SIS epidemics on Networks

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in collaboration with Eric Cator, Ruud van de Bovenkamp, Cong Li, Stojan Trajanovski, Dongchao Guo, Annalisa Socievole and Huijuan Wang
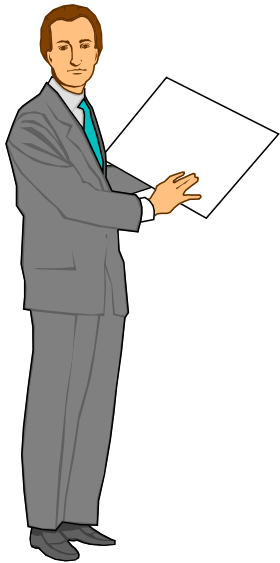
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Outline

Exact SIS model

NIMFA: N-intertwined MF approximation

Expected survival time

Non-Markovian epidemics

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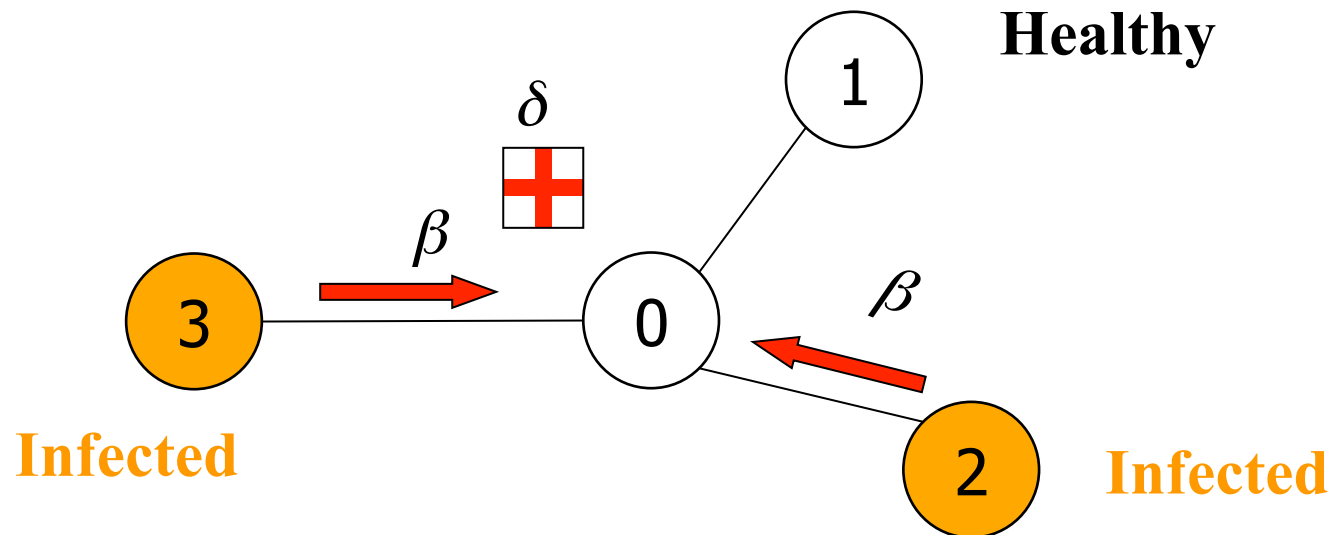
Simple SIS model on networks

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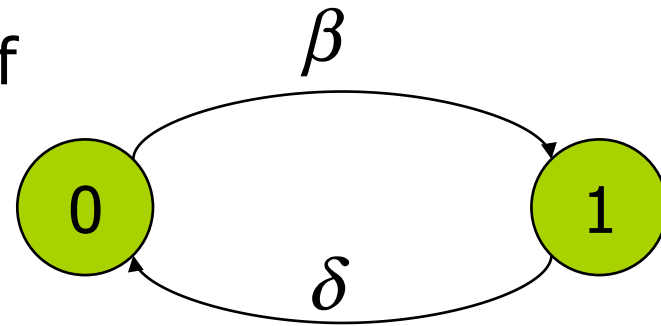- Homogeneous death (curing) rate δ for infected nodes

$\tau = \beta / \delta$: 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
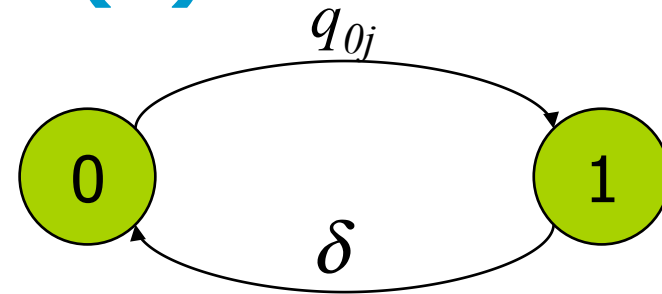 - curing rate δ
- At time t:
  - $X_j(t)$ is the state of node j
  - infinitesimal generator $Q_j(t) = \begin{bmatrix} -q_{0j} & q_{0j} \\ q_{1j} & -q_{1j} \end{bmatrix} = \begin{bmatrix} -q_{0j} & q_{0j} \\ \delta & -\delta \end{bmatrix}$

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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

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

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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

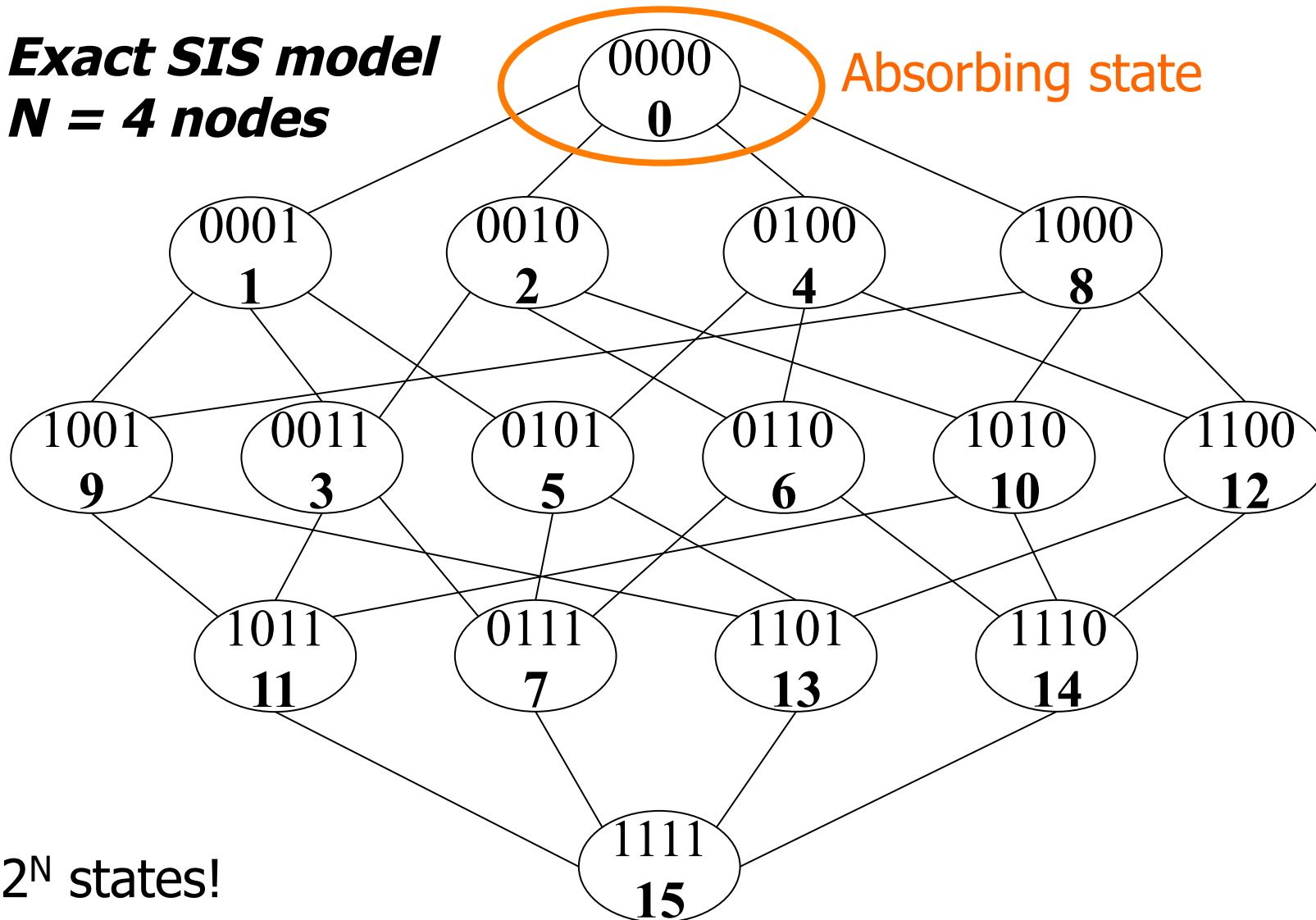- *Drawback*: this exact model has 2^N states, where N is the number of nodes in the network.

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SIS Markovian process on a graph

$$\begin{cases} \text{for } j \notin I : I \rightarrow I \cup \{j\} \text{ at rate } \beta \sum_{k \in I} a_{ki} + \varepsilon \\ \text{for i} \in I : I \rightarrow I \setminus \{i\} \text{ at rate } \delta \end{cases}$$

I: infected subgraph (containing infected nodes)
ε: nodal self-infection

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Exact SIS model N = 4 nodes

Absorbing state

2^N states!

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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

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

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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$_i$X$_j$X$_k$]...

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

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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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Non-Markovian epidemics

NIMFA: N-intertwined mean-field approxim.

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

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

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

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

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

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NIMFA non-linear equations

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

where the viral probability of infection is

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

In matrix form:

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

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

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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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Lower bound for the epidemic threshold

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

Ignoring the correlation terms

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

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

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

The NIMFA epidemic threshold is precisely

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

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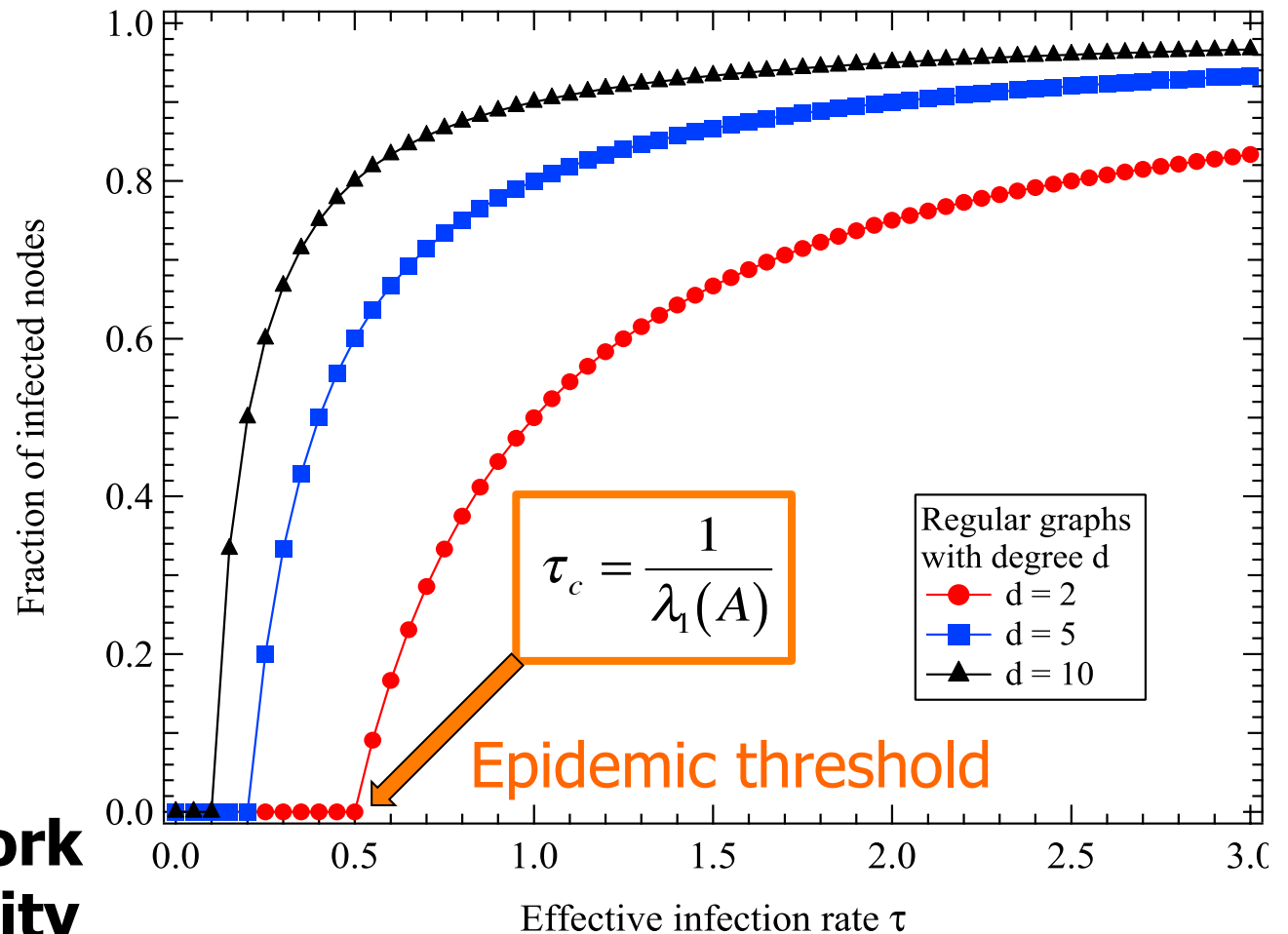# What is so interesting about epidemics?

network protection

self-replicating
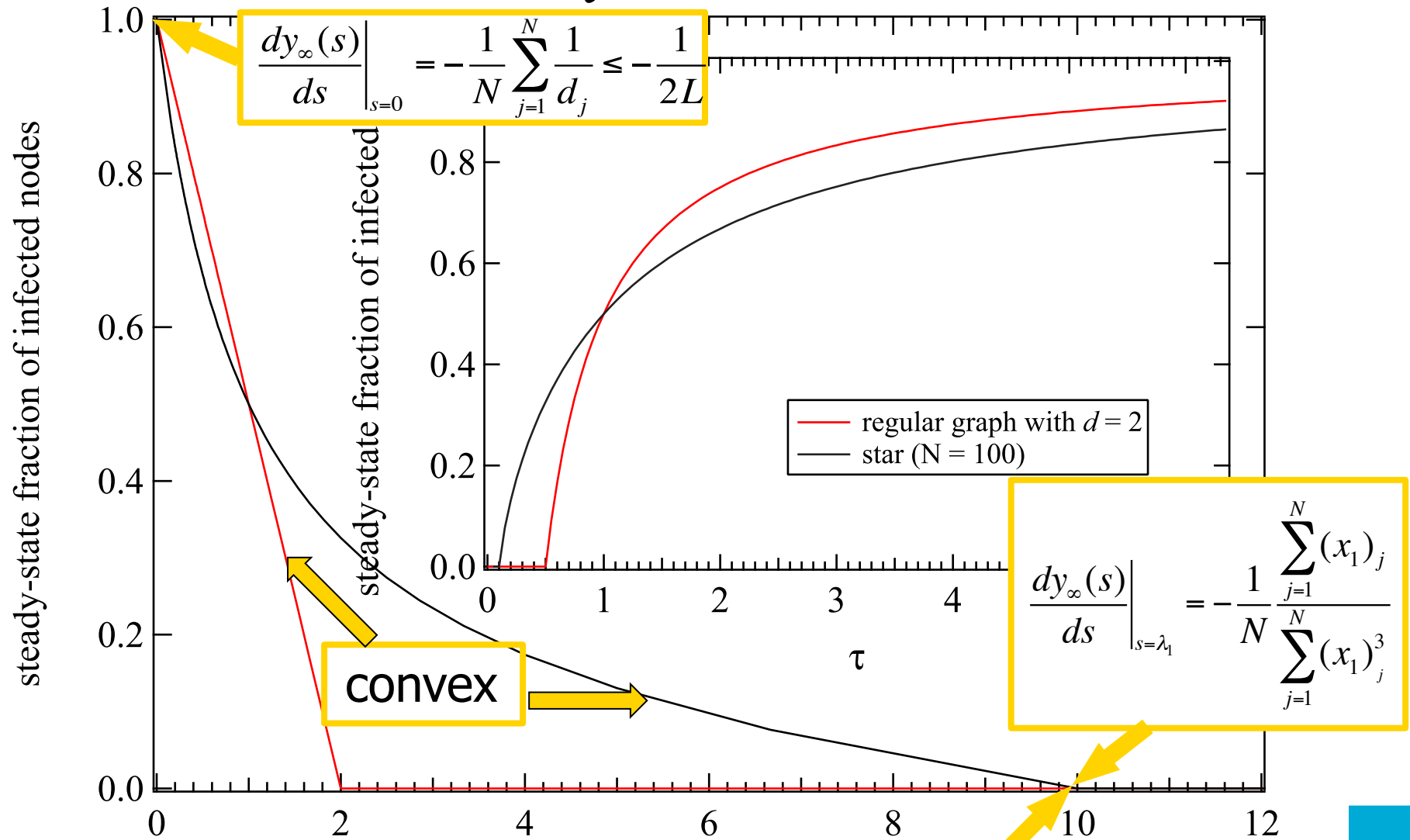objects (worms)

propagation errors

rumors (social nets)

epidemic algorithms
(gossiping)

**cybercrime : network
robustnes & security**

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

Epidemic threshold

Regular graphs with degree d
- d = 2
- d = 5
- d = 10

Fraction of infected nodes

Effective infection rate τ

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

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

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

steady-state fraction of infected nodes

steady-state fraction of infected

convex

— regular graph with $d = 2$
— star ($N = 100$)

τ

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

$s = 1/\tau$

$s_c = \lambda_1$

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

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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.

- **GEMF**: very general extension: 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.

- 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.
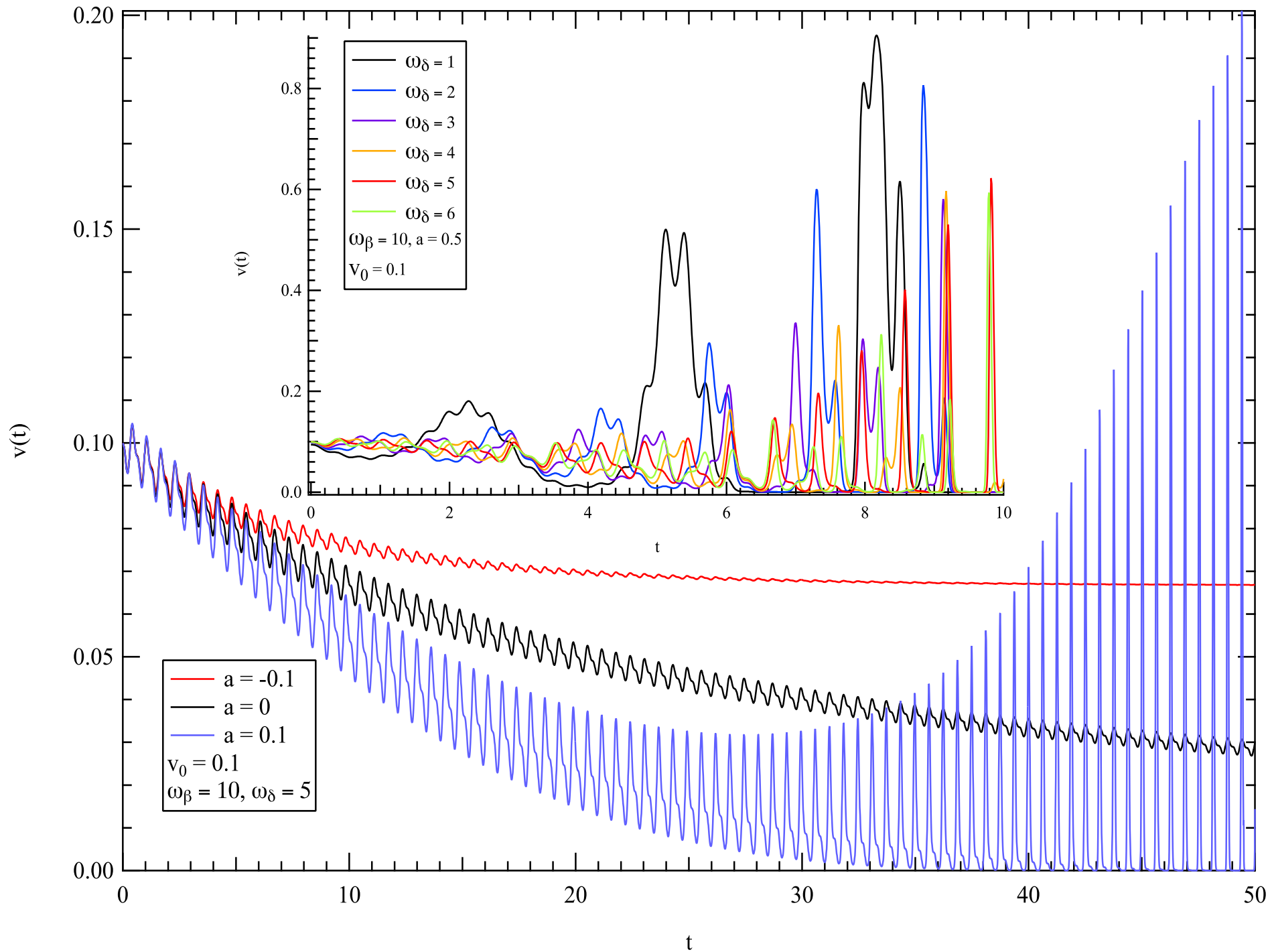
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Time-dependent rates in NIMFA for regular graphs

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

$$v(t) = \frac{\exp\left(\int_0^t \{r\beta(u) - \delta(u)\}\,du\right)}{\frac{1}{v(0)} + \int_0^t r\beta(s)\exp\left(\int_0^s \{r\beta(u) - \delta(u)\}\,du\right)ds}$$
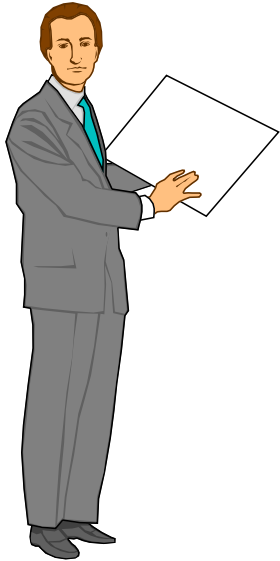
Classical case (constant rates): Kephart & White (1992)

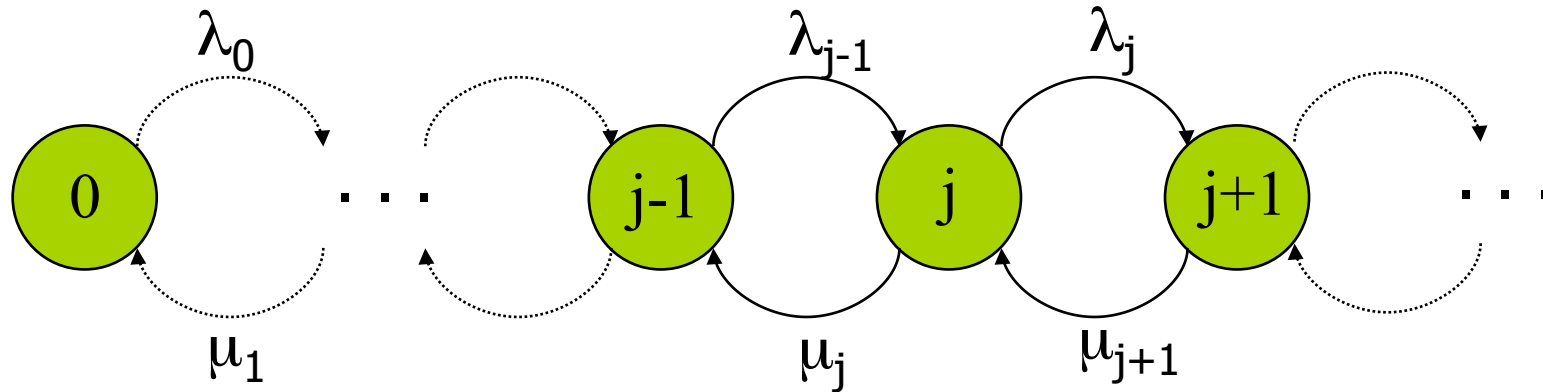$$v(t) = \frac{\exp(\{r\beta - \delta\}t)}{\frac{1}{v(0)} + \frac{1}{\left\{1 - \frac{1}{r\tau}\right\}}\left(\exp(\{r\beta - \delta\}t) - 1\right)}$$

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SIS epidemics on the complete graph

$$\begin{cases} \lambda_j = (\beta j + \varepsilon)(N - j) \\ \mu_j = \delta j \end{cases}$$

Birth-death processes *quadratic* in state j

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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: $\quad E[T] \cong \dfrac{1}{|\zeta|}$ with $\quad -\zeta = \dfrac{1}{F(\tau)} + O\left(\dfrac{N^2 \log N}{x^{2N-1}}\right)$

$$x = \tau N \approx \frac{\tau}{\tau_c}$$

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

$$F\left(\frac{x}{N}\right) \sim \frac{1}{\delta} \frac{x\sqrt{2\pi}}{(x-1)^2} \frac{e^{N\left(\log x + \frac{1}{x} - 1\right)}}{\sqrt{N}}$$
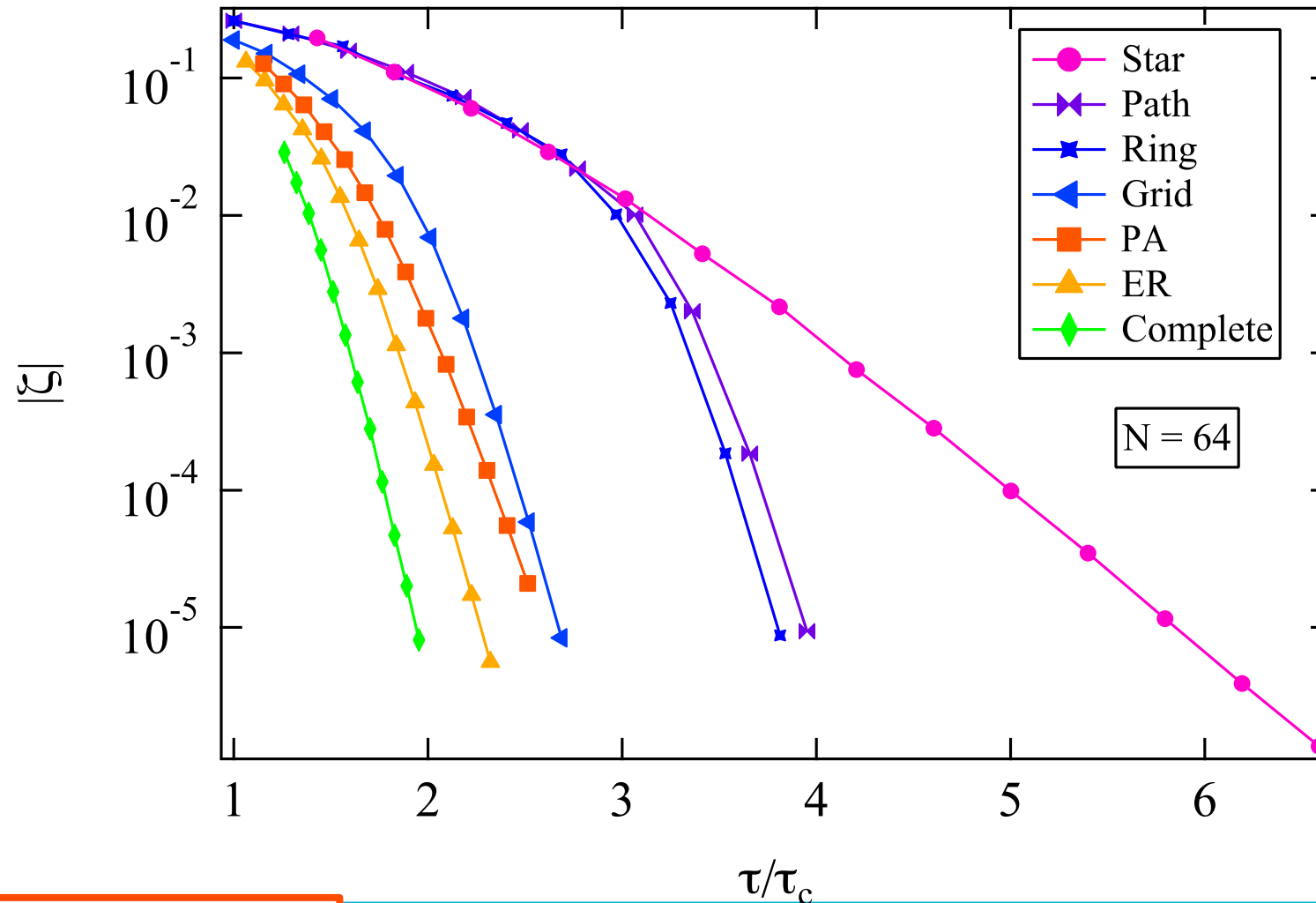
Hitting time (on K_N) for all τ: $\qquad E[T] = F(\tau)$
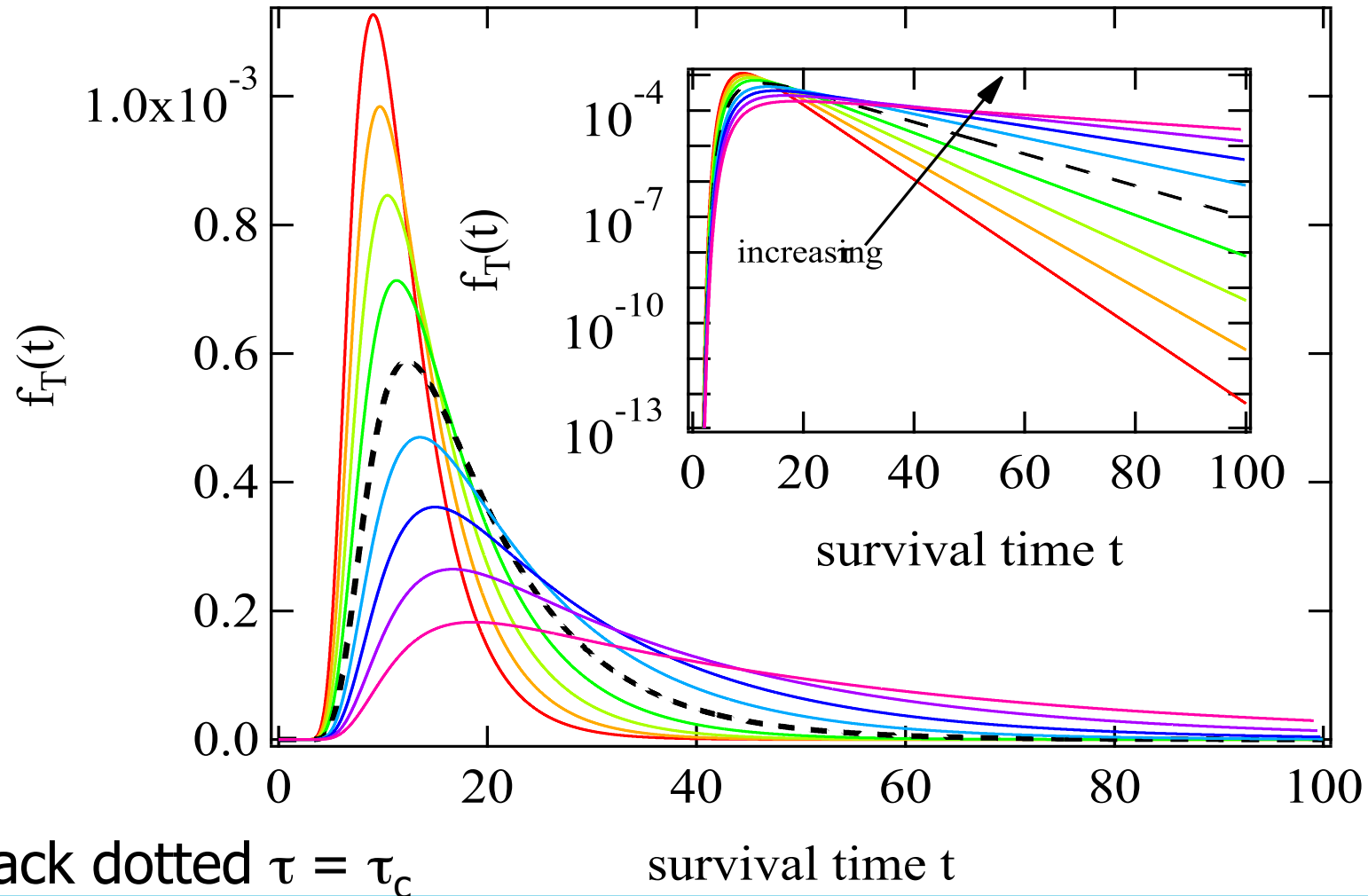
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Average survival time in K$_N$
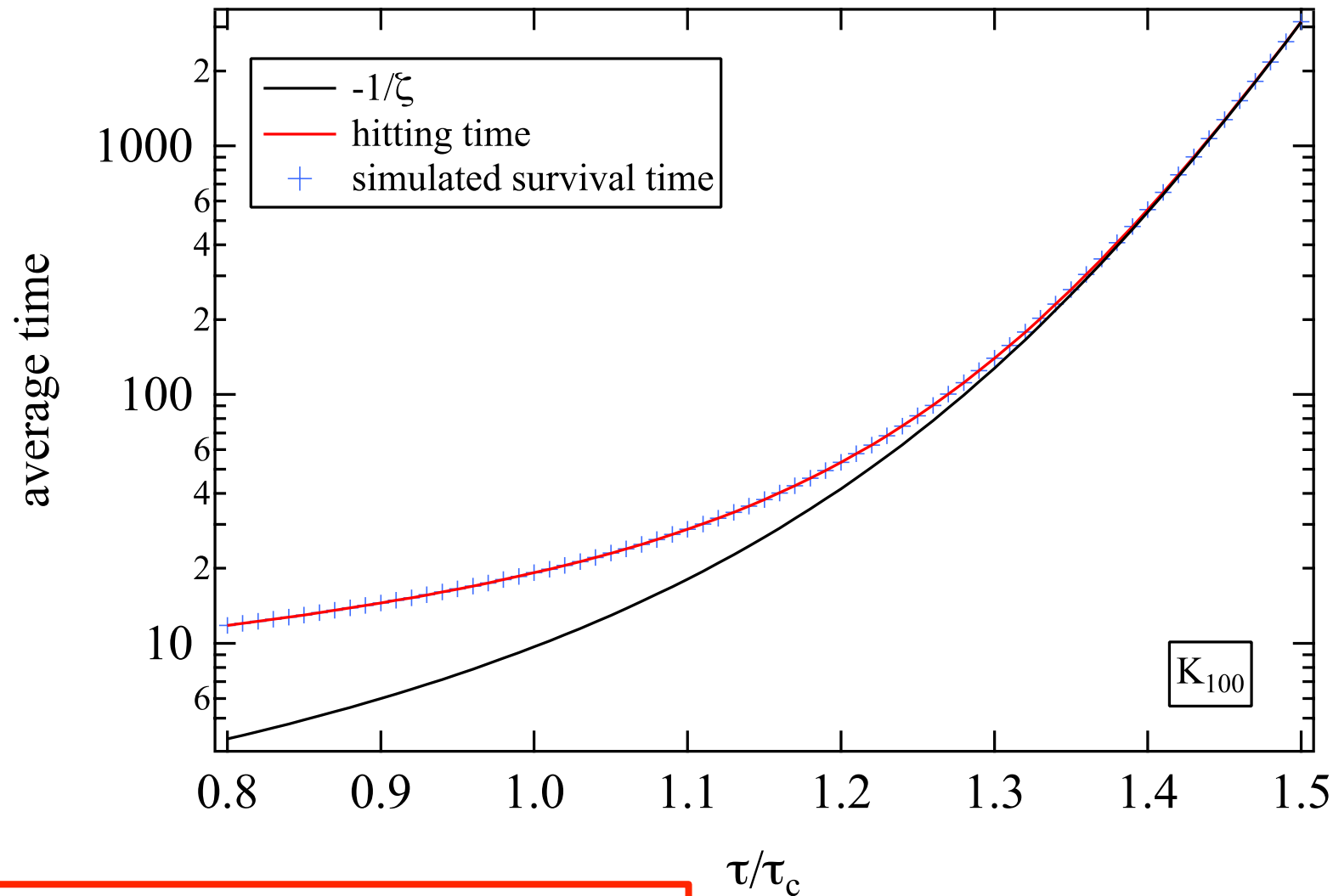
$$E[T] = F(\tau) = \frac{1}{\delta} \sum_{j=1}^{N} \sum_{r=0}^{j-1} \frac{(N-j+r)!}{j(N-j)!}$$
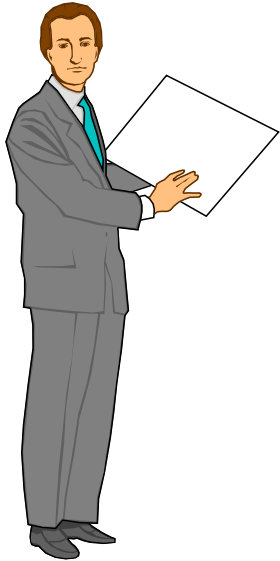
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Second smallest eigenvalue Q in graphs

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

Pdf survival time in K$_{100}$

Black dotted $\tau = \tau_c$

$$f_T\left(t \mid \beta = 0\right) = \delta I \left(1 - e^{-\delta t}\right)^{I-1} e^{-\delta t} \quad \text{(Max I i.i.d. exp.)}$$

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Expected survival time

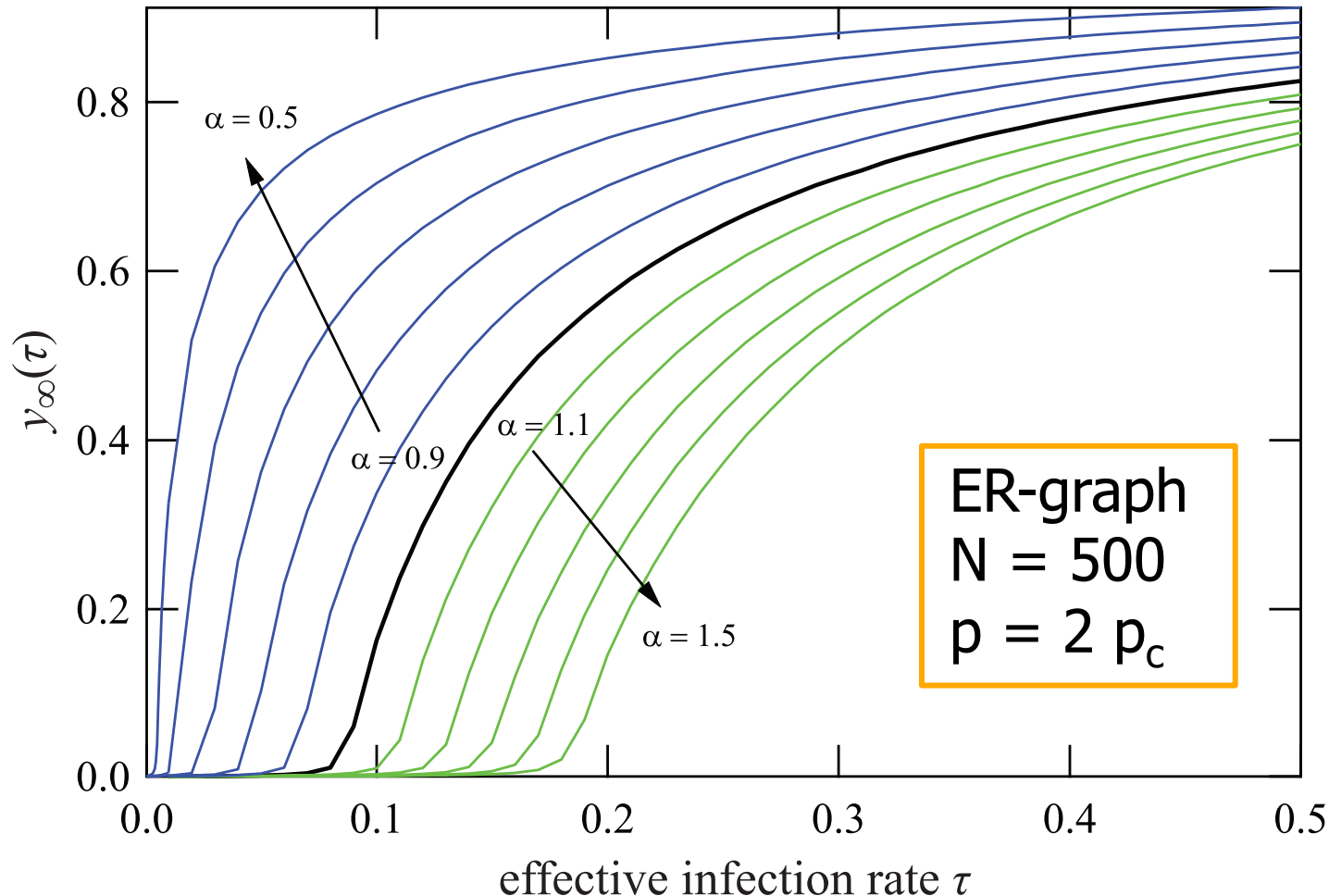Non-Markovian epidemics

Epidemic times are not exponential

Time until retweet r in seconds
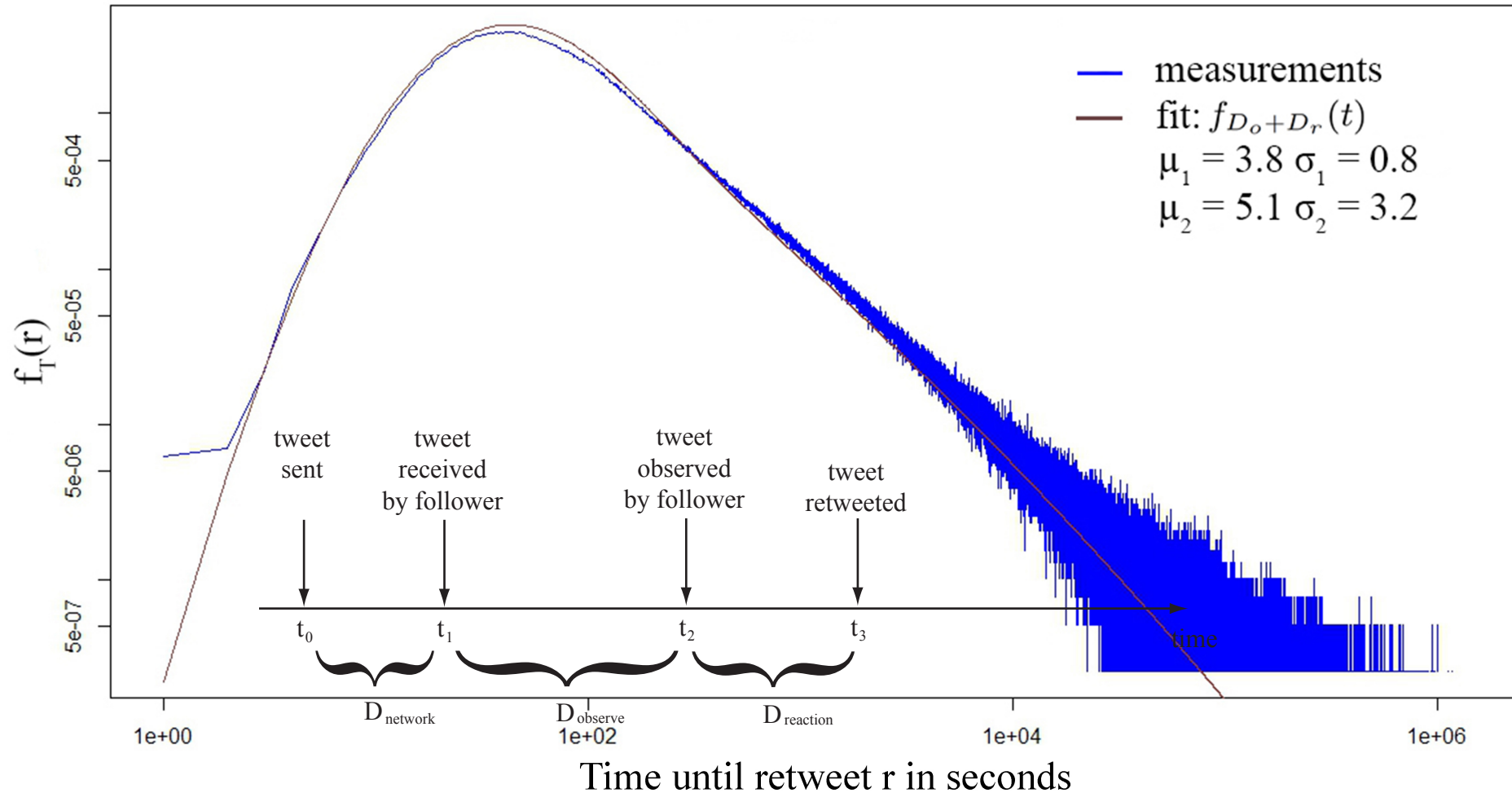
Non-Markovian infection times

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

Weibull pdf

Same mean
E[T]:

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

$\alpha = 0.9$ $\alpha = 1.1$ $\alpha = 1.5$

$\alpha = 0.5$
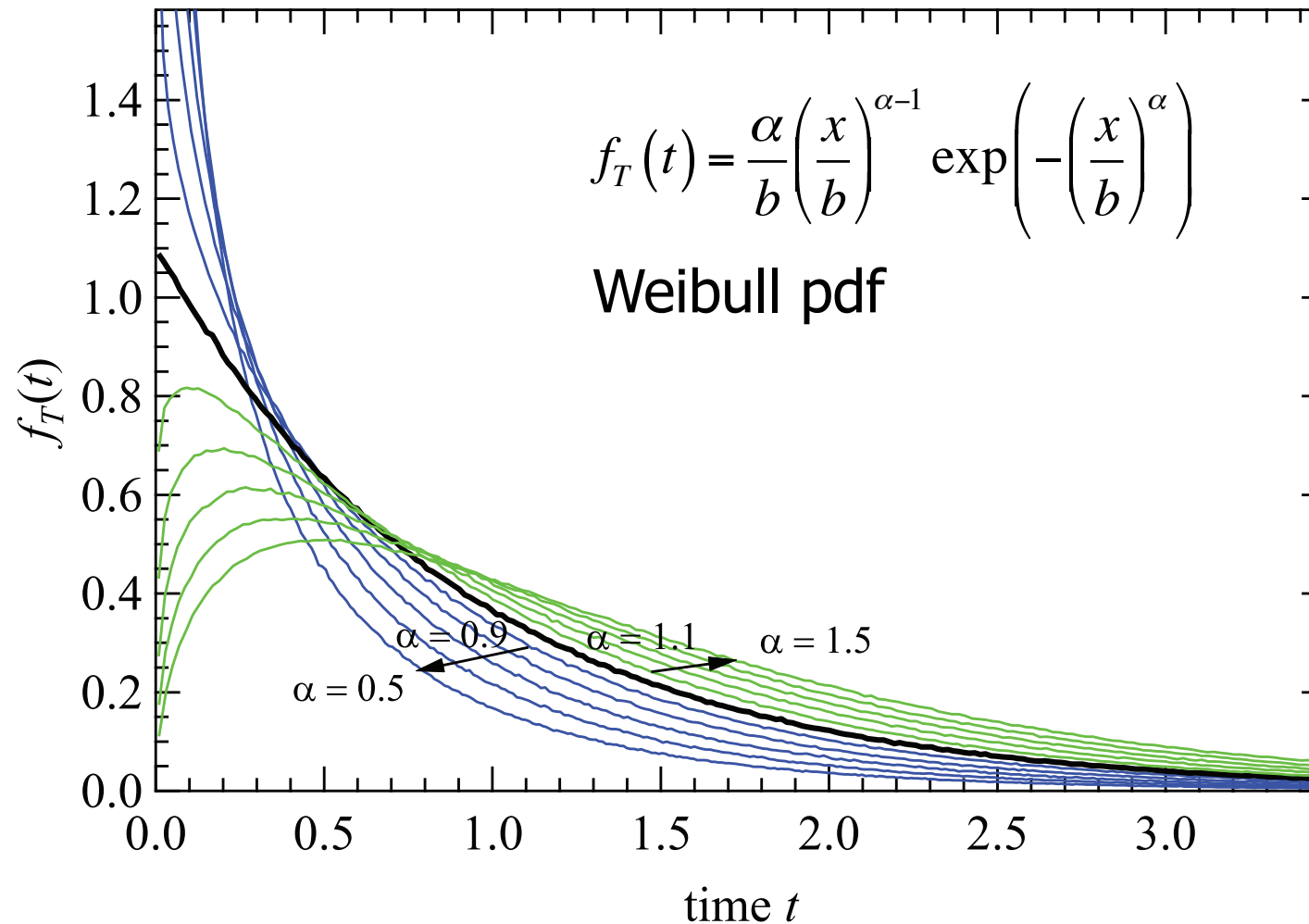
T is the time to infect a neighboring node

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Non-Markovian epidemic threshold

Non-exponential infection time has a dramatic influence!

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GSIS: SIS with general infection times

NIMFA is valid provided the effective infection rate $\tau = \beta/\delta$ is replaced by the **averaged number $E[M]$ of infection events during a healthy period**:

$$E[M] = \frac{1}{2\pi i} \int_{c-i\infty}^{c+i\infty} \frac{\phi_T(z)\phi_R(-z)}{1-\phi_T(z)} \frac{dz}{z} \qquad \phi_X(z) = E[e^{-zX}]$$
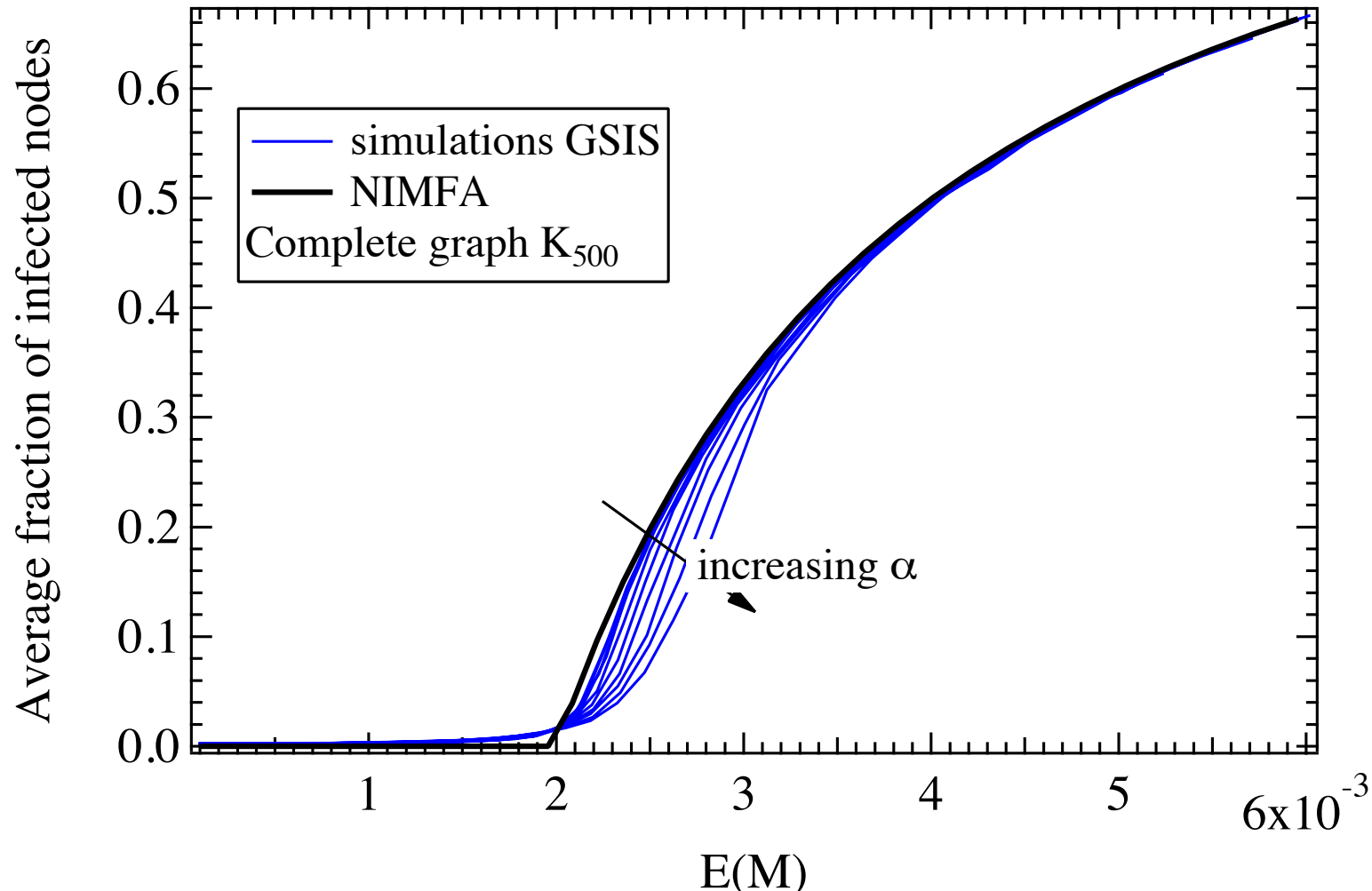
Generalized criterion for the epidemic threshold: $\quad E[M_c] = \dfrac{1}{\lambda_1}$

Scaling law for large N
When infection time T is Weibullian: $\quad \tau_c = \dfrac{q(\alpha)}{\lambda_1^{1/\alpha}} \quad q(\alpha) = O(1)$

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E. Cator, R. van de Bovenkamp and P. Van Mieghem, "SIS epidemics on networks with general infection and curing times", Physical Review E, Vol. 87, No. 6, p. 062816, 2013.

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GSIS: E[M] gives the right scaling

E[*M*]: averaged number of infection events
received during a healthy period

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Pdf survival time K_{100} (Weibull)

Increasing α
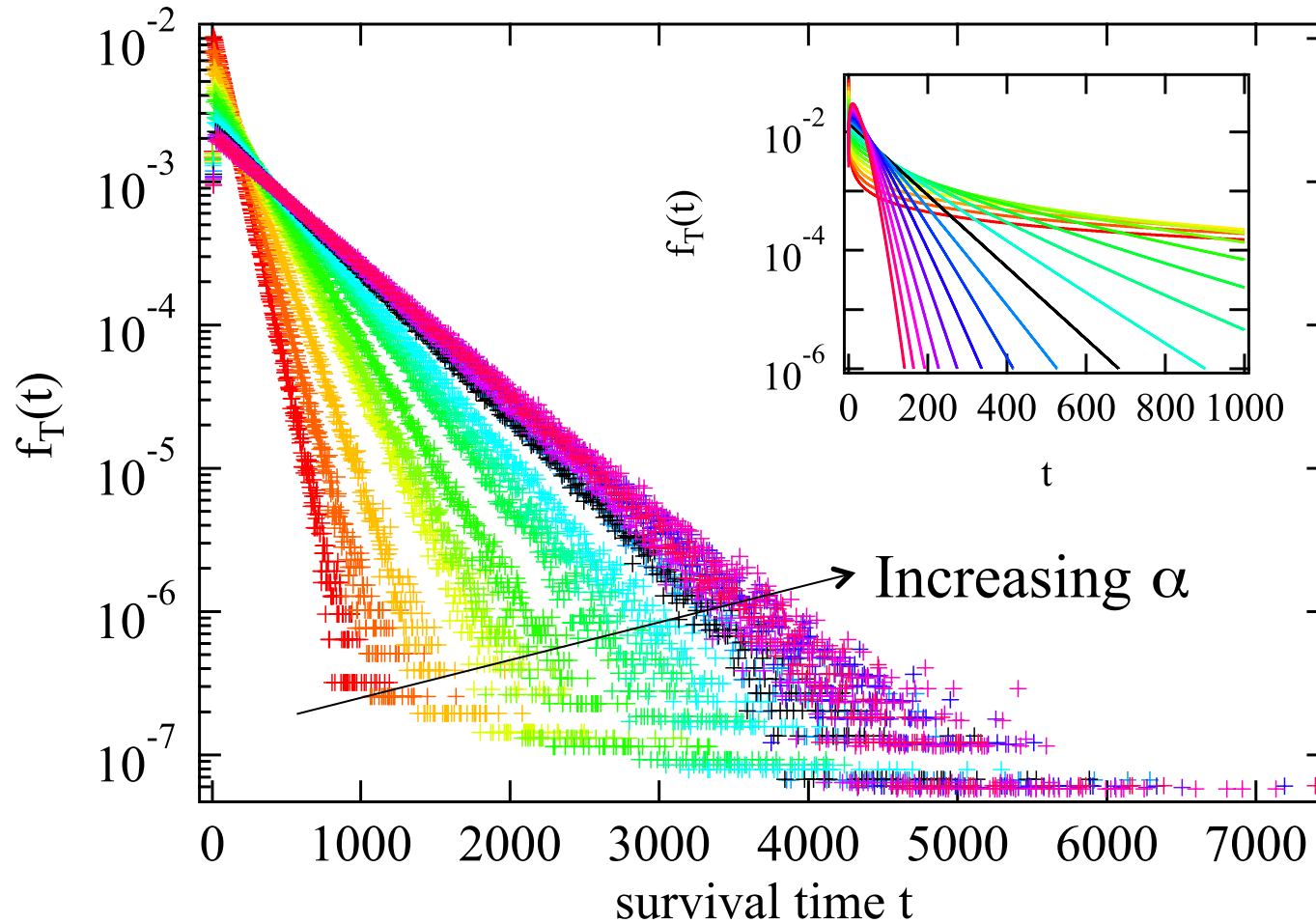
E[M]=0.014

$$f_{\text{infection time}}(t) = \frac{\alpha}{b}\left(\frac{t}{b}\right)^{\alpha-1}\exp\left(-\left(\frac{t}{b}\right)^{\alpha}\right)$$

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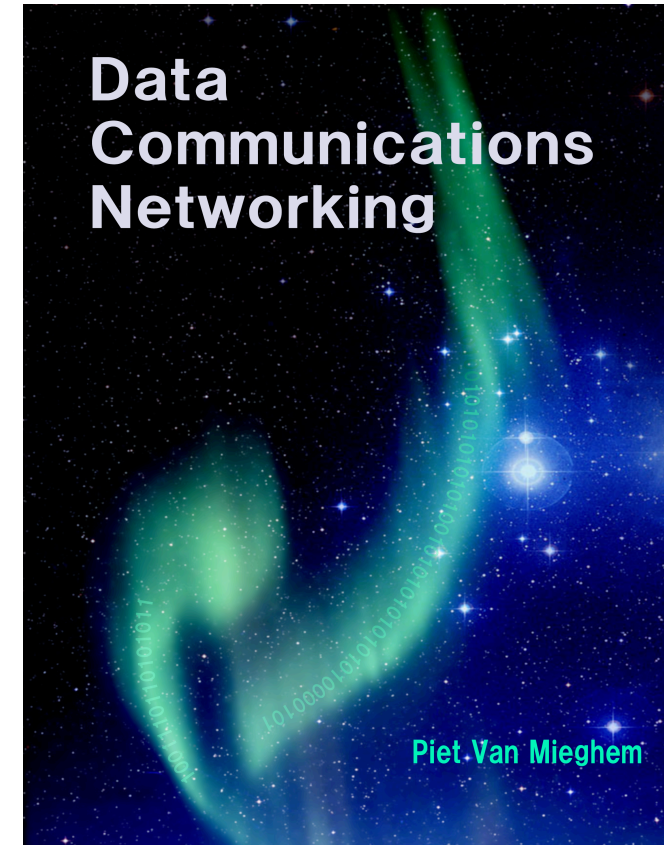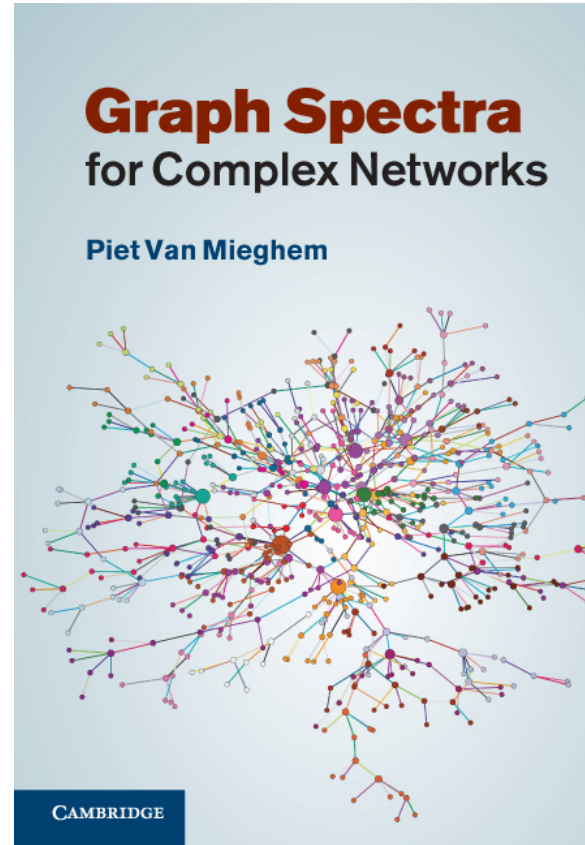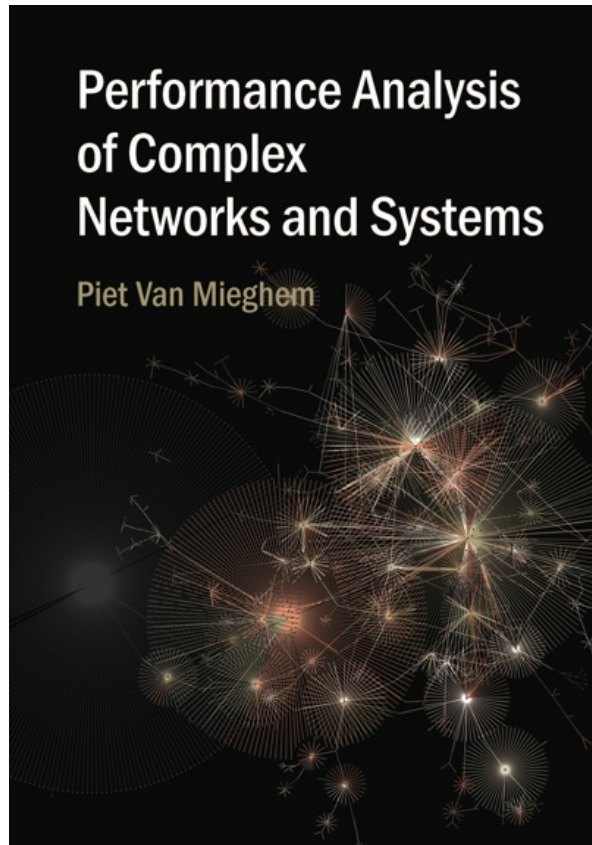
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More to read

General overviews

- P. Van Mieghem, *Performance Analysis of Complex Networks and Systems*, Cambridge University Press, 2014 (Chapter 17: Epidemics in Networks)

- R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani, "Epidemic processes in complex networks", Review of Modern Physics, 2014

Specialized recent topics (see my website):

- Adaptive SIS on networks

- Competing viruses

- Average survival time of a virus in a network (decay time towards absorption)

- SIS Epidemics in (two-level) communities

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Books

Performance Analysis of Complex Networks and Systems — Piet Van Mieghem

Graph Spectra for Complex Networks — Piet Van Mieghem — CAMBRIDGE

Data Communications Networking — Piet Van Mieghem

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Thank You

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