1.022 Introduction to Network Models

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Lecture 20

Outline

- Models of diffusion with network structure
  - Networked Susceptible-Infected-Susceptible (SIS) Model: In a general network, nodes can become infected and then recover in such a way that they become susceptible again
- Models of diffusion without network structure
  - The classic SIS Epidemic Model: Individuals can become infected and then recover in such a way that they become susceptible again (the underlying structure is a complete graph).
  - The classic Susceptible-Infected-Removed Epidemic (SIR) Model: the diffusion takes place between infected nodes and susceptible nodes over a complete graph. Once a node reaches the "removed" state, it has either recovered and is no longer susceptible or contagious, or it has died.

Optional Readings:
Ch. 21 [Easley-Kleinberg]
C. 17 [M.E.J. Newman]
Ch. 7.1 and 7.2 [Matthew O. Jackson]

Introduction

- We are interested in the following questions:
  - Under what conditions will an initial outbreak spread to a nontrivial portion of the population?
  - What percentage of the population will eventually become infected?
  - What is the effect of immunization policies?
  - How do contagions spread in populations?
  - Will a disease become an epidemic?
  - Who are the best people to vaccinate?
  - Will a given YouTube video go viral?
  - What individuals should we market to for maximizing product penetration?

Epidemics

- Epidemiology is where Biology meets Social science
  - McKendrick & Kermack (1927): "Mathematical Theory of Epidemics"
- Spread of an epidemic depends on the pathogen carrying it
  - As well as the "contagion" network structure
- Goal of studying epidemics
  - Understand how to outbreaks happen
  - Use it to design intervention to curb / prevent the outbreak
- Similar to "information spreading"
  - Spread of opinions in society
  - Adoption of new technology

A Networked Susceptible-Infected-Susceptible Model

- SIS epidemic model over a network with n agents

  the network of contacts is given by adjacency matrix $A = [a_{ij}]$
  the set of the neighbors of node i: $N_i = \{j \mid a_{ij} \neq 0\}$
  probability of contact between individuals i and j during the time interval $[t, t + \Delta)$:Δa_{ij}.

- Each individual (or node) is in one of the two states $X_i(t) \in \{0, 1\}$
  - Susceptible: the state $X_i(t) = 0$ means that node i doesn't have the disease at time t, but could catch it via contact
  - Infected: the state $X_i(t) = 1$ means that node i has the disease at time t; can pass it on to susceptible via contact

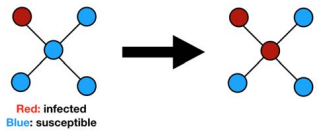
A Networked SIS Model (continued)

- Dynamics
  - a susceptible individual comes in contact with his/her neighbor
  - if the neighbor is infected, susceptible becomes infected
  - infected nodes recover in such a way that they become susceptible again

- Each node can switch to the infected state during the time interval $[t, t + \Delta)$ with a probability that depends on:
  - an infection rate β
  - the probability of contact with a neighbor in this interval (Δa_{ij})
  - their states

A Networked SIS Model (continued)

- Probability of transition from susceptible to infected:
  $\Pr[X_i(t+\Delta) = 1 | X_j(t) = 1, X_i(t) = 0, X_k(t) = 0 \text{ for all } k \neq j] = \beta \Delta a_{ij}$.

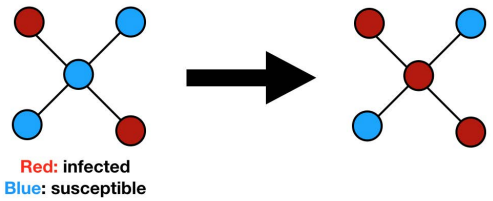


  Hence,

$$\Pr[X_i(t+\Delta) = 0 | X_j(t) = 1, X_i(t) = 0, X_k(t) = 0 \text{ for all } k \neq j] = 1 - \beta \Delta a_{ij}$$

- Let $X(t) := (X_1(t), \ldots, X_n(t))^\top$ be the state vector:

$$\Pr[X_i(t+\Delta) = 0 | X_i(t) = 0, X(t)] = \Pi_{j \in \{j | X_j(t)=1\}} (1 - \beta \Delta a_{ij})$$



- Finally

$$\Rightarrow \Pr[X_i(t+\Delta) = 1 | X_i(t) = 0, X(t)] = 1 - \Pi_{j \in \{j | X_j(t)=1\}} (1 - \beta \Delta a_{ij})$$

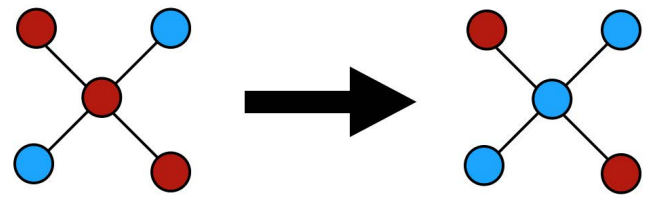
A Networked SIS Model (continued)

- Using the first-order approximation ($\Delta \ll 1$)

$$\Pr[X_i(t+\Delta) = 1 | X_i(t) = 0, X(t)] = \sum_{j \in N_i} \beta \Delta a_{ij} X_j(t)$$

Will see in your project!

- Assume node i is infected, the probability of i recovering back to the susceptible state in the time interval $[t, t+\Delta)$ is given by



$$\Pr[X_i(t+\Delta) = 0 | X_i(t) = 1] = \Delta\gamma$$

$0 \leq \gamma \leq 1$ is the curing rate.

A Networked SIS Model (continued)

This spread model is still hard to analyze for large-scale networks (it has 2^n states). One standard approach is to use a mean-field approximation.

- Transitional probabilities:

$$\Pr[X_i(t+\Delta) = 1 | X_i(t) = 0, X(t)] = \sum_{j \in N_i} \beta \Delta a_{ij} X_j(t)$$

$$\Pr[X_i(t+\Delta) = 1 | X_i(t) = 1] = 1 - \Delta\gamma$$

- Define $p_i(t) = \Pr[X_i(t) = 1] = \mathbb{E}[X_i(t)]$. Then, applying Bayes rule

$$p_i(t+\Delta) \approx p_i(t)(1-\Delta\gamma) + (1 - p_i(t)) \sum_{j \in N_i} \beta \Delta a_{ij} p_j(t)$$

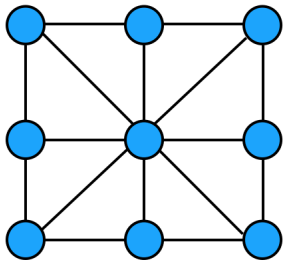
- Shifting $\Delta \to 0$, the dynamics of $p_i(t)$ can be written as

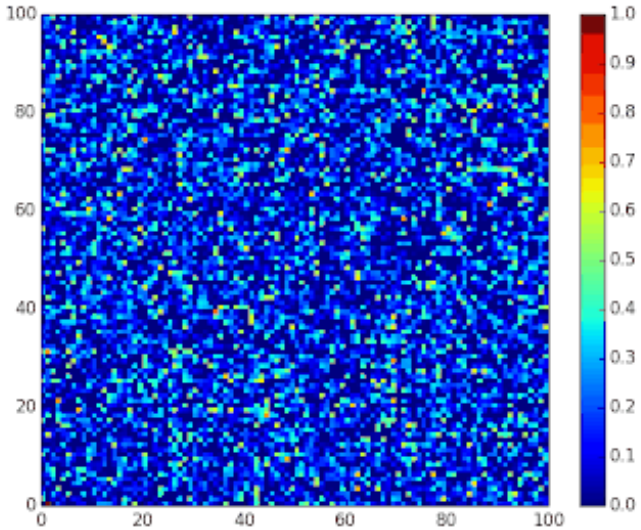
$$\frac{dp_i(t)}{dt} = \beta(1 - p_i(t)) \sum_{j=1}^{n} a_{ij} p_j(t) - \gamma p_i(t)$$

This approximation is widely used in the field of epidemic analysis and control, since it performs numerically well for many realistic network topologies.

Example: Spatial Epidemic Model Simulation

- In this example, we consider the epidemic model on a 2-d square lattice; each cell can infect any of the eight immediate neighbors.





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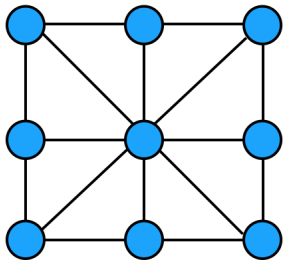

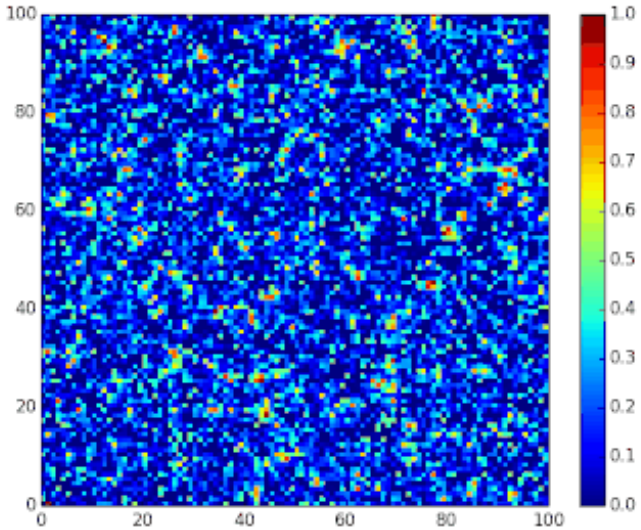

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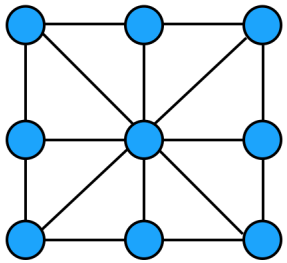

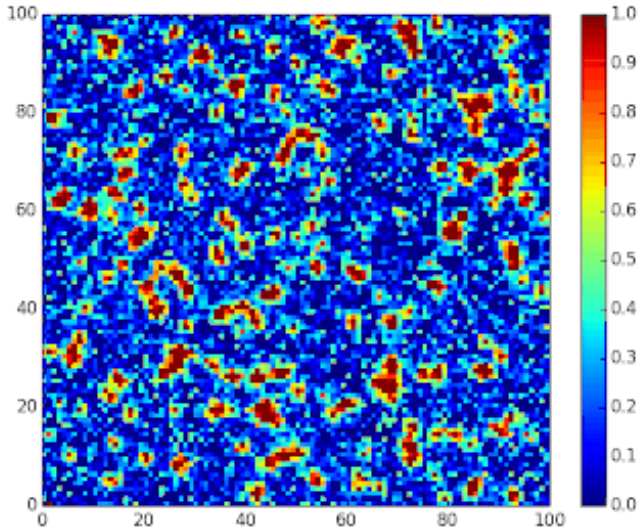

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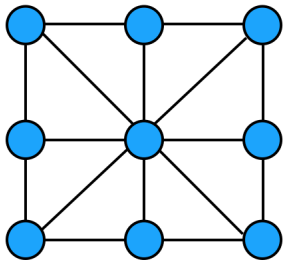

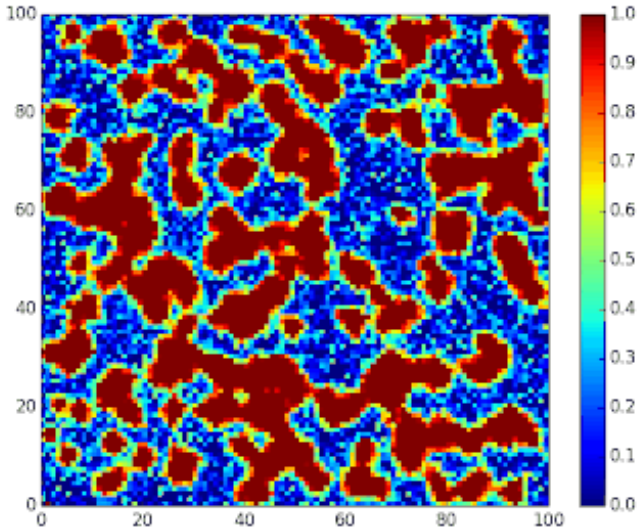

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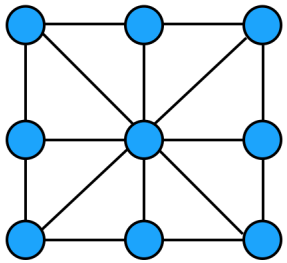

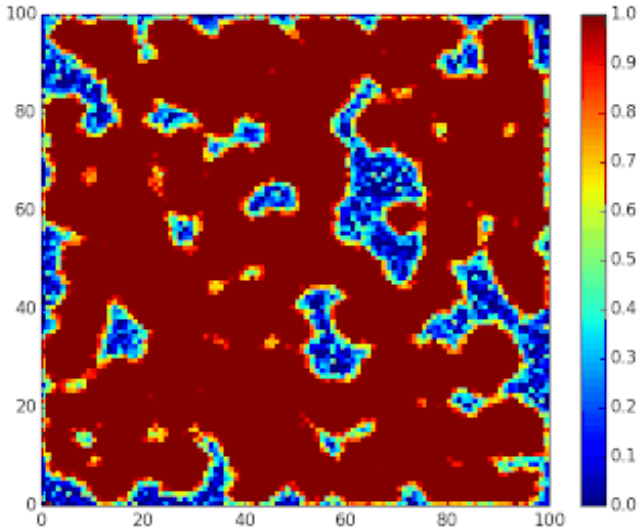

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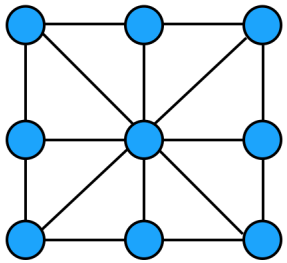

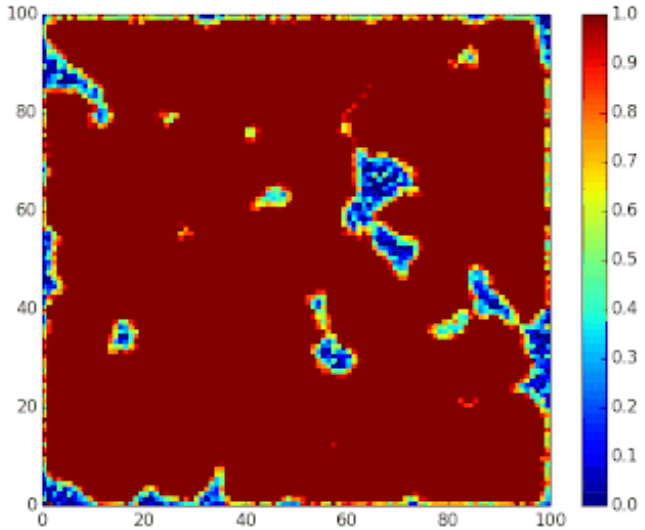

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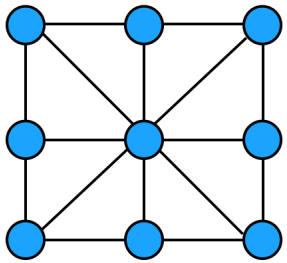

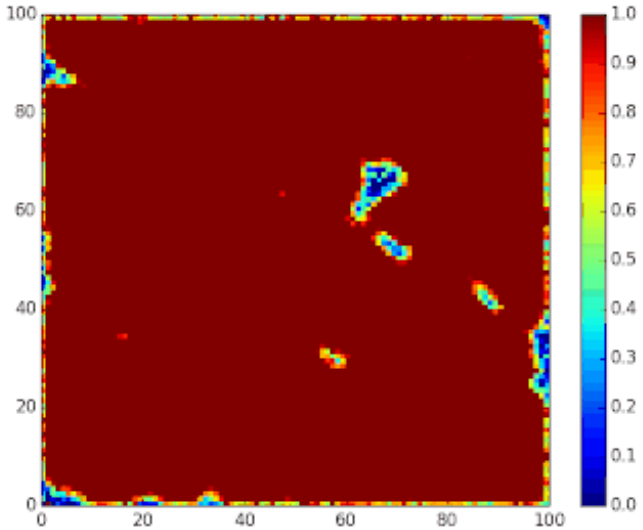

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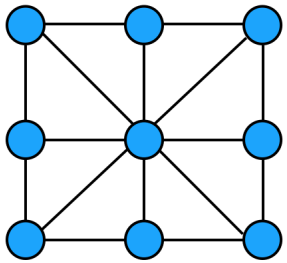

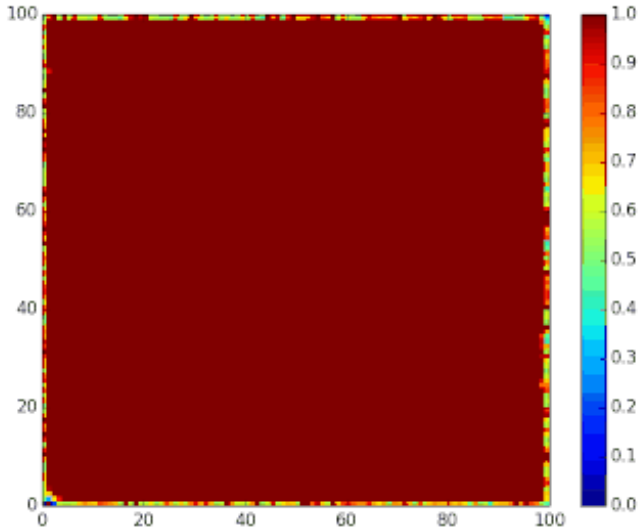

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Full mixing in classic Epidemiological models

- Full mixing assumption

  In classic epidemiology, it is assumed that each individual can potentially have contact with any other in the population (= complete underlying graph).

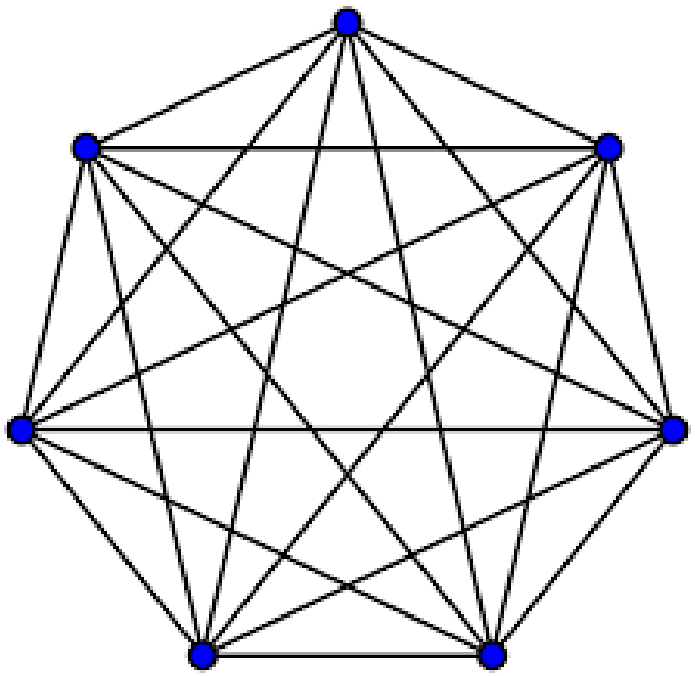


Image by David Benbennick. Source: Wikimedia Commons. This image is in the public domain.

Classic SIS Model

- Traditional approach in mathematical epidemiology: *no contact network*
  - *fully mixed* : each individual contacts any other random individual
- That is, contact graph is *complete*
  - due to symmetry, we can study it more carefully
- Using the full mixing assumption ($a_{ij} = 1/(n-1)$ for $i \neq j$) and the dynamics

$$\frac{dp_i(t)}{dt} = \beta(1 - p_i(t)) \sum_{j=1}^{n} a_{ij} p_j(t) - \gamma p_i(t)$$

it follows that

$$\frac{dp_i(t)}{dt} = \beta(1 - p_i(t)) p_i(t) - \gamma p_i(t)$$

Because of the full mixing assumption and symmetry, all p_i's are the same.

Classic SIS Model (continued)

$$\frac{dp_i(t)}{dt} = \beta(1 - p_i(t))p_i(t) - \gamma p_i(t)$$

- $p_i(t)$ and $1 - p_i(t)$ are the fraction of susceptible and infected individuals
- Let's define $x(t) := 1 - p_i(t)$ and $s(t) := p_i(t)$
- Then, we get the exact classic SIS model

$$\begin{aligned} \frac{ds(t)}{dt} &= \gamma x(t) - \beta s(t)x(t), \\ \frac{dx(t)}{dt} &= \beta s(t)x(t) - \gamma x(t), \quad s(t) + x(t) = 1. \end{aligned}$$

Classic SIS Model (continued)

- The size of infection is given by

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

- Rearranging the terms we get

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

Integrating both sides and after some simplifications we arrive at

$$x(t) = \frac{\beta - \gamma}{\beta + (\beta - \gamma)Ce^{-(\beta-\gamma)t}}$$

where

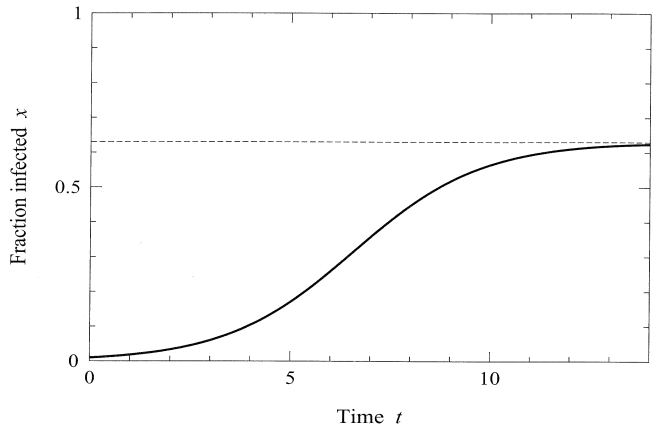
$$C = \frac{(\beta - \gamma) - \beta x(0)}{(\beta - \gamma)x(0)}$$

Classic SIS Model (continued)

- The size of infection $x(t)$ is thus

$$x(t) = x(0)\frac{(\beta-\gamma)e^{(\beta-\gamma)t}}{\beta-\gamma+\beta x(0)(e^{(\beta-\gamma)t}-1)}$$

- Assuming $\beta > \gamma$, the steady state value of $x(t)$ is $(\beta-\gamma)/\beta$, which is called an endemic state.



The fraction of infected individuals in the SIS model grows with time following a logistic curve. The fraction infected never reaches unity, tending instead to an intermediate value at which the rates of infection and recovery are balanced.

SI Model

- In the SI model, individuals once infected are infected forever ($\gamma = 0$).
- An infected never recovers and stays infected and infectious to others.
- The parameters of the SI model are
  - β infection rate: probability of contagion after contact per unit time
  - Zero recovery rate ($\gamma = 0$) !
- Dynamics: $s(t)$ and $x(t)$ be the fraction of individuals in susceptible, and infected state

$$\begin{aligned} \frac{ds(t)}{dt} &= -\beta s(t)x(t), \\ \frac{dx(t)}{dt} &= \beta s(t)x(t) \end{aligned}$$

where $s(t) + x(t) = 1$ for all t.

SIR Model

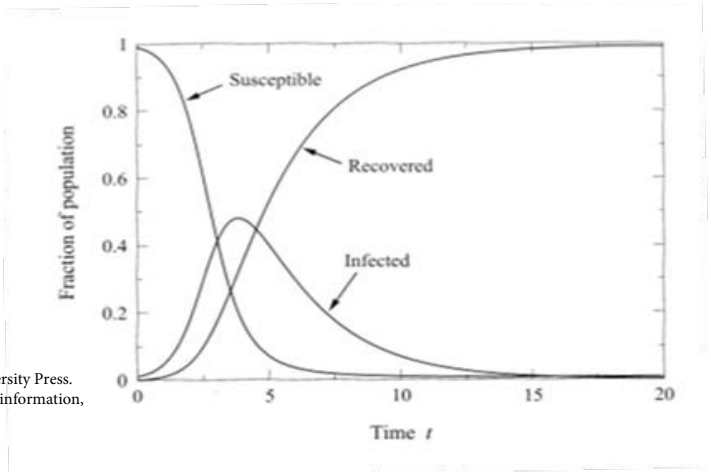
- For many real diseases, people recover from infection
  - Moreover, they retain immunity to the disease after recovery (e.g., chickenpox).
- This motivates SIR model
  - Three states: susceptible, infected, and recovered.
- Dynamics: $s(t)$, $x(t)$ and $r(t)$ be the fraction of individuals in susceptible, infected and recovered state

$$\begin{aligned}
\frac{ds(t)}{dt} &= -\beta s(t)x(t), \\
\frac{dx(t)}{dt} &= \beta s(t)x(t) - \gamma x(t), \\
\frac{dr(t)}{dt} &= \gamma x(t),
\end{aligned}$$

where γ is the recovery rate and $s(t) + x(t) + r(t) = 1$ for all t.

SIR Model

- Solving these equations, we obtain $\frac{dr(t)}{dt} = \gamma(1 - r - s(0)e^{-\beta r(t)/\gamma})$.



- Assume $s(0) \approx 1$. The steady state value of $r(t)$ satisfies

$$r = 1 - e^{-\beta r/\gamma}.$$

- For $\beta/\gamma < 1$, this has a unique solution at $r = 0$: there is no epidemic (infected individuals recover faster than susceptible ones become infected).
- The transition between epidemic and non-epidemic regimes happen at the point $\beta = \gamma$, called the epidemic threshold or transition.

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