N-Intertwined Mean-Field Approximation (NIMFA) versus exact SIS epidemics on Networks

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STAR workshop on random graphs
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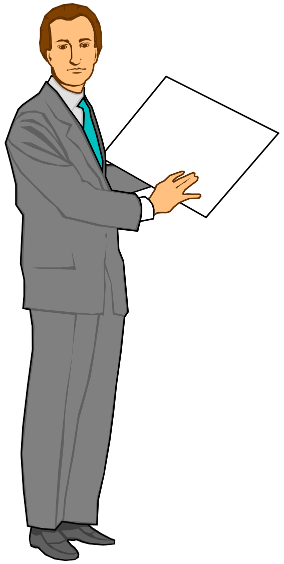
Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

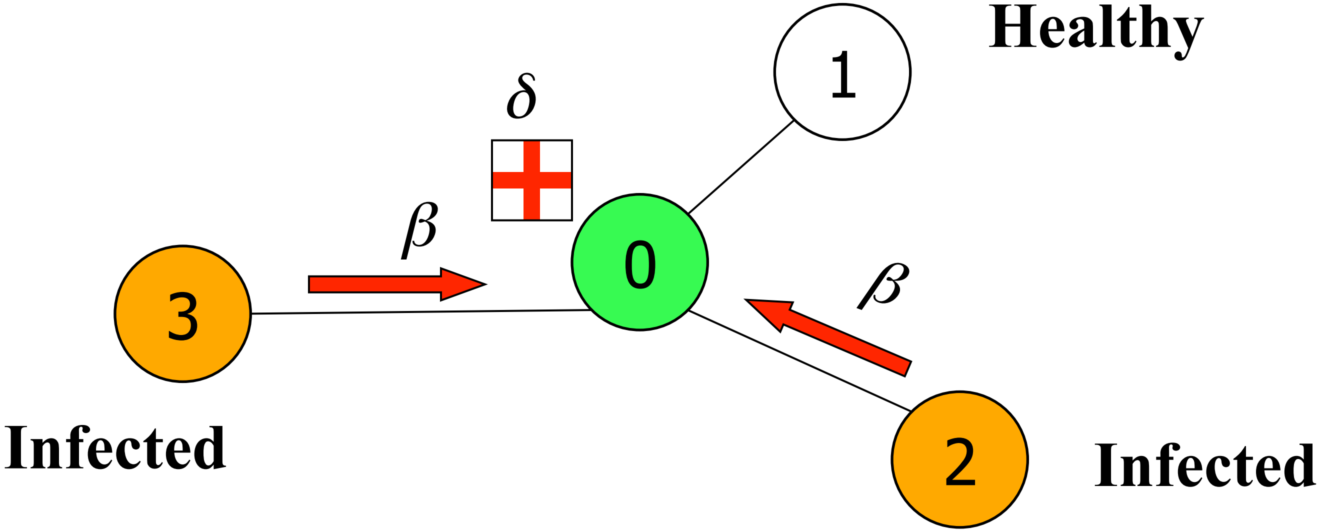
Defining the SIS epidemic threshold

Future research

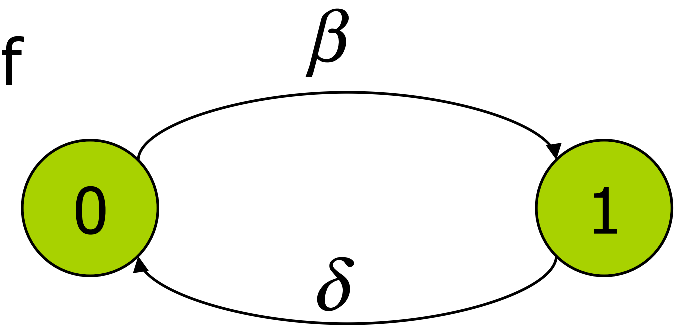
Simple SIS model on networks

- Homogeneous birth (infection) rate β on all edges between infected and susceptible nodes
- Homogeneous death (curing) rate δ for infected nodes

$\tau = \beta / \delta$: effective spreading rate



Definition of the states in SIS



- Each node *j* can be in either of the two states:
  - "0": healthy
  - "1": infected
- **Markov continuous time**:
  - infection rate β
  - curing rate δ
- Mathematically:
  - X_j is the state of node j
  - infinitesimal generator $Q_j(t) = \begin{bmatrix} -q_{1j} & q_{1j} \\ q_{2j} & -q_{2j} \end{bmatrix} = \begin{bmatrix} -q_{1j} & q_{1j} \\ \delta & -\delta \end{bmatrix}$

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

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

Joint probabilities

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

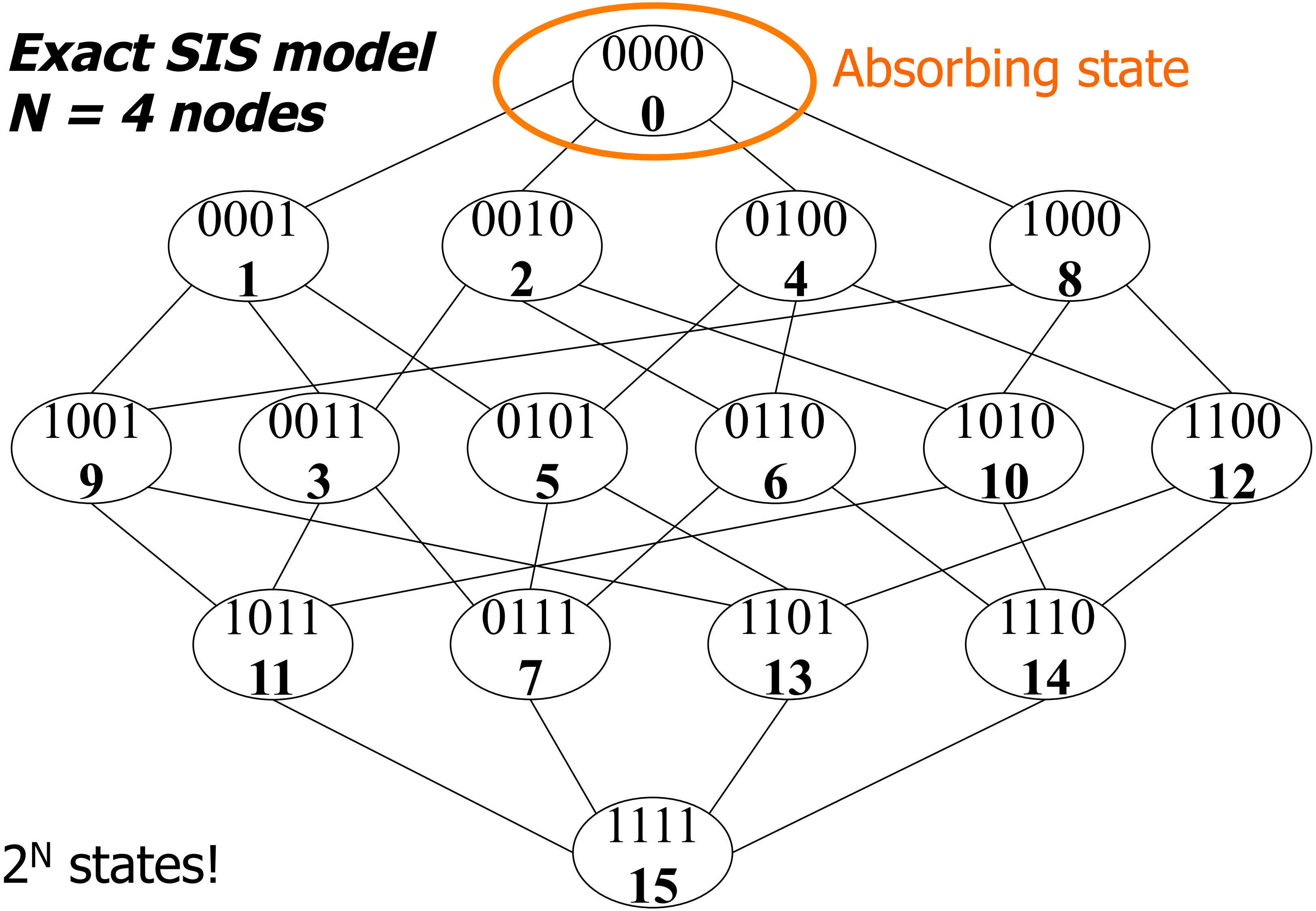
$$= -2\delta E\left[X_iX_j\right] + \beta\sum_{k=1}^{N} a_{ik}E\left[X_jX_k\right] + \beta\sum_{k=1}^{N} a_{jk}E\left[X_iX_k\right] - \beta\sum_{k=1}^{N}\left(a_{jk}+a_{ik}\right)E\left[X_iX_jX_k\right]$$

Next, we need the $\binom{N}{3}$ differential equations for $E[X_iX_jX_k]$...

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

E. Cator and P. Van Mieghem, 2012, "Second-order mean-field susceptible -infected-susceptible epidemic threshold", Physical Review E, vol. 85, No. 5, May, p. 056111.

Exact SIS model
N = 4 nodes

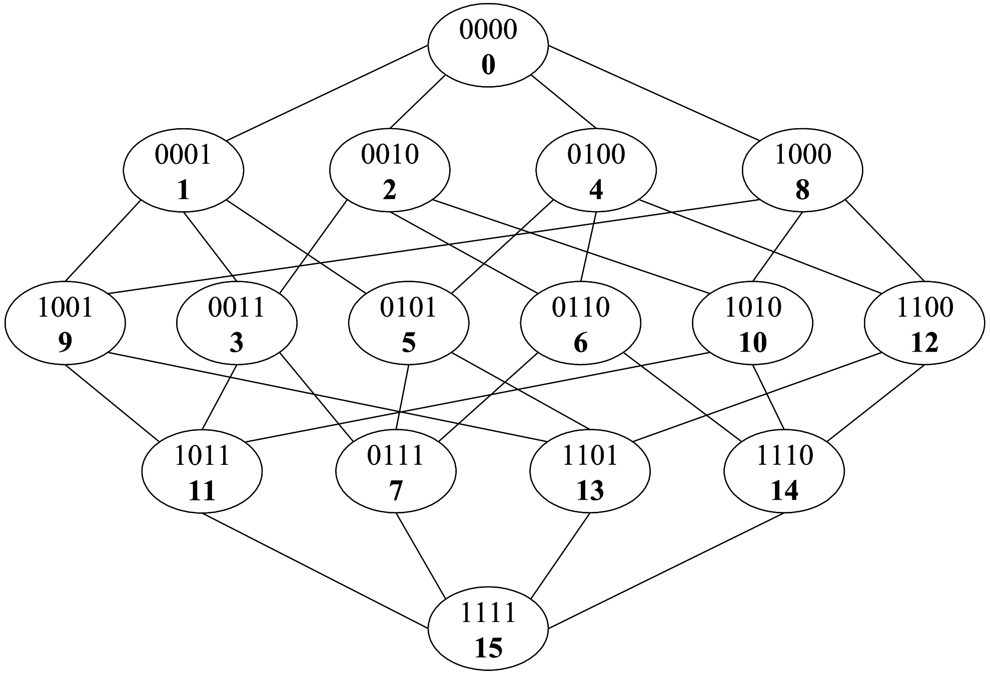


Absorbing state

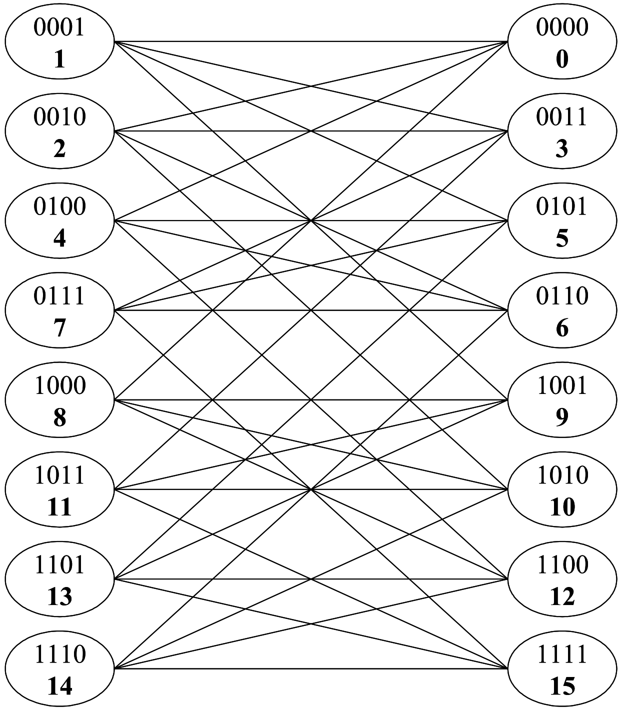
2^N states!

P. Van Mieghem, J. Omic, R. E. Kooij, “Virus Spread in Networks”, IEEE/ACM Transaction on Networking, Vol. 17, No. 1, pp. 1-14, (2009).

Markov theory



Regular bipartite Markov graph



Recursive structure of infinitesimal general Q_N

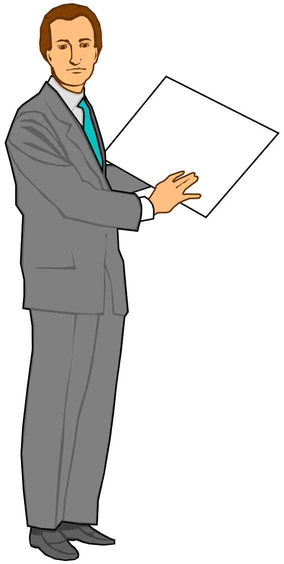
Simon, P., M. Taylor and I. Z. Kiss, Exact epidemic models on graphs using graph-automorphism driven lumping, Mathematical Biology, Vol. 62, pp. 479-508, 2011

Van Mieghem, P. and E. Cator, ε-SIS epidemics and the epidemic threshold, Physical Review E, vol. 86, No. 1, July, p. 016116, 2012

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

Defining the SIS epidemic threshold

Future research

NIMFA: N-intertwined mean-field approxim.

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

$E\left[X_j X_k\right] = \Pr\left[X_j = 1, X_k = 1\right] = \Pr\left[X_j = 1 \middle| X_k = 1\right]\Pr\left[X_k = 1\right]$ and $\Pr\left[X_j = 1 \middle| X_k = 1\right] \geq \Pr\left[X_j = 1\right]$

$$\Longrightarrow \quad E\left[X_i X_k\right] \geq \Pr\left[X_i = 1\right]\Pr\left[X_k = 1\right] = E\left[X_i\right]E\left[X_k\right]$$

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

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

E. Cator and P. Van Mieghem, 2012, "Second-order mean-field susceptible -infected-susceptible epidemic threshold", Physical Review E, vol. 85, No. 5, May, p. 056111.

NIMFA non-linear equations

$$\begin{cases} \dfrac{dv_1}{dt} = (1-v_1)\beta\sum_{k=1}^{N} a_{1k}v_k - \delta v_1 \\ \dfrac{dv_2}{dt} = (1-v_2)\beta\sum_{k=1}^{N} a_{2k}v_k - \delta v_2 \\ \vdots \\ \dfrac{dv_N}{dt} = (1-v_N)\beta\sum_{k=1}^{N} a_{Nk}v_k - \delta v_N \end{cases}$$

where the viral probability of infection is

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

In matrix form:

$$\boxed{\frac{dV(t)}{dt} = \beta A.V(t) - diag(v_i(t))(\beta A.V(t) + \delta u)}$$

where the vector u^T =[1 1 ... 1] and V^T = [v_1 v_2 ... v_N]

P. Van Mieghem, J. Omic, R. E. Kooij, “Virus Spread in Networks”, IEEE/ACM Transaction on Networking, Vol. 17, No. 1, pp. 1-14, (2009).

Lower bound for the epidemic threshold

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

Ignoring the quadratic terms

$$\frac{dV(t)}{dt} \leq \left(-\delta I + \beta A\right) V(t) \quad \Longrightarrow \quad V(t) \leq \mathrm{e}^{(-\delta I + \beta A)t}\, V(0)$$

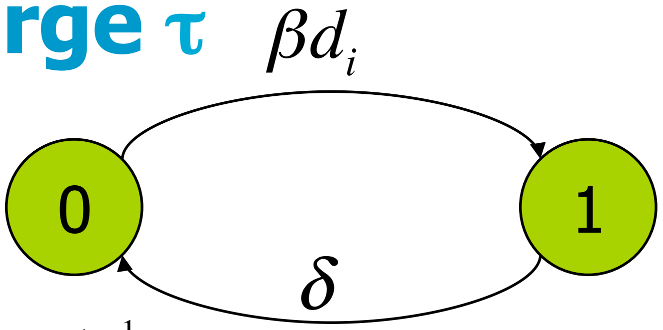
If all eigenvalues of $\beta A - \delta I$ are negative, v_j tends exponentially fast to zero with *t*. Hence, if

$$\beta \lambda_1(A) - \delta < 0 \quad \Longrightarrow \quad \tau = \frac{\beta}{\delta} < \frac{1}{\lambda_1(A)} < \tau_c$$

The NIMFA epidemic threshold is precisely

$$\boxed{\tau_c^{(1)} = \frac{1}{\lambda_1(A)} < \tau_c} \qquad \boxed{\tau_c^{(1)} = \frac{1}{\lambda_1(A)} < \tau_c^{(2)} = \frac{1}{\lambda_1(H)} < \tau_c}$$

Exact in steady-state for large τ



Almost all neighbors of node *j* are infected: independence

$$\Pr\left[X_j = 1\right] \cong \frac{\beta d_j}{\delta + \beta d_j} = \left(1 + \frac{1}{\tau d_j}\right)^{-1} = \left(1 + \frac{s}{d_j}\right)^{-1}$$

Exact steady-state average fraction of infected nodes:

$$y_\infty(s) \cong \frac{1}{N}\sum_{j=1}^{N} \Pr\left[X_j = 1\right] = \frac{1}{N}\sum_{j=1}^{N}\left(1 + \frac{s}{d_j}\right)^{-1}$$

Slope: $$\left.\frac{dy_\infty(s)}{ds}\right|_{s=0} = \frac{1}{N}\sum_{j=1}^{N}\frac{1}{d_j} = E\left[\frac{1}{D}\right]$$

P. Van Mieghem, 2012, “The Viral Conductance in Networks”, Computer Communications, Vol 35, No. 12, pp. 1494-1509.

What is so interesting about epidemics?

network protection

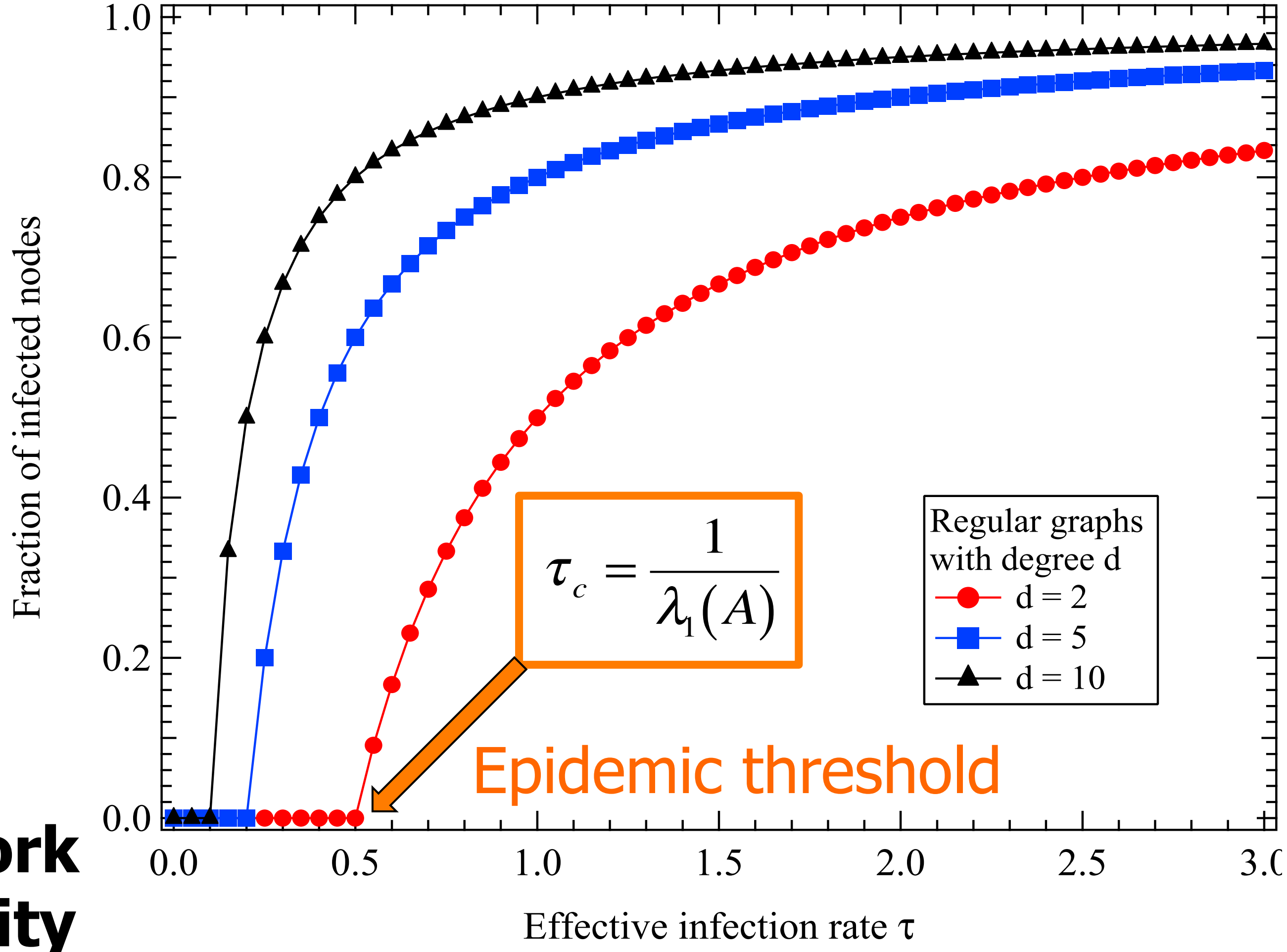
self-replicating objects (worms)

propagation errors

rumors (social nets)

epidemic algorithms (gossiping)

cybercrime : network robustnes & security

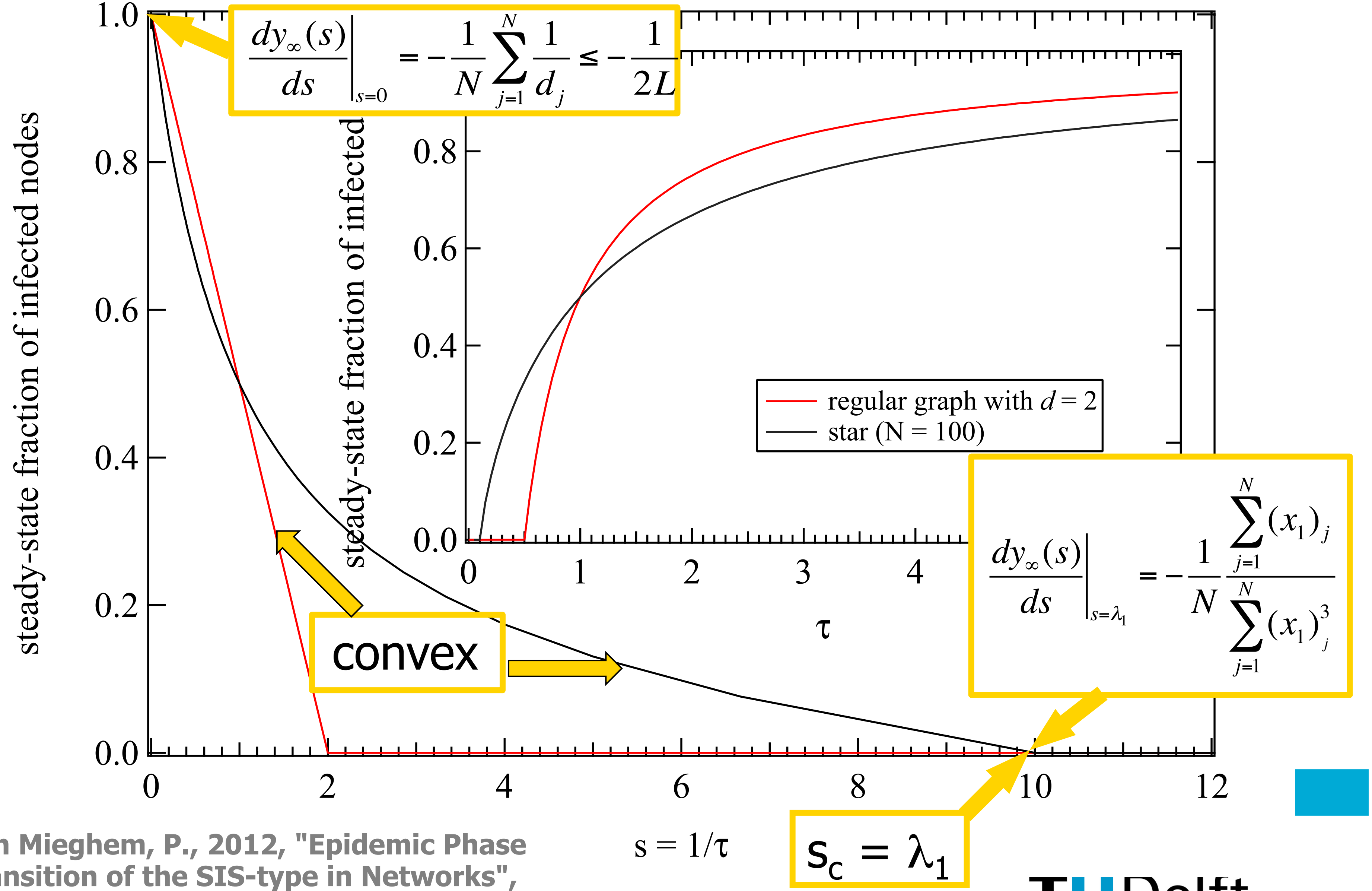


$$\tau_c = \frac{1}{\lambda_1(A)}$$

Epidemic threshold

$$\max\left(E[D]\sqrt{1+\frac{Var[D]}{\left(E[D]\right)^2}}, \sqrt{d_{\max}}\right) \le \lambda_1(A) \le d_{\max}$$

Transformation $s = \frac{1}{\tau}$ & principal eigenvector



$$\left.\frac{dy_\infty(s)}{ds}\right|_{s=0} = -\frac{1}{N}\sum_{j=1}^{N}\frac{1}{d_j} \le -\frac{1}{2L}$$

convex

$$\left.\frac{dy_\infty(s)}{ds}\right|_{s=\lambda_1} = -\frac{1}{N}\frac{\sum_{j=1}^{N}(x_1)_j}{\sum_{j=1}^{N}(x_1)_j^3}$$

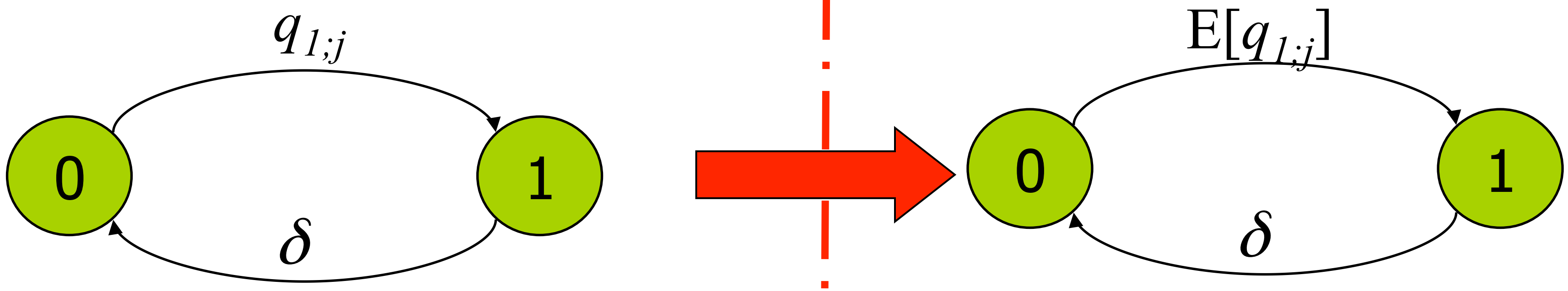
$s_c = \lambda_1$

Van Mieghem, P., 2012, "Epidemic Phase Transition of the SIS-type in Networks", Europhysics Letters (EPL), Vol. 97, Februari, p. 48004.

Extensions of the N-intertwined model

- In-homogeneous: each node i has own β_i and δ_i:
  - P. Van Mieghem and J. Omic, "In-homogeneous Virus Spread in Networks", TUDelft report (see http://www.nas.ewi.tudelft.nl/people/Piet/)
- SAIS instead of SIS:
  - From 2 states (Infected and Susceptible) to a 3-states (Infected, Susceptible, Alert)
  - "Epidemic Spread in Human Networks", F. Darabi Sahneh and C. Scoglio, 50th IEEE Conf. Decision and Contol, Orlando, Florida (2011)
- SIR instead of SIS:
  - "An individual-based approach to SIR epidemics in contact networks", M. Youssef and C. Scoglio, Journal of Theoretical Biology 283, pp. 136-144, (2011).
- Very general extension: m compartments (includes both SIS, SAIS, SIR,...):
  - "Generalized Epidemic Mean-Field Model for Spreading Processes over Multi-Layer Complex Networks", F. Darabi Sahneh, C. Scoglio, P. Van Mieghem, submitted IEEE/ACM Transactions on Networking

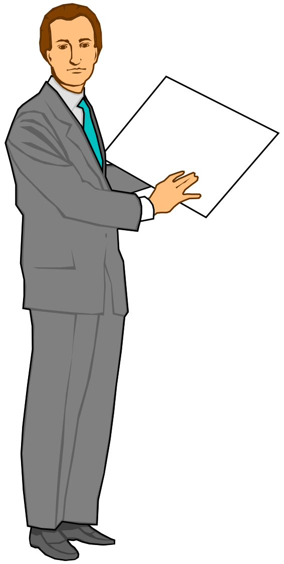
Mean-field approximation (NIMFA)



- 2^N linear equations
- Steady-state
  - absorbing (healthy) state
  - reached after unrealistically long time
- difficult to analyze

- N non-linear equations
- Meta-stable state:
  - phase-transition
  - epidemic threshold
  - realistic
- analytically tractable
- lower bound epidemic threshold

Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

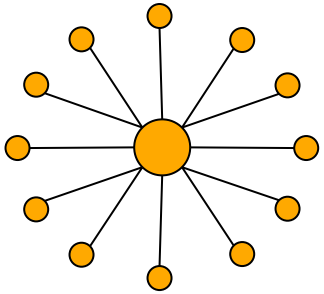
Future research

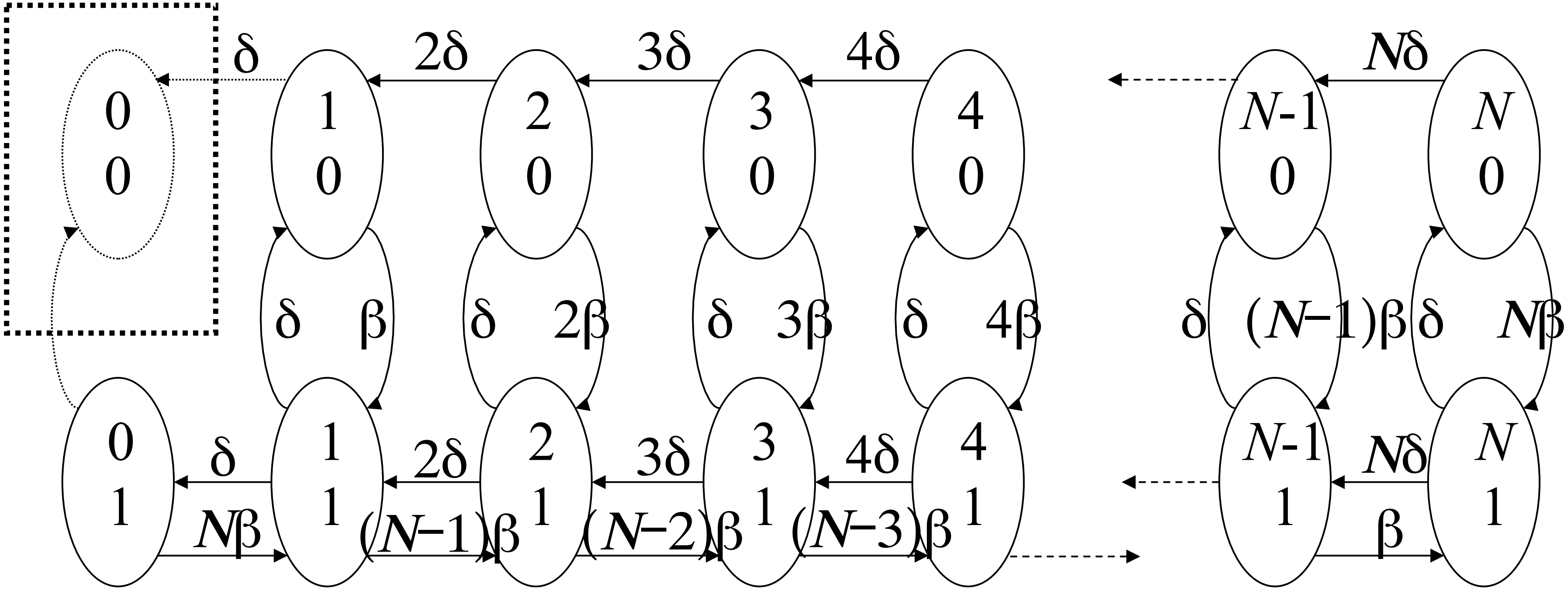
Defining the SIS epidemic threshold

- Exact SIS steady-state (finite N):
  - overall healthy state (physically not interesting)
- Metastable (or quasi-stationary) state:
  - not defined, but physically interesting
- Two approaches:
  - modified SIS Markov chain (excluding overall healthy state)
  - ε-SIS Markov model

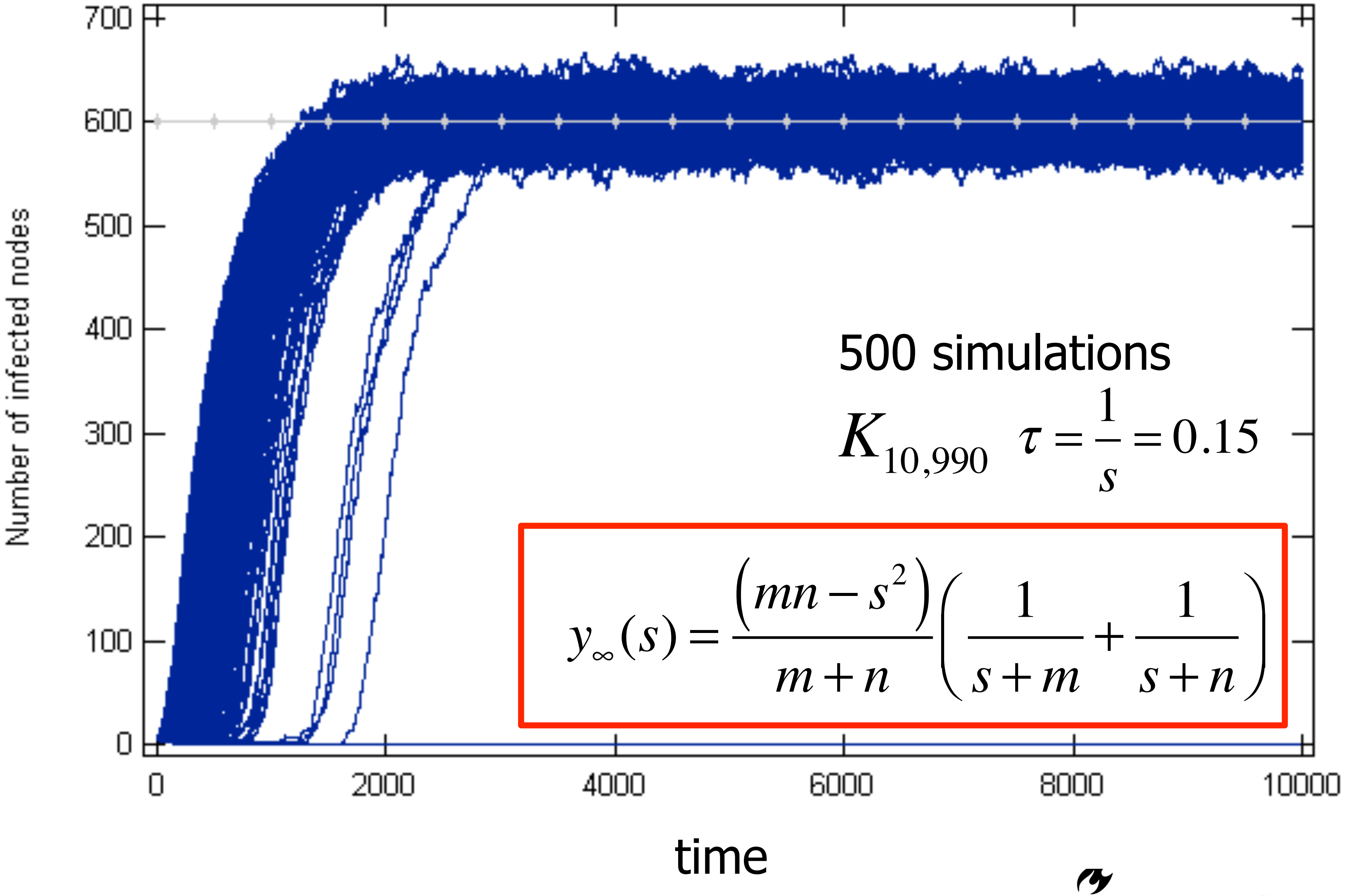
E. Cator and P. Van Mieghem, 2012, "**SIS epidemics on the complete graph and the star graph: exact analysis**", PRE, submitted.

MSIS Markov Chain Star





Simulations

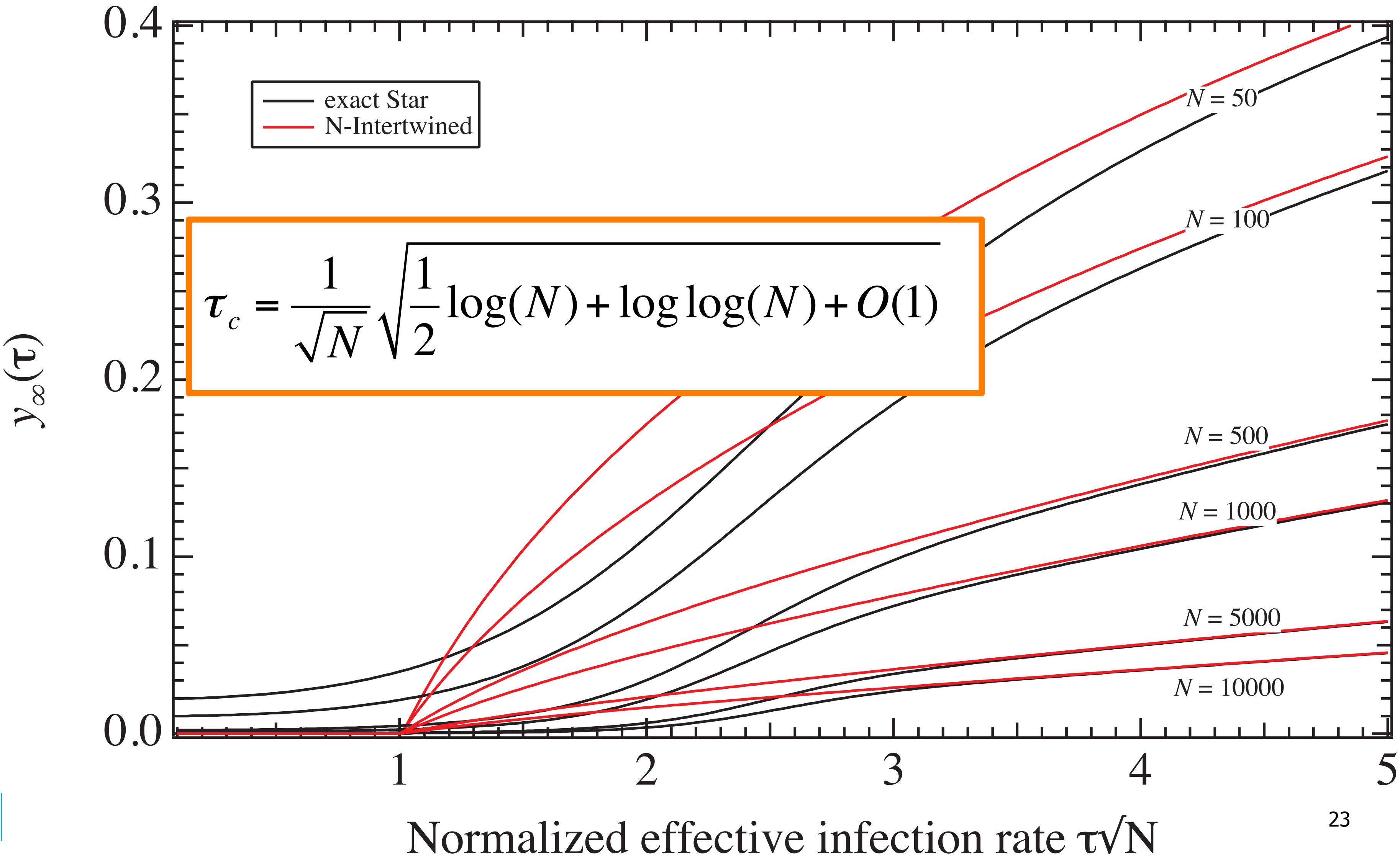


500 simulations

$K_{10,990} \quad \tau = \frac{1}{s} = 0.15$

$$\boxed{y_\infty(s) = \frac{\left(mn - s^2\right)}{m+n}\left(\frac{1}{s+m} + \frac{1}{s+n}\right)}$$

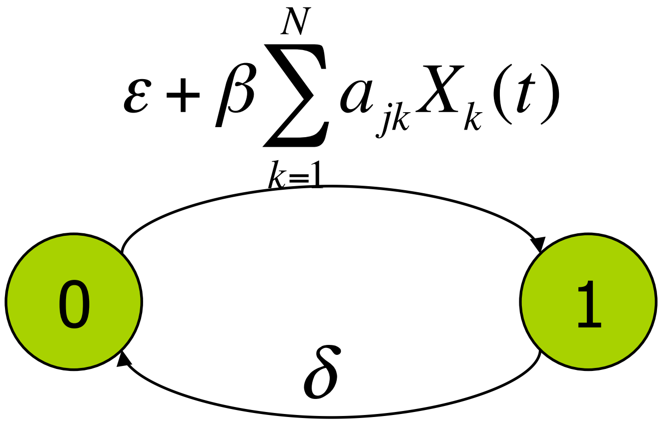
Star graph



$$\tau_c = \frac{1}{\sqrt{N}}\sqrt{\frac{1}{2}\log(N)+\log\log(N)+O(1)}$$

E. Cator and P. Van Mieghem, 2012, **“SIS epidemics on the complete graph and the star graph: exact analysis”**, PRE, submitted.

ε-SIS epidemics



due to self-infection with rate $\varepsilon > 0$, the steady-state is **not** the absorbing state!

↓

epidemic threshold & meta-stable state in SIS can be defined for a given $0 < \varepsilon < \delta/N$

ε-SIS epidemics on the complete graph

$$\pi_j = \pi_0 \binom{N}{j} \tau^j \frac{\Gamma\left(\frac{\varepsilon^*}{\tau} + j\right)}{\Gamma\left(\frac{\varepsilon^*}{\tau}\right)} \qquad \pi_0^{-1} = \sum_{k=0}^{N} \binom{N}{k} \tau^k \frac{\Gamma\left(\frac{\varepsilon^*}{\tau} + k\right)}{\Gamma\left(\frac{\varepsilon^*}{\tau}\right)}$$

$$\varepsilon^* = \frac{\varepsilon}{\delta}$$

$$\tau = \frac{\beta}{\delta}$$

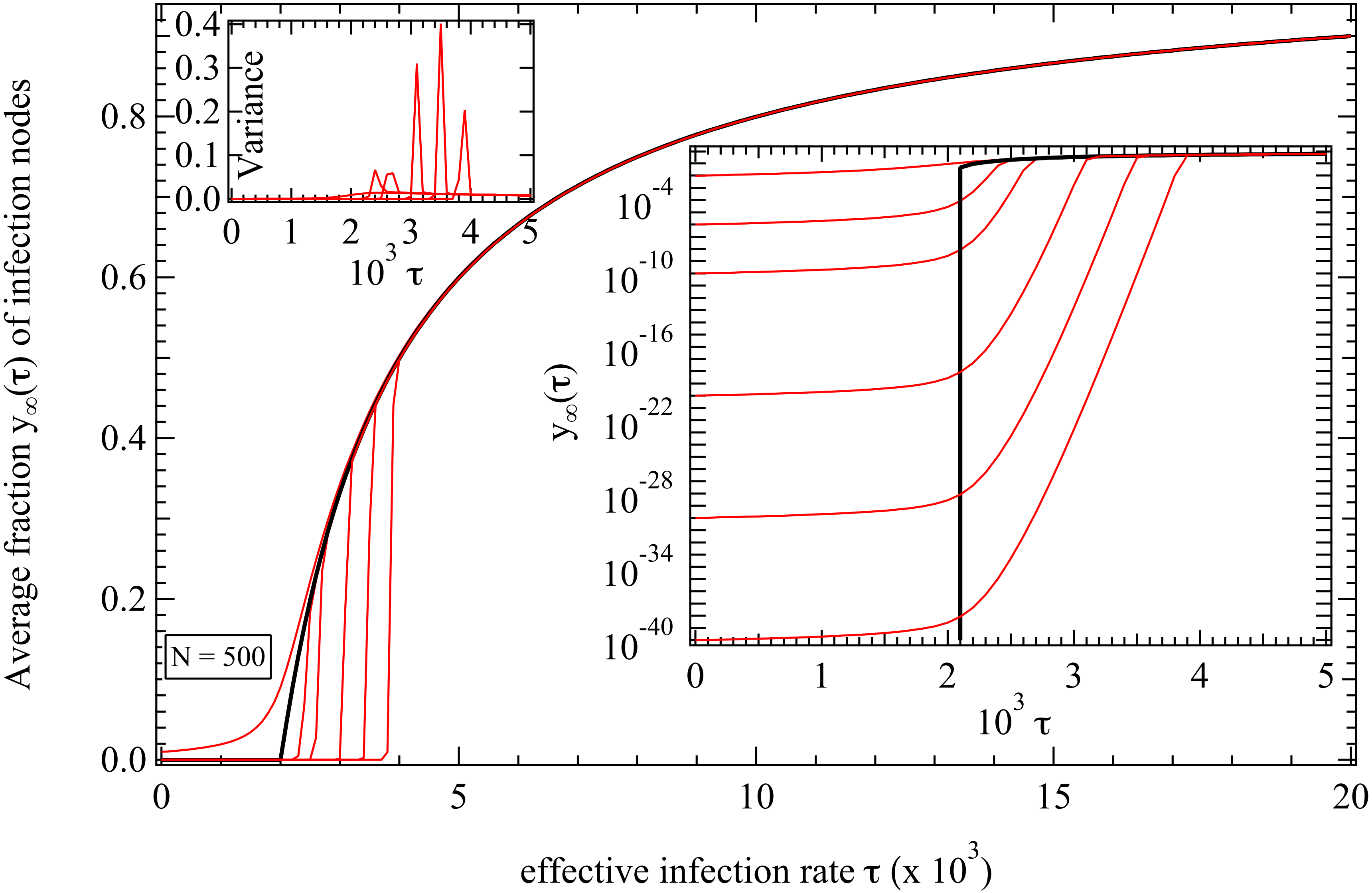
average steady-state fraction of infected nodes is $y_\infty(\tau \mid \varepsilon^*) = \frac{1}{N}\sum_{j=1}^{N} j\pi_j$

epidemic threshold $\tau_c = \frac{1}{N}\left(1 + \frac{2}{\sqrt{N}} + O\left(\frac{1}{N}\right)\right)$

NIMFA epidemic threshold $\tau_c^{(1)} = \frac{1}{N-1} = \frac{1}{N}\left(1 + \frac{1}{N} + O\left(\frac{1}{N^2}\right)\right)$

Van Mieghem, P. and E. Cator, ε-SIS epidemics and the epidemic threshold, Physical Review E, vol. 86, No. 1, July 2012, p. 016116

ε-SIS epidemics on the complete graph



HMF mean-field approximation

governing eq.:

$$\frac{d\rho_k(t)}{dt} = -\delta\rho_k(t) + \beta k\left(1-\rho_k(t)\right)\Theta(\rho(t))$$

steady-state:

$$\rho_k(\tau) = \frac{\tau k\Theta(\tau)}{1+\tau k\Theta(\tau)}$$

$$\tau = \frac{\beta}{\delta}$$

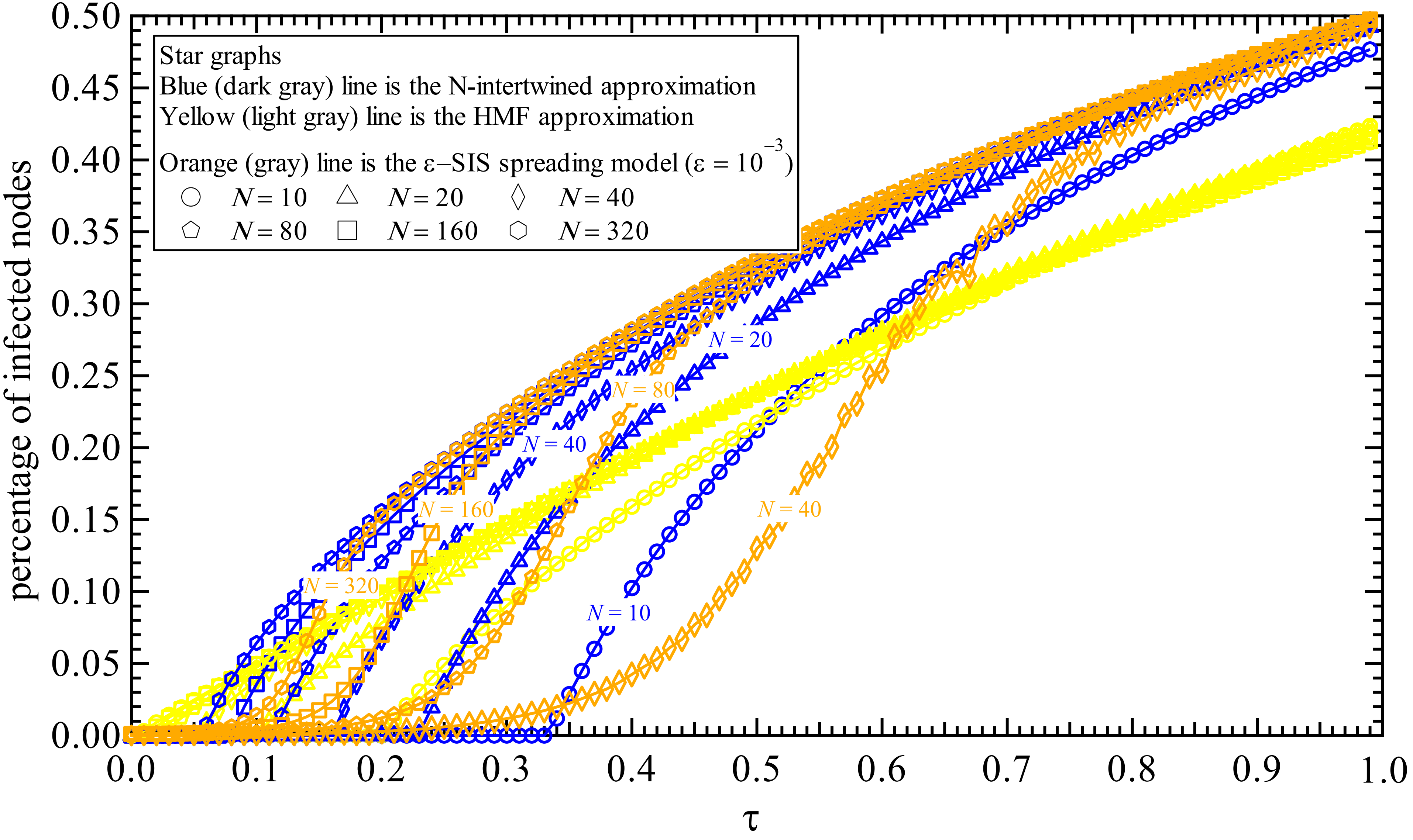
$$\Theta(\tau) = \frac{1}{E[D]}\sum_{k=1}^{N-1} k\,\Pr[D=k]\rho_k(\tau)$$

HMF epidemic threshold:

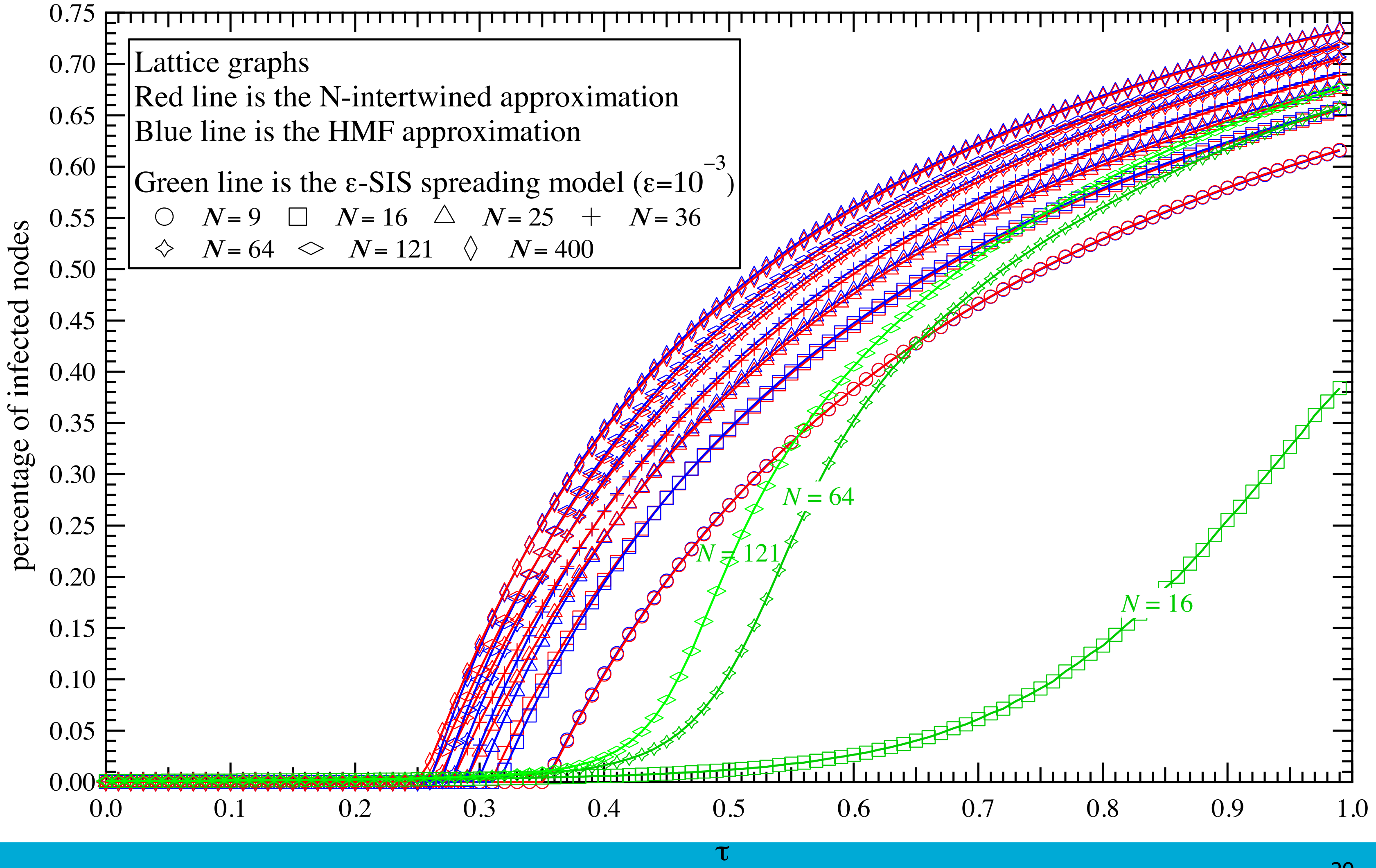
$$\tau_{c;HMF} = \frac{E[D^2]}{E[D]}$$

Pastor-Satorras, R. and Vespignani, A., Epidemic dynamics and endemic states in complex networks, Phys. Rev. E 63, 066117, 2001.

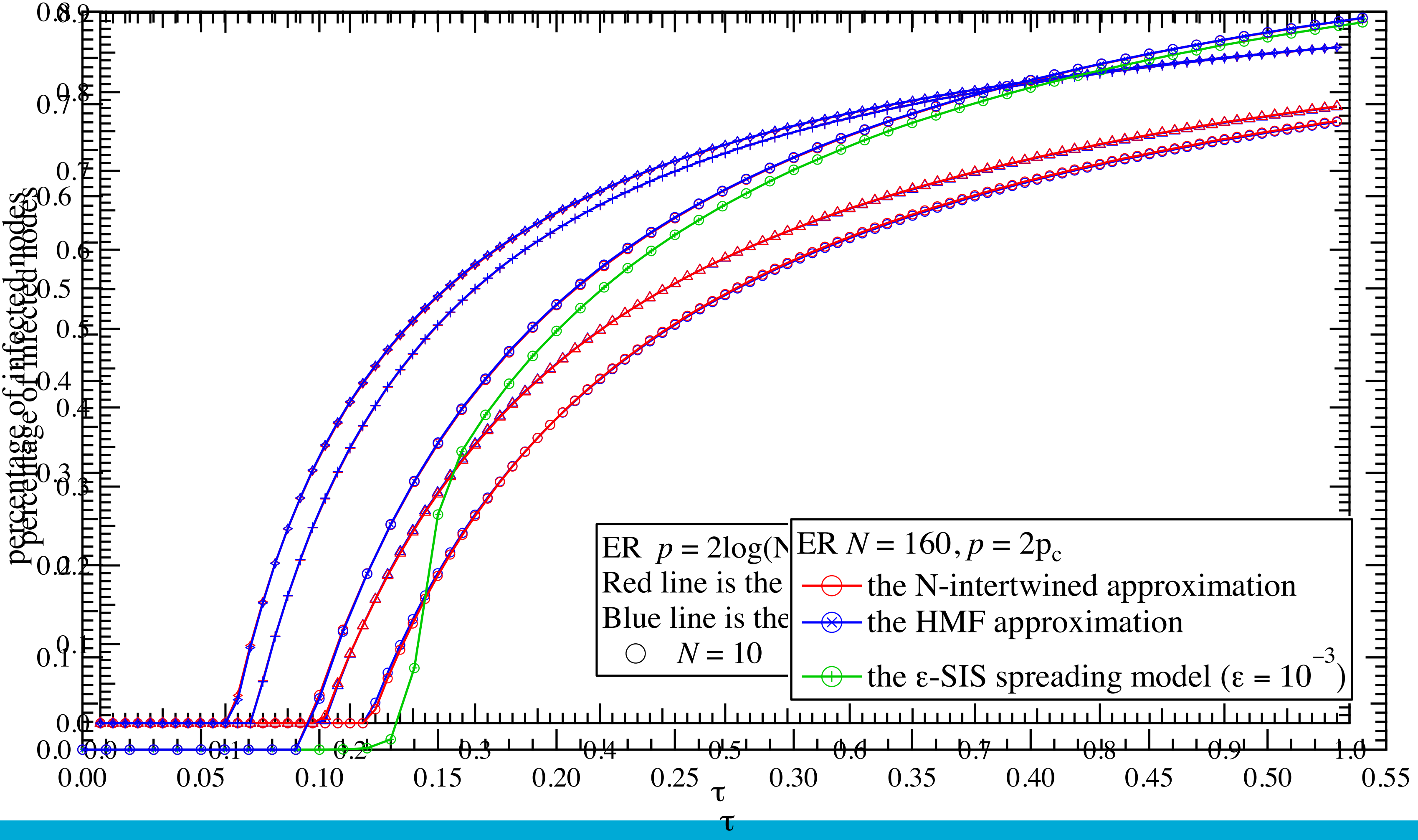
Comparison: star graph



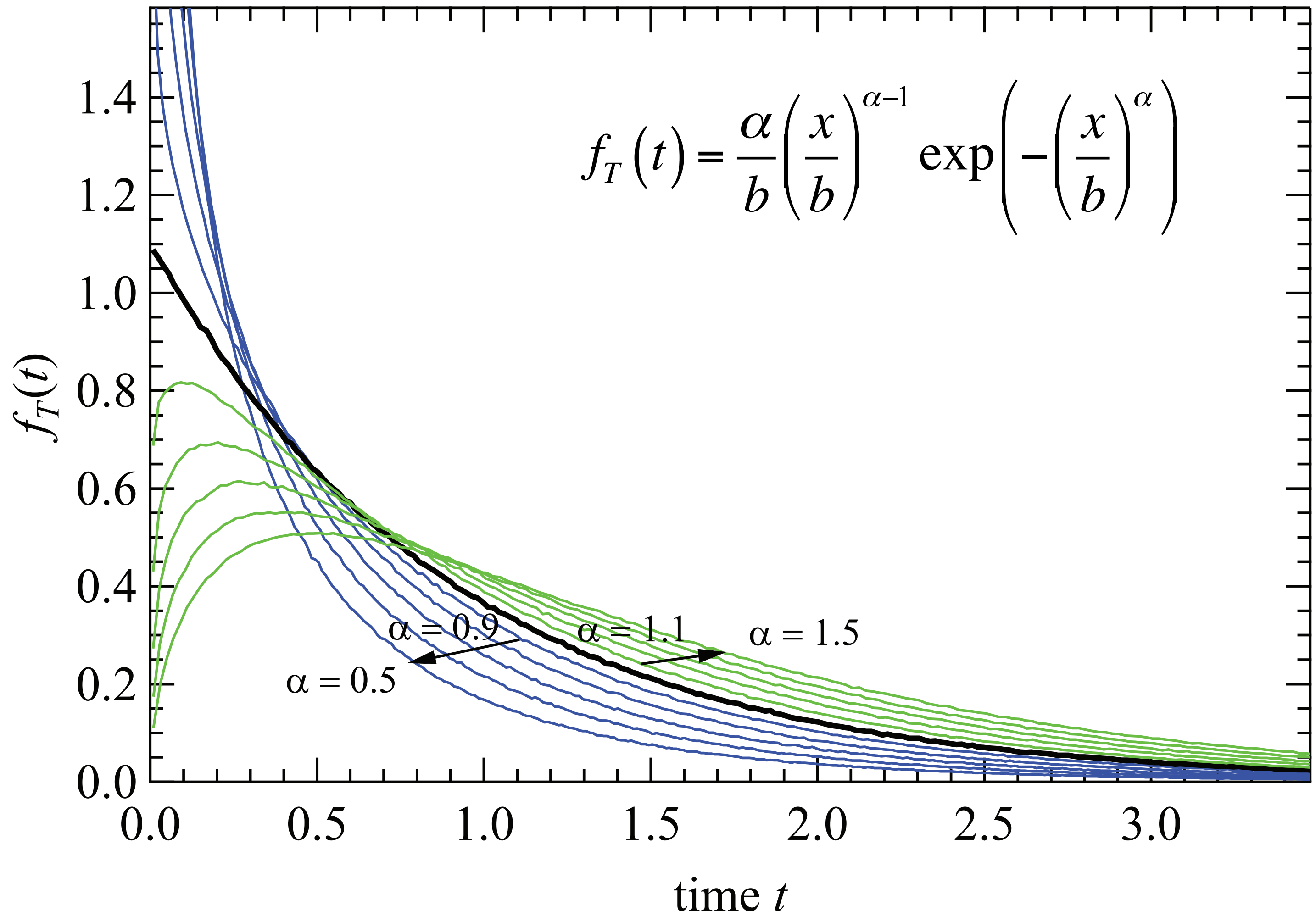
Comparison: Lattice



Comparison: ER graph (close to p_c)



Non-Markovian infection

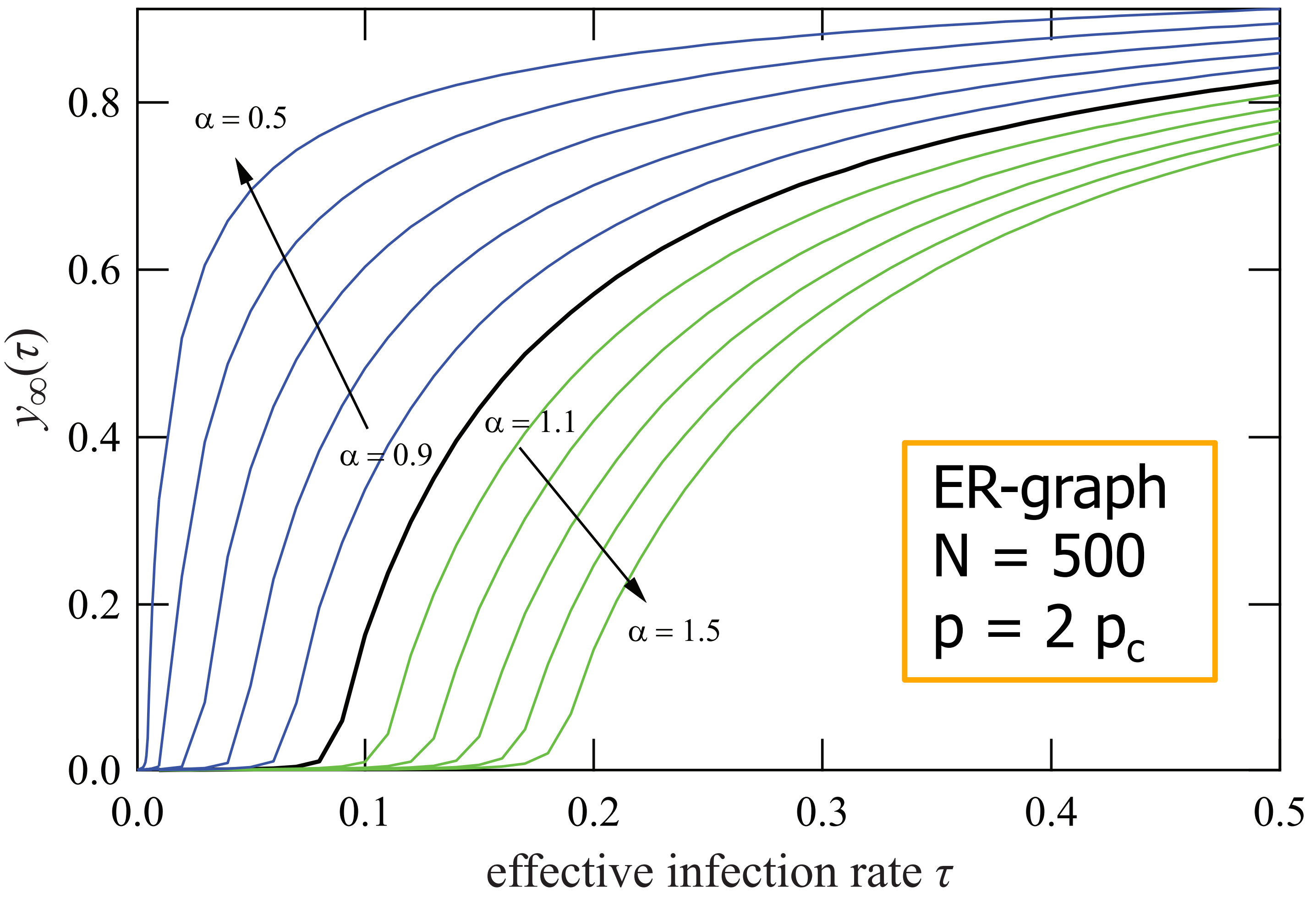


Same mean E[*T*]:

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

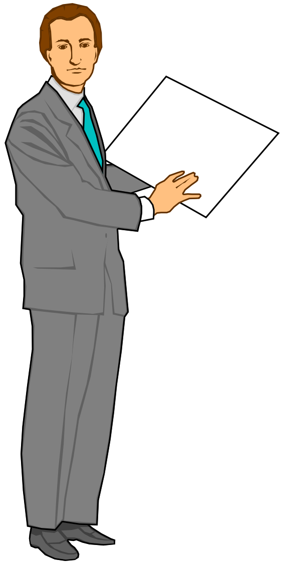
T is the time to infected a neighboring node

Non-Markovian epidemic threshold



Non-exponential infection time has a dramatic influence!

Outline



Exact SIS model

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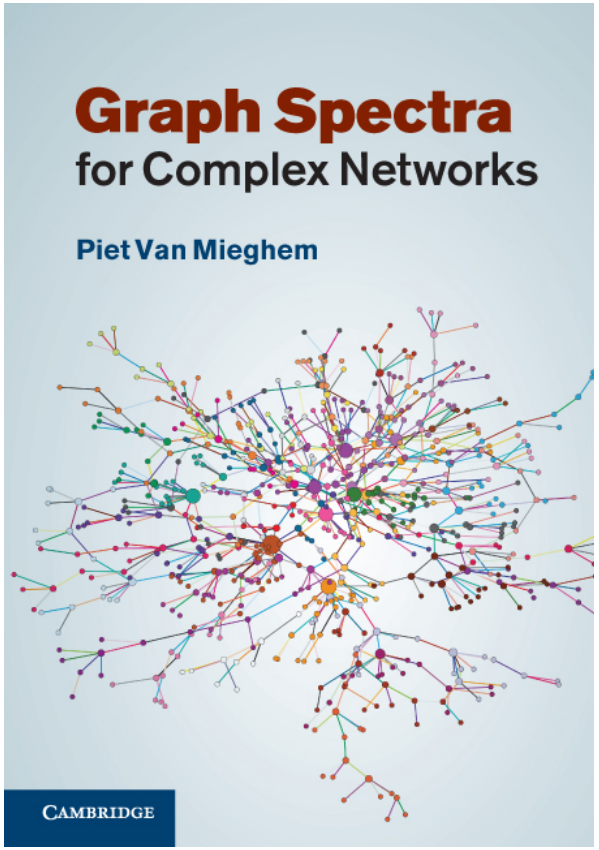
Future research

Agenda for future research

- Determine for which graphs NIMFA is accurate
- Can we compute/estimate the epidemic threshold for non-exponential infection times?
- Impact of directionality of the graph on the epidemic threshold
- **Wider scope**:
  - Epidemics in adaptive networks
  - Epidemics & Games (OPEN POSITION EU CONGAS)

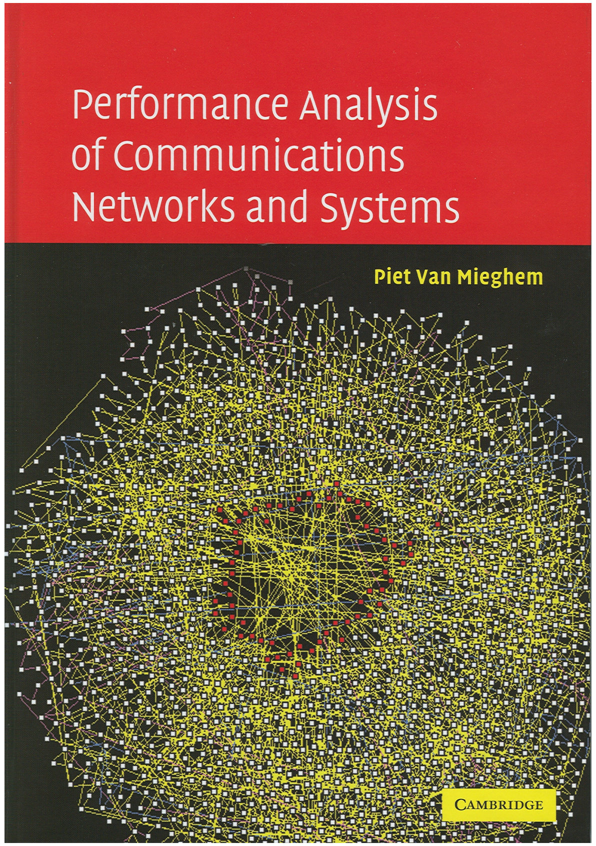
Books



Graph Spectra
for Complex Networks

Piet Van Mieghem

CAMBRIDGE



Performance Analysis
of Communications
Networks and Systems

Piet Van Mieghem

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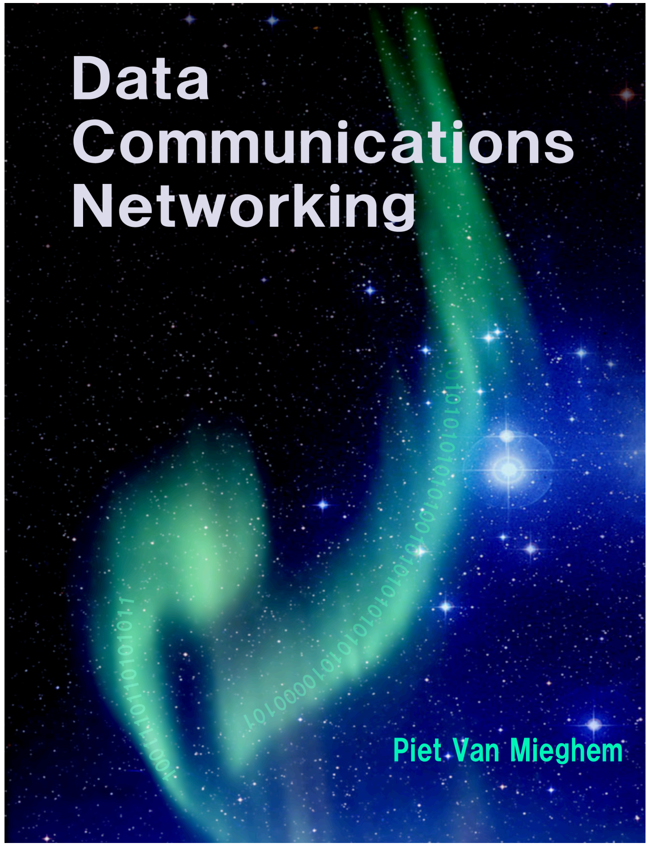

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Thank You

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