

Complex Networks epidemics

2016.1.25(Mon)

Goal

metrics

algorithms

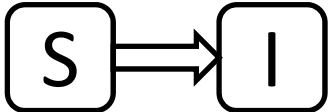
models

processes

contents of this chapter

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

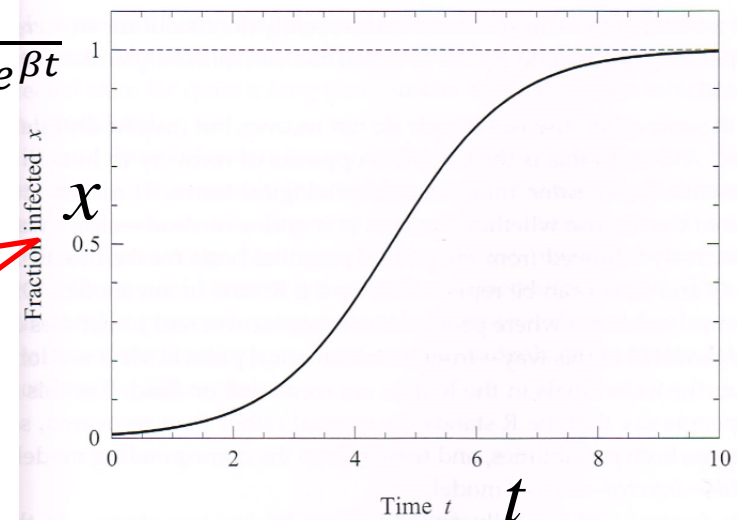
SI model

- Two states
 - Susceptible (S) : not infected
 - Infected (I)
- 
- The diagram consists of two rounded rectangular boxes. The left box contains the letter 'S' and the right box contains the letter 'I'. A horizontal arrow points from the 'S' box to the 'I' box, indicating a transition from the susceptible state to the infected state.
- $S(t)$: # 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

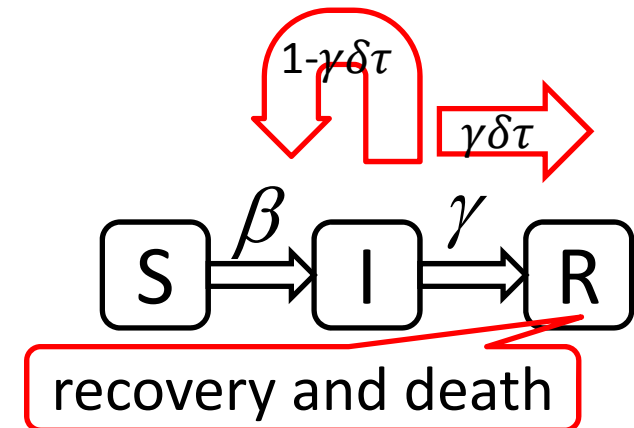
Differential equation of SI model

- $\frac{dX}{dt} = \beta \frac{SX}{n}$: 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 wither 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

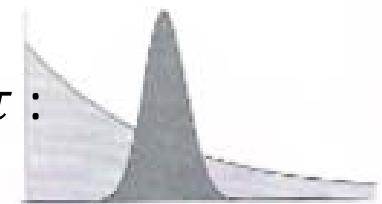


SIR model



- 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 :

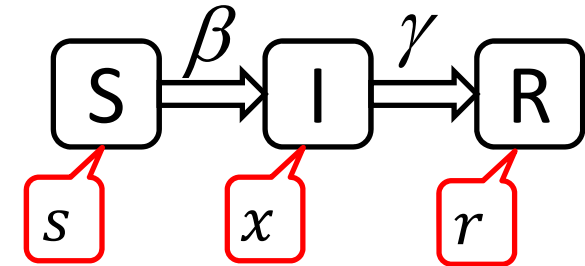
$$\lim_{\delta t \rightarrow 0} (1 - \gamma\delta\tau)^{\tau/\delta\tau} = e^{-\gamma\tau}$$
- Probability $p(\tau)d\tau$ that the individual remains infected for τ and then recovers between τ and $\tau + d\tau$: $p(\tau)d\tau = \gamma e^{-\gamma\tau}d\tau$



not realistic for most real disease

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

Equations for the SIR model



- $\frac{ds}{dt} = -\beta sx$
- $\frac{dx}{dt} = \beta sx - \gamma x$
- $\frac{dr}{dt} = \gamma x$
- $s + x + r = 1$

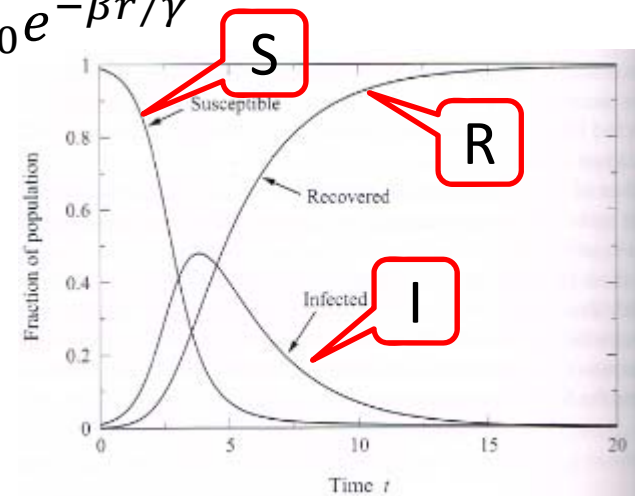
- Eliminate x : $\frac{1}{s} \frac{ds}{dt} = -\frac{\beta}{\gamma} \frac{dr}{dt}$

- Integrate both sides with respect to t : $s = s_0 e^{-\beta r/\gamma}$

- Put this equation and $x = 1 - s - r$ into $\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\beta r/\gamma})$

- $t = \frac{1}{\gamma} \int_0^r \frac{du}{1 - r - s_0 e^{-\beta r/\gamma}}$

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



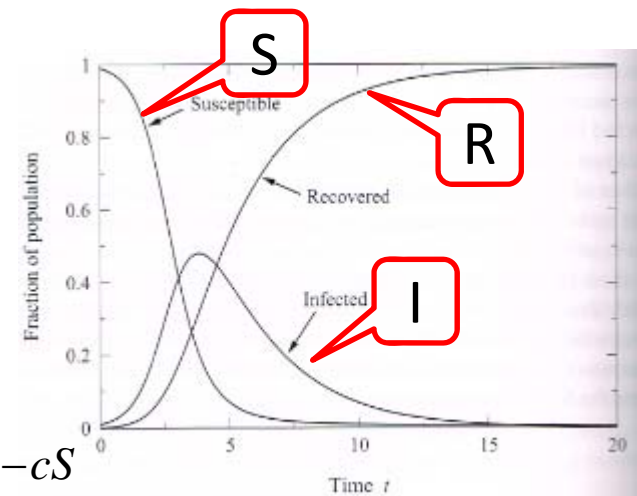
Time evolution of the SIR model

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

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

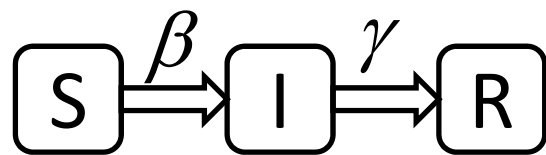
Size of the giant component
of a Poisson random graph
($c = \beta/\gamma$)

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



size

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

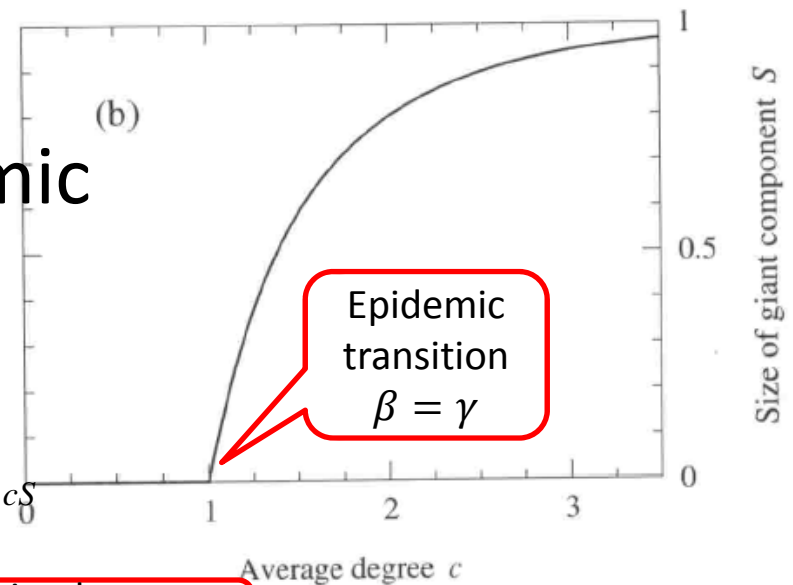
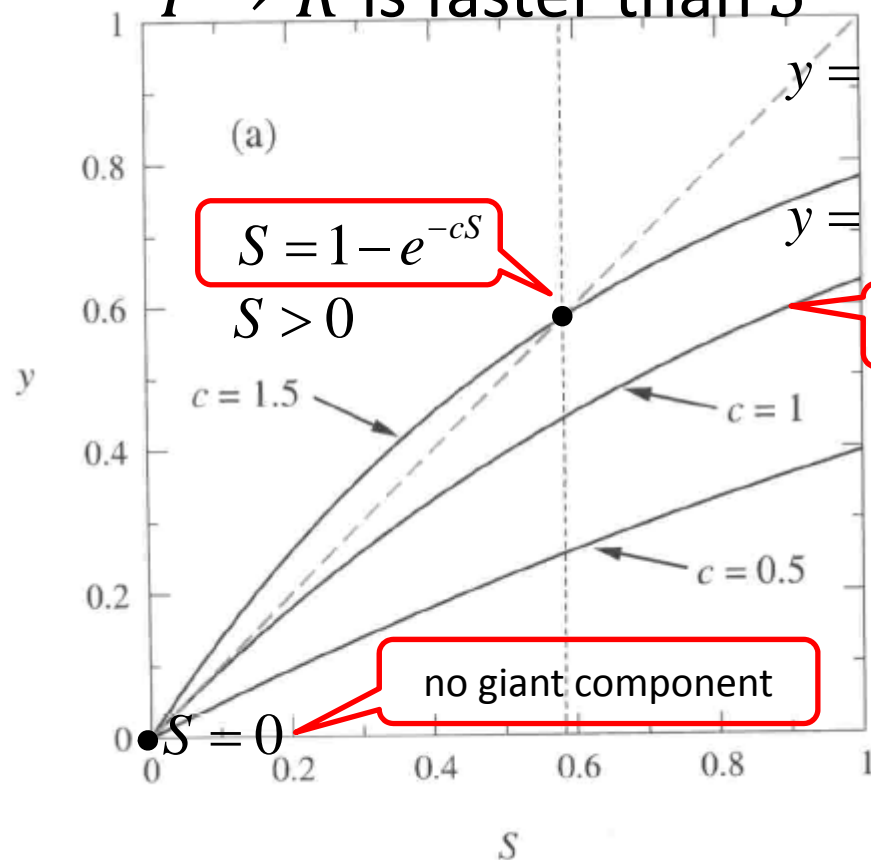


Size of epidemics

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

$$c = \beta/\gamma$$

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



transition between
two regimes

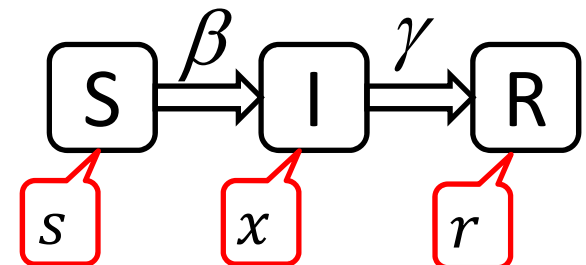
$$\frac{d}{dS}(1 - e^{-cS}) = 1$$

$$ce^{-cS} = 1$$

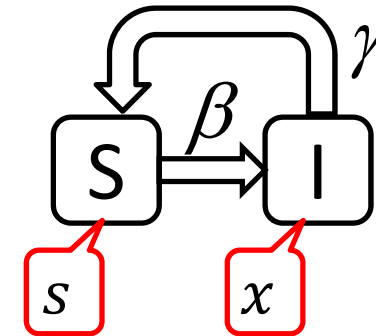
$$S = 0 \rightarrow c = 1$$

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

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

- $s + x = 1$

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

Initial population
of x

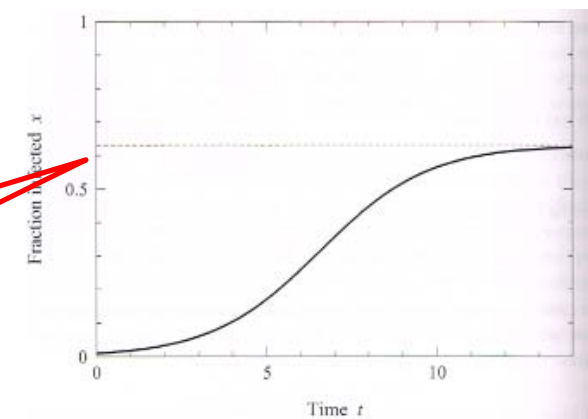
- $x(t) = (1 - \gamma/\beta) \frac{C e^{(\beta-\gamma)t}}{1 + C e^{(\beta-\gamma)t}}, C = \frac{\beta x_0}{\beta - \gamma - \beta x_0}$

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

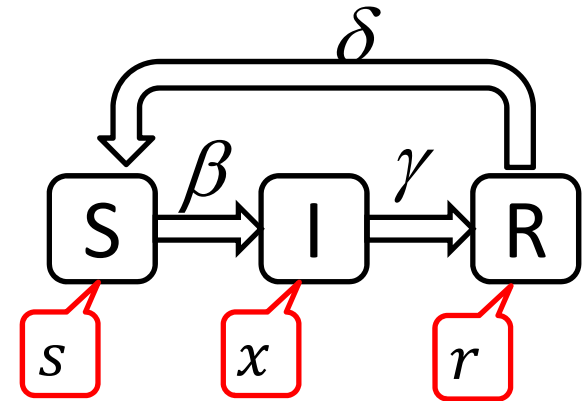
- $x(t) = x_0 \frac{(\beta - \gamma) e^{(\beta - \gamma)t}}{\beta - \gamma + \beta x_0 e^{(\beta - \gamma)t}}$

- We never have the whole population infected

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



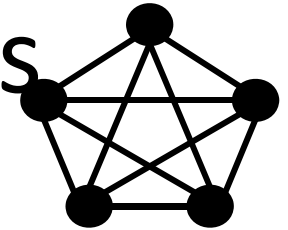
SIRS model



- $\frac{ds}{dt} = \delta r - \beta sx$
- $\frac{dx}{dt} = \beta sx - \gamma x$
- $\frac{dr}{dt} = \gamma x - \delta r$
- $s + x + r = 1$

- 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

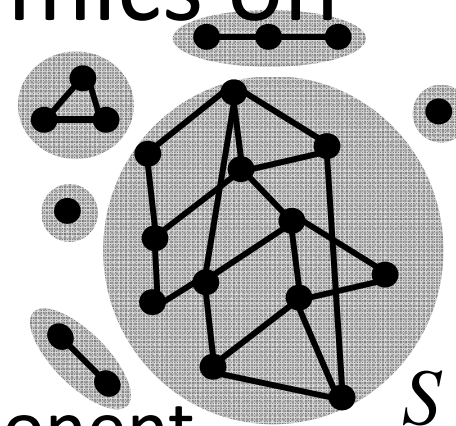
Epidemic model + network model

Network disease model

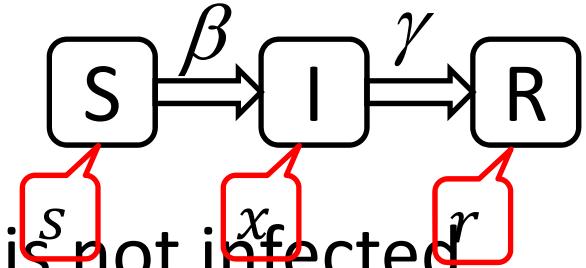
- Transmission rate : probability per unit time (β) that infection will be transmitted between ~~S and I~~ two individuals connected by an edge

Late-time properties of epidemics on networks

- SI model on a network as $t \rightarrow \infty$
 - 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



Late-time properties of the SIR model



- SIR model
- The probability that the individual is not infected after a total time τ : $e^{-\beta\tau}$
- 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 $\rightarrow \phi$ 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

