Complex Networks
epidemics

2019.1.28(Mon)

Goal

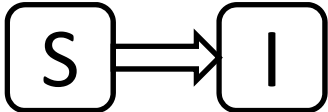|	
metrics	algorithms
models	processes

contents of this chapter

- Models of spread of disease
    - SI model
    - SIR model
   - SIS model
    - SIRS model
- Epidemic models on networks

SI model

- Two states
  - Susceptible (S) : not infected
  - Infected (I)

- $S(t)$: # of susceptible individuals at time t
- $X(t)$: # of infected individuals at time t
- β: average # of contacts per unit time
- S/n: average probability of susceptible
- $\beta S/n$: # of susceptible individuals an infected contact with
- $\beta SX/n$: average rate of new infections

Differential equation of SI model

- $\frac{dX}{dt} = \beta \frac{SX}{n}$: the rate of change of X

- $\frac{dS}{dt} = -\beta \frac{SX}{n}$: the rate of change of S

- Fractions of susceptible and infected individuals : $s = \frac{S}{n}, x = \frac{X}{n}$

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

- Every individual must be either susceptible or infected : $S + X = n, s + x = 1$

- Eliminate s by writing $s = 1 - x \rightarrow \frac{dx}{dt} = \beta(1 - x)x$

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

  - x_0 is the value of x at $t = 0$

there aren't many disease that really saturate their population like this because of immune system / death of infected individuals

x

Fraction infected x

t

Time t

1

0.5

0

0   2   4   6   8   10
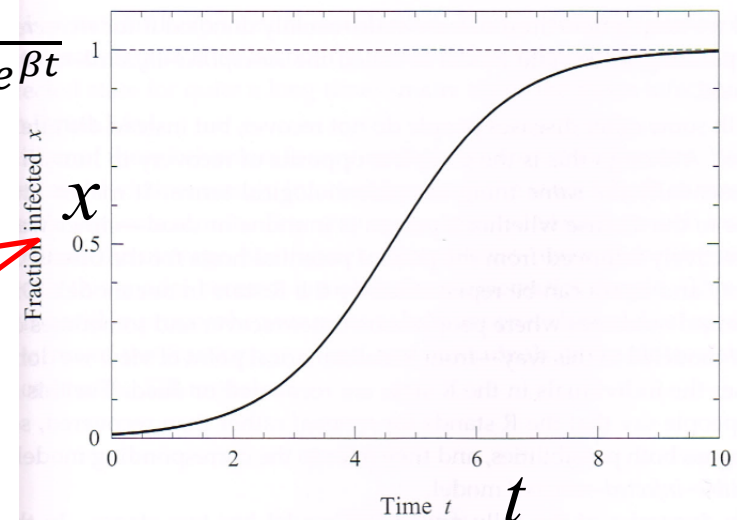
SIR model
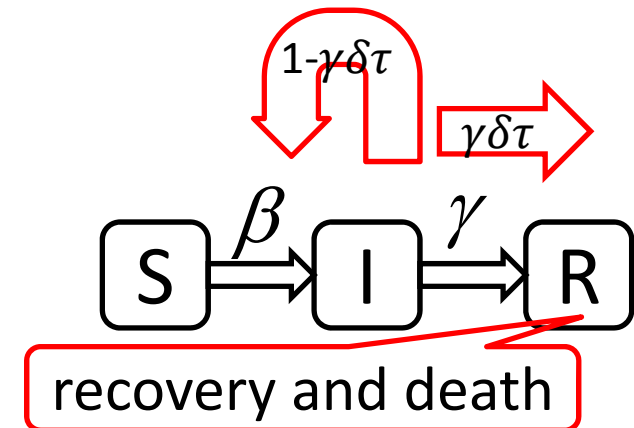
- three states
  - Susceptible (S) : not infected
  - Infected (I)
  - Recovered (removed) (R)
- It makes little difference to the disease whether a person is immune or dead
- τ : the length of time that infected individual is likely to remain infected before they recover
- $\gamma\delta\tau$: probability of recovering in time interval $\delta\tau$
- $1 - \gamma\delta\tau$: probability of not doing so
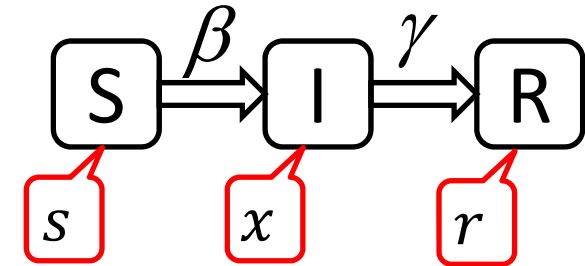- Probability that the individual is still infected after time τ :
  $$\lim_{\delta t \to 0}(1 - \gamma\delta\tau)^{\tau/\delta\tau} = e^{-\gamma\tau}$$
- Probability $p(\tau)d\tau$ that the individual remains infected for and then recovers between τ and $\tau + d\tau$: $p(\tau)d\tau = \gamma e^{-\gamma\tau}d\tau$

recovery and death

not realistic for most real disease

Exponential distribution: some might remain in I state for a long time

Equations for the SIR model

- $\dfrac{ds}{dt} = -\beta s x$
- $\dfrac{dx}{dt} = \beta s x - \gamma x$
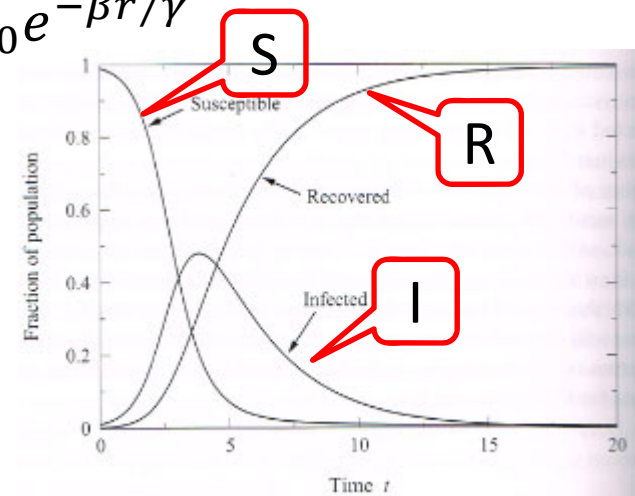- $\dfrac{dr}{dt} = \gamma x$
- $s + x + r = 1$
- Eliminate x : $\dfrac{1}{s}\dfrac{ds}{dt} = -\dfrac{\beta}{\gamma}\dfrac{dr}{dt}$
- Integrate both sides with respect to t : $s = s_0 e^{-\beta r/\gamma}$
- Put this equation and $x = 1 - s - r$:
  $\dfrac{dr}{dt} = \gamma\left(1 - r - s_0 e^{-\beta r/\gamma}\right)$
- $t = \dfrac{1}{\gamma}\int_0^r \dfrac{du}{1 - r - s_0 e^{-\beta r/\gamma}}$

Time evolution of the SIR model
$\beta = 1, \gamma = 0.4, s_0 = 0.99, x_0 = 0.01, r_0 = 0$

Time evolution of the SIR model

- S decreases / R increases monotonically
- S does not go to zero (because no I left as $t \to \infty$)
- R: total size of the outbreak
- $\frac{dr}{dt} = \gamma\left(1 - r - s_0 e^{-\beta r/\gamma}\right) = 0$
- $r = 1 - s_0 e^{-\beta r/\gamma}$
- Initial condition:
  - c infected and n-c susceptible
  - $s_0 = 1 - c/n,\ x_0 = c/n,\ r_0 = 0$
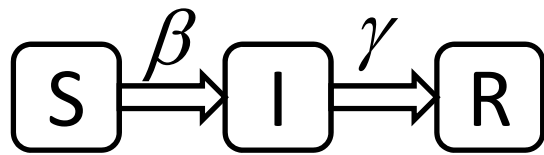 - When $n \to \infty, s_0 \cong 1$
- $r = 1 - e^{-\beta r/\gamma}$

Time evolution of the SIR model
$\beta = 1, \gamma = 0.4, s_0 = 0.99, x_0 = 0.01, r_0 = 0$

S

R

I

Size of the giant component
of a Poisson random graph
$(c = \beta/\gamma)$

size

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

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$
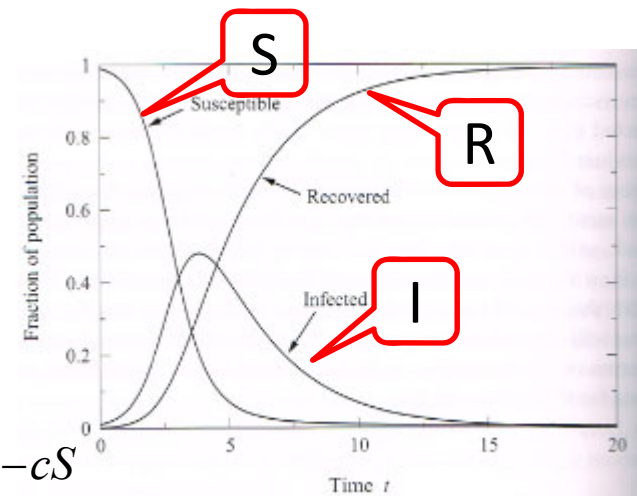
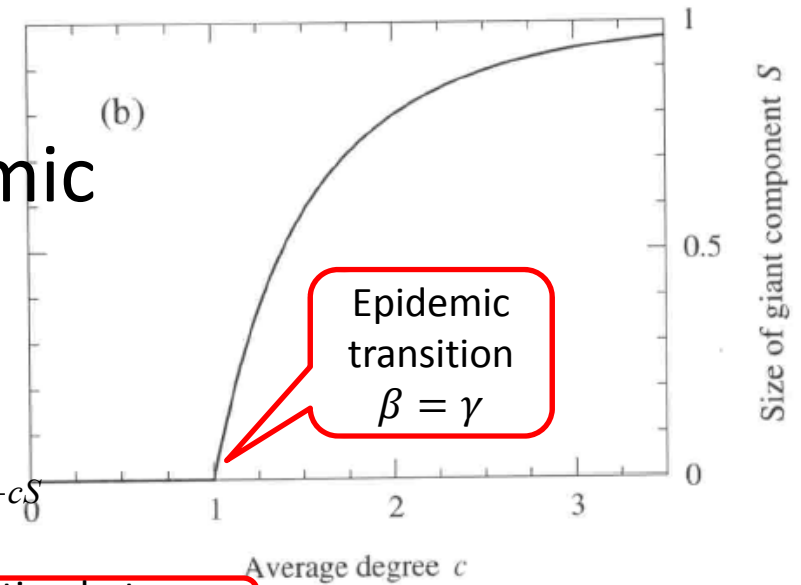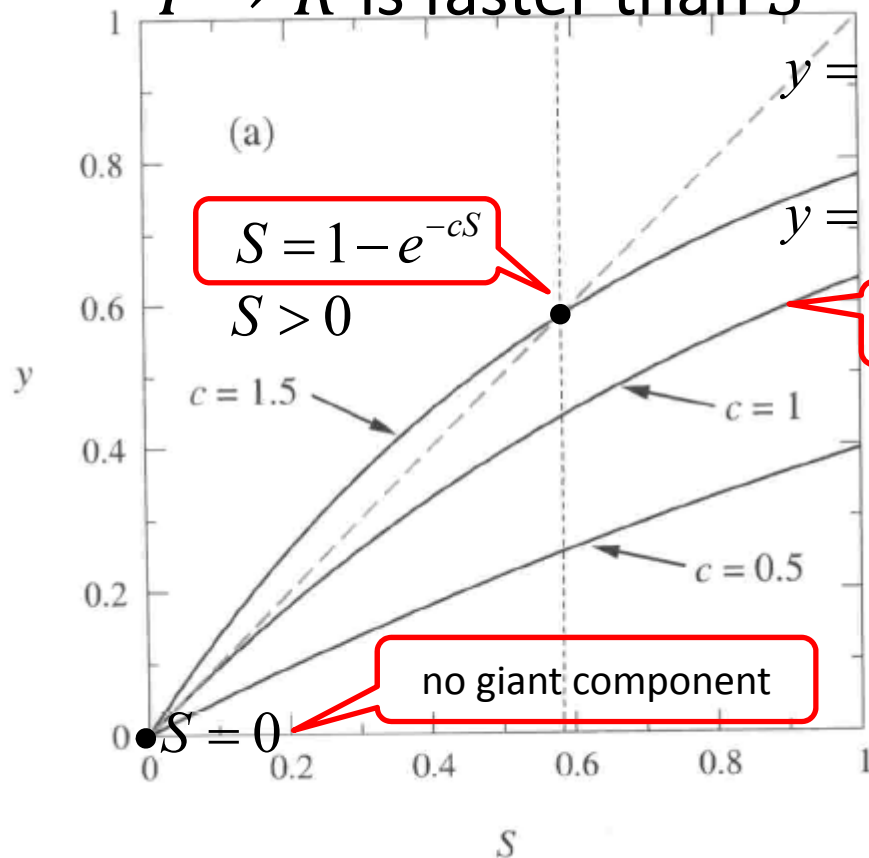# Size of epidemics

$$S = 1 - e^{-cS}$$
$$c = \beta/\gamma$$

- If $\beta \leq \gamma$ there is no epidemic
  - $I \to R$ is faster than $S \to I$

(a)

$y = S$

$y = 1 - e^{-cS}$

$S = 1 - e^{-cS}$
$S > 0$

$c = 1.5$

$c = 1$

$c = 0.5$

no giant component

$S = 0$

(b)

Epidemic transition
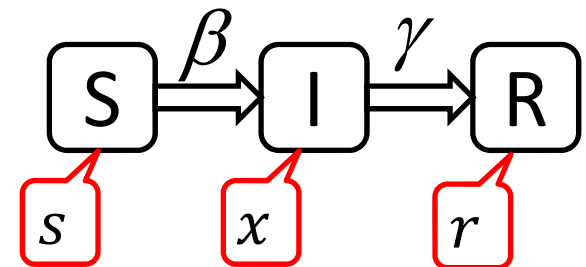$\beta = \gamma$

transition between two regimes
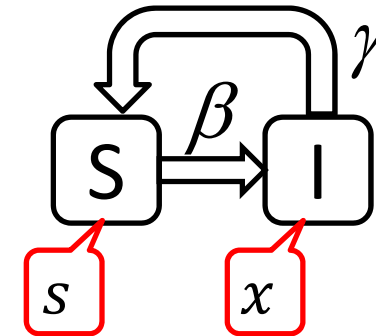
$$\frac{d}{dS}(1 - e^{-cS}) = 1$$

$$ce^{-cS} = 1$$
$$S = 0 \to c = 1$$

Basic reproduction number

- The average number of additional I people
  - If each I person passes disease to two others on average, then $R_0 = 2 \rightarrow$ disease will grow exponentially
  - If $R_0 = 1/2 \rightarrow$ disease will die exponentially
  - If $R_0 = 1 \rightarrow$ epidemic threshold $(\beta = \gamma)$

SIS model

- Individuals can be infected more than once

- $\begin{cases} \dfrac{ds}{dt} = \gamma x - \beta s x \\[2mm] \dfrac{dx}{dt} = \beta s x - \gamma x \\[2mm] s + x = 1 \end{cases}$
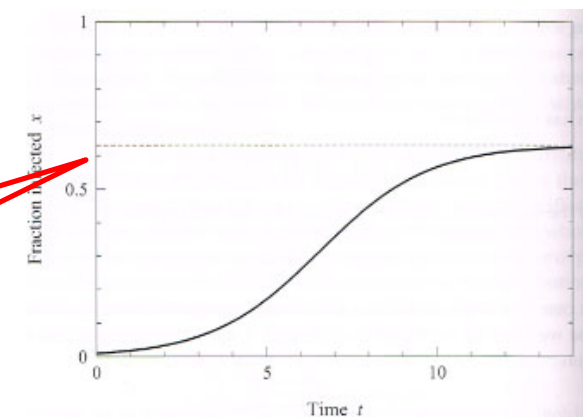
- $\dfrac{dx}{dt} = (\beta - \gamma - \beta x)x$

- $x(t) = (1 - \gamma/\beta)\dfrac{Ce^{(\beta-\gamma)t}}{1+Ce^{(\beta-\gamma)t}}, \; C = \dfrac{\beta x_0}{\beta-\gamma-\beta x_0}$

Initial population of x

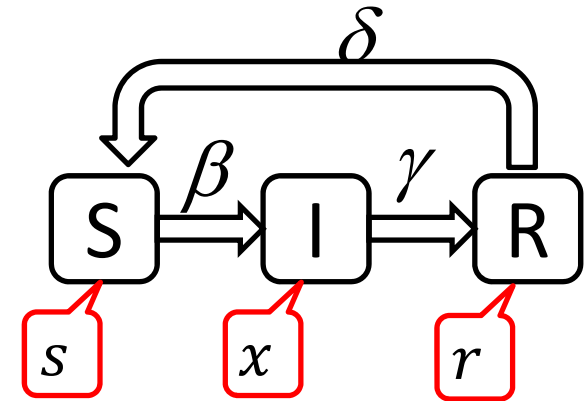- Large population and a small number of initial carriers: $x_0 \to 0, C = \beta x_0/(\beta - \gamma)$

- $x(t) = x_0 \dfrac{(\beta-\gamma)e^{(\beta-\gamma)t}}{\beta-\gamma+\beta x_0 e^{(\beta-\gamma)t}}$

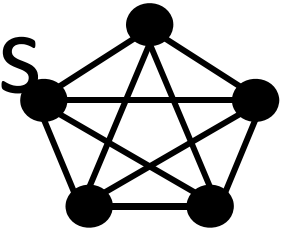- We never have the whole population infected

$x = (\beta - \gamma)/\beta$

SIRS model

- $\left[\dfrac{ds}{dt} = \delta r - \beta s x \right.$
- $\dfrac{dx}{dt} = \beta s x - \gamma x$
- $\dfrac{dr}{dt} = \gamma x - \delta r$
- $s + x + r = 1$
- Rich behaviors depending on the values of the three parameters
  - Disease persists in an endemic state
  - Disease die out
  - Disease oscillates between outbreaks and periods of remission

Epidemic models on networks

- Previous epidemic models assumes "full mixing": each individual can potentially have contact with any other and transmit disease with probability β

- In the real world, however, most people have a set of regular acquaintances, neighbors, and so forth. Most other members can be ignored.

- The set of a person's potential contacts can be represented as a network

- The structure of that network can have a strong effect on the way a disease spread

Epidemic model + network model

Network disease model

- Transmission rate : probability per unit time (β) that infection will be transmitted between ~~S and I~~ two individuals connected by an edge

Late-time properties of epidemics on networks

- SI model on a network as $t \to \infty$
  - All reachable individuals will be infected
- Most networks have a one large component
- If initial carrier is chosen at random, it will infect the large component with probability S, and it will fall in one of the small components with probability 1-S
- New types of behaviors not seen in fully mixed models
  - Parameters of disease model + network structure + position of the initial carrier in the network

S
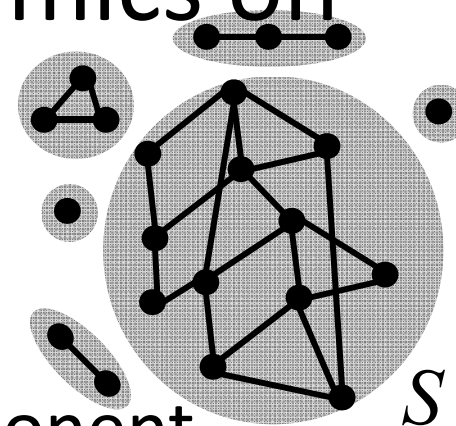
Late-time properties of the SIR model
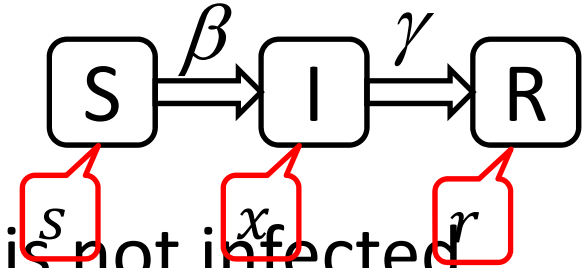
- SIR model
- The probability that the individual is not infected after a total time $\tau : e^{-\beta\tau}$
- The probability that the disease is infected : $\phi = 1 - e^{-\beta\tau}$
- Assumption for simplicity: every infected individuals remains infectious for the same length of time $\to \phi$ is constant across the whole network
- "Color in" or "occupy" each edge with probability ϕ or not with probability $1 - \phi$

Bond percolation

- Disease spread in this model is precisely the set connected to the initial infected vertex by any path of occupied edges
  - Bond percolation cluster to which the initial carrier belongs
- Similar to percolation process (epidemics)
  - percolation transition corresponds to epidemic threshold
  - Size of outbreaks corresponds to the size of percolation clusters

(a) $\phi = 0.2$　　　(b) $\phi = 0.5$　　　(c) $\phi = 1$