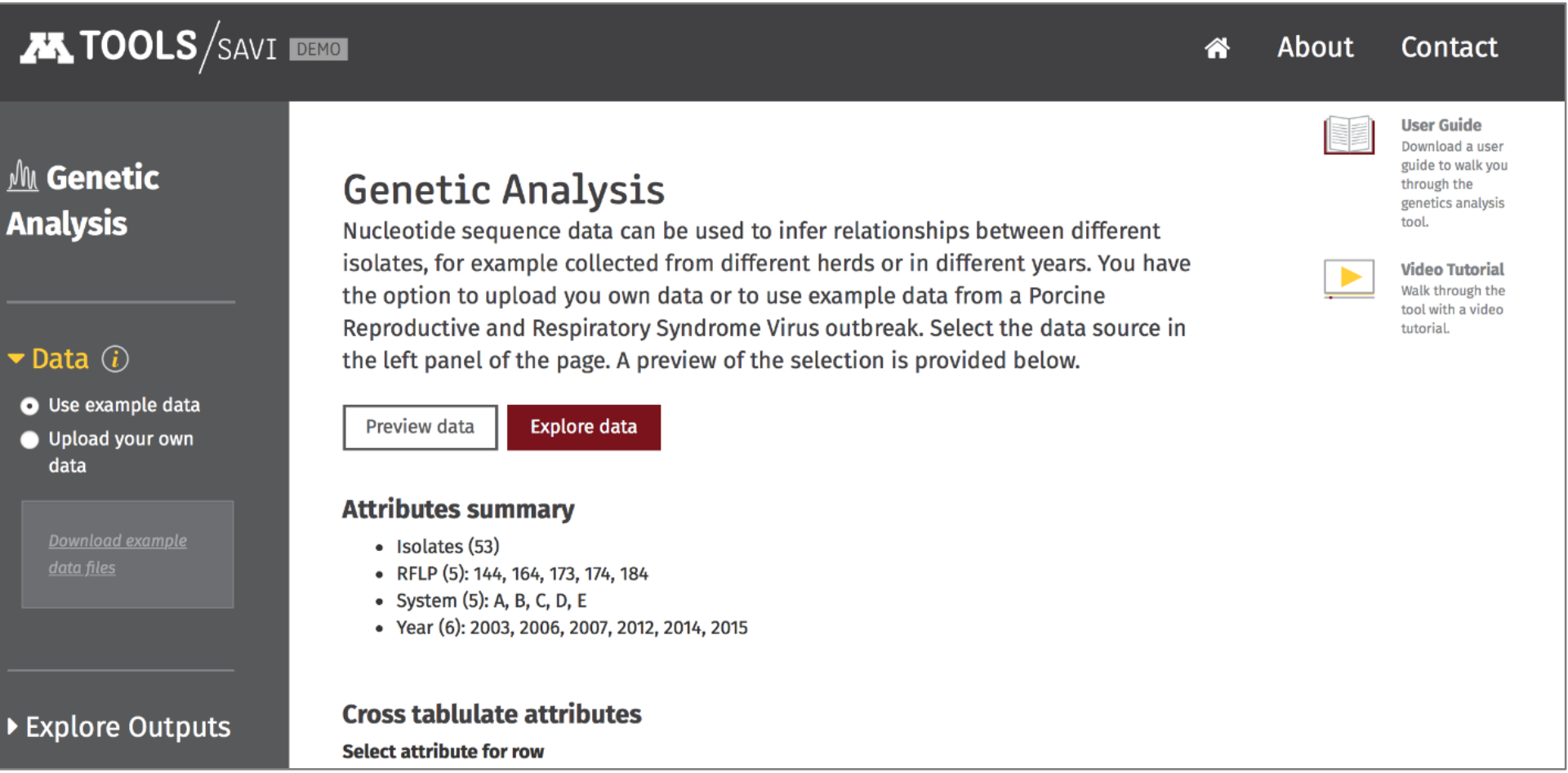
## Optisample™ Beta

Optimize the strategy of sampling for each farm in order to substantiate the freedom of infection considering also the costs of testing.



## Network K-Test

Performs network k-test on the epidemiological relevance of a network.


TOOLS/SAVI DEMO
About
Contact
Genetic Analysis
Data
Use example data
Upload your own data
Download example data files
Explore Outputs
Genetic Analysis
Nucleotide sequence data can be used to infer relationships between different isolates, for example collected from different herds or in different years. You have the option to upload you own data or to use example data from a Porcine Reproductive and Respiratory Syndrome Virus outbreak. Select the data source in the left panel of the page. A preview of the selection is provided below.
Preview data
Explore data
Attributes summary
Isolates (53)
RFLP (5): 144, 164, 173, 174, 184
System (5): A, B, C, D, E
Year (6): 2003, 2006, 2007, 2012, 2014, 2015
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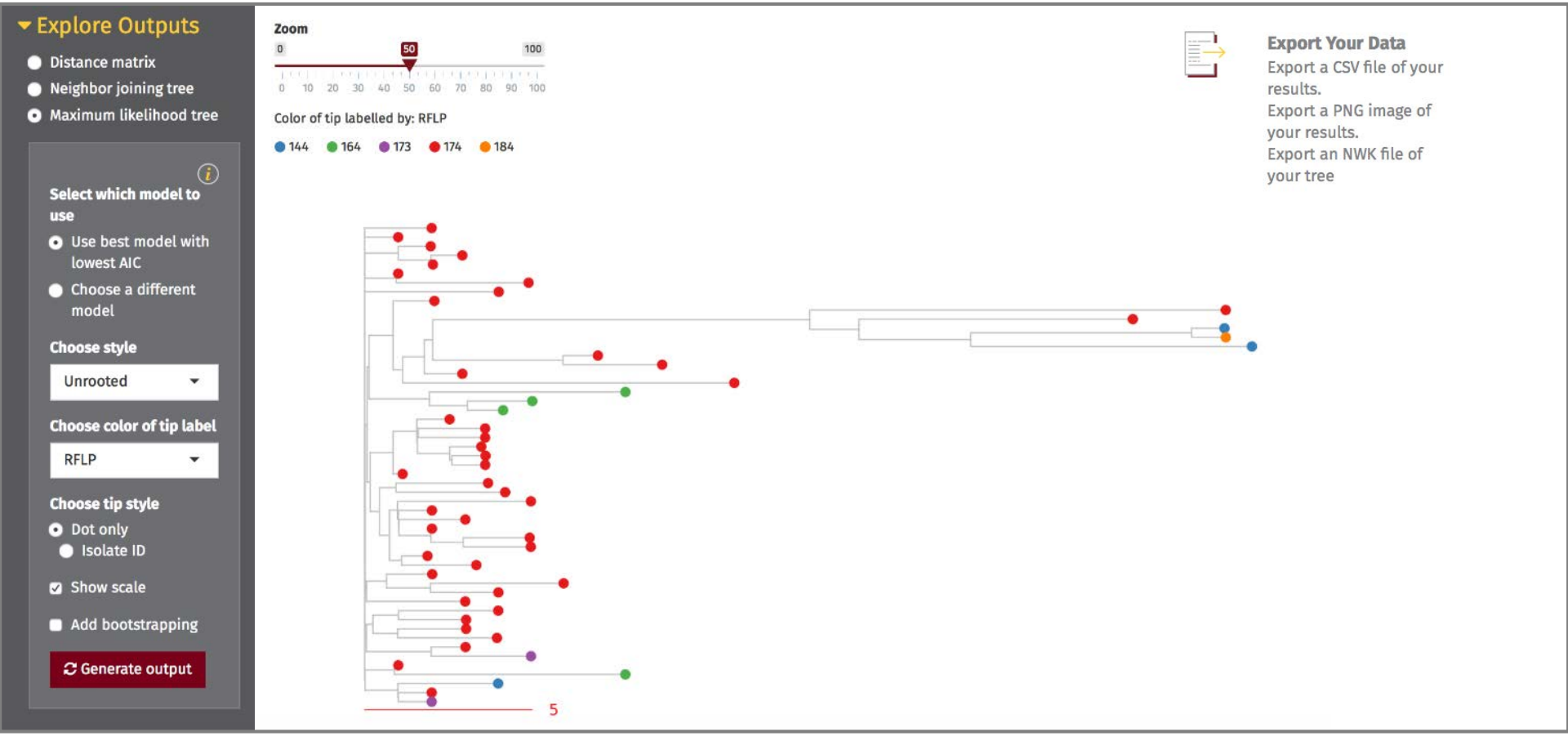
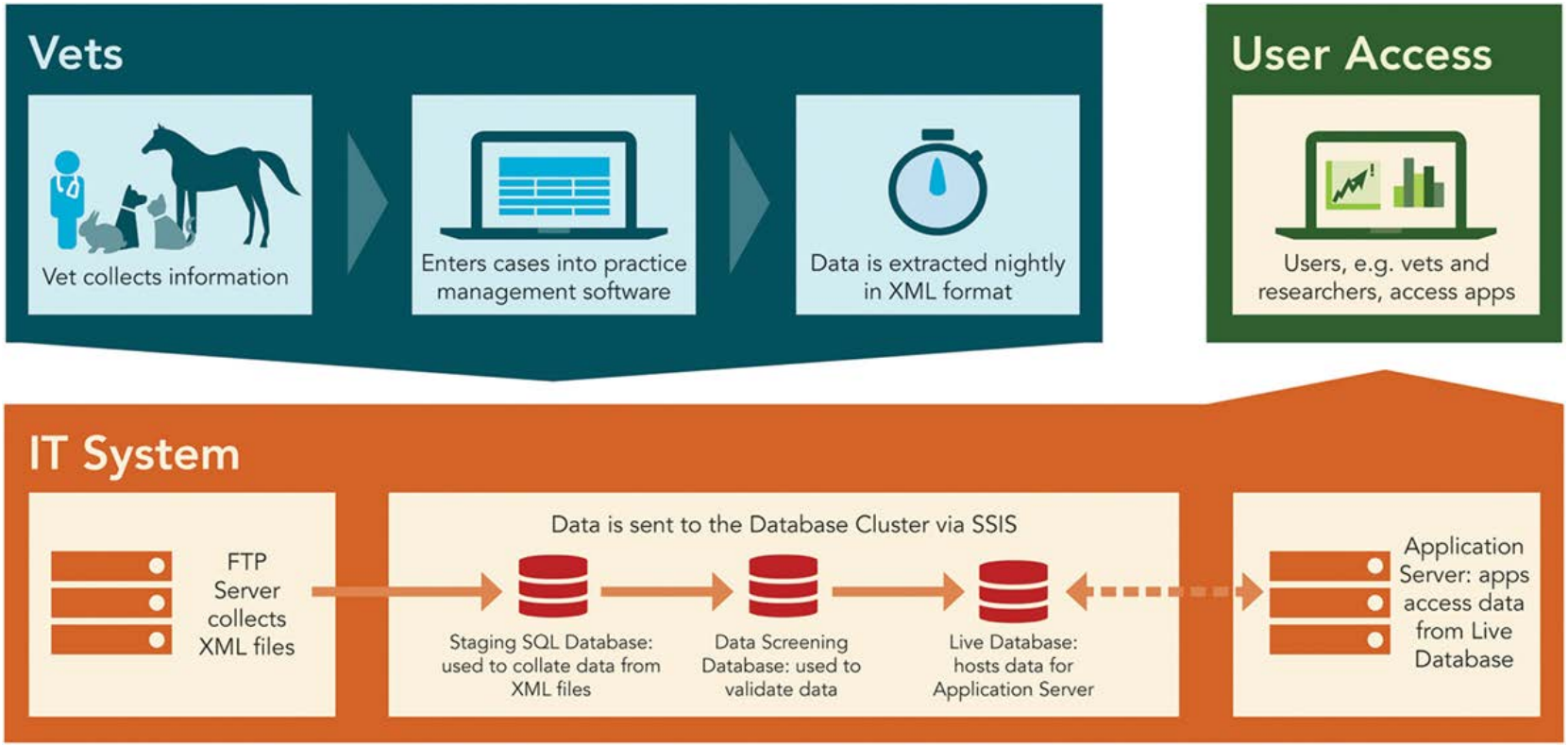
Select attribute for row
User Guide
Download a user guide to walk you through the genetics analysis tool.
Video Tutorial
Walk through the tool with a video tutorial.


Explore Outputs
Distance matrix
Neighbor joining tree
Maximum likelihood tree
Select which model to use
Use best model with lowest AIC
Choose a different model
Choose style
Unrooted
Choose color of tip label
RFLP
Choose tip style
Dot only
Isolate ID
Show scale
Add bootstrapping
Generate output
Zoom
0
50
100
0 10 20 30 40 50 60 70 80 90 100
Color of tip labelled by: RFLP
144
164
173
174
184
Export Your Data
Export a CSV file of your results.
Export a PNG image of your results.
Export an NWK file of your tree
5

# New data sources


**Muellner P**, **Muellner U**, Gates M, Pearce T, **Ahlstrom C**, O'Neill D, Brodbelt D and Cave NJ. Evidence in practice – a pilot study leveraging companion animal and equine health data from primary care veterinary clinics in New Zealand. *Frontiers in Veterinary Science* 3:116. doi: 10.3389/fvets.2016.00116, 2016.

# New data sources – primary care data



VetIntel Equine

About Contact

Baseline statistics | National data | My practice data

# Baseline Statistics

**49** Clinics enrolled in VetIntel

**305** Total of patients recorded

**64%** Average coding rate in the last three months

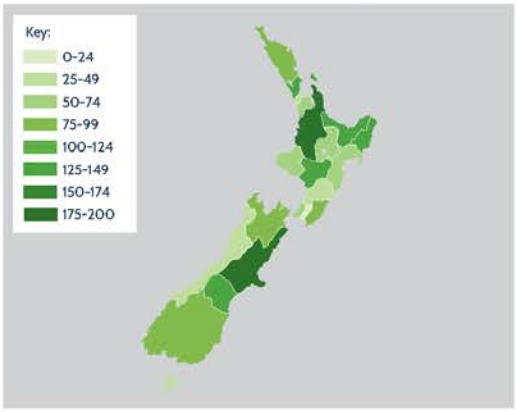
Top 3 presentation reasons

| | | |
|---|---|---|
| 1 | Wound - laceration | Significant increase ▲ |
| 2 | Traumatic episode | Significant increase ▲ |
| 3 | Lameness - bilateral forelimb | No significant change = |

Top 3 diagnosis

| | | |
|---|---|---|
| 1 | Periodontal disease | Significant increase ▲ |
| 2 | Aquired overgrowth of cheek ... | Significant increase ▲ |
| 3 | Solar penetration | No significant change = |

## Number of recorded visits per region



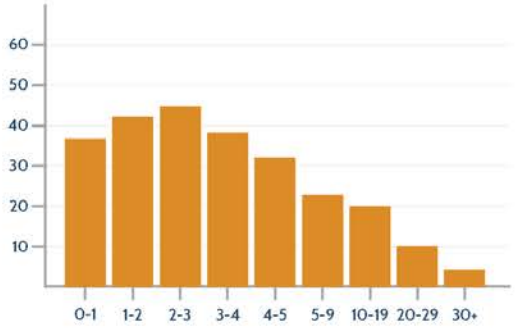

## Number of recorded visits

Past 12 months

Total number of recorded visits in the past year: 1,579 visits


## Age distribution

Average age of patients: 4.5 years




With support from the New Zealand Equine Health Association

Powered by Epi-interactive

# National data

## Data type

Select category:

- ○ Presentation reason
- ◉ Diagnosis
- ○ Procedure
- ○ Vaccinations

Select: Laminitis

## Time

Choose time range: 01-01-2016 to 31-12-2016

Select time interval:

- ○ Daily
- ○ Weekly
- ◉ Monthly

## Filters

Select breed: All

Select age range: All

Select gender: All

## Diagnosis

Chart | Map | Data Table

Total of 1,386 patients in the selected time period

Category: Diagnosis

Diagnosis: Laminitis

Time range: 01-01-2016 to 31-12-2016

Time internal: Monthly

Filters: None


## Top 10 diagnoses

Past three months

| | | |
|---|---|---|
| 1 | Periodontal disease | Significant increase ▲ |
| 2 | Aquired overgrowth of cheek teeth (sharp enamel points) | Significant increase ▲ |
| 3 | Solar penetration | No significant change = |
| 4 | Cellulitis | Significant increase ▲ |
| 5 | Inflammatory airway disease (IAD) | Significant decrease ▼ |
| 6 | Colic - spasmodic/undifferentiatied | Significant increase ▲ |
| 7 | White line disease | No significant change = |
| 8 | Pyrexia of unknown origin (PUO) | Significant increase ▲ |
| 9 | Pregnancy - single | Significant decrease ▼ |
| 10 | Wave mouth | Significant increase ▲ |

## Top 10 presentation reasons

Past three months

| | | |
|---|---|---|
| 1 | Wound - laceration | Significant increase ▲ |
| 2 | Traumatic episode | Significant increase ▲ |
| 3 | Lameness - bilateral forelimb | No significant change = |
| 4 | Lameness | Significant increase ▲ |
| 5 | Lameness - right fore | Significant decrease ▼ |
| 6 | Lameness - left fore | Significant increase ▲ |
| 7 | Wound - puncture | No significant change = |
| 8 | Wound | Significant increase ▲ |
| 9 | Pain - on eating/chewing | Significant decrease ▼ |
| 10 | Lameness left hind | Significant increase ▲ |

## Data type

Select category:

- ○ Presentation reason
- ◉ Diagnosis
- ○ Procedure
- ○ Vaccinations

Select: Laminitis

## Time

Choose time range: 01-01-2016 to 31-12-2016

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- ○ Daily
- ○ Weekly
- ◉ Monthly

## Filters

Select breed: All

Select age range: All

Select gender: All

# National data

## Diagnosis

Chart | Map | Data Table

Total of 1,386 patients in the selected time period

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Diagnosis: Laminitis

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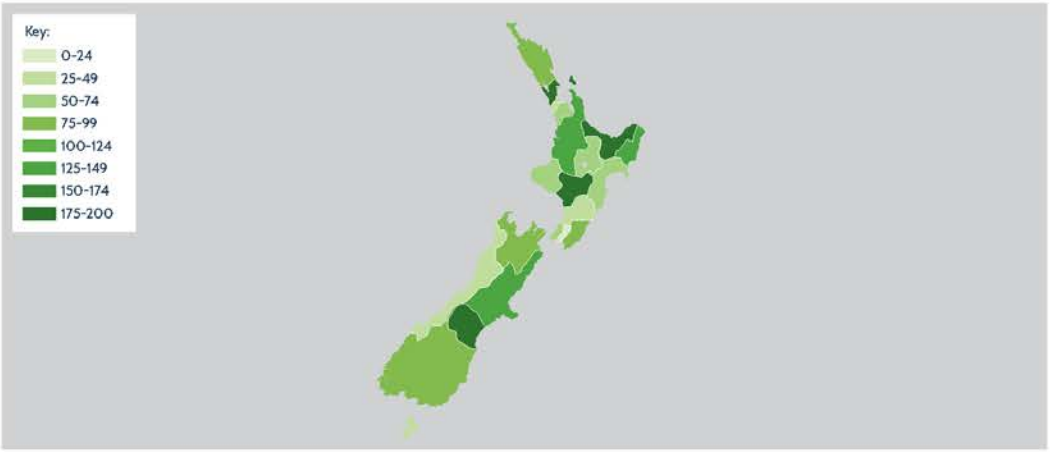
Filters: None




## Top 10 diagnoses

Past three months

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## Top 10 presentation reasons

Past three months

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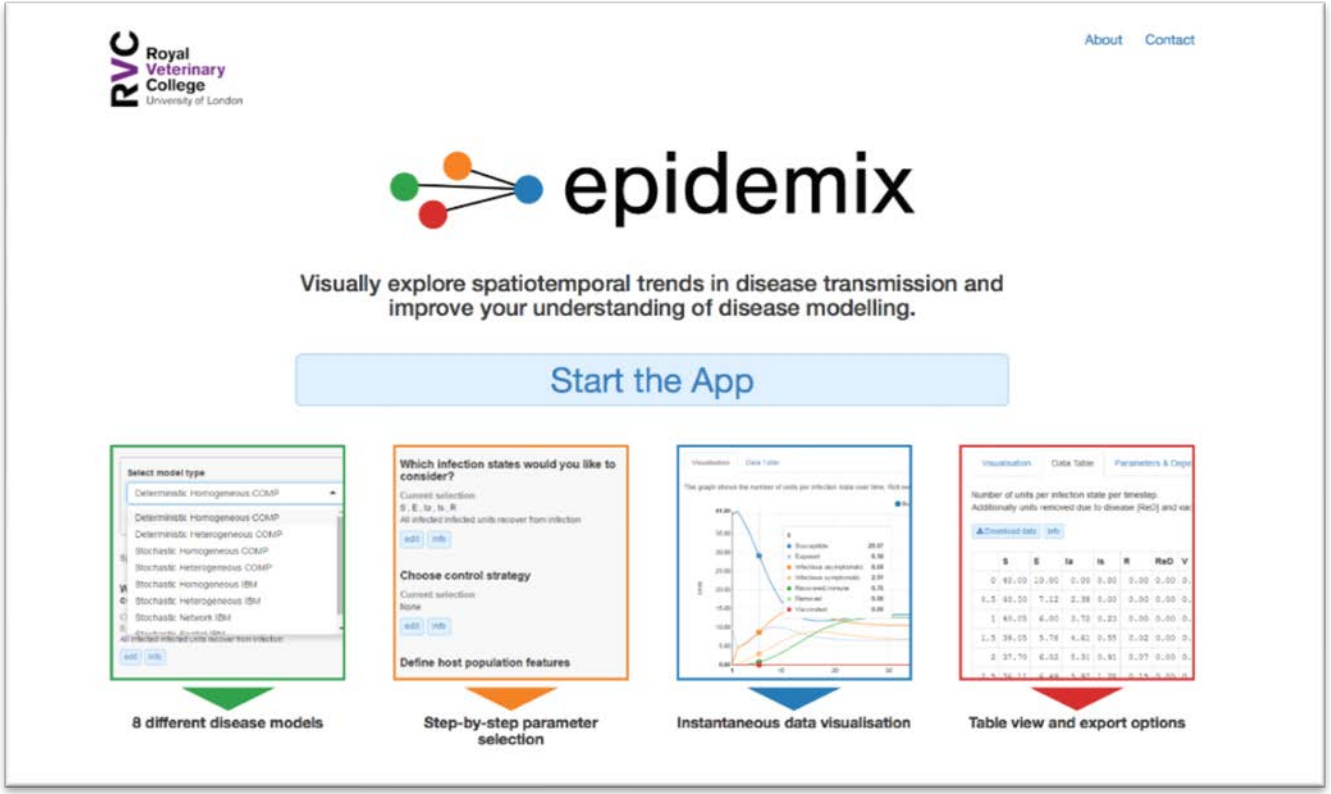
| 8 | Wound | Significant increase ▲ |
| 9 | Pain - on eating/chewing | Significant decrease ▼ |
| 10 | Lameness left hind | Significant increase ▲ |

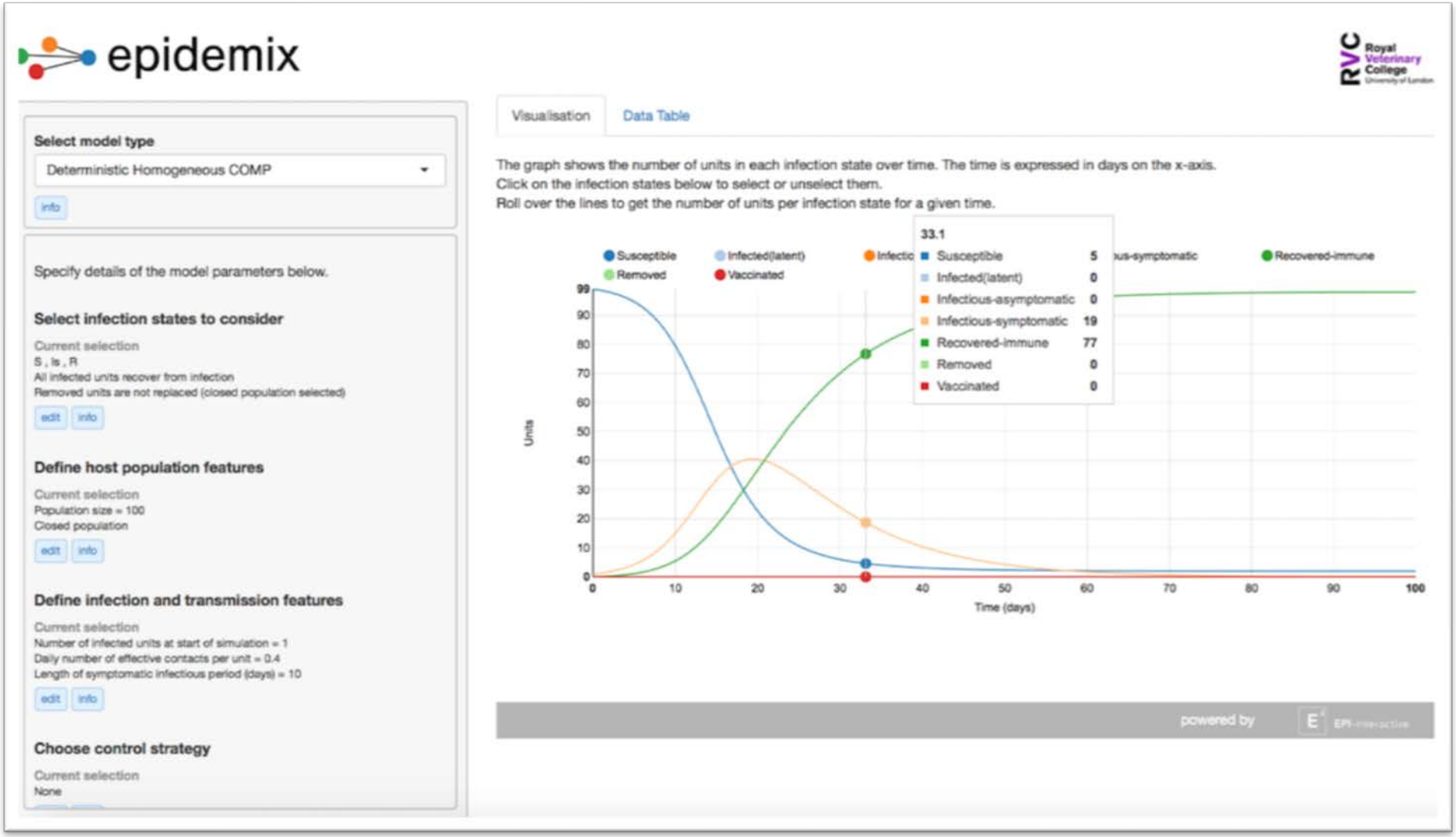
# … for vet clinics

# Decision-support




**Muellner U**, Fournie G, **Muellner P**, **Ahlstrom C**, Pfeiffer D. epidemix - an Interactive Multi-Model Application for Teaching and Visualizing Infectious Disease Transmission. *Epidemics*, In press, 2017.

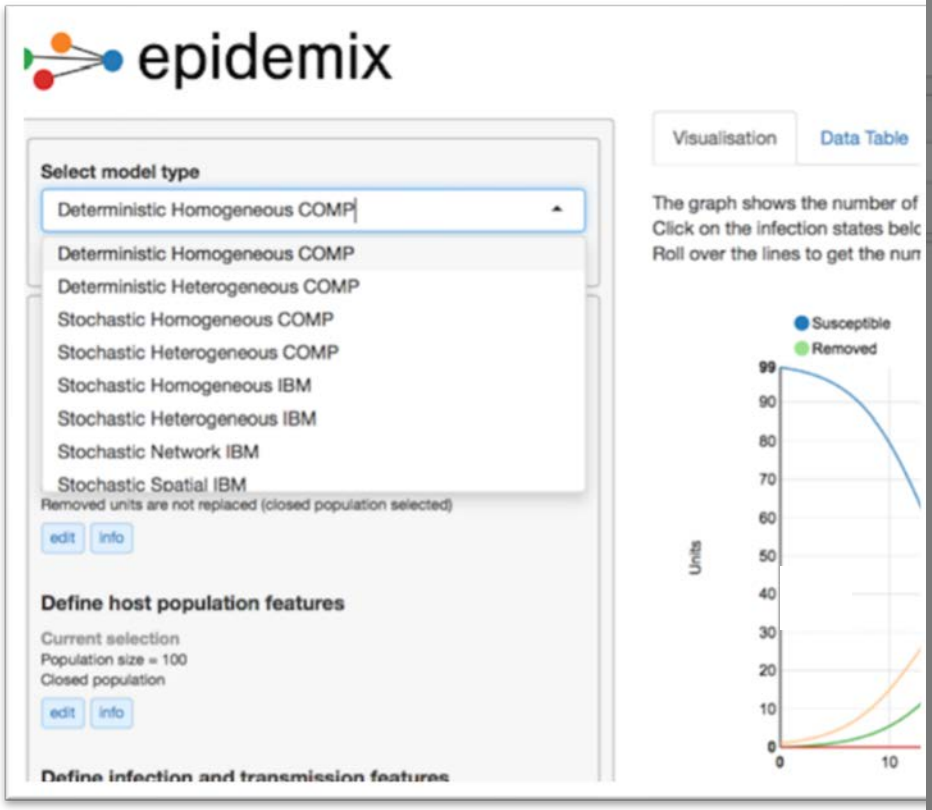
# Interactive & layering

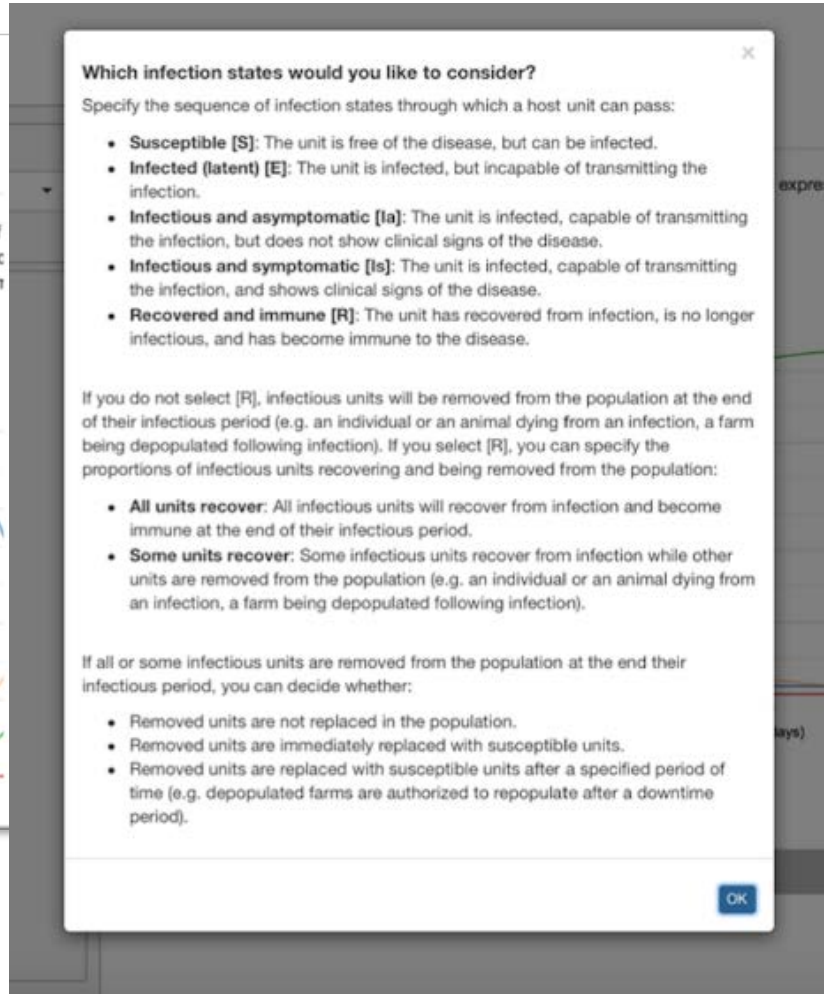


# Animation

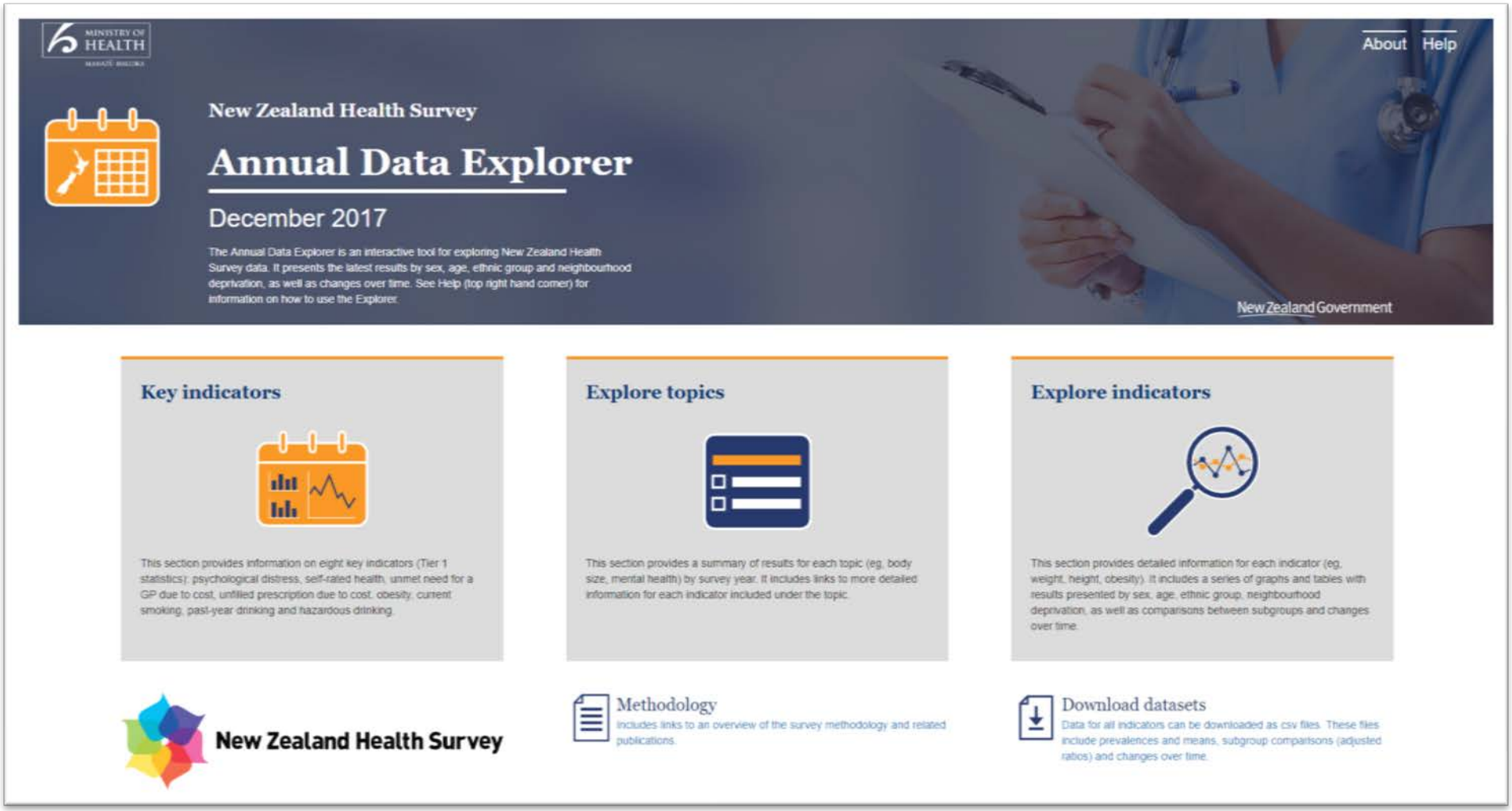

Choose control strategy
Current selection
Vaccination
Proportion of vaccinated units = 0.5
Random vaccination strategy (network model)
edit
info
Vaccination
Culling
Proportion of vaccinated units
0.5
Vaccination strategy (network model)
Random
Targeted
Set simulation parameters
Current selection
Number of simulations = 10
Length of a simulation (days) = 100
Number of timesteps per day = 1
edit
info
units' infection states over the course of a simulation by pressing the play button (triangle at the right bottom of the slider).
Click to update the graph when changing a parameter in the left sidebar.
Show graph
Choose time (in timesteps)
1
57
100
1 11 21 31 41 51 61 71 81 91 100
Select a simulation by moving the slider
1
10
1 2 3 4 5 6 7 8 9 10
Infection states:
Susceptible
Infected (latent)
Infectious asymptomatic
Infectious symptomatic
Recovered
Removed
Vaccinated

# Context-sensitive information



# Health data reporting



**Population and indicator**

Show indicator overview

Choose a population

Adults (aged 15 years and ove

Choose a topic

Self-rated health

Choose an indicator

Excellent, very good or good s

## Indicator: Excellent, very good or good self-rated health

**Adults**
**Topic:** Self-rated health

**Indicator Definition:**

Adult respondents (aged 15+ years) are categorised as having good or better self-rated health if they answered 'excellent', 'very good' or 'good' to

Full definition

**Download**
Charts (zip)

### Most adults reported that they were in good, very good or excellent health

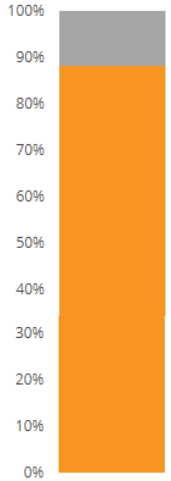
Self-rated health is a widely used indicator of a population's health status. Interviewers asked adults taking part in the survey whether they considered their health to be 'excellent, very good, good, fair or poor'. The term 'good health' means good, very good or excellent health. Ratings of 'fair or poor'…

More information

Overview | Prevalence / mean | Subgroups comparison | Changes over time

# 2016/17

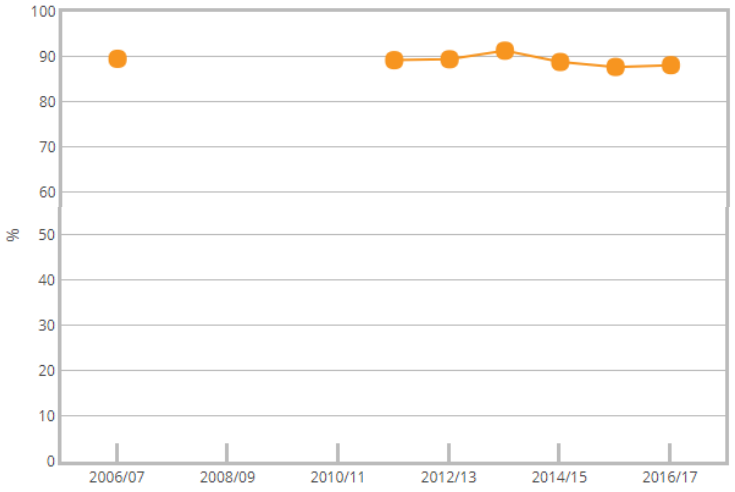
**Show:**
Total




The prevalence was
**88.2%**
which is an estimated
**3,379,000 adults**

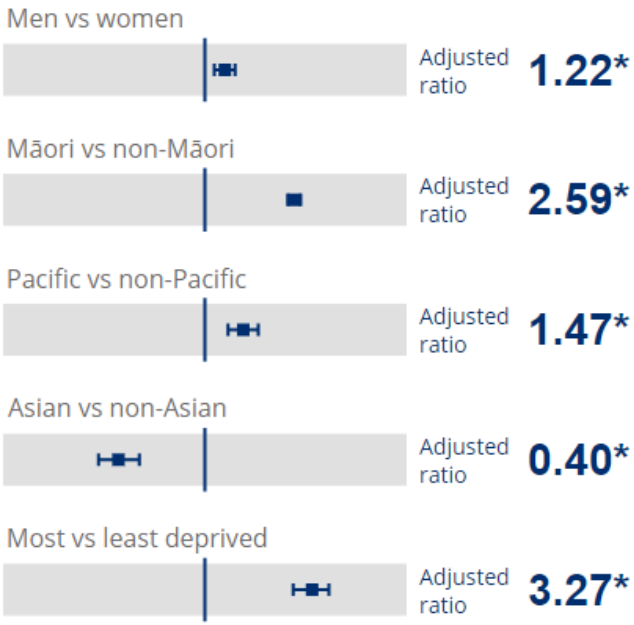
## Time series

This chart presents unadjusted results; that is, the prevalence estimates reflect the actual percentage of the population affected in each time period.



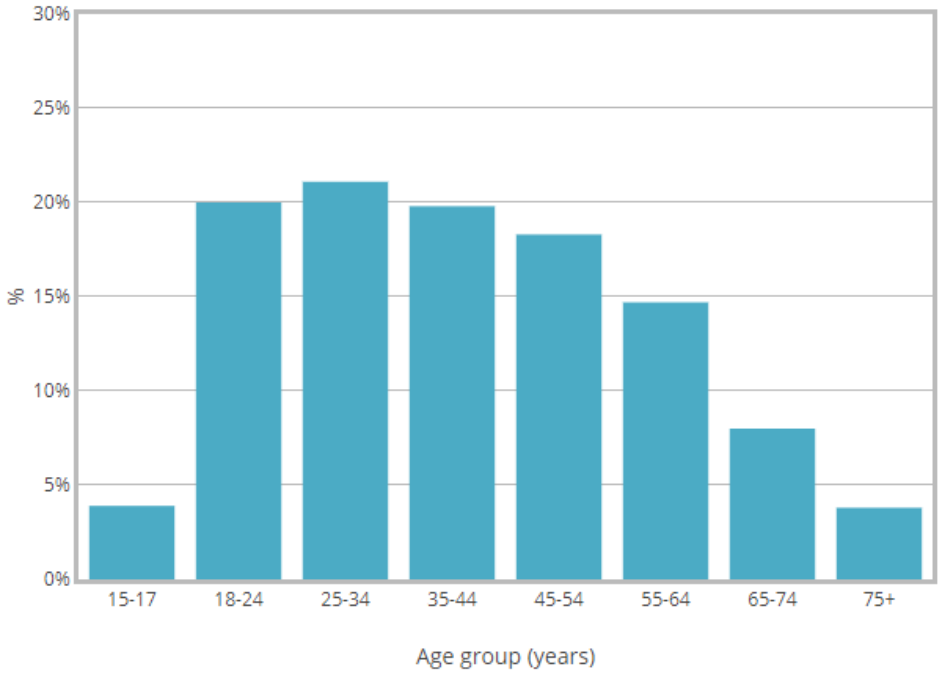
## Subgroups comparison

This chart gives comparisons by sex, ethnic group and neighbourhood deprivation. Adjusted ratios above 1 mean the indicator is more likely in the group of interest than the comparison group; adjusted ratios below 1 mean the indicator is less likely.



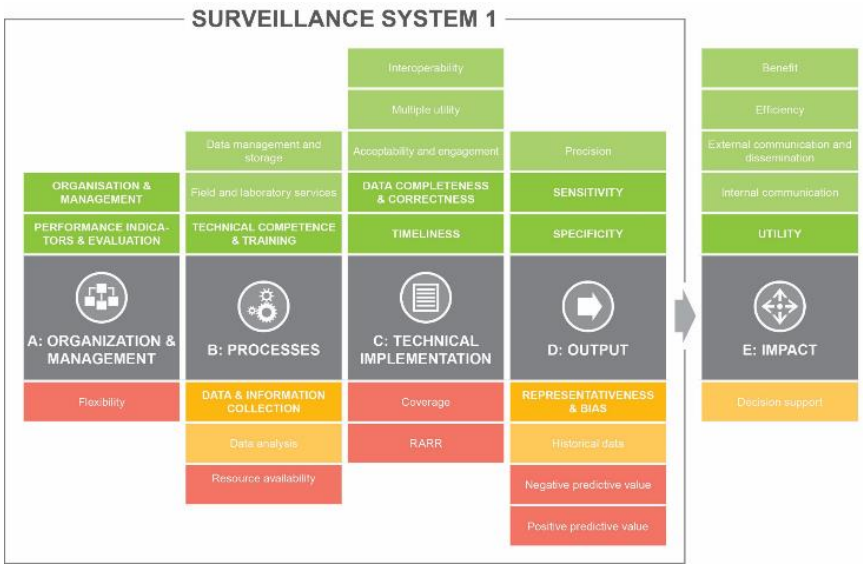

An asterisk (*) indicates that the adjusted ratio is statistically significant.

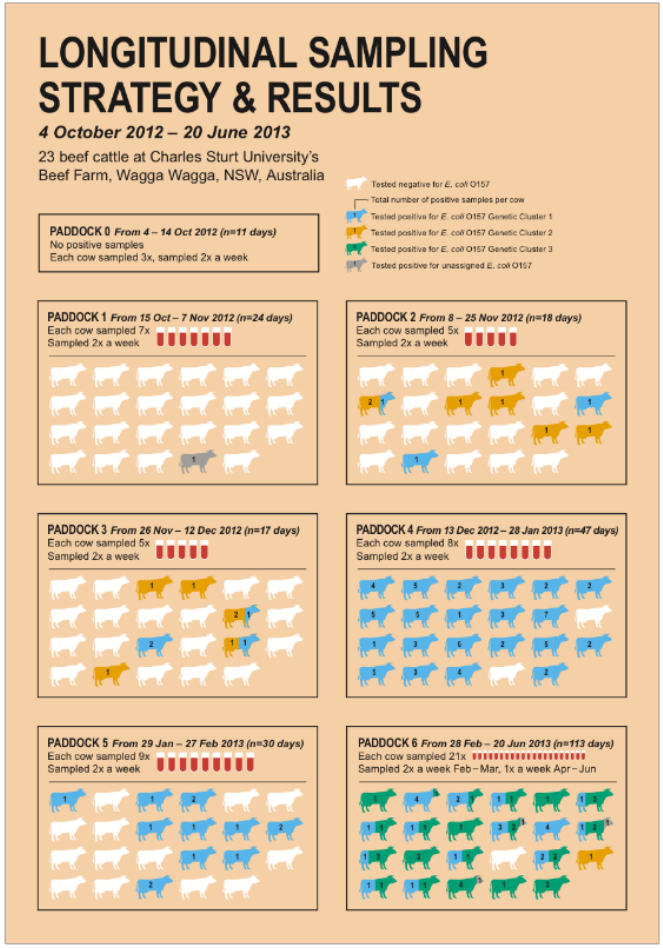
## Age distribution



# Infographics

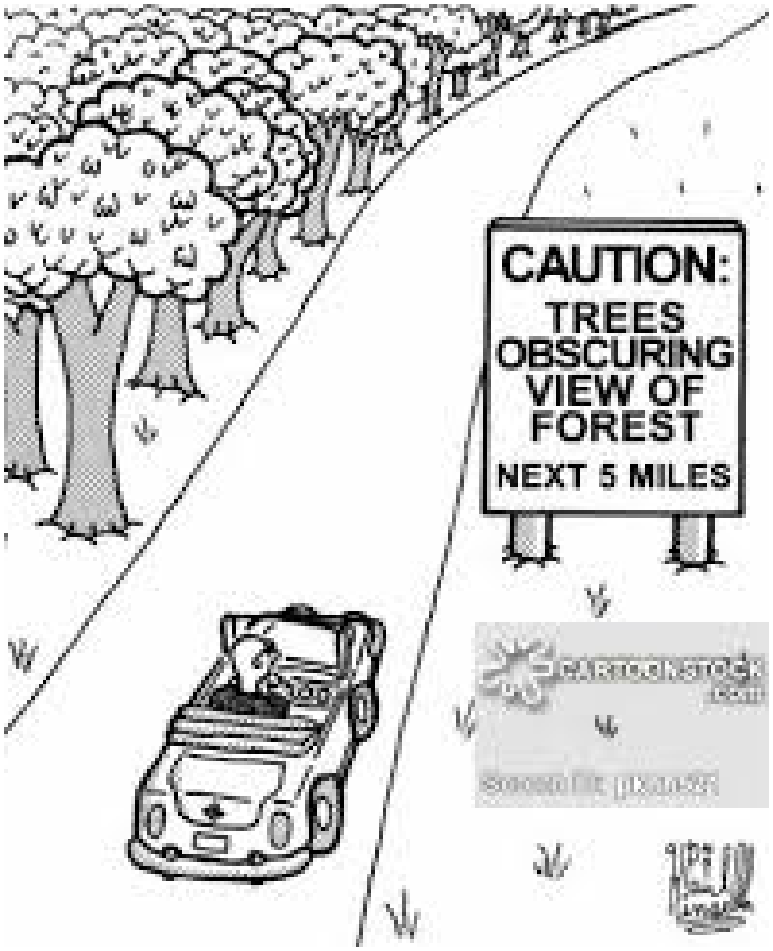
- Providing a visual summary of technical reports, strategies…
- Lots of fun to make and often what people remember



# Why are we struggling?

- Its complicated!
- Easy is hard
- Forest for the trees



# Let go of the “Wolpertinger model”

- Don’t need “web-programming-epidemiologist-designer-veterinarians”
  - Things are getting way to complex!
- In-depth collaboration / multidisciplinary approach needed
  - Need connectors
  - Can be painful

# Conclusion

- Try out new ways to communicate research

"We have interesting stories, beautiful information and above all information that holds the key to improving human and animal health and well being – let's do a better job at getting the message across."

# Thank you for listening

EPI-interactive

**uli@epi-interactive.com**
**petra@epi-interactive.com**

**Acknowledgements**
Epi-interactive team: Petra Muellner, Anna Poulin, Christina Ahlstrom, Geoff Longuett, Shanna Tervoort-McLeod, Kara Dawson