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
SIS 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 $Q_j(t) =$
    $$
    Q_j(t) = \begin{bmatrix}
    -q_{0j} & q_{0j} \\
    q_{1j} & -q_{1j} \\
    \end{bmatrix} = \begin{bmatrix}
    -q_{0j} & q_{0j} \\
    \delta & -\delta \\
    \end{bmatrix}
    $$
SIS 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 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.
SIS Markovian process on a graph

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

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

Absorbing state

$2^N$ states!

Governning 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

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

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

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
NIMFA: N-intertwined mean-field approxim.

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

\[E[X_jX_k] = \Pr[X_j = 1, X_k = 1] = \Pr[X_j = 1|X_k = 1] \Pr[X_k = 1]\]

and \[\Pr[X_j = 1|X_k = 1] \geq \Pr[X_j = 1]\]

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

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

NIMFA (= equality above) upper bounds the prob. of infection

NIMFA 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

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

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

\[
\beta \lambda_1(A) - \delta < 0 \quad \Rightarrow \quad \tau = \frac{\beta}{\delta} < \frac{1}{\lambda_1(A)} < \tau_c
\]

The NIMFA epidemic threshold is precisely

\[
\tau_c^{(1)} = \frac{1}{\lambda_1(A)} < \tau_c < \tau_c^{(2)} = \frac{1}{\lambda_1(H)} < \tau_c
\]
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 $\delta_i$:
  P. Van Mieghem and J. Omic, 2008, "In-homogeneous Virus Spread in Networks", (arxiv.org/1306.2588)

• **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 NIMFA for regular graphs

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

\[
v(t) = \frac{\exp\left(\int_0^t \{r\beta(u) - \delta(u)\} \, du\right)}{\frac{1}{v(0)} + \int_0^t r\beta(s)\exp\left(\int_0^s \{r\beta(u) - \delta(u)\} \, du\right) \, ds}
\]

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

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

Outline

Exact SIS model

NIMFA: N-intertwined MF approximation

Expected survival time

Non-Markovian epidemics
SIS epidemics on the complete graph

\[
\begin{align*}
\lambda_j &= (\beta j + \epsilon)(N - j) \\
\mu_j &= \delta j
\end{align*}
\]

Birth-death processes quadratic in state \( j \)

Average Time to Absorption (Survival time)

Ganesh, Massoulié, Towsley (2005):

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

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

\( \tau < \tau_c \)

\( \tau > \tau_c \)

Mountford et al. (2013):

(regular trees w. bounded degree)

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

Complete graph \( K_N \):

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

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

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

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

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

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

Average survival time in $K_N$

$$E[T] = F(\tau) = \frac{1}{\delta} \sum_{j=1}^{N} \sum_{r=0}^{j-1} \frac{(N-j+r)!}{j(N-j)!}$$
Second smallest eigenvalue $Q$ in graphs

\[ \xi \approx 1 \]

$E[T]$
Black dotted $\tau = \tau_c$ survival time $t$.

$$f_T(t \mid \beta = 0) = \delta I \left(1 - e^{-\delta t}\right)^{I-1} e^{-\delta t} \quad \text{(Max I i.i.d. exp.)}$$
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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 \( \mathbb{E}[T] \):

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

\( T \) 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

NIMFA is valid provided the effective infection rate $\tau = \frac{\beta}{\delta}$ 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:

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

$q(\alpha) = O(1)$
GSIS: $E[M]$ gives the right scaling

Average fraction of infected nodes

- simulations GSIS
- NIMFA
- Complete graph $K_{500}$

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

$E[M]=0.014$

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

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