Epidemics on Networks

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in collaboration with

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Outline

Exact SIS model

NIMFA: N-Intertwined MF Approximation

Recent developments
Continuous-time Markovian SIS epidemics on networks

- Constant infection rate $\beta$ on all links
- Constant curing rate $\delta$ for all nodes

\[ \tau = \beta / \delta \] effective spreading or infection rate

\( X_j(t) = 1 \) node $j$ is infected at time $t$

\( X_j(t) = 0 \) node $j$ is healthy at time $t$

Infection and curing are independent Poisson processes

Markov graph of the exact SIS model on $N = 4$ nodes

Absorbing state

$2^N$ states!

Markov theory

Regular bipartite Markov graph

Recursive structure of infinitesimal general $Q_N$


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 

\[E[X_j] = \text{Pr}[X_j = 1],\] probability that node $j$ is infected

if infected: probability of curing per unit time

if not infected (healthy): probability of infection per unit time

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

Outline

Exact SIS model

NIMFA: N-Intertwined MF Approximation

Recent developments

NIMFA: replace \( \text{rv} \) by its mean

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

NIMFA

\[
X_j \Rightarrow E[\tilde{X}_j]
\]

\[
\frac{dE[E[\tilde{X}_j]]}{dt} = E[-\delta E[\tilde{X}_j] + (1 - E[\tilde{X}_j]) \beta \sum_{k=1}^{N} a_{kj} E[\tilde{X}_k]]
\]

Bernoulli \( \text{rv} \)

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

in normalized time \( t^* = \delta t \):

\[
\frac{dv_j(t^*)}{dt^*} = -v_j(t^*) + (1 - v_j(t^*)) \sum_{k=1}^{N} a_{kj} v_k(t^*)
\]

\[
\tau = \frac{\beta}{\delta}
\]
NIMFA: \(N\)-intertwined mean-field approxim.

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

\[
\text{Cov}[X_j X_k] = E[X_j X_k] - E[X_j] E[X_k] \geq 0
\]


E. Cator, P. Donnelly and P. Van Mieghem, 2018, "Reply to "Comment on 'Nodal infection in Markovian SIS and SIR epidemics on networks are non-negatively correlated'"", Physical Review E, Vol. 98, No. 2, August, p. 026302.

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

NIMFA: upper bounds SIS

R\(_j\) > 0

Lower bound for the epidemic threshold

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

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

Ignoring the last summation:

\[
\frac{dV(t)}{dt} \leq (-\delta I + \beta A) V(t)
\]

\(V(t) \leq e^{(-\delta I + \beta A)t} V(0)\)

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

\[
\beta \lambda_\ell(A) - \delta < 0
\]

\(\tau = \frac{\beta}{\delta} < \frac{1}{\lambda_\ell(A)} < \tau_c\)

The NIMFA epidemic threshold is precisely

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

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

- Network protection
- Self-replicating objects (worms)
- Propagation errors
- Rumors (social nets)
- Epidemic algorithms (gossiping)
- Cybercrime: network robustness & security

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

\[
\max \left( E[D] \sqrt{1 + \frac{\text{Var}[D]}{E[D]^2}} \cdot d_{\text{max}} \right) \leq \lambda_1(A) \leq d_{\text{max}}
\]

**Exact vs. Mean-field approx. (NIMFA)**

- $2^N$ linear equations
- Steady-state
  - Absorbing (healthy) state
  - Reached after unrealistically long time
  - Difficult to analyze
- Only for exponential infection and curing times

- $N$ non-linear equations
- Meta-stable state:
  - Phase-transition
  - Epidemic threshold
  - Realistic
  - Analytically tractable
  - Lower bound epidemic threshold
  - Valid for any infection and curing time distribution

Extensions of NIMFA

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

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

- Generalized Epidemic mean-field model (**GEMF**): extension of NIMFA to $m$ compartments (includes both SIS, SAIS, SIR,...):
  

- **NIMFA on Interdependent networks**
  

- **Universal SIS mean-field framework**: NIMFA is close to optimal
  

Outline

Exact SIS model

NIMFA: N-Intertwined MF Approximation

Recent developments

- **Non-Markovian epidemics**
- Tanh-approximation
- Inferring the graph
Epidemic times are not exponential

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

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

NIMFA: valid provided the effective infection rate \( \tau \) is replaced by the av. number \( E[M] \) of infection events during a healthy period (via renewal theory assuming existence of metastable state):

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

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

NIMFA steady state:

\[
0 = -v_{j\infty} + \tau (1 - v_{j\infty}) \sum_{k=1}^{N} a_{kj} v_{k\infty} \quad \tau = \frac{\beta}{\delta}
\]

\[
0 = -v_{j\infty} + E[M] (1 - v_{j\infty}) \sum_{k=1}^{N} a_{kj} v_{k\infty}
\]

GSIS: SIS with general infection times

Generalized criterion for the NIMFA epidemic threshold: \( E[M_c] = \frac{1}{\lambda_1} \)

If the recovery time \( R \) is exponential, then \( E[M] = \frac{\phi_T(\delta)}{1-\phi_T(\delta)} \)
and the epidemic threshold obeys: \( \phi_T(\delta) = \frac{1}{1+\lambda_1} \)

When the infection time \( T \) is Weibullian: \( \phi_T \left( \frac{1}{\tau T(1+1/\alpha)}; \alpha \right) = \frac{1}{1+\lambda_1} \)
with pgf \( \phi_T(w; \alpha) = \alpha \int_0^\infty e^{-\frac{wx-x^\alpha}{\lambda_1}} d\alpha \)

Scaling law for large \( N \)
When infection time \( T \) is Weibullian: \( q(\alpha) = O(1) \)

\[
E[M] = \frac{1}{2\pi i} \int_{L(-\infty)}^{L(\infty)} \frac{\phi_T(z) \phi_R(-z) dz}{1 - \phi_T(z) z}
\]
Epidemic threshold $\tau_c^{(1)}(\alpha)$ versus $\alpha$

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

\[
\frac{1}{\tau_c^{(3)}(\alpha)} = \ln(1 + \lambda_1) + \frac{1}{2} \left( \psi'(1) - \psi'(\alpha) \right) \ln^2(1 + \lambda_1) + O\left( \frac{1}{\alpha^7} \right)
\]

\[
\eta(\alpha, \rho)
\]

Given that 1 infection event has occurred in $[0, \rho]$, what is the prob. of its occurrence at time $\sigma$?
**GSIS: infection time T is Gamma**

The infection time \( T \) is Gamma distributed: 
\[
f_T(x; \xi) = \frac{(x/b_T)^{\xi-1} e^{-x/b_T}}{b_T^\xi \Gamma(\xi)}
\]
with mean \( E[T] = \beta r \xi \) and pgf \( \phi_T(z; \xi) = (1 + b_T z)^{-\xi} \)

Comparison requires \( E[T] = \frac{1}{\beta} \) so that \( b_T = 1/(\xi \beta) \)

If the recovery time \( R \) is exponential, then \( E[M] = \frac{\phi_T(\delta)}{1-\phi_T(\delta)} \)

The NIMFA epidemic threshold obeys \( E[M_C] = \frac{1}{\lambda_1} \), so \( \phi_T(\delta) = \frac{1}{1+\lambda_1} \)

\[
\tau^{(1)}_{C\Gamma}(\xi) = \frac{1}{\xi \left( 1 + \frac{1}{\lambda_1} \right)^{\xi-1}} = \frac{1}{\xi \left( \ln(1+\lambda_1) \right)^{\xi-1}}
\]

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

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**Epidemic threshold \( \tau^{(1)}_{C\Gamma}(\xi) \) versus \( \xi \)**

One-to-one relation infection time of viral item and its global endemic effect in a graph

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Time-dependent prevalence $\alpha \to \infty$

$\lim_{\alpha \to \infty} \tau_c^{(1)}(\alpha) = \frac{1}{\ln(1 + \lambda_1)}$

$\alpha \to \infty$ represents a synchronized infection

Epidemic threshold: $\frac{1}{1-p}$

$p$: fraction of nodes being cured

If $\ln\left(\frac{1}{1-p}\right) = 1$ or $p = 0.632$, then pulse curing is comparable with Poisson curing:


Challenges for epidemics on networks

- Tight upper bound of the epidemic threshold (for any graph), or near to exact determination of $t_c$
- Time-dependent analysis of SIS epidemics: beyond the tanh-formula
- Non-Markovian epidemics
- Epidemics on evolving, adaptive and temporal networks
- Competing and mutating viruses on networks
- Modeling of social contagion
- Control of epidemics on networks
- **Measured data** of epidemics (e.g. fraction of infected nodes, the underlying topology of the ‘contact’ network) in real-world networks!

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](http://www.nas.ewi.tudelft.nl)
Thank You

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