

influence models
infection models

SYSTEM 6302

CLASS 21

Infection Models: Population-Level **SI** Model

↑ Infected
↑ Susceptible

Let x = fraction of people infected

↳ $1-x$ = fraction of people not infected

(solvable by separation of variables and partial fractions)

Assume a "well-mixed" population

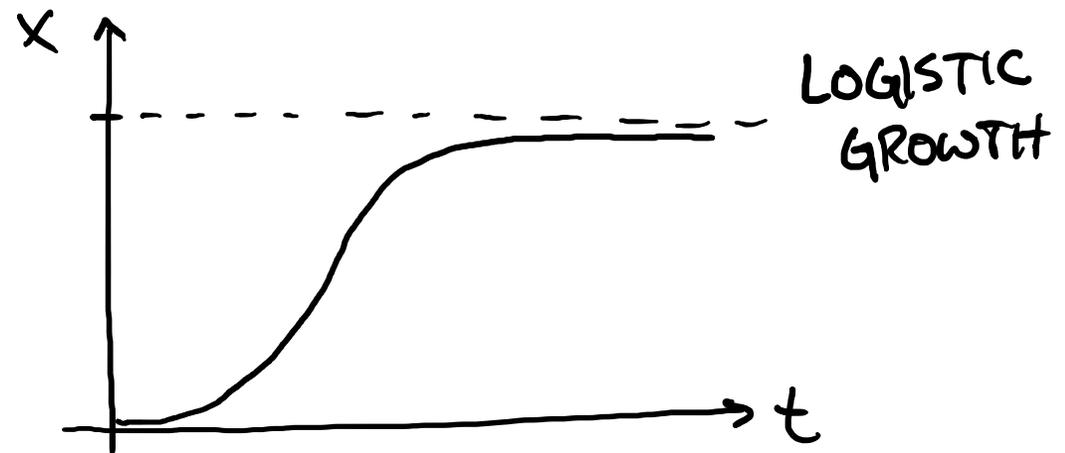
$$\frac{dx}{dt} = \beta (1-x)x$$

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

the mixing of sick people meeting healthy people

⇒

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



Infection Models: Population-Level **SI** Model

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↑ Susceptible

Let x = fraction of people infected

↳ $1-x$ = fraction of people not infected
= s

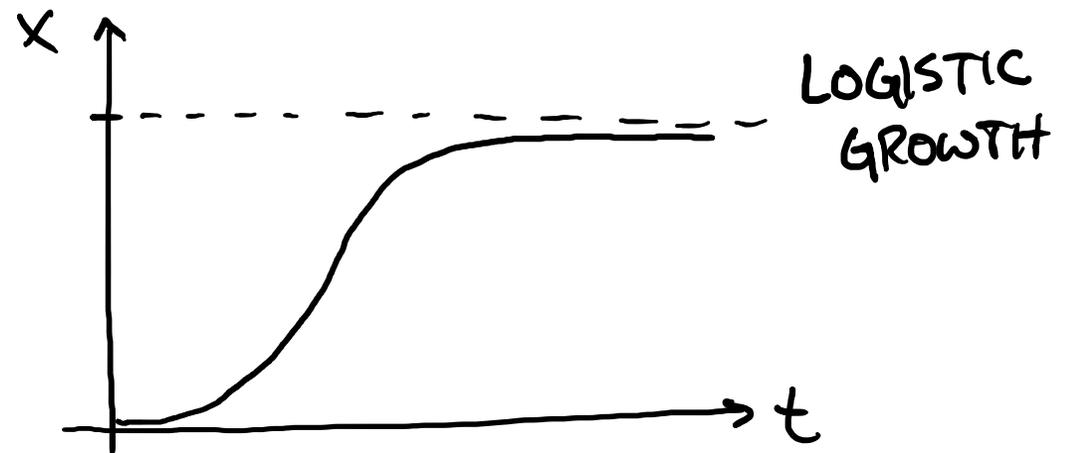
Assume a "well-mixed" population

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

$$\frac{dx}{dt} = \beta s x$$

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

⇒ equal & opposite!



Infection Models: Population-Level **SIR Model**
↑ recovered (removed!)

SIS Models exist too!

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

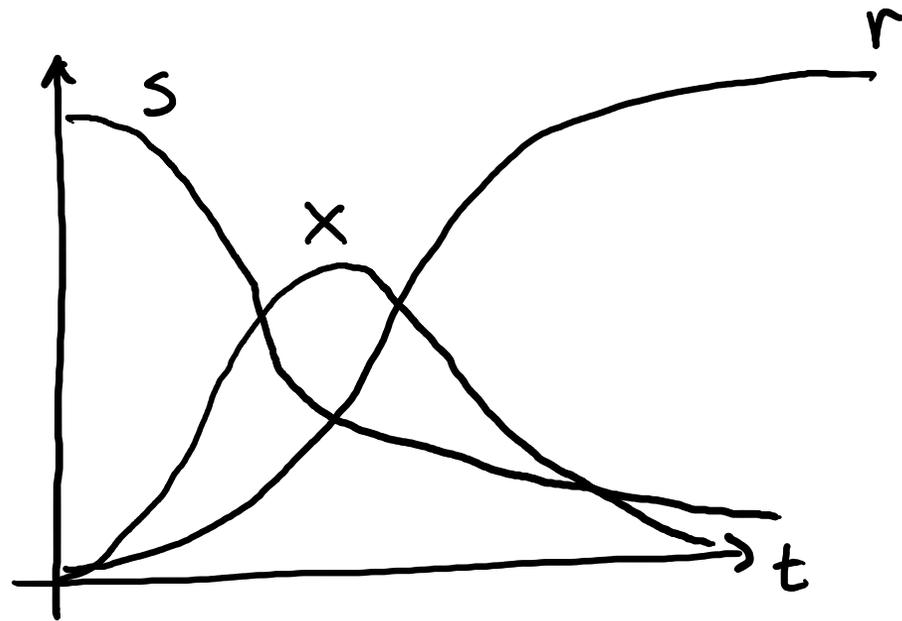
infected people recover (die!)
(proportional to the fraction of infected people)

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

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

$$\frac{dr_i}{dt} = 0 \stackrel{x+s+r=1}{=} \gamma(1-s-r)$$
$$= \gamma(1 - s_0 e^{-\frac{\beta}{\gamma} r} - r)$$

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

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

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

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

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

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

↓

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

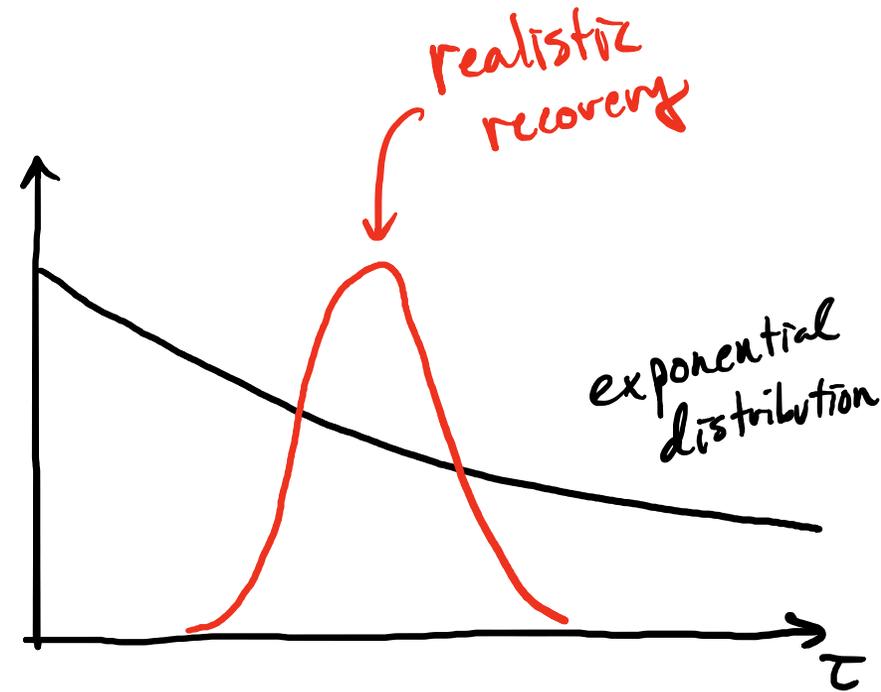
How long do people stay infected in the SIR model?

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

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

$(1 - \gamma\delta\tau)(1 - \gamma\delta\tau) \dots (1 - \gamma\delta\tau)$
 $\frac{\tau}{\delta\tau}$ 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 $d\tau$

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

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 ← adjacency matrix

$\left. \begin{matrix} x_i \\ s_i \\ r_i \end{matrix} \right\}$ probability that node i is $\left\{ \begin{matrix} \text{infected} \\ \text{susceptible} \\ \text{recovered} \end{matrix} \right.$

$$dx_i = \sum_{j=1}^n s_i \cdot \underbrace{\beta dt}_{\substack{\text{probability that} \\ \text{disease is} \\ \text{transmitted}}} \cdot \underbrace{A_{ij}}_{\substack{\text{node } i \text{ \& } j \\ \text{are connected}}} \cdot \underbrace{x_j}_{\substack{\text{probability that} \\ \text{node } j \text{ is} \\ \text{infected}}} - \underbrace{\gamma dt \cdot x_i}_{\substack{\text{recovery is not} \\ \text{dependant on} \\ \text{neighbors}}}$$

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

Infection Models with Network Effects

→ Heterogeneous connectivity: A ← adjacency matrix

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

→ early on, $s \approx 1$

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

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

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

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

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

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

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

→ 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-0 (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 ϕ (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

- ⑤ 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

- ⑤ 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 .
↑ $x_j = \begin{cases} 1 & \text{if } j \text{ is active} \\ 0 & \text{if } j \text{ is inactive} \end{cases}$ ← node specific threshold
- $\sum_{j \in N_i} A_{ij} \leq 1$ → thresholds are selected randomly (rest is deterministic)