

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

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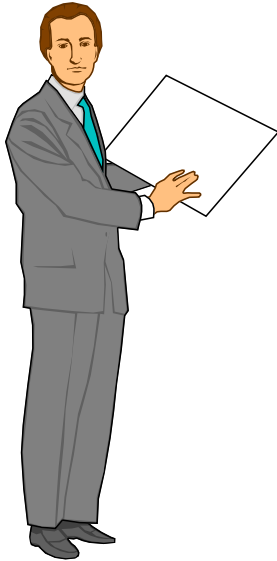
Outline

Exact SIS model

NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

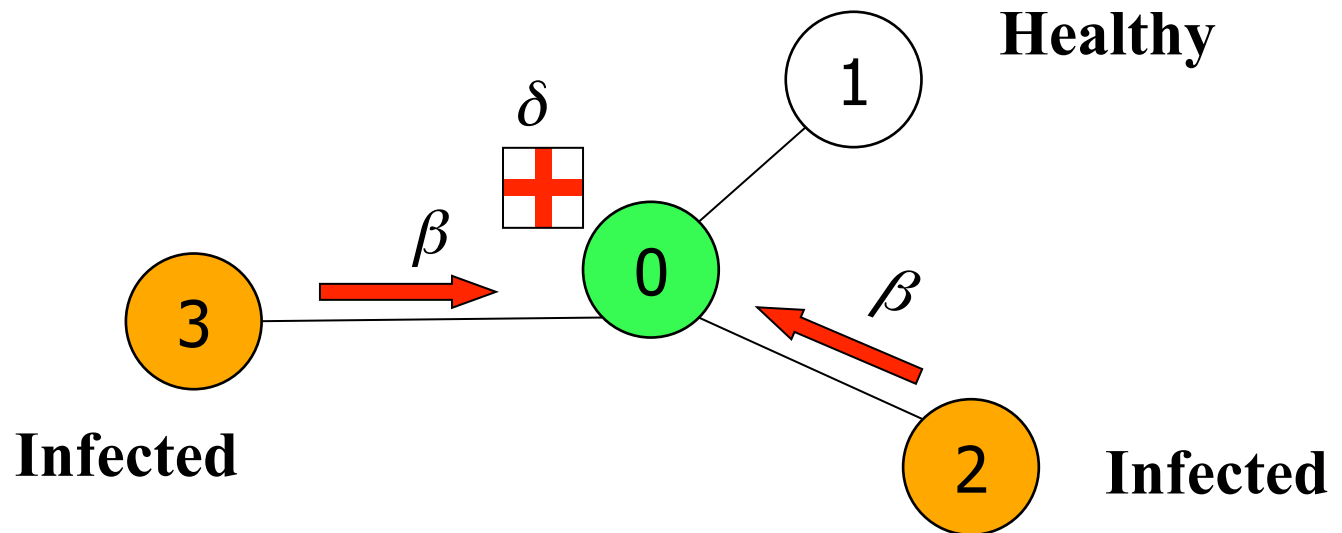
Summary



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

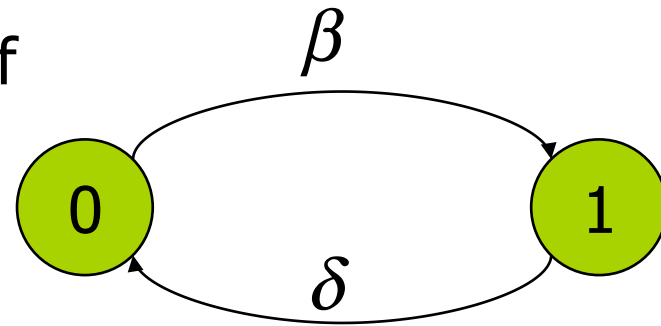
$\tau = \beta / \delta$: effective spreading rate



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

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

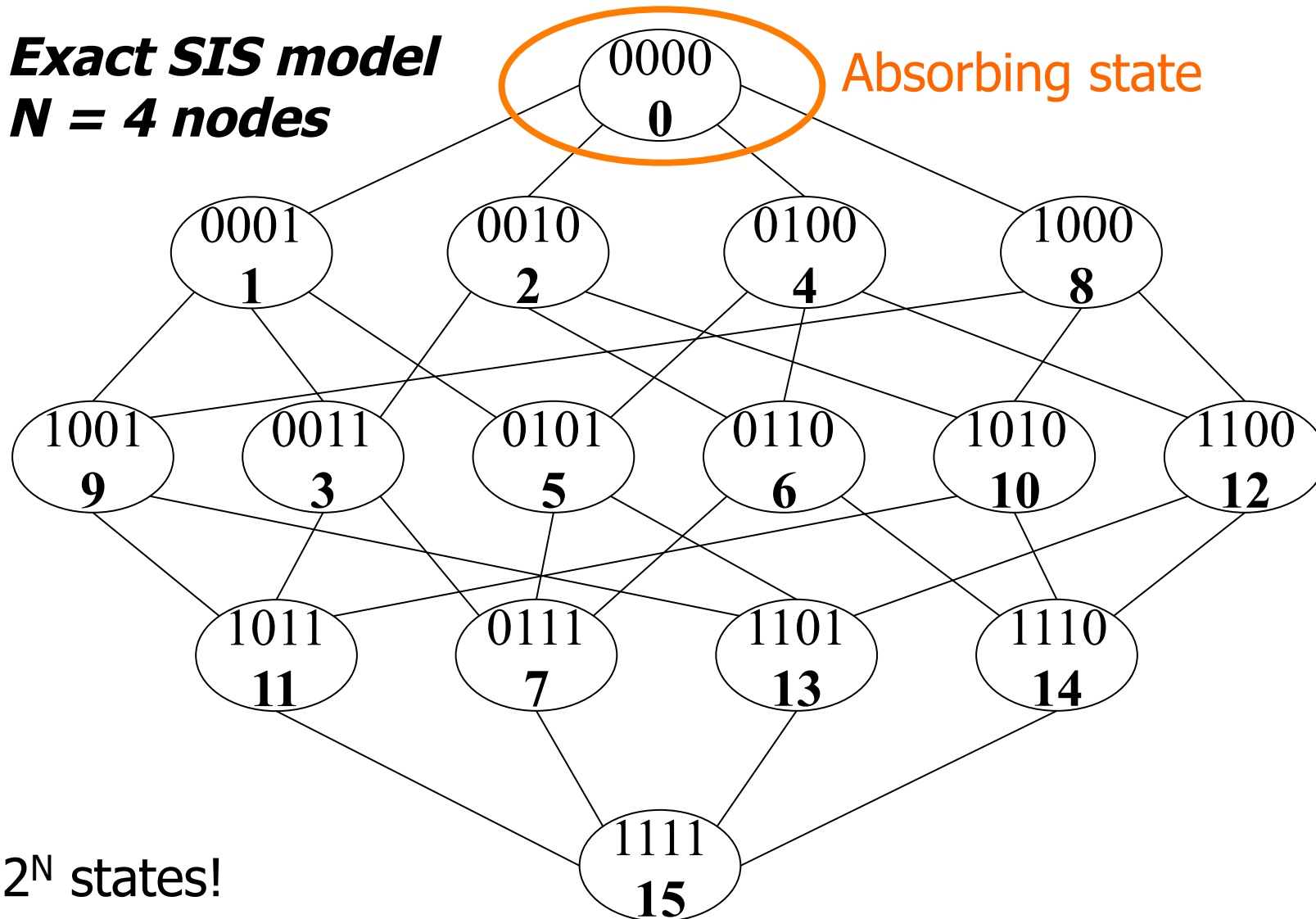
Joint probabilities

$$\begin{aligned} \frac{dE[X_i X_j]}{dt} &= E \left[-2\delta X_i X_j + X_j \beta (1 - X_i) \sum_{k=1}^N a_{ik} X_k + X_i \beta (1 - X_j) \sum_{k=1}^N a_{jk} X_k \right] \\ &= -2\delta E[X_i X_j] + \beta \sum_{k=1}^N a_{ik} E[X_j X_k] + \beta \sum_{k=1}^N a_{jk} E[X_i X_k] - \beta \sum_{k=1}^N (a_{jk} + a_{ik}) E[X_i X_j X_k] \end{aligned}$$

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

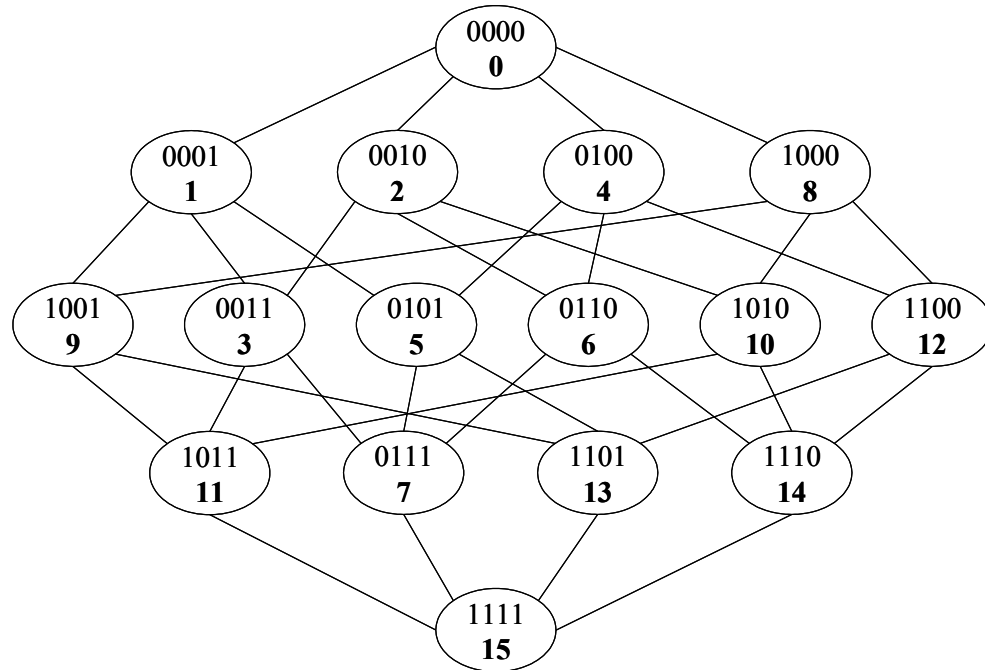
In total, the SIS process is defined by $2^N = \sum_{k=1}^N \binom{N}{k} + 1$ linear equations

Exact SIS model
 $N = 4$ nodes

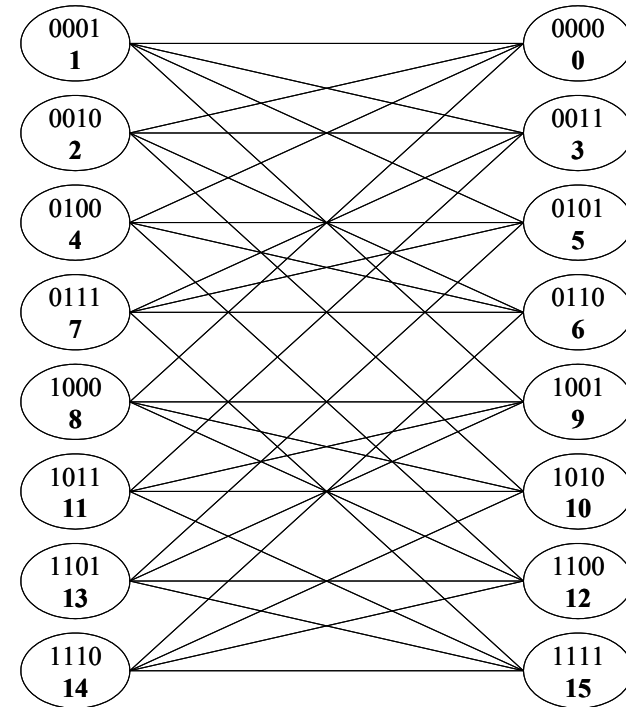


2^N states!

Markov theory



bi-partite Markov graph



Recursive structure of infinitesimal general Q_N

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

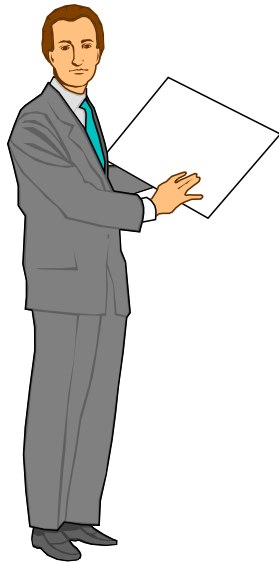
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Exact SIS model

NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

Summary



NIMFA: N-intertwined mean-field approxim.

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

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

$$\longrightarrow E[X_j X_k] \geq \Pr[X_j = 1] \Pr[X_k = 1] = E[X_j] E[X_k]$$

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

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

NIMFA non-linear equations

$$\left\{ \begin{array}{l} \frac{dv_1}{dt} = (1-v_1)\beta \sum_{k=1}^N a_{1k}v_k - \delta v_1 \\ \frac{dv_2}{dt} = (1-v_2)\beta \sum_{k=1}^N a_{2k}v_k - \delta v_2 \\ \vdots \\ \frac{dv_N}{dt} = (1-v_N)\beta \sum_{k=1}^N a_{Nk}v_k - \delta v_N \end{array} \right.$$

where the viral probability of infection is

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

In matrix form:

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

where the vector $u^T = [1 \ 1 \ \dots \ 1]$ and $V^T = [v_1 \ v_2 \ \dots \ v_N]$

Lower bound for the epidemic threshold

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

Ignoring the quadratic terms

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

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

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

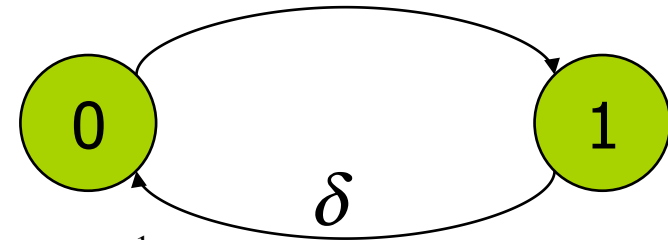
The NIMFA epidemic threshold is precisely

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

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

Exact in steady-state for large τ βd_i

Almost all neighbors of node j are infected: independence



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

Exact steady-state average fraction of infected nodes:

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

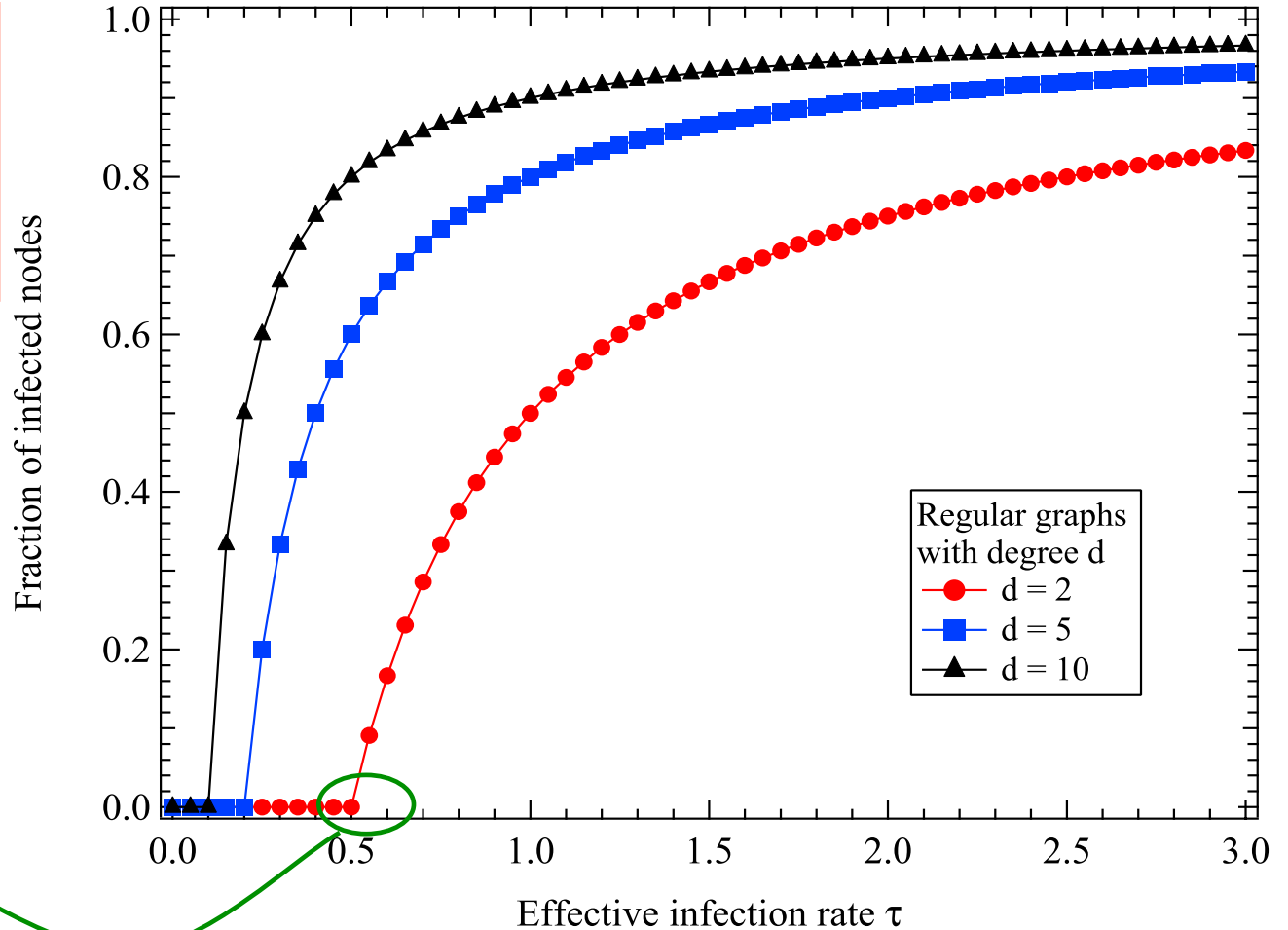
Slope: $\left. \frac{dy_\infty(s)}{ds} \right|_{s=0} = \frac{1}{N} \sum_{j=1}^N \frac{1}{d_j} = E\left[\frac{1}{D}\right]$

What is so interesting about epidemics?

β : infection rate per link
 δ : curing rate per node
 $\tau = \beta / \delta$: effective spreading rate

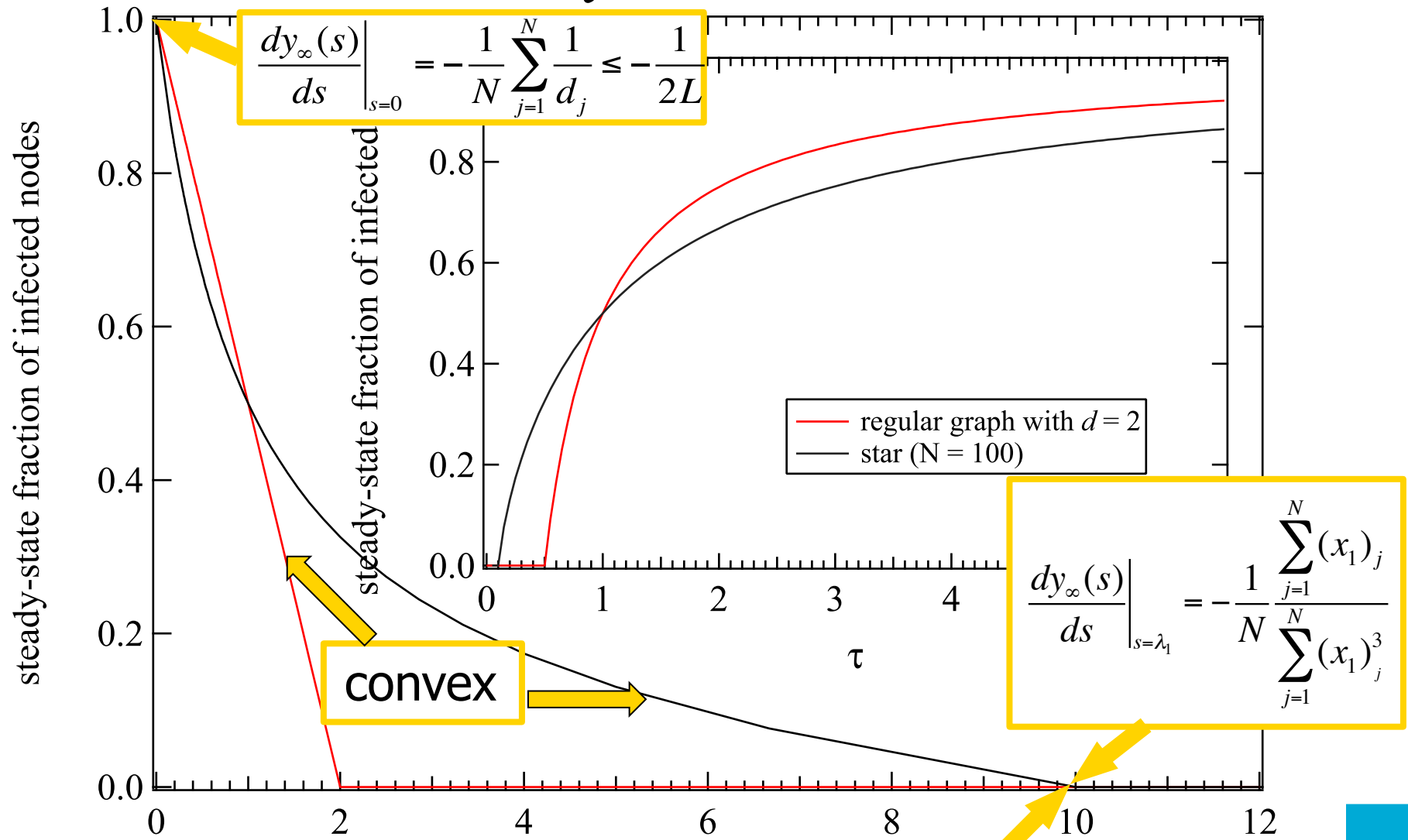
- Final epidemic state
- Rate of propagation
- Epidemic threshold

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



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

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

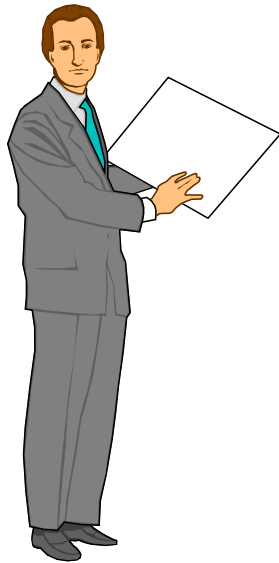


Van Mieghem, P., 2012, "Epidemic Phase Transition of the SIS-type in Networks", *Europhysics Letters (EPL)*, Vol. 97, Februari, p. 48004.

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 my website)
- 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 Control, 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

Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

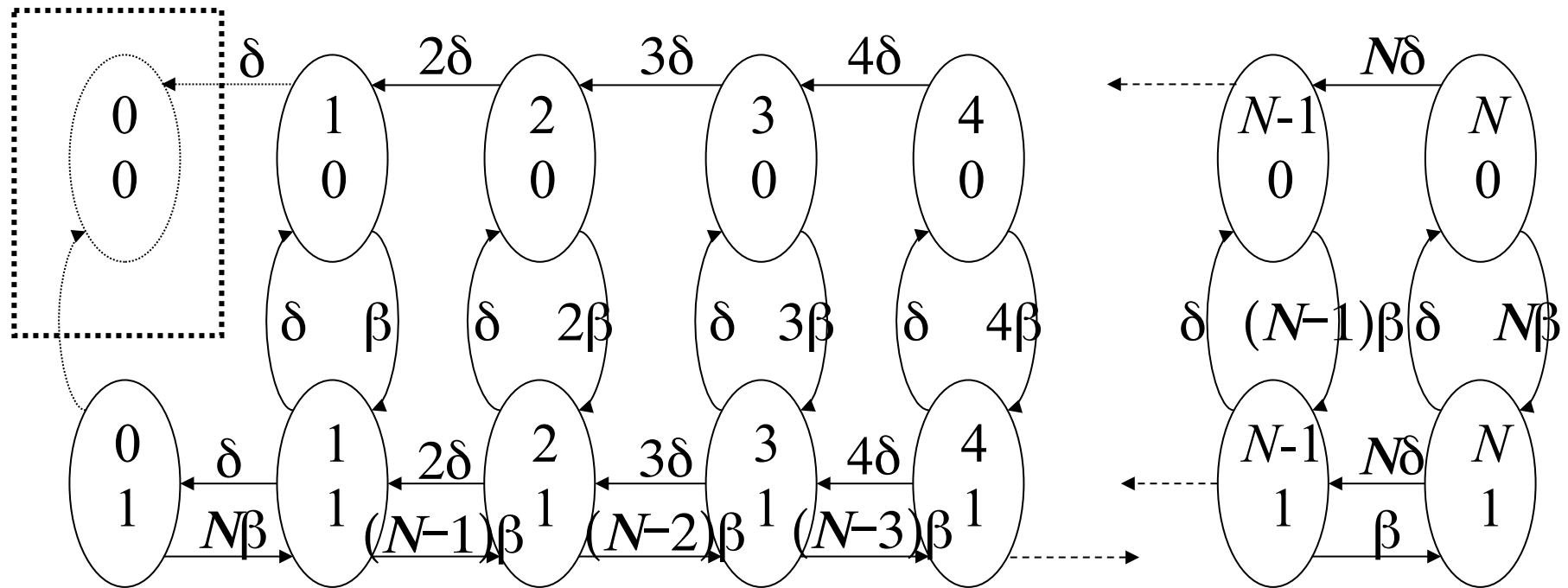
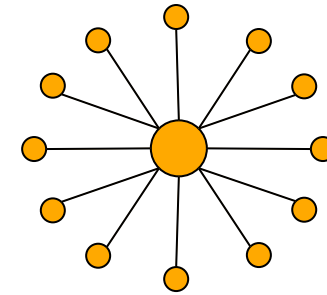
Defining the SIS epidemic threshold

Summary

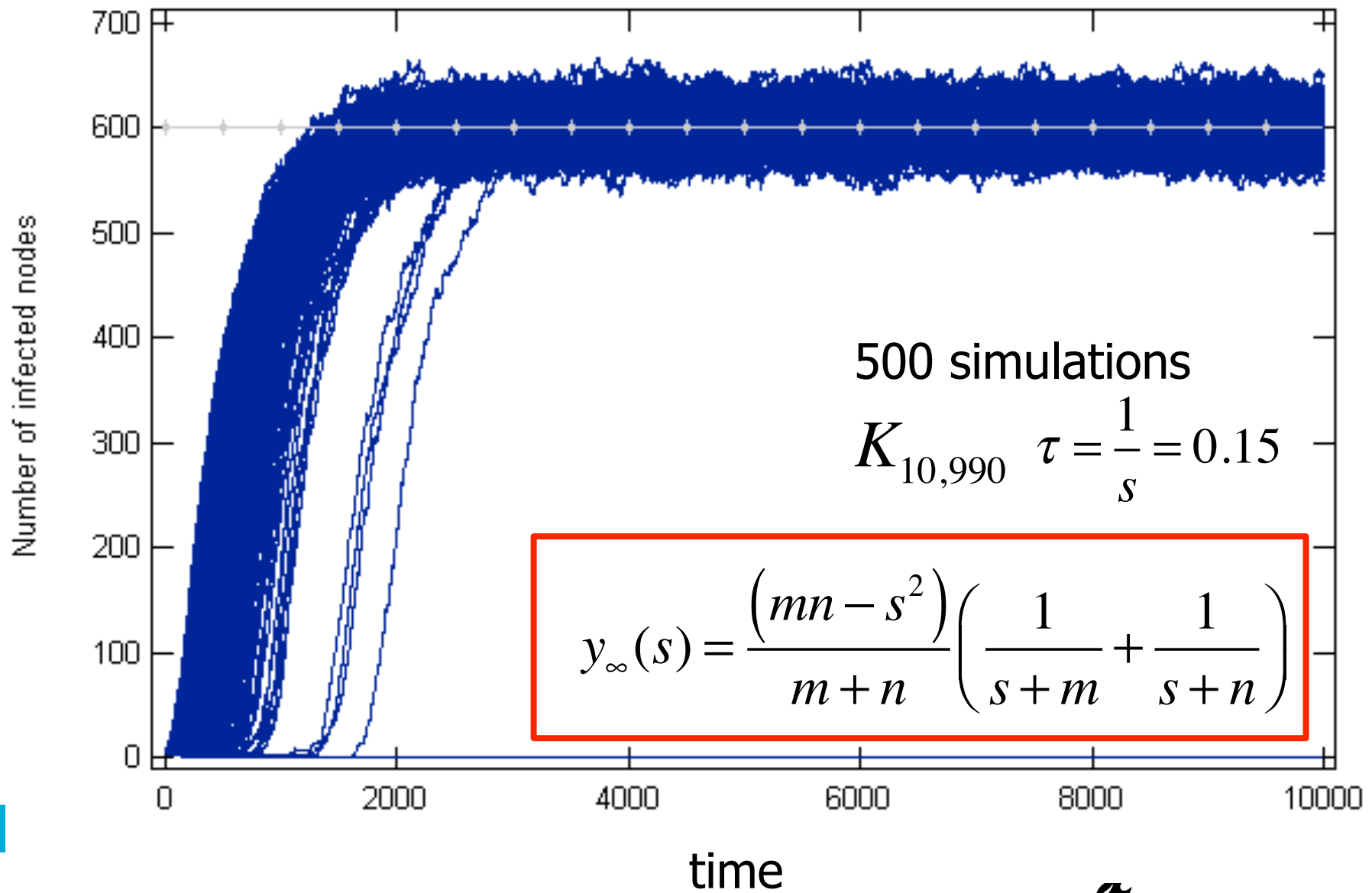
Defining the SIS epidemic threshold

- 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

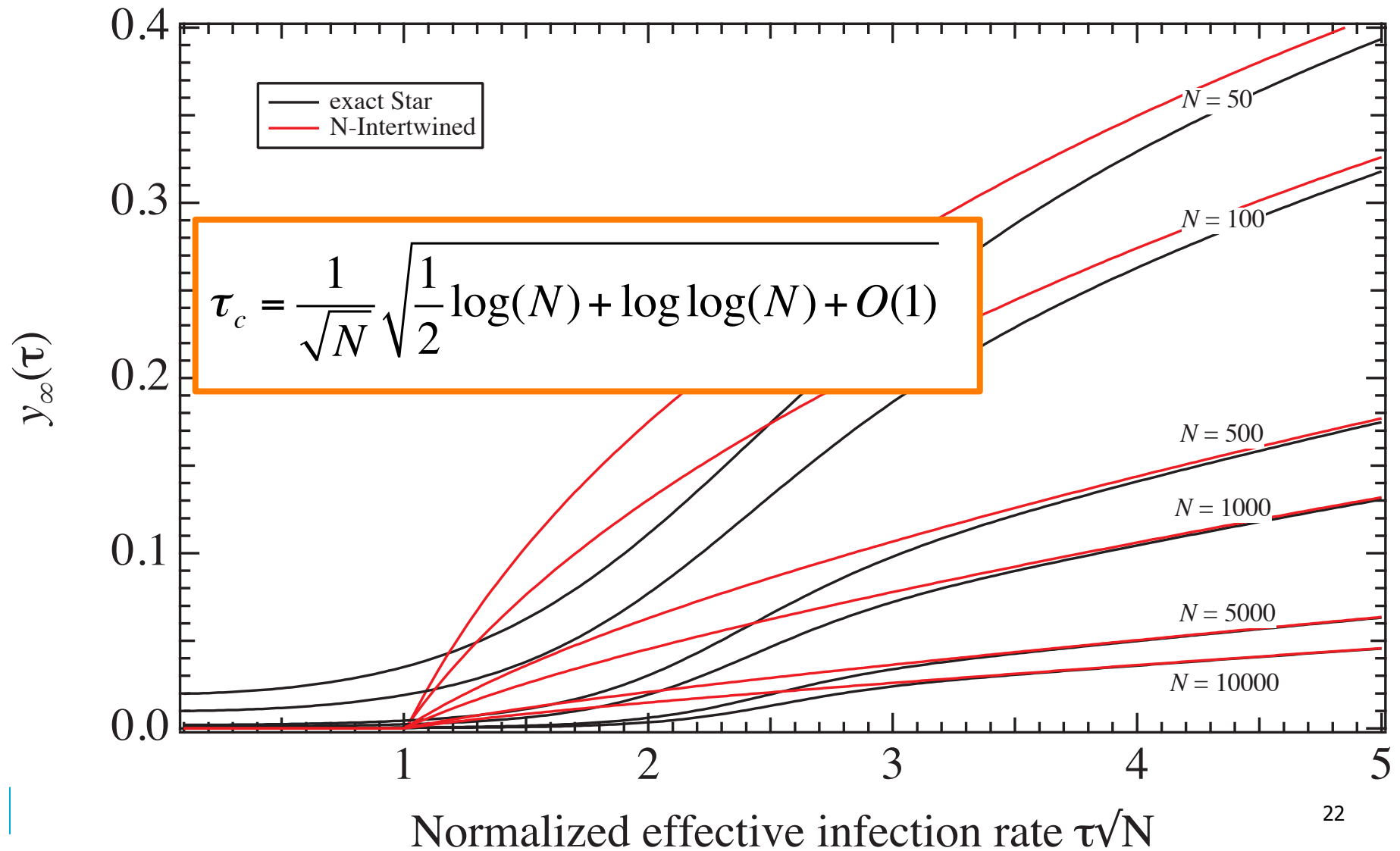
MSIS Markov Chain Star



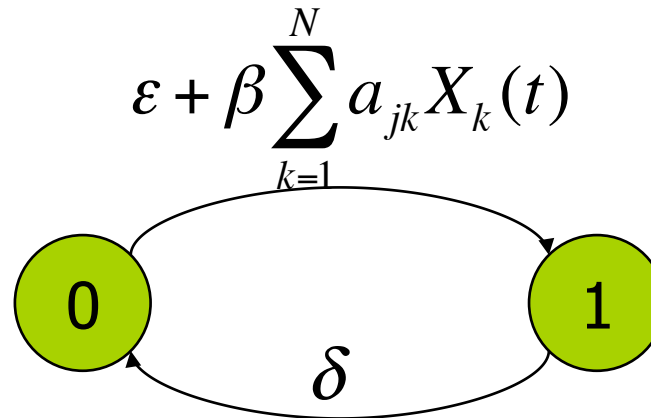
Simulations



Star graph



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

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

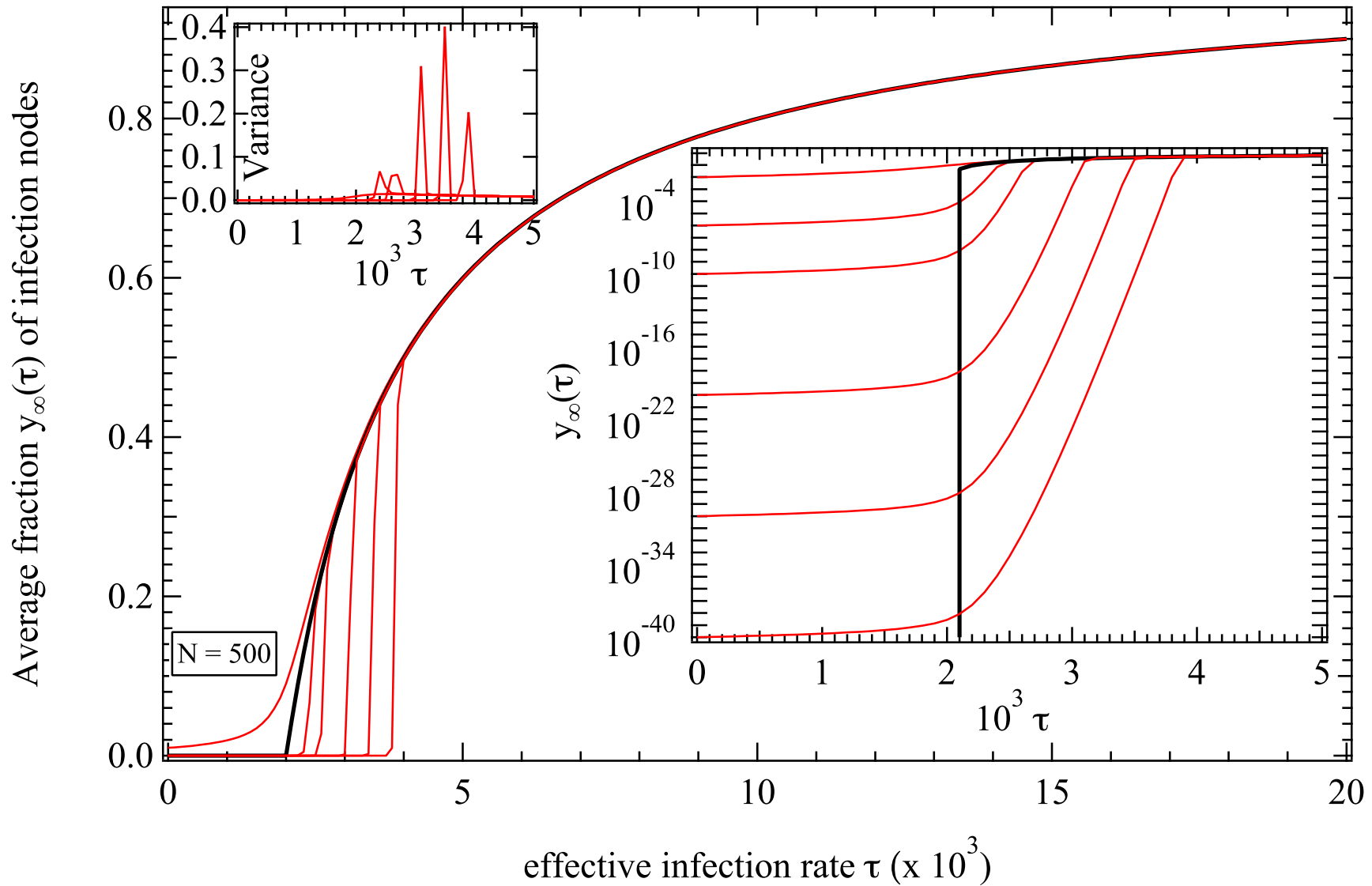
$$\tau = \frac{\beta}{\delta}$$

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

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

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

ε -SIS epidemics on the complete graph



HMF mean-field approximation

governing eq.:

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

steady-state:

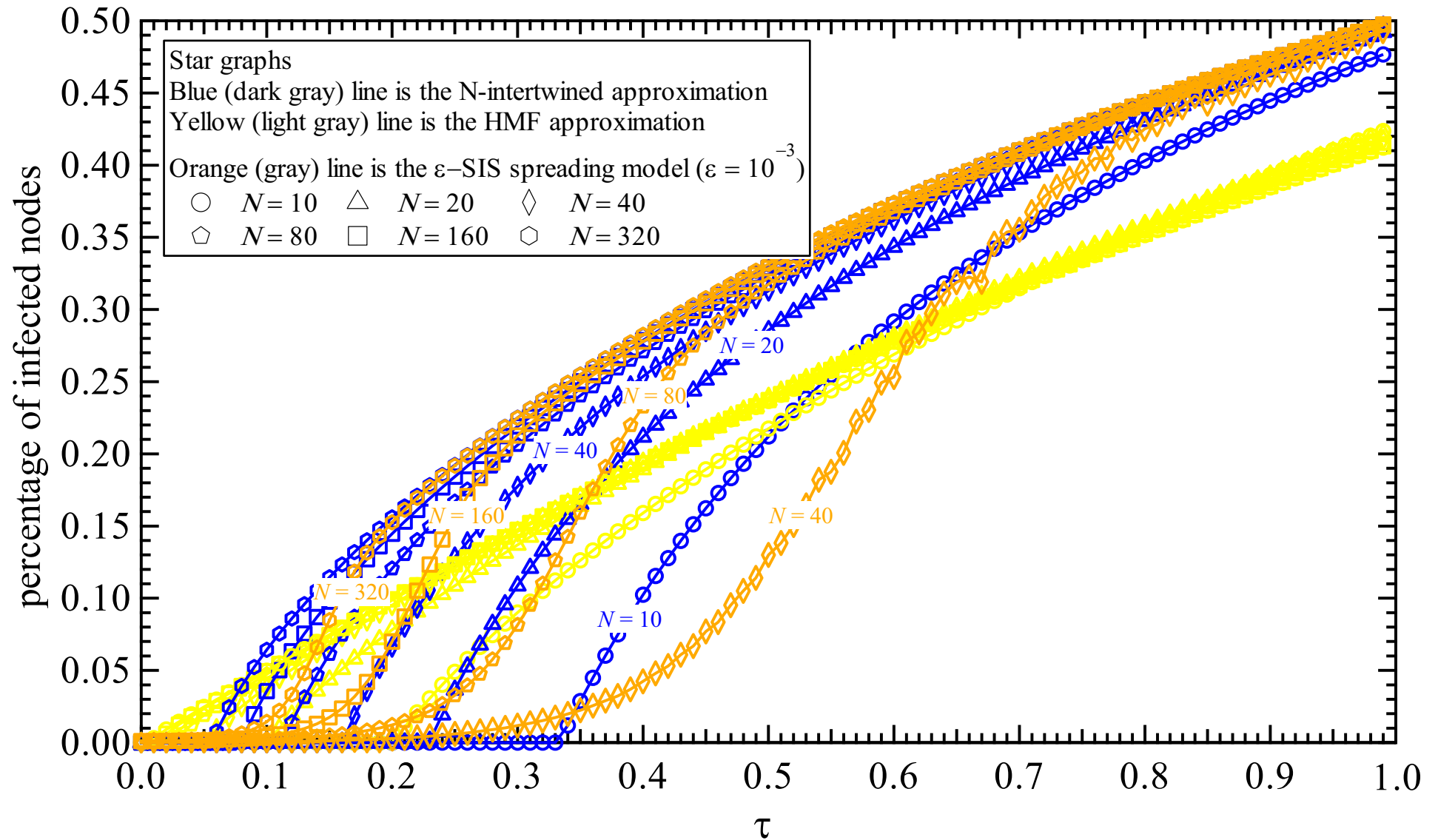
$$\rho_k(\tau) = \frac{\tau k \Theta(\tau)}{1 + \tau k \Theta(\tau)} \quad \tau = \frac{\beta}{\delta}$$

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

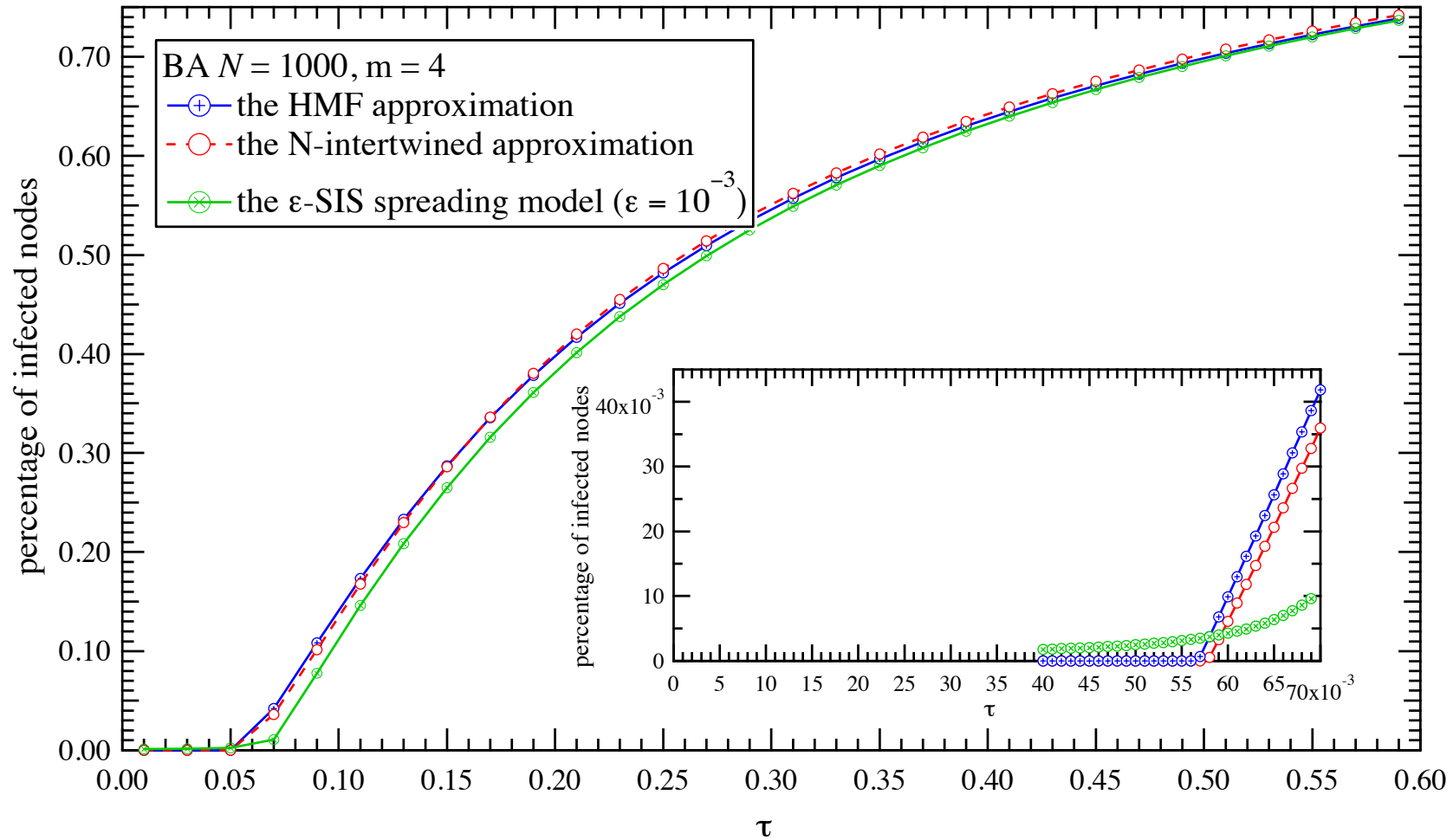
HMF epidemic threshold:

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

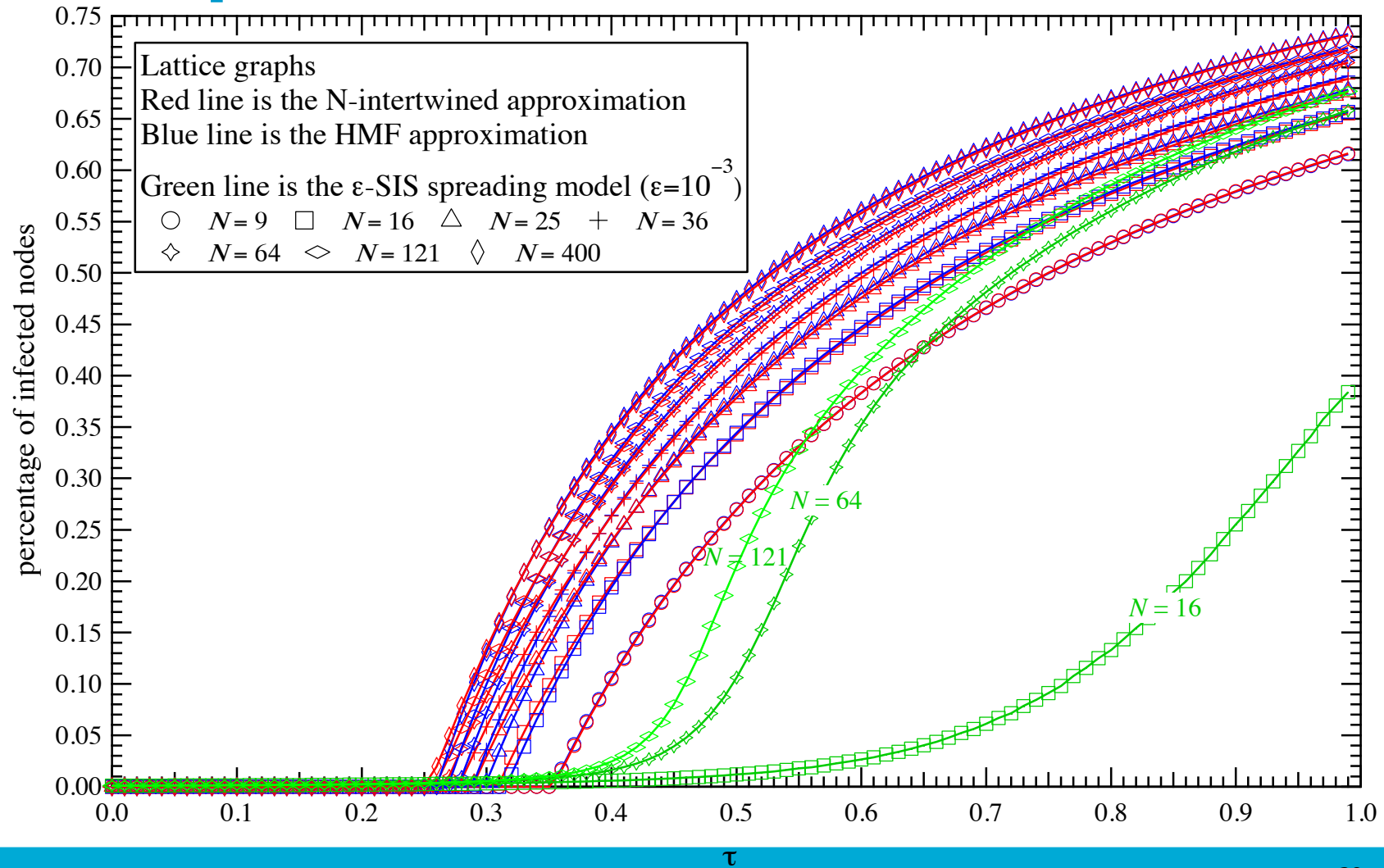
Comparison: star graph



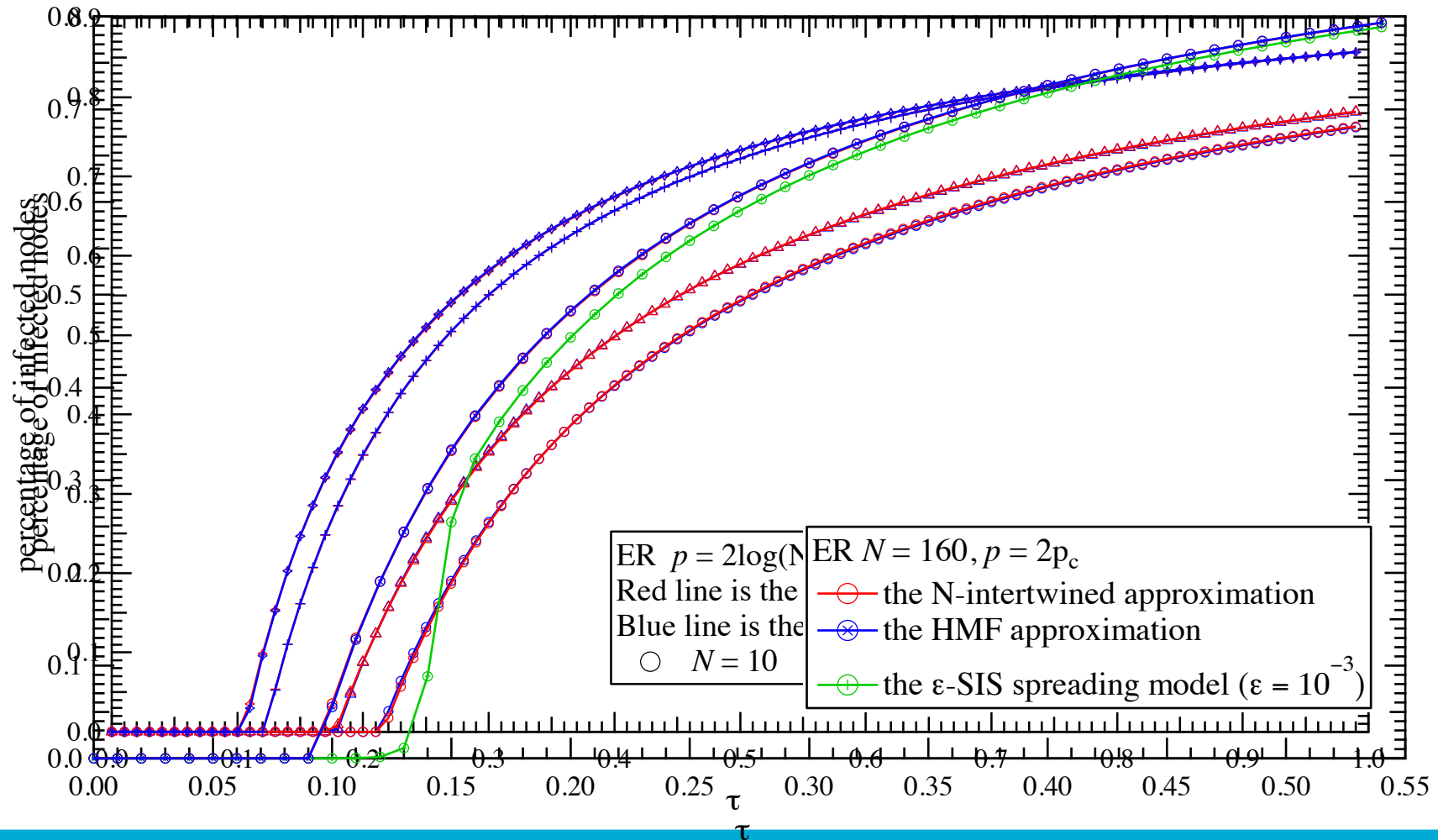
Comparison: BA



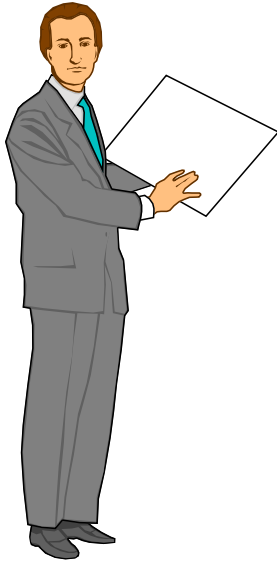
Comparison: Lattice



Comparison: ER graph (close to p_c)



Outline



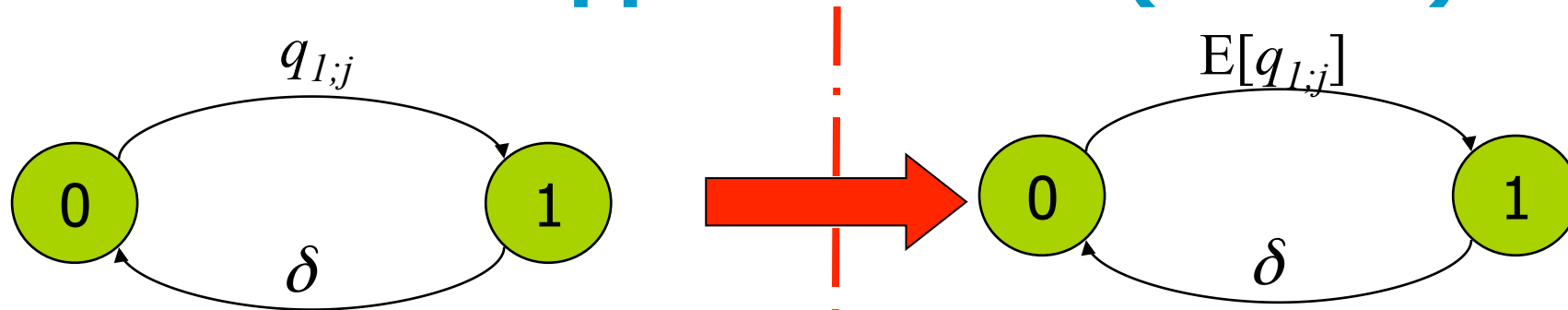
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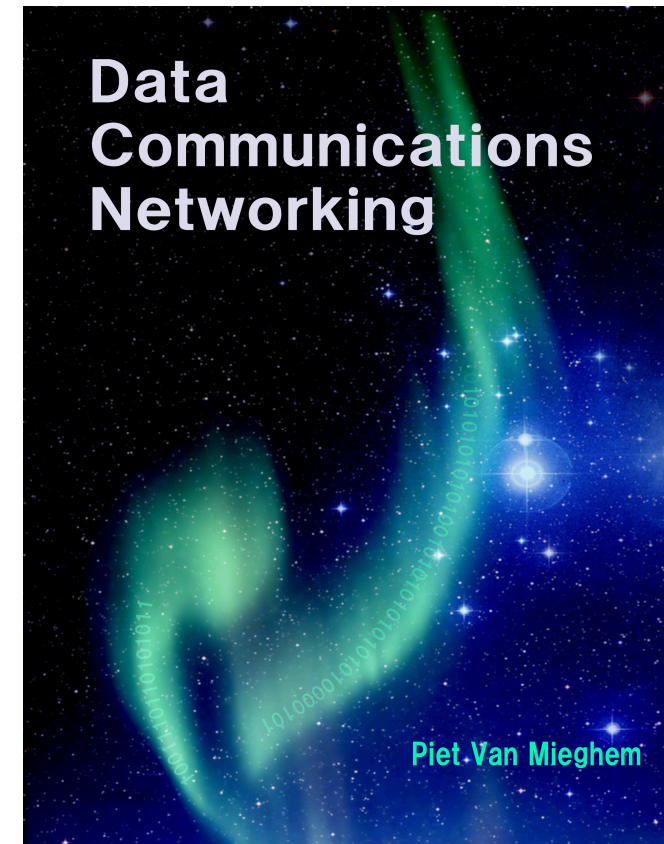
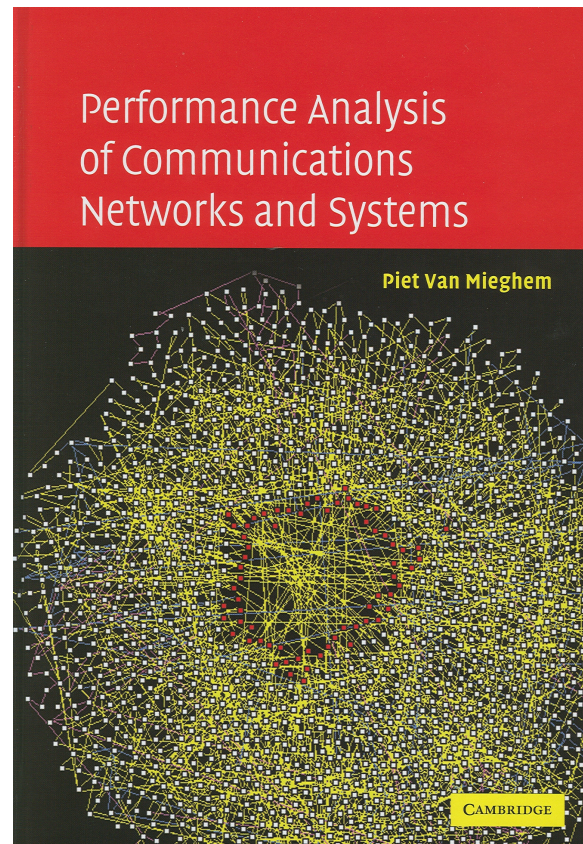
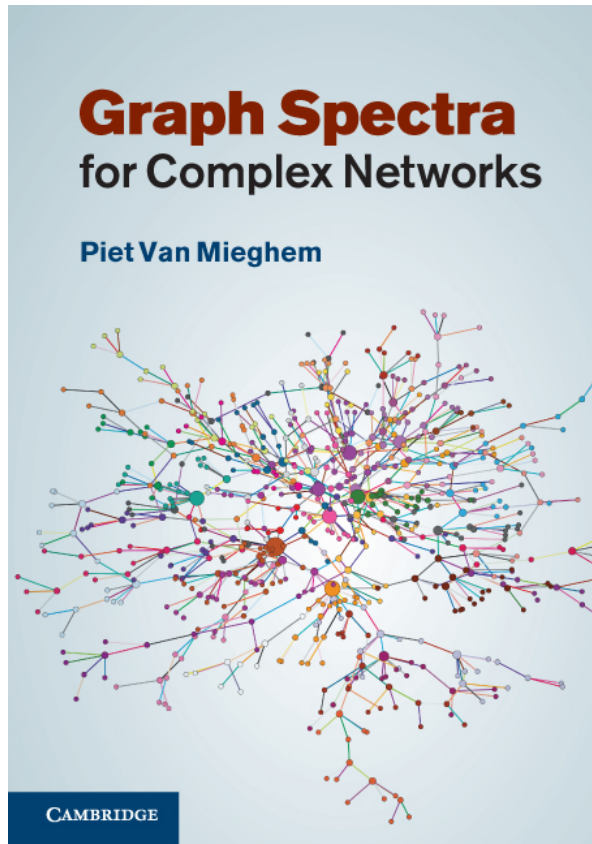
Mean-field approximation (NIMFA)



- 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

Books



Articles: <http://www.nas.ewi.tudelft.nl>

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A photograph of a modern architectural structure, likely a library or lecture hall, featuring a prominent conical roof with a metal framework. The building is situated on a green hillside with a wide, sloping ramp or walkway. The sky is blue with scattered white clouds. The text "Thank You" is overlaid in the center of the image.

Thank You

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