

# Epidemic models over networks

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# Epidemic models

Epidemic models attempt to capture the **dynamics in the spreading of a disease** (or idea, computer virus, product adoption).

Central questions they try to answer are:

- ▶ 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?

# In today's lecture

## Classic epidemic models (full mixing)

The SI model

The SIR model

The SIS model

## Epidemic models over networks

Homogeneous models

A general network model for SIS

Scale-free network model for SIS

# Full mixing in classic epidemiological models

## Full mixing assumption

In classic epidemiology, it is assumed that every individual has an equal chance of coming into contact with every other individual in the population

# Full mixing in classic epidemiological models

## Full mixing assumption

In classic epidemiology, it is assumed that every individual has an equal chance of coming into contact with every other individual in the population

*Dropping this assumption by making use of an underlying **contact network** leads to the more realistic models over networks (second half of the lecture)!*

# The SI model (fully mixing susceptible – infected)

Notation (following [Newman, 2010])

- ▶ Let  $S(t)$  be the number of individuals who are *susceptible* to sickness at time  $t$
- ▶ Let  $X(t)$  be the number of individuals who are *infected* at time  $t$ <sup>1</sup>
- ▶ Total population size is  $n$
- ▶ Contact with infected individuals causes a susceptible person to become infected
- ▶ An infected **never recovers** and stays infected and infectious to others

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<sup>1</sup>Well, really  $S$  and  $X$  are random variables and we want to capture number of infected and susceptible *in expectation*.

# The SI model

In the SI model, individuals can be in one of two states:

- ▶ *susceptible* (S), or
- ▶ *infective* (I)



The parameters of the SI model are

- ▶  $\beta$  infection rate: probability of contagion after contact per unit time



# The SI model

## Dynamics

$$\frac{dX}{dt} = \beta \frac{SX}{n} \quad \text{and} \quad \frac{dS}{dt} = -\beta \frac{SX}{n}$$

where

- ▶  $S/n$  is the probability of meeting a susceptible person at random per unit time
- ▶  $XS/n$  is the average number of susceptible people that infected nodes meet per unit time
- ▶  $\beta XS/n$  is the average number of susceptible people that become infected from all infecteds per unit time

# The SI model

## Logistic growth equation and curve

Define  $s = S/n$  and  $x = X/n$ , since  $S + X = n$  or equivalently  $s + x = 1$ , we get:

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

The solution to the differential equation (known as the “*logistic growth equation*”) leads to the *logistic growth curve*

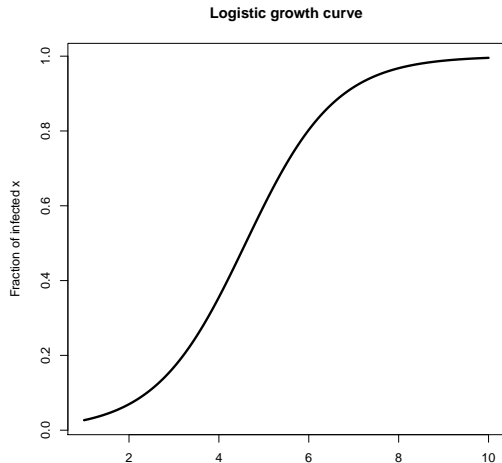
$$x(t) = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$$

where  $x(0) = x_0$

# The SI model

## Logistic growth equation and curve

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



# Solving the logistic growth equation I

$$\begin{aligned} \frac{dx}{dt} &= \beta(1-x)x \\ \Leftrightarrow \int_{x_0}^x \frac{1}{(1-x)x} dx &= \int_0^t \beta dt \\ \Leftrightarrow \int_{x_0}^x \frac{1}{(1-x)} dx + \int_{x_0}^x \frac{1}{x} dx &= \beta t - \beta 0 \\ \Leftrightarrow \int_{x_0}^x \frac{1}{(1-x)} dx + \int_{x_0}^x \frac{1}{x} dx &= \beta t \\ \Leftrightarrow \ln \frac{1-x_0}{1-x} + \ln \frac{x}{x_0} &= \beta t \\ \Leftrightarrow \ln \frac{(1-x_0)x}{(1-x)x_0} &= \beta t \end{aligned}$$

## Solving the logistic growth equation II

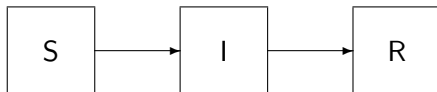
$$\begin{aligned} \ln \frac{(1-x_0)x}{(1-x)x_0} &= \beta t \\ \Leftrightarrow \frac{(1-x_0)x}{(1-x)x_0} &= e^{\beta t} \\ \Leftrightarrow \frac{x}{1-x} &= \frac{x_0 e^{\beta t}}{1-x_0} \\ \Leftrightarrow \frac{1-x}{x} &= \frac{1-x_0}{x_0 e^{\beta t}} \\ \Leftrightarrow \frac{1}{x} &= \frac{1-x_0}{x_0 e^{\beta t}} + 1 = \frac{1-x_0 + x_0 e^{\beta t}}{x_0 e^{\beta t}} \\ \Leftrightarrow x &= \frac{x_0 e^{\beta t}}{1-x_0 + x_0 e^{\beta t}} \end{aligned}$$

# The SIR model

Allowing *recovery* and *immunity*

In the SIR model, individuals can be in one of two states:

- ▶ *susceptible* (S), or
- ▶ *infective* (I), or
- ▶ *recovered* (R)



The parameters of the SIR model are

- ▶  $\beta$  infection rate: probability of contagion after contact per unit time
- ▶  $\gamma$  recovery rate: probability of recovery from infection per unit time

# The SIR model

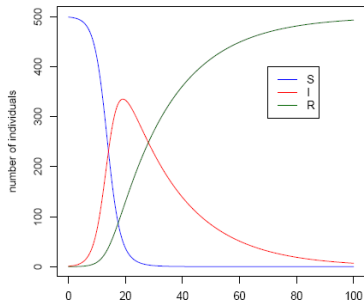
## Dynamics

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

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

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

The solution to this system (with  $s + x + r = 1$ ) is not analytically tractable, but solutions look like the following:



# The SIR model I

## A threshold phenomenon

Now we are interested in considering the *fraction of the population that will get sick* (i.e. size of the epidemic), basically captured by  $r(t)$  as  $t \rightarrow \infty$

Substituting  $dt = \frac{dr}{\gamma x}$  from the third equation into  $ds = -\beta s x dt$  and solving for  $s$  (assuming  $r_0 = 0$ ), we obtain that

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

and so

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



# The SIR model II

## A threshold phenomenon

As  $t \rightarrow \infty$ , we get that  $r(t)$  stabilizes and so  $\frac{dr}{dt} = 0$ , thus:

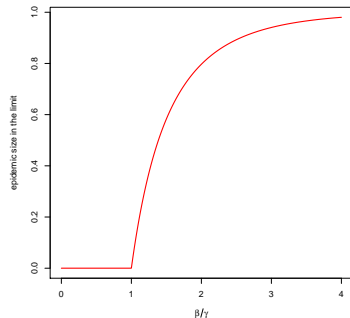
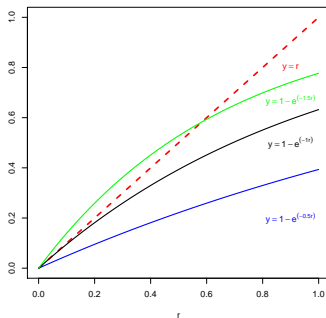
$$r = 1 - s_0 e^{-\frac{\beta}{\gamma} r}$$

Assume that  $s_0 \approx 1$ , since typically we start with a small nr. of infected individuals and we are considering large populations, and

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

# The SIR model III

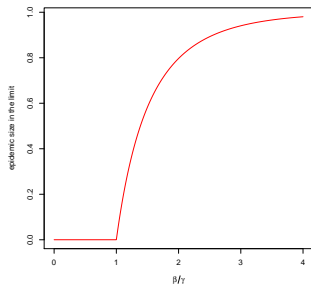
A threshold phenomenon



# The SIR model IV

## A threshold phenomenon

- ▶ if  $\frac{\beta}{\gamma} \leq 1$  then no epidemic occurs
- ▶ if  $\frac{\beta}{\gamma} > 1$  then epidemic occurs
- ▶  $\beta = \gamma$  is the *epidemic transition*



# The SIR model

The basic reproduction number  $R_0$

## Basic reproduction number $R_0$

$R_0$  is the average number of additional people that a newly infected person passes the disease onto before they recover<sup>2</sup>.

- ▶  $R_0 > 1$  means each infected person infects more than 1 person and hence the epidemic grows exponentially (at least at the early stages)
- ▶  $R_0 < 1$  makes the epidemic shrink
- ▶  $R_0 = 1$  marks the *epidemic threshold* between the growing and shrinking regime

In the SIR model,  $R_0 = \frac{\beta}{\gamma}$

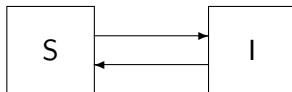
<sup>2</sup>It is defined for the early stages of the epidemic and so one can assume that most people are in the susceptible state.

# The SIS model

People can cure but do not become immune

In the SIS model, individuals can be in one of two states:

- ▶ *susceptible* (S), or
- ▶ *infective* (I)



The parameters of the SI model are

- ▶  $\beta$  infection rate: probability of contagion after contact per unit time
- ▶  $\gamma$  recovery rate: probability of recovery from infection per unit time

# The SIS model

## Dynamics

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

Using  $s + x = 1$ , we can solve the system analytically obtaining

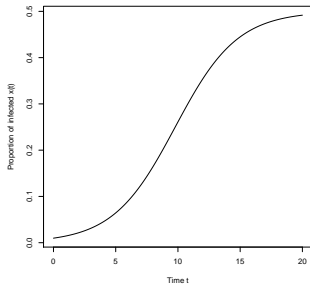
$$x(t) = x_0 \frac{(\beta - \gamma)e^{(\beta - \gamma)t}}{\beta - \gamma + \beta x_0 e^{(\beta - \gamma)t}}$$

Intuition: The SIS models the *flu*  
while the SIR models the *mumps*

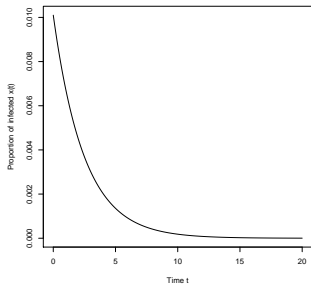
# The SIS model

## Examples

$$\beta = 0.8, \gamma = 0.4$$



$$\beta = 0.4, \gamma = 0.8$$



- ▶ *logistic* growth curve
- ▶ *steady state* at  $x = \frac{\beta - \gamma}{\beta}$

- ▶ *exponential decay*

# The SIS model

The basic reproduction number  $R_0$

- ▶ The point  $\beta = \gamma$  marks the epidemic transition
- ▶ In the SIS model,  $R_0 = \frac{\beta}{\gamma}$



# In today's lecture

## Classic epidemic models (full mixing)

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The SIR model

The SIS model

## Epidemic models over networks

Homogeneous models

A general network model for SIS

Scale-free network model for SIS

# Homogeneous network models

All nodes have degree very close to  $\langle k \rangle$  (e.g. Erdős-Rényi networks or regular lattices)

We can re-write the equation of the epidemic models taking into account that individuals have approximately  $\langle k \rangle$  possibilities of contagion from neighbors

# Homogeneous SI model

## Equations of dynamics

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

$$\frac{ds}{dt} = -\beta \langle k \rangle s(1-s)$$

## Solution

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

## Observations

- ▶ Same behavior as in the non-networked model
- ▶ Growth of infecteds depends on  $\langle k \rangle$  as well as  $\beta$

# Homogeneous SIR model

## Equations of dynamics

$$\frac{ds}{dt} = -\beta \langle k \rangle sx \qquad \frac{dx}{dt} = \beta \langle k \rangle sx - \gamma x \qquad \frac{dr}{dt} = \gamma x$$

## Epidemic threshold

- ▶ if  $\frac{\beta}{\gamma} \leq \frac{1}{\langle k \rangle}$  then no epidemic occurs
- ▶ if  $\frac{\beta}{\gamma} > \frac{1}{\langle k \rangle}$  then epidemic occurs

## Observations

- ▶ Same behavior as in the non-networked model

# Homogeneous SIS model

## Equations of dynamics

$$\frac{ds}{dt} = \gamma x - \beta \langle k \rangle s x \qquad \frac{dx}{dt} = \beta \langle k \rangle s x - \gamma x$$

## Solution

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

## Observations

- ▶ Same behavior as in the non-networked model
- ▶ Epidemic threshold at  $\beta \langle k \rangle - \gamma = 1$ 
  - ▶ Equivalent to  $\frac{\beta}{\gamma} \leq \frac{1}{\langle k \rangle}$ , same as SIR

# A general network model for SIS [Chakrabarti et al., 2008]

Now we need to consider that infection can be through existing connections

- ▶  $\mathbf{A}$  is the adjacency matrix of the underlying contact network, and  $A_{ij}$  is the entry corresponding to the potential edge between nodes  $i$  and  $j$
- ▶ Assume  $\mathbf{A}$  is symmetric (contagion goes in both ways) and has dimension  $n \times n$  ( $n$  is the population size)
- ▶  $s_i(t)$  is the probability of node  $i$  being susceptible to disease at time  $t$
- ▶  $x_i(t)$  is the probability of node  $i$  being infected at time  $t$

# Model dynamics I

From [Chakrabarti et al., 2008]

“During each time interval  $\Delta t$ , an infected node  $i$  tries to infect its neighbors with probability  $\beta$ . At the same time,  $i$  may be cured with probability  $\gamma$ .”

## Model dynamics II

### Notation

- ▶ Let  $x_i(t)$  be the probability that node  $i$  is infected at time  $t$
- ▶ Let  $\zeta_i(t)$  be the probability that a node  $i$  will not receive infections from its neighbors in the next time step

$$\begin{aligned} \zeta_i(t) &= \prod_{j:i-j} \overbrace{x_j(t-1)(1-\beta)}^{j \text{ fails to pass infection}} + \overbrace{(1-x_j(t-1))}^{j \text{ is not infected}} \\ &= \prod_{j:i-j} 1 - x_j(t-1)\beta \end{aligned}$$



## Model dynamics III

Then, the probability that a node  $i$  is uninfected is:

$$1-x_i(t) = \underbrace{\zeta_i(t)}_{\text{neighbors fail to infect}} \left( \underbrace{((1-x_i(t-1)))}_{\text{node is healthy}} + \underbrace{\gamma x_i(t-1)}_{\text{node is infected and cures}} \right)$$

Finally, the fraction of infecteds is computed as:

$$x(t) = \sum_i x_i(t)$$

# Threshold phenomenon I

## Theorem

*The epidemic threshold of the SIS model over arbitrary networks is  $\frac{1}{\lambda_1}$ , where  $\lambda_1$  is the largest eigenvalue of the underlying contact network, that is:*

- ▶ If  $\frac{\beta}{\gamma} > \frac{1}{\lambda_1}$  then epidemic occurs
- ▶ If  $\frac{\beta}{\gamma} < \frac{1}{\lambda_1}$  then no epidemic occurs

## Threshold phenomenon II

$$\begin{aligned}\zeta_i(t) &= \prod_{j:i-j} 1 - x_j(t-1)\beta \\ &\geq 1 - \beta \sum_{j:i-j} x_j(t-1) \\ &= 1 - \beta \sum_j A_{ij} x_j(t-1)\end{aligned}$$

## Threshold phenomenon III

$$\begin{aligned}
 x_i(t) &= 1 - (1 - (1 - \gamma)x_i(t-1))\zeta_i(t) \\
 &\leq 1 - (1 - (1 - \gamma)x_i(t-1))(1 - \beta \sum_j A_{ij}x_j(t-1)) \\
 &= 1 - (1 - (1 - \gamma)x_i)(1 - \beta \sum_j A_{ij}x_j) \\
 &= 1 - \left( 1 - (1 - \gamma)x_i - \beta \sum_j A_{ij}x_j + (1 - \gamma)x_i\beta \sum_j A_{ij}x_j \right) \\
 &= (1 - \gamma)x_i + \beta \sum_j A_{ij}x_j - (1 - \gamma)x_i\beta \sum_j A_{ij}x_j \\
 &\leq (1 - \gamma)x_i(t-1) + \beta \sum_j A_{ij}x_j(t-1)
 \end{aligned}$$

## Threshold phenomenon IV

In matrix notation:

$$\mathbf{x}(t) \leq ((1 - \gamma)\mathbf{I} + \beta\mathbf{A})\mathbf{x}(t - 1)$$

Define  $\mathbf{S} = \beta\mathbf{A} + (1 - \gamma)\mathbf{I}$ , then

$$\mathbf{x}(t) \leq \mathbf{S}\mathbf{x}(t - 1) \leq \mathbf{S}^2\mathbf{x}(t - 2) \leq \dots \leq \mathbf{S}^t\mathbf{x}(0)$$

Assuming that  $\mathbf{x}(0) = \sum_r a_r \mathbf{v}_r$ , where  $\mathbf{v}_r$  are the eigenvectors of  $\mathbf{S}$

$$\mathbf{x}(t) \leq \mathbf{S}^t \sum_r a_r \mathbf{v}_r = \sum_r (\lambda_r)^t a_r \mathbf{v}_r$$

From linear algebra we know that  $\lambda_1 > 0$  (matrix  $\mathbf{S}$  is symmetric and real) and also  $\lambda_1 > \lambda_2 > \dots > \lambda_r$ . For  $t \rightarrow \infty$ , the sum is dominated by the first eigenvalue and so

# Threshold phenomenon $V$

$$\mathbf{x}(t) \leq (\lambda_1)^t a_1 \mathbf{v}_1$$

If  $\lambda_1 < 1$ , then the epidemic must vanish (the other direction also holds, check [Chakrabarti et al., 2008]).

Finally, the relation between the eigenvalues of  $\mathbf{S} = (1 - \gamma)\mathbf{I} + \beta\mathbf{A}$  matrix and the ones of  $\mathbf{A}$  matrix is, for all  $r$ :

$$\lambda_r^S = 1 - \gamma + \beta\lambda_r^A$$

## Threshold phenomenon VI

So the final threshold (w.r.t. leading eigenvalue of  $\mathbf{A}$ )

$$\begin{aligned} & \lambda_1^S < 1 \\ \iff & 1 - \gamma + \beta \lambda_1^A < 1 \\ \iff & 1 + \beta \lambda_1^A < 1 + \gamma \\ \iff & \beta \lambda_1^A < \gamma \\ \iff & \frac{\beta}{\gamma} < \frac{1}{\lambda_1^A} \end{aligned}$$



# Scale-free network model for SIS.

Recap: Homogeneous SIS model

Equations of dynamics

$$\frac{ds}{dt} = \gamma x - \beta \langle k \rangle s x \qquad \frac{dx}{dt} = \beta \langle k \rangle s x - \gamma x$$

Solution

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

Observations

- ▶ Same behavior as in the non-networked model
- ▶ Epidemic threshold at  $\beta \langle k \rangle - \gamma = 1$ 
  - ▶ Equivalent to  $\frac{\beta}{\gamma} \leq \frac{1}{\langle k \rangle}$ , same as SIR



# The scale-free model of epidemics for SIS I

From [Pastor-Satorras and Vespignani, 2001]

Instead of assuming homogeneous mixing, have a different equation for all nodes of same degree  $k$ :

$$\frac{dx_k}{dt} = \beta k(1 - x_k)\Theta(\beta) - \gamma x_k$$

where

- ▶  $(1 - x_k)$  is the probability that a node of degree  $k$  is not infected
- ▶  $\Theta(\beta)$  is the probability that a neighbor is infected
- ▶  $\beta k\Theta(\beta)$  is the probability of contagion of a  $k$ -degree node from an infected neighbor

## The scale-free model of epidemics for SIS II

From [Pastor-Satorras and Vespignani, 2001]

Imposing stationarity ( $\frac{dx_k}{dt} = 0$ , for all  $k$ ), we obtain

$$x_k = \frac{k\beta\Theta(\beta)}{\gamma + k\beta\Theta(\beta)}$$

and so nodes with higher degree are more susceptible to being infected. W.l.o.g. may assume  $\gamma = 1$ .

The probability that any edge points to an  $s$ -degree node is proportional to  $sP(s)$ , and by def.  $\sum_s sP(s) = \langle k \rangle$ . Therefore

$$\Theta(\beta) = \frac{\sum_k kP(k)x_k}{\sum_s sP(s)} = \frac{1}{\langle k \rangle} \sum_k kP(k)x_k$$

# The scale-free model of epidemics for SIS III

From [Pastor-Satorras and Vespignani, 2001]

Plug in the expression for  $x_k$  to obtain

$$\Theta(\beta) = \frac{1}{\langle k \rangle} \sum_k k P(k) \frac{k \beta \Theta(\beta)}{1 + k \beta \Theta(\beta)}$$

A non-zero stationary prevalence ( $x_k \neq 0$ ) is obtained when both sides of previous eq., taken as funct. of  $\Theta$ , cross in  $0 < \Theta \leq 1$ .

This corresponds to

$$\left. \frac{d}{d\Theta} \left( \frac{1}{\langle k \rangle} \sum_k k P(k) \frac{k \beta \Theta}{1 + k \beta \Theta} \right) \right|_{\Theta=0} \geq 1$$

# The scale-free model of epidemics for SIS IV

From [Pastor-Satorras and Vespignani, 2001]

The critical epidemic threshold  $\beta_c$  is the value  $\beta$  which yields equality above. This is given by

$$\frac{1}{\langle k \rangle} \sum_k k P(k) \beta_c k = \frac{\langle k^2 \rangle}{\langle k \rangle} \beta_c = 1$$

Hence,  $\beta = \frac{\langle k \rangle}{\langle k^2 \rangle}$

This implies that in scale-free networks, for which  $\langle k^2 \rangle \rightarrow \infty$ , we have  $\beta_c = 0$ .

# The scale-free model of epidemics for SIS V




From [Pastor-Satorras and Vespignani, 2001]

So, **there is no epidemic threshold** for (infinite) scale-free networks. In practice, the epidemic threshold in scale-free networks is going to be very small. As a consequence, viruses can spread and proliferate at any rate. However, this spreading rate is in general exponentially small.

( In the scale-free model of [Barabasi and Albert, 1999] we have  $P(k) = 2m^2/k^3$  and so we obtain in this case (w.l.o.g.  $\gamma = 1$ )

$$\Theta(\beta) = \frac{e^{-\frac{1}{m\beta}}}{\beta m} \quad \text{and} \quad x \approx 2e^{-\frac{1}{m\beta}} \quad )$$

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