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

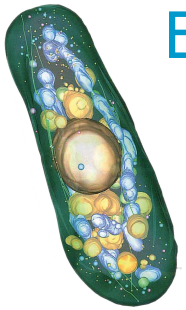
Piet Van Mieghem

in collaboration with Eric Cator, Ruud van de Bovenkamp, Cong Li

Informatik-Kolloquium, 25 Febr. 2013
University of Göttingen

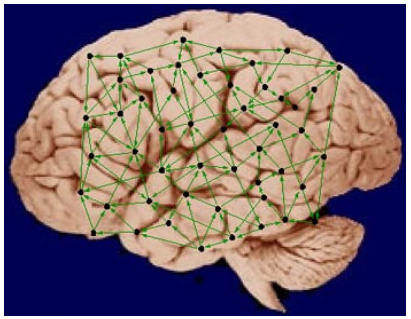
TU Delft

Effect of Network on Function



Biology

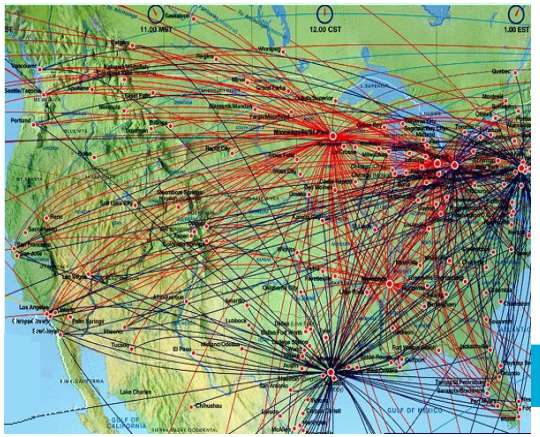
Brain



Economy

Network Science

Social networking

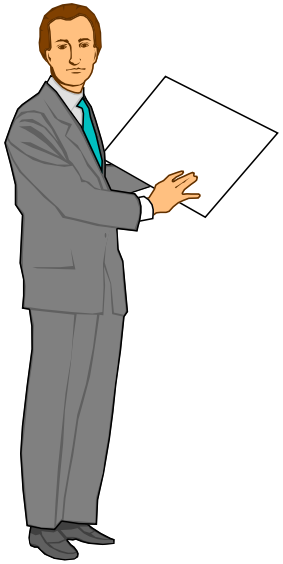


Man-made Infrastructures
Internet, power-grid

Nature-inspired Networking
to design superior man-made
robust networks/systems

TU Delft

Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

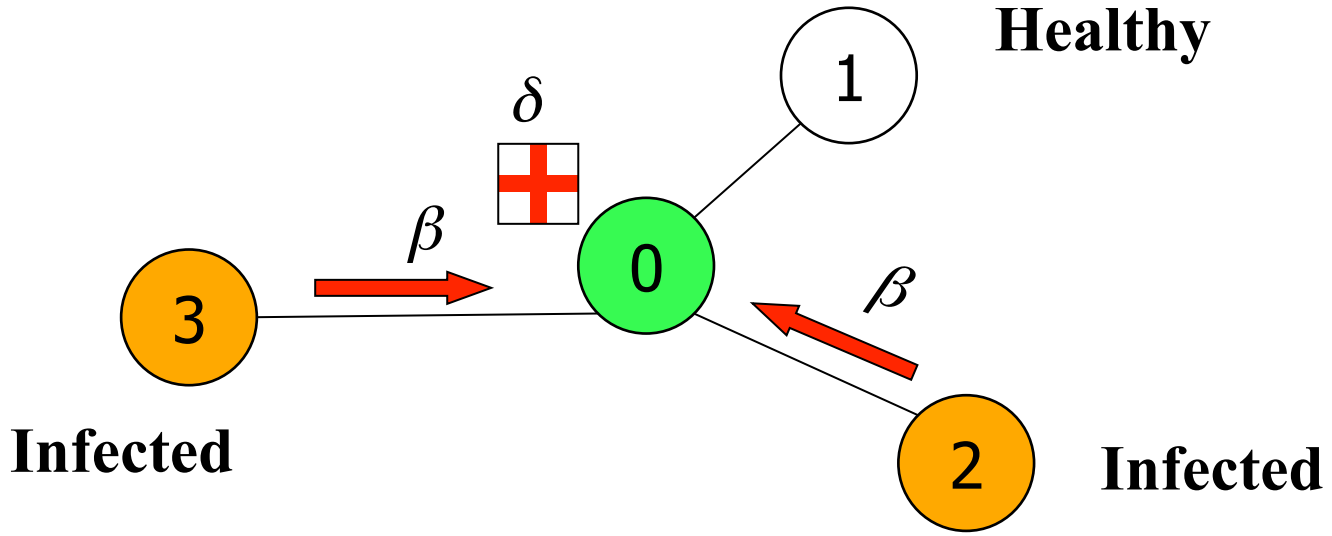
Defining the SIS epidemic threshold

Non-Markovian epidemics

Simple SIS model on networks

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

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

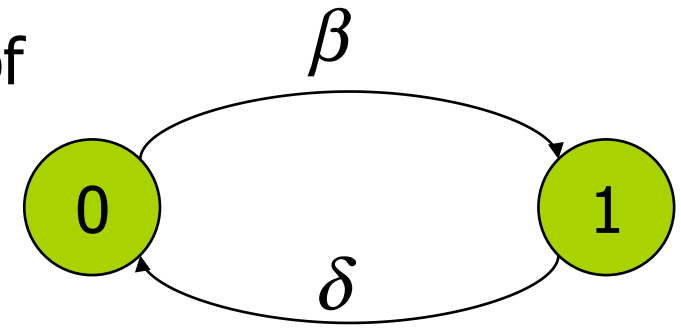


Infection and curing are independent Poisson processes

TU Delft

Definition of the states in SIS

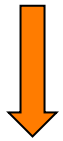
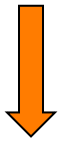
- Each node *j* can be in either of the two states:
  - "0": healthy
  - "1": infected
- **Markov continuous time**:
  - infection rate β
  - curing rate δ
- Mathematically:
  - X_j is the state of node j
  - infinitesimal generator $Q_j(t) = \begin{bmatrix} -q_{1j} & q_{1j} \\ q_{2j} & -q_{2j} \end{bmatrix}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



TU Delft

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

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

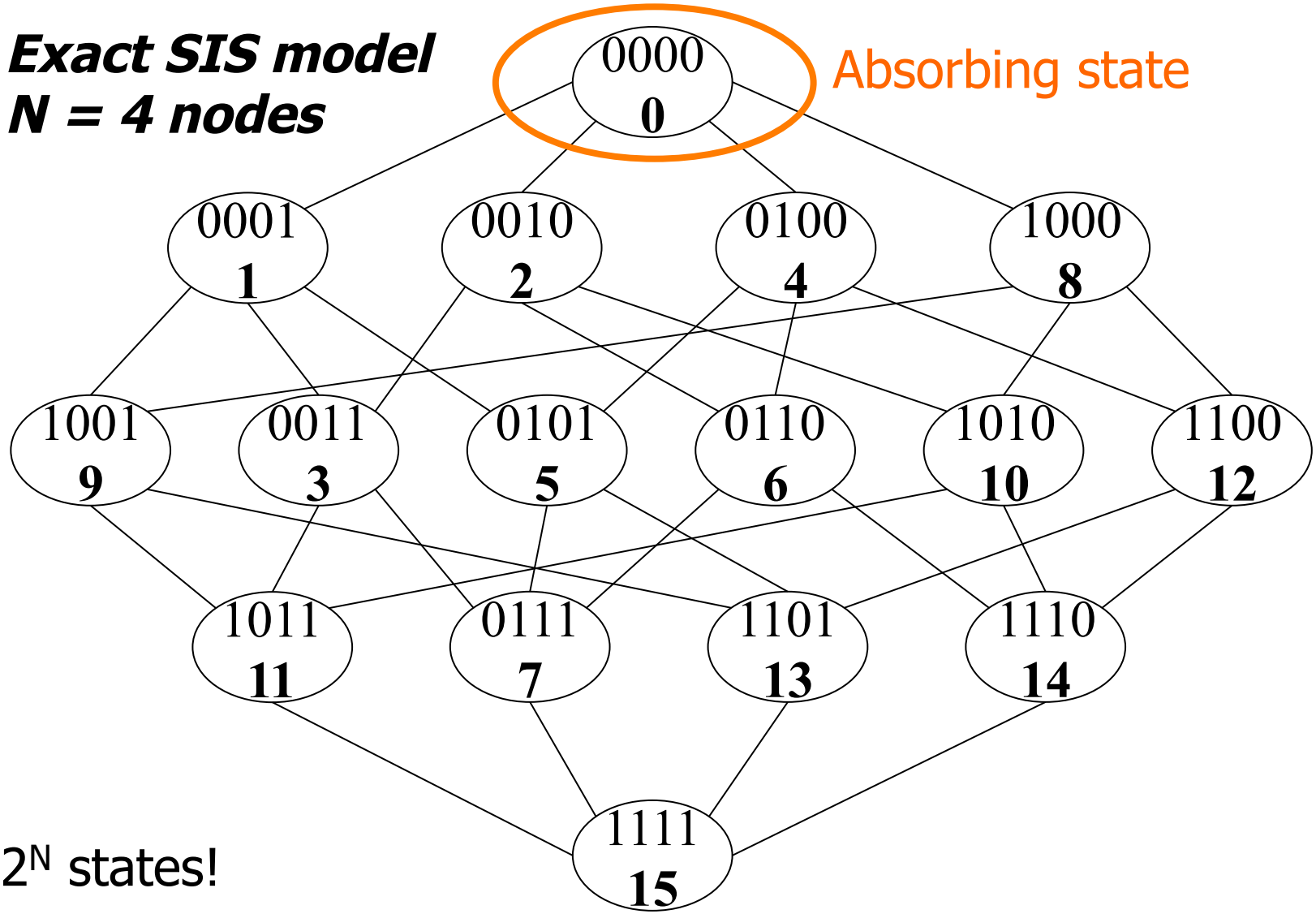
$$= -2\delta E[X_iX_j] + \beta\sum_{k=1}^{N} a_{ik}E[X_jX_k] + \beta\sum_{k=1}^{N} a_{jk}E[X_iX_k] - \beta\sum_{k=1}^{N}(a_{jk}+a_{ik})E[X_iX_jX_k]$$

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

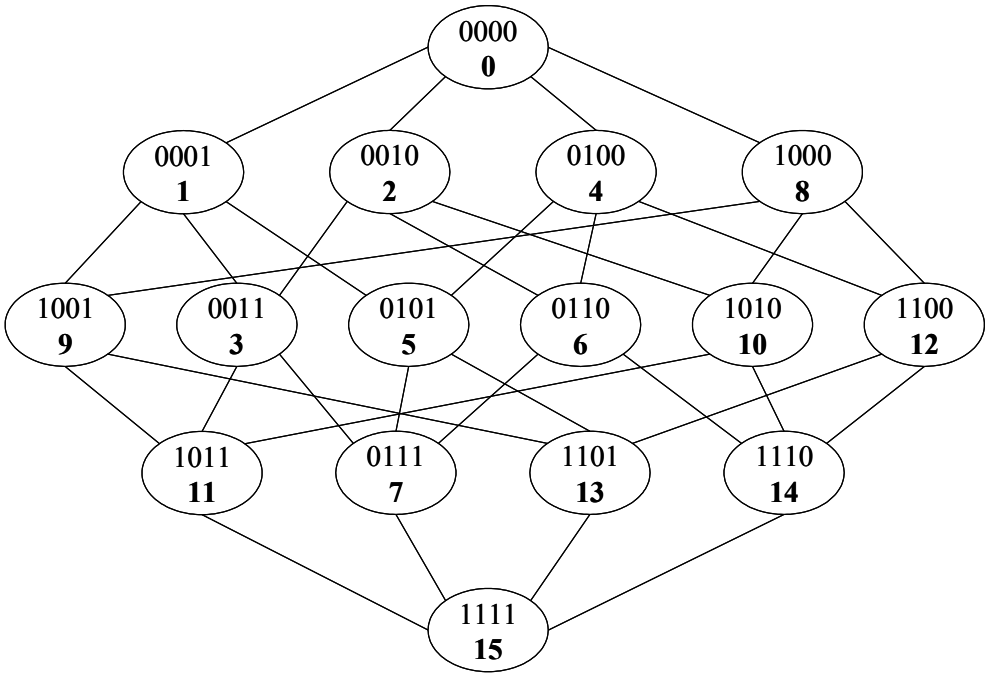


2^N states!

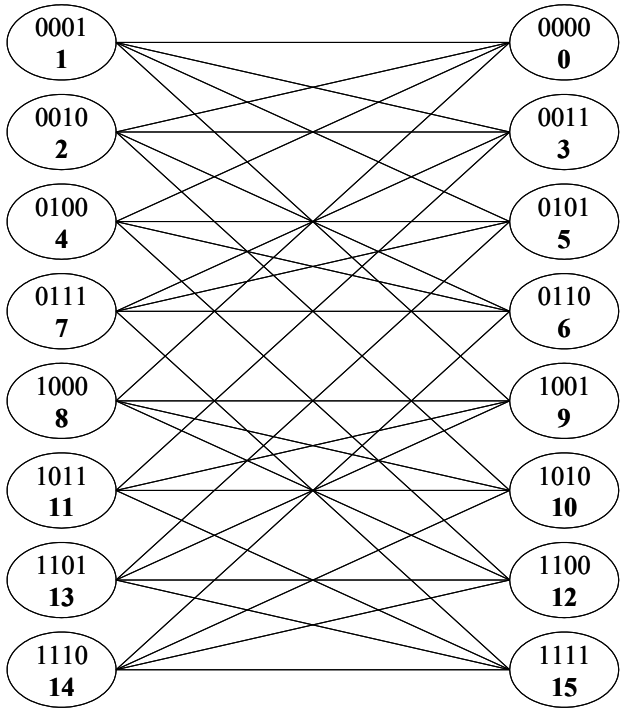
P. Van Mieghem, J. Omic, R. E. Kooij, "Virus Spread in Networks", IEEE/ACM Transaction on Networking, Vol. 17, No. 1, pp. 1-14, (2009).

TU Delft

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

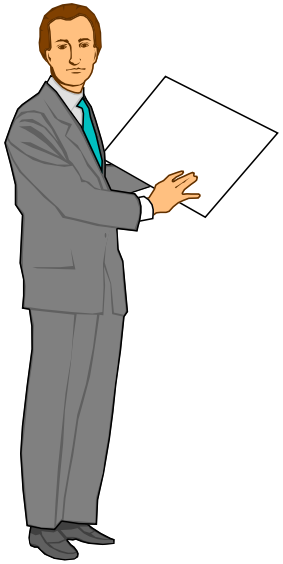
Van Mieghem, P. and E. Cator, ε-SIS epidemics and the epidemic threshold, Physical Review E, vol. 86, No. 1, July, p. 016116, 2012

TU Delft

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

Non-Markovian epidemics

TU Delft

NIMFA: N-intertwined mean-field approxim.

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

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

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

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

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.

TU Delft

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:

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

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

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

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

Ignoring the quadratic terms

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

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

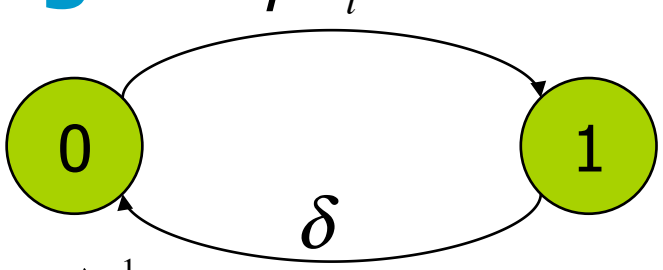
$$\beta \lambda_1(A) - \delta < 0 \quad \Longrightarrow \quad \tau = \frac{\beta}{\delta} < \frac{1}{\lambda_1(A)} < \tau_c$$

The NIMFA epidemic threshold is precisely

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

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

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

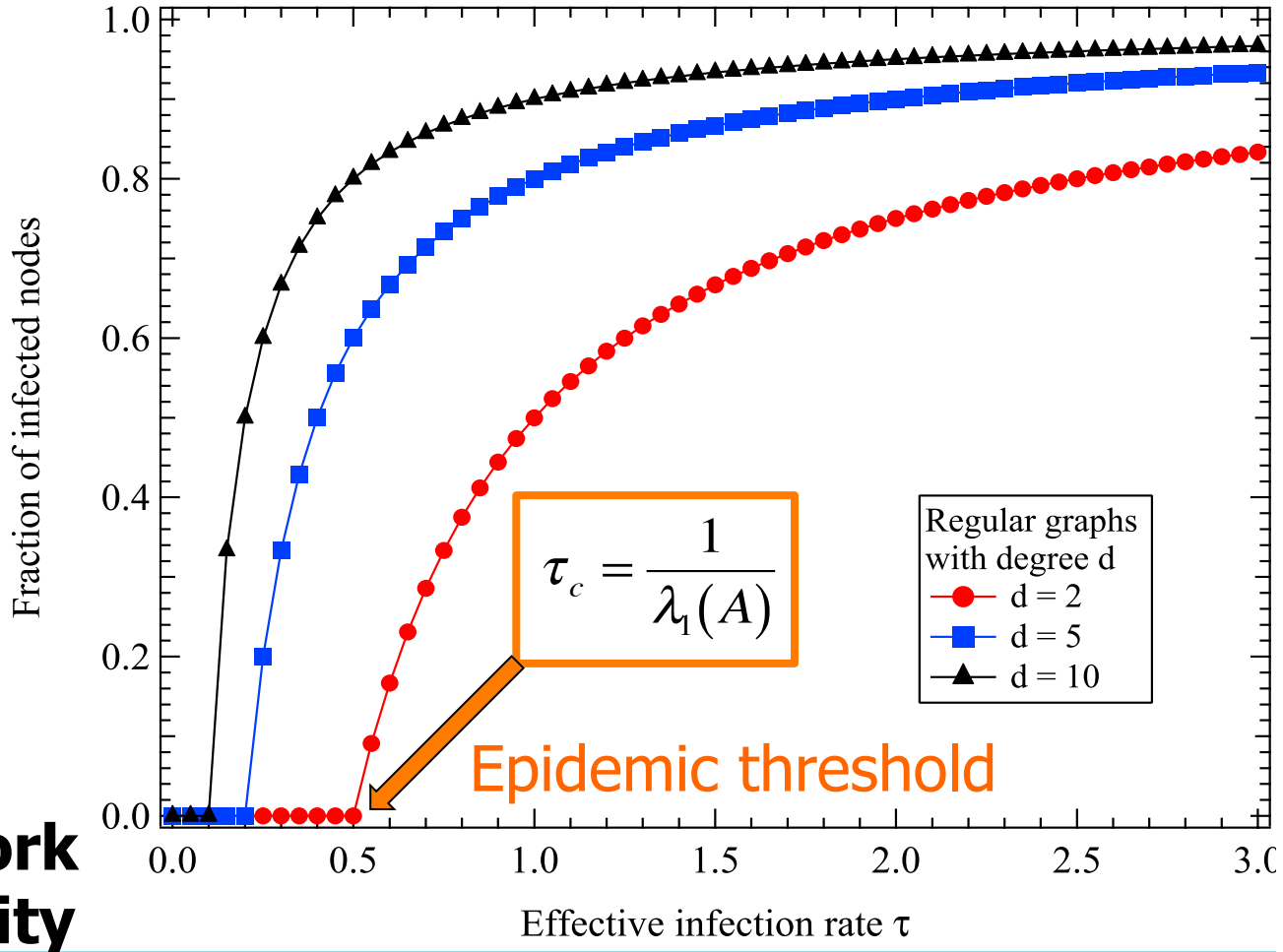
self-replicating objects (worms)

propagation errors

rumors (social nets)

epidemic algorithms (gossiping)

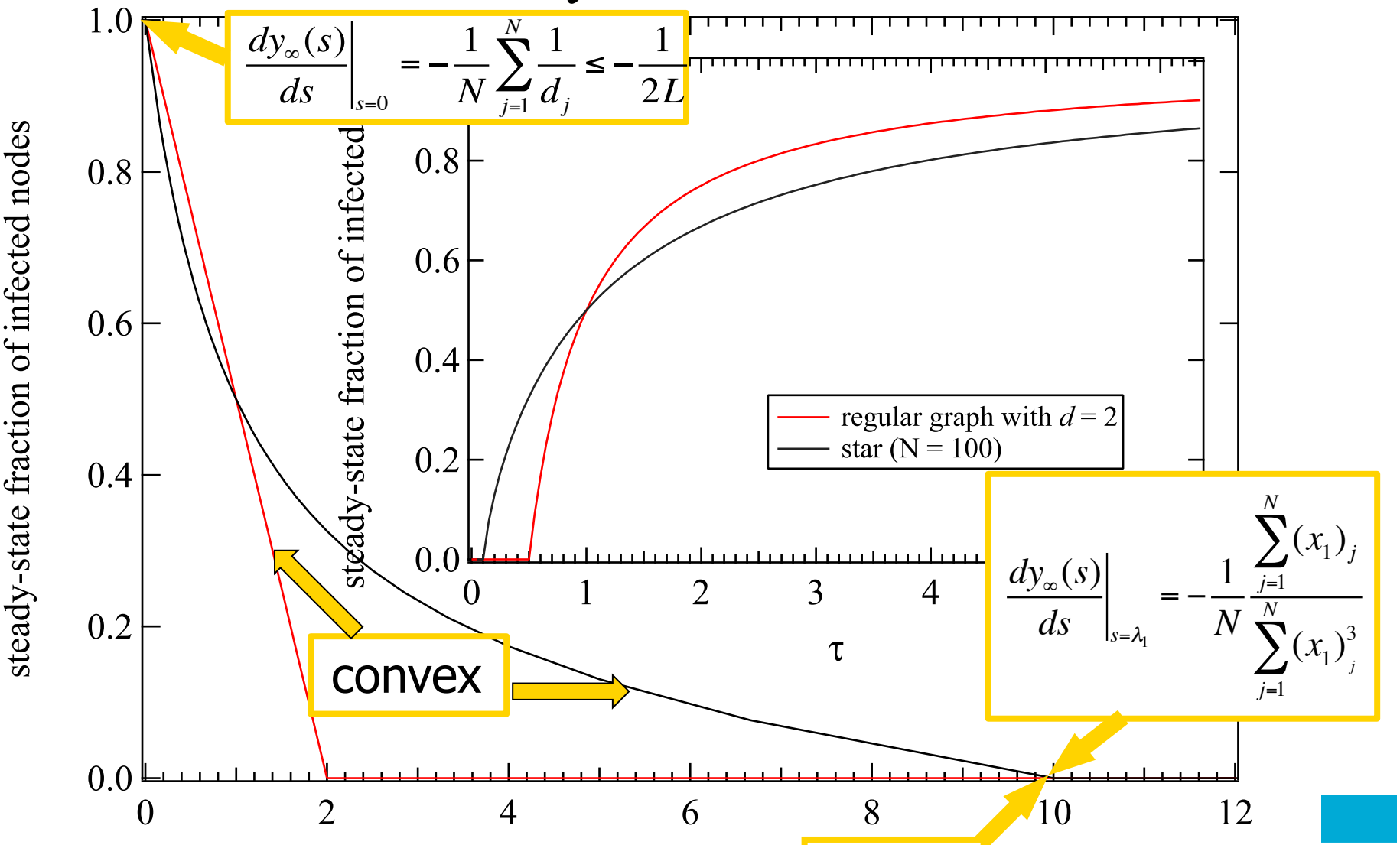
cybercrime : network robustnes & security



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

TU Delft

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



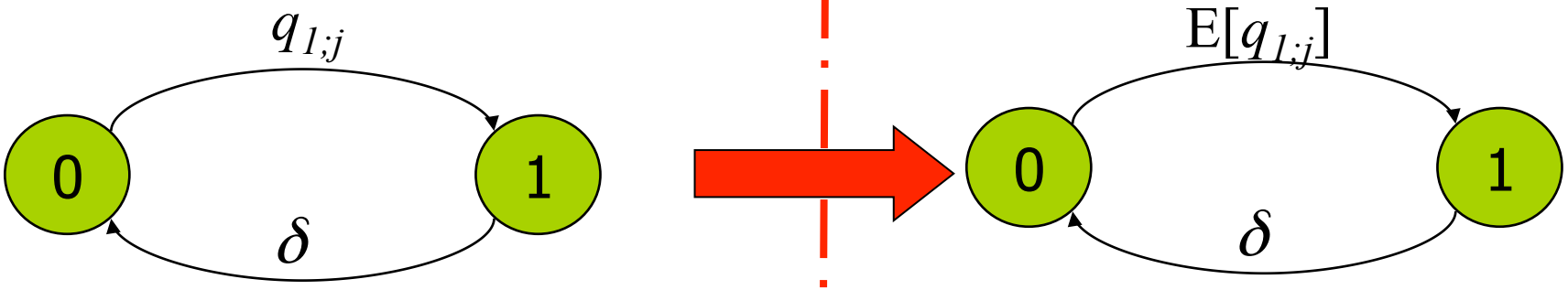
Van Mieghem, P., 2012, "Epidemic Phase Transition of the SIS-type in Networks", Europhysics Letters (EPL), Vol. 97, Februari, p. 48004.

TU Delft

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, IEEE/ACM Transactions on Networking, to appear

Mean-field approximation (NIMFA)

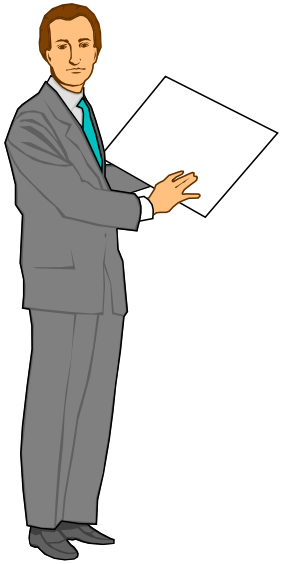


- 2^N linear equations
- Steady-state
  - absorbing (healthy) state
  - reached after unrealistically long time
- difficult to analyze

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

TU Delft

Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

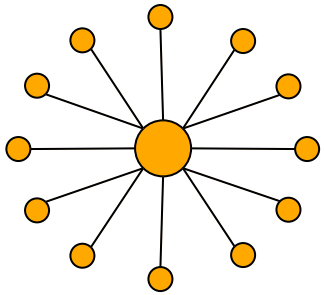
Non-Markovian epidemics

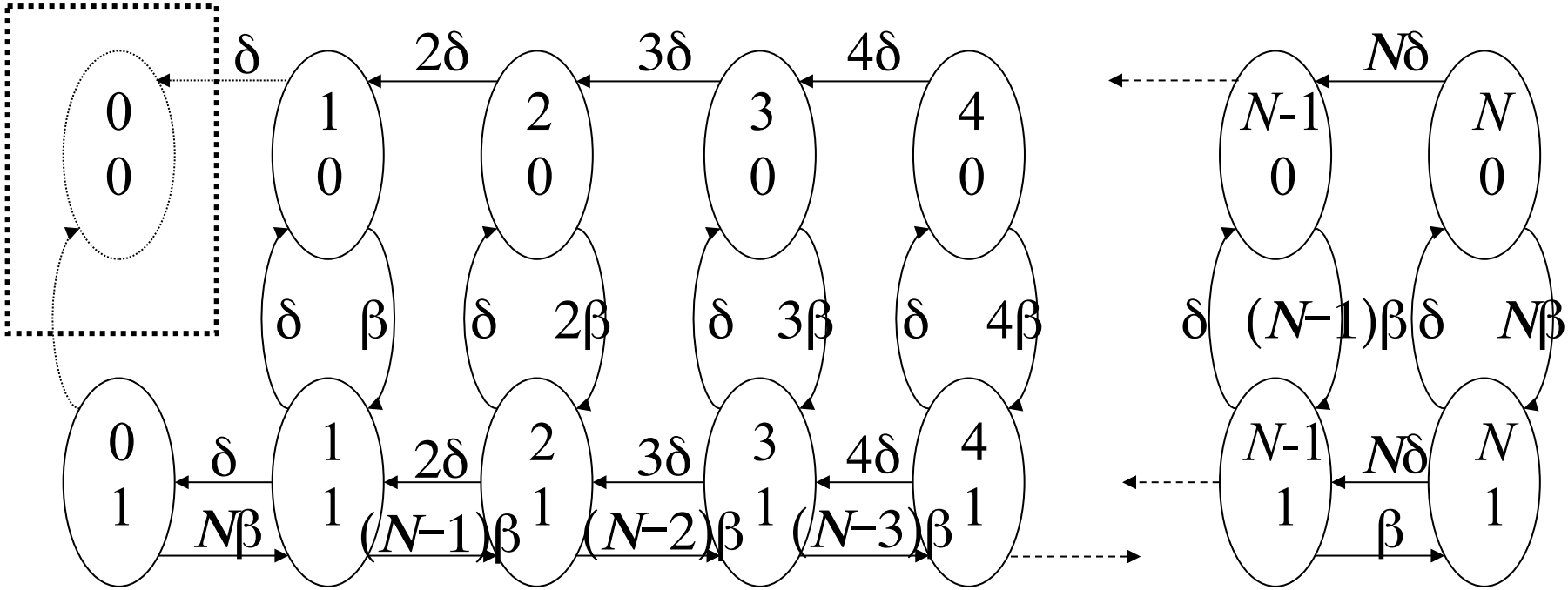
Defining the SIS epidemic threshold

- 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

E. Cator and P. Van Mieghem, 2012, "SIS epidemics on the complete graph and the star graph: exact analysis", PRE, vol. 87, p. 012811.

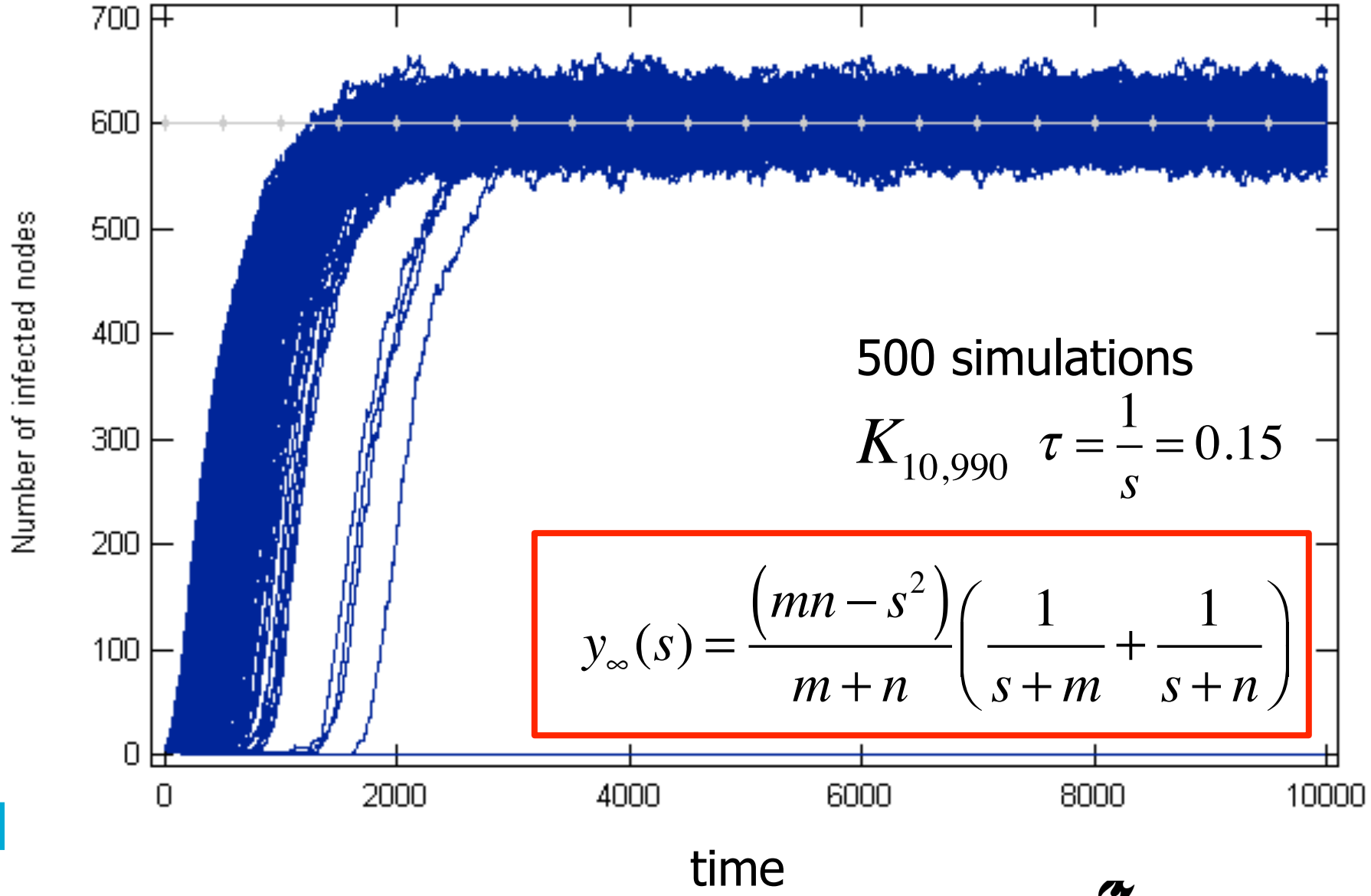
MSIS Markov Chain Star





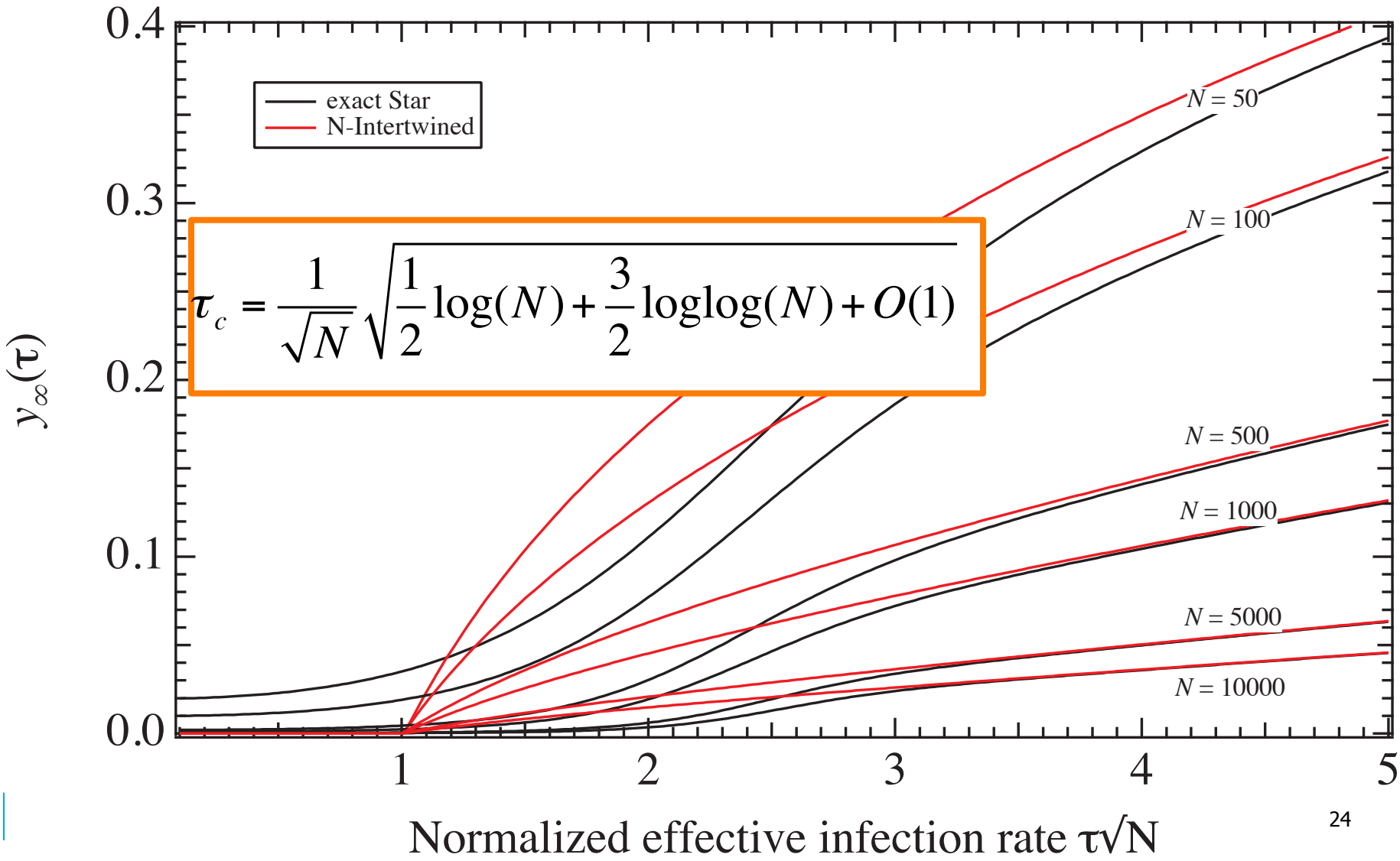
TU Delft

Simulations



TU Delft

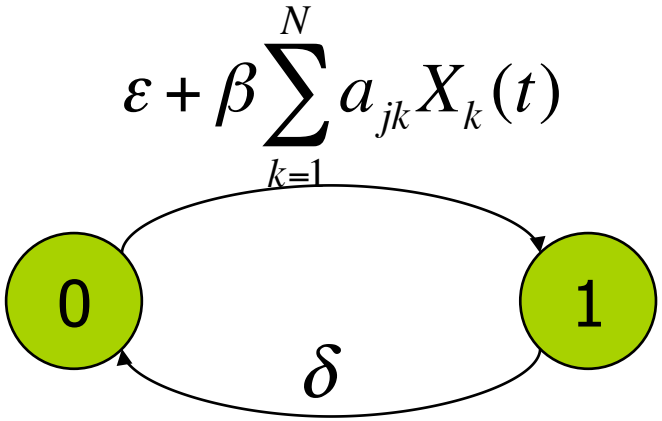
Star graph



E. Cator and P. Van Mieghem, 2012, "SIS epidemics on the complete graph and the star graph: exact analysis", PRE, vol. 87, p. 012811.

TU Delft

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

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

$$\varepsilon^* = \frac{\varepsilon}{\delta} \qquad \tau = \frac{\beta}{\delta}$$

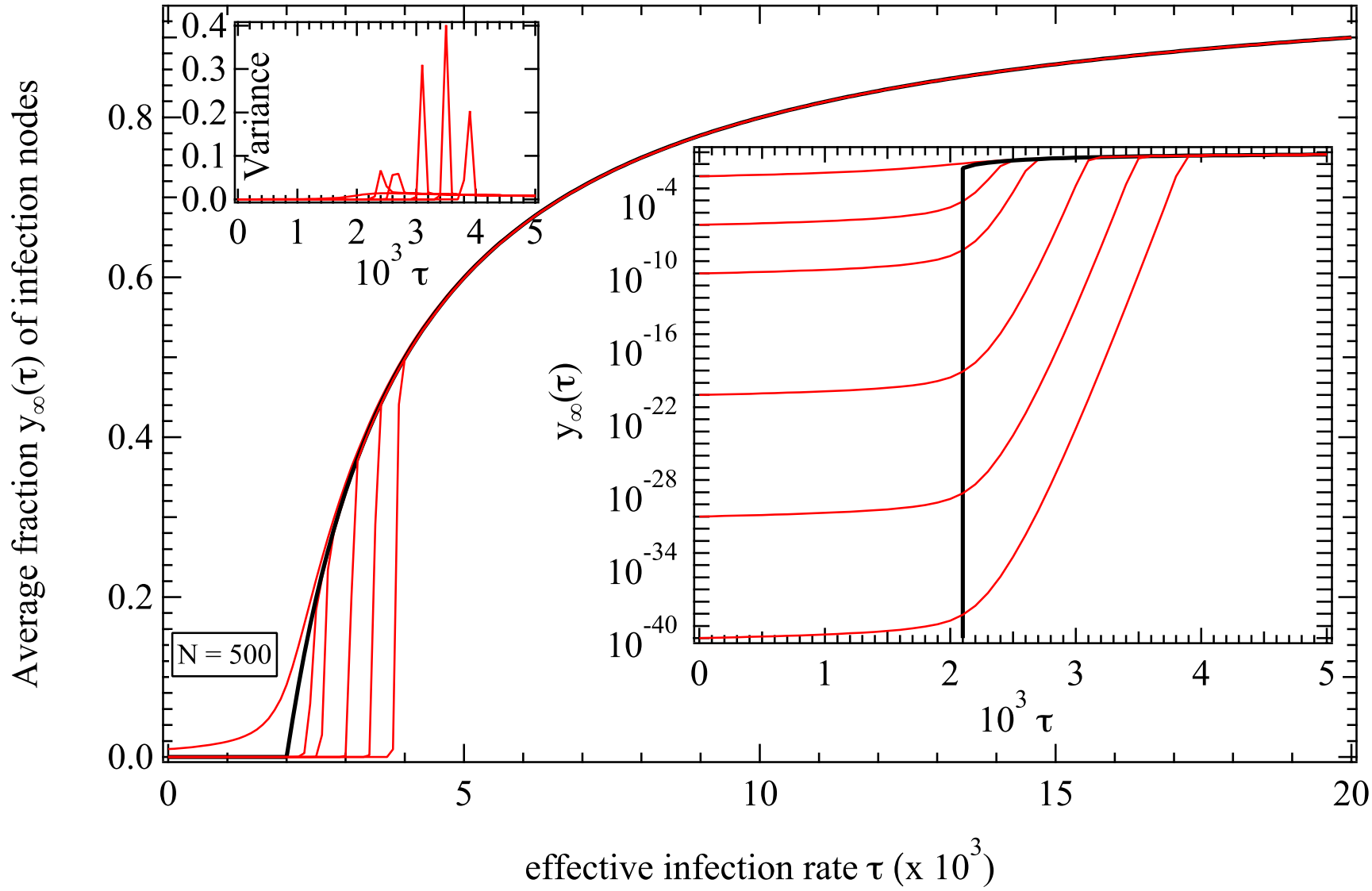
average steady-state fraction of infected nodes is $y_\infty(\tau \mid \varepsilon^*) = \frac{1}{N} \sum_{j=1}^{N} j\pi_j$

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



TU Delft

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:

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

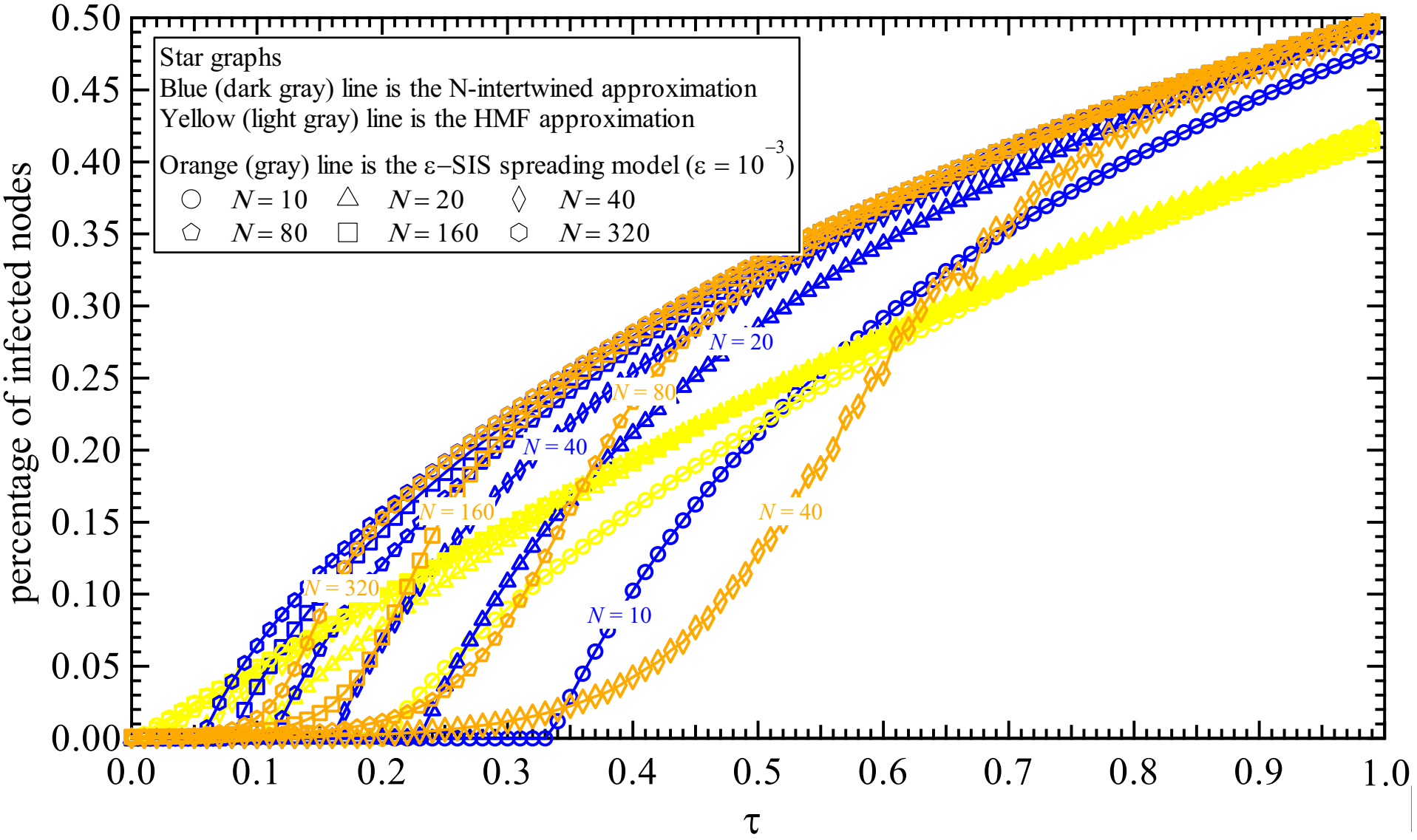
$$\Theta(\tau) = \frac{1}{E[D]}\sum_{k=1}^{N-1} k\,\Pr[D=k]\rho_k(\tau)$$

HMF epidemic threshold:

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

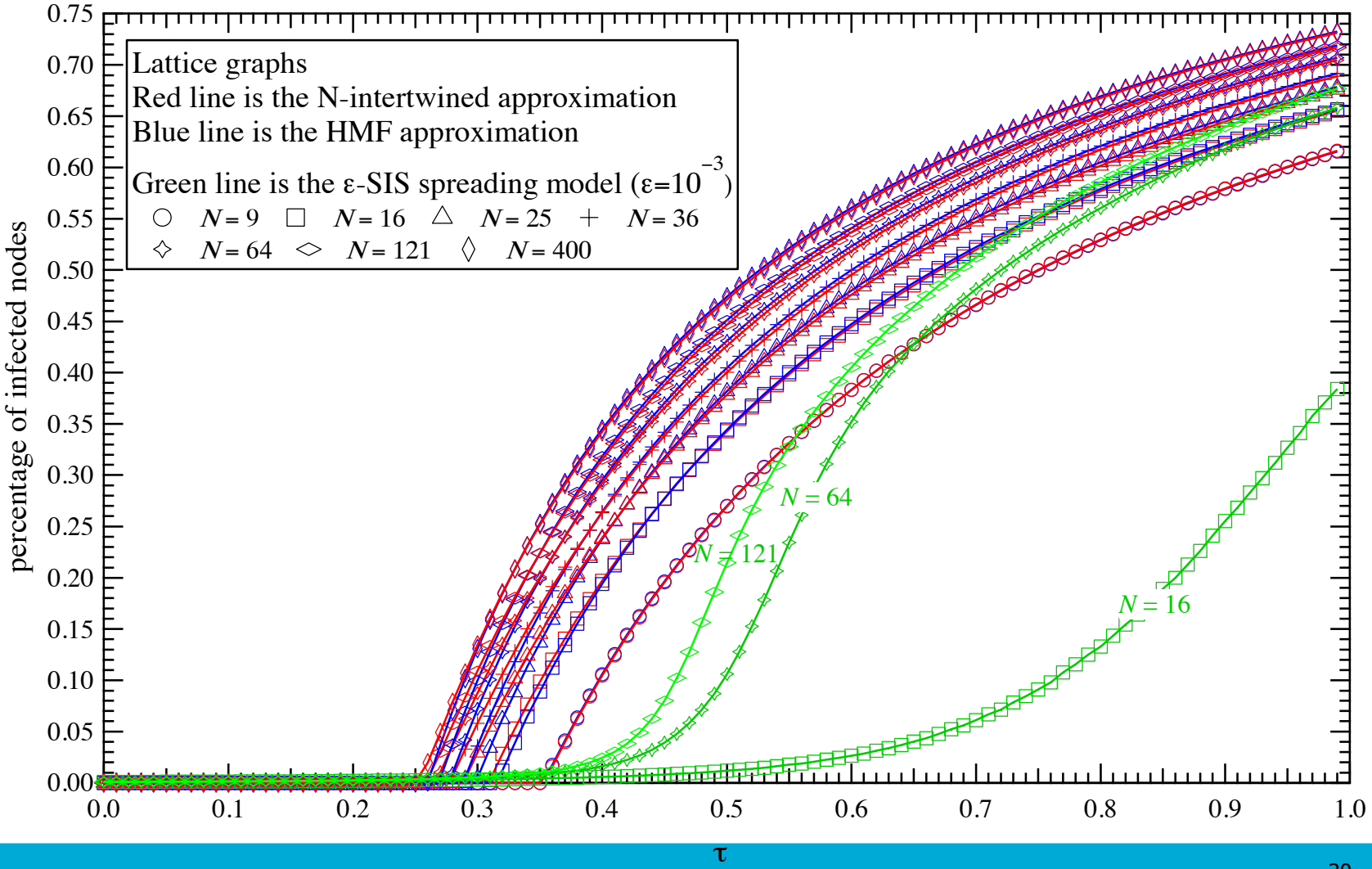
Pastor-Satorras, R. and Vespignani, A., Epidemic dynamics and endemic states in complex networks, Phys. Rev. E 63, 066117, 2001.

Comparison: star graph



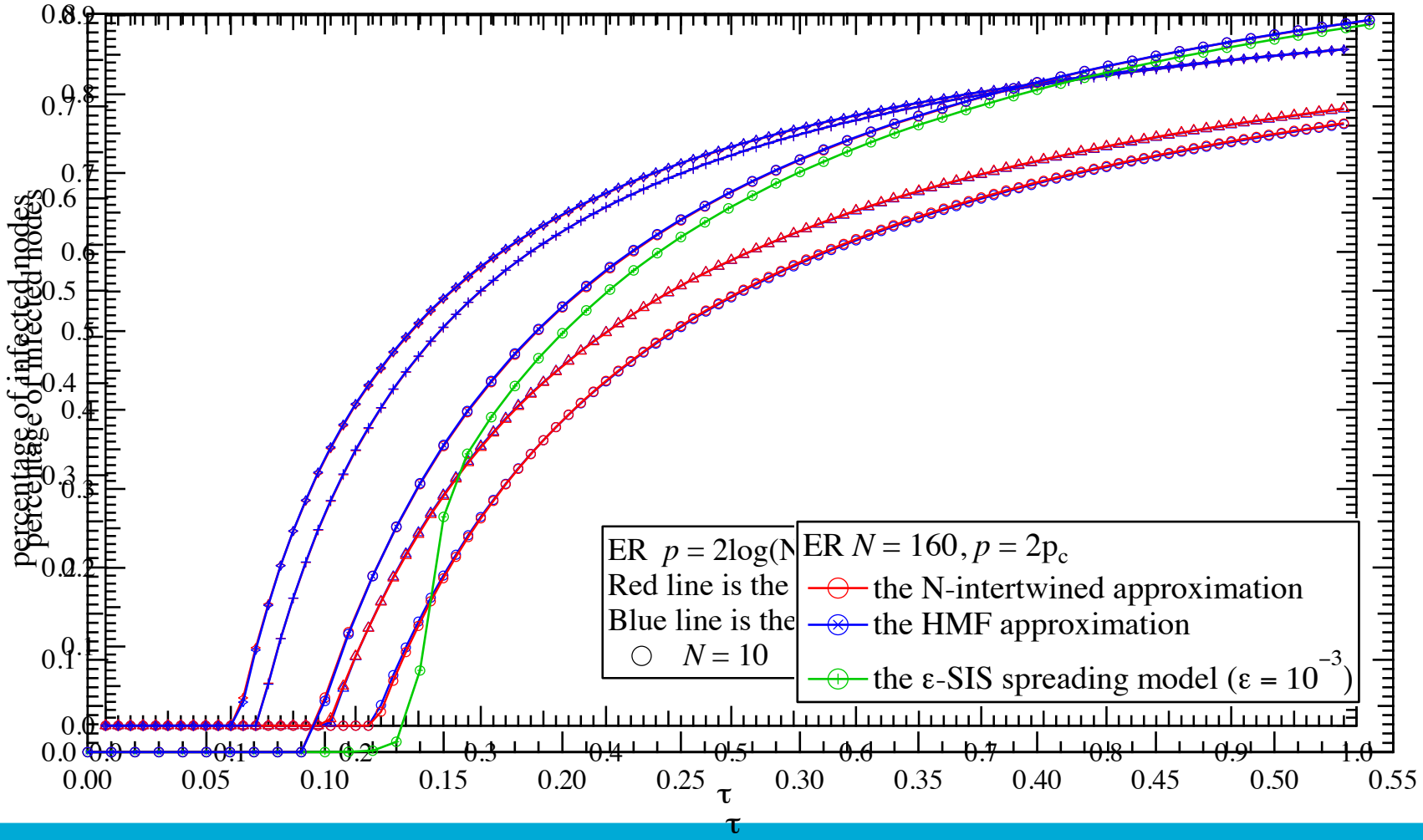
TU Delft

Comparison: Lattice



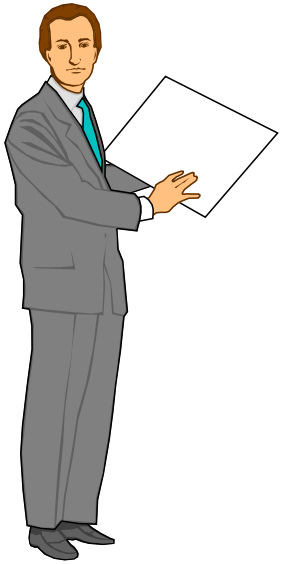
TU Delft

Comparison: ER graph (close to p_c)



TU Delft

Outline



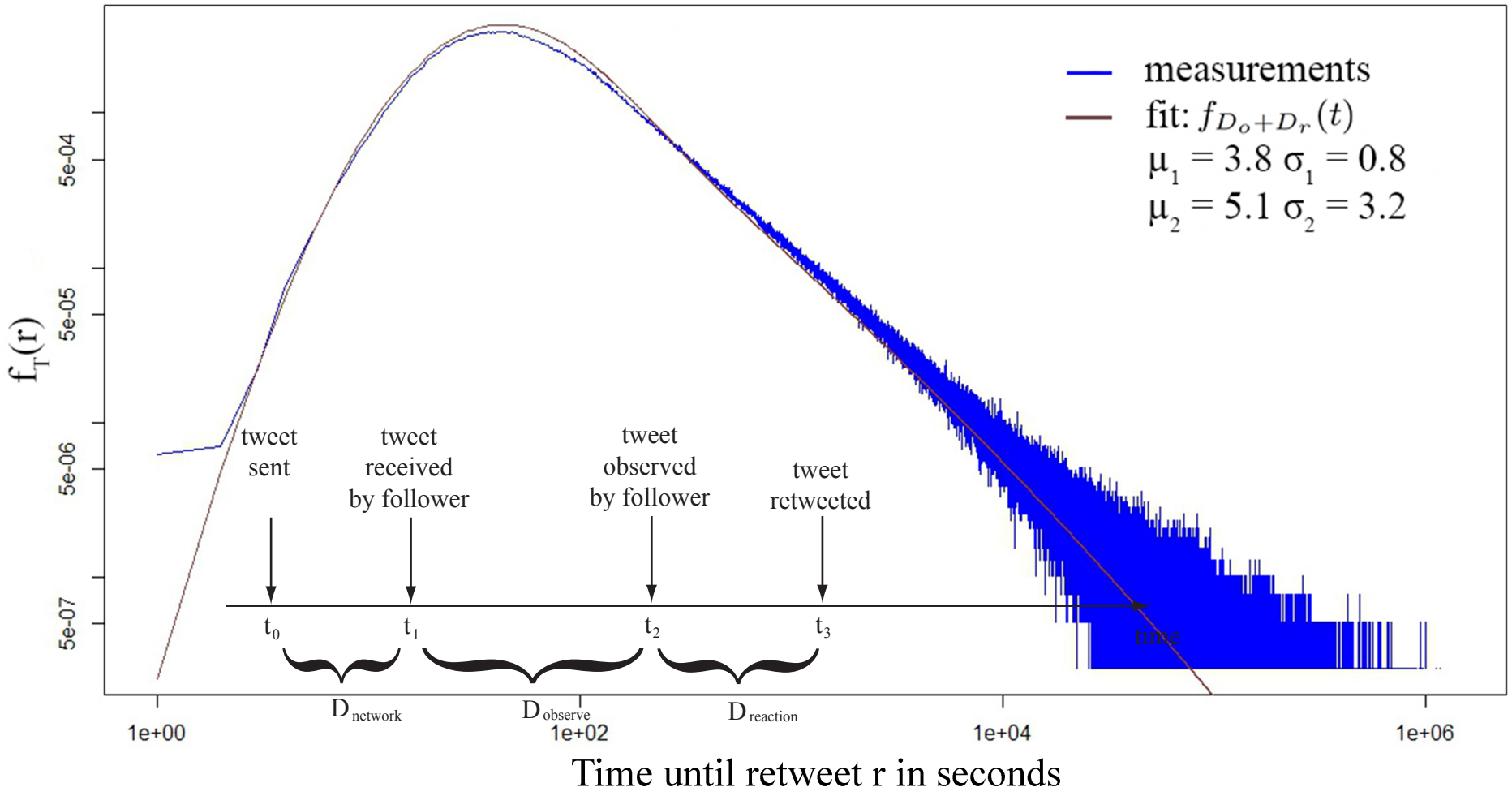
Exact SIS model

NIMFA: N-intertwined MF approximation

Defining the SIS epidemic threshold

Non-Markovian epidemics

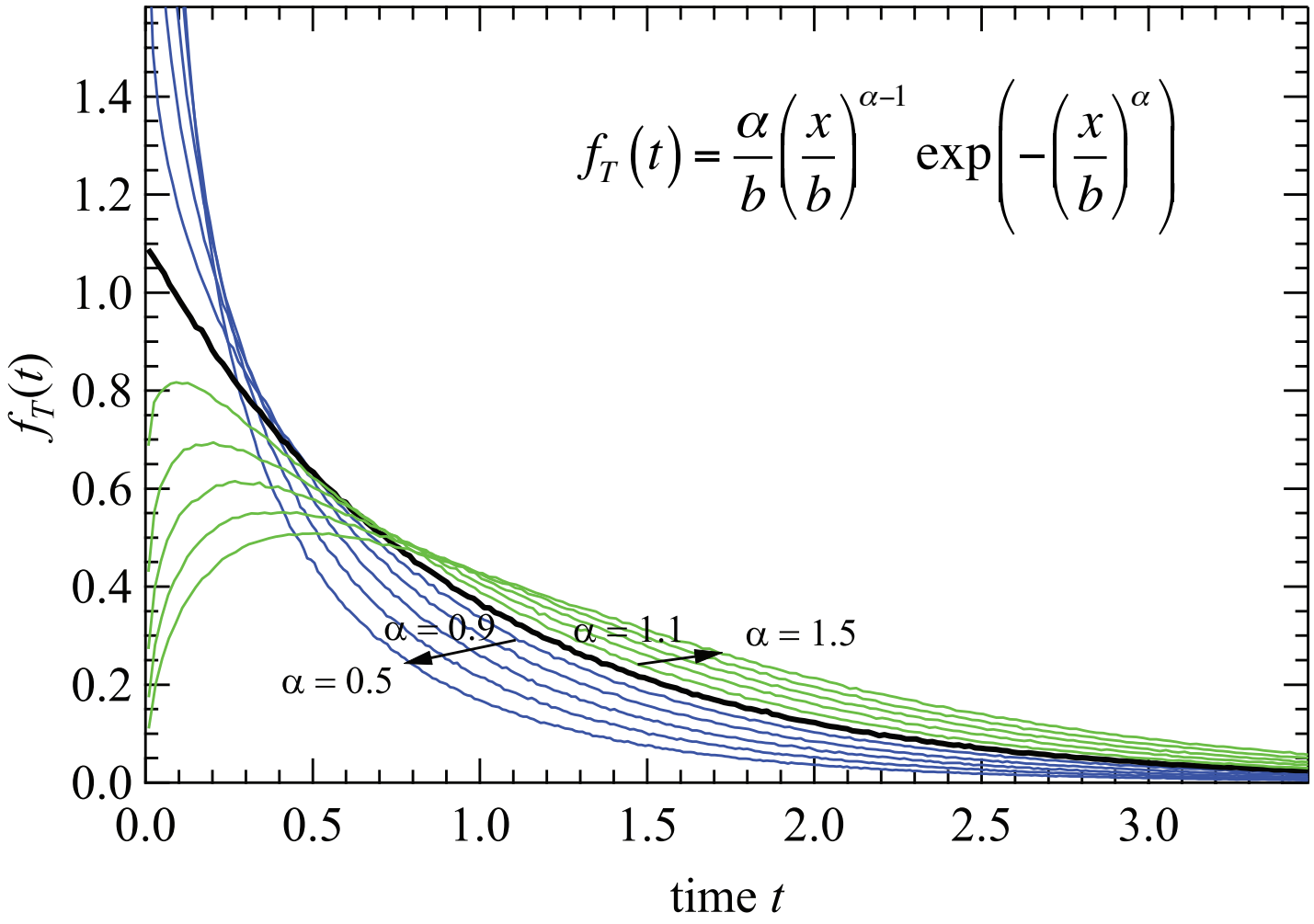
Epidemic times are not exponential



C. Doerr, N. Blenn and P. Van Mieghem, "Lognormal infection times of Online information spread", PLoS ONE, submitted

TU Delft

Non-Markovian infection times



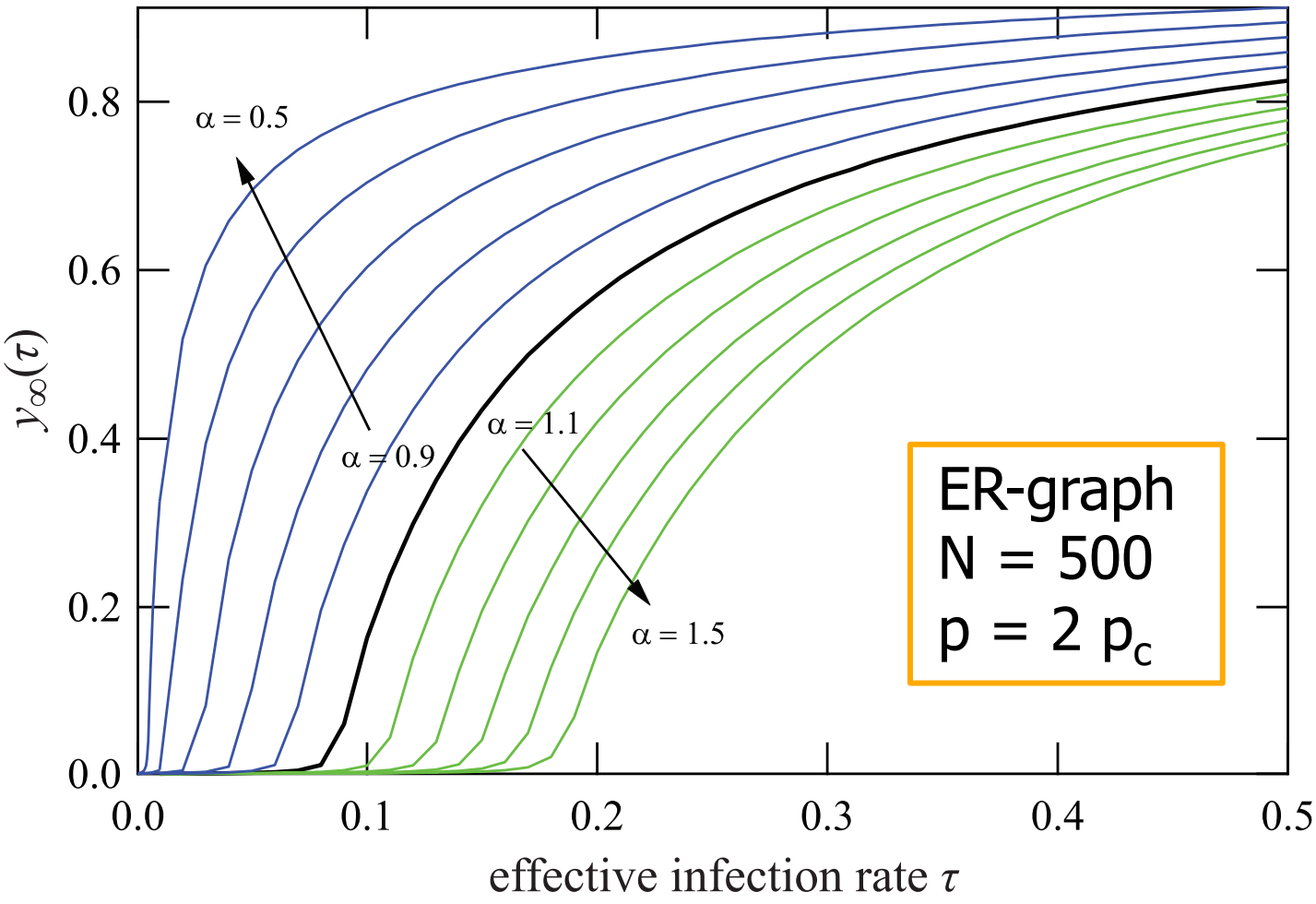
Same mean E[*T*]:

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

T is the time to infect a neighboring node

TU Delft

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, to appear.

TU Delft

GSIS: SIS with general infection times

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

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

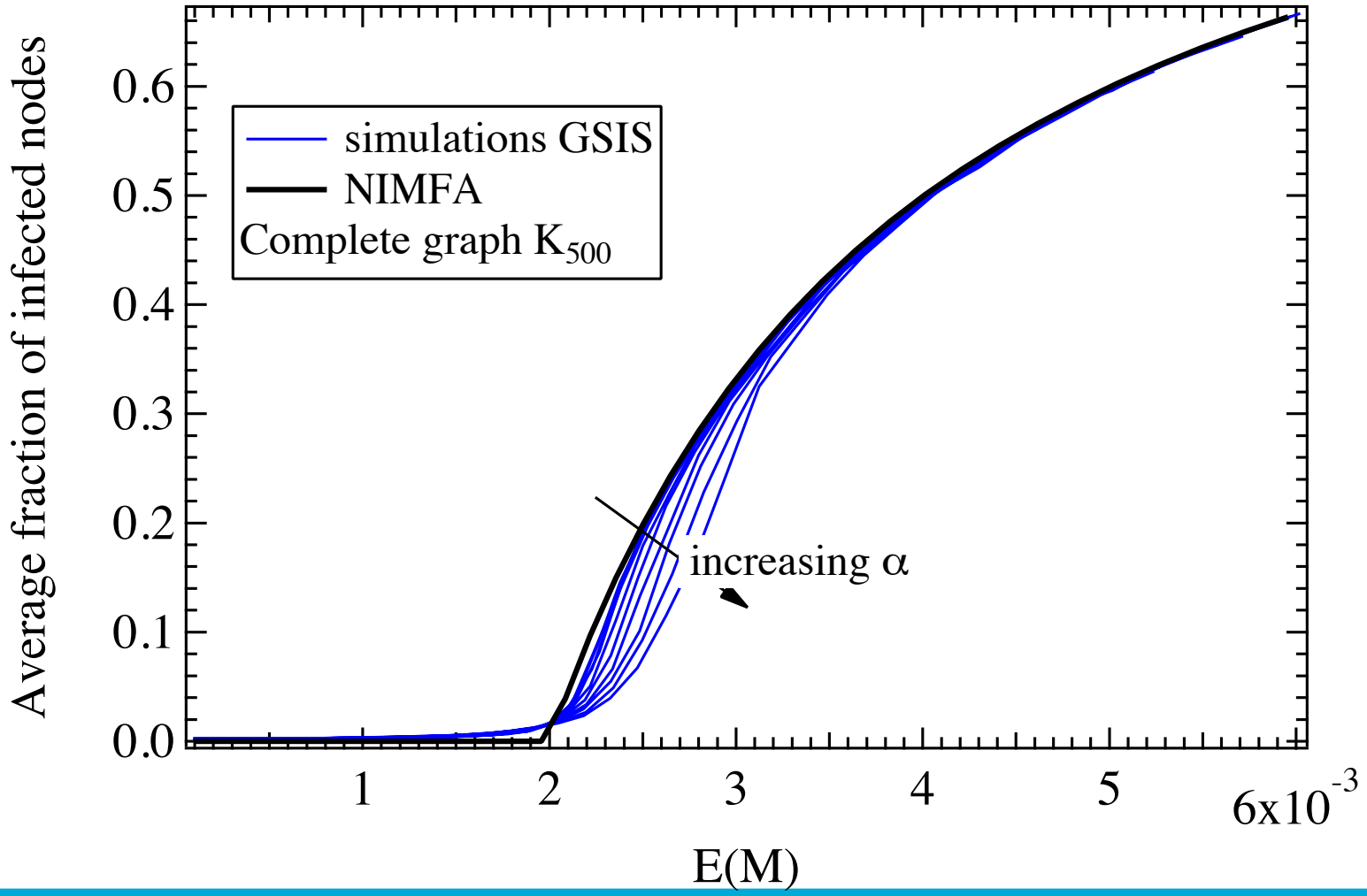
Generalized criterion for the epidemic threshold: $E[M_c] = \frac{1}{\lambda_1}$

Scaling law for large N
When infection time T is Weibullian:

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

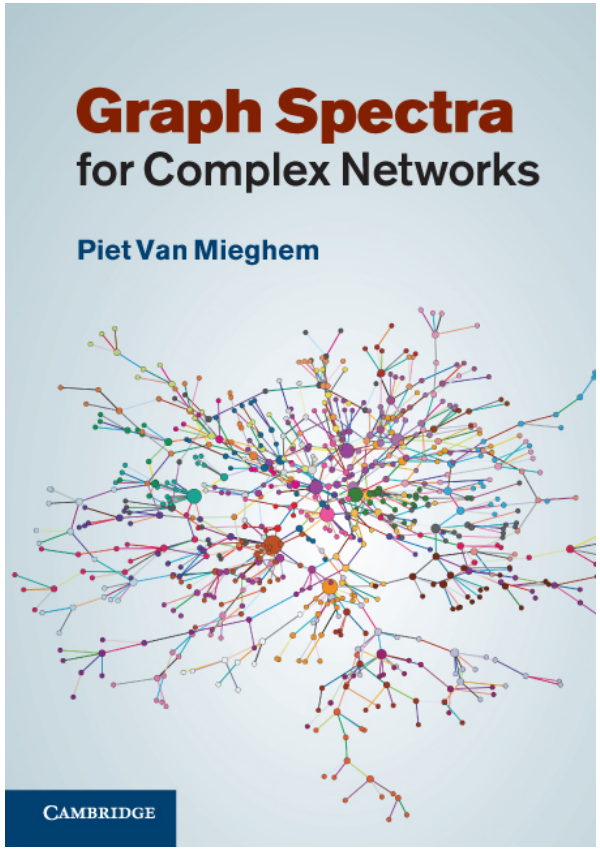
E. Cator, R. van de Bovenkamp and P. Van Mieghem, "SIS epidemics on networks with general infection and curing times", Physical Review X, submitted

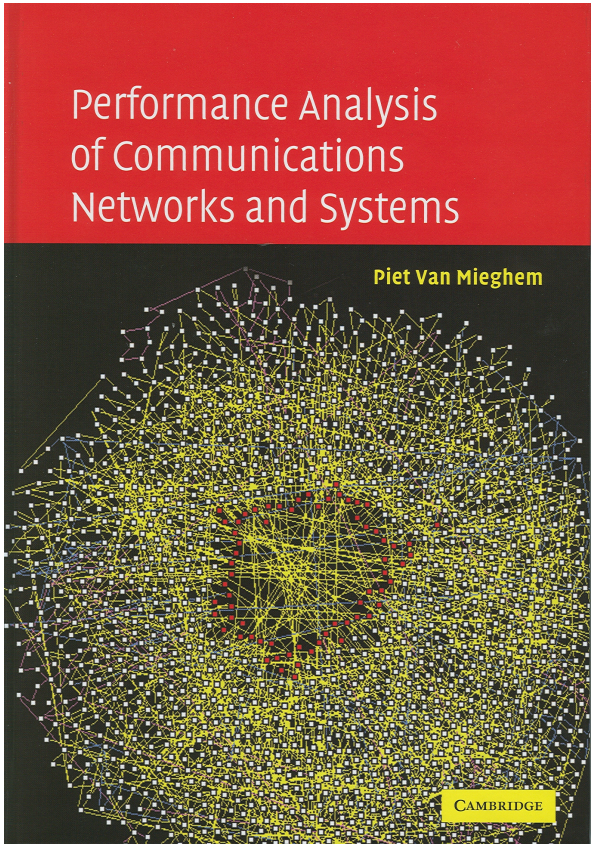
GSIS: E[M] gives the right scaling

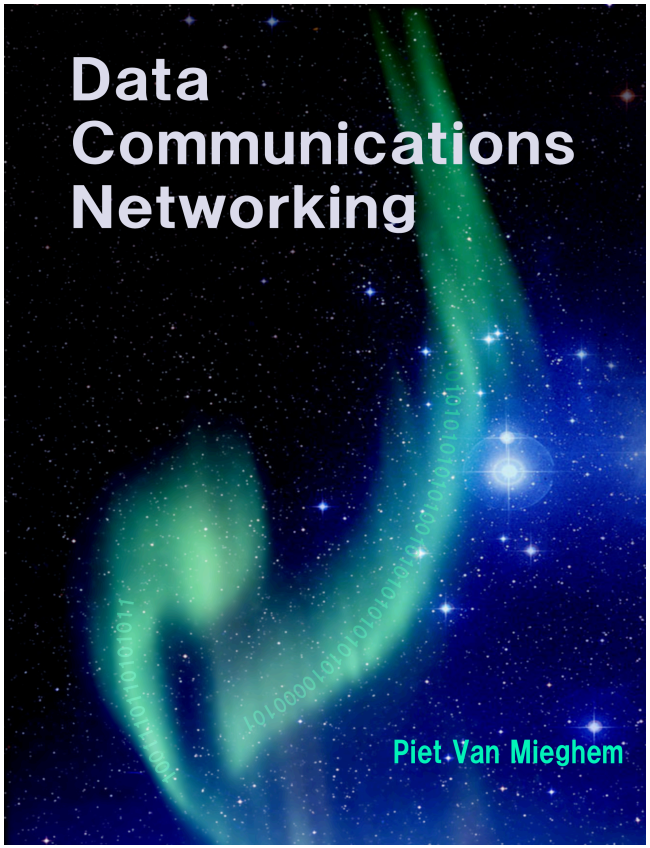


TU Delft

Books







Articles: **http://www.nas.ewi.tudelft.nl**

TU Delft


Thank You
Piet Van Mieghem
NAS, TUDelft
P.F.A.VanMieghem@tudelft.nl

TU Delft