

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

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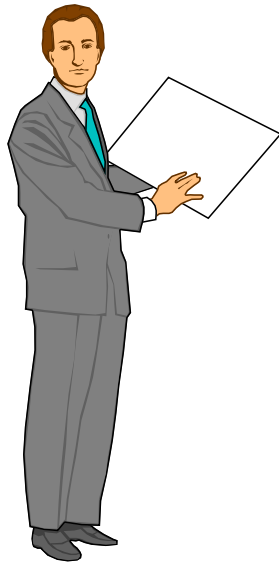
Outline

Exact SIS model

NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

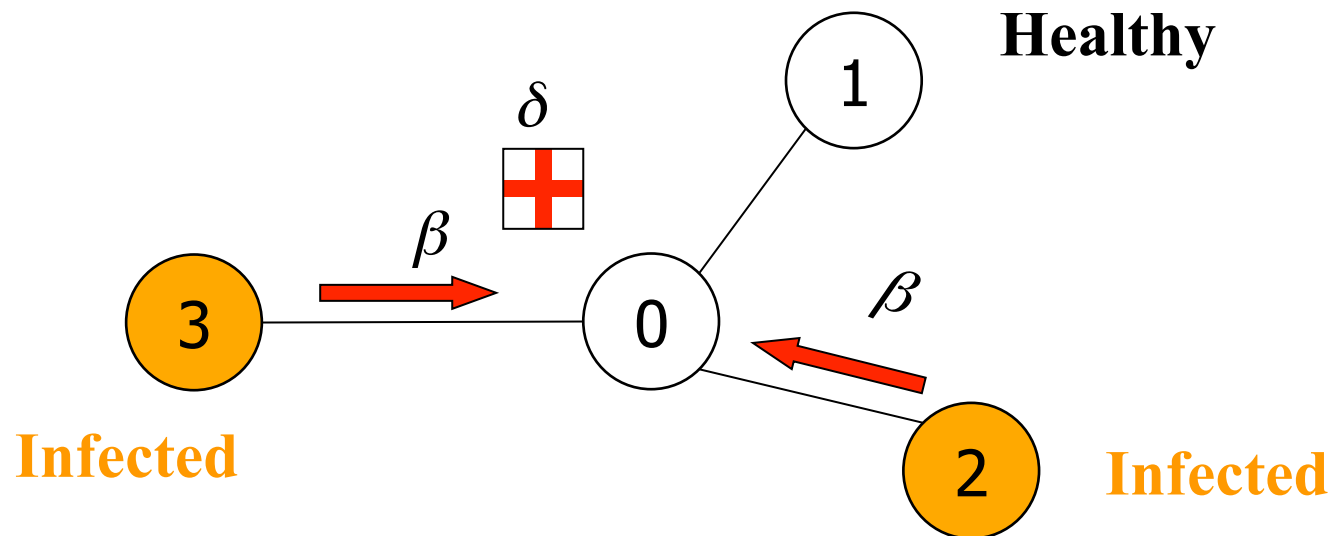
Non-Markovian epidemics



Simple SIS model on networks

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

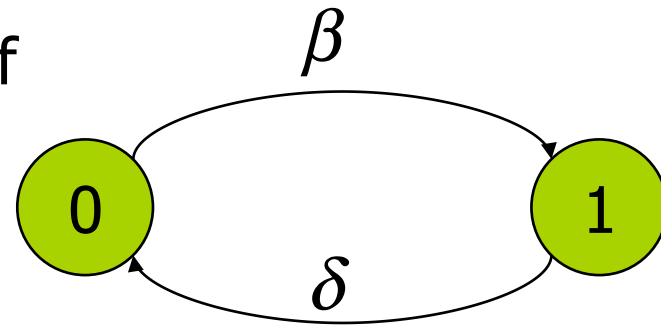
$\tau = \beta / \delta$: effective spreading rate



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 β
 - curing rate δ
- At time t :

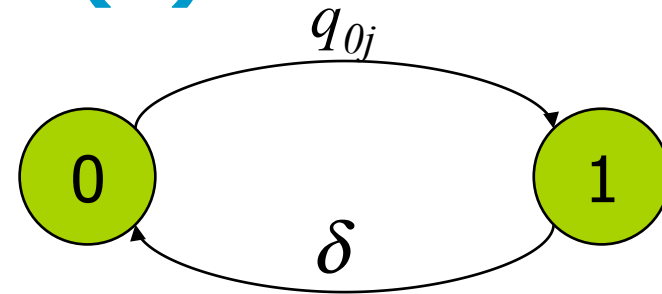


- $X_j(t)$ is the state of node j
- infinitesimal generator $Q_j(t) = \begin{bmatrix} -q_{0j} & q_{0j} \\ q_{1j} & -q_{1j} \end{bmatrix} = \begin{bmatrix} -q_{0j} & q_{0j} \\ \delta & -\delta \end{bmatrix}$

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

$$A = \begin{bmatrix} a_{11} & a_{12} & \dots & a_{1N} \\ a_{21} & a_{22} & \dots & a_{2N} \\ \vdots & \vdots & \ddots & \vdots \\ a_{N1} & a_{N2} & \dots & a_{NN} \end{bmatrix}$$

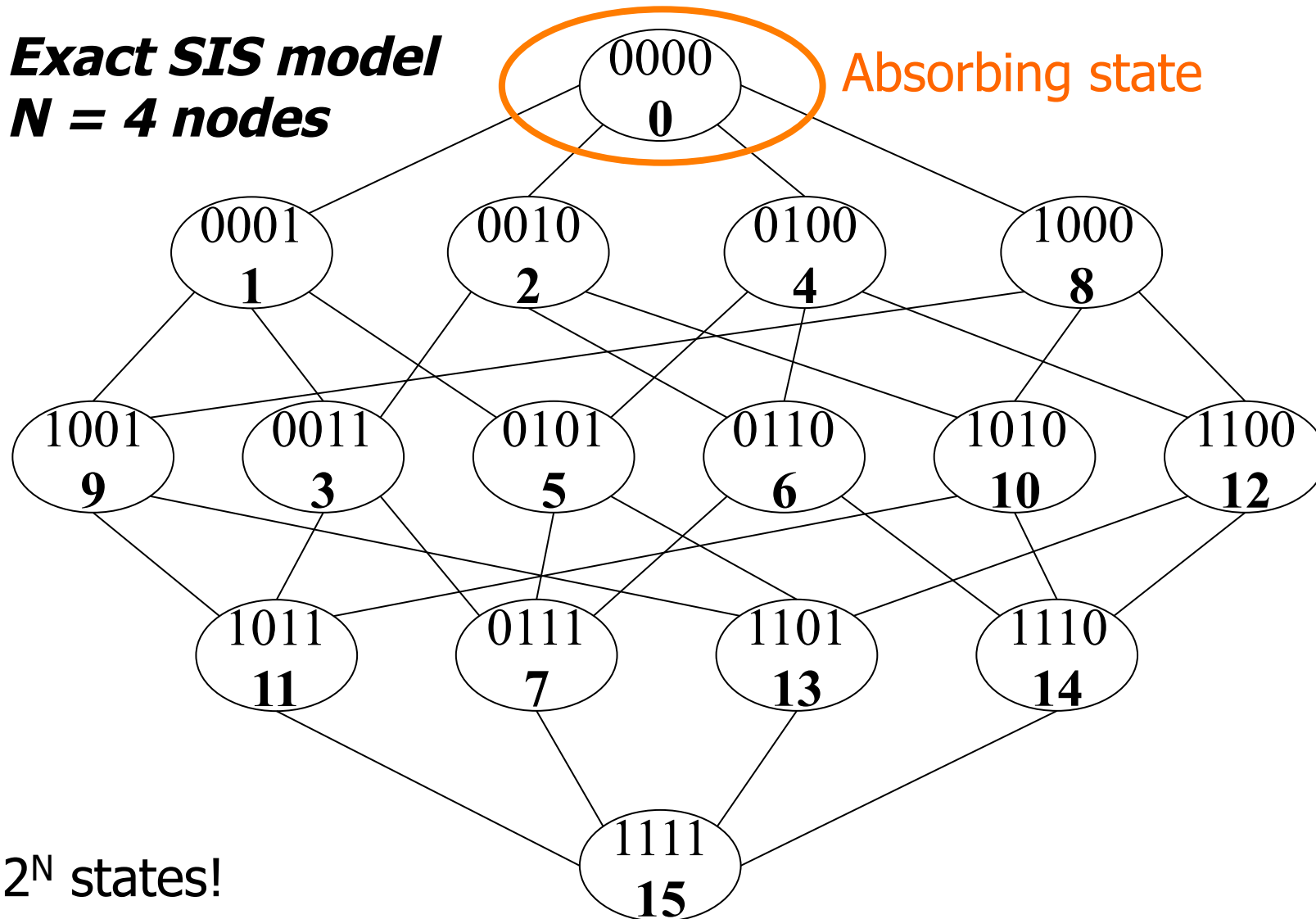
SIS model on networks (3)

- 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.

Exact SIS model
 $N = 4$ nodes



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

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

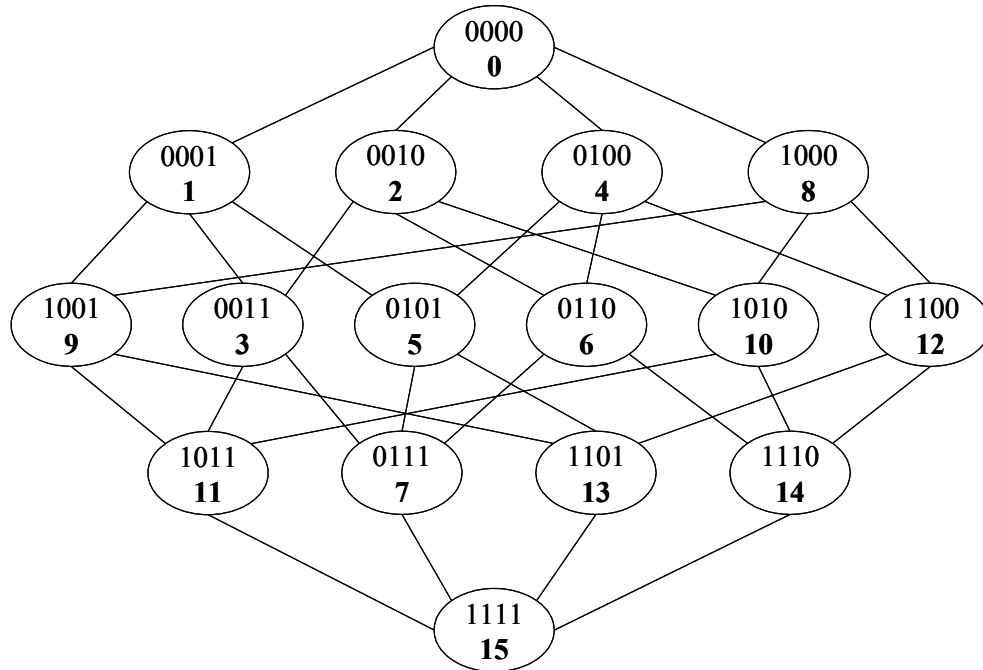
Joint probabilities

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

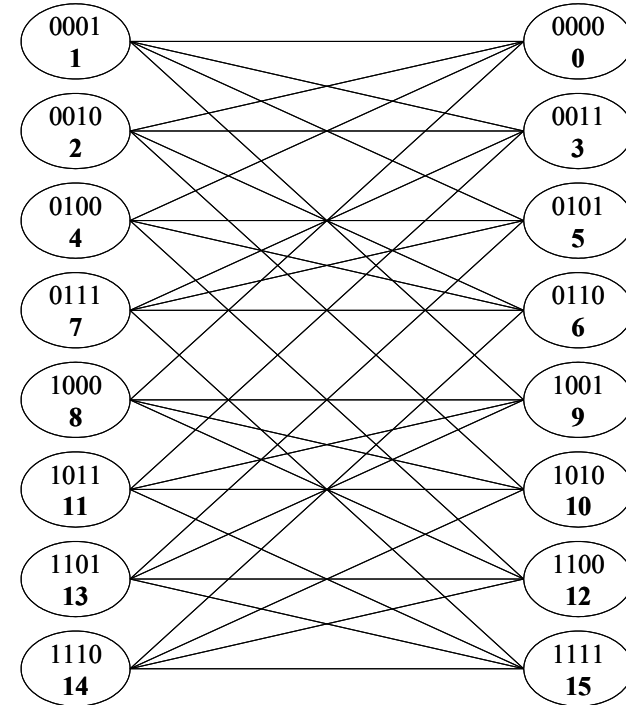
Next, we need the $\binom{N}{3}$ differential equations for $E[X_i X_j X_k] \dots$

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

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



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NIMFA: N-intertwined MF approximation

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NIMFA: N-intertwined mean-field approxim.

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

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

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

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

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

NIMFA non-linear equations

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

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

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

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

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

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

What is so interesting about epidemics?

network protection

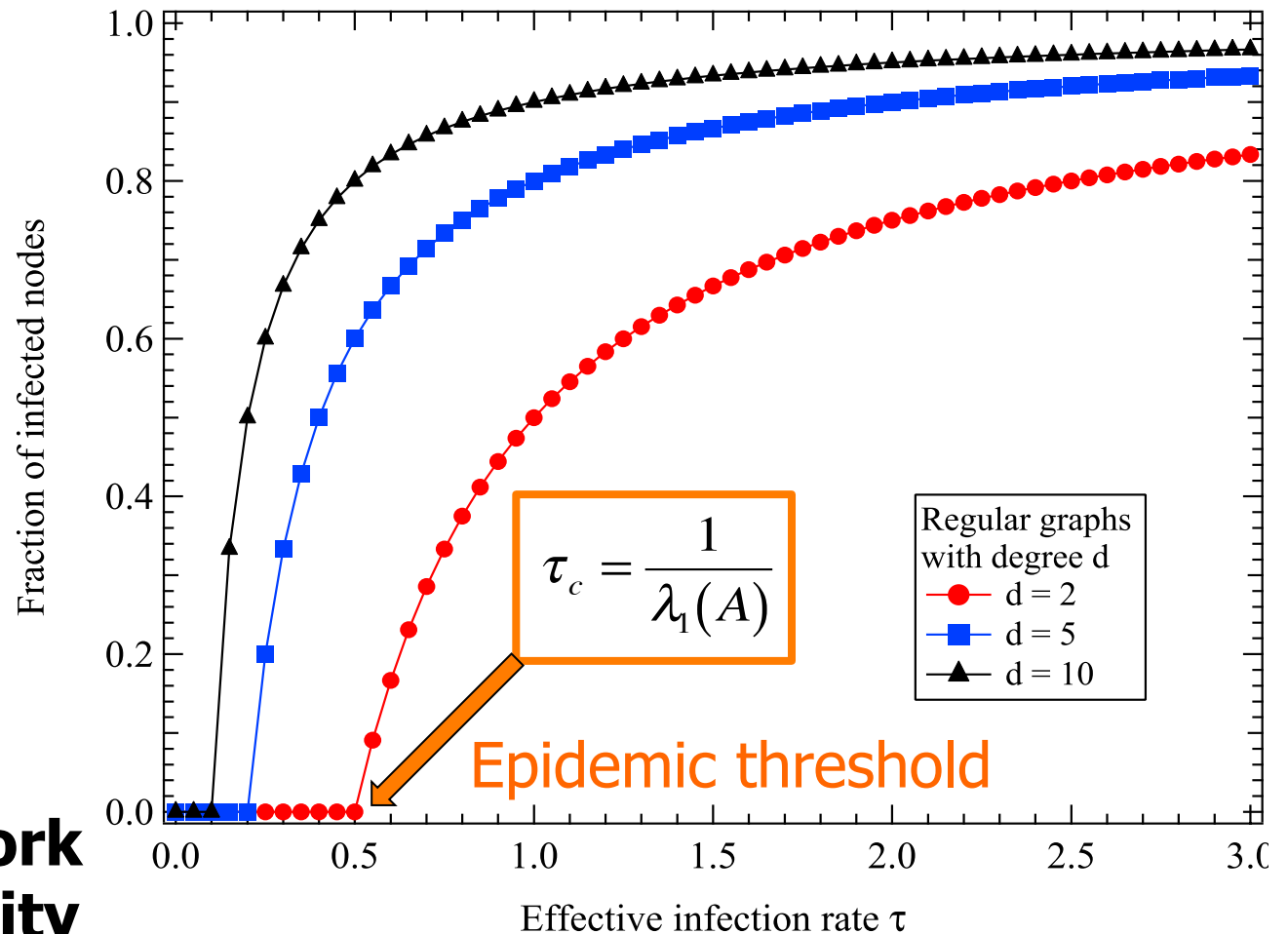
self-replicating
objects (worms)

propagation errors

rumors (social nets)

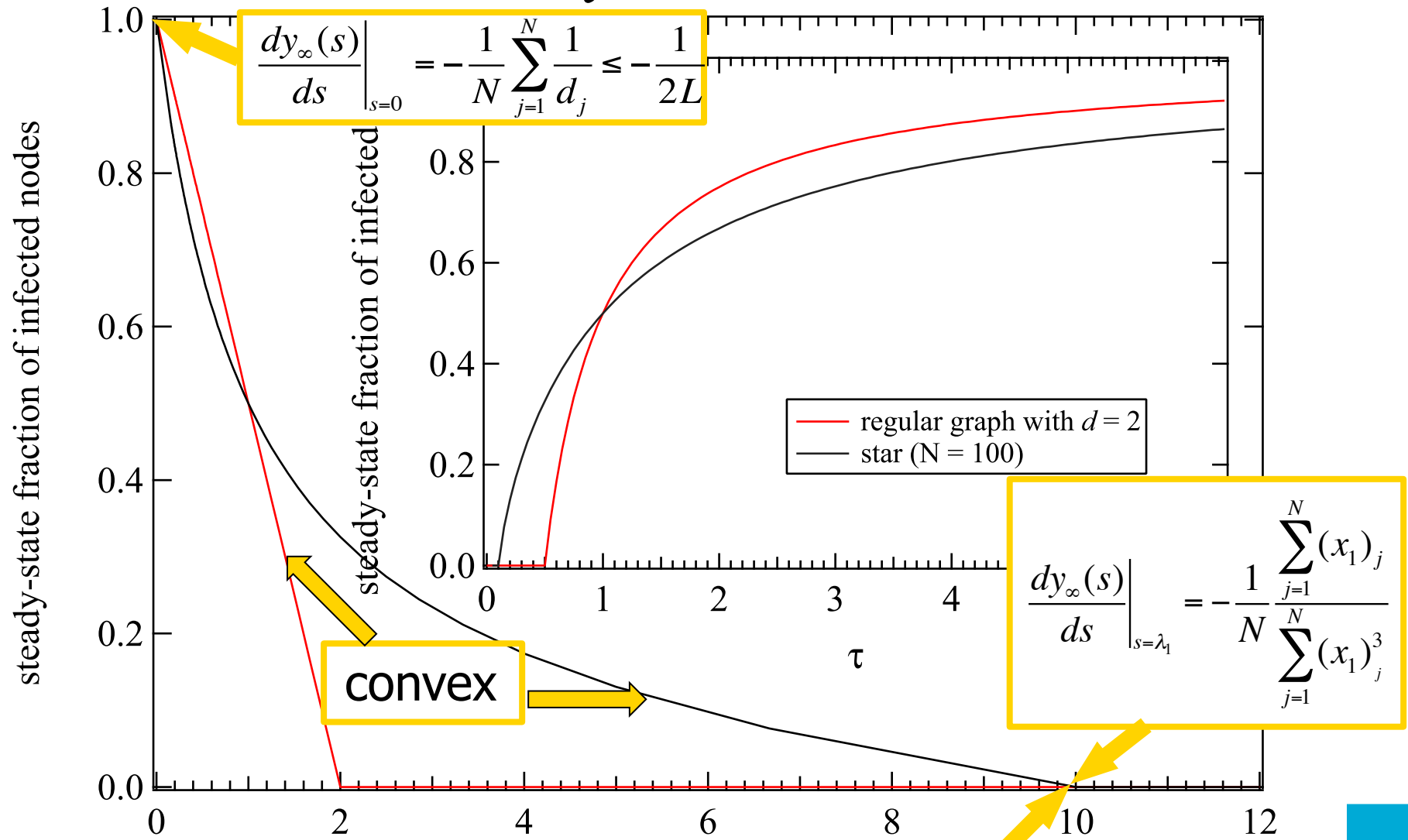
epidemic algorithms
(gossiping)

**cybercrime : network
robustnes & security**



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

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

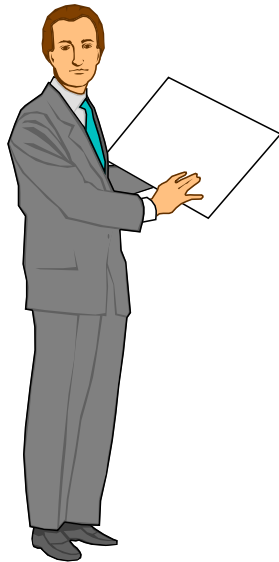


Van Mieghem, P., 2012, "Epidemic Phase Transition of the SIS-type in Networks", *Europhysics Letters (EPL)*, Vol. 97, Februari, p. 48004.

Extensions of the NIMFA

- In-homogeneous: each node i has own β_i and δ_i :
P. Van Mieghem and J. Omic, "In-homogeneous Virus Spread in Networks", (arxiv.org/1306.2588)
- SAIS (Infected, Susceptible, Alert) instead of SIS:
"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, *IEEE/ACM Transactions on Networking*, 2013 (on-line 10.1109/TNET.2013.2239658)
- Interdependent networks
Wang, H., Q. Li, G. D'Agostino, S. Havlin, H. E. Stanley and P. Van Mieghem, 2013, "Effect of the Interconnected Network Structure on the Epidemic Threshold", *PRE*, to appear.

Outline



Exact SIS model

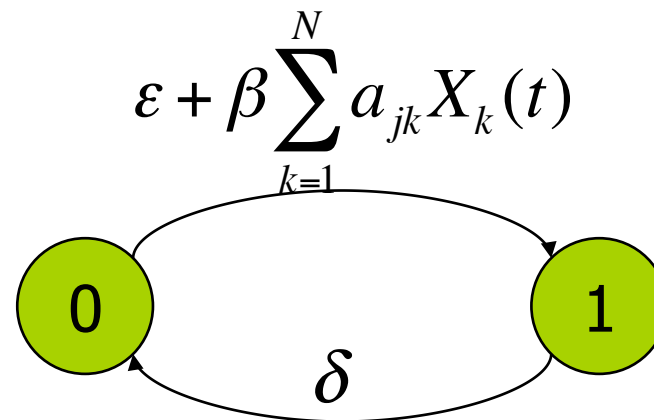
NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

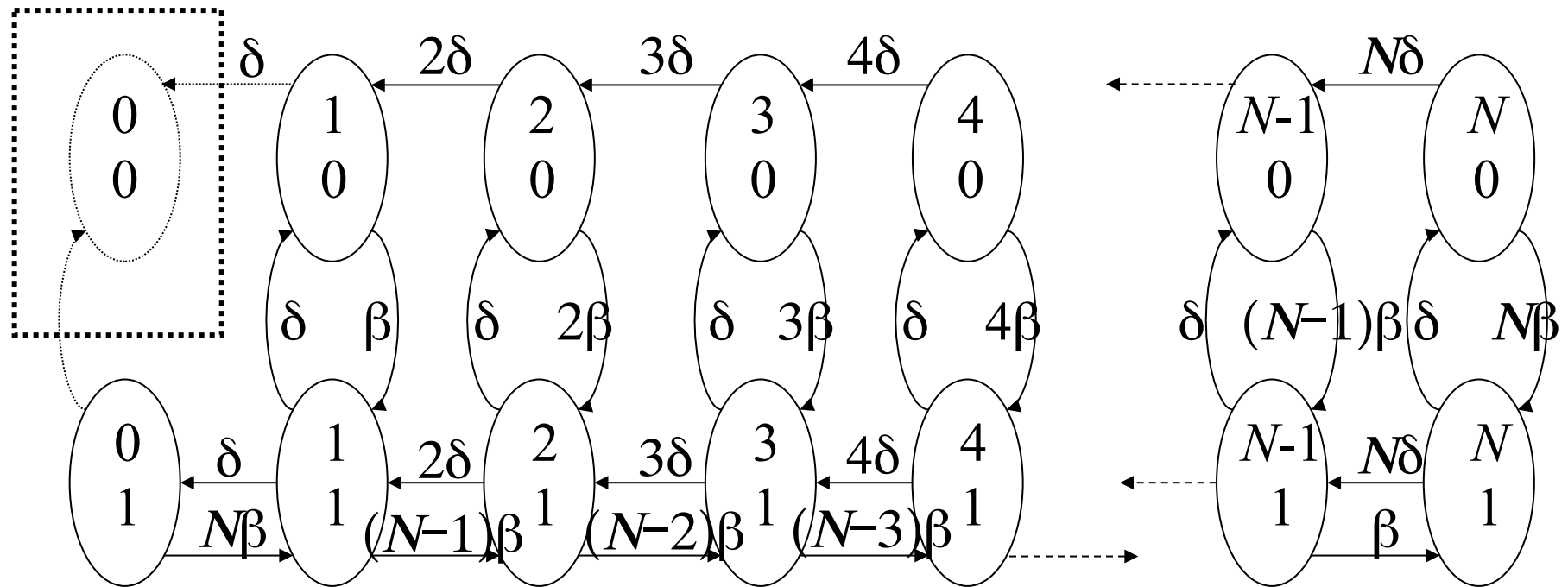
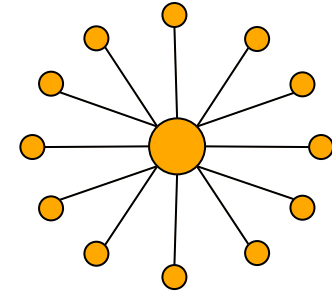
Non-Markovian epidemics

Defining the SIS epidemic threshold

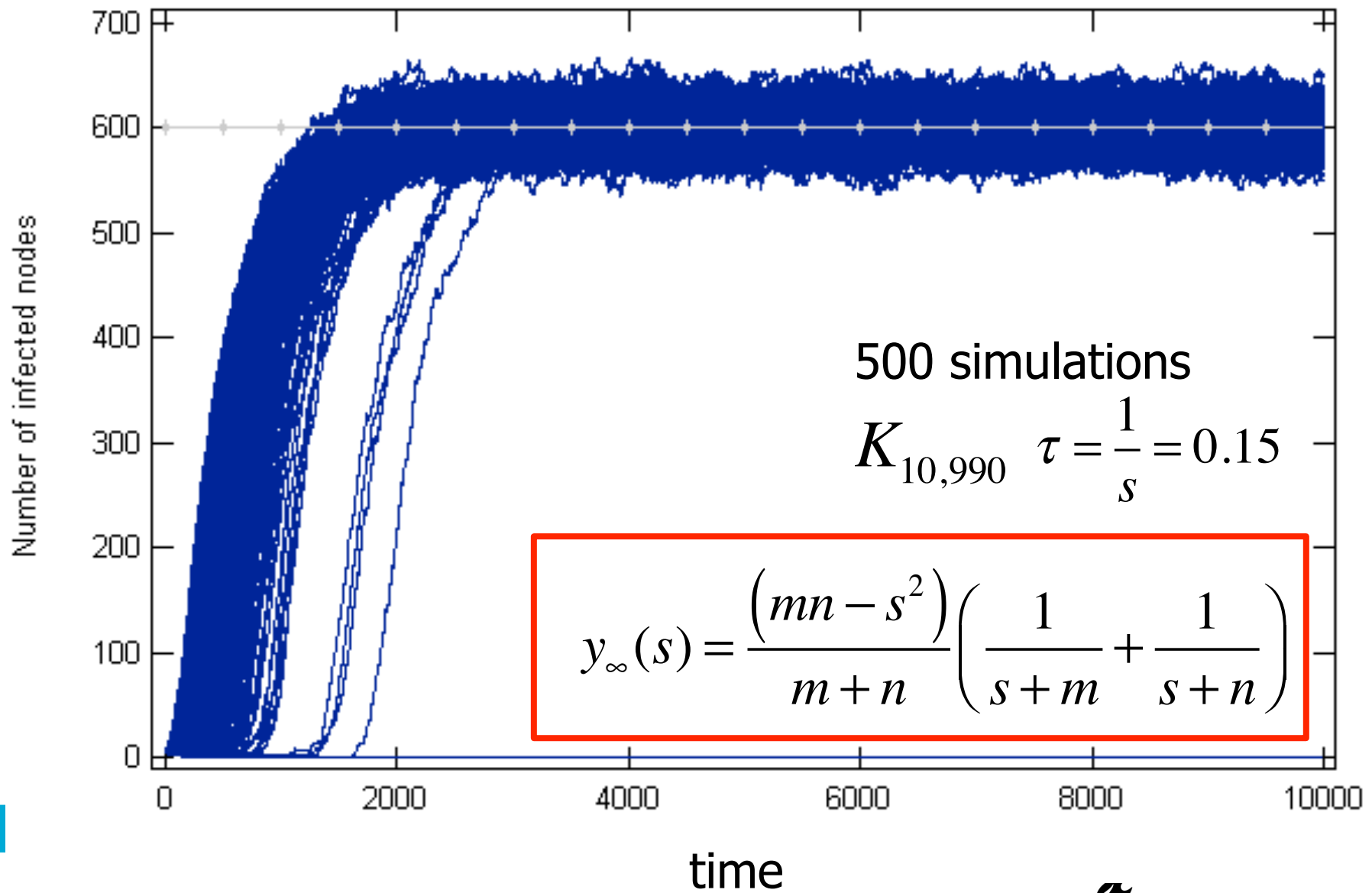
- Exact SIS steady-state (finite N):
 - overall healthy state (physically not interesting)
- Metastable (or quasi-stationary) state:
 - not defined, but physically interesting
- **Two approaches:**
 - modified SIS Markov chain (excluding overall healthy state)
 - ε -SIS Markov model



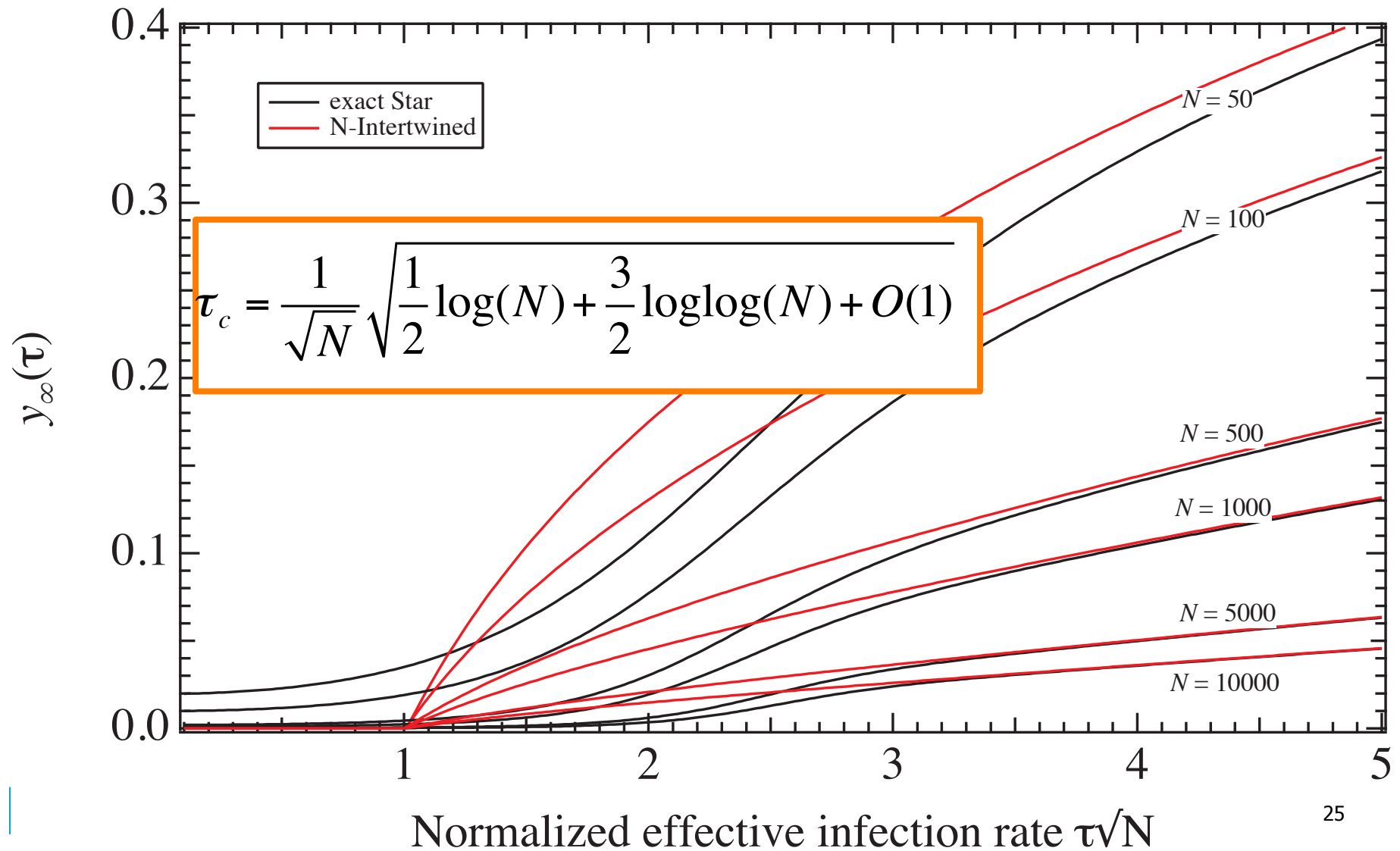
MSIS Markov Chain Star



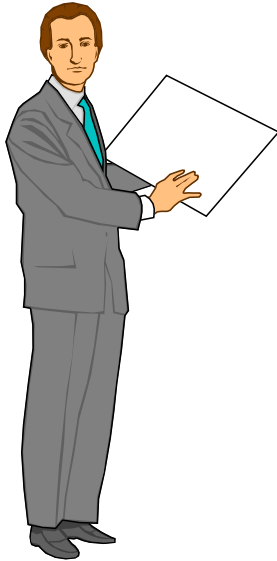
Simulations



Star graph



Outline



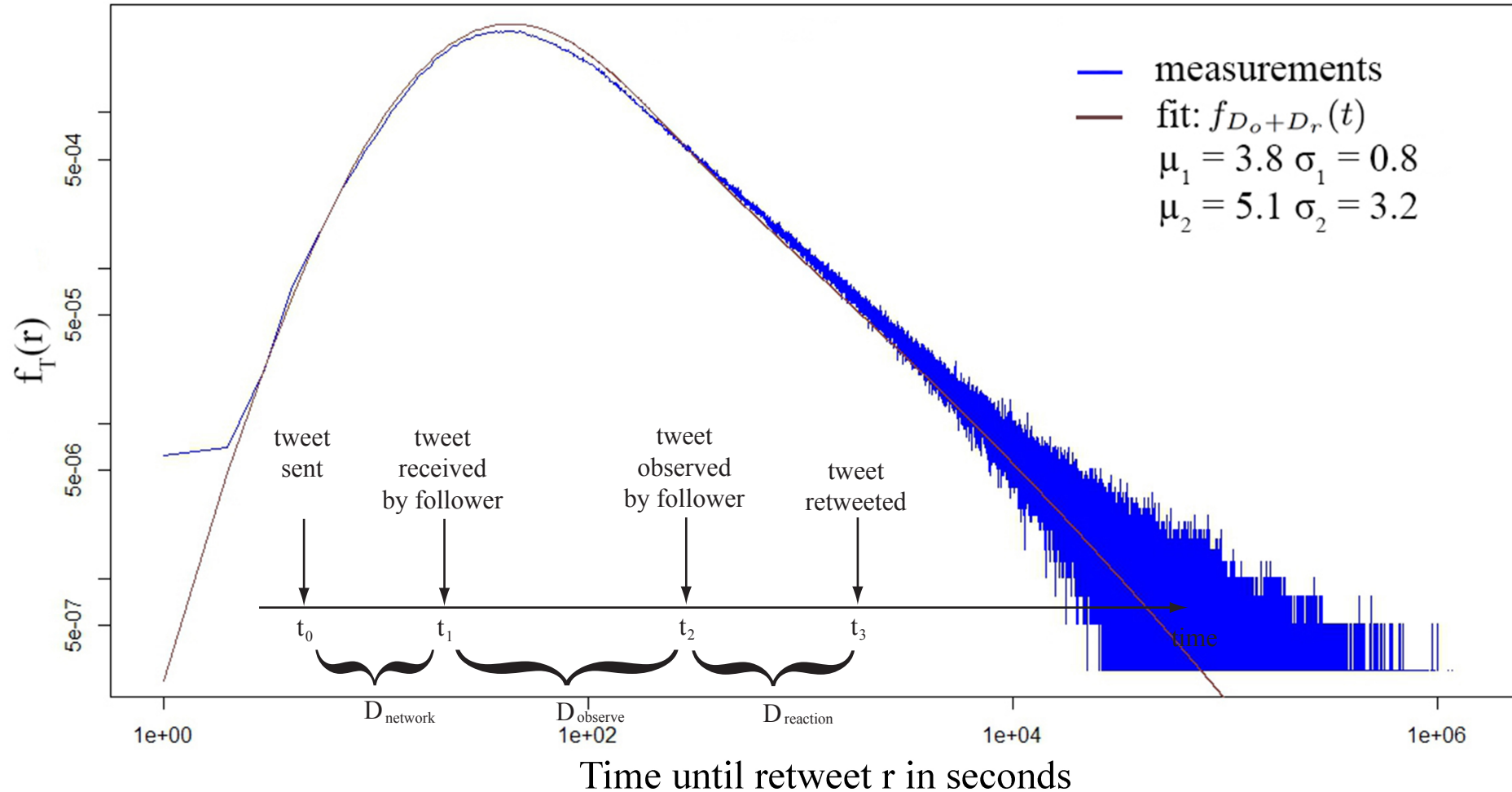
Exact SIS model

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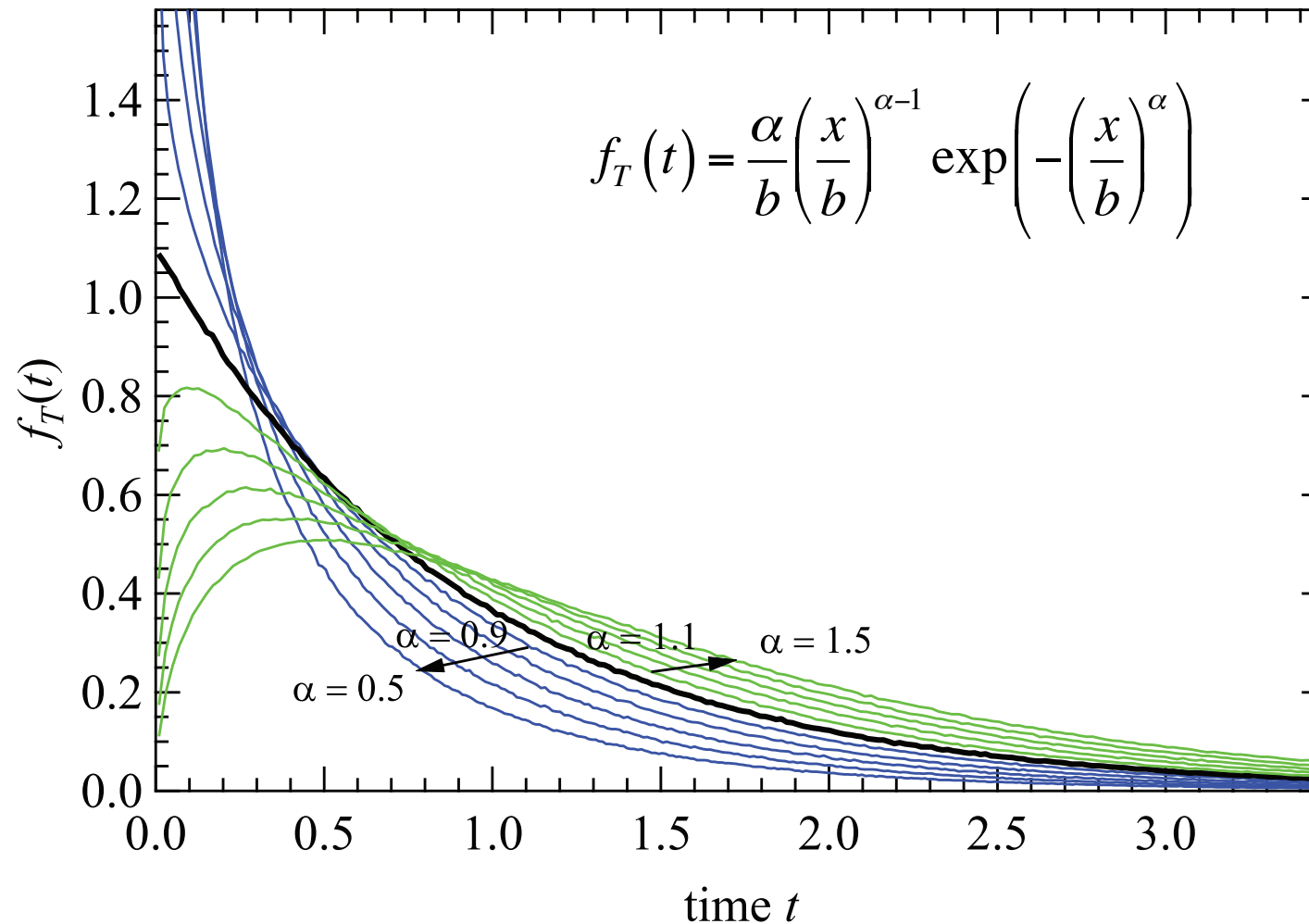
Defining the SIS epidemic threshold

Non-Markovian epidemics

Epidemic times are not exponential



Non-Markovian infection times

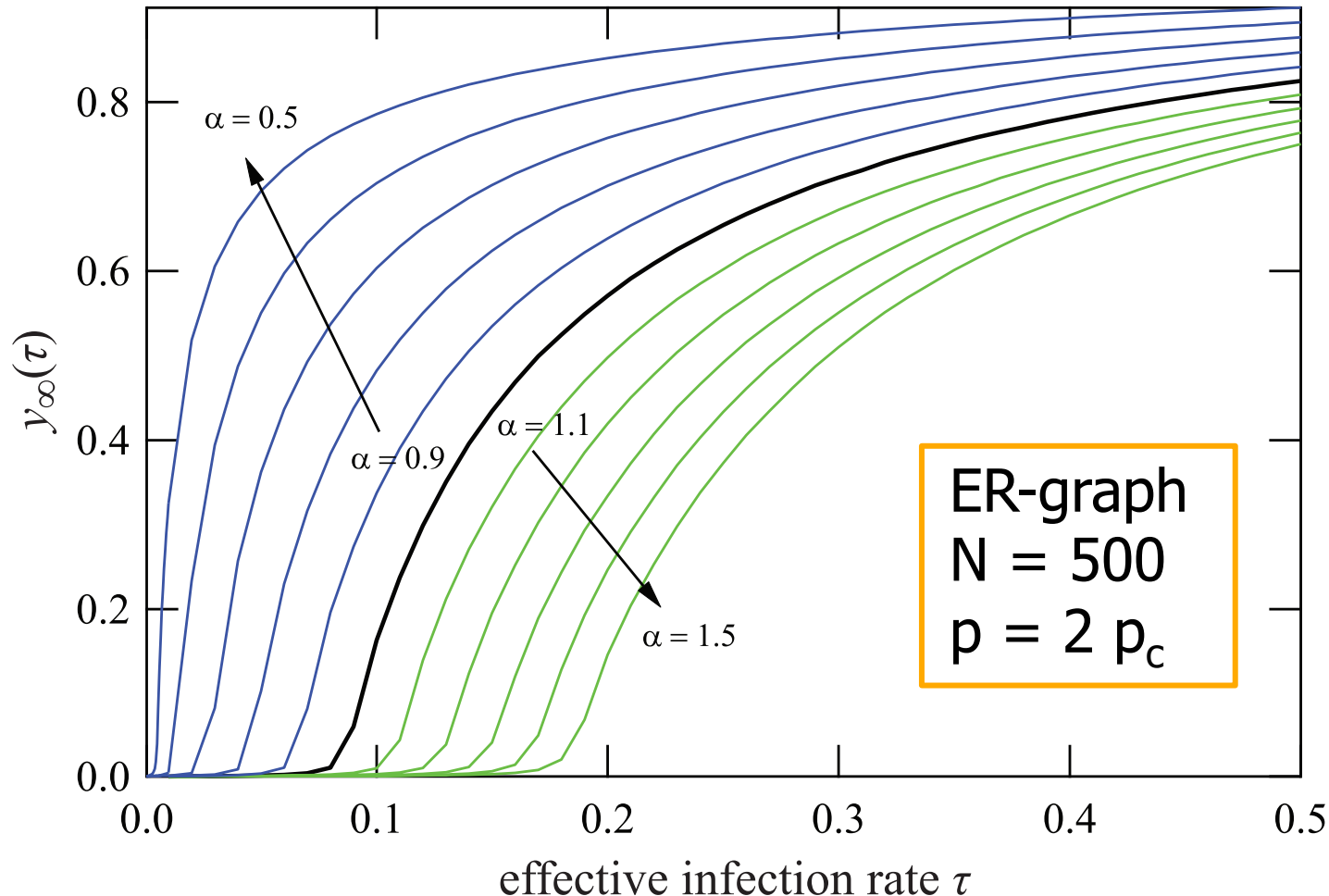


Same mean
 $E[T]$:


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

T is the time to infect a neighboring node

Non-Markovian epidemic threshold



Non-exponential infection time has a dramatic influence!

P. Van Mieghem and R. van de Bovenkamp, "Non-Markovian infection spread Dramatically alters the SIS epidemic threshold", Physical Review Letters, vol. 110, No. 10, March, p. 108701. 

GSIS: SIS with general infection times

NIMFA is valid provided the effective infection rate τ is replaced by the av. number $E[M]$ of infection events during a healthy period:

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

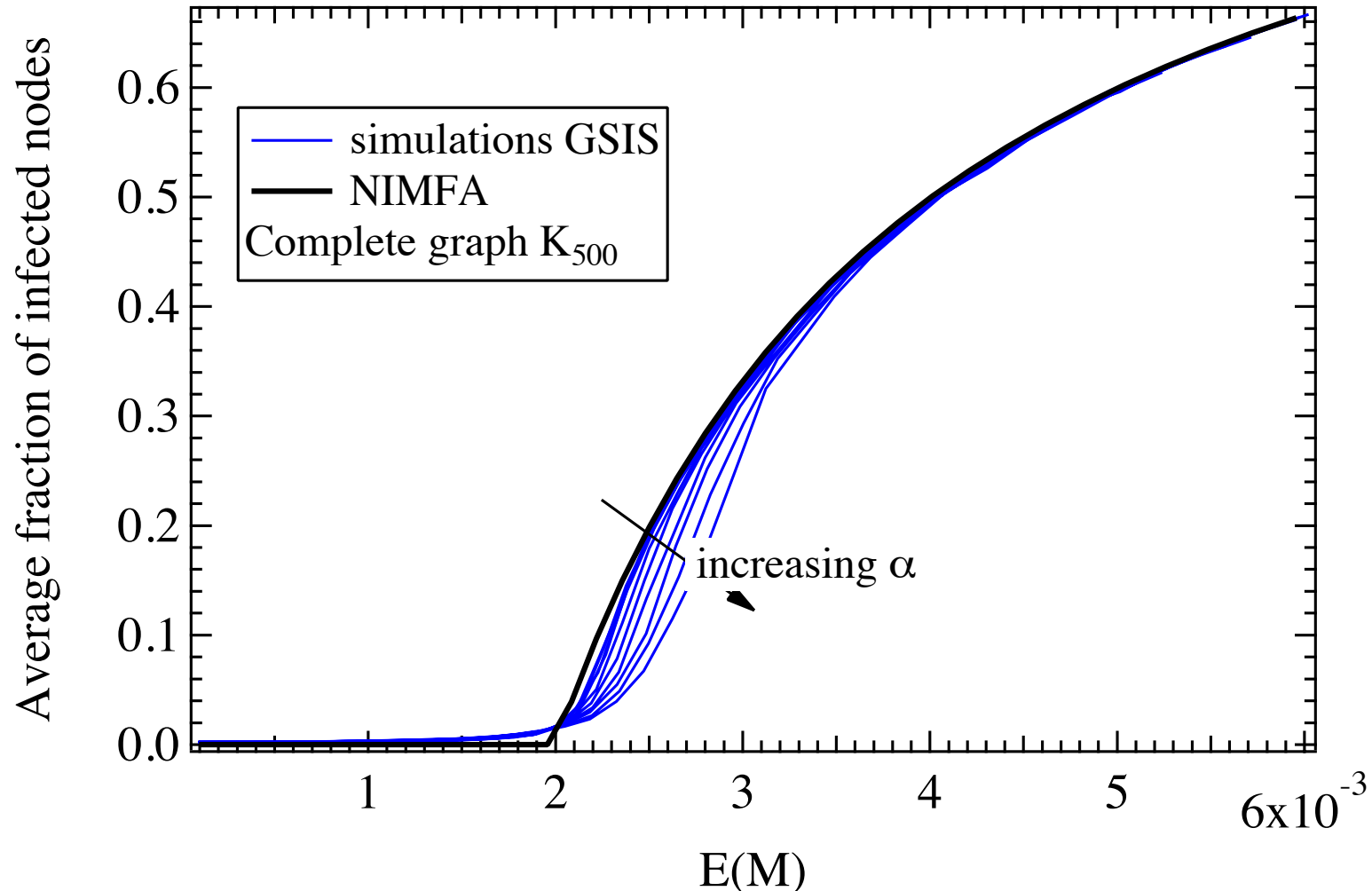
Generalized criterion for the epidemic threshold: $E[M_c] = \frac{1}{\lambda_1}$

Scaling law for large N

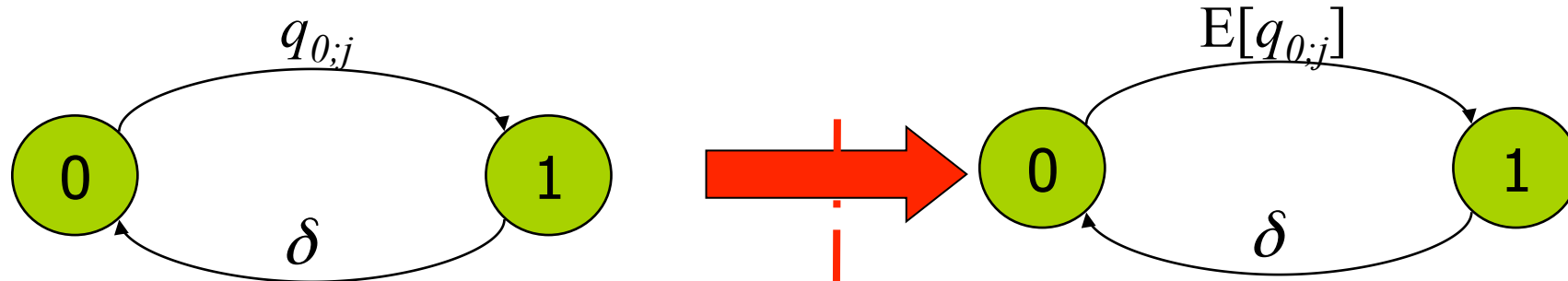
When infection time T is Weibullian:

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

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



Mean-field approximation (NIMFA)



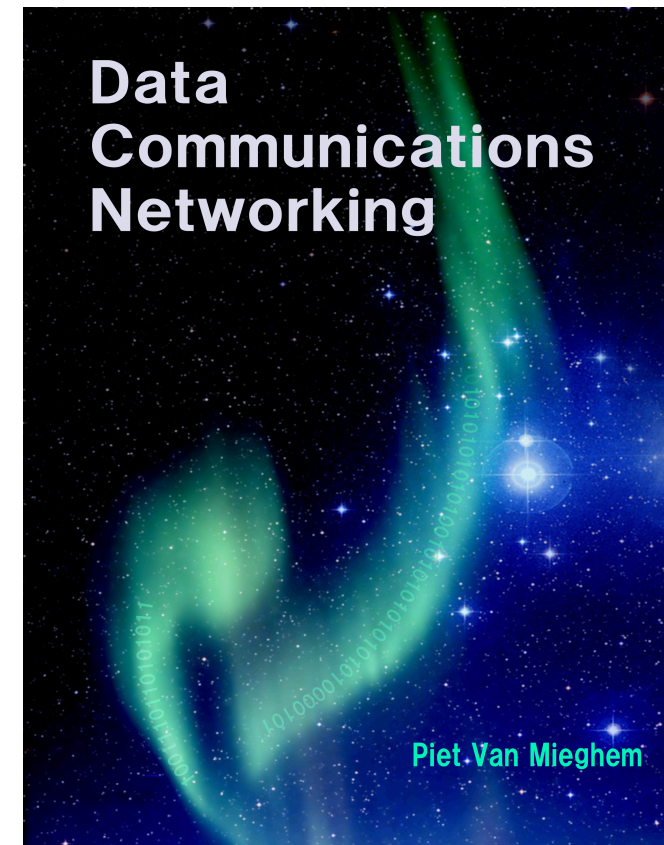
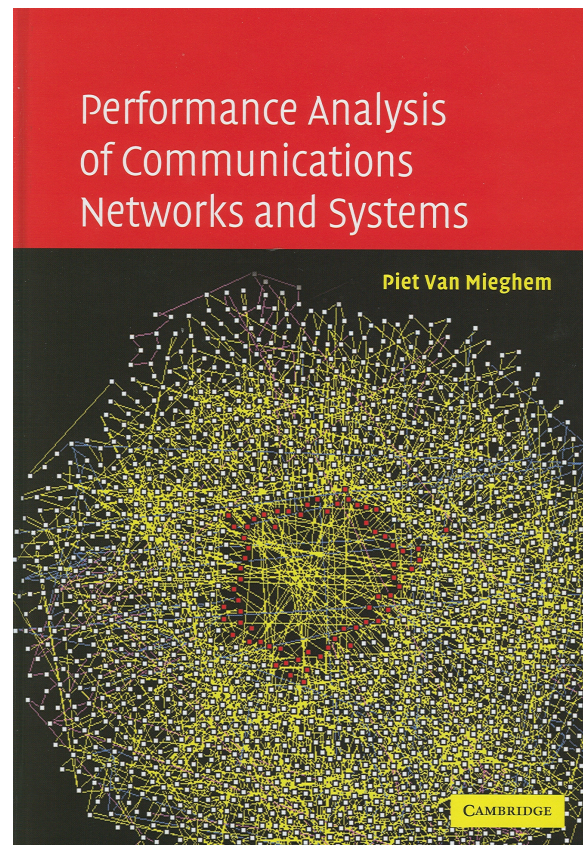
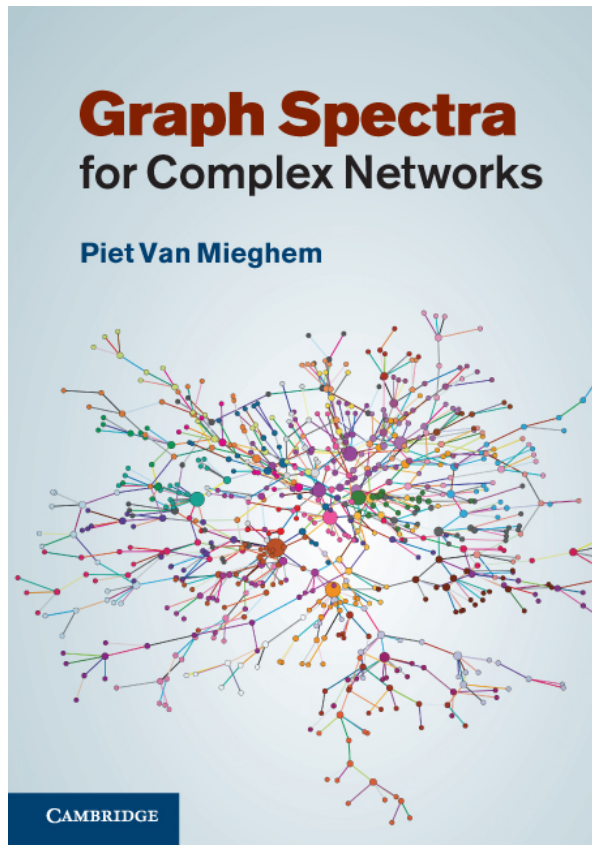
- 2^N linear equations
- Steady-state
 - absorbing (healthy) state
 - reached after unrealistically long time
- difficult to analyze
- **only** for exponential infection and curing times

- N non-linear equations
- Meta-stable state:
 - phase-transition
 - epidemic threshold
 - realistic
- analytically tractable
- lower bound epidemic threshold
- valid for **any** infection and/or curing time distribution

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 viruses on networks
- Measurements of epidemics (e.g. fraction of infected nodes) in real-world networks are scarce

Books



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

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A photograph of a modern architectural structure, likely a library or university building, featuring a prominent conical roof with a metal framework. The building is situated on a green hillside with a paved walkway and a person walking. The sky is blue with scattered white clouds.

Thank You

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