

Forecasting the spread and impacts of invaders

Top of the South Marine Biosecurity,
NIWA and Cawthron Joint Workshop

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New Zealand Government

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OVERVIEW

Introduction

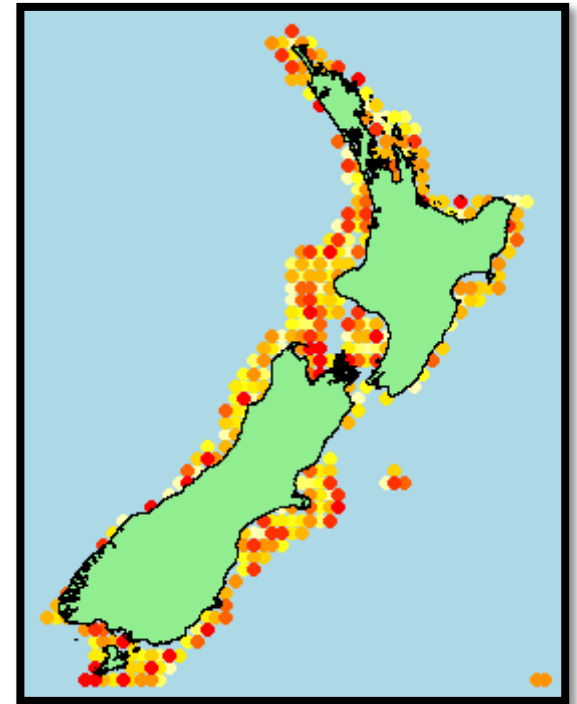
- Motivation
- Data available

Methods

- Dynamic range model
- Epidemiological model
- MCMC scheme

Results

- Measuring spread of invasive species



1.

INTRODUCTION

- Over 360 invasive species have been recorded in New Zealand waters.
- These species can have detrimental effects on existing species, e.g. by outcompeting them for resources or predated upon them.
- Important to understand the dynamics of their spread, for effective management strategies to reduce epidemic sizes.



1.

INTRODUCTION

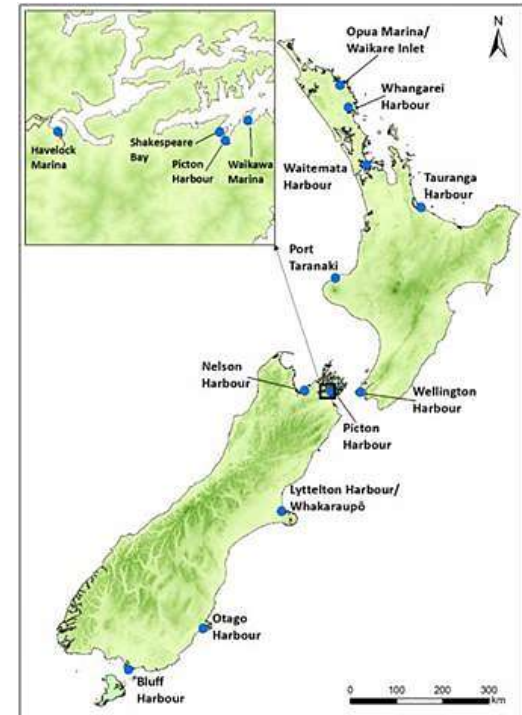
- Data available on the incidence of different invasive species are from a range of sources. These are of two forms.

1. Baseline distributions:

- a) Herbarium / museum records
- b) Literature
- c) Port Biological Baseline Surveys (2001 -2008)

2. Monitoring:

- a) Marine High Risk Site Surveillance (MHRSS) program (2002 – current)
- b) Marine Invasives Taxonomic Service (2005 – current)



The 11 sites included in the MHRSS program.

1.

INTRODUCTION

There are eleven key species of interest:

1. *Arcuatula senhousia* (Asian date mussel)
2. *Charybdis japonica* (Asian paddle crab)
3. *Eudistoma elongatum* (Australian droplet tunicate)
4. *Ficopomatus enigmaticus* (Australian tubeworm)
5. *Limaria orientalis* (file shell)
6. *Magallana gigas* (Pacific oyster)
7. *Metapenaeus Bennettiae* (greentail prawn)
8. *Pyura doppelgangera* (sea squirt)
9. *Sabella spallanzanii* (Mediterranean fanworm)
10. *Theora lubrica* (Asian semele)
11. *Undaria pinnatifida* (wakame, edible seaweed)

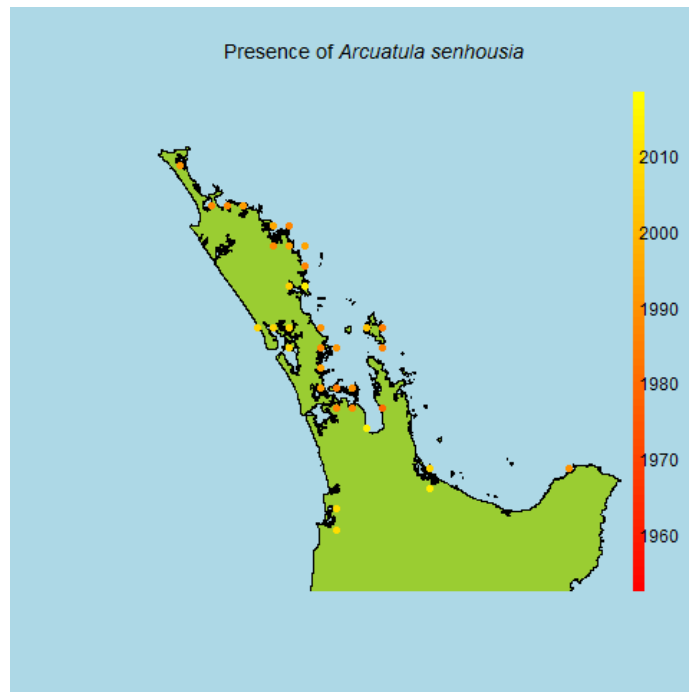


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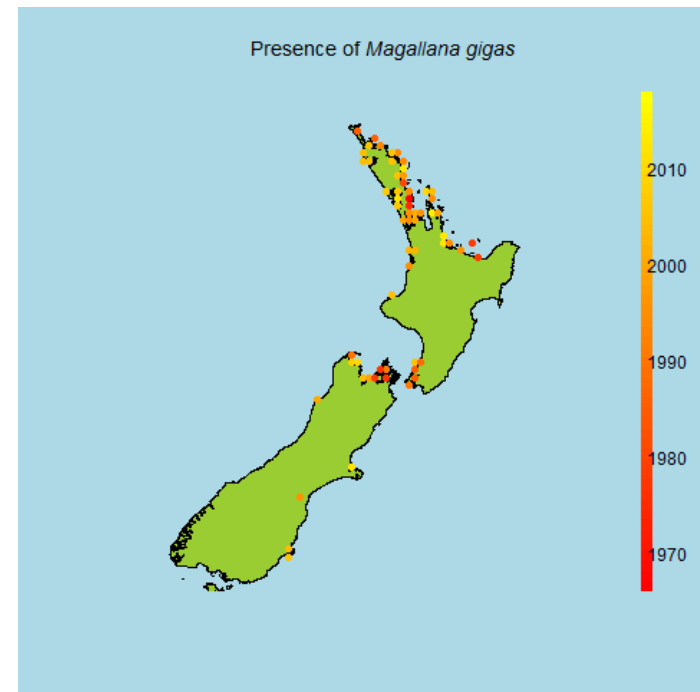
INTRODUCTION

Examples of presence maps over time are shown below:

Asian date mussel



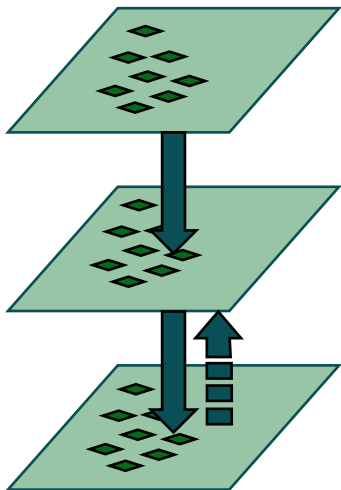
Pacific oyster



2.

METHODS

- Dynamic range models (DRMs): used to forecast the time course of spread and impacts, that incorporate global occurrence data, environmental suitability, spread dynamics, demography and impact data.

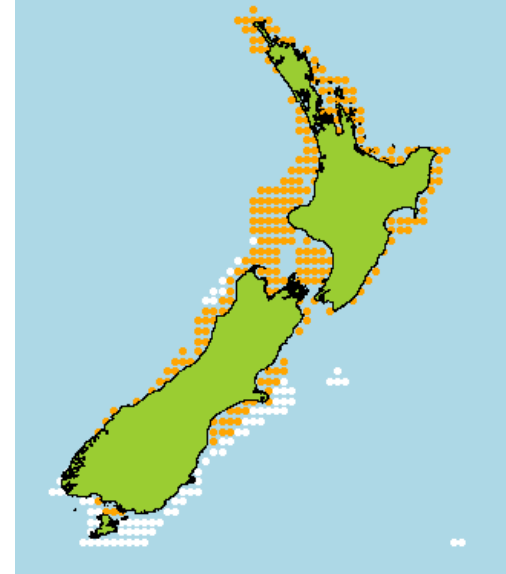


Area of potential establishment
climate and host

Spread
Point of entry, population biology
and spread mechanisms

Impacts
Economic data and host

Area of potential establishment

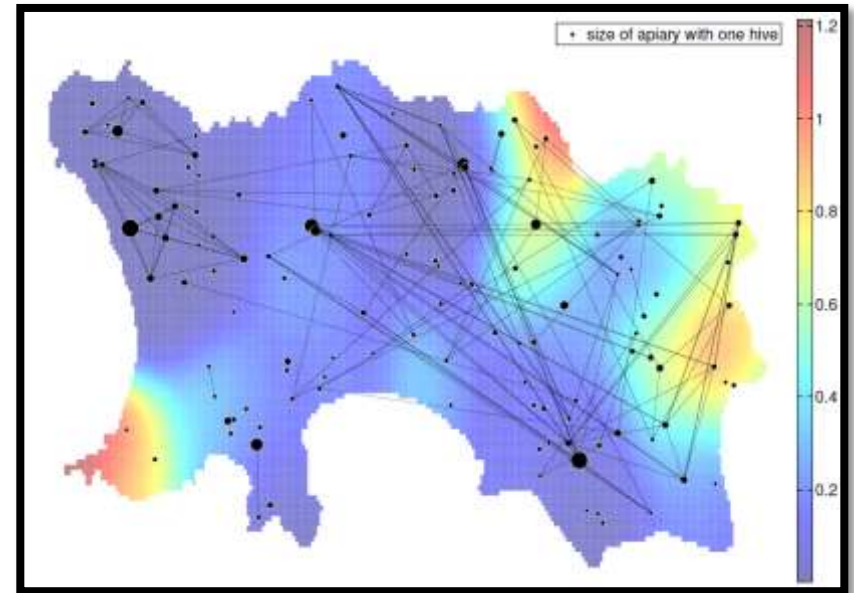


The areas of potential establishment for the Mediterranean fanworm.

2.

METHODS

- We have adapted the DRM to a previous **individual-based epidemiological model**, used to simulate the spread of infection in **honeybees** in the UK and abroad.
- This model used **presence / absence data of infection** (including date of inspection, location and owner information) as the input, and **Bayesian methods** (an MCMC scheme) to fit unknown parameter values.
- The output parameters can be used to **simulate epidemics in a stochastic individual-based model**, to recreate the epidemic and test management strategies.



A map of the island of Jersey (south of the UK mainland), with links shown between hives owned by the same individual. Heat map shows the likely origin of the epidemic.

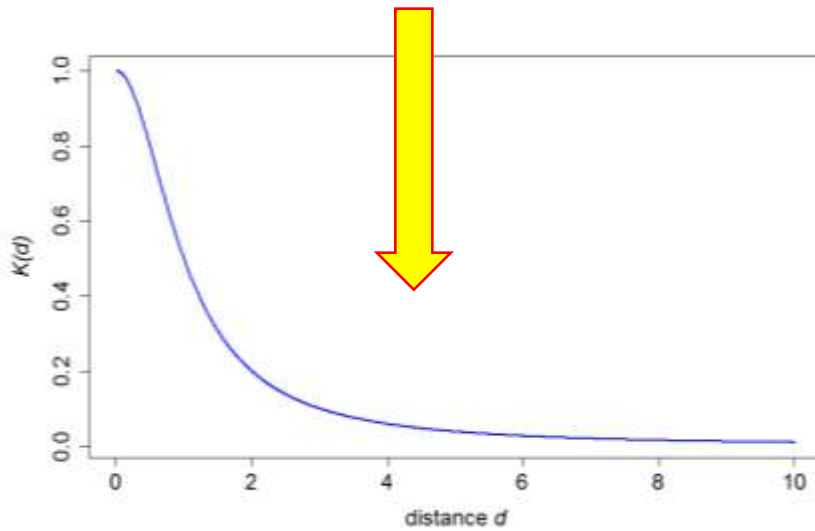
2.

METHODS

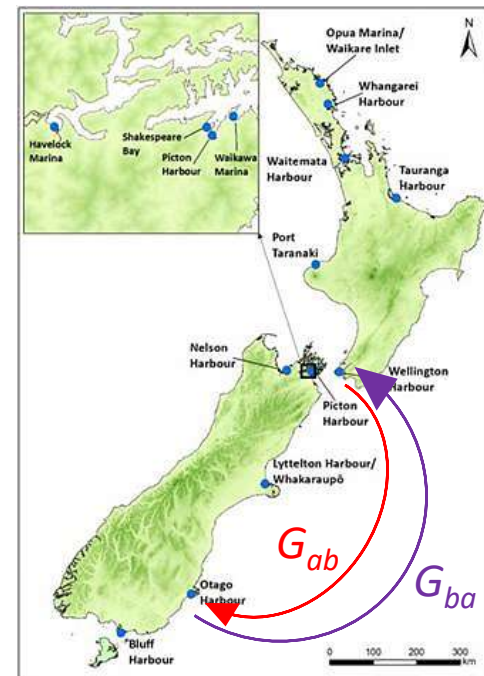
Two methods of spread in the model:

1) Spatial (diffusive) spread

$$K_{ij} = \frac{1}{d_{ij}^2 + \alpha^2}$$



2) Network (saltative) spread



2.

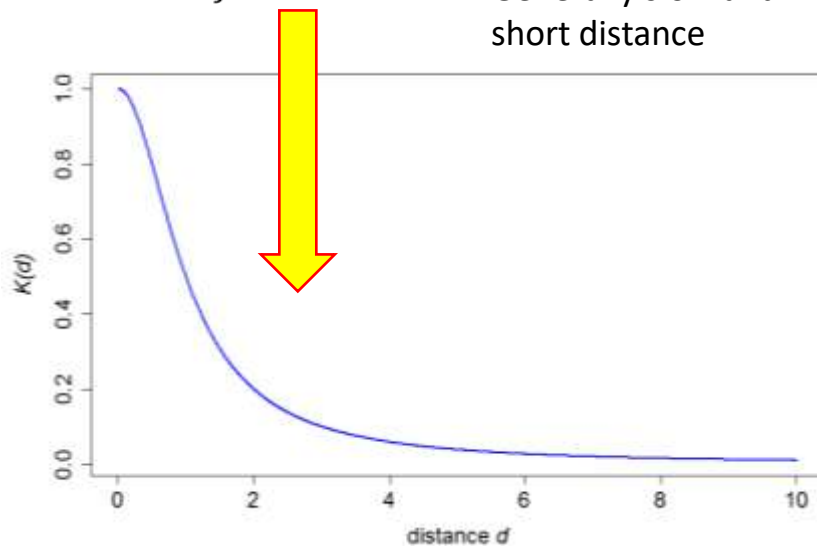
METHODS

Two methods of spread in the model:

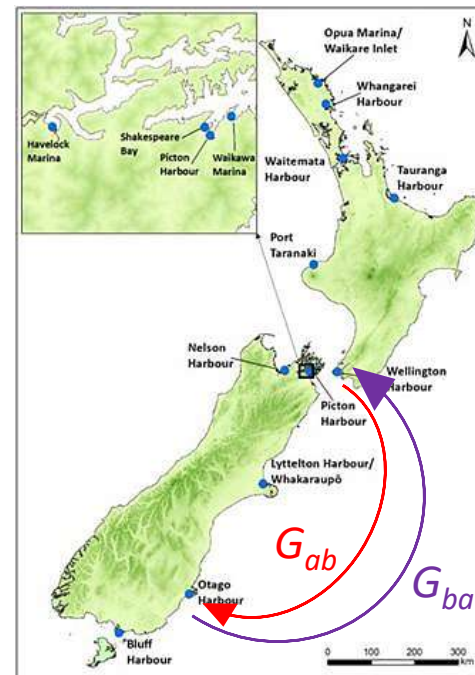
1) Spatial (diffusive) spread

$$K_{ij} = \frac{1}{d_{ij}^2 + \alpha^2}$$

- Movement of organism
- Water currents
- Generally slow and short distance



2) Network (saltative) spread

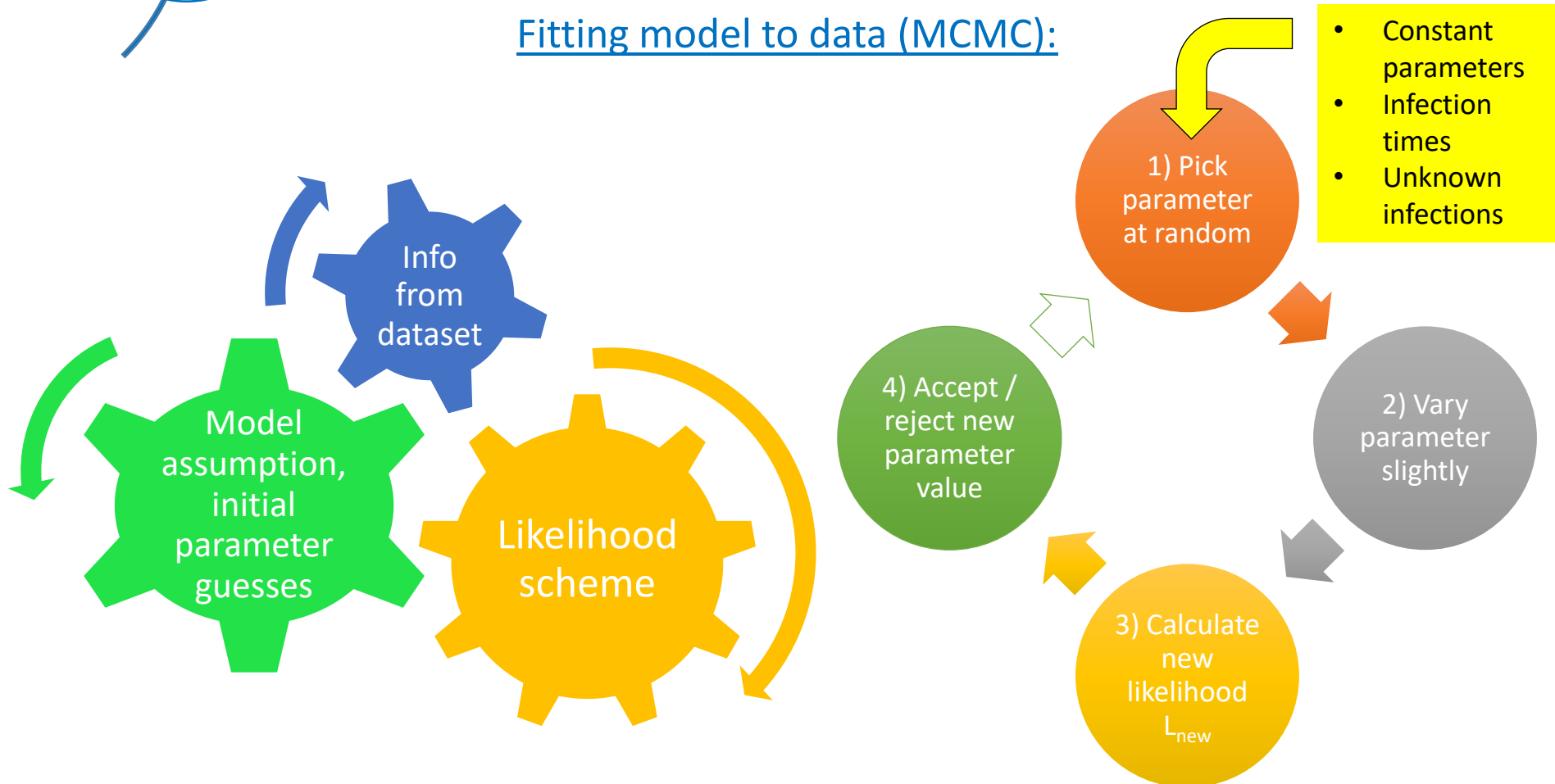


- Commercial vessel traffic data
- Recreational boat movement
- Can be rapid and independent of distance (e.g. size of ports)

2.

METHODS

Fitting model to data (MCMC):

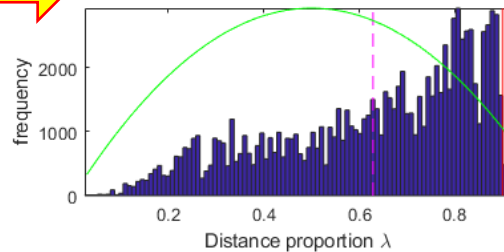
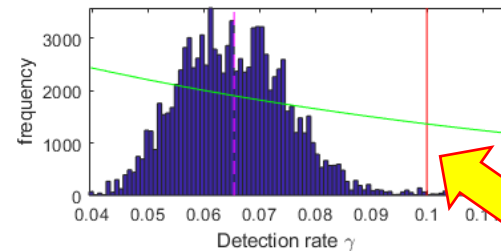
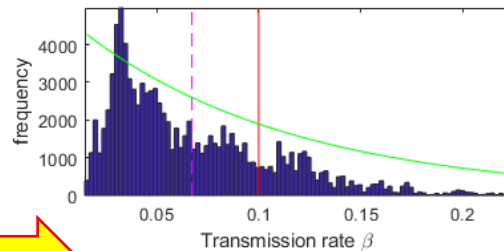


3.

RESULTS

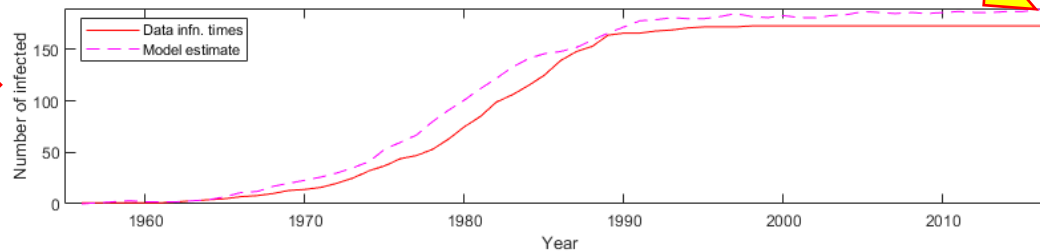
Outputs from MCMC scheme

Histograms:
parameter
distributions



Red lines:
estimates from
simulating data

Bottom plot:
infections
across time

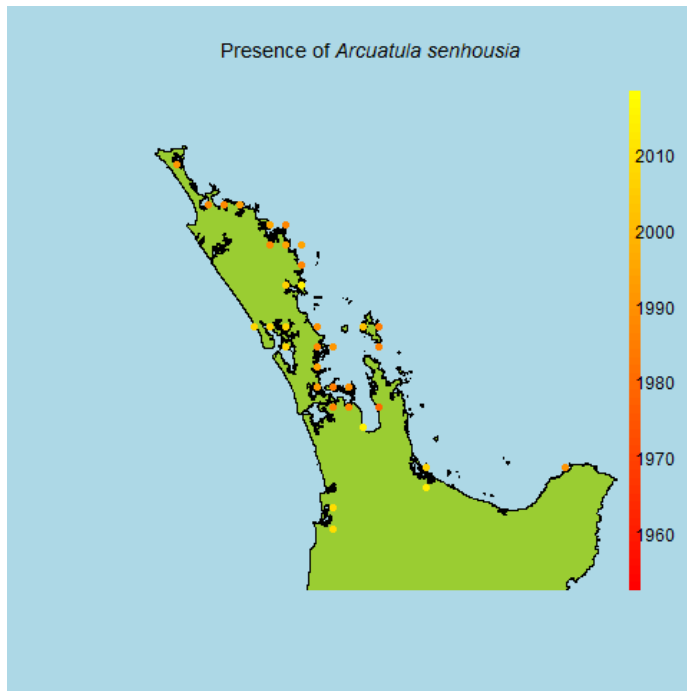


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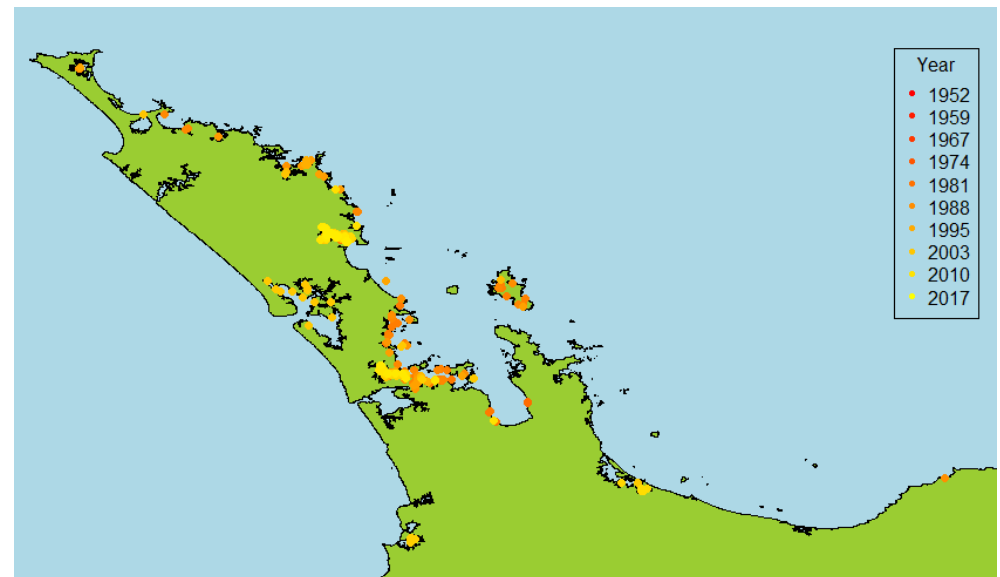
RESULTS

Comparing simulated epidemics with data - map

Data



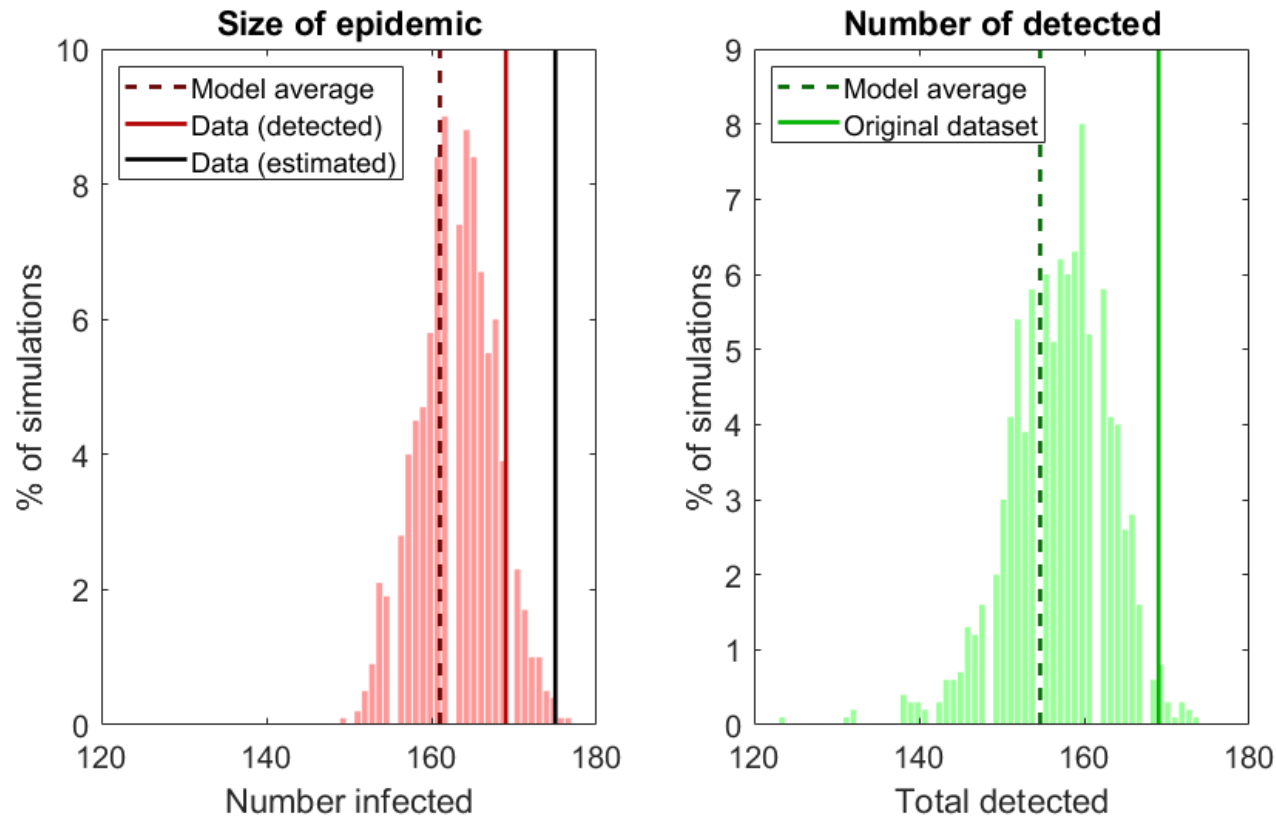
Model (example simulation)



3.

RESULTS

Comparing simulated epidemics with data – proxies for goodness of fit



4.

NEXT STEPS

The next steps for the project include:

- Supplement current presence-only data with presence / absence data, to limit spread.
- Observation bias: Lag in detection, unquantified survey effort in space and time.
- Add in up-to-date vessel movement data for network (long-distance) spread of invasive species.
- Consult with experts to verify model assumptions are appropriate, and prior distributions for unknown parameters are biologically reasonable.
- Carrying out the full analysis on all eleven datasets.
- Simulate possible management strategies to detect and / or mitigate spread of invasive species.



Acknowledgements

- This research was funded by the Ministry of Business, Innovation and Employment, through contract C01X1511.
- Graeme Inglis and Kim Seaward assembled the data and developed the conceptual basis for the project.
- Thanks to Tarek Soliman and Dong Wang, who developed the initial dynamic range models for use in the project.



Source: Serena Cox

QUESTIONS?



Source: K Seaward