

Midterm report

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December 11, 2018

1 Introduction

Measles is one of the most extensively studied systems in theoretical epidemiology. Over the last few decades, much of the literature have been devoted to explaining wide range of dynamical behaviours it can exhibit, ranging from simple annual cycles to near-chaotic dynamics (Bolker and Grenfell, 1993). These investigations have provided us important theoretical foundation in population dynamics and useful statistical tools for analyzing epidemic time series.

One of the simplest, yet widely used, model is the Time series Susceptible-Infected-Recovered (TSIR) model (Bjornstad et al., 2002).

This thesis aims to extend the TSIR framework to estimate temporally and spatially varying transmission rates of measles. First, I review the TSIR framework along with other useful statistical frameworks that provide necessary bases for building the spatial framework. Second, I extend the TSIR model by incorporating Bayesian hierarchical structure in epidemiological parameters and spatial mixing among geographically distant regions. Finally, I discuss results of my analysis and their implications.

2 Review - TSIR model

The basic TSIR model describes dynamics of susceptible S_t and infected I_t individuals with the following set of equations:

$$\begin{aligned} S_t &= S_{t-1} + B_{t-1} - I_t \\ I_t &= \beta_w S_{t-1} \times \frac{I_{t-1}^\alpha}{N_{t-1}} \end{aligned} \tag{1}$$

where B_t represents number of births, β_w represents transmission rate for bi-week w , N represents total population size, and α represents a heterogeneity parameter. The main idea behind the TSIR model is that the dynamical system can be linearized by taking a log transformation:

$$\log I_t = \log \beta_w + \log S_{t-1} + \alpha \log I_{t-1} - \log N_{t-1}. \tag{2}$$

After linearization, inference becomes a two-step process. First, *relative* susceptible dynamics $Z_t = S_t - \bar{S}$ is reconstructed from incidence and birth time series. Second, given the *true* susceptible dynamics S_t , time varying transmission rates β_w and heterogeneity parameter α is estimated using a generalized linear model (Bjornstad et al., 2002). Inferred parameters can be used to simulate epidemics and make predictions about future epidemics.

2.1 Susceptible reconstruction

In this section, we describe the susceptible reconstruction method introduced by

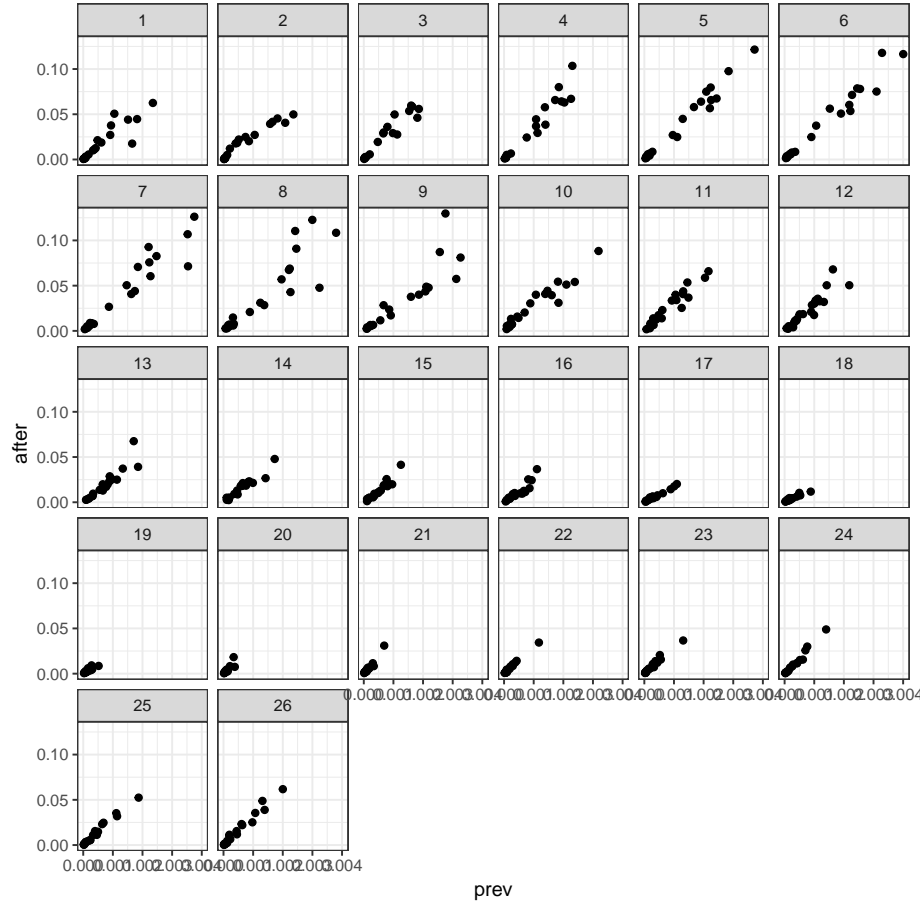
Figure ??? provides an analysis of measles time series from London

```
library(tsiR)
library(ggplot2); theme_set(theme_bw())
london <- twentymeas$London
rr <- runtsir(london, nsim=1)
```

##	alpha	mean beta	mean rho	mean sus
##	9.60e-01	1.19e-05	4.57e-01	1.14e+05
##	prop. init. sus. prop. init. inf.			
##	3.01e-02	6.12e-05		

```
tmpdf <- data.frame(
  prev=head(london$cases*rr$rho/london$pop, -1), ## I/N
  after=tail(london$cases*rr$rho/rr$simS[,1], -1), ## I/S
  period=rep(1:26, 100)[1:(nrow(london)-1)]
)

ggplot(tmpdf) +
  geom_point(aes(prev, after)) +
  facet_wrap(~period)
```



2.2 Splines

2.3 Hierarchical structure

3 Methods

References

- Bjornstad, O. N., B. F. Finkenstadt, and B. T. Grenfell (2002). Dynamics of measles epidemics: estimating scaling of transmission rates using a time series sir model. *Ecological Monographs* 72(2), 169–184.
- Bolker, B. and B. T. Grenfell (1993). Chaos and biological complexity in measles dynamics. *Proc. R. Soc. Lond. B* 251(1330), 75–81.