

Fitting a Managed Population Model using Approx. Bayesian Computation

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Introduction

The Cardiff University Pathogen Lab has been maintaining different strains of the *Gyrodactylus* parasite for over 25 years. They are closely managed to avoid parasite extinction.

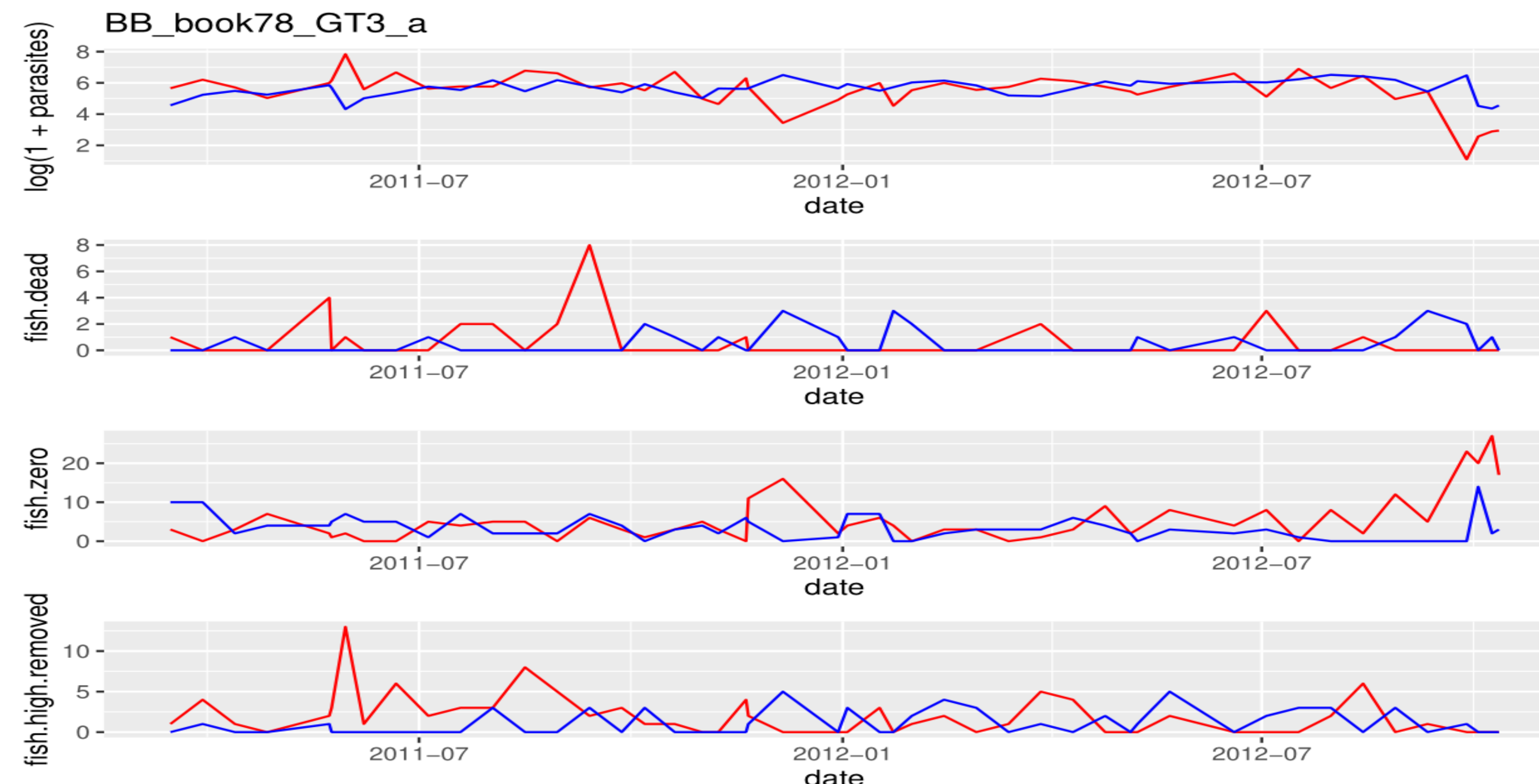
We use ABC to estimate the virulence of different *Gyrodactylus* strains, using lab records of parasite population numbers and deaths of host fish. Only total population numbers summed over all host fish are known.

Gyrodactylus

Gyrodactylus is a piscine ectoparasite, length around 0.5mm. Gyrodactylids are common fish parasites and cause problems for all teleosts, including farmed salmonids and aquarium fish.



- *Gyrodactylus* can reproduce asexually and individuals are born pregnant, allowing parasite populations to grow very quickly. **BOOM**
- Large *Gyrodactylus* populations will kill their hosts, though they will attempt to migrate when the current host gets too crowded. **BUST**
- In the laboratory setting, fish with high parasite counts are removed and rehabilitated, though some fish still die.
- The point at which fish are removed varies, generally depending on whether *Gyrodactylus* numbers are being built up for some experiment, or if the population is just being maintained.



Sample data for lab bred *Gyrodactylus turnbulli* in red, and a realisation from the fitted model in blue.

Population dynamics

Let x be the parasite population on a single fish, then we have:

- λ individual birth rate
- μ individual death rate
- m equilibrium population
- $(\lambda - \mu)x/m$ individual emigration rate
- α emigration survival probability
- δx host death rate

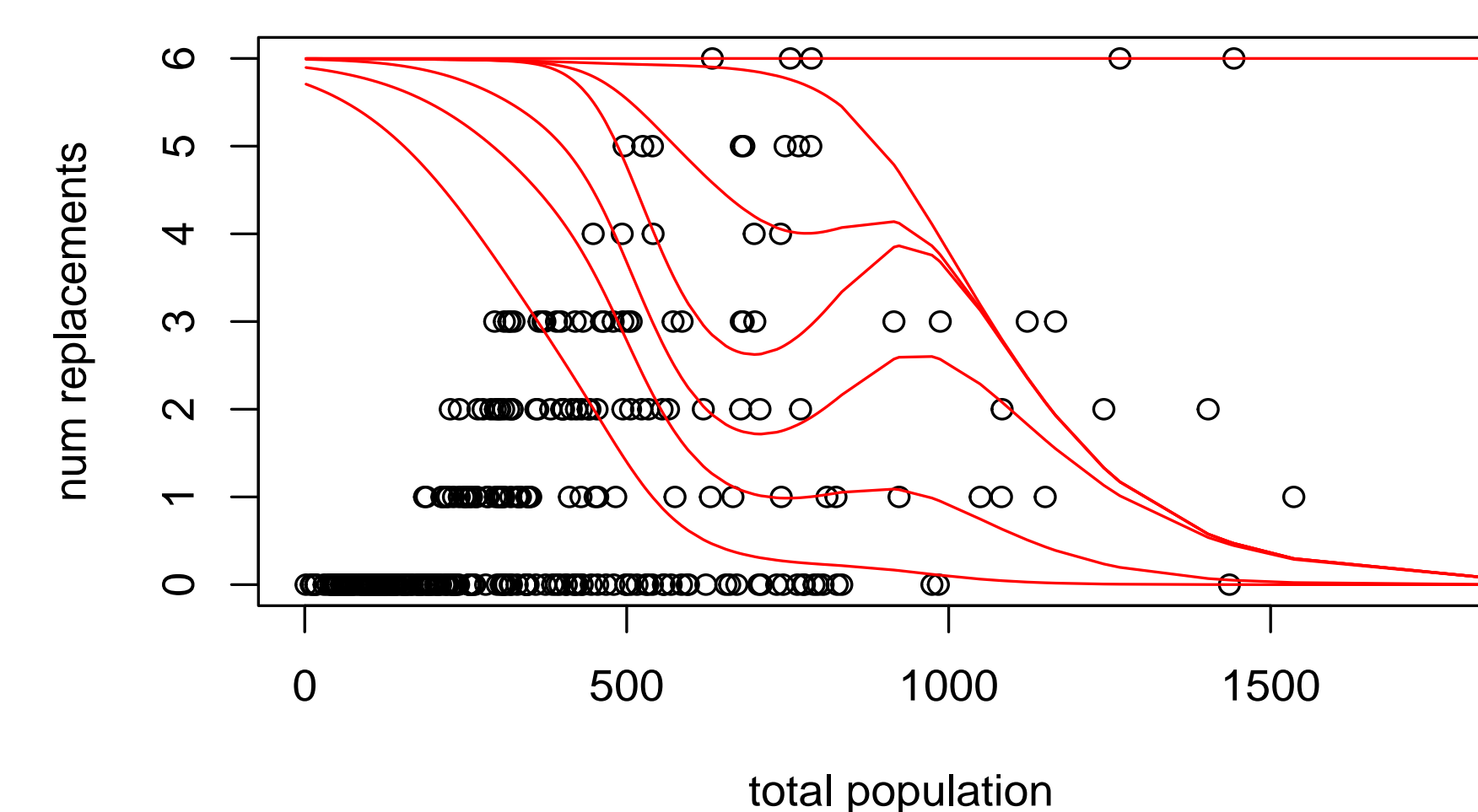
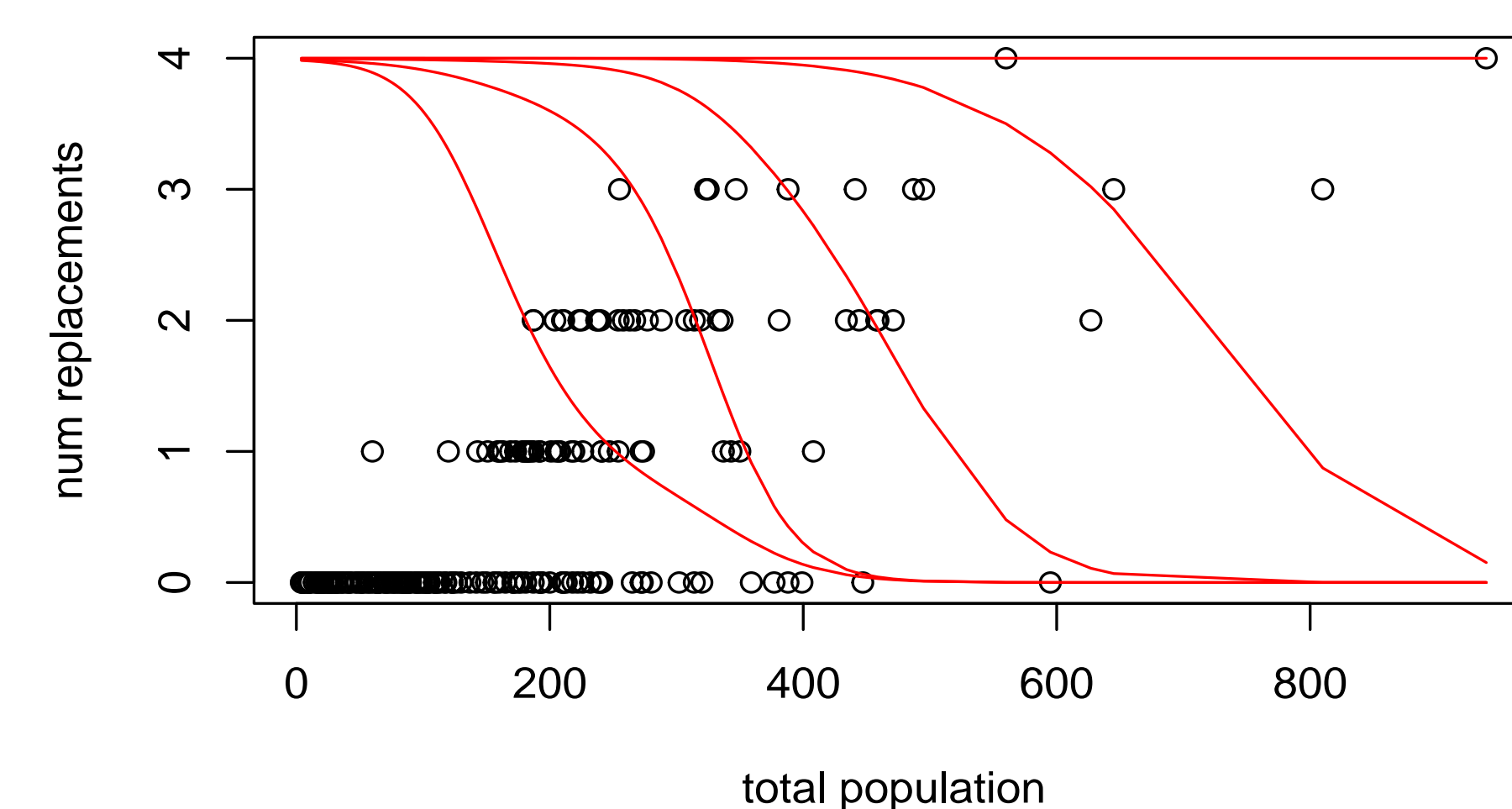
We also have immigration from other fish. Surviving émigrés choose from the available hosts with equal probabilities.

Population management

Each day we replace any dead fish, and on **screening** days we also:

- Replace some of the most infected fish with uninfected fish.
- Change the total number of host fish by introducing new fish.

We consider two management régimes—**high** and **low**—depending on whether the lab is building up parasite numbers for an experiment, or just maintaining the population.



Fitted probabilities of 0, 1, 2, ... replacements: low régime on the left and high régime on the right. Probabilities are given by the widths of the stacked bands, as a function of total parasite population.

ABC fitting

We used the sequential sampling approach of Toni et al. (2009), as described by Kypraios, Neal & Prangle (2017).

For the **summary statistic** we used, for each observed sequence:

- mean of $\log(1 + \text{total population})$
- standard deviation of $\log(1 + \text{total population})$
- mean parasites per live fish
- mean fish deaths
- mean number of uninfected fish

Each sequence was sampled on fixed screening days.

Summaries of simulated and real data were compared using weighted least squares, with weights proportional to sequence length and the perceived importance of each statistic.

Priors were moderately informative, based on an understanding of birth rates, death rates and host mortality coming from more detailed studies.

Posteriors

The model was unable to distinguish between m and α , so the latter was fixed at 0.5.

Using the lab records we have digitised so far, we have been able to fit models to a lab bred and a wild strain of *Gyrodactylus turnbulli*.

There is evidence of differences in the birth rate and the host death rate, and hopefully the credible intervals will shrink as we are able to incorporate more data.

<i>Gyrodactylus turnbulli</i>						
	Lab bred			Wild		
	5%	median	95%	5%	median	95%
λ	0.08	0.19	0.55	0.06	0.11	0.29
μ	0.05	0.10	0.35	0.05	0.08	0.20
m	315	460	660	310	460	650
δ	3.6e-8	0.0041	0.027	2.8e-9	0.00098	0.018