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

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])

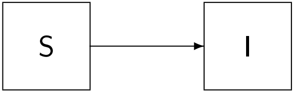
- Let $S(t)$ be the number of individuals who are *susceptible* to sickness at time t
- Let $X(t)$ be the number of individuals who are *infected* at time t[1]
- Total population size is n
- Contact with infected individuals causes a susceptible person to become infected
- An infected never recovers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

[1] 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:

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



The parameters of the SI model are

- β infection rate: probability of contagion after contact per unit time

The SI model

Dynamics

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

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*

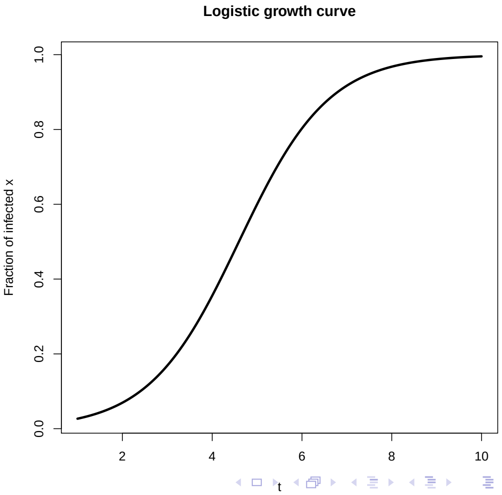
$$x(t) = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$$

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

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

Solving the logistic growth equation II

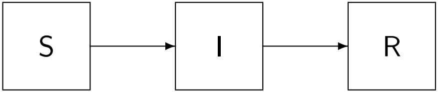
$$
\begin{aligned}
\ln \frac{(1-x_0)x}{(1-x)x_0} &= \beta t \\
\iff \frac{(1-x_0)x}{(1-x)x_0} &= e^{\beta t} \\
\iff \frac{x}{1-x} &= \frac{x_0 e^{\beta t}}{1-x_0} \\
\iff \frac{1-x}{x} &= \frac{1-x_0}{x_0 e^{\beta t}} \\
\iff \frac{1}{x} = \frac{1-x_0}{x_0 e^{\beta t}} + 1 &= \frac{1-x_0+x_0 e^{\beta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

The SIR model

Allowing *recovery* and *immunity*

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

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



The parameters of the SIR model are

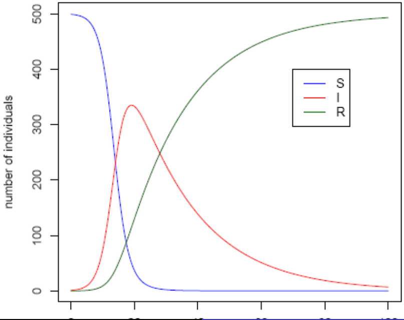
- β infection rate: probability of contagion after contact per unit time
- γ recovery rate: probability of recovery from infection per unit time

The SIR model

Dynamics

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

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 $t \to \infty$

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

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

The SIR model II

A threshold phenomenon

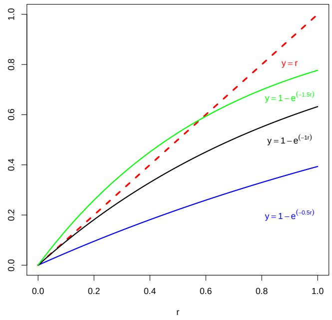
As $t \to \infty$, we get that $r(t)$ stabilizes and so $\frac{dr}{dt} = 0$, thus:

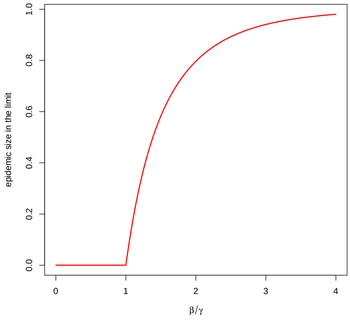
$$r = 1 - s_0 e^{-\frac{\beta}{\gamma} r}$$

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

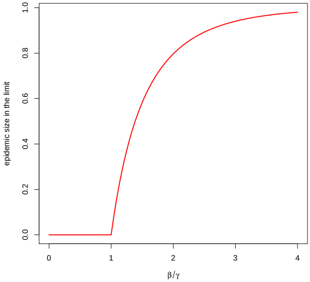




The SIR model IV

A threshold phenomenon

- if $\frac{\beta}{\gamma} \leqslant 1$ 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[2].

- $R_0 > 1$ 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, $R_0 = \frac{\beta}{\gamma}$

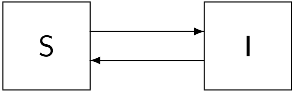
[2] It is defined for the early stages of the epidemic and so one can assume that most people are in the susceptible state.

The SIS model

People can cure but do not become immune

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

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



The parameters of the SI model are

- β infection rate: probability of contagion after contact per unit time
- γ recovery rate: probability of recovery from infection per unit time

The SIS model

Dynamics

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

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

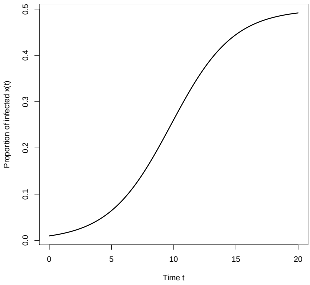
$$x(t) = x_0 \frac{(\beta - \gamma) e^{(\beta - \gamma) t}}{\beta - \gamma + \beta x_0 e^{(\beta - \gamma) t}}$$

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

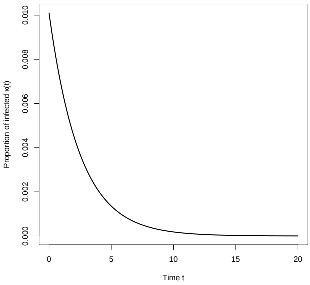
The SIS model

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

Homogeneous network models

All nodes have degree very close to $\langle k \rangle$ (e.g. Erdös-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

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

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 β

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 $\frac{\beta}{\gamma} \leqslant \frac{1}{\langle k\rangle}$ 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

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

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 $\frac{\beta}{\gamma} \leqslant \frac{1}{\langle k\rangle}$, 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 Δt, an infected node i tries to infect its neighbors with probability β. At the same time, i may be cured with probability γ."

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:

$$1 - x_i(t) = \overbrace{\zeta_i(t)}^{\text{neighbors fail to infect}} \Big(\overbrace{(1 - x_i(t-1))}^{\text{node is healthy}} + \overbrace{\gamma x_i(t-1)}^{\text{node is infected and cures}} \Big)$$

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 λ_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

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

Threshold phenomenon III

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

Threshold phenomenon IV

In matrix notation:

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

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

$$\mathbf{x}(t) \leqslant \mathbf{S}\mathbf{x}(t-1) \leqslant \mathbf{S}^2\mathbf{x}(t-2) \leqslant \ldots \leqslant \mathbf{S}^t\mathbf{x}(0)$$

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

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

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

Threshold phenomenon V

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

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 **A**)

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

□

References I

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