Social Networks & Recommendation Systems

XI. Agent-based models.

Grzegorz Siudem

Warsaw University of Technology



Warsaw University of Technology



MSc program in Data Science has been developed as a part of task 10 of the project "NERW PW. Science - Education - Development - Cooperation" co-funded by European Union from European Social Fund.

Lecture

SIR model (Kermack, McKendrick, 1932)

• We assume a constant size of the population over time.

SIR model (Kermack, McKendrick, 1932)

- We assume a constant size of the population over time.
- Each individual is in one of three states:

SIR model (Kermack, McKendrick, 1932)

- · We assume a constant size of the population over time.
- Each individual is in one of three states:
 - · S susceptible,
 - I infected,
 - · R recovered/ removed.

SIR model (Kermack, McKendrick, 1932)

- · We assume a constant size of the population over time.
- Each individual is in one of three states:
 - · S susceptible,
 - I infected,
 - · R recovered/ removed.
- We only allow the following transitions: $S \rightarrow I \rightarrow R$.

SIR model (Kermack, McKendrick, 1932)

- We assume a constant size of the population over time.
- Each individual is in one of three states:
 - · S susceptible,
 - I infected,
 - · R recovered/ removed.
- We only allow the following transitions: $S \rightarrow I \rightarrow R$.
- Classically we assume that every agent is in contact with each other, and then the variables describe the system in which $\beta, \gamma > 0$

$$\begin{cases} \frac{dS}{dt} &= -\beta SI, \\ \frac{dI}{dt} &= \beta SI - \gamma I, \\ \frac{dR}{dt} &= \gamma I. \end{cases}$$

Epidemics – other variants of the model

· SIRS model (e.g. computer viruses)

$$S \rightarrow I \rightarrow R \rightarrow S$$
.

Epidemics – other variants of the model

• SIRS model (e.g. computer viruses)

$$S \rightarrow I \rightarrow R \rightarrow S$$
.

· SEIR model (e.g. rubella, sexually transmitted diseases)

$$S \to E \to I \to R.$$

Epidemics – other variants of the model

• SIRS model (e.g. computer viruses)

$$S \rightarrow I \rightarrow R \rightarrow S$$
.

· SEIR model (e.g. rubella, sexually transmitted diseases)

$$S \rightarrow E \rightarrow I \rightarrow R$$
.

· SIS model

$$S \to I \to S.$$

 \cdot I(t) number of infected nodes,

- \cdot I(t) number of infected nodes,
- S(t) nmber of susceptible nodes, wherein

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

- \cdot I(t) number of infected nodes,
- \cdot S(t) nmber of susceptible nodes, wherein

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

• β probability that in a single time step a healthy individual will become infected from a sick neighbor.

- \cdot I(t) number of infected nodes,
- · S(t) nmber of susceptible nodes, wherein

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

- β probability that in a single time step a healthy individual will become infected from a sick neighbor.
- γ the probability that the sick agent will recover in a single time step.

- \cdot I(t) number of infected nodes,
- \cdot S(t) nmber of susceptible nodes, wherein

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

- β probability that in a single time step a healthy individual will become infected from a sick neighbor.
- γ the probability that the sick agent will recover in a single time step.
- · Model can be described, in the mean-field approach, as follows

$$\frac{dI(t)}{dt} = \left[\beta\left(\langle k \rangle \frac{I(t)}{N}\right)\right] S(t) - \gamma I(t).$$

SIS model on the graphs: analysis

Let's change variables

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

where i(t) = I(t)/N and s(t) = S(t)/N

SIS model on the graphs: analysis

Let's change variables

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

where i(t) = I(t)/N and s(t) = S(t)/N

Let us ask two questions:

- Under what conditions does an epidemic burst?
- What happens to the number of infected people in the large time limit?

SIS model on the graphs: steady state

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

Under what conditions does an epidemic burst?

• Let us compute $di(t)/dt|_{t=0}$.

SIS model on the graphs: steady state

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

Under what conditions does an epidemic burst?

- Let us compute $di(t)/dt|_{t=0}$.
- · Received epidemic threshold

$$\lambda_c = \frac{1}{\langle k \rangle s(0)},$$

should be compared with the model parameters

$$\lambda = \frac{\beta}{\gamma}.$$

SIS model on the graphs: steady state

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

Under what conditions does an epidemic burst?

- Let us compute $di(t)/dt|_{t=0}$.
- · Received epidemic threshold

$$\lambda_c = \frac{1}{\langle k \rangle s(0)},$$

should be compared with the model parameters

$$\lambda = \frac{\beta}{\gamma}.$$

Conclusions?

SIS model on the graphs: epidemic threshold

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

What happens to the number of infected people in the large time limit?

• We are looking for stable solutions:

$$\frac{di(t)}{dt}|_{t\to\infty}=0.$$

SIS model on the graphs: epidemic threshold

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

What happens to the number of infected people in the large time limit?

• We are looking for stable solutions:

$$\frac{di(t)}{dt}|_{t\to\infty}=0.$$

· We get two solutions

$$i_{\infty} = 0, \quad i_{\infty} = 1 - \frac{\gamma}{\beta \langle k \rangle}.$$

SIS model on the graphs: epidemic threshold

$$\frac{di(t)}{dt} = i(t) \left[\beta \langle k \rangle s(t) - \gamma \right],$$

What happens to the number of infected people in the large time limit?

• We are looking for stable solutions:

$$\frac{di(t)}{dt}|_{t\to\infty}=0.$$

· We get two solutions

$$i_{\infty} = 0, \quad i_{\infty} = 1 - \frac{\gamma}{\beta \langle k \rangle}.$$

The analysis needs to be a bit more subtle

• $i_k(t)$, $I_k(t)$ number (ratio) of infected nodes with degree k,

The analysis needs to be a bit more subtle

- $i_k(t)$, $I_k(t)$ number (ratio) of infected nodes with degree k,
- $s_k(t)$, $S_k(t)$ number (ratio) of susceptible nodes with degree k,

The analysis needs to be a bit more subtle

- \cdot $i_k(t)$, $I_k(t)$ number (ratio) of infected nodes with degree k,
- $s_k(t)$, $S_k(t)$ number (ratio) of susceptible nodes with degree k,
- Q_l probability that any random network's edge is connected to infected vertex (for ER graphs $Q_l(t) = I(t)/N$).

The analysis needs to be a bit more subtle

- $i_k(t)$, $I_k(t)$ number (ratio) of infected nodes with degree k,
- $s_k(t)$, $S_k(t)$ number (ratio) of susceptible nodes with degree k,
- Q_l probability that any random network's edge is connected to infected vertex (for ER graphs $Q_l(t) = I(t)/N$).
- · Furthermore we assume

$$I_k(t) + S_k(t) = N_k = N\mathcal{P}(k).$$

The analysis needs to be a bit more subtle

- $i_k(t)$, $I_k(t)$ number (ratio) of infected nodes with degree k,
- $s_k(t)$, $S_k(t)$ number (ratio) of susceptible nodes with degree k,
- Q_l probability that any random network's edge is connected to infected vertex (for ER graphs $Q_l(t) = I(t)/N$).
- · Furthermore we assume

$$I_k(t) + S_k(t) = N_k = N\mathcal{P}(k).$$

Then the equation takes the form

$$\frac{di_k(t)}{dt} = \beta k Q_l s_k(t) - \gamma i_k(t).$$

SIS model on scale-free networks – asymptotic

$$\frac{di_k(t)}{dt} = \beta k Q_l s_k(t) - \gamma i_k(t).$$

We are looking for the stable asymptotic solutions

$$\frac{di_k(t)}{dt}|_{t\to\infty}=0 \ \Rightarrow \ i_k=\frac{\lambda kQ_l}{1+\lambda kQ_l}.$$

SIS model on scale-free networks – asymptotic

$$\frac{di_k(t)}{dt} = \beta k Q_l s_k(t) - \gamma i_k(t).$$

We are looking for the stable asymptotic solutions

$$\frac{di_k(t)}{dt}|_{t\to\infty}=0 \ \Rightarrow \ i_k=\frac{\lambda kQ_l}{1+\lambda kQ_l}.$$

Analysis of the solution leads to

$$\lambda_{c} = \frac{\langle k \rangle}{\langle k^{2} \rangle}.$$

SIS model on scale-free networks – asymptotic

$$\frac{di_k(t)}{dt} = \beta k Q_l s_k(t) - \gamma i_k(t).$$

We are looking for the stable asymptotic solutions

$$\frac{di_k(t)}{dt}|_{t\to\infty}=0 \ \Rightarrow \ i_k=\frac{\lambda kQ_l}{1+\lambda kQ_l}.$$

Analysis of the solution leads to

$$\lambda_{c} = \frac{\langle k \rangle}{\langle k^{2} \rangle}.$$

Which is very bad news...

Why?

Very simple bibliometric model

BA algorithm modification

• We are looking for citations vector of scientists with *C* citations and *N* publications.

Very simple bibliometric model

BA algorithm modification

- We are looking for citations vector of scientists with *C* citations and *N* publications.
- At each time step, the agent publishes works that are cited according to the rich get richer.

Very simple bibliometric model

BA algorithm modification

- We are looking for citations vector of scientists with *C* citations and *N* publications.
- At each time step, the agent publishes works that are cited according to the rich get richer.
- · Is it consistent with empirical data? (visualization)

Voter model

• In every graph's node we put variable $\sigma_i = \pm 1$ (opinion, prefferences, etc.).

Voter model

- In every graph's node we put variable $\sigma_i = \pm 1$ (opinion, prefferences, etc.).
- At every time step random vertex change its opinion according neighbors' opinions

$$m_i = \sum_{j \in \mathcal{N}(i)} \sigma_j,$$

due to the formula

$$S_i := S(m_i) = \operatorname{sgn}(m_i).$$

Voter model

- In every graph's node we put variable $\sigma_i = \pm 1$ (opinion, prefferences, etc.).
- At every time step random vertex change its opinion according neighbors' opinions

$$m_i = \sum_{j \in \mathcal{N}(i)} \sigma_j,$$

due to the formula

$$S_i := S(m_i) = \operatorname{sgn}(m_i).$$

Illustration

Thank you for your attention!

Warsaw University of Technology



MSc program in Data Science has been developed as a part of task 10 of the project "NERW PW. Science - Education - Development - Cooperation" co-funded by European Union from European Social Fund.