Modeling Infectious Diseases

Chapter 2: Introduction to Simple Epidemic Models Part 3

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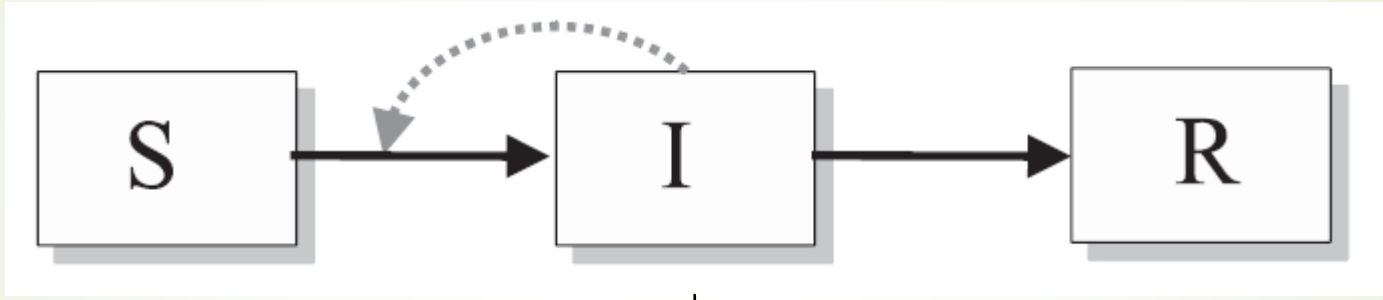
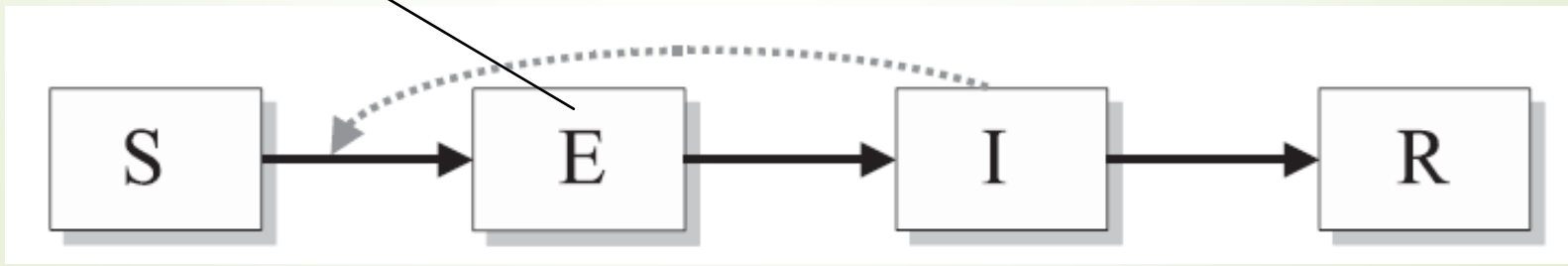
SEIR Model



infected but not yet infectious



(Exposed)

$$\frac{dS}{dt} = \mu - \beta SI - \mu S,$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I,$$

$$\frac{dR}{dt} = \gamma I - \mu R.$$

$$\frac{dS}{dt} = \mu - (\beta I + \mu)S,$$

$$\frac{dE}{dt} = \beta SI - (\mu + \boldsymbol{\sigma})E,$$

$$\frac{dI}{dt} = \boldsymbol{\sigma}\ E - (\mu + \gamma)I,$$

$$\frac{dR}{dt} = \gamma I - \mu R.$$

$$S + E + I + R = 1$$

the average duration of the latent period is given by $1/\boldsymbol{\sigma}$

Fixed points:

$$S^* = \frac{(\mu+\gamma)(\mu+\sigma)}{\beta\sigma} = \frac{1}{R_0}$$

$$E^* = \frac{\mu(\mu+\gamma)}{\beta\sigma}(R_0 - 1).$$

$$I^* = \frac{\mu}{\beta}(R_0 - 1),$$

Endemic

$$S^* = 1$$
$$E^* = 0$$
$$I^* = 0$$
$$R^* = 0$$

Disease Free

$$R_0 = \frac{\beta\,\sigma}{(\mu+\gamma)(\mu+\sigma)} \xrightarrow{\sigma/(\mu+\sigma)\sim 1} R_0 = \frac{\beta}{(\mu+\gamma)}$$

the latent is far smaller that the expected lifespan

death of some individuals in the exposed class who do not contribute to the chain of transmission

$\sigma \to \infty$

endemic equilibrium to be feasible and stable $\longrightarrow$ $R_0 > 1$

$$\det J - \Lambda I = 0$$

$$\Lambda = -\mu$$

$$\Lambda^3 + (\mu R_0 + 2\mu + \sigma + \gamma)\Lambda^2 + \mu R_0(2\mu + \sigma + \gamma)\Lambda + \mu(R_0 - 1)(\mu + \sigma)(\mu + \gamma) = 0.$$

in many cases σ and γ will be much larger than μ and μR_0. ⟶ $\Lambda \sim -(\sigma + \gamma)$

$$\Lambda^2 + \mu R_0 \Lambda + \frac{\gamma\sigma}{\sigma + \gamma}\mu(R_0 - 1) \approx 0.$$

SIR ⟶ $\Lambda^2 + \mu R_0 \Lambda + (\mu + \gamma)\mu(R_0 - 1) = 0,$

$$T \sim 2\pi\sqrt{A|\bar{G}|}$$

$$G = \frac{1}{\mu+\gamma} + \frac{1}{\mu+\sigma}$$

$$(\beta SIR/\gamma SIR = \beta SEIR/\gamma SEIR), (1/\gamma SIR = 1/\gamma SEIR + 1/\sigma SEIR)$$

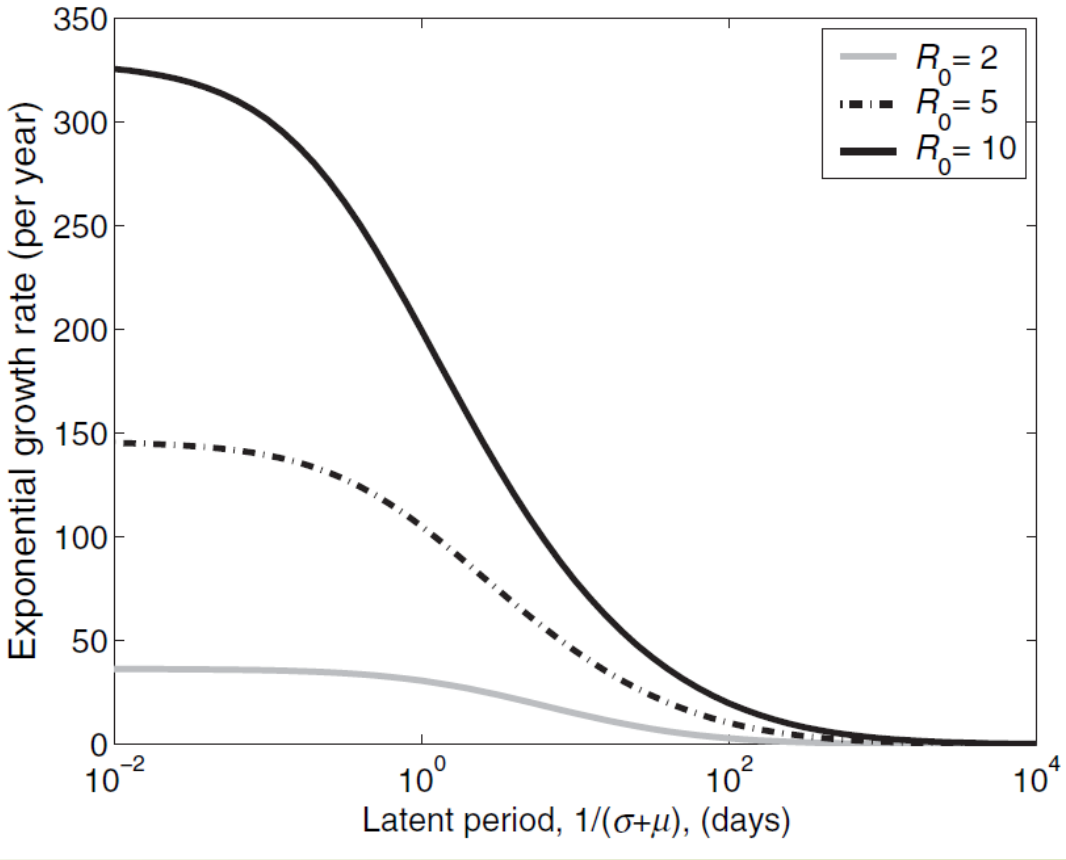
SIR ~ SEIR

However, the two models behave very differently at invasion:

$$I_{SEIR}(t) \approx I(0)\exp\left(\frac{1}{2}\left[\sqrt{4(R_0-1)\sigma\gamma+(\sigma+\gamma)^2}-(\sigma+\gamma)\right]t\right),$$

$$\left\{\approx I(0)\exp\left([(\sqrt{R_0}-1)\gamma]t\right) \qquad \text{if } \sigma=\gamma\right\}$$

$$I_{SIR}(t) \approx I(0)\exp([(R_0-1)\gamma]t)$$

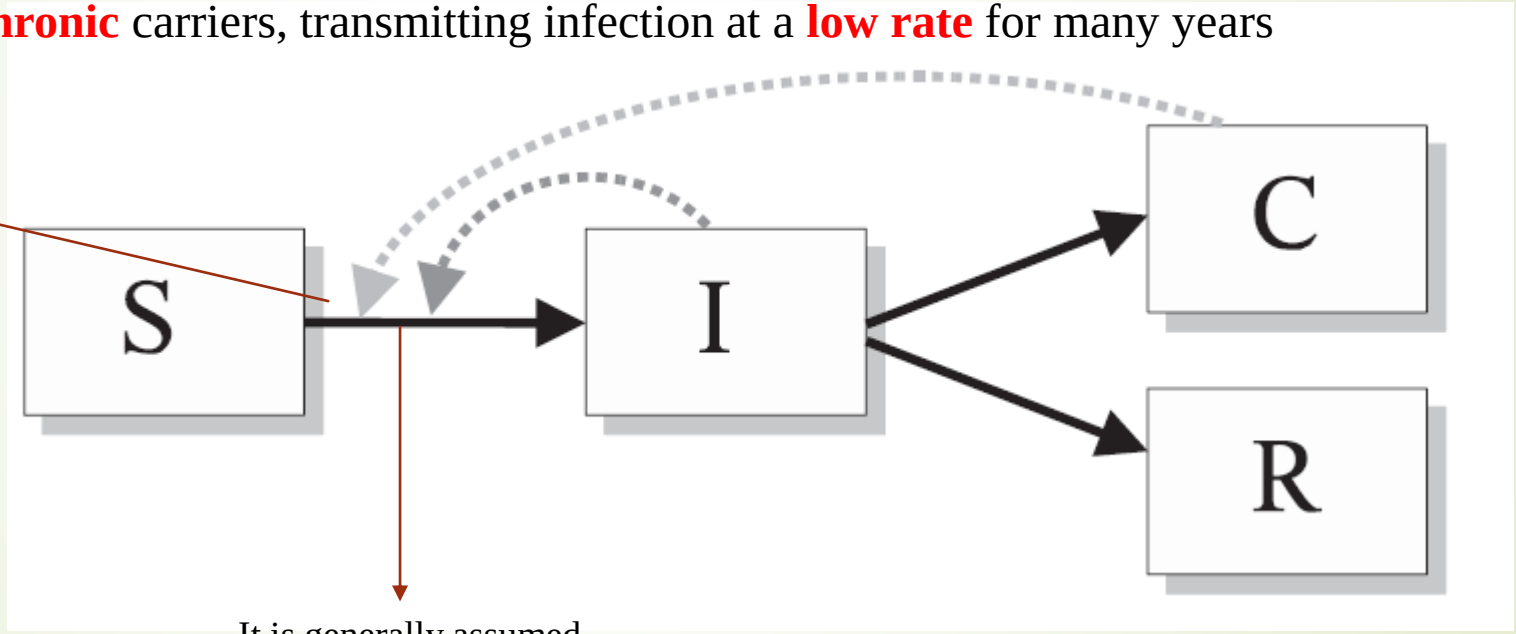


Infections with a carrier state

Hepatitis B

Chronic carriers, transmitting infection at a **low rate** for many years

susceptible individuals can be infected by either carriers or acutely infectious individuals



It is generally assumed that the progress of infection within an individual is independent of their source of infection

ε is the reduced transmission rate from chronic carriers compared to acute infectious individuals

$$\frac{dS}{dt} = \mu - (\beta I + \varepsilon\beta C)S - \mu S,$$

$$\frac{dI}{dt} = (\beta I + \varepsilon\beta C)S - \gamma I - \mu I,$$

$$\frac{dC}{dt} = \gamma q I - \Gamma C - \mu C,$$

$$\frac{dR}{dt} = \gamma(1-q)I + \Gamma C - \mu R.$$

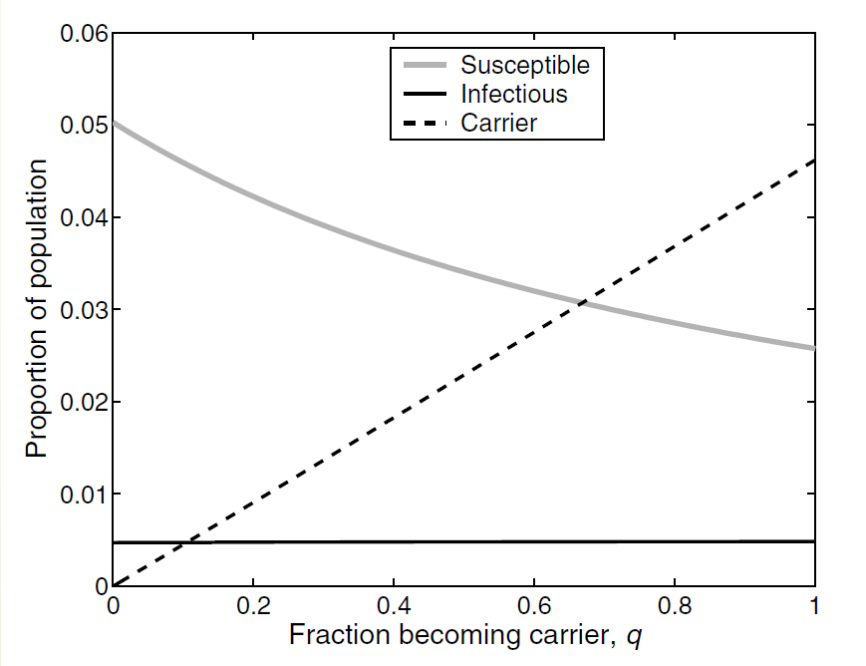
Γ is the rate at which individuals leave the carrier class

q is the proportion of acute infections that become carriers while a fraction (1−q) simply recover

$$R_0 = \frac{\beta}{\gamma + \mu} + \frac{q\gamma}{(\gamma + \mu)} \frac{\varepsilon\beta}{(\Gamma + \mu)}$$

$$S^* = \frac{\gamma + \mu}{\beta + \frac{q\gamma\varepsilon\beta}{\Gamma + \mu}} = \frac{1}{R_0},$$

$$I^* = \frac{\mu(1 - S^*)}{\gamma + \mu}, \qquad C^* = \frac{\gamma q \mu (1 - S^*)}{(\gamma + \mu)(\Gamma + \mu)}$$



Discrete-time models

- The inherent assumption has been that the processes of disease transmission occur in real time and that variability in factors such as the infectious period may be dynamically important.

~ constant factors → Discrete-time

what a time increment represents?

Ideally, units of time should represent the "**generation**" length of the infection through a host, though in some cases this can lead to some difficulty especially if latent and infectious periods differ markedly.

Latent period= 1 week

$$S_{t+1} = \mu - S_t e^{-\beta I_t},$$

$$E_{t+1} = S_t(1 - e^{-\beta I_t})$$

$$I_{t+1} = E_t,$$

per capita probability of *not* contracting the infection given It infectives with transmission β

β, very much analogous to R0 in the continuous-time models. Thus, as before, for the infection to invade, we require β >1.

$$S^* = S_{t+1} = S_t,\ E^* = E_{t+1} = E_t$$

$$S_{t+1} = S_t + \mu - \beta S_t I_t$$

$$S^* = \frac{\mu}{1 - e^{-\beta\mu}},$$

$$E^* = \mu,$$

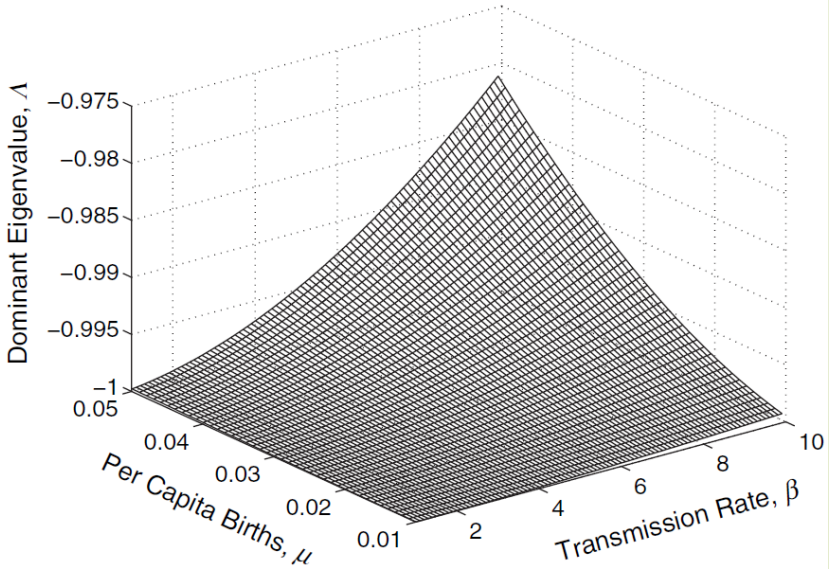
$$I^* = \mu.$$

$$S_{t+1} = S_t + \mu - \beta S_t^{\alpha} I_t^{\phi}$$

$$(S^* < 1) \longrightarrow \beta > \frac{-\log(1-\mu)}{\mu}$$

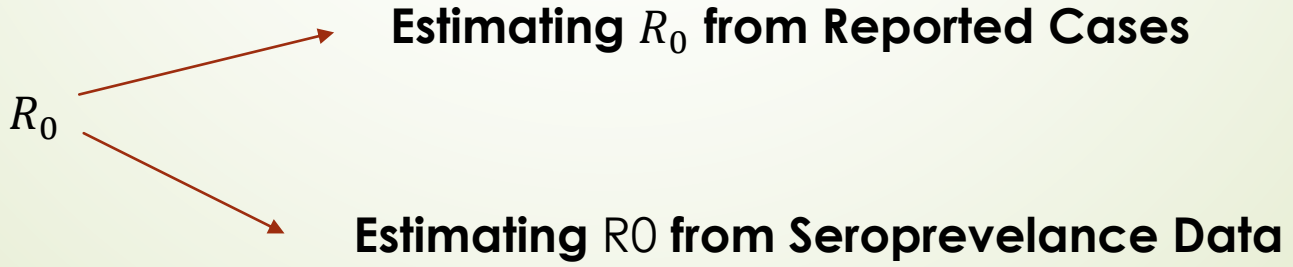
$$\boldsymbol{J} = \begin{pmatrix} e^{-\beta I^*} & 0 & -\beta S^* e^{-\beta I^*} \\ 1 - e^{-\beta I^*} & 0 & \beta S^* e^{-\beta I^*} \\ 0 & 1 & 0 \end{pmatrix}$$

Stability of the equilibrium solution requires the dominant eigenvalue to have magnitude less than one



Parameterization

- A good understanding of the host's biology, for example, will provide accurate estimates of the birth and death rates
- The infectious period can usually be estimated independently via clinical monitoring of infecteds, either by observation of transmission events or by more detailed techniques measuring the amount of pathogen excreted.
- β?



Estimating R_0 from Reported Cases

$$I^* = \frac{\mu}{\beta}(R_0 - 1) = \frac{\mu}{\gamma + \mu}\left[1 - \frac{1}{R_0}\right]$$

we are unlikely to record every case within a population as many infections will go unreported.

$$I(t) \sim I(0)\exp([R_0 - 1](\gamma + \mu)t)$$

(1) this method can work only if there is an epidemic to be observed, and cannot provide information on endemic diseases;

(2) in the early stages of an epidemic, due to the low number of cases, the dynamics may be highly stochastic.

(3) The final difficulty with this approach is that unless the pathogen is novel to the population, some individuals are likely to be immune

Y(t) in models vs epidemiological data typically available

In general, it is reasonable to assume that case reports take place once an individual leaves the infectious class

$$K(T) = \int_{T-1}^{T} \gamma I \, dt$$

the number of new cases reported at time point T

Age of infection is given by $A \approx 1/[\mu(R_0 - 1)]$

The average age of infection is generally estimated by simply finding the average age of all reported cases.

Estimating R_0 from Seroprevelance Data

- Estimating R0 from case report data is problematic in humans because reporting is often patchy and biased because not all infected individuals seek medical advice.

- serological information → $S = 1/R_0$

The complication with this approach is that we need to make sure that our sample represents of the entire population

age-dependent nature of the likelihood of being susceptible → $P(a) \approx \exp(-a\mu(R_0 - 1))$

$$L(R_0) = \prod_{i=1}^{n} \exp(-a_i \mu(R_0 - 1)) \prod_{i=1}^{m} [1 - \exp(-b_i \mu(R_0 - 1))]$$