Parametrisation and Identification Methods for Epidemic Systems

Provisional Year Review Seminar

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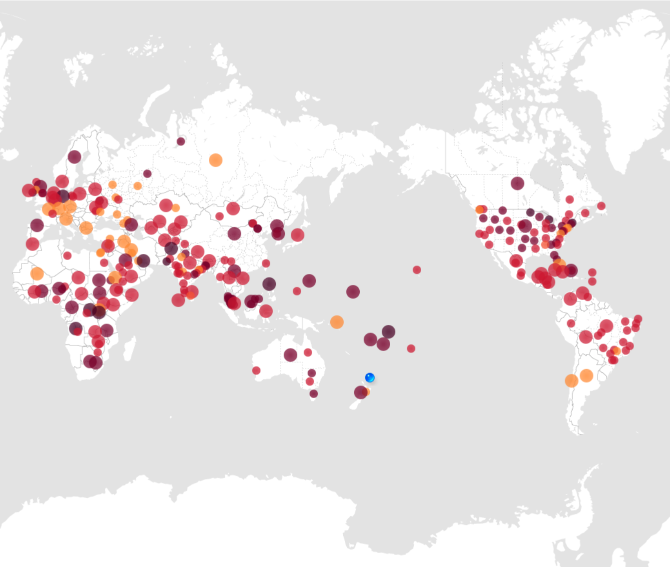
Motivation



Courtesy of HealthMap

Problem Setup

Modelling

The classical SIR model*

*Kermack and McKendrick, "A Contribution to the Mathematical Theory of Epidemics".

Modelling

The classical SIR model*

Analytical Results:

- $\mathcal{R}_0$: threshold parameter
- Asymptotic behaviour

*Kermack and McKendrick, "A Contribution to the Mathematical Theory of Epidemics".

Why Parameter Estimation?

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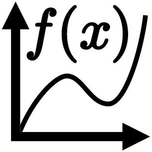
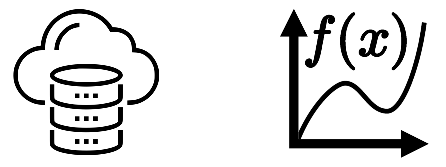


Why Parameter Estimation?



- Prediction
- Control

Problem Formulation

Given a (forward) process model

$$\mathcal{D}(x) = f(x; \theta)$$

and the observation model

$$y = g(x; \theta)$$

determine the value of θ that best fits some given data y.

Forward Problem

To solve the model

$$\mathcal{D}(x) = f(x; \theta)$$

we will typically integrate the right-hand side:

$$x = \mathcal{I}(f(x; \theta))$$

For example, when $\mathcal{D} = \frac{d}{dt}$:

$$x(t) = \int_0^t f(x(\tau); \theta) d\tau$$

Forward Problem

To solve the model

$$\mathcal{D}(x) = f(x;\theta)$$

we will typica

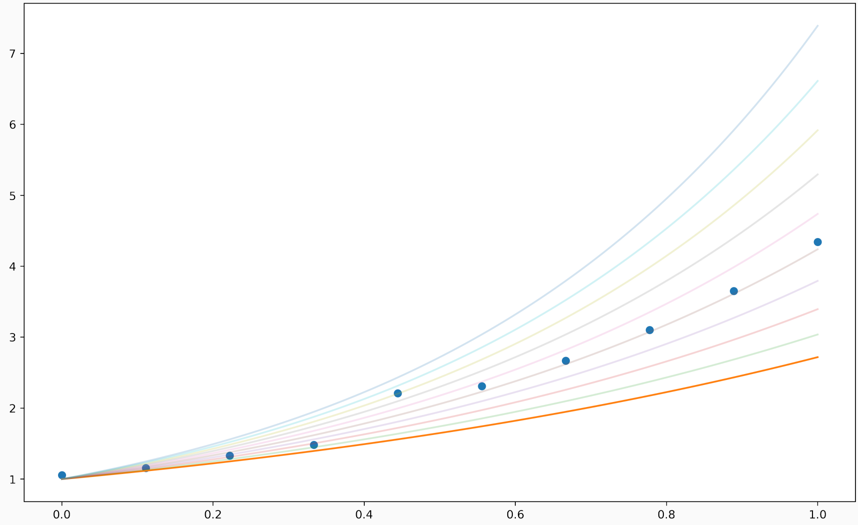
Problem

This is computationally expensive to do!

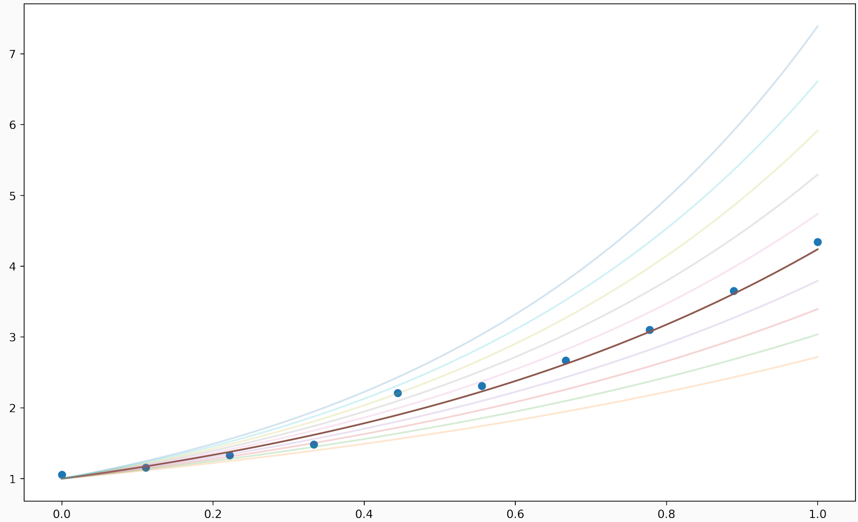
For example, when $\mathcal{D} = \frac{d}{dt}$:

$$x(t) = \int_0^t f(x(\tau);\theta)d\tau$$

Standard Approach



Standard Approach



Standard Approach

Form and solve the constrained minimisation problem:

$$\begin{aligned} \underset{x}{\text{minimize}} \quad & \|y - g(x)\|^2 \\ \text{subject to} \quad & \mathcal{D}(x) - f(x;\theta) = 0. \end{aligned}$$

Constraint is often formulated as

$$x - \mathcal{I}(f(x;\theta)) = 0$$

and directly substituted into the objective.

This is the ordinary least-squares method, or *trajectory matching*.

Pitfalls

1. Computation Expense

Solving the forward model multiple times in OLS can be expensive

Pitfalls

1. Computation Expense
2. Model Error

The forward models solves enforce that the model is (entirely) correct, even if this may not be true

Pitfalls

1. Computation Expense
2. Model Error
3. Identifiability

We make the implicit assumption that we *can* recover adequate estimates of the parameters

Identifiability

Different parameter values $\implies$ different observations

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Structural Identifiability

1. Uniqueness of the parameter estimation problem
2. Perfect, infinite data

Identifiability

$$\text{Different parameter values} \implies \text{different observations}$$

Structural Identifiability

1. Uniqueness of the parameter estimation problem
2. Perfect, infinite data

Practical Identifiability

1. Well-posedness of the parameter estimation problem
2. Noisy, finite data

Methods

Generalised Profiling[†]

Combine *state estimation* and *parameter estimation*

$$\mathcal{L}(\theta) = \underbrace{\|y - g(x)\|^2}_{\substack{\text{state estimation}\\ \text{data misfit}}} + \rho \underbrace{\|\mathcal{D}(x) - f(x;\theta)\|^2}_{\substack{\text{parameter estimation}\\ \text{model misfit}}} + \lambda \underbrace{R(\theta)}_{\text{regularisation}}$$

[†] Ramsay et al., "Parameter estimation for differential equations: a generalized smoothing approach".

Generalised Profiling[†]

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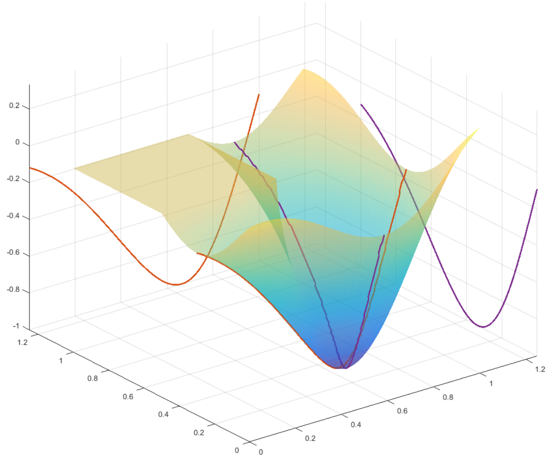
- Does not require a forward model solve
- Does not strictly enforce the model — allows for model error
- Deals with partially observed systems

[†] Ramsay et al., “Parameter estimation for differential equations: a generalized smoothing approach”.

Profile Likelihood

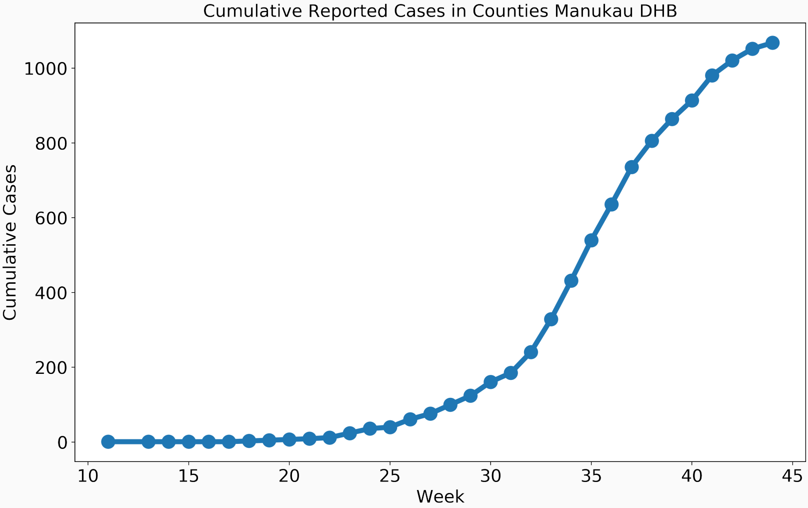
A method used to detect practical identifiability

$$\mathcal{L}_{p,\Omega}(\theta) = \min_{\theta \mid \Omega(\theta)=\omega} \mathcal{L}(\theta)$$

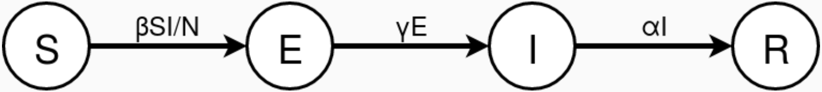


Case Study: Measles

Measles in Auckland 2019



Model



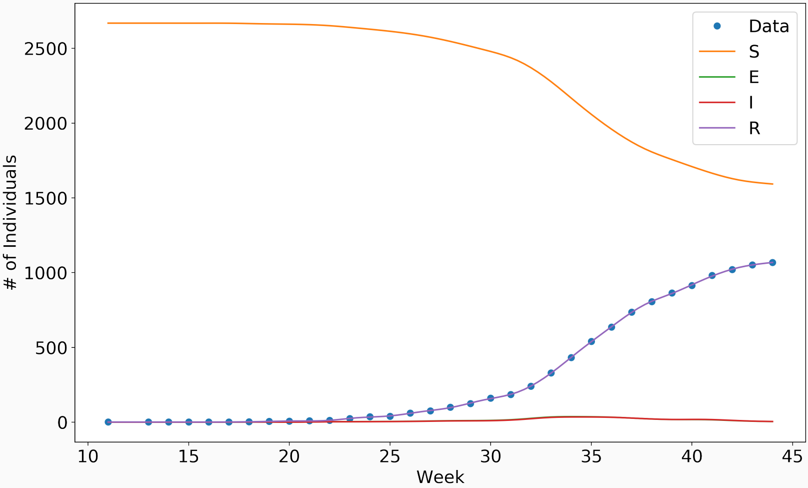
Parameters

α **:** 1/infection period (week^{-1})

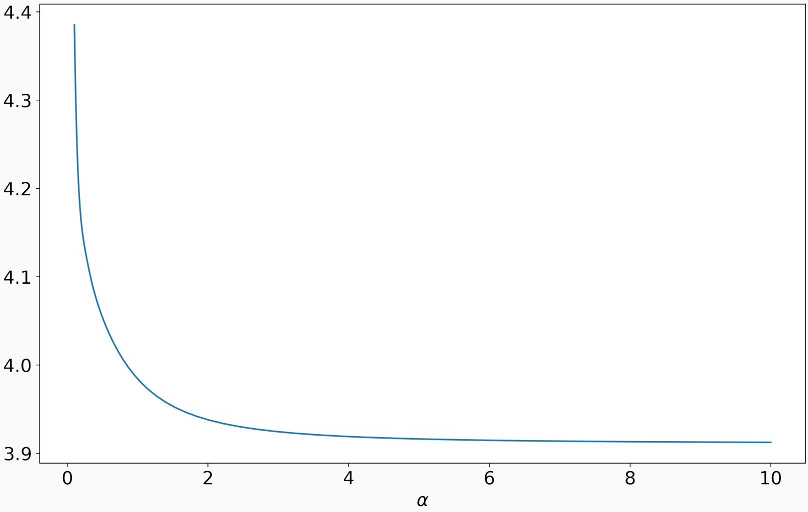
β **:** Effective contact rate (week^{-1})

γ **:** 1/incubation period (week^{-1})

Estimated Trajectory and Parameters



Profile Likelihoods



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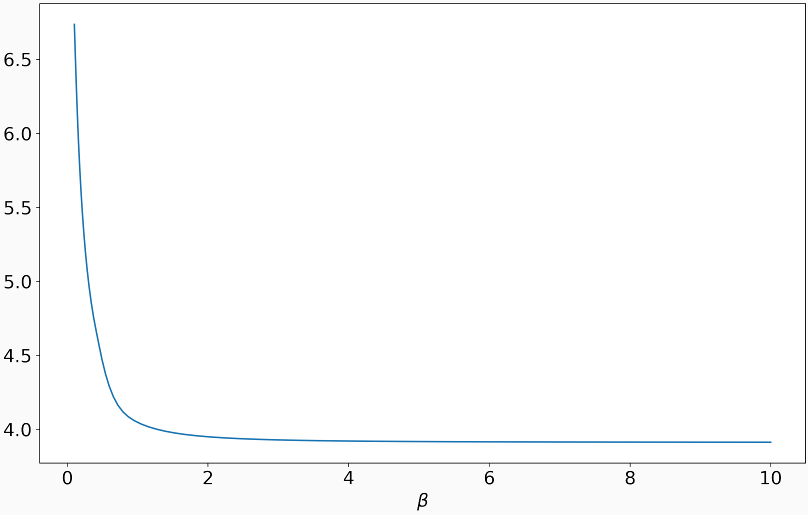
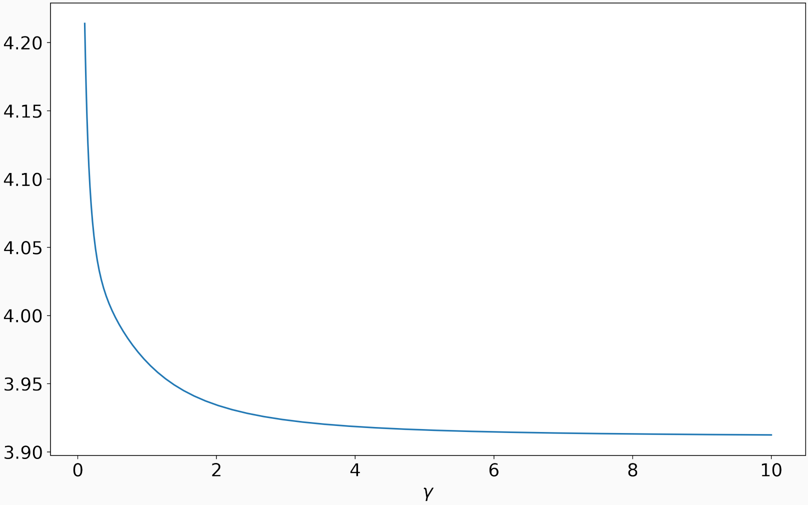
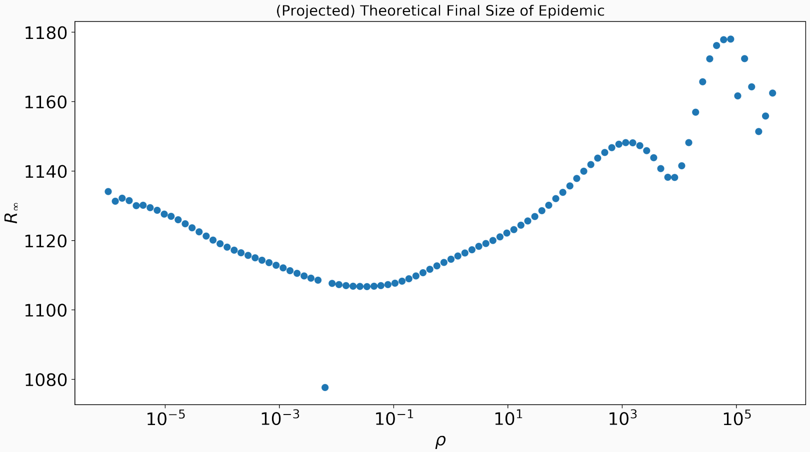


Profile Likelihoods



Interesting Tidbit



Learnings

- The SEIR model can fit the cumulative case data

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- The parameters are not practically identifiable

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- The parameters are not practically identifiable
- The final size of the epidemic is identifiable and stable

Future Work

Directions

1. WDHB Project — Mumps and Measles
2. Spatio-temporal Models
3. Bayesianisation

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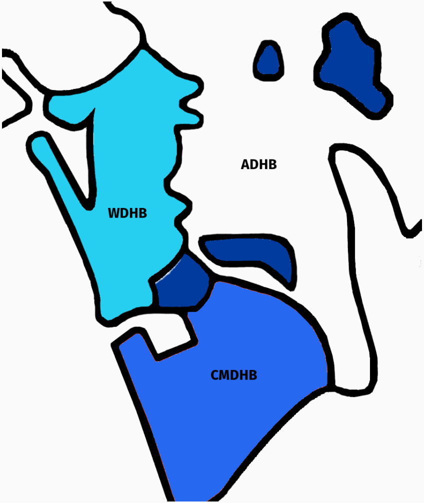
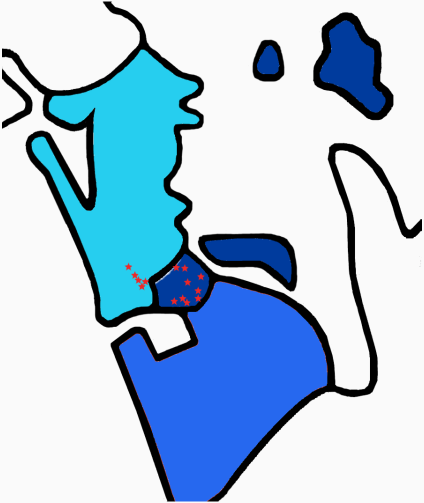
WDHB Project



Map of DHBs in Auckland region[‡]

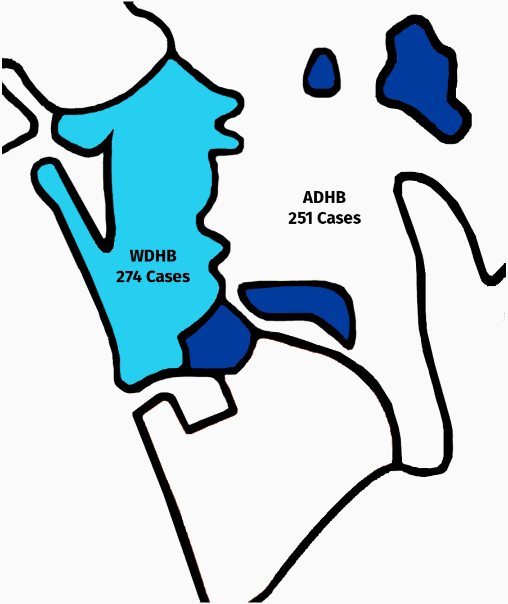
[‡] Adapted from `https://strokenetwork.org.nz/uploads/sites/strokenetwork/files/study_days_and_workshops/DHB-MapNorth.png`

WDHB Project



School immunisation campaigns

WDHB Project



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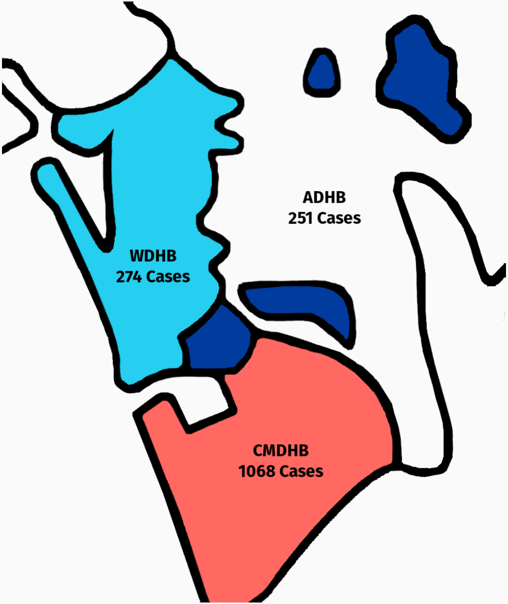

WDHB Project

How effective was the secondary schools programme in response to the 2017 mumps outbreak in mitigating the spread of measles?

Spatio-temporal Models

PDE Models

$$\mathcal{D}(x) := \frac{\partial x}{\partial t} - \nabla \cdot D\nabla(x)$$

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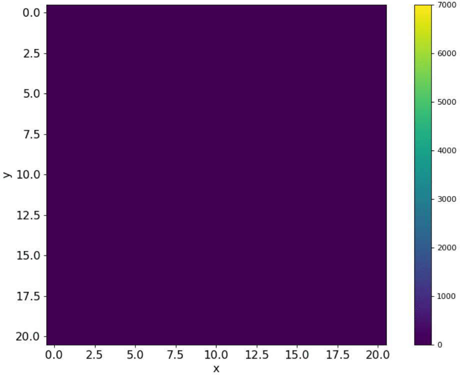
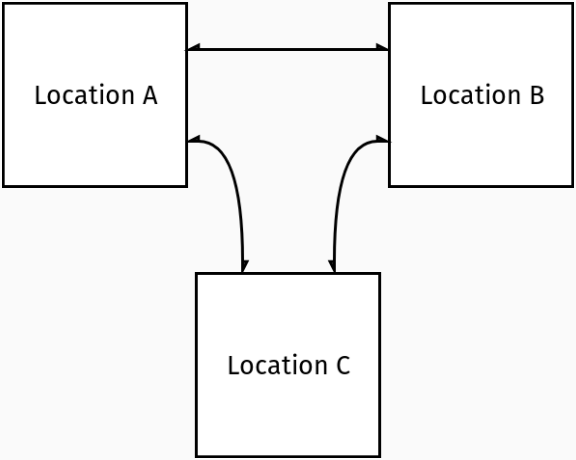


Spatio-temporal Models

Metapopulation models



Spatio-temporal Models

How does generalised profiling extend to these types of models?

Bayesianisation

Bayes' Rule:

$$\pi(\theta|y) = \pi(y|x)\pi(x|\theta)\pi(\theta)$$

Generalised profiling is equivalent to assuming additive iid observation and process error:

$$\begin{aligned} y &= x + \epsilon_o, & \epsilon_o &\sim \mathcal{N}(0, \sigma_o^2) \\ \mathcal{D}(x) &= f(x; \theta) + \epsilon_m, & \epsilon_m &\sim \mathcal{N}(0, \sigma_m^2) \end{aligned}$$

Bayesianisation

1. What happens for other error structures, and can we recover estimators of the posterior?

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1. What happens for other error structures, and can we recover estimators of the posterior?

2. Can we use optimisation methods to speed up the process of Bayesian sampling procedures?

Summary

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  - the data can be fit
  - but the parameters are not identifiable

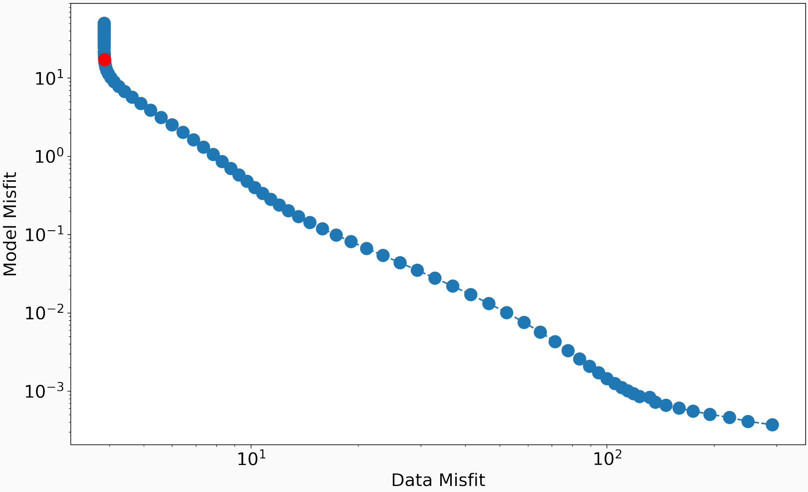
Summary

- Standard methods for parameter estimation have pitfalls
  - computational expense
  - model error
  - identifiability problems
- Problems can be mitigated with generalised profiling and profile likelihood
- These methods have been applied to a measles case study
  - the data can be fit
  - but the parameters are not identifiable
- Future directions include
  - further analysis of measles
  - extension to spatial models
  - comparison with Bayesian methods

Thank you!

Questions?

Measles L-Curve in ρ



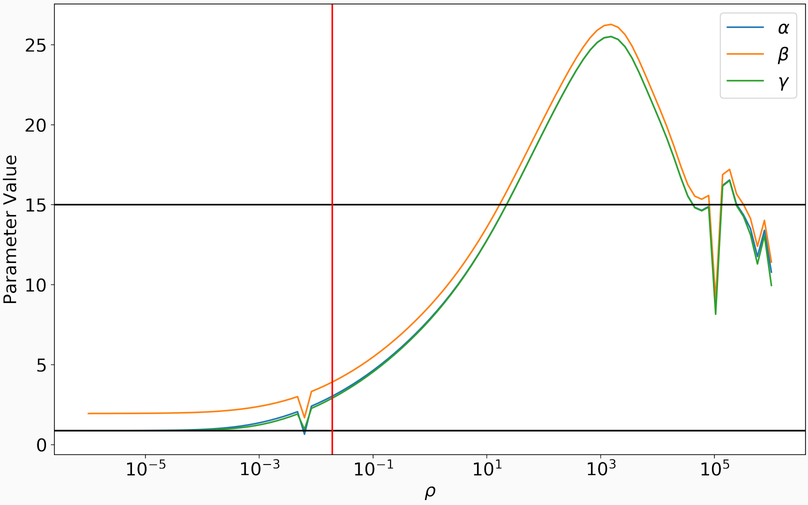
Final Size Relation

$$\log\left(\frac{S(0)}{S_\infty}\right) = \mathcal{R}_0\left(1 - \frac{S_\infty}{N}\right)$$
$$R_\infty = N - S_\infty$$

SEIR Model (ODE Form)

$$\begin{aligned}
\dot{S} &= -\beta S \frac{I}{N} \\
\dot{E} &= \beta S \frac{I}{N} - \gamma E \\
\dot{I} &= \gamma E - \alpha I \\
\dot{R} &= \alpha I
\end{aligned}$$

Measles Parameter Value Trace in ρ



Measles $\mathcal{R}_0$ Trace in ρ