SIS epidemics on Networks

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Outline

- Exact SIS model
- NIMFA: N-intertwined MF approximation
- Expected survival time
- Non-Markovian epidemics
**Simple SIS model on networks**

- Homogeneous birth (infection) rate $\beta$ on all links between infected and susceptible nodes
- Homogeneous death (curing) rate $\delta$ for infected nodes

$$\tau = \frac{\beta}{\delta} : \text{effective spreading rate}$$

Infection and curing are independent Poisson processes
**SI S model on networks (1)**

- Each node $j$ can be in either of the two states:
  - “0”: healthy
  - “1”: infected

- **Markov continuous time**:
  - infection rate $\beta$
  - curing rate $\delta$

- At time $t$:
  - $X_j(t)$ is the state of node $j$
  - infinitesimal generator $Q_j(t) = \begin{bmatrix} -q_{0j} & q_{0j} \\ q_{1j} & -q_{1j} \end{bmatrix} = \begin{bmatrix} -q_{0j} & q_{0j} \\ \delta & -\delta \end{bmatrix}$
**SI S model on networks (2)**

- Nodes are interconnected in graph:
  \[ Q_j(t) = \begin{bmatrix} -q_{0j} & q_{0j} \\ \delta & -\delta \end{bmatrix} \]
  
  where the infection rate is due to all infected neighbors of node \( j \):
  \[ q_{0j}(t) = \beta \sum_{k=1}^{N} a_{jk} X_k(t) \]

  and where the adjacency matrix of the graph is
  \[
  A = \begin{bmatrix}
  a_{11} & a_{12} & \cdots & a_{1N} \\
  a_{21} & a_{22} & \cdots & a_{2N} \\
  \vdots & \vdots & \ddots & \vdots \\
  a_{N1} & a_{N2} & \cdots & a_{NN}
  \end{bmatrix}
  \]
SIS model on networks (3)

• Markov theory requires that the infinitesimal generator is a matrix whose elements are not random variables.
• However, this is not the case in our simple model:

\[ q_{0j}(t) = \beta \sum_{k=1}^{N} a_{jk} X_k(t) \]

• By conditioning to each possible combination of infected states, we finally arrive to the exact Markov continuous SIS model.
• **Drawback:** this exact model has \(2^{N}\) states, where \(N\) is the number of nodes in the network.
SI S Markovian process on a graph

\[
\begin{align*}
\text{for } j \notin I &: I \to I \cup \{j\} \text{ at rate } \beta \sum_{k \in I} a_{ki} + \epsilon \\
\text{for } i \in I &: I \to I \setminus \{i\} \text{ at rate } \delta
\end{align*}
\]

I: infected subgraph (containing infected nodes)  
\(\epsilon\): nodal self-infection
Exact SIS model
N = 4 nodes

Absorbing state

2^N states!

Governing SIS equation for node $j$

\[
\frac{dE[X_j]}{dt} = E \left[ -\delta X_j + (1 - X_j) \beta \sum_{k=1}^{N} a_{kj} X_k \right]
\]

- time-change of $E[X_j] = Pr[X_j = 1]$, probability that node $j$ is infected
- if infected: probability of curing per unit time
- if not infected (healthy): probability of infection per unit time

\[
\frac{dE[X_j]}{dt} = -\delta E[X_j] + \beta \sum_{k=1}^{N} a_{kj} E[X_k] - \beta \sum_{k=1}^{N} a_{kj} E[X_j X_k]
\]
Joint probabilities

\[
\frac{dE[X_i X_j]}{dt} = E \left[ \left\{ -\delta X_i + \beta (1 - X_i) \sum_{k=1}^{N} a_{ik} X_k \right\} X_j + X_i \left\{ -\delta X_j + \beta (1 - X_j) \sum_{k=1}^{N} a_{jk} X_k \right\} \right]
\]

\[
= -2\delta E[X_i X_j] + \beta \sum_{k=1}^{N} a_{ik} E[X_j X_k] + \beta \sum_{k=1}^{N} a_{jk} E[X_i X_k] - \beta \sum_{k=1}^{N} (a_{jk} + a_{ik}) E[X_i X_j X_k]
\]

Next, we need the \( \binom{N}{3} \) differential equations for \( E[X_i X_j X_k] \)...

In total, the SIS process is defined by \( 2^N = \sum_{k=1}^{N} \binom{N}{k} + 1 \)
linear equations

Markov Theory

- SIS model is exactly described as a continuous-time Markov process on $2^N$ states, with infinitesimal generator $Q_N$.

- **Drawbacks:**
  - no easy structure in $Q_N$
  - computationally intractable for $N>20$
  - steady-state is the absorbing state (reached after unrealistically long time)
  - very few exact results...

- The mathematical community (e.g. Liggett, Durrett,...) uses:
  - duality principle & coupling & asymptotics
  - graphical representation of the Poisson infection and recovery events
Outline

Exact SIS model

NIMFA: N-intertwined MF approximation

Expected survival time

Non-Markovian epidemics
NI MFA: N-intertwined mean-field approxim.

\[ \frac{dE[X_j]}{dt} = -\delta E[X_j] + \beta \sum_{k=1}^{N} a_{kj} E[X_k] - \beta \sum_{k=1}^{N} a_{kj} E[X_j X_k] \]

\[ E[X_j X_k] = \Pr[X_j = 1, X_k = 1] = \Pr[X_j = 1|X_k = 1] \Pr[X_k = 1] \text{ and } \Pr[X_j = 1|X_k = 1] \geq \Pr[X_j = 1] \]

\[ E[X_i X_k] \geq \Pr[X_i = 1] \Pr[X_k = 1] = E[X_i] E[X_k] \]

NI MFA (= equality above) \textbf{upper bounds} the prob. of infection

NI MFA non-linear equations

\[
\begin{align*}
\frac{dv_1}{dt} &= (1-v_1)\beta \sum_{k=1}^{N} a_{1k}v_k - \delta v_1 \\
\frac{dv_2}{dt} &= (1-v_2)\beta \sum_{k=1}^{N} a_{2k}v_k - \delta v_2 \\
&\vdots \\
\frac{dv_N}{dt} &= (1-v_N)\beta \sum_{k=1}^{N} a_{Nk}v_k - \delta v_N
\end{align*}
\]

where the viral probability of infection is

\[v_k(t) = E[X_k(t)] = \Pr[X_k(t) = 1]\]

In matrix form:

\[
\frac{dV(t)}{dt} = \beta A V(t) - \text{diag}(v_i(t))(\beta A V(t) + \delta u)
\]

where the vector \(u^T = [1 \ 1 \ \ldots \ 1]\) and \(V^T = [v_1 \ v_2 \ \ldots \ v_N]\)

**Lower bound for the epidemic threshold**

\[
\frac{dv_j(t)}{dt} = -\delta v_j + \beta \sum_{k=1}^{N} a_{kj} v_k - \beta \sum_{k=1}^{N} a_{kj} E[X_i X_k]
\]

\[v_k(t) = E[X_k(t)]\]

Ignoring the correlation terms

\[
\frac{dV(t)}{dt} \leq (-\delta I + \beta A)V(t) \quad \Rightarrow \quad V(t) \leq e^{(-\delta I + \beta A)t} V(0)
\]

If all eigenvalues of \(\beta A - \delta I\) are negative, \(v_j\) tends exponentially fast to zero with \(t\). Hence, if

\[\beta \lambda_1(A) - \delta < 0\]

\[\tau = \frac{\beta}{\delta} < \frac{1}{\lambda_1(A)} < \tau_c\]

The NIMFA epidemic threshold is precisely

\[\tau_c^{(1)} = \frac{1}{\lambda_1(A)} < \tau_c\]

\[\tau_c^{(1)} = \frac{1}{\lambda_1(A)} < \tau_c^{(2)} = \frac{1}{\lambda_1(H)} < \tau_c\]
What is so interesting about epidemics?

network protection
self-replicating objects (worms)
propagation errors
rumors (social nets)
epidemic algorithms (gossiping)
cybercrime: network robustness & security

\[
\tau_c = \frac{1}{\lambda_1(A)}
\]

\[
\max \left( E[D] \sqrt{1+\frac{\text{Var}[D]}{(E[D])^2}}, \sqrt{d_{\text{max}}} \right) \leq \lambda_1(A) \leq d_{\text{max}}
\]
Transformation \( s = \frac{1}{\tau} \) & principal eigenvector

\[
\frac{dy_\infty(s)}{ds} \bigg|_{s=0} = -\frac{1}{N} \sum_{j=1}^{N} \frac{1}{d_j} \leq -\frac{1}{2L}
\]

Extensions of the NIMFA

- In-homogeneous: each node $i$ has own $\beta_i$ and $\delta_i$:

- SAIS (Infected, Susceptible, Alert) and SIR instead of SIS:

- GEMF: very general extension: $m$ compartments (includes both SIS, SAIS, SIR,...):

- Interdependent networks
Time-dependent rates in NI MFA for regular graphs

\[
\frac{dv(t)}{dt} = r \beta(t) v(t) (1 - v(t)) - \delta(t) v(t)
\]

\[
v(t) = \frac{\exp\left(\int_0^t \{r \beta(u) - \delta(u)\} du\right)}{1 + \int_0^t r \beta(s) \exp\left(\int_0^s \{r \beta(u) - \delta(u)\} du\right) ds}
\]

Classical case (constant rates): Kephart & White (1992)

\[
v(t) = \frac{\exp(\{r \beta - \delta\} t)}{1 + \frac{1}{v(0)} \left(\exp(\{r \beta - \delta\} t) - 1\right)} \left(1 - \frac{1}{r \tau}\right)
\]

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Expected survival time

Non-Markovian epidemics
SIS epidemics on the complete graph

\[
\lambda_j = (\beta_j + \epsilon)(N - j)
\]
\[
\mu_j = \delta j
\]

Birth-death processes \textit{quadratic} in state \( j \)

Average Time to Absorption (Survival time)

Ganesh, Massoulie, Towsley (2005):

\[ E[T] \leq \frac{1}{\delta} \frac{\log N + 1}{\tau \lambda} \]

- \( \tau < \tau_c \)

\[ E[T] = O\left(e^{bN^a}\right) \]

- \( \tau > \tau_c \)

Mountford et al. (2013):

(regular trees w. bounded degree)

\[ E[T] = O\left(e^{cN}\right) \]

Complete graph \( K_N \):

\[ E[T] \approx \frac{1}{|\xi|} \quad \text{with} \quad -\xi = \frac{1}{F(\tau)} + O\left(\frac{N^2 \log N}{x^{2N-1}}\right) \]

\[ x = \tau N \approx \frac{\tau}{\tau_c} \]

\[ F(\tau) = \frac{1}{\delta} \sum_{j=1}^{N} \sum_{r=0}^{j-1} \frac{(N - j + r)!}{j!(N - j)!} \]

\[ F\left(\frac{x}{N}\right) \sim \frac{1}{\delta} \frac{x\sqrt{2\pi} e^{N\left(\log x + \frac{1}{x} - 1\right)}}{\sqrt{N}} \]

Hitting time (on \( K_N \)) for all \( \tau \):

\[ E[T] = F(\tau) \]

Average survival time in $K_N$

\[ E[T] = F(\tau) = \frac{1}{\delta} \sum_{j=1}^{N} \sum_{r=0}^{j-1} \frac{(N - j + r)!}{j (N - j)!} \]

\[ \tau / \tau_c \]

-1/\zeta

- hitting time

+ simulated survival time
Second smallest eigenvalue $Q$ in graphs

\[ |\xi| \approx \frac{1}{E[T]} \]
Pdf survival time in $K_{100}$

Black dotted $\tau = \tau_c$

$f_T(t | \beta = 0) = \delta I \left(1 - e^{-\delta t}\right)^{I-1} e^{-\delta t}$ (Max I i.i.d. exp.)
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Epidemic times are not exponential

Non-Markovian infection times

\[ f_T(t) = \frac{\alpha}{b} \left( \frac{x}{b} \right)^{\alpha-1} \exp \left( -\left( \frac{x}{b} \right)^\alpha \right) \]

Weibull pdf

Same mean \( E[T] \):

\[ b = \frac{1}{\beta \Gamma \left( 1 + \frac{1}{\alpha} \right)} \]

\( T \) is the time to infect a neighboring node
Non-Markovian epidemic threshold

Non-exponential infection time has a dramatic influence!

GSIS: SIS with general infection times

NI MFA is valid provided the effective infection rate $\tau = \beta/\delta$ is replaced by the **averaged number $E[M]$ of infection events during a healthy period**:

$$E[M] = \frac{1}{2\pi i} \int_{c-i\infty}^{c+i\infty} \frac{\phi_T(z)\phi_R(-z)}{1 - \phi_T(z)} \frac{dz}{z}$$

$$\phi_X(z) = E[e^{-zX}]$$

Generalized criterion for the epidemic threshold:

$$E[M_c] = \frac{1}{\lambda_1}$$

Scaling law for large $N$

When infection time $T$ is Weibullian:

$$\tau_c = \frac{q(\alpha)}{\lambda_1^{1/\alpha}}$$

$q(\alpha) = O(1)$

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GSIS: $E[M]$ gives the right scaling

$E[M]$: averaged number of infection events received during a healthy period
Pdf survival time $K_{100}$ (Weibull)

$$f_{\text{infection time}}(t) = \frac{\alpha}{b} \left( \frac{t}{b} \right)^{\alpha-1} \exp \left( -\left( \frac{t}{b} \right)^\alpha \right)$$

Increasing $\alpha$

$E[M] = 0.014$
Challenges for SIS epidemics on nets

- Tight upper bound of the epidemic threshold (for any graph)
- A general mean-field criterion that specifies the graphs for which NIMFA is accurate
- Time-dependent analysis of SIS epidemics
- Epidemics on evolving and adaptive networks
- Competing and mutating viruses on networks
- Measurements of epidemics (e.g. fraction of infected nodes) in real-world networks are scarce
More to read

General overviews
• P. Van Mieghem, *Performance Analysis of Complex Networks and Systems*, Cambridge University Press, 2014 (Chapter 17: Epidemics in Networks)

Specialized recent topics (see my website):
• Adaptive SIS on networks
• Competing viruses
• Average survival time of a virus in a network (decay time towards absorption)
• SIS Epidemics in (two-level) communities
Books

Performance Analysis of Complex Networks and Systems
Piet Van Mieghem

Graph Spectra for Complex Networks
Piet Van Mieghem

Data Communications Networking
Piet Van Mieghem

Articles: http://www.nas.ewi.tudelft.nl
Thank You

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