

influence models

infection models

SYSM 6302

CLASS 21

Infection Models : Population-Level SI Model

SI Model

Let x = fraction of people infected

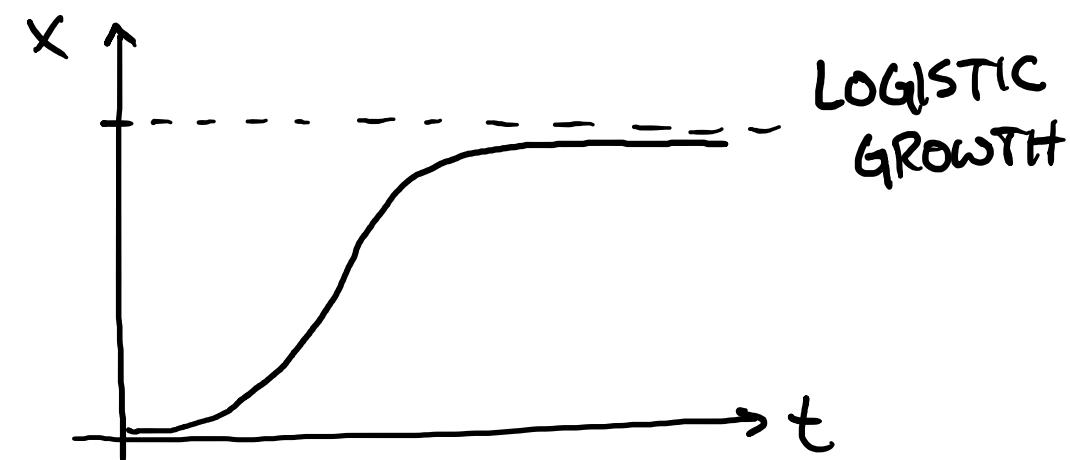
$\hookrightarrow 1-x$ = fraction of people not infected

Assume a "well-mixed" population

$$\frac{dx}{dt} = \beta \underbrace{(1-x)x}_{\text{the mixing of sick people meeting healthy people}} \quad \Rightarrow$$

contagiousness of the disease
(infection rate)
(mobility rate)

$$x(t) = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$$



Infection Models : Population-Level

SI Model

↑
Infected
Susceptible

Let x = fraction of people infected

↪ $\underline{1-x}$ = fraction of people not infected
 "S"

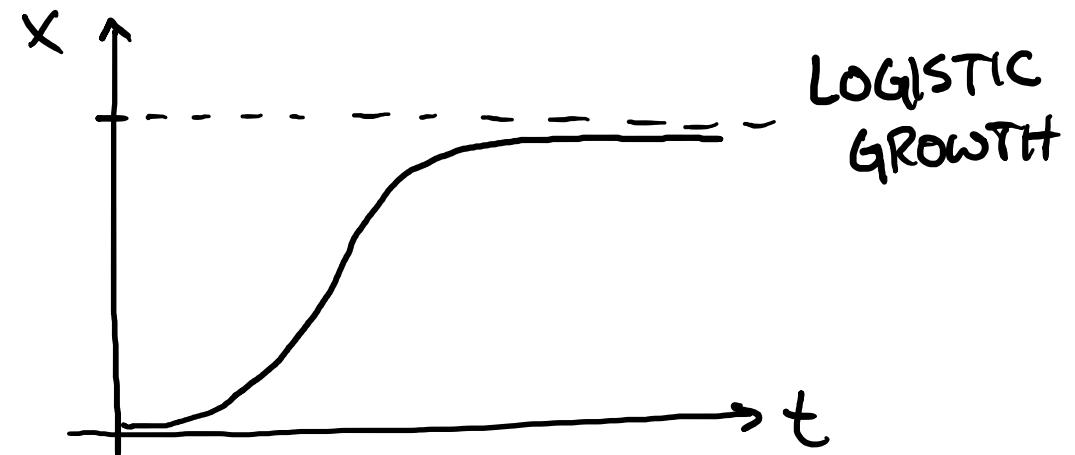
Assume a "well-mixed" population

$$\frac{dx}{dt} = \beta S X$$

↑ equal & opposite!

$$\frac{ds}{dt} = -\beta S X$$

$$x(t) = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$$



Infection Models : Population-Level SIR Model

SIR Model

↑ recovered (removed!)

SIS Models exist too!

$$\frac{dx}{dt} = \beta sx - \gamma x$$

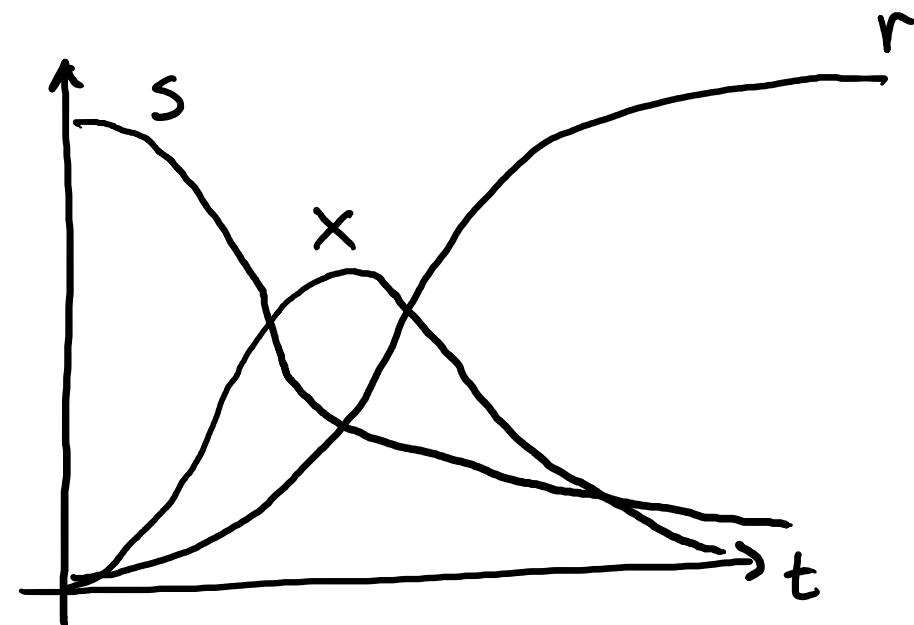
infected people
 recover (die!)
 (proportional to the
 fraction of infected people)

$$\frac{ds}{dt} = -\beta sx$$

equal &
 opposite!

$$\frac{dr}{dt} = \gamma x$$

recovery rate



Note that as $t \rightarrow \infty$, $r(t)$ is the # of people who have had the disease

$$\frac{dr}{dt} = 0 = \gamma(1-s-r)$$

$$= \gamma(1-s_0 e^{-\frac{\beta r}{\gamma}} - r)$$

$$\Rightarrow 0 = 1 - s_0 e^{-\frac{\beta r}{\gamma}} - r$$

$$r = 1 - s_0 e^{-\frac{\beta}{\gamma} r}$$

\uparrow plays the role of c
 $s_0 \approx 1$ usually

Giant Component

$$S = 1 - e^{-CS}$$

$\frac{\beta}{\gamma} > 1$ Epidemic!
 $\frac{\beta}{\gamma} < 1$ No epidemic

$\leftarrow \beta = \gamma$: epidemic threshold

$$\frac{ds}{dt} = -\beta s x$$

$$\frac{dr}{dt} = \gamma x$$

$$\Rightarrow -\frac{1}{\beta s} \frac{ds}{dt} = \frac{1}{\gamma} \frac{dr}{dt}$$

$$\frac{1}{s} \frac{ds}{dt} = -\frac{\beta}{\gamma} \frac{dr}{dt}$$

↓

$$-\frac{\beta r}{\gamma}$$

$$S(t) = s_0 e$$

How long do people stay infected in the SIR model?

↳ what is the probability that someone is still infected after time τ ?

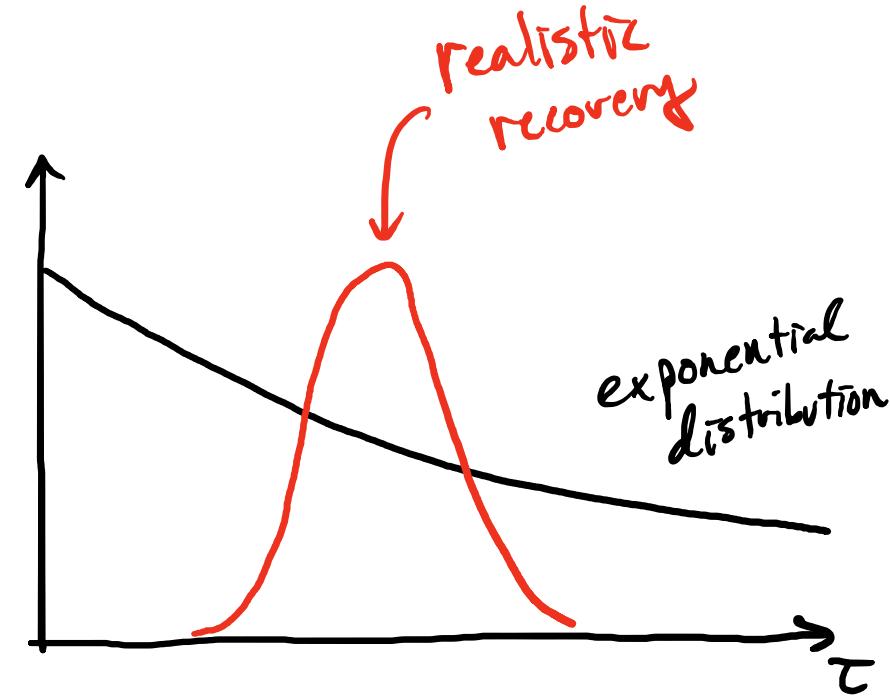
$$\lim_{\delta\tau \rightarrow 0} (1 - \gamma \delta\tau)^{\frac{\tau}{\delta\tau}} = e^{-\gamma\tau}$$

$(1 - \gamma \delta\tau)$ $(1 - \gamma \delta\tau)$ \dots $(1 - \gamma \delta\tau)$

\uparrow

$\frac{\tau}{\delta\tau}$ times

probability of not
recovering in $\delta\tau$ time interval
($\gamma \delta\tau$ = prob. of recovering)



Probability of not recovering for τ , and then recovering between τ and $\tau + d\tau$

$$P(\tau) d\tau = \gamma e^{-\gamma\tau} d\tau$$

Reproduction Number R_0 = average # of people an infected person will pass the disease onto

→ $R_0 = 1$ is the epidemic threshold

→ Suppose someone stays infected (infectious!) for time τ ,

↳ At $s=1$ (naive population), $\beta\tau$ = expected # of people infected

$$R_0 = \int_0^\infty \beta\tau \cdot \gamma e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

Infection Models with Network Effects

→ Heterogeneous connectivity: $A \xleftarrow{\text{adjacency matrix}}$

x_i
 s_i
 r_i

probability that node i is

infected
susceptible
recovered

$$dx_i = \sum_{j=1}^n s_i \cdot \beta dt \cdot A_{ij} \cdot x_j - \gamma dt \cdot x_i$$

probability that node i is susceptible

probability that disease is transmitted

node i & j are connected

probability that node j is infected

recovery is not dependant on neighbors

$$\frac{dx_i}{dt} = \beta s_i \sum_{j=1}^n A_{ij} x_j - \gamma x_i$$

Infection Models with Network Effects

→ Heterogeneous connectivity: $A \xleftarrow{\text{adjacency matrix}}$

x_i
 s_i
 r_i

probability that node i is
 infected
 susceptible
 recovered

$$\frac{dx_i}{dt} = \beta s_i \sum_{j=1}^n A_{ij} x_j - \gamma x_i \quad \rightarrow \text{early on, } S \approx 1$$

$$\frac{ds_i}{dt} = -\beta s_i \sum_{j=1}^n A_{ij} x_j$$

$$\frac{dr_i}{dt} = \gamma x_i$$

$$\frac{dx_i}{dt} = \sum_{j=1}^n (\underbrace{(\beta A_{ij} - \gamma s_j)}_{M_{ij}}) x_j$$

$$\frac{dx}{dt} = \beta M x, \quad M = A - \frac{\gamma}{\beta} I$$

$$\frac{dx}{dt} = \beta Mx \quad , \quad M = A - \frac{\gamma}{\beta} I$$

→ Note $M \neq A$ share eigenvectors: $Av_i = \lambda_i v_i$

$$Mv_i = \left(A - \frac{\gamma}{\beta} I\right)v_i = Av_i - \frac{\gamma}{\beta} v_i = \left(\lambda_i - \frac{\gamma}{\beta}\right)v_i$$

$$\rightarrow \text{Let } X(t) = \sum_{i=1}^n a_i(t) v_i \rightarrow \frac{da_i}{dt} = \beta \left(\lambda_i - \frac{\gamma}{\beta}\right) a_i \rightarrow a_i(t) = a_i(0) e^{(\beta\lambda_i - \gamma)t}$$

$$X(t) = \sum_{i=1}^n a_i(0) v_i e^{(\beta\lambda_i - \gamma)t}$$

response is dominated by most positive eig.value λ_1

Epidemic threshold: $\beta\lambda_1 - \gamma = 0 \rightarrow \lambda_1$

small	harder for disease to spread
large	easier for disease to spread

Late time properties of SI

- ① start with patient- \emptyset (or some set of initially infected people): set S
 - ② infected people infect their neighbors with probability $P = \beta dt$
- As long as $\beta > 0$, for $t \rightarrow \infty$, every node reachable from set S will become infected
- Infection is contained by the components of the network.

Late time properties of SIR

- ① start with patient- \emptyset (or some set of initially infected people): set S
- ② infected people infect their neighbors with probability P ($P = 1 - e^{-\beta \tau}$)
- ③ an infected node stays infected (infectious!) for time τ . ← same for everyone

→ This process can be simulated online, but if we only care about $t \rightarrow \infty$:

→ flip all coins (for all edges) ahead of time → **Heads**: disease would be communicated if it reaches this far

↳ Percolation-tails flips effectively remove edge from the network

Tails: disease would not be communicated

→ nodes in R (recovered) are all nodes reachable from S in the percolated graph.
→ $\beta/\gamma > 1$ doesn't necessarily mean epidemic

→ repeat this stochastic process to understand the expected behavior

Beyond Simple Diffusion

- used to model diffusion of innovation, product adoption, voting behavior
- generalizes SIR + other methods → e.g., includes edge-specific probabilities
- late-time properties / discrete active vs. inactive / only inactive → active transitions

Independent Cascade

- ② Activate all nodes in the seed set, S .
- ① For all newly activated nodes, u , attempt to activate each neighbor, v , with probability A_{vu} only once.
i.e. each edge is tried only once

Linear Threshold

- ② Activate all nodes in the seed set, S .
 - ① If $\sum_{j \in N_i} A_{ij} x_j \geq \Theta_i$ activate node i .
 $\begin{cases} 1 & \text{if } j \text{ is active} \\ 0 & \text{if } j \text{ is inactive} \end{cases}$ node specific threshold
- $\sum_{j \in N_i} A_{ij} \leq 1$ ↳ thresholds are selected randomly (rest is deterministic)