Network Science (VU) (706.703)

Epidemics

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Outline

Introduction

Models of the spread of disease

- Mathematical representation of epidemics predates network science
- In a typical model we classify individuals into one of the categories
    1. **Susceptible** (S): someone who does not have disease but can catch it if they come in contact with an infected person
    2. **Infected** (I): someone who has the disease and can pass it on if they come in contact with a susceptible person
    3. **Recovered** (R): someone who was infected and has cured the disease and is now immune to it

Models of the spread of disease

- These states abstract all the biological details of catching a disease
- However, they capture some of the gross diseases dynamics
- Numbers of S, I, R persons in time
- The time component
- The models also abstract the individual tendency to catch the disease by assuming that each individual catches the disease if it comes into contact with an infected person

Models of the spread of disease

- Models are probabilistic, i.e. there is a chance that an individual comes in contact with another individual
- All the numbers are therefore random, and if the disease spreads more than once the numbers will be a bit different each time
- Thus, we are interested in expected or average numbers of S, I, R persons in time
- Additional simplification for the beginning: complete networks
- Everyone is connected to everyone and has the equal chance of getting in contact to every other person per unit times
- Fully mixed, mass-action approximation, or mean-field theory

SI model

- We have only susceptible (S) and infected (I) individuals
- Let $S(t)$ be the number of susceptible individuals at time t
- Let $X(t)$ be the number of infected individuals at time t
- Because of randomness we are interested in expectations and denote them with S and X

SI model

- The number of infected individuals goes up when susceptible individuals contract the disease from the infected ones
- Suppose that in a fully mixed model people meet with other people at random with a rate β
- This means that each individual has, on average, β contacts per unit time with randomly chosen other individuals
- The diseases is transmitted only when a susceptible person has a contact with an infected person

SI model

- The total population consists of n people
- The average probability of meeting a susceptible person: $\frac{S}{n}$
- An infected person meets therefore $\beta\frac{S}{n}$ susceptible people per unit time
- We have on average X infected persons
- Thus, the overall average rate of new infections per unit time is given by $\beta\frac{SX}{n}$

SI model

- The rate of change of X in time is then given by the following differential equation:

$$\dot{X} = \beta \frac{SX}{n}$$

- At the same time the number of susceptible individuals goes down at the same rate:

$$\dot{S} = -\beta \frac{SX}{n}$$

SI model

- Let us define the variables representing the fractions of S and I individuals: $s = \frac{S}{n}$ and $x = \frac{X}{n}$
- We can then rewrite the previous equations:

$$\begin{aligned} \dot{x} &= \beta s x \\ \dot{s} &= -\beta s x \end{aligned}$$

SI model

- We have $S + X = n$ or $s + x = 1$
- Thus, $s = 1 - x$, and after eliminating s we obtain:

$$\dot{x} = \beta(1 - x)x$$

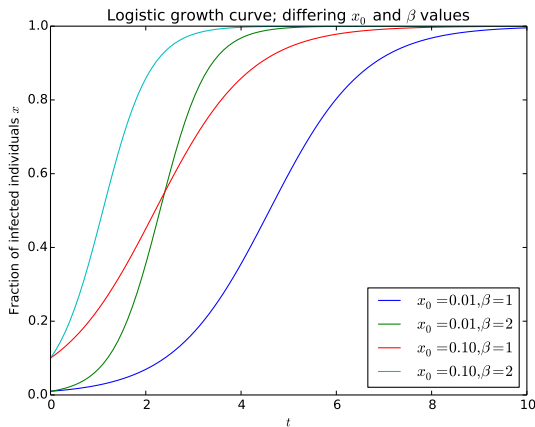- This is *logistic growth equation*
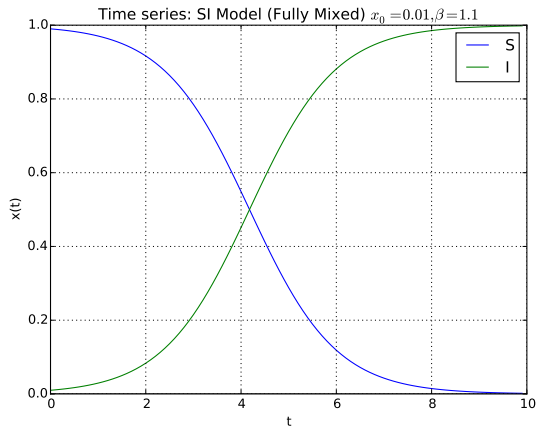
SI model

$$\dot{N} = rN(1 - \frac{N}{K})$$

$$\dot{x} = \beta(1 - x)x$$

- K carrying capacity now equals 1 (all individuals are infected)
- r growth rate is now β

Logistic growth curve

Logistic growth curve; differing x_0 and β values

SI model: numerical solution

SIR Model

Modeling recovery

SIR model

- Now we have susceptible (S), infected (I), and recovered (R) individuals
- Recovered individuals retain their immunity and can not get infected anymore
- As before, let $S(t)$ be the number of susceptible individuals at time t
- Let $X(t)$ be the number of infected individuals at time t
- Let $R(t)$ be the number of recovered individuals at time t
- Because of randomness we are interested in expectations and denote them with S, X, and R respectively

SIR model

- The dynamics of the fully mixed SIR model has two stages
- In the first stage S individuals become I individuals when they have contact with I individuals
- Contacts between individuals happen at average rate β per person as before
- In the second stage infected individuals recover at some constant average rate γ

SIR model

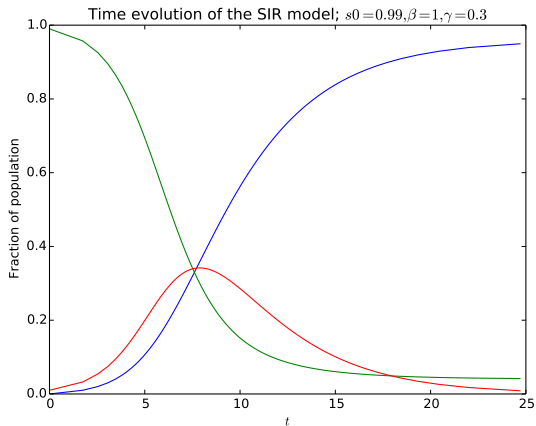- In terms of the fractions s, x, and r we can write our equations:

$$
\begin{aligned}
\dot{s} &= -\beta s x \\
\dot{r} &= \gamma x \\
\dot{x} &= \beta s x - \gamma x
\end{aligned}
$$

- s, x, and r satisfy:

$$s + x + r = 1$$

Time evolution of the SIR model

Time evolution of the SIR model; $s0 = 0.99, \beta = 1, \gamma = 0.3$

Time evolution of the SIR model

- The fraction of S individuals decreases monotonically
- S individuals become infected
- I individuals recover at constant rate
- The number of R individuals increases monotonically
- The fraction of I individuals goes up at first, and then down as people recover

Time evolution of the SIR model

- The number of S individuals does not go to zero
- When $x \to 0$ there are no infected people to pass the disease
- Any individuals who do not get the disease until late will most probably never get the disease at all
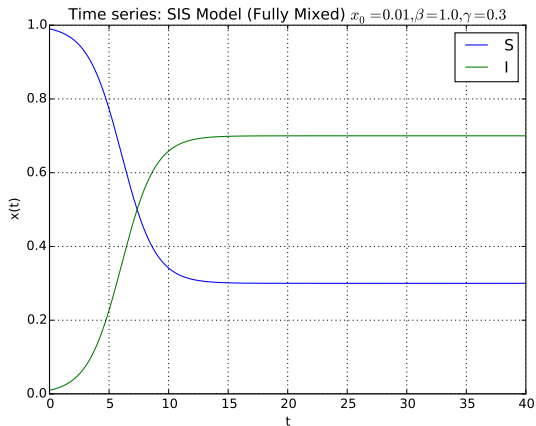- Similarly, the fraction of R individuals does not quite reach 1

Outbreak size

- The size of the epidemics is the function of β (contact rate) and γ (recovery rate)
- The size goes continuously to zero as β/γ approaches 1 from above
- Also, for $\beta/\gamma \leq 1$ there is no epidemic at all
- The simple explanation is that if $\beta \leq \gamma$ then infected individuals recover faster than they meet with susceptible individuals
- The number of infected persons starts small and goes down, and the disease dies out instead of spreading out
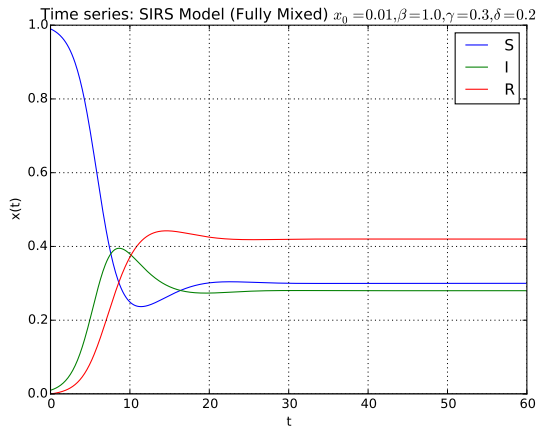
Further extensions of the SI model

- A different extension would be to allow for reinfection
- E.g. after recovering the individuals go into susceptible S state
- SIS model (with some consant rate γ the people become susceptible again (e.g. bacteria)
- Another possibility the individuals recover only temporary
- SIRS model (with some sonstant rate δ the people move from recovered to susceptible)
- Epidemics models from the jupyter notebook

SIS model: numerical solution

Time series: SIS Model (Fully Mixed) $x_0 = 0.01, \beta = 1.0, \gamma = 0.3$

SIRS model: numerical solution

Summary: Epicemic models

- Fully mixed models: no network involved
- Everybody can meet anybody else
- Depending on the model various behaviors
- E.g. SIR model: large outbreak possible depending on the ratios of parameters
- Some people do not get infected at all
- E.g. SIRS model: damped waves of small outbreaks, endemic states
- Behavior dependent only on the parameters of the dynamics

Epidemics on Networks

Modeling adjacency

Epidemic models on networks

- In the real world, the networks have strong effect on the way a disease spreads through the population
- E.g. through regular acquaintances, friends, neighbors, etc.
- Network models of epidemics take into account the underlying network
- But in principle they work in the same way as fully mixed models

Epidemic models on networks

- We will define *transmission rate* or *infection rate* to be the probability per unit time that the infection will be transmitted from an infected to a susceptible individual, who are connected by a link in the network
- The transmission rate is the property of disease
- But it is also a property of the social and behavioral parameters of the population
- Given a value of transmission rate β and the initial number of infected individuals x_0 we can generalize all the models to the network case
- However, it is difficult to solve these models for a general network
- Typically, we simulate the spread on a computer

Late-time properties of epidemics on networks

- There is one respect in which the model is straightforward
- In the case $t \rightarrow \infty$ (late-time properties)
- For example, SI model on networks
- Since nobody recovers, in the end (regardless how small is β), everyone connected to the initially infected nodes will get infected
- Everyone in the component to which the initial carriers belong
- Most networks have one large component that typically contains a significant fraction of nodes
- Thus, if we start with a single infected individual and that node belongs to the large component we will have a large outbreak

Late-time properties of epidemics on networks

- That is the difference between fully mixed and network models of epidemics
- Fully mixed: the size of the outbreak determined by the model parameters
- Network: disease behavior determined by
  1. Model parameters
  2. **Network structure** and the **position of the initial carrier**

Time-dependent properties of epidemics on networks

- We are interested in the average (expected) probabilities $s_i(t)$, $x_i(t)$, or $r_i(t)$ of a node i being in a given state
- Given the adjacency matrix we can write down the equations for these quantities
- An SI outbreak starting on a randomly chosen node will eventually spread to all members of the component
- We are now interested only in the case of giant component
- All other outbreaks have non-significant effects and die out

Time-dependent properties of the SI model

- Suppose i is in the giant component
- What is the probability that i gets infected between times t and $t + dt$
- To become infected i has to catch the disease from an infected neighbor j
- Probability that j is already infected: $x_j = 1 - s_j$
- Probability that the disease is transmitted: βdt
- Additionally we require that i is in S state beforehand (the probability of this: s_i)

Time-dependent properties of the SI model

- Multiplying these probabilities and summing over all neighbors of i
- The total probability of becoming infected is given by:

$$ds_i = -s_i \sum_j A_{ij} x_j \beta dt = -\beta s_i \sum_j A_{ij}(1 - s_j)dt$$

$$\frac{ds_i}{dt} = \dot{s}_i = -\beta s_i \sum_j A_{ij}(1 - s_j)$$

- Minus: the probability of being susceptible goes down when nodes become infected

Time-dependent properties of the SI model

- Similarly:

$$\dot{x}_i = \beta s_i \sum_j A_{ij} x_j = \beta(1 - x_i) \sum_j A_{ij} x_j$$

- Those two equations are really same equations since $s_i + x_i = 1$

Time-dependent properties of the SI model

- We use the same initial conditions as before
- We start with a single infected node chosen uniformly at random, or a small fraction of nodes
- In the limit of large network size the initial conditions are: $x_i = 0$, and $s_i = 1$
- The equations are coupled set of n non-linear differential equations
- Can not be solved in closed form for general A_{ij}
- Let us therefore consider suitable limits

Time-dependent properties of the SI model

$$\dot{x}_i = \beta(1 - x_i) \sum_j A_{ij} x_j = \beta \sum_j A_{ij} x_j - x_i \sum_j A_{ij} x_j$$

- For large n and assuming initial conditions as above x_i will be small
- We can ignore terms of quadratic order in small quantities

$$\dot{x}_i = \beta \sum_j A_{ij} x_j$$

Time-dependent properties of the SI model

$$\dot{\mathbf{x}} = \beta \mathbf{A} \mathbf{x}$$

- Linear system, which we know how to solve!
- We write $\mathbf{x}$ as the linear combination of the eigenvectors, where $\mathbf{v}_r$ is the eigenvector with eigenvalue κ_r

$$\mathbf{x}(t) = \sum_{r=1}^{n} a_r(t) \mathbf{v}_r$$

Time-dependent properties of the SI model

$$\dot{\mathbf{x}} = \sum_{i=1}^{n} \frac{da_r}{dt} \mathbf{v}_r = \beta \mathbf{A} \sum_{i=1}^{n} a_r(t) \mathbf{v}_r = \beta \sum_{i=1}^{n} \kappa_r a_r(t) \mathbf{v}_r$$

- Then comparing terms in $\mathbf{v}_r$:

$$\dot{a}_r = \beta \kappa_r a_r$$

Time-dependent properties of the SI model

- Substituting in the previous equation:

$$\mathbf{x}(t) = \sum_{i=1}^{n} a_r(0) e^{\beta \kappa_r t} \mathbf{v}_r$$

- The fastest growing term corresponds to κ_1 and assuming that it dominates over the others:

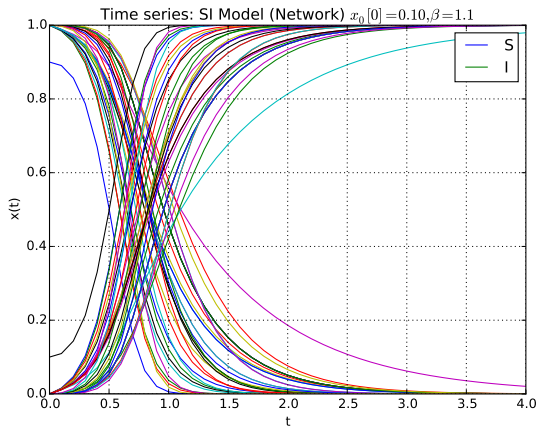$$\mathbf{x}(t) \sim e^{\beta \kappa_1 t} \mathbf{v}_1$$

Time-dependent properties of the SI model

- We expect the number of I individuals to grow exponentially
- Similarly to the fully mixed model
- Now, the exponential constant depends not just on β
- It also depends on the leading eigenvalue of the adjacency matrix (structure of the network)
- Moreover, the probability infection in this early period varies from node to node roughly as the corresponding element of the leading eigenvector

Time-dependent properties of the SI model

- What are the corresponding elements of the leading eigenvector?
- Eigenvector centrality!
- Thus, eigenvector centrality is an approximate measure of the probability of the early infection of a node
- At late times this probability tends to 1
- At early times the nodes with higher eigenvector centralities become infected faster
- Epidemics models from the jupyter notebook

SI network model: numerical solution

Time-dependent properties of the SIR model

- We can extend these techniques to the SIR model
- Again, we concentrate on outbreaks taking place in the giant component
- We define s_i, x_i, and r_i to be the probabilities that node i is in S, I, or R state
- The evolution of s_i is (approximately) governed by the same equation as before:

$$\dot{s}_i = -\beta s_i \sum_j A_{ij} x_j$$

Time-dependent properties of the SIR model

- x_i (γ is the recovery rate):

$$\dot{x}_i = \beta s_i \sum_j A_{ij} x_j - \gamma x_i$$

- r_i:

$$\dot{r}_i = \gamma x_i$$

Time-dependent properties of the SIR model

- We use the same initial conditions as before
- We start with a single infected node chosen uniformly at random, or a small fraction of nodes
- In the limit of large network size the initial conditions are: $x_i = 0$, and $s_i = 1$
- This simplifies the equation for x_i:

$$\dot{x}_i = \beta \sum_j A_{ij} x_j - \gamma x_i = \sum_j (\beta A_{ij} - \gamma \delta_{ij}) x_j$$

Time-dependent properties of the SIR model

$$\dot{\mathbf{x}} = \beta \mathbf{M} \mathbf{x}$$

- Linear system, which we know how to solve!
- $\mathbf{M}$ is a symmetric $n \times n$ matrix:

$$\mathbf{M} = \mathbf{A} - \frac{\gamma}{\beta} \mathbf{I}$$

Time-dependent properties of the SIR model

- We write $\mathbf{x}$ as the linear combination of the eigenvectors of $\mathbf{M}$, where $\mathbf{v}_r$ is the eigenvector with eigenvalue κ_r
- Since $\mathbf{M}$ differs from $\mathbf{A}$ only in a multiple of $\mathbf{I}$ it has the same eigenvectors as $\mathbf{A}$

$$\mathbf{M}\mathbf{v}_r = \mathbf{A}\mathbf{v}_r - \frac{\gamma}{\beta}\mathbf{I}\mathbf{v}_r = (\kappa - \frac{\gamma}{\beta})\mathbf{v}_r$$

- The eigenvalue has shifted by $\frac{\gamma}{\beta}$

Time-dependent properties of the SIR model

- We can solve as previously:

$$\mathbf{x}(t) = \sum_{i=1}^{n} a_r(0) e^{(\beta \kappa_r - \gamma)t} \mathbf{v}_r$$

- The exponential constant depends on β (infection rate), γ (recovery rate), and κ (network structure)
- The faster people recover the less chance they have to pass the disease on the others
- Again, the fastest growing term corresponds to κ_1 and assuming that it dominates over the others:

$$\mathbf{x}(t) \sim e^{(\beta \kappa_1 - \gamma)t} \mathbf{v}_1$$

Time-dependent properties of the SIR model

- Again, eigenvector centrality is an approximate measure of the probability of the early infection of a node
- However, it is possible now for γ to be sufficiently large that the exponential constant in the leading term is negative
- Then, the term **decays** exponentially rather than grows
- The total number of infected individuals will decay over times
- The disease dies out

Time-dependent properties of the SIR model

- The point at which this happens:

$$\beta\kappa_1 - \gamma = 0$$
$$\frac{\beta}{\gamma} = \frac{1}{\kappa_1}$$

- The position of epidemic threshold depends on the leading eigenvalue of the adjacency matrix
- If the leading eigenvalue is small then β must be large, or γ must be small for an outbreak
- In other words: small value of κ_1 makes it harder for disease to spread
- Sparse networks have smaller κ_1, dense networks have larger κ_1