

Fitting ODE-based models to hospitalization data

Deterministic ODE-based SIR

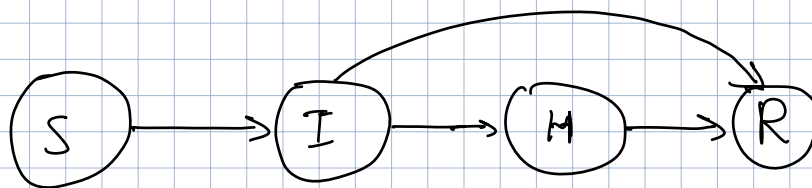
When population size $N \rightarrow \infty$, stochastic SIR approaches its deterministic limit, governed by the following system of ordinary differential equations:

$$\frac{dS(t)}{dt} = -\frac{\beta}{N} S(t) I(t)$$

$$\frac{dI(t)}{dt} = \frac{\beta}{N} S(t) I(t) - \gamma I(t)$$

$$\frac{dR(t)}{dt} = \gamma \cdot (1-g) I(t) + \lambda H(t)$$

$$\frac{dH(t)}{dt} = \gamma \cdot g I(t) - \lambda H(t)$$



β = transmission rate, γ - removal or hospitalization rate

g = infection-to-hospitalization ratio (probability) or IHR

$1/\lambda$ - average length of hospital stay

Hospitalization can be reported as incidence (new hospitalizations per day or week) or as prevalence (number of hospital beds occupied at a particular time). Prevalence reporting is common in US right now.

Suppose y_1, \dots, y_n are hospital beds reported at times t_1, \dots, t_n . We can assume a negative binomial distribution as before

$$y_i \sim \text{Negative-binomial} \left(\mu = H(t_i), \sigma^2 = \mu \left(1 + \frac{\mu}{\varphi} \right) \right)$$

$\mu > 0$ mean of the negative binomial

$\varphi > 0$ - overdispersion parameter

Why negative binomial — Poisson could also work, but it is better to have a more flexible mean-variance relationship.

Note: $H(t_i) = H(t_i, \beta, \gamma, q, \alpha)$ - deterministic function of transmission model parameters

Since we now have a full data generating process described, we know what the likelihood function is

$$\Pr(y_1, \dots, y_n | \beta, \gamma, \phi, \alpha, \varphi) = \prod_{i=1}^n \Pr(y_i | \beta, \gamma, \phi, \alpha, \varphi), \text{ where}$$

$\Pr(y | \beta, \gamma, \phi, \alpha, \varphi)$ is negative binomial probability mass function.

So the posterior distribution becomes

$$\Pr(\beta, \gamma, \phi, \alpha, \varphi | y_1, \dots, y_n) \propto \Pr(y_1, \dots, y_n | \beta, \gamma, \phi, \alpha, \varphi) \times \underbrace{\Pr(\beta, \gamma, \phi, \alpha, \varphi)}_{\text{need to specify priors}}$$

Fitting ODE-based models to case data

$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t)$$

$$\frac{dR(t)}{dt} = \gamma I(t)$$

$$\frac{dN_{SI}(t)}{dt} = \beta S(t) I(t)$$



But, we observe cases as incidence data

y_1, \dots, y_n , where y_i is number of new cases in interval $[t_i, t_{i+1}]$

$I(t_{i+1}) - I(t_i) \neq \#$ of new infections

$N_{SI}(t)$ = cumulative incidence or the total number of infections up to time t .

$$\Delta N_{SI}^{(i)} = N_{SI}(t_{i+1}) - N_{SI}(t_i) = \# \text{ of new infections in time period } [t_i, t_{i+1})$$

$$y_i \sim \text{Negative-binomial}(\mu = \mathcal{D} \Delta N_{SI}^{(i)}, \sigma^2 = \mu(1 + \frac{\mu}{\varphi}))$$

\mathcal{D} - case detection probability

$$\Pr(y_1, \dots, y_n | \beta, \gamma, \mathcal{D}, \varphi) = \prod_{i=1}^n \Pr(y_i | \beta, \gamma, \mathcal{D}, \varphi), \text{ where}$$

$\Pr(y_i | \beta, \gamma, \mathcal{D}, \varphi)$ is negative binomial probability mass function.

As before, the posterior becomes

$$\Pr(\beta, \gamma, \mathcal{D}, \varphi | y_1, \dots, y_n) \propto \Pr(y_1, \dots, y_n | \beta, \gamma, \mathcal{D}, \varphi) \times \underbrace{\Pr(\beta, \gamma, \mathcal{D}, \varphi)}_{\text{need to specify priors}}$$

We can use R-H algorithm to approximate this posterior distribution