

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

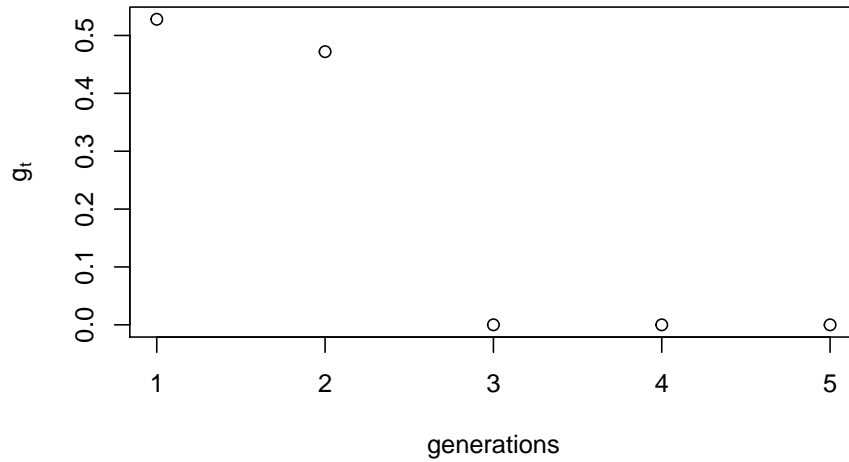
We can extend this framework such that infection lasts for more than one generation (see Fraser (2007)?).

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

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 approximate that with a gamma distribution, we can approximate g_t .



So we can say that most of infection occur within the first two generations (and assume that transmission rate stays constant?):

$$i_{t+1} = S_t(\beta_t i_t g_1 + \beta_{t-1} i_{t-1} g_2). \quad (5)$$

```
library(tsiR)
g_t_adj <- c(g_t[1], 1-g_t[1])

london <- twentymeas[["London"]]

IP <- 2

cumcases <- cumsum(london$cases)
cumbirth <- cumsum(london$births)

X <- cumcases
Y <- cumbirth

Yhat <- lowess(X,Y,f = 2/3, iter = 1)$y

rho <- derivative(X,Yhat)

Z <- residual.cases(Yhat,Y)
adj.rho <- rho

period <- rep(1:(52/IP), round(nrow(london)+1))[2:(nrow(london)-1)]
```

```

Iadjusted <- london$cases * adj.rho
Inew <- tail(Iadjusted,-2)
Iminus1 <- tail(head(Iadjusted,-1), -1)
Iminus2 <- head(Iadjusted,-2)
Zminus <- tail(head(Z, -1), -1)

lIminus <- log(head(Iadjusted,-1)+1)
Zminus <- head(Z,-1)

pop <- data$pop

## Error in data$pop: object of type 'closure' is not subsettable

minSmean <- max(0.01*pop,-(min(Z)+1))

## Error in eval(expr, envir, enclos): object 'pop' not found

Smean <- seq(minSmean, 0.4*mean(pop), length=250)

## Error in seq(minSmean, 0.4 * mean(pop), length = 250): object 'minSmean'
not found

loglik <- rep(NA, length(Smean))

## Error in eval(expr, envir, enclos): object 'Smean' not found

```

References

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