Notes

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1 Discrete time model

We are interested in estimating transmission rate (potentially time varying) across space. First, let's begin with a simple example.

$$\begin{aligned} S_{t+1} &= S_t - \beta_t S_t I_t \\ I_{t+1} &= \beta_t S_t I_t \end{aligned} \tag{1}$$

In this particular case, we have

$$i_{t+1} = \beta S_{t+1} I_{t+1} = \beta S_{t+1} i_t. \tag{2}$$

This is essentially the framework for the TSIR model. The implicit assumption is that all infection occurs in one generation.

1.1 Multiple time step

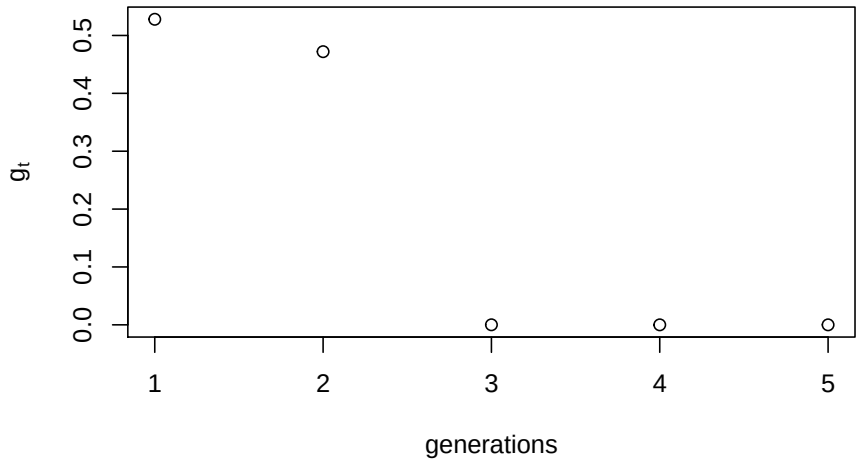
We can extend this framework such that infection lasts for more than one generation (see Fraser (2007)?).

$$S_{t+1} = S_t - S_t \sum_{k=1}^{t} \beta_{t,k} i_k g_{t+1-k} \tag{3}$$

Incidence is given by

$$i_{t+1} = S_t \sum_{k=1}^{t} \beta_{t,k} i_k g_{t+1-k}. \tag{4}$$

Measles has mean generation interval of 15 days and CV of 0.21. If we approximte that with a gamma distribution, we can approximate g_t.



However, there is probably some censoring that we have to take into account and more infection must occur than 52%. In fact, we have to calculate the probability that a person infected within the first two weeks will infected another person during the next two weeks. Given that the distribution of infection time follows some distribution $f(t)$, where $0 \leq t \leq 14$ and generation time $g(t)$, we want to compute the following:

$$\int_0^1 4f(t) \int_{14-t}^{28-t} g(s)dsdt$$

Assume that $f(t)$ is a uniform distribution...

```
library(pracma)
integral2(function(x, y) dunif(x, min=0, max=14) *
                         dgamma(y, shape=1/gcv^2, scale=gbar*gcv^2),
                  xmin=0,
                  xmax=14,
                  ymin=function(x) 14-x,
                  ymax=function(x) 28-x)

## $Q
## [1] 0.8160168
##
## $error
## [1] 1.693841e-11
```

We obtain 81.6%.

Assume that most of infection occur within the first two generations:

$$i_{t+1} = S_t(\beta_{t,1} i_t g_1 + \beta_{t-1,2} i_{t-1} g_2). \tag{5}$$

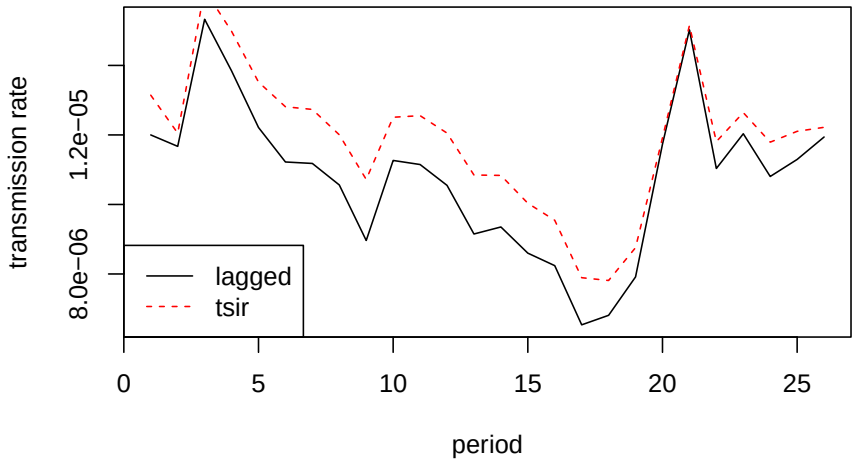
If we know S_t, we can solve for β by minimizing sum of squares. In particular, we can write the above equation as matrix form:

$$\begin{bmatrix} i_3 \\ i_4 \\ \vdots \\ i_2 8 \\ i_2 9 \\ \vdots \end{bmatrix} = \begin{bmatrix} S_2 i_1 g_2 & S_2 i_2 g_1 & 0 & \cdots & 0 \\ 0 & S_3 i_2 g_2 & S_3 i_3 g_1 & \cdots & 0 \\ \vdots & & \ddots & & \vdots \\ S_2 7 i_2 7 g_1 & 0 & \cdots & 0 & S_2 7 i_2 6 g_2 \\ S_2 8 i_2 7 g_2 & S_2 8 i_2 8 g_1 & 0 \cdots & 0 & \\ \vdots & & & & \vdots \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \vdots \\ \beta_{25} \\ \beta_{26} \end{bmatrix} \tag{6}$$

We can probably even use tensors to make this cleaner (or not)...

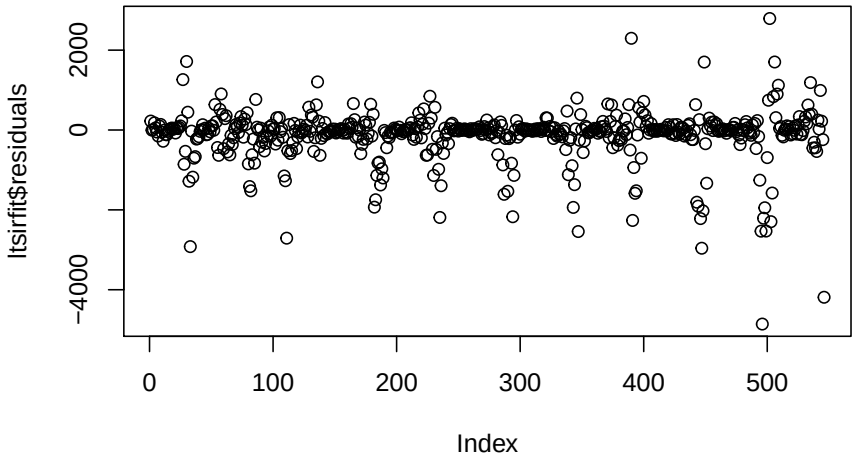
We can compare transmission rates inferred from this model vs. those inferred from the tsir model:

```
london <- twentymeas[["London"]]

g_t_adj <- c(0.816, 1-0.816)

ltsirfit <- runltsir(london, g_t_adj)
tsirfit <- runtsir(data=london, method="pois", nsim=100, IP=2, inits.fit=FALSE)

##            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
```



However, We run into residual issuses.

```
plot(ltsirfit$residuals)
```



For the case of measles, changes in transmission rates are mostly driven by changes in contact rates. Hence, we can simplify the model such that

$$i_{t+1} = \beta_{t,1} S_t((1-\epsilon)i_t + \epsilon i_{t-1}). \tag{7}$$

Then, we can even include the heterogeneity parameter and perform a log transformation to obtain a linear problem:

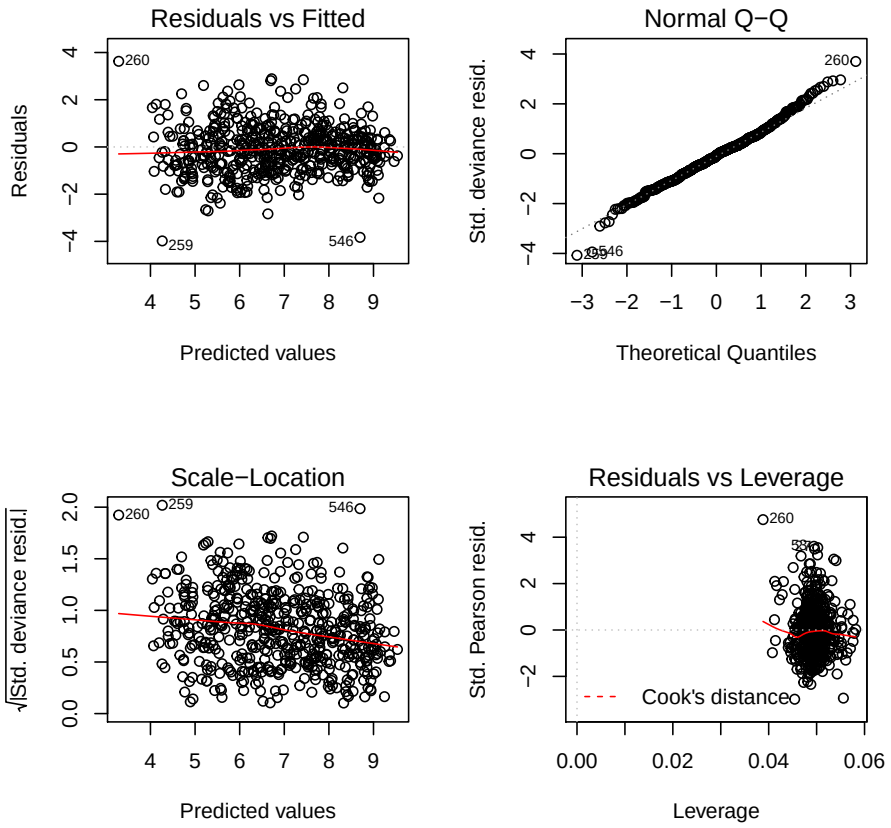
$$\log i_{t+1} = \log \beta_t + \log S_t + \alpha \log((1-\epsilon)i_t + \epsilon i_{t-1}). \tag{8}$$

We can assume Gaussian error but we can also use negative binomial with log linik:

$$i_{t+1} = \text{NegBin}\left(\exp\left(\log \beta_t + \log S_t + \alpha \log((1-\epsilon)i_t + \epsilon i_{t-1})\right)\right) \tag{9}$$

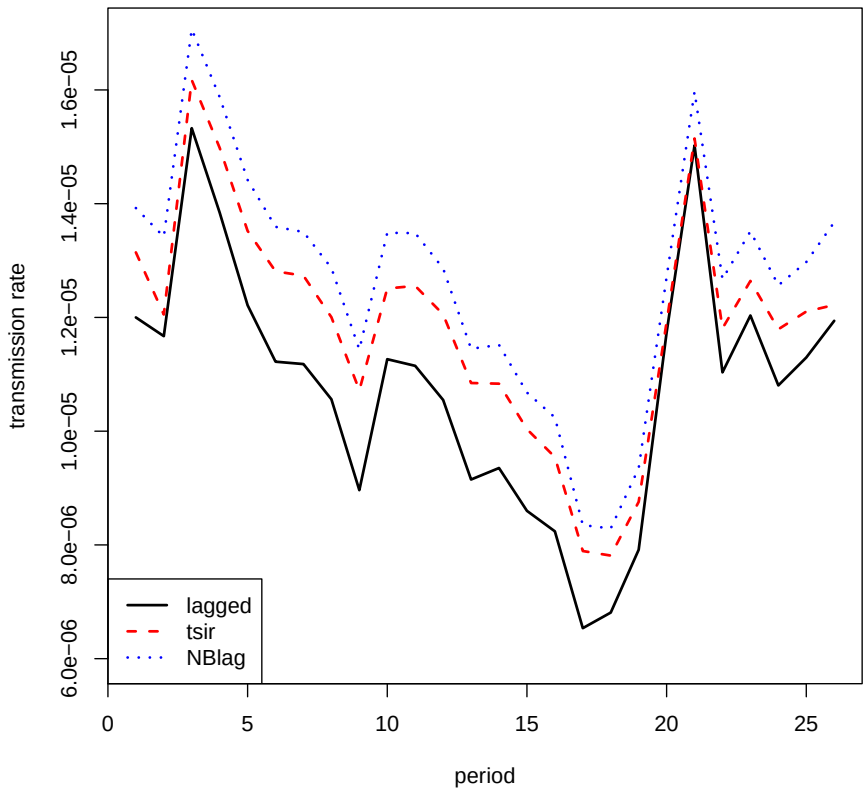
and perform a two dimensional optimization on ϵ and $\bar{S}$. Then, our residuals are much better:

```
ltsirfit_NB <- runltsir_NB(london, predict=TRUE, nsim=100)
par(mfrow=c(2, 2))
plot(ltsirfit_NB$fit)
```



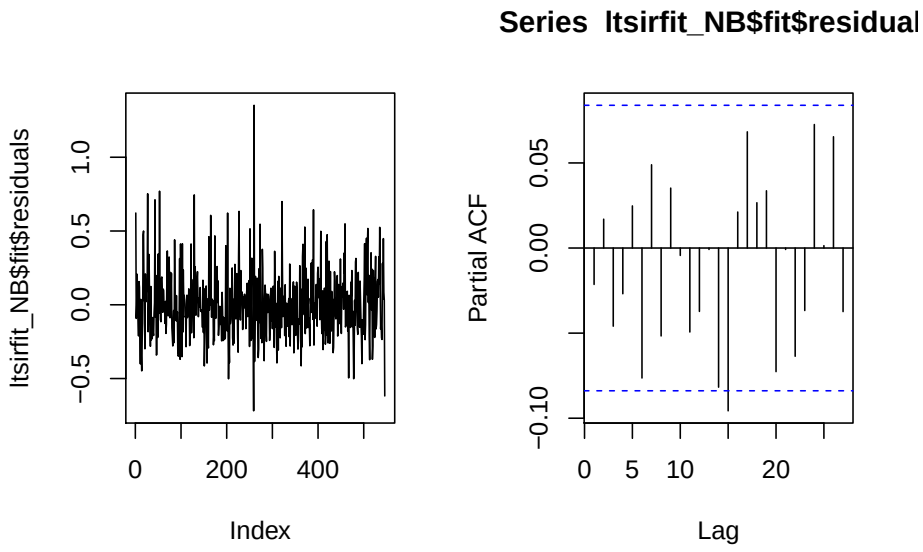
```
par(mfrow=c(1,1))
```

Looking at the estimates of the transmission rates:



However, it appears that there might be weak underlying structures in the residuals that we might have to deal with? Might be too weak to care about?

```
par(mfrow=c(1, 2))
plot(ltsirfit_NB$fit$residuals, type="l")
pacf(ltsirfit_NB$fit$residuals)
```



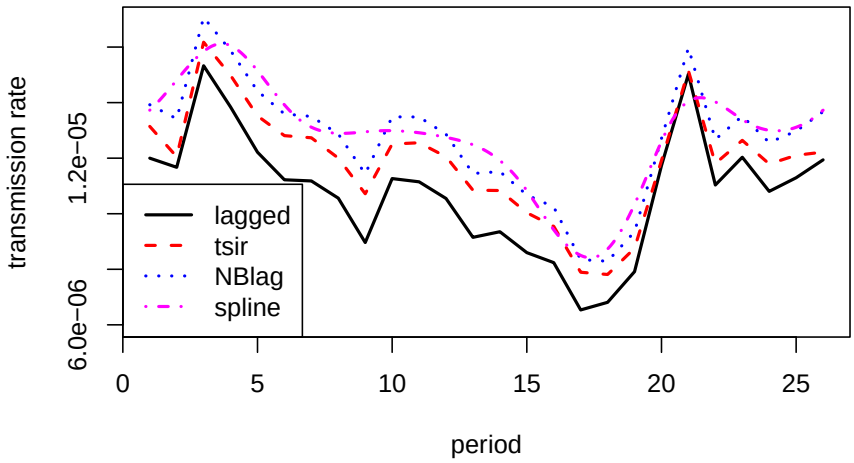

```
par(mfrow=c(1,1))
```

1.2 Splines

We can try to smooth transmission rate over time using cyclic splines (`s(period, bs=''cc'')`) with GAM.

```
ltsirfit_spline <- runltsir_NB(london, spline=TRUE, predict=TRUE, nsim=100)
```

Transmission rates?



Note that ϵ estimated by the model is fairly small (1.4%):

```
ltsirfit_spline$epsilon
```

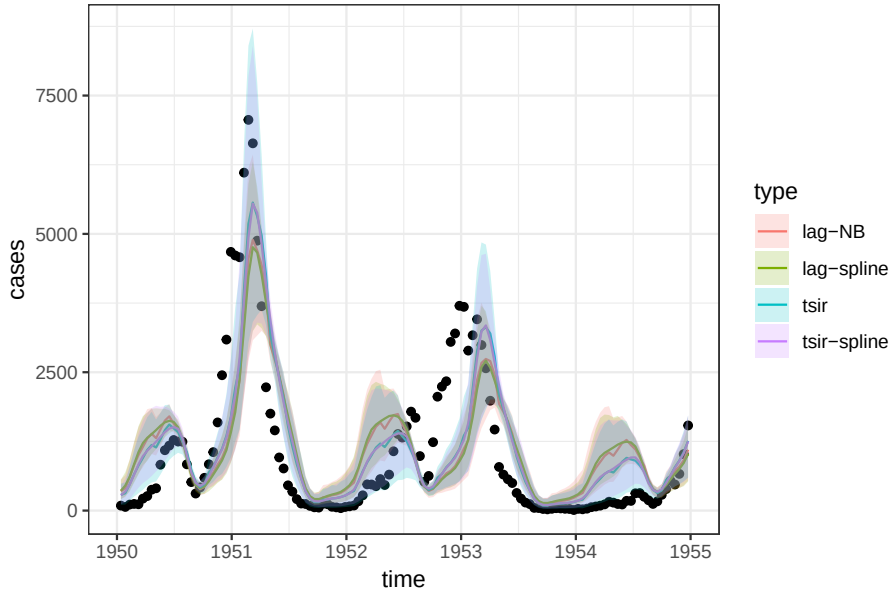
```
##    epsilon
## 0.01434702
```

There's another spline fit that I built inside tsiR...

```
tsirfit2 <- runtsir.spline(london, method="pois", nsim=100, IP=2, inits.fit=FALSE)
```

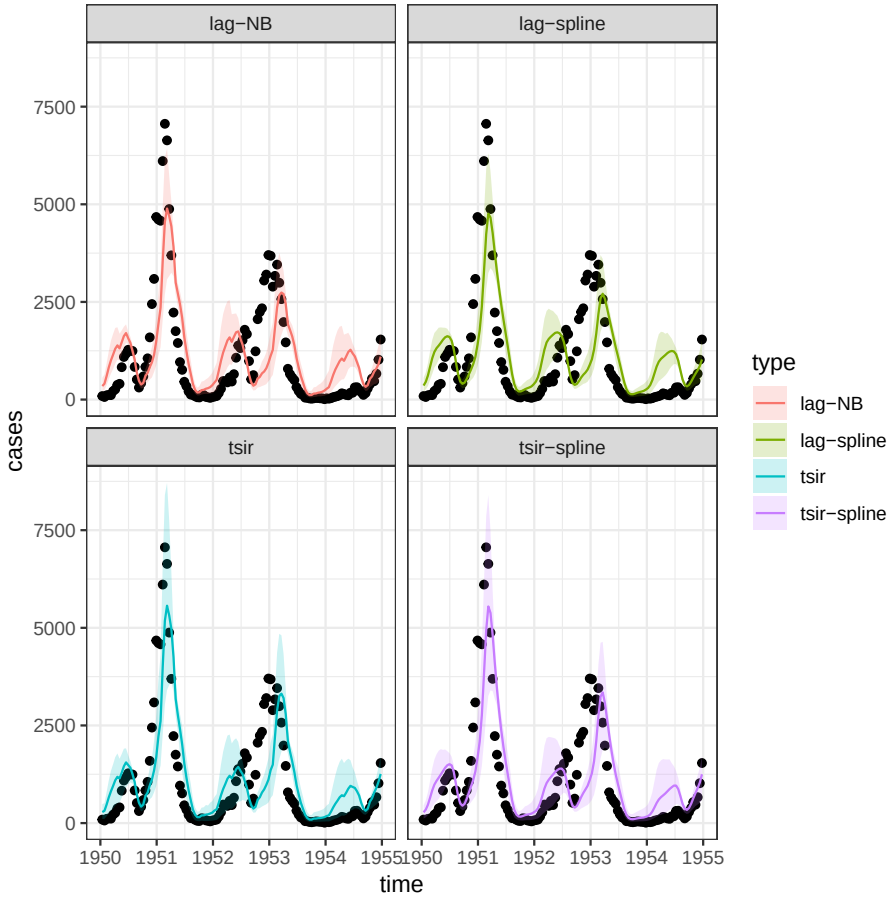
```
##            alpha        mean beta         mean rho         mean sus
##         9.60e-01         1.19e-05         4.57e-01         1.14e+05
## prop. init. sus. prop. init. inf.
##         3.01e-02         6.12e-05
```

Now, we want to compare how each model predicts the time series:



facet?

```
gcomp +
        facet_wrap(~type)
```



Misc

See Vehtari - Slick time series... (Andrew Gelman); see the cover of third edition of Bayesian analysis.

```
library(MASS)

# glm.fit(family=negative.binomial(theta=10, link="identity"))
```

References

Fraser, C. (2007). Estimating individual and household reproduction numbers in an emerging epidemic. *PloS one 2*(8), e758.