Notes on network/generation interval

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1 Censored generation interval distributions

Following Champredon and Dushoff (2015), we can write the number of infection occuring at time t caused by infectors who were themselves infected at time s as

$$i_s(t) = K(t-s)i(s)S(t) \tag{1}$$

Writing the kernel as the product of the intrinsic genreation distributions and $\mathcal{R}_0$, we get

$$i_s(t) = \mathcal{R}_0 g(t-s)i(s)S(t) \tag{2}$$

The censored generation interval distributions is what is often measured and we have to account for all infections that happen before time t. Note that number of infection occuring at time s caused by infectors who were themselves infected at time $s-\tau$ is given by

$$i_{s-\tau}(s) = \mathcal{R}_0 i(s-\tau)g(\tau)S(s) \tag{3}$$

Normalizing this gives the backward generation interval distributions of the cohorts at time s but we are interested in all infections that are τ time steps apart before time t:

$$\mathcal{R}_0 \int_\tau^t i(s-\tau)g(\tau)S(s)ds. \tag{4}$$

Then, the censored generation interval is given by

$$c_t(\tau) = \frac{\int_\tau^t i(s-\tau)g(\tau)S(s)ds}{\int_0^t \int_x^t i(s-x)g(x)S(s)dsdx}. \tag{5}$$

We note that the denominater is basically cumulative incidence up to time t divided by $\mathcal{R}_0$. The stragihtforward intuition behind this is that we are normalizing by all incidence before time t. Mathematically, we have the following:

$$\begin{aligned}\mathcal{R}_0 \int_0^t \int_x^t i(s-x)g(x)S(s)dsdx &= \int_0^t \mathcal{R}_0 S(s) \int_0^s i(s-x)g(x)dxds \\ &= \int_0^t i(s)ds\end{aligned} \tag{6}$$

Then,

$$c_t(\tau) = \frac{\mathcal{R}_0 \int_\tau^t i(s-\tau) S(s) ds}{\int_0^t i(s) ds} g(\tau)$$

During an early outbreak, incidence grows exponentially ($i(t) = i(0)\exp(rt)$) and proportion susceptible doesn't change very much. So we can write this as

$$c_t(\tau) = \mathcal{R} g(\tau) \exp(-r\tau) \frac{\int_\tau^t \exp(rs) ds}{\int_0^t \exp(rs) ds},$$

where $\mathcal{R} = \mathcal{R}_0 S$. What does this mean?

We're also interested in $c_\infty(\tau)$. This is something people can study after the outbreak.

$$c_\infty(\tau) = \frac{\mathcal{R}_0 \int_\tau^\infty i(s-\tau) S(s) ds}{\int_0^\infty i(s) ds} g(\tau)$$

2 SIR model

First, let's start with the simplest case: SIR model.

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta}{N} SI \\ \frac{dI}{dt} &= \frac{\beta}{N} SI - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned} \tag{7}$$

For this model, intrinsic generation interval distributions follows an exponential distribution with rate parameter γ.

What is often measured is *censored* generation interval distributions:

```
library(deSolve)

## Warning:  package 'deSolve' was built under R version 3.3.3

sir <- function(t, y, parms) {
    with(as.list(c(y, parms)), {
        dS <- -beta/N*S*I
        dI <- beta/N*S*I - gamma*I
        list(c(dS, dI))
    })
}

parms <- c(beta=2, gamma=1, N=1000)
y <- c(S = 999, I=1)

ode(y, 0:10, sir, parms)
```

```
##    time        S          I
## 1     0 999.0000   1.000000
## 2     1 995.5805   2.705102
## 3     2 986.4422   7.232768
## 4     3 962.7806  18.754753
## 5     4 906.1829  45.060231
## 6     5 792.7542  91.625025
## 7     6 626.8697 140.122109
## 8     7 464.1079 152.572969
## 9     8 349.8662 125.531861
## 10    9 283.0737  86.402452
## 11   10 246.4744  53.777136
```

```
sir.incidence <- function(t) {
    t <- seq(0, t, by=0.1)

}
```

References

Champredon, D. and J. Dushoff (2015). Intrinsic and realized generation intervals in infectious-disease transmission. *Proceedings. Biological sciences 282*(1821), 20152026–20152026.