Epidemics on Networks

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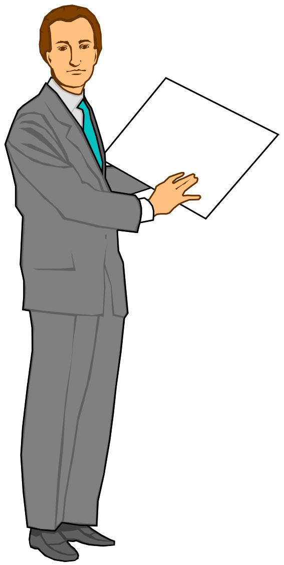
Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

Recent developments

Local rule – Global emergent property models on networks

- Opinion models
- Synchronization
- Automata
- Ising-Spin model
- Sandpile models
- …
- **Epidemics on networks**

Many feature a phase transition

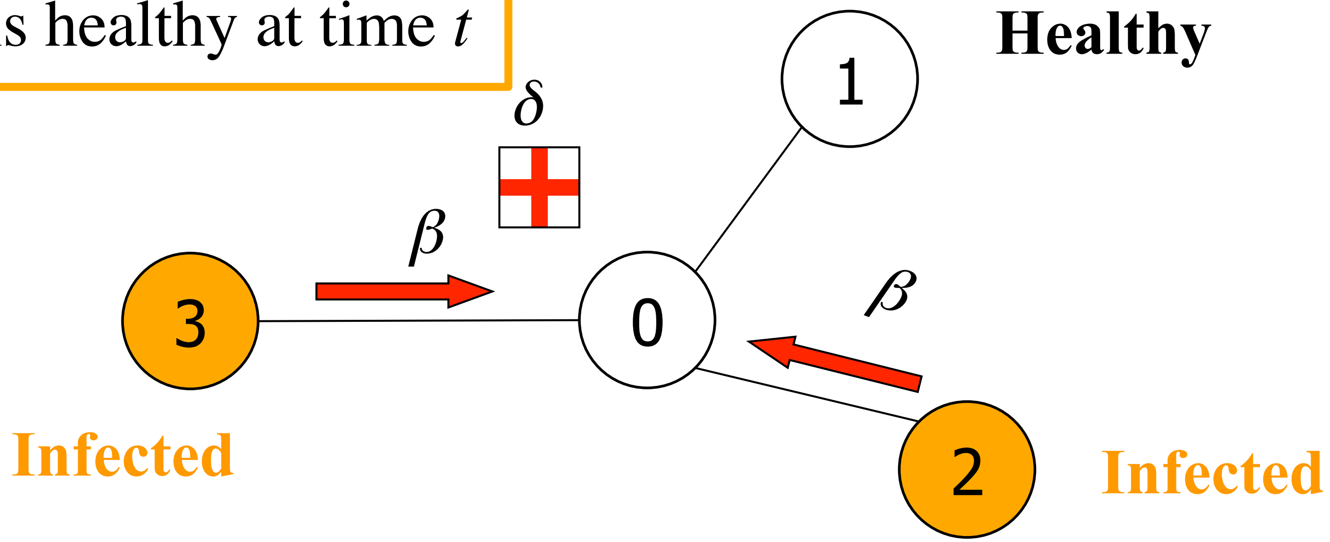
All crucially depend on the graph

Continuous-time SIS model on networks

- Constant infection rate β on all links
- Constant curing rate δ for all nodes

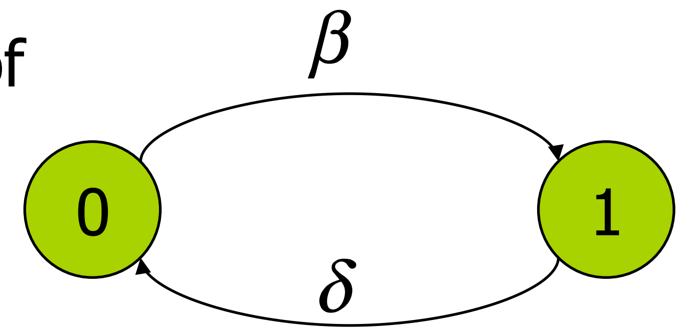
$\tau = \beta / \delta$: effective spreading rate

$X_j(t) = 1$	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

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 $Q_j(t) = \begin{bmatrix} -q_{0j} & q_{0j} \\ q_{1j} & -q_{1j} \end{bmatrix} = \begin{bmatrix} -q_{0j} & q_{0j} \\ \delta & -\delta \end{bmatrix}$

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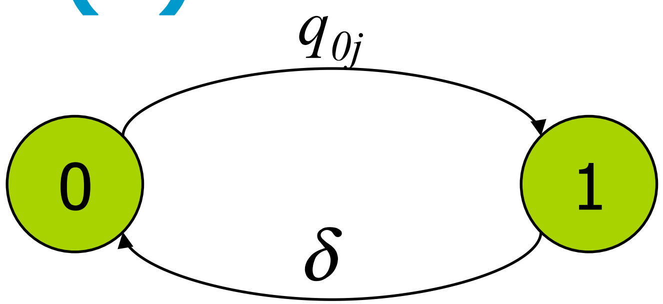
SIS model on networks (2)

- 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

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

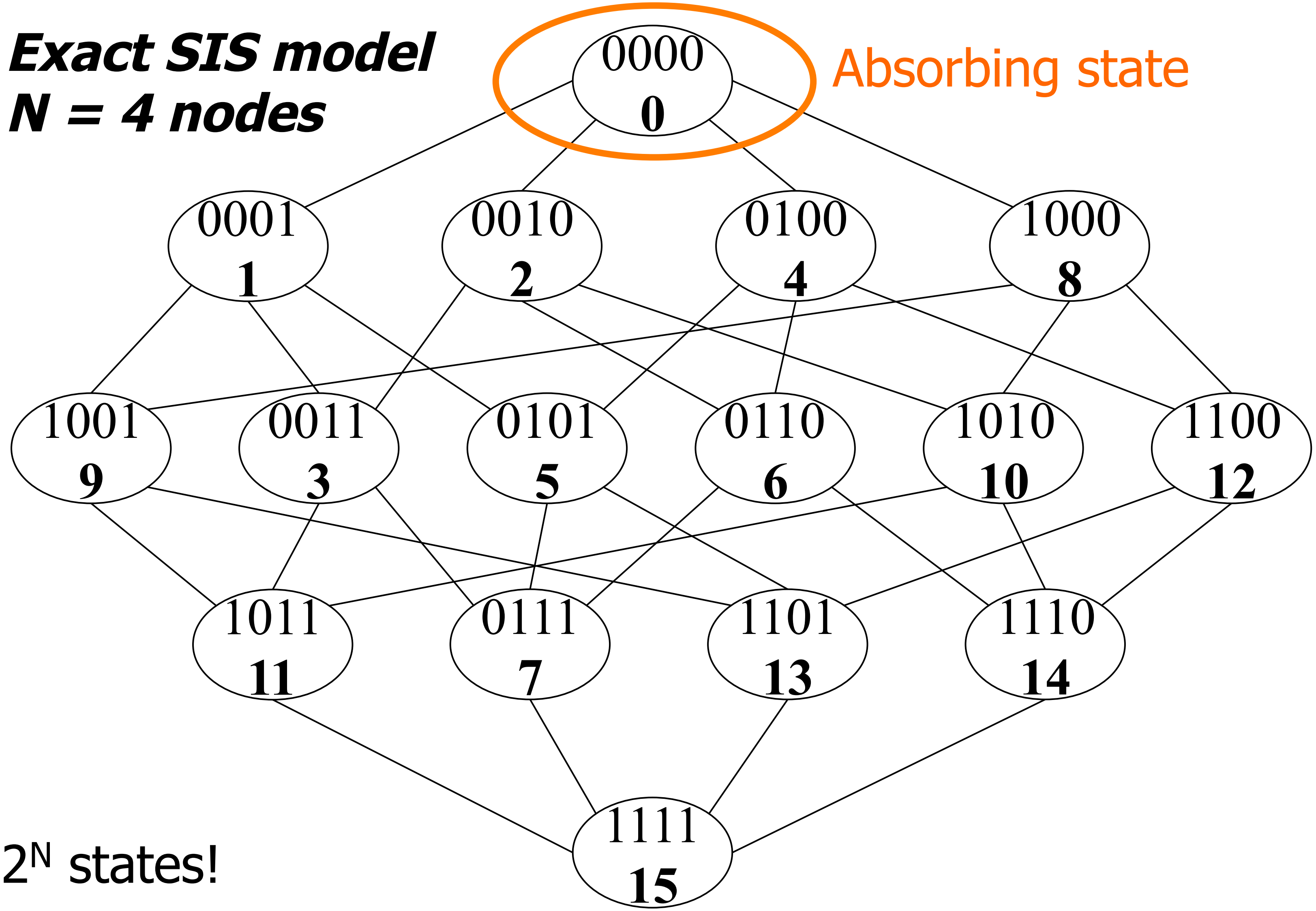
SIS model on networks (3)

- 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:

$$q_{0j}(t) = \beta \sum_{k=1}^{N} a_{jk} X_k(t) \xrightarrow{\text{NIMFA}} q_{0j}(t) = \beta \sum_{k=1}^{N} a_{jk} E\left[X_k(t)\right]$$

- 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!

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).

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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

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

R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani, "Epidemic processes in complex networks", Review of Modern Physics, Vol. 87, No. 3, pp. 925-979, 2015

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 SIS epidemic threshold", Physical Review E, vol. 85, No. 5, May, p. 056111.

Outline

Exact SIS model

NIMFA: N-intertwined MF approximation

Recent developments

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NIMFA: N-intertwined mean-field approxim.

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

$$\Rightarrow \quad Cov\left[X_j X_k\right] = E\left[X_j X_k\right] - E\left[X_j\right] E\left[X_k\right] \geq 0$$

E. Cator and P. Van Mieghem, 2014, "Nodal infection in Markovian SIS and SIR epidemics on networks are non-negatively correlated," Physical Review E, Vol. 89, No. 5, p. 052802.

$$\frac{dE[X_j]}{dt} = \underbrace{-\delta E\left[X_j\right] + \beta\left(1 - E\left[X_j\right]\right) \sum_{k=1}^{N} a_{kj} E\left[X_k\right]}_{\text{NIMFA: upper bounds SIS}} \underbrace{- \beta \sum_{k=1}^{N} a_{kj} Cov\left[X_j X_k\right]}_{R_j > 0}$$

NIMFA: upper bounds SIS

$R_j > 0$

P. Van Mieghem and R. van de Bovenkamp, 2015, "Accuracy criterion for the mean-field approximation in SIS epidemics on networks," Physical Review E, Vol. 91, No. 3, p. 032812.

NIMFA: replace rv by its mean

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

NIMFA

$$X_j \Rightarrow E\left[\breve{X}_j\right]$$

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

Bernoulli rv

$$E\left[\breve{X}_j\right] = \Pr\left[\breve{X}_j = 1\right] = v_j$$

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

Lower bound for the epidemic threshold

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

Ignoring the correlation terms

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

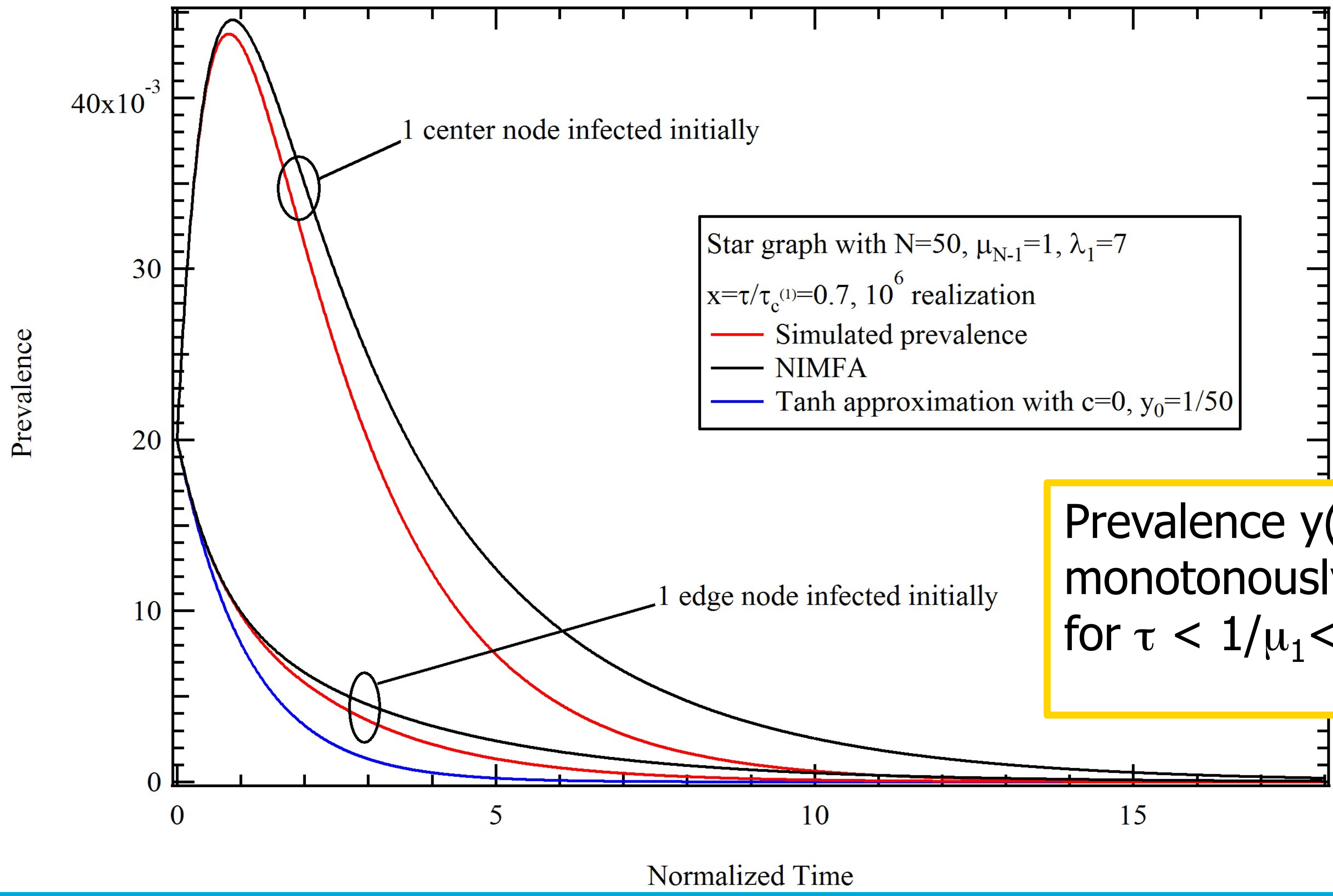
If all eigenvalues of $\beta A - \delta I$ are negative, v_j tends exponentially fast to zero for sufficiently large time *t*. Hence, if

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

The NIMFA epidemic threshold is precisely

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

Below the epidemic threshold: $x = \lambda_1 \tau < 1$



Prevalence y(t) decreases monotonously
for $\tau < 1/\mu_1 < 1/\lambda_1$

P. Van Mieghem, 2016, "Approximate formula and bounds for the time-varying SIS prevalence in networks", Physical Review E, Vol. 93 No. 5, p. 052312.

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What is so interesting about epidemics?

network protection

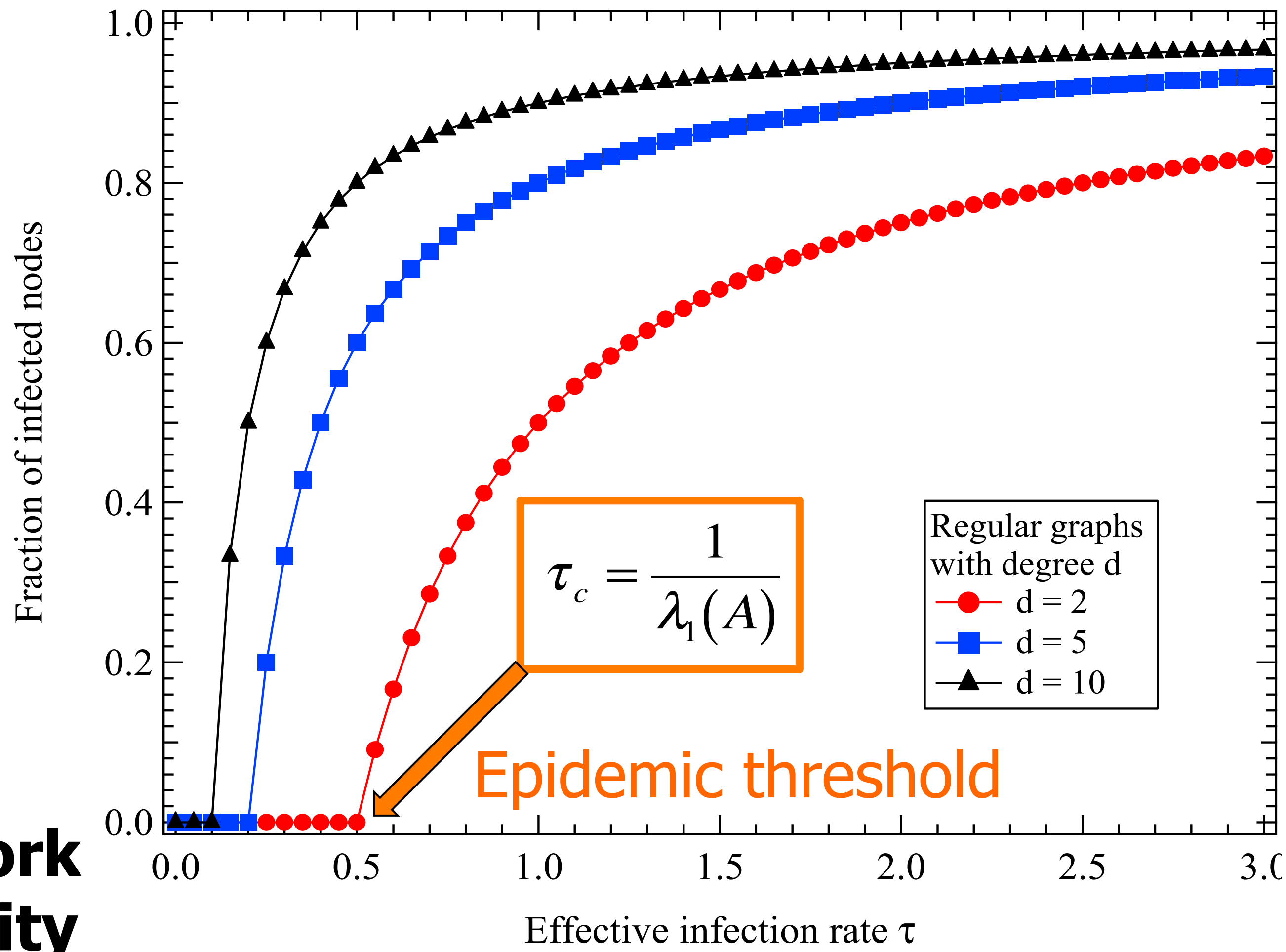
self-replicating objects (worms)

propagation errors

rumors (social nets)

epidemic algorithms (gossiping)

cybercrime : network robustnes & security



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

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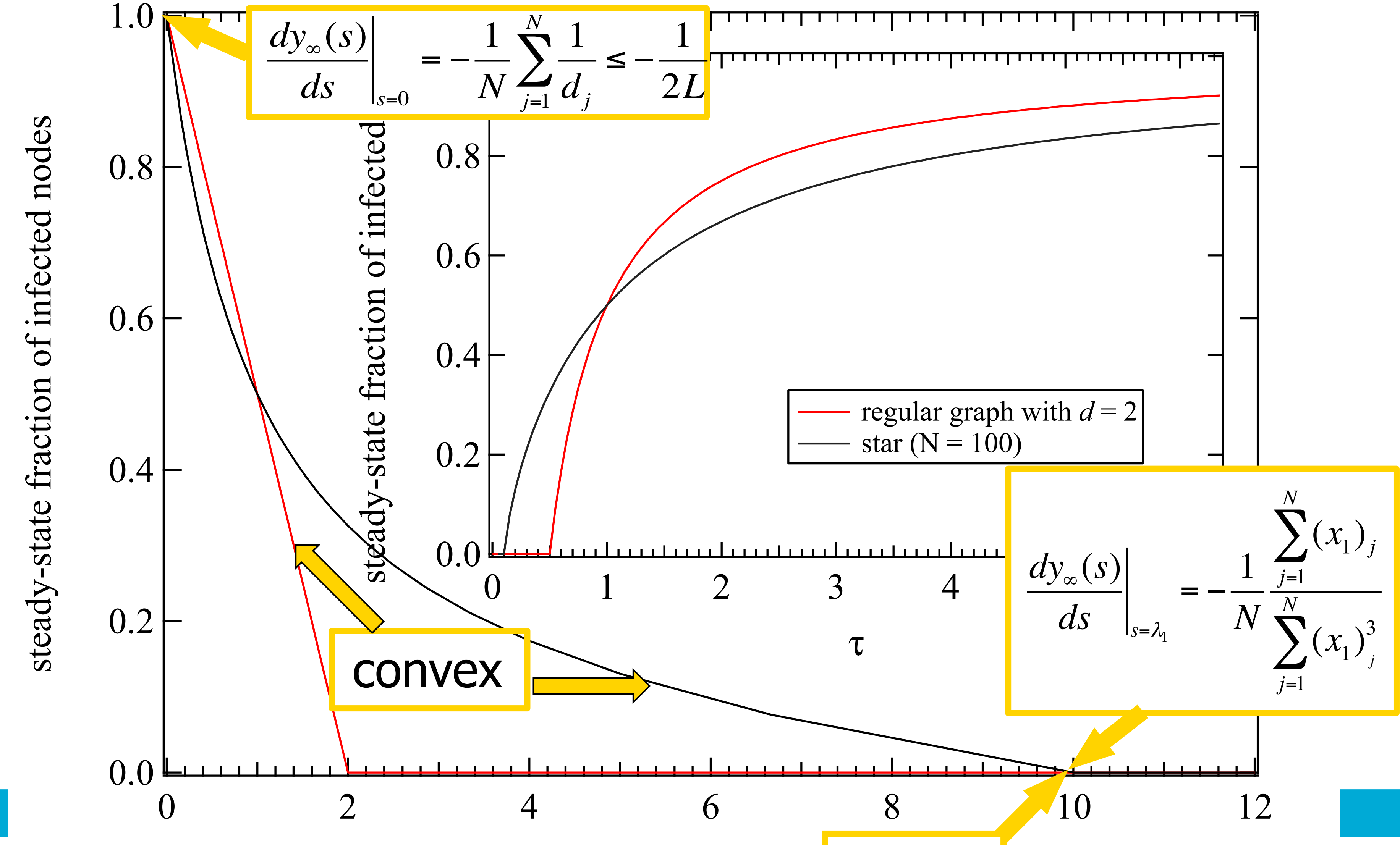
Transformation $s = \frac{1}{\tau}$ & principal eigenvector



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

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

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

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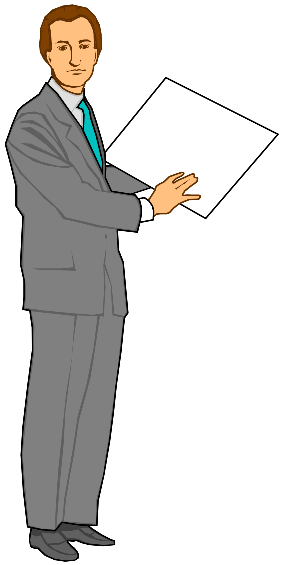
Extensions of the NIMFA

- **In-homogeneous**: each node i has own β_i and δ_i:
  P. Van Mieghem and J. Omic, 2008, "In-homogeneous Virus Spread in Networks", (arxiv.org/ 1306.2588)
- **SAIS** (Infected, Susceptible, Alert) and **SIR** instead of SIS:
  F. Darabi Sahneh and C. Scoglio, 2011,"Epidemic Spread in Human Networks", 50th IEEE Conf. Decision and Contol, Orlando, Florida.
  "M. Youssef and C. Scoglio, 2011, An individual-based approach to SIR epidemics in contact networks" Journal of Theoretical Biology 283, pp. 136-144.
- Generalized Epidemic mean-field model (**GEMF**): general extension of NIMFA to m compartments (includes both SIS, SAIS, SIR,...):
  F. Darabi Sahneh, C. Scoglio, P. Van Mieghem, 2013, "Generalized Epidemic Mean-Field Model for Spreading Processes over Multi-Layer Complex Networks",, IEEE/ACM Transactions on Networking, Vol. 21, No. 5, pp. 1609-1620.
- NIMFA on **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", Physical Review E, Vol. 88, No. 2, August, p. 022801.

Outline



Exact SIS model

NIMFA: N-intertwined MF approximation

Recent developments

- **Accuracy Criterion NIMFA**
- Non-Markovian epidemics
- Time-dependent rates
- Upper bound SIS epidemic τ_c
- Survival time

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Accuracy criterion

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

NIMFA: upper bounds SIS

R_j

For each node *j*, R_j assesses the deviation of NIMFA from exact

$$R_j = \sum_{k=1}^{N} a_{jk} c_{kj} \qquad c_{kj} = Cov\left[X_j X_k\right] \geq 0$$

Choose the norm $\|R\|_1$ to assess accuracy of the graph

$$\|R\|_1 = \sum_{j=1}^{N} \left|R_j\right| = \sum_{j=1}^{N}\sum_{k=1}^{N} a_{jk} c_{kj} = trace(AC) = \sum_{k=1}^{N} \lambda_k(AC)$$

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Accuracy criterion

Since: $$\|R\|_1 = \sum_{j=1}^{N}\sum_{k=1}^{N} a_{jk} c_{kj} \le \frac{1}{4}\sum_{j=1}^{N}\sum_{k=1}^{N} a_{jk} = \frac{L}{2}$$

Normalized criterion: $$r_T = \frac{2\|R\|_1}{L}$$

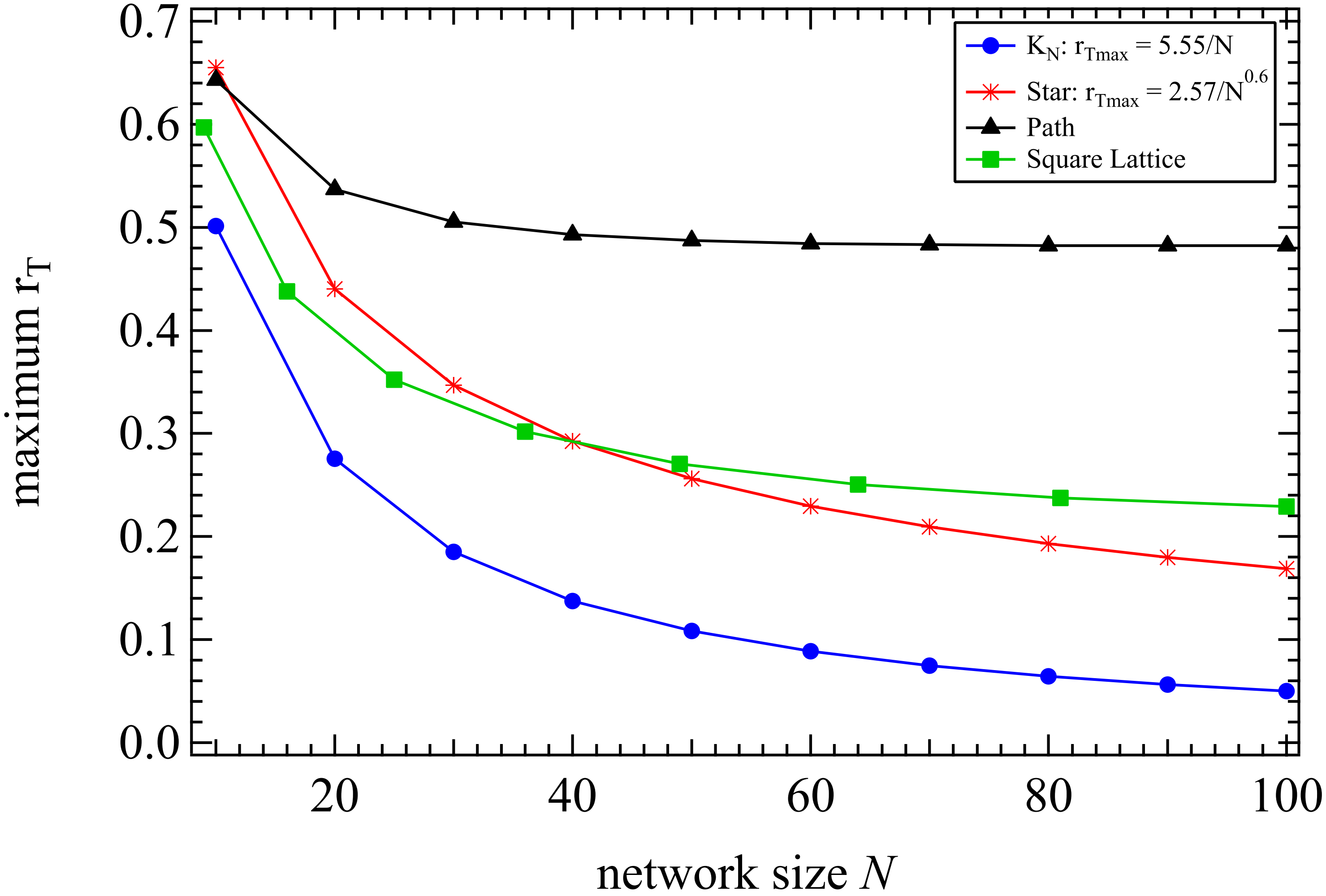
Bounds for $\|R\|_1 = \sum_{k=1}^{N} \lambda_k (AC)$

Wielandt-Hoffman : $$\sum_{k=1}^{N} \lambda_k (AC) \le \sum_{k=1}^{N} \lambda_k (A) \lambda_k (C)$$

Graph energy: $$\sum_{k=1}^{N} \lambda_k (A) \lambda_k (C) \le \frac{E_G}{2} \left(\lambda_1 (C) - \lambda_N (C) \right)$$

$\max_\tau r_T$

$$r_T = \frac{2\|R\|_1}{L}$$



Conjecture $\max_\tau r_T = O\left(\frac{1}{\lambda_1(A)}\right)$

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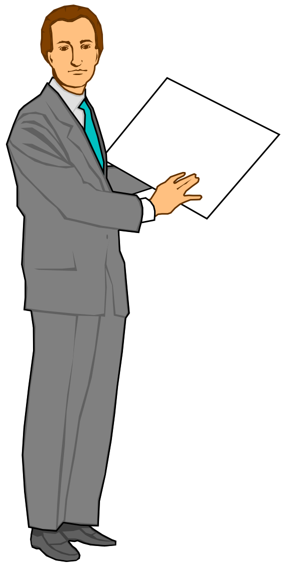
Outline



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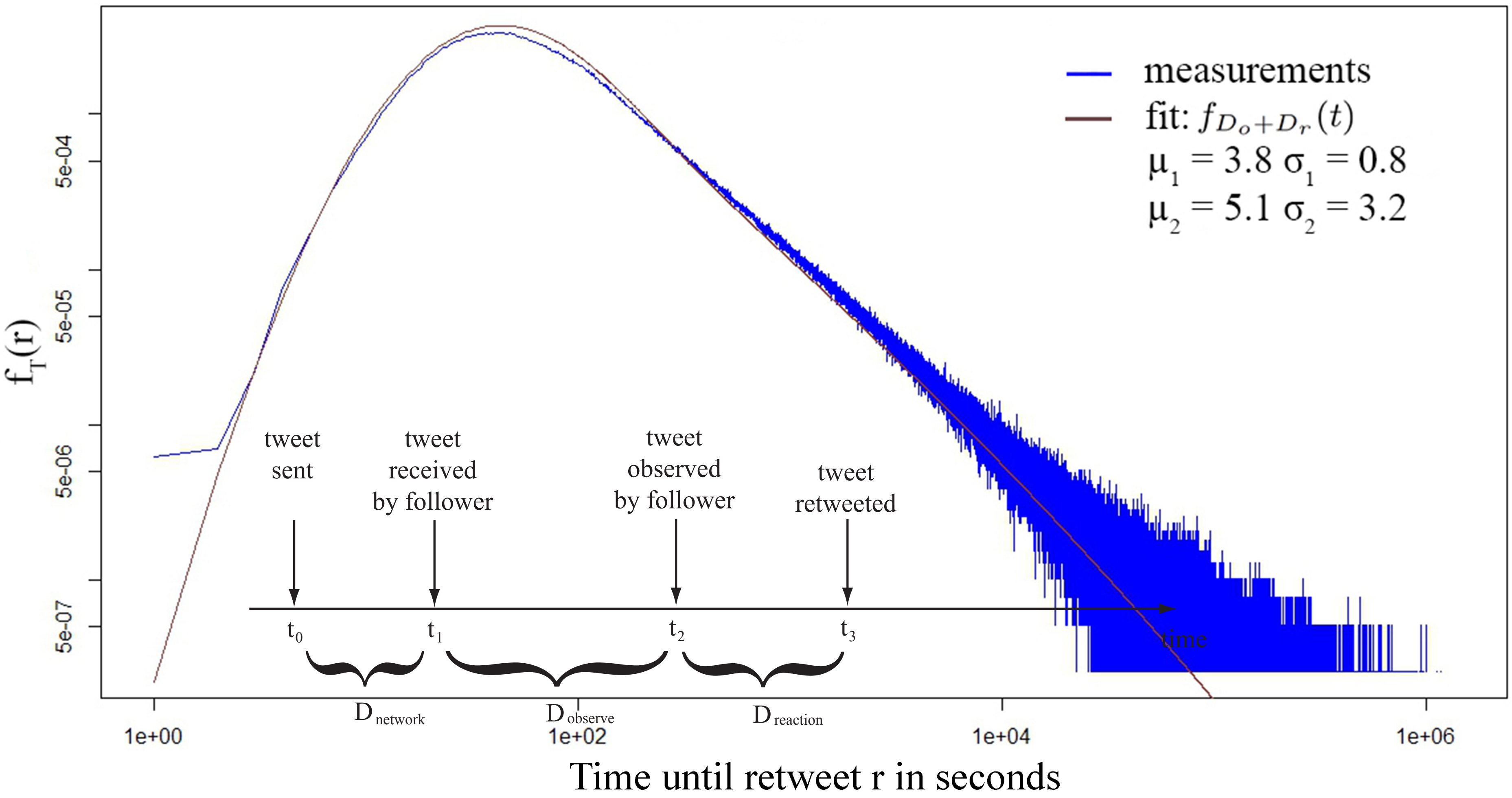
Epidemic times are not exponential



C. Doerr, N. Blenn and P. Van Mieghem, "Lognormal infection times of Online information spread", PLOS ONE, Vol. 8, No. 5, p. e64349, 2013

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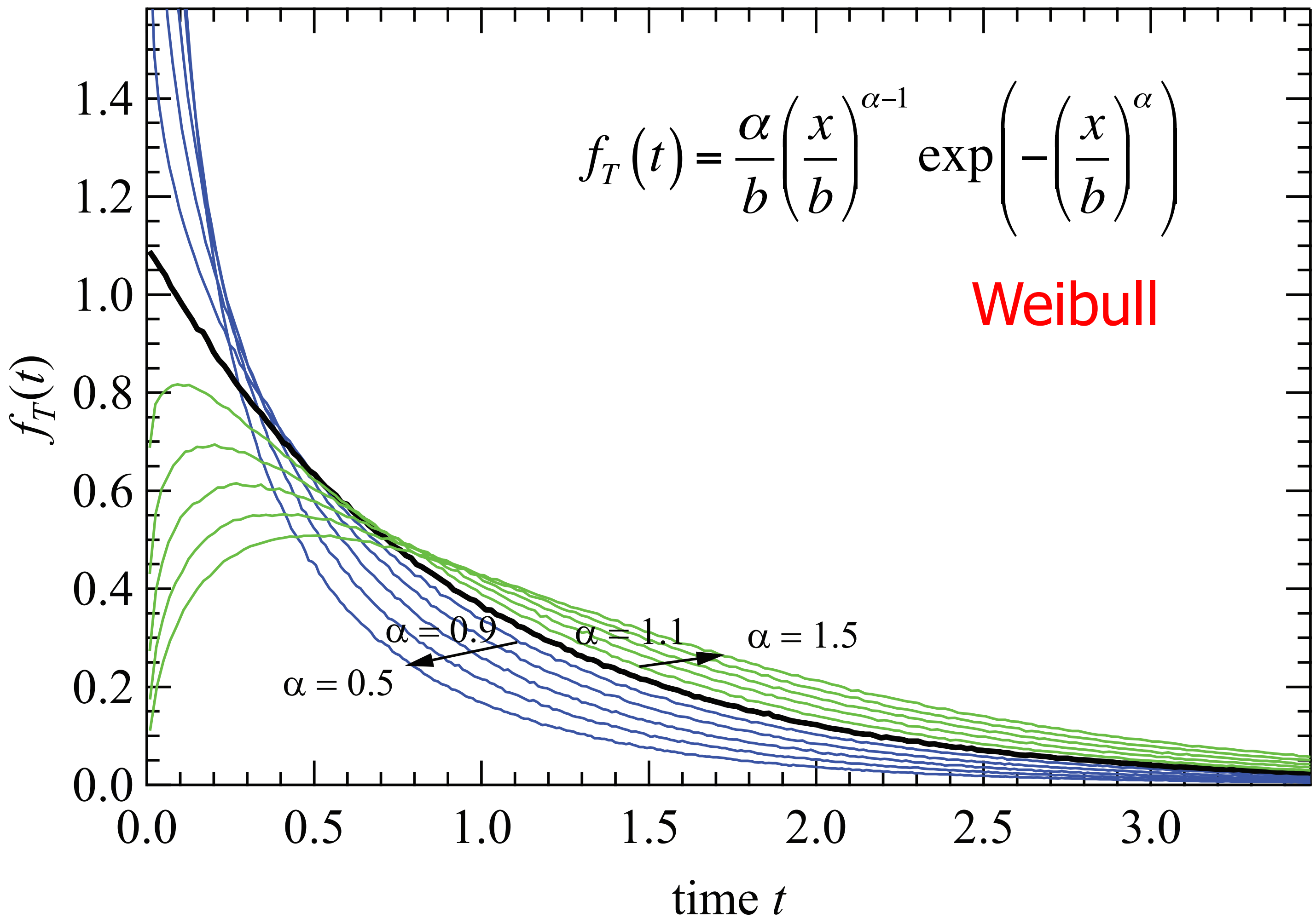
Non-Markovian infection times



$$f_T(t) = \frac{\alpha}{b}\left(\frac{x}{b}\right)^{\alpha-1} \exp\left(-\left(\frac{x}{b}\right)^{\alpha}\right)$$

Same mean E[*T*]:

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

T is the time to infect a neighboring node

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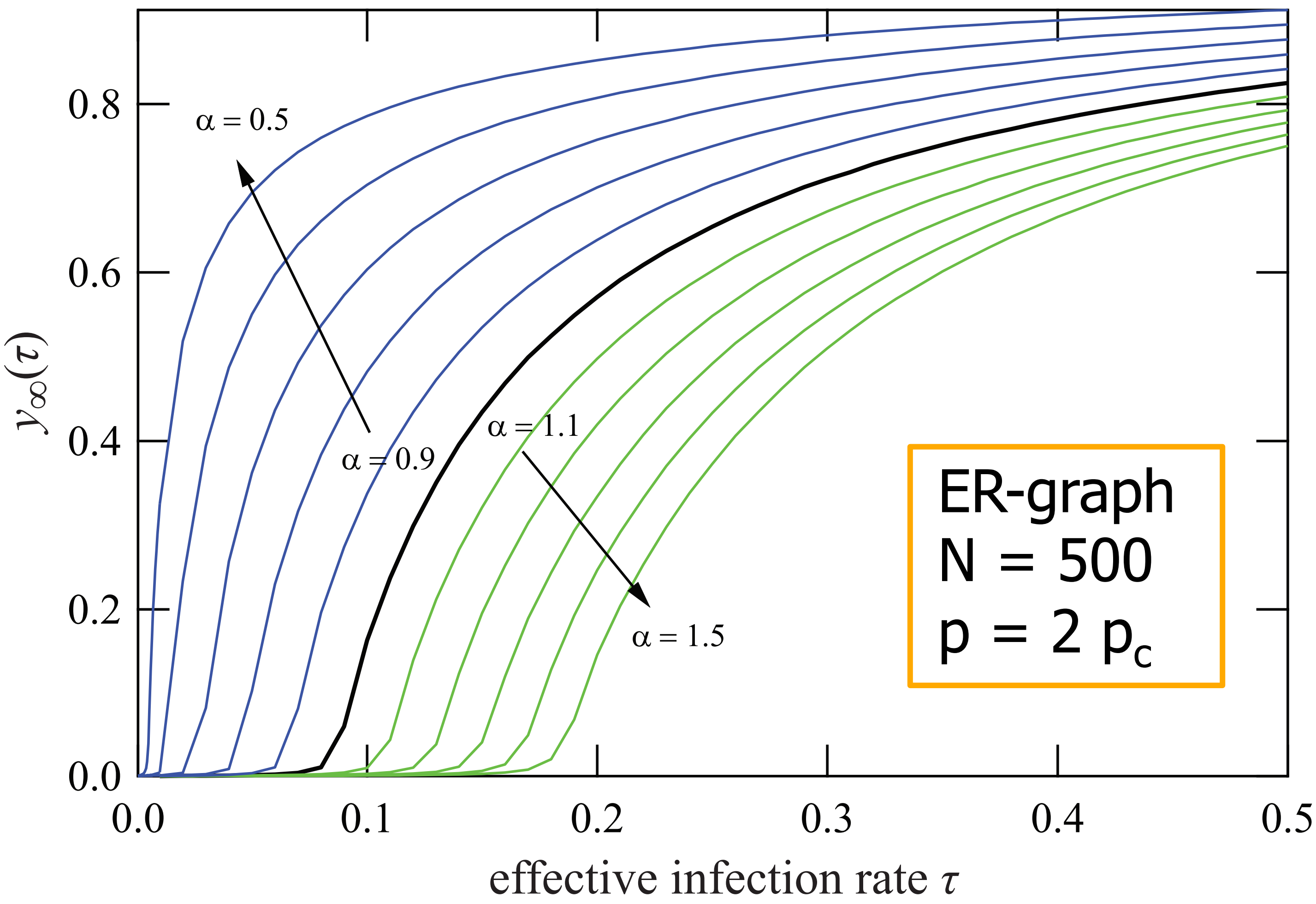
Non-Markovian epidemic threshold



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.

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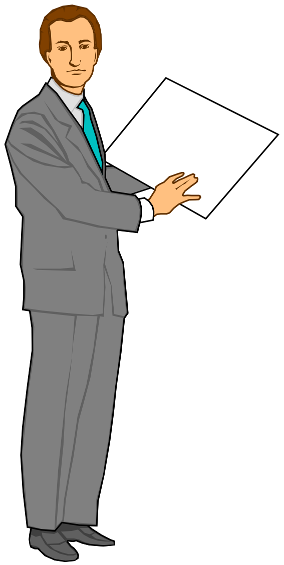
Outline



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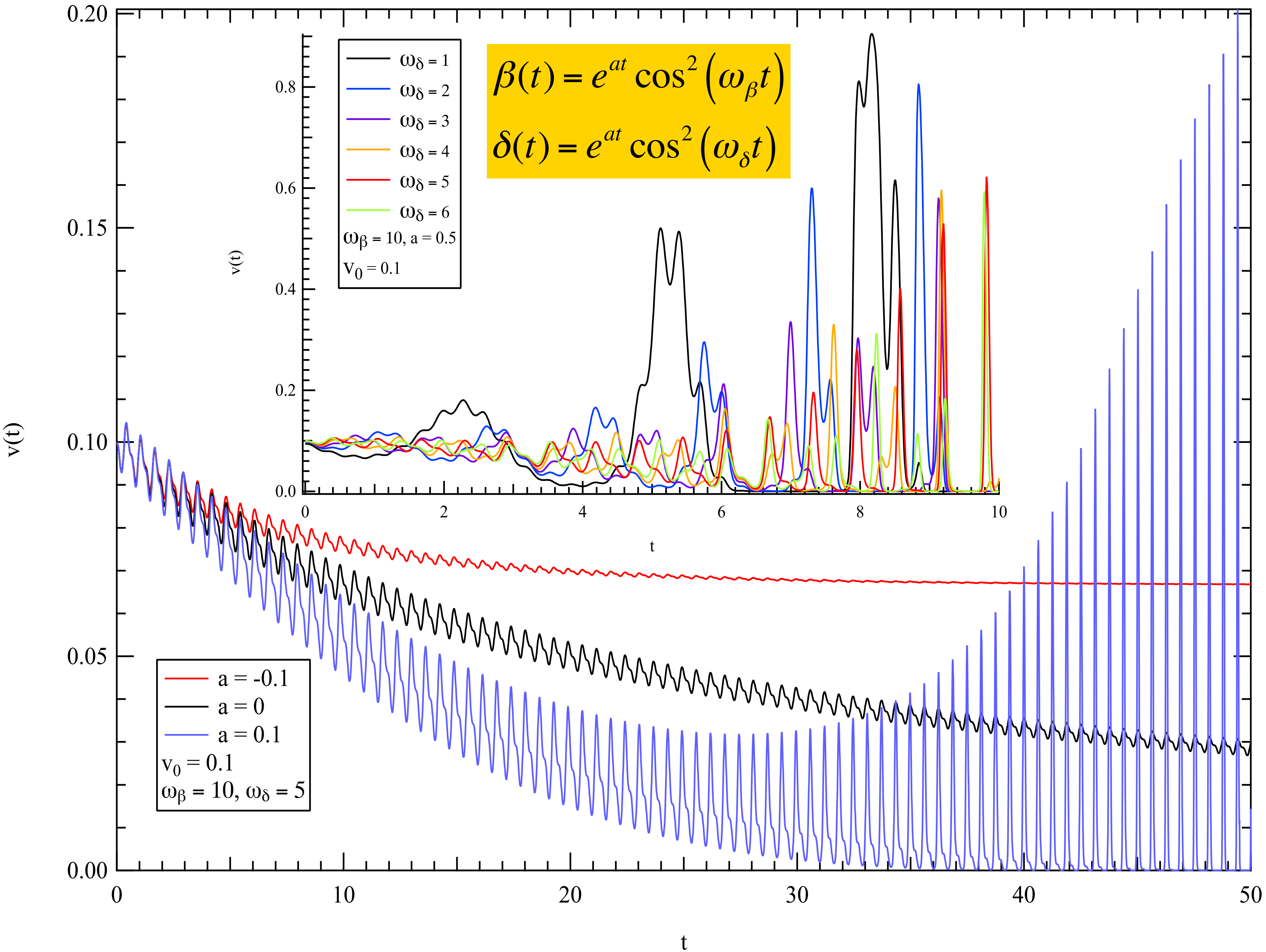
Time-dependent rates in NIMFA for regular graphs

$$\frac{dv(t)}{dt} = r\beta(t)v(t)(1 - v(t)) - \delta(t)v(t)$$

$$v(t) = \frac{\exp\left(\int_0^t \{r\beta(u) - \delta(u)\}du\right)}{\frac{1}{v(0)} + \int_0^t r\beta(s)\exp\left(\int_0^s \{r\beta(u) - \delta(u)\}du\right)ds}$$

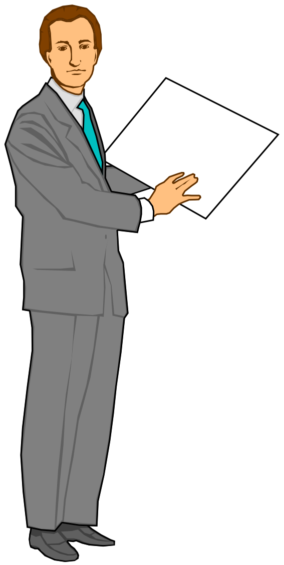
Application: modeling of the time evolution of the Internet Conficker worm (submitted)

P. Van Mieghem, 2014, "SIS epidemics with time-dependent rates describing ageing of information spread and mutation of pathogens", Delft University of Technology, report20140615.



$\beta(t) = e^{at}\cos^2(\omega_\beta t)$
$\delta(t) = e^{at}\cos^2(\omega_\delta t)$
$\omega_\delta = 1$
$\omega_\delta = 2$
$\omega_\delta = 3$
$\omega_\delta = 4$
$\omega_\delta = 5$
$\omega_\delta = 6$
$\omega_\beta = 10$, a = 0.5
$v_0 = 0.1$
v(t)
t
a = -0.1
a = 0
a = 0.1
$v_0 = 0.1$
$\omega_\beta = 10$, $\omega_\delta = 5$

Outline



Exact SIS model

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- Time-dependent rates
- **Upper bound SIS epidemic τ_c**
- Survival time

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Upper bounds for τ_c

From $$\frac{dy(t^*)}{dt^*} = -y(t^*) + \frac{\tau}{N} E\left[w^T Q w\right]$$

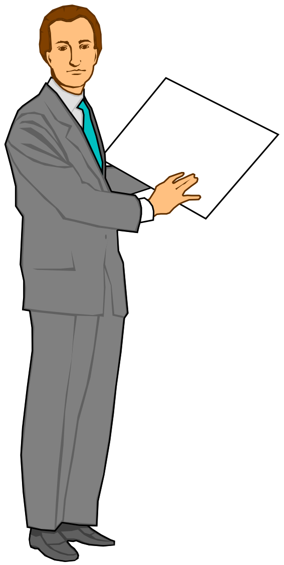
where the fraction of infected nodes is $S = \frac{1}{N}\sum_{j=1}^{N} X_j = \frac{u^T w}{N}$
and y = E[S]

we have $$\tau_c \leq \frac{1}{\mu_{N-1}\left(1 - 2\sqrt{Var[S_\infty(\tau_c)]}\right)}$$

Ring/Cycle graph: $$(\tau_c)_C = \frac{1}{2\left(1 - 2\sqrt{Cov[X_{1\infty}, X_{2\infty}]}\right)}$$

P. Van Mieghem, 2016, "Approximate formula and bounds for the time-varying SIS prevalence in networks", Physical Review E, Vol. 93 No. 5, p. 052312.

Outline



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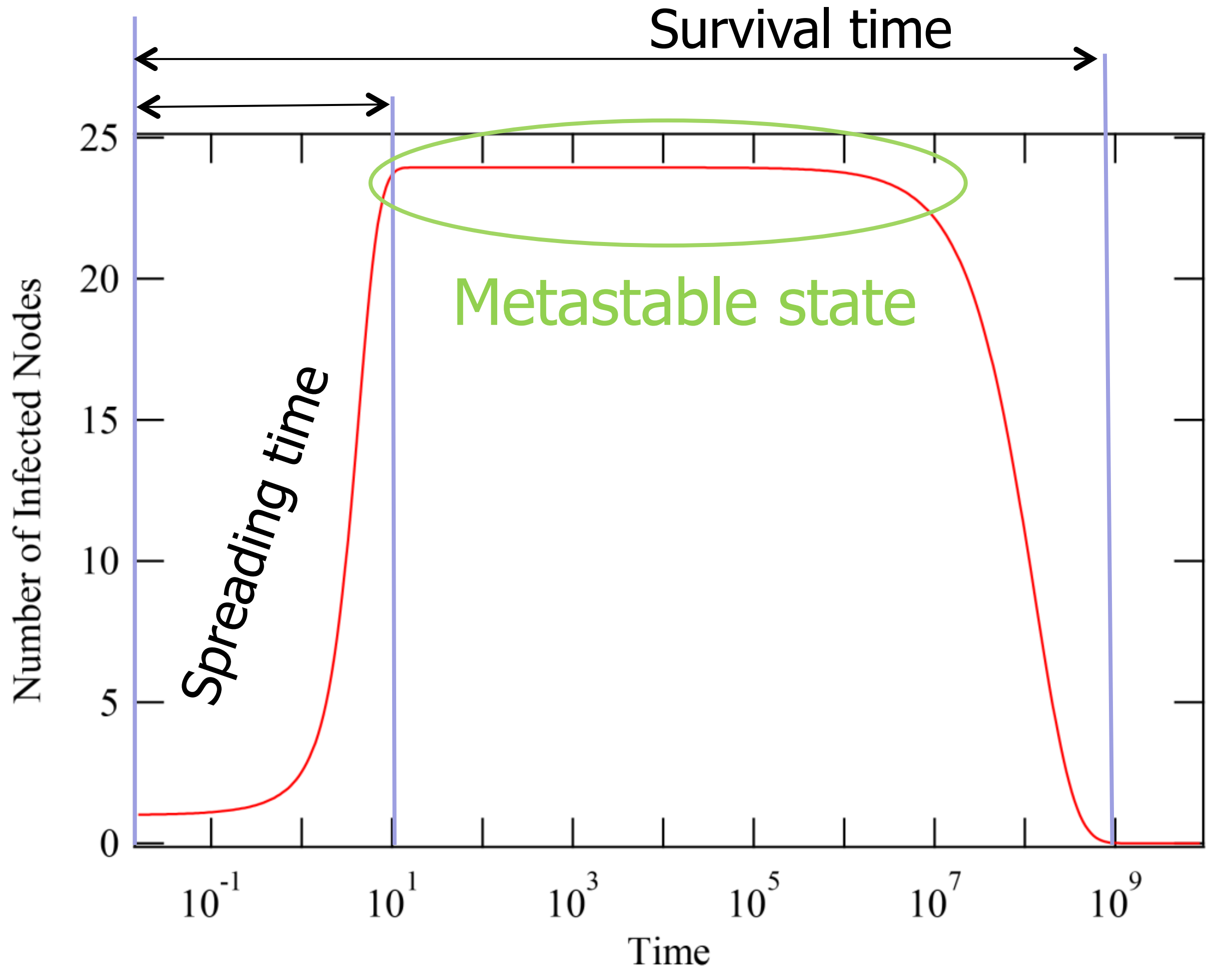
- Upper bound SIS epidemic τ_c
- **Survival time**

Spreading and survival time



For the effect of different initial conditions, see also Fig. 17.2 on p. 457 in P. Van Mieghem, *Performance Analysis of Complex Networks and Systems*, Cambridge University Press, 2014.

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Average Time to Absorption (Survival time)

Ganesh,Massoulie,Towsley (2005):

$$E[T] \leq \frac{1}{\delta} \frac{\log N + 1}{(1 - \tau\lambda)_1} \qquad \tau < \tau_c$$

$$E[T] = O\left(e^{bN^a}\right) \qquad \tau > \tau_c$$

Mountford *et al.* (2013):
(regular trees w. bounded degree)

$$E[T] = O\left(e^{cN}\right)$$

Complete graph K_N:

$$E[T] = F(\tau) = \frac{1}{\delta} \sum_{j=1}^{N} \sum_{r=0}^{j-1} \frac{(N-j+r)!}{j(N-j)!}$$

$$x = \tau N \approx \frac{\tau}{\tau_c} > 1 \qquad F\left(\frac{x}{N}\right) \sim \frac{1}{\delta} \frac{x\sqrt{2\pi}}{(x-1)^2} \frac{e^{N\left(\log x + \frac{1}{x} - 1\right)}}{\sqrt{N}}$$

P. Van Mieghem, "Decay towards the overall-healthy state in SIS epidemics on networks", arxiv1310.3980 (2013).
R. van de Bovenkamp and P. Van Mieghem, "Survival time of the SIS infection process on a graph", PRE, vol. 92, p. 032806 (2015).

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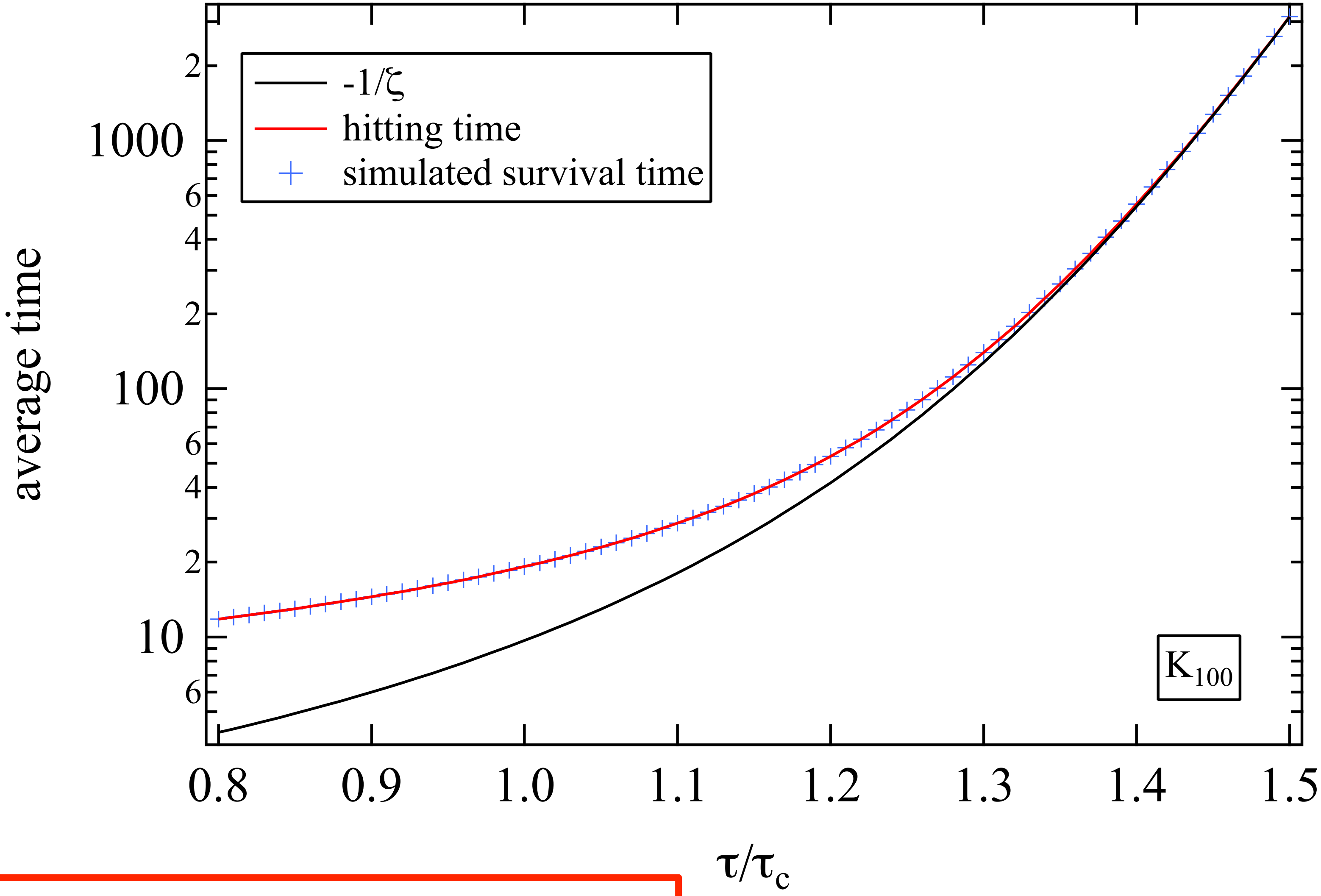
Average survival time in K_N



$$E[T] = F(\tau) = \frac{1}{\delta}\sum_{j=1}^{N}\sum_{r=0}^{j-1}\frac{(N-j+r)!}{j(N-j)!}$$

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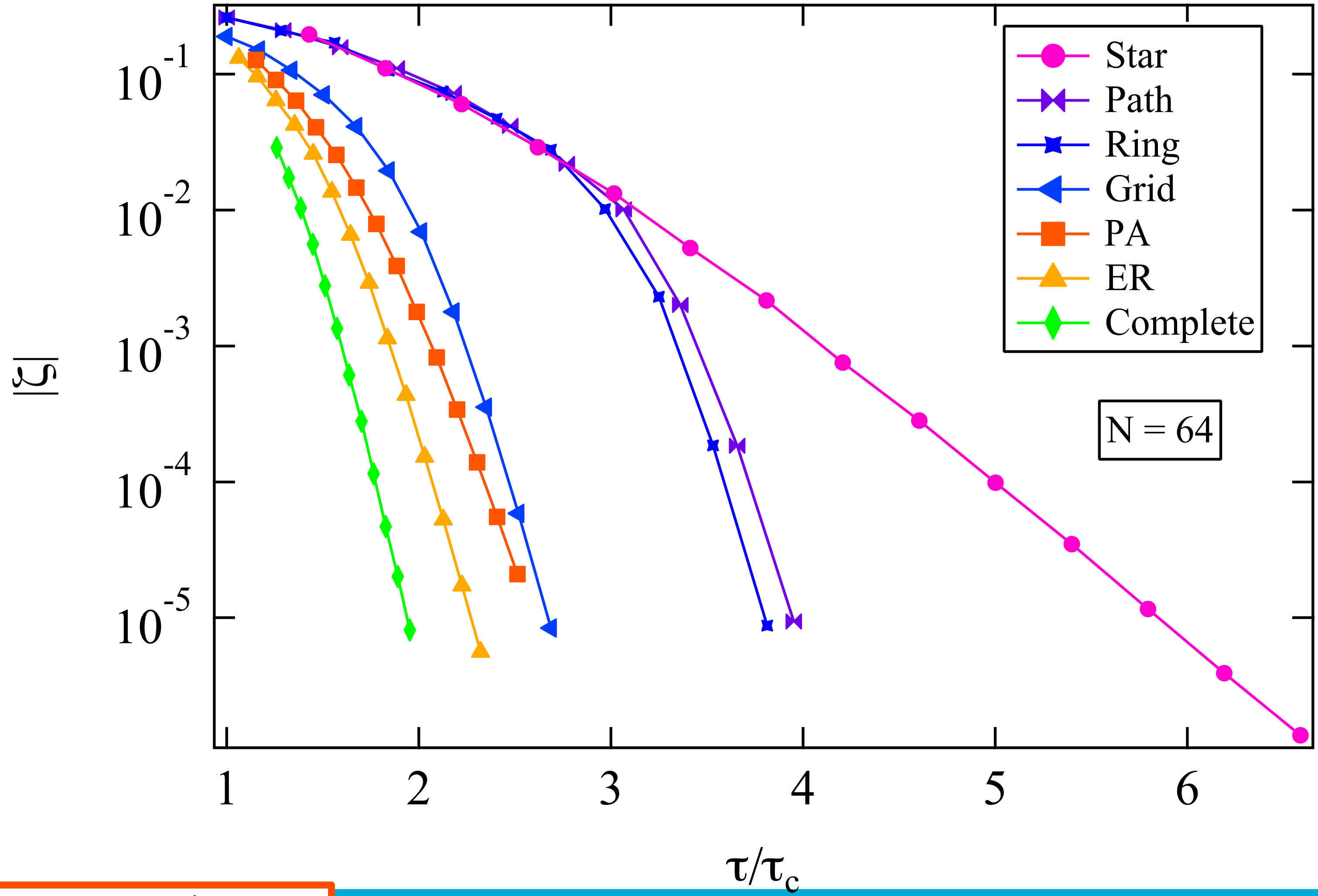
Second smallest eigenvalue Q in graphs



$$|\zeta| \approx \frac{1}{E[T]}$$

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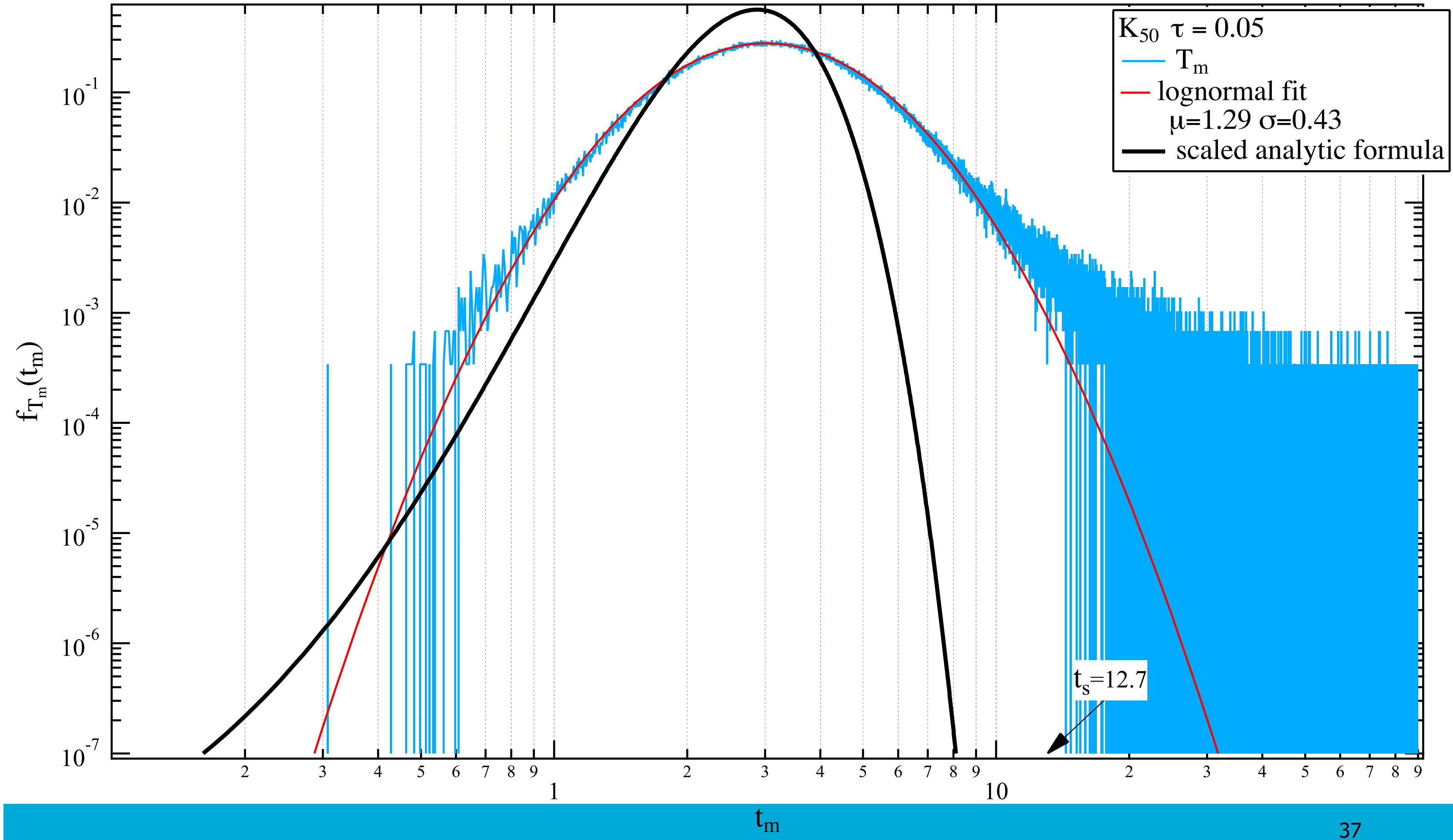
Pdf of the spreading time



With Zhidong He: in preparation

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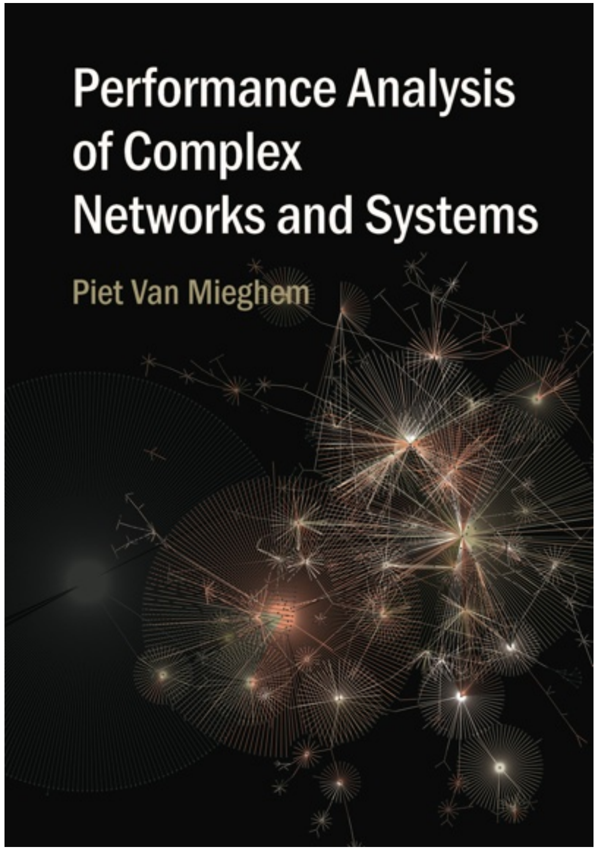
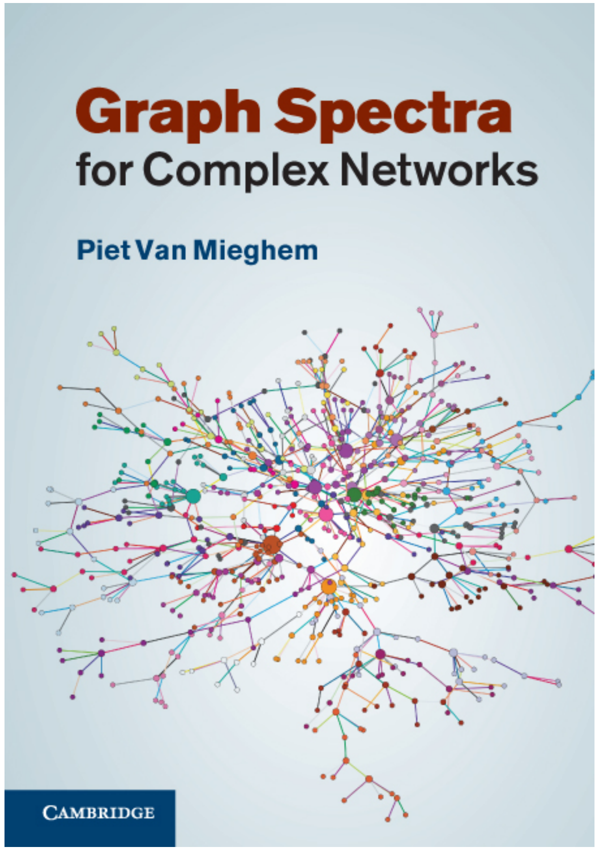
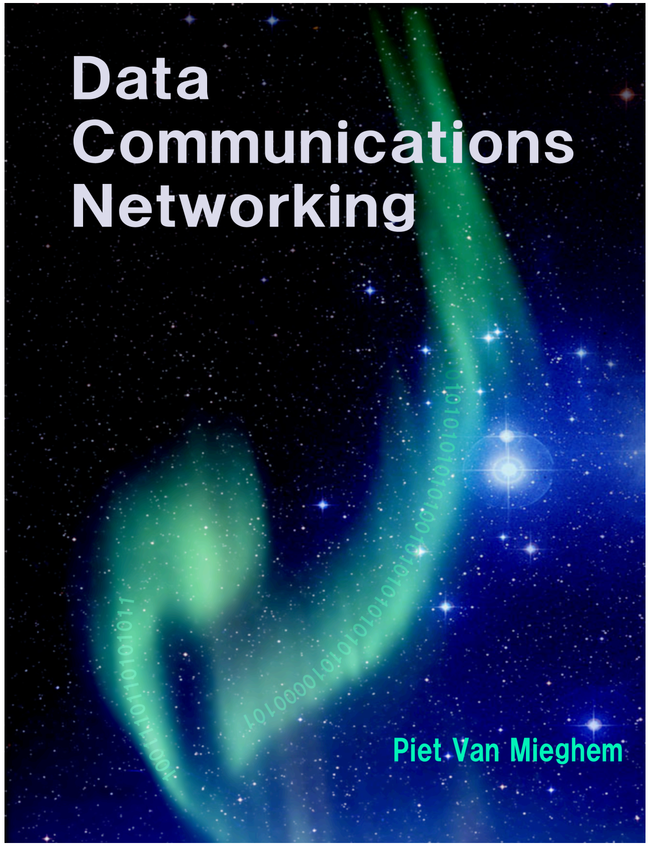
Challenges for epidemics on networks

- A general mean-field criterion: for which graphs is NIMFA accurate? Is the conjecture true?
- Tight upper bound of the epidemic threshold (for any graph), or near to exact determination of τ_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







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Thank You

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