Network Dynamics

Network Application Diagnostics
BE2M32DSAA

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Outline

1. Epidemics
   - Compartment Models
   - SI Model
   - SIS Model
   - SIR Model

2. Epidemics on Networks
   - Network Properties
   - SI Network Model
   - SIR Network Model

Acknowledgments

This presentation is a clone of the original presentations created by Leonid Zhukov in 2015.

Outline

1. Epidemics
   - Compartment Models
   - SI Model
   - SIS Model
   - SIR Model
2. Epidemics on Networks
   - Network Properties
   - SI Network Model
   - SIR Network Model

Network Dynamics

- How networks change over time.
- Changes in parameters and topological structures
- Applications:
  - virus, disease spreading
  - computer virus spreading
  - information spreading
  - influence spreading

Multi-compartment Model

- **A multi-compartment model:** is a type of mathematical model used for describing the way materials or energies are transmitted among the compartments of a system.
- Each **compartment** is assumed to be a homogeneous entity within which the entities being modelled are equivalent.
- The **lumped-element model** (also called lumped-parameter model, or lumped-component model) (CZ model se soustředěnými prvky) simplifies the description of the behaviour of spatially distributed physical systems into a topology consisting of discrete entities that approximate the behaviour of the distributed system under certain assumptions.
  - The simplification reduces the state space of the system to a finite dimension,
  - and the partial differential equations (PDEs) of the continuous (infinite-dimensional) time and space model of the physical system into ordinary differential equations (ODEs) with a finite number of parameters.

Compartment Model in Systems Theory

- A description of a network whose components are compartments
  - that represent a population of elements that are equivalent with respect to the manner in which they process input signals to the compartment.
- Instant homogeneous distribution of materials or energies within a "compartment".
- The exchange rate of materials or energies among the compartments is related to the densities of these compartments.
- Usually, it is desirable that the materials do not undergo chemical reactions while transmitting among the compartments.
- When concentration of the cell is of interest, typically the volume is assumed to be constant over time, though this may not be totally true in reality.

Kermack–McKendrick Theory

- **Kermack–McKendrick theory** (1927) is a hypothesis that predicts the number and distribution of cases of an infectious disease as it is transmitted through a population over time.
- Kermack–McKendrick theory is indeed the source of SIR models and their relatives.
- Kermack–McKendrick theory is a compartmental differential-equation model that structures the infectioned population in terms of age-of-infection, while using simple compartments for people who are susceptible (S) and recovered/removed (R).

Disease States[New10]

- The within-host dynamics of the disease is reduced to changes between a few basic disease states.
- The simplest version there are just two states, susceptible and infected.
- An individual in the **susceptible** (CZ náchylný) state is someone who does not have the disease yet but could catch it if they come into contact with someone who does.
- An individual in the **infected** (CZ infikovaný) state is someone who has the disease and can, potentially, pass it on if they come into contact with a susceptible individual.
- An individual in the **recovered** (CZ uzdravený) state is someonewho have been infected and then recovered from the disease, can't be infected again or to transmit the infection to others.

Model Assumptions[New10]

- A *fully mixed* or *mass-action approximation*, in which it is assumed that every individual has an equal chance, per unit time, of coming into contact with every other—people mingle and meet completely at random in this approach.
- Closed population (no birth, death, migration), population size N.
- Models: SI, SIS, SIR, SIRS, . . .

Outline

Formal Model[?]

- $S(t)$ …susceptible,
- $I(t)$ …infected

$$S \longrightarrow I$$

$$S(t) + I(t) = N$$

- β …infection/contact rate, number of contacts per unit time
- Infection equation:

$$I(t + \delta t) = I(t) + \beta \frac{S(t)}{N} I(t) \delta t$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t)$$

Fractions[?]

- Fractions
  - $i(t) = I(t)/N$,
  - $s(t) = S(t)/N$,
- Equations

$$\frac{di(t)}{dt} = \beta s(t)i(t)$$

$$\frac{ds(t)}{dt} = -\beta s(t)i(t)$$

$$s(t) + i(t) = 1$$

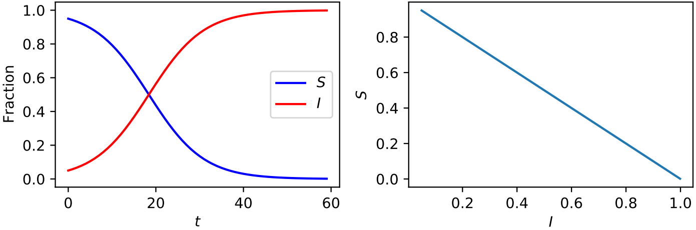
- Differential equation, $i(t = 0) = i_0$

$$\frac{di(t)}{dt} = \beta(1 - i(t))i(t)$$

Logistic growth function[?]

- Solution

$$i(t) = \frac{i_0}{i_0 + (1 - i_0)\mathrm{e}^{-\beta t}}$$



1

- Limit $t \to \infty$

$$i(t) \to 1$$

$$s(t) \to 0$$

[1] in image $i_0 = 0.05, \beta = 0.8$

Outline

Formal Model[?]

- $S(t)$ ... susceptible,
- $I(t)$ ... infected

$$S \longrightarrow I \longrightarrow S$$

$$S(t) + I(t) = N$$

- β ... infection/contact rate, number of contacts per unit time
- γ ... recovery rate
- Infection equation:

$$\frac{ds}{dt} = -\beta s i + \gamma i$$

$$\frac{di}{dt} = \beta s i - \gamma i$$

$$s + i = 1$$

- Differential equation, $i(t = 0) = i_0$

$$\frac{di}{dt} = (\beta - \gamma - i)i$$

SIS Model Solution[?]

- Solution

$$i(t) = (1 - \frac{\gamma}{\beta})\frac{C}{C + \mathrm{e}^{-(\beta-\gamma)t}}$$

where

$$C = \frac{\beta i_0}{\beta - \gamma - \beta i_0}$$

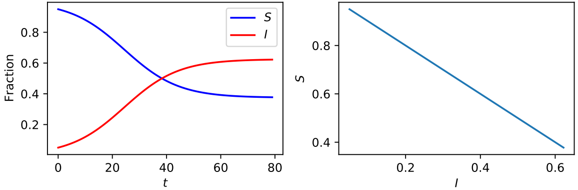
- Limit $t \to \infty$

$$\beta > \gamma : \qquad i(t) \to (1 - \frac{\gamma}{\beta}) \tag{1}$$

$$\beta < \gamma : \qquad i(t) = i_0 \mathrm{e}^{(\beta-\gamma)t} \to 0 \tag{2}$$

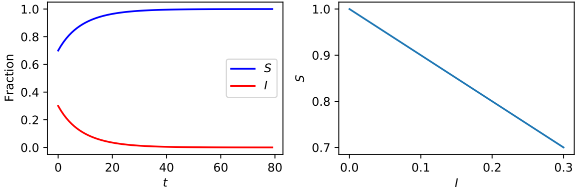
Logistic Function[?]

- $\beta > \gamma: \ i(t) \rightarrow (1 - \frac{\gamma}{\beta})$



[1]

- $\beta < \gamma: \ i(t) = i_0 e^{(\beta-\gamma)t} \rightarrow 0$



[2]

[1] in image $i_0 = 0.05, \beta = 0.8, \gamma = 0.3$
[2] in image $i_0 = 0.3, \beta = 0.3, \gamma = 0.8$

Outline

Formal Model[New10, ?]

- $S(t)$ ... susceptible,
- $I(t)$ ... infected
- $R(t)$ ... recovered or died

$$S \longrightarrow I \longrightarrow R$$

$$S(t) + I(t) + R(t) = N$$

- β ... infection/contact rate, number of contacts per unit time
- γ ... recovery rate
- Infection equation:

$$\frac{ds}{dt} = -\beta si \quad (3)$$

$$\frac{di}{dt} = \beta si - \gamma i \quad (4)$$

$$\frac{dr}{dt} = \gamma i \quad (5)$$

$$s + i + r = 1 \quad (6)$$

SIR Model Solution[New10, ?]

- From (3) and (5)

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

- By integration

$$s = s_0 \mathrm{e}^{-\frac{\beta}{\gamma} r} \tag{7}$$

- From (5), (6) and (7)

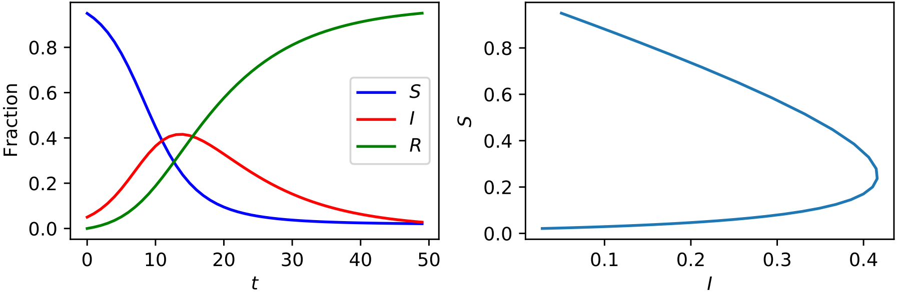
$$\frac{dr}{dt} = \gamma(1 - r - s_0 \mathrm{e}^{-\frac{\beta}{\gamma} r}) \tag{8}$$

- Solution

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

  - A closed form cannot be evaluated.

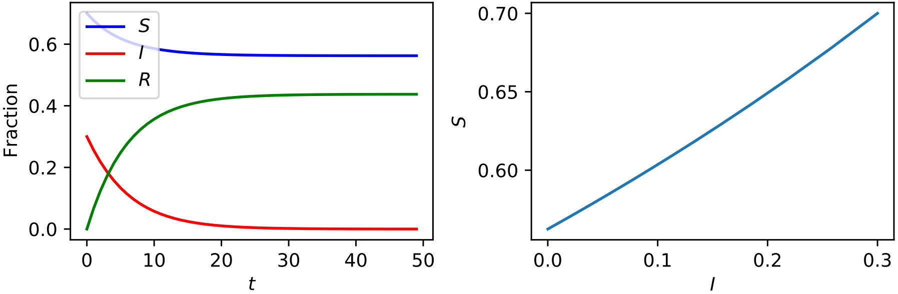
A SIR Model Evolution I [New10, ?]



[1]

[1] in image $i_0 = 0.05, \beta = 2.0, \gamma = 0.5 \implies \frac{\beta}{\gamma} = 4.0$

A SIR Model Evolution II[New10, ?]



[1]

- The number of susceptibles does not go to zero.
  - Any individuals who survive to late enough times without being infected will probably never get the disease at all.

[1] in image $i_0 = 0.3, \beta = 0.6, \gamma = 1.2 \implies \frac{\beta}{\gamma} = 0.5$

Total size of the outbreak[New10, ?]

- It is the total number of individuals who ever catch the disease during the entire course of the epidemic.

$$\frac{dr}{dt} = 0, t \to \infty, r_\infty = \text{const.}$$

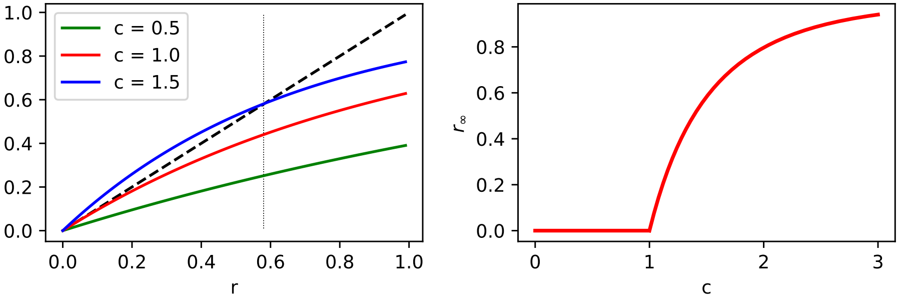
- From (8)

$$r_\infty = 1 - s_0 \mathrm{e}^{-\frac{\beta}{\gamma} r_\infty}$$

  - No closed form solution.
  - Search for giant component conditions of a Poisson random graph leads to the same equation.
- Assuming initial conditions $r(0) = 0, i(0) = c/N, s(0) = 1 - c/N \approx 1$ for a small number c of initially infected individuals.

Critical Point[New10, ?]

$$r_\infty = 1 - s_0 \mathrm{e}^{-R_0 r_\infty}, R_0 = \frac{\beta}{\gamma}$$



$$(r_\infty)'|_{r_\infty=0} = (1 - s_0 \mathrm{e}^{-R_0 r_\infty})'|_{r_\infty=0}$$

- critical point: $R_0 = 1$

Epidemic Threshold[New10, ?]

- r_∞ ... the total size of the outbreak
- **Epidemic threshold**

$$\text{Epidemics:} \quad R_0 > 1, \beta > \gamma, \quad r_\infty = \text{const.} > 0 \tag{9}$$

$$\text{No epidemics:} \quad R_0 < 1, \beta < \gamma, \quad r_\infty \to 0 \tag{10}$$

$$\text{Epidemic transition:} \quad R_0 = 1, \beta = \gamma, \tag{11}$$

$$\tag{12}$$

Basic Reproduction Number[New10, ?]

- **Basic reproduction number**

$$R_0 = \frac{\beta}{\gamma}$$

  - It is the average number of people infected by a person before his recovery.
  - An individual remains infectious for a time τ.
  - The expected number of others they will have contact with during that time is $\beta\tau$.
  - The average over the distribution of τ (the standard exponential distribution)

$$R_0 = \beta\gamma \int_0^\infty \tau \mathrm{e}^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

Outline

Network Environment[New10, ?]

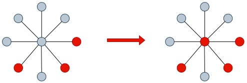
- The “full mixing” assumption is not good in the real word.
  - Most people have a set of regular contacts and the rest of members of the world population can be safely ignored.
  - Network models of spreading make use a network structure of possible contacts (adjacency matrix $\mathbf{A}$).
- Probabilistic model (state of a node):
  - $s_i(t)$ . . . probability that at t node i is susceptible $x_i(t)$ . . . probability that at t node i is infected $r_i(t)$ . . . probability that at t node i is recovered
- β . . . infection rate
  - probability to get infected on a contact in time δt

  γ . . . recovery rate
  - probability to recover in a unit time δt
- from deterministic to probabilistic description
- connected component - all nodes reachable
- network is undirected (matrix $\mathbf{A}$ is symmetric)

Spreading Processes[New10, ?]

Two processes

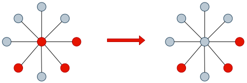
- Node infection:



  - j neighbor is infected with probability $x_j(t)$ and
  - must transmit the disease during the given time interval (with probability $\beta\delta t$)

$$P_{\text{inf}} = s_i(t)\left(1 - \prod_{j\in\mathcal{N}(i)}\left(1 - \beta x_j(t)\delta t\right)\right) \approx \beta s_i(t)\sum_{j\in\mathcal{N}(i)} x_j(t)\delta t$$

- Node recovery:



$$P_{\text{rec}} = \gamma x_i(t)\delta t$$

Outline

Formal SI Network Model[New10, ?]

- SI model

$$S \longrightarrow I$$

- Probabilities tied with node i: $s_i(t)$ - susceptible, $x_i(t)$ - infected at t

$$s_i(t) + x_i(t) = 1$$

- β ... infection rate, a probability to get infected in a unit time

$$x_i(t+\delta t) = x_i(t) + \beta s_i \sum_j A_{ij} x_j \delta t$$

- Infection equations:

$$\frac{x_i(t)}{dt} = \beta s_i \sum_j A_{ij} x_j(t)$$

$$s_i(t) + x_i(t) = 1$$

SI Model Solving[New10, ?]

- Differential equation

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i(t)) \sum_j A_{ij} x_j(t)$$

- Early time approximation, $t \to 0$, $x_i(t) \ll 1$

$$\frac{dx_i(t)}{dt} = \beta \sum_j A_{ij} x_j(t)$$

$$\frac{d\mathbf{x}(t)}{dt} = \beta \mathbf{A}\mathbf{x}(t)$$

- A solution in the eigenvector basis

$$\mathbf{A}\mathbf{v}_k = \lambda_k \mathbf{v}_k$$

$$\mathbf{x}(t) = \sum_k a_k(t) \mathbf{v}_k$$

SI Model Solution[?]

$$\sum_k \frac{da_k(t)}{dt}\mathbf{v}_k = \beta \sum_k \mathbf{A} a_k(t)\mathbf{v}_k = \beta \sum_k a_k(t)\lambda_k \mathbf{v}_k$$

$$\frac{da_k(t)}{dt} = \beta\lambda_k a_k(t)$$

$$a_k(t) = a_k(0)\mathrm{e}^{\beta\lambda_k t}, a_k(0) = \mathbf{v}_k^T \mathbf{x}(0)$$

- Solution

$$\mathbf{x}(t) = \sum_k a_k(0)\mathrm{e}^{\beta\lambda_k t}\mathbf{v}_k$$

- $t \to 0, \lambda_{\max} = \lambda_1 > \lambda_k \ldots$ the fastest growing term

$$\mathbf{x}(t) = \mathbf{v}_1 \mathrm{e}^{\beta\lambda_1 t}$$

- growth rate of infections depends on λ_1
- probability of infection of nodes depends on $\mathbf{v}_1$, i.e. v_{1i}

SI Model Late-Time Solution[?]

- Late-time approximation: $t \to \infty, x_i(t) \to \text{const.}$

$$\frac{dx_i(t)}{dt} = \beta(1 - x_i(t)) \sum_j A_{ij} x_j(t) = 0$$

  $\mathbf{Ax} \neq 0$ since $\lambda_{\min} \neq 0$, $1 - x_i(t) \approx 0$

- All nodes in the connected component get infected for $t \to \infty$: $x_i(t) \to 1$
- Vertices of higher eigenvector centrality becoming infected faster than those of lower

Outline

Formal SIR Network Model[New10, ?]

- SIR model

$$S \longrightarrow I \longrightarrow R$$

- Probabilities tied with node i:
  $s_i(t)$ - susceptible, $x_i(t)$ - infected, $r_i(t)$ - recovered at t
- β ... infection rate, γ ... recovery rate
- Infection equations:

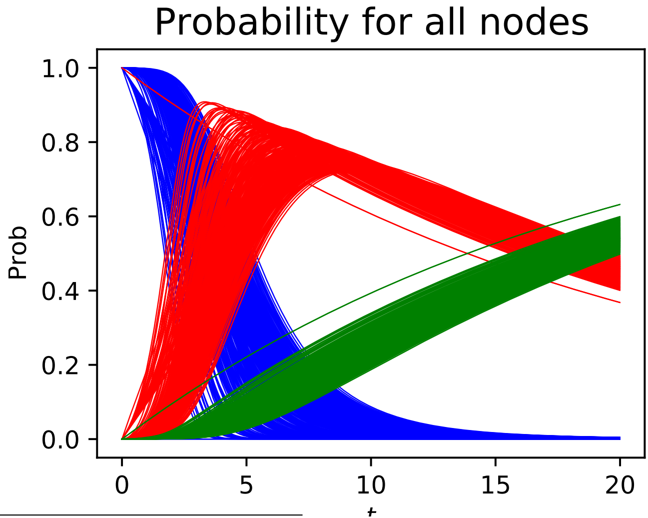
$$\frac{s_i(t)}{dt} = -\beta s_i \sum_j A_{ij} x_j(t) \quad (13)$$

$$\frac{x_i(t)}{dt} = \beta s_i \sum_j A_{ij} x_j(t) - \gamma x_i \quad (14)$$

$$\frac{r_i(t)}{dt} = \gamma x_i \quad (15)$$

$$s_i(t) + x_i(t) + r_i(t) = 1$$

SIR Network Model Evolution Example[New10, ?]



[1]

[1] in image $\beta = 0.1, \gamma = 0.05$, Barabasi-Albert network with 350 nodes, 2 initially infected

Summary

- Compartment models
- SI, SIS, SIR models
- SI Network model
- How to identify model parameters?

Competencies

- Define compartment model.
- Describe SI model.
- Describe SIS model.

References I

[New10] M. Newman. *Networks: an introduction*. Oxford University Press, Inc., 2010.