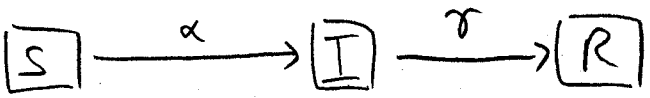
6 Infectious disease modeling

SIR Model

- N people
- 3 states: Susceptible
  Infected
  Recovered
- Transition: 

- $S_t + I_t + R_t = N$.
- No births or deaths
- Population is homogeneously mixed.

This is just one example. These assumptions can be changed in other similar models.

Goal in modeling disease transmission: How to control it.

ODEs

$$\begin{cases} S' = -\alpha SI \\ I' = \alpha SI - \gamma I \\ R' = \gamma R \end{cases}$$

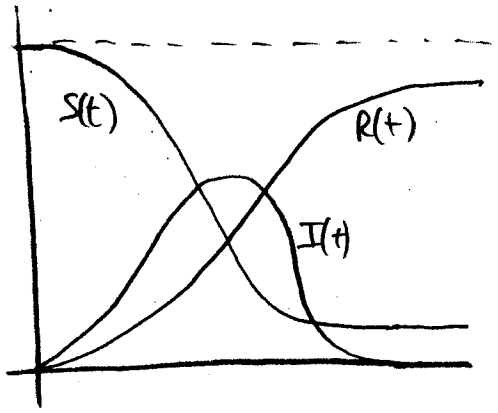
Difference eqns

$$\begin{cases} \Delta S = -\alpha SI \\ \Delta I = \alpha SI - \gamma I \\ \Delta R = \gamma R \end{cases}$$

(2)

What we should expect:

(model validation)



pos. or neg.?

Key aspect: $I' = (\alpha S - \gamma) I = \gamma\left(\frac{\alpha}{\gamma} S - 1\right) I$

If $S > \gamma/\alpha$, then $I' > 0$ (epidemic growing)

If $S < \gamma/\alpha$, then $I' < 0$ (epidemic shrinking).

The value $p := \gamma/\alpha$ is a threshold, the "relative removal rate"

Initially: $I_0' = (\alpha S_0 - \gamma) I$

Define $\boxed{R_0 := \frac{\alpha}{\gamma} S_0}$, the basic reproductive number.

If $R_0 > 1$, then $I'(0) > 0 \implies$ epidemic occurs.

If $R_0 < 1$ then $I'(0) < 0 \implies$ no epidemic.

* R_0 represents the expected # of people an initially infected person will infect.

Approximates:

$R_0 =$ 12-18	for measles
5-7	for smallpox, polio
2-5	for HIV, SARS
2-3	for 1918 Spanish flu

Analysis of R_0:

$\alpha S_0 I_0$ = # of people infected in the first timestep.

αS_0 = # of people infected per capita in the first timestep.

$\frac{1}{\gamma} \approx$ ave. duration of infection.

$$\Rightarrow R_0 = \frac{\alpha}{\gamma} S_0 = (\alpha S_0)\left(\frac{1}{\gamma}\right)$$

$$= \begin{pmatrix} \text{\# new infections} \\ \text{per person per day} \end{pmatrix} \begin{pmatrix} \text{ave. duration} \\ \text{of infection} \end{pmatrix}$$

= # secondary infections from one sick person.

Policy goal: Enact steps to reduce $R_0 < 1$.

Example: Timestep = 1 day
500 susceptibles ($S_0 = 500$)
0.1% chance of transmission ($\alpha = 0.001$)
10 day illness. ($\gamma = 0.1$)

$$R_0 = \frac{\alpha}{\gamma} S_0 = \frac{.001}{.1}(500) = 5.$$

$$I_1 = \alpha S_0 I_0 + (1-\gamma) I_0 = .001(500)(1) + .9(1) = 1.4$$

[Note: If $S_0 = 50$, then $R_0 = 0.5$. No epidemic.]

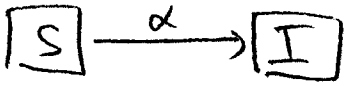
Epidemic subsides when $S_t < \rho = \frac{\gamma}{\alpha} = 100$

(i.e, $\frac{4}{5}^{th}$ of population contracts disease)

Computationally, $\lim_{t\to\infty} S_t = 2.15$ (not everyone gets sick!)

Other epidemic models

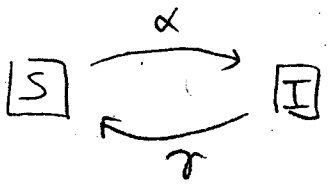
SI model. (e.g, herpes)



$$\begin{cases} S' = -\alpha SI \\ I' = \alpha SI \end{cases}$$

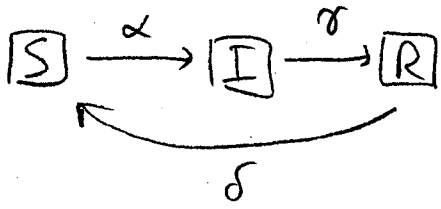
SIS model. Disease w/o immunity (e.g., chlamydia)

$$\begin{cases} S' = -\alpha SI + \gamma I \\ I' = \alpha SI - \gamma I \end{cases}$$

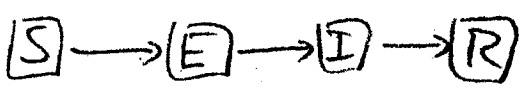


SIRS model. Finite time immunity.

$$\begin{cases} S' = -\alpha SI + \delta R \\ I' = \alpha SI - \gamma I \\ R' = \gamma I + \delta R \end{cases}$$

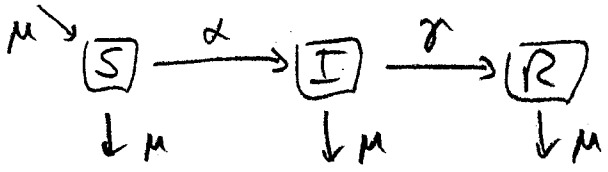


SEIR model. E = exposed (incubation period, no symptoms)



SIR model with birth & death rate

$$\begin{cases} S' = -\beta SI + \mu(N-S) \\ I' = \beta SI - \gamma I - \mu I \\ R' = \gamma I - \mu R \end{cases}$$



(many other ways to do this).

etc...

Other approaches

Differential equations are continuous time, continuous space

Difference equations are discrete time, continuous space.

Consider an SIR model that is discrete time & discrete space.

Let X be a social network:

- Vertices: people
- Edges: contact
- Edge weights (optional): contact hours.

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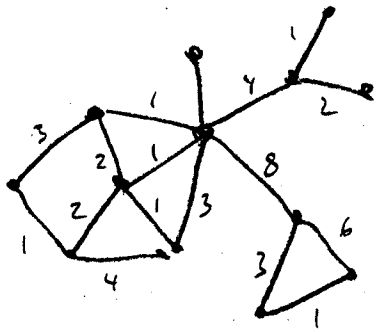


Every person (node) has a state,

S, I, or R.

How to model disease transmission?

Two possible ways:

① Bernoulli trials ("coin flips")

Suppose i is infectious, j is susceptible $(X_i = I,\ X_j = S)$.

If i & j spend [1 hour] together, then say

$$\Pr(i \text{ infects } j) = p. \quad \Rightarrow \quad \Pr(i \text{ doesn't infect } j) = 1-p.$$

If i & j spend [t hours] together, then

$$\Pr(i \text{ infects } j) = 1 - \Pr(i \text{ doesn't infect } j)$$

$$= \boxed{1-(1-p)^t} \quad \left(\begin{array}{l}\text{assuming each hour is an}\\ \text{independent event.}\end{array}\right)$$

If j spends $t_1, \dots, t_k$ hrs with $i_1, \dots, i_k$, all infectious, then during the next time step:

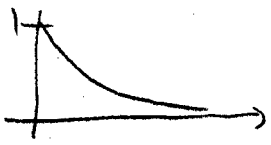
$$\Pr(j \text{ gets infected}) = 1 - \Pr(\text{nobody infects } j)$$

$$= 1 - \prod_{i=1}^{k} (1-p)^{t_i}$$

(2) Exponential dist.

Suppose i is in contact with j for t_{ij} hours.

$$Pr(i \text{ infects } j) = 1 - e^{-rt_{ij}}$$



Prob. person getting infected by 2 different people are independent events.

$$Pr(i \text{ not infected}) = \prod_{j:(i,j) \text{ in } X} \left(1 - \left(1 - e^{-rt_{ij}}\right)\right)$$

$$P(i \text{ infected}) = 1 - \prod_{j:(i,j) \text{ in } X} \left(1 - \left(1 - e^{-rt_{ij}}\right)\right)$$

Think: What are the pros & cons of using an agent-based model over a continuous-space, DE model?