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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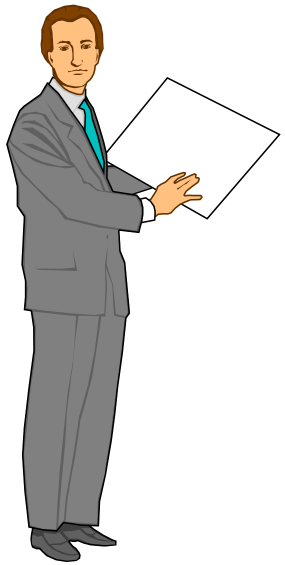
Outline



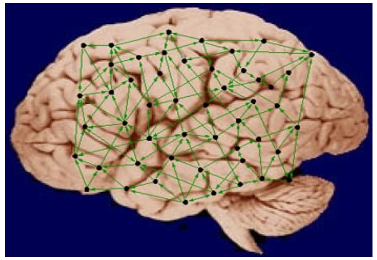
Network Science in brief

Exact SIS model

NIMFA: N-intertwined MF approximation

Recent developments

Understanding Network Function & Topology



Biology

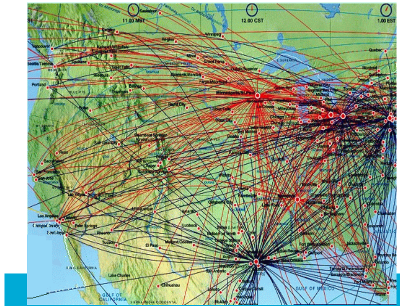
Brain

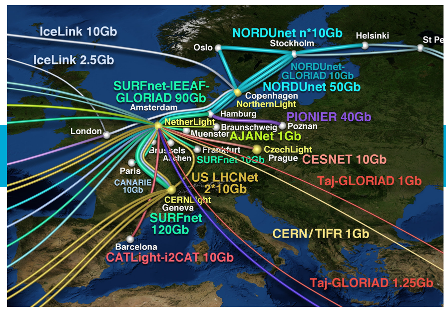
Economy

Network Science

Social networking

Designing robust infrastructures Internet, electricity grid, ...





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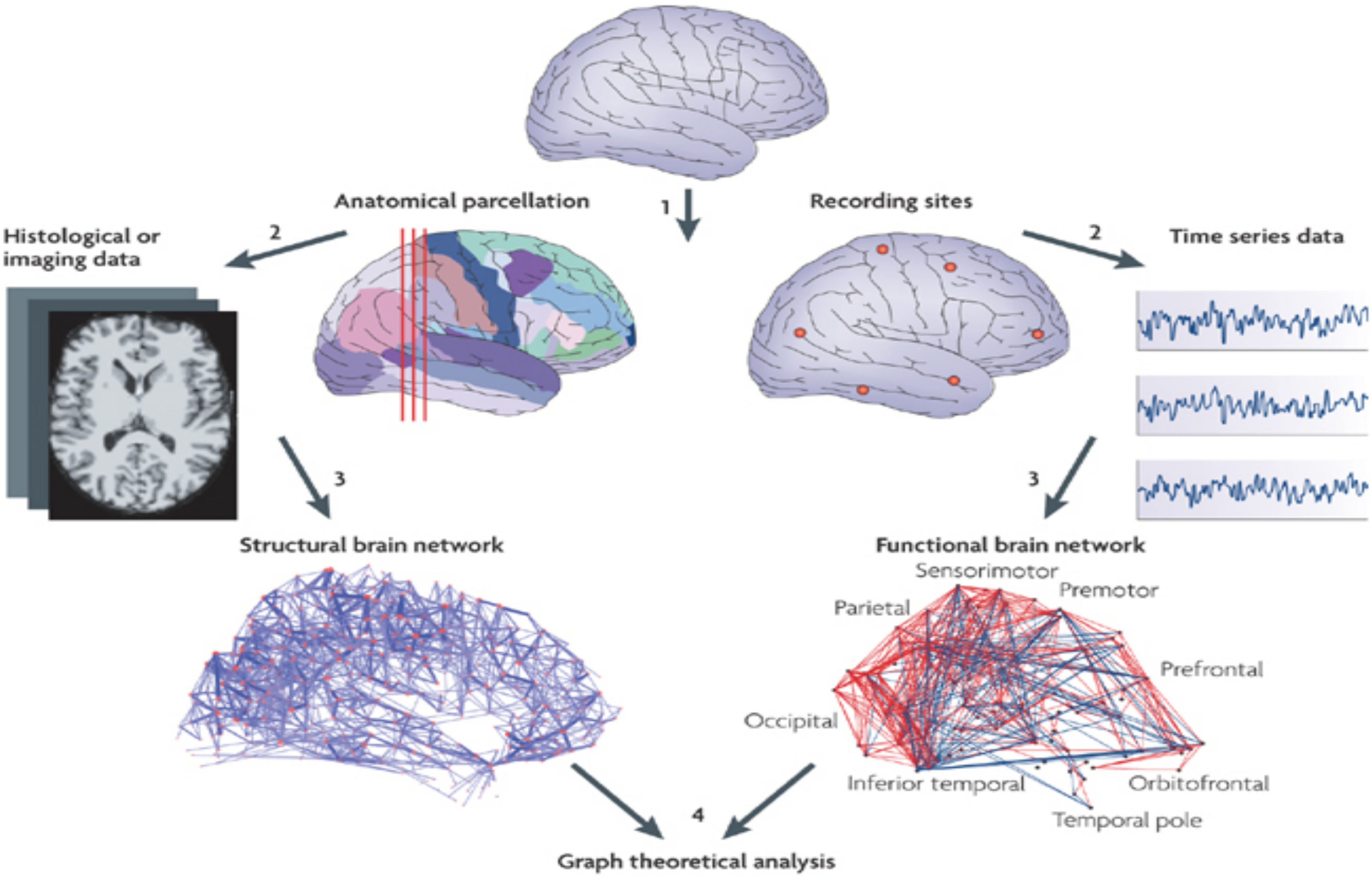
Functional brain network



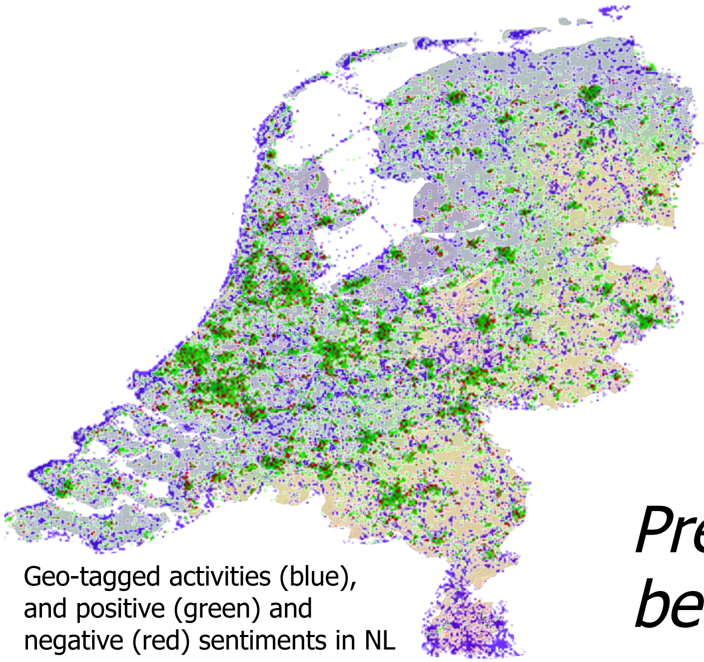
Collaboration with VU Medical Center, Amsterdam
(http://home.kpn.nl/stam7883/index.html)

Nature Reviews | Neuroscience

Trends in Social Networks

Monitoring **entire** communities (>1.5 billion relations)

Evolution of social networks: organic growth, saturation or dying out?



Geo-tagged activities (blue), and positive (green) and negative (red) sentiments in NL

How does content spread? Keys to success?

Your friends' influence on your opinions and decisions

Predicting patterns of human behavior

How much does the Net know about you?

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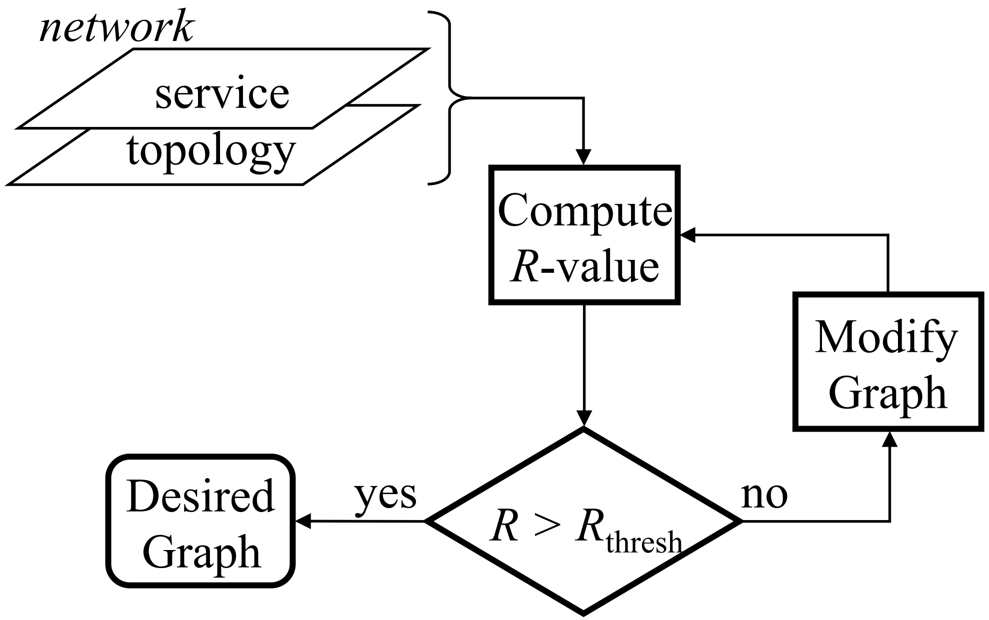
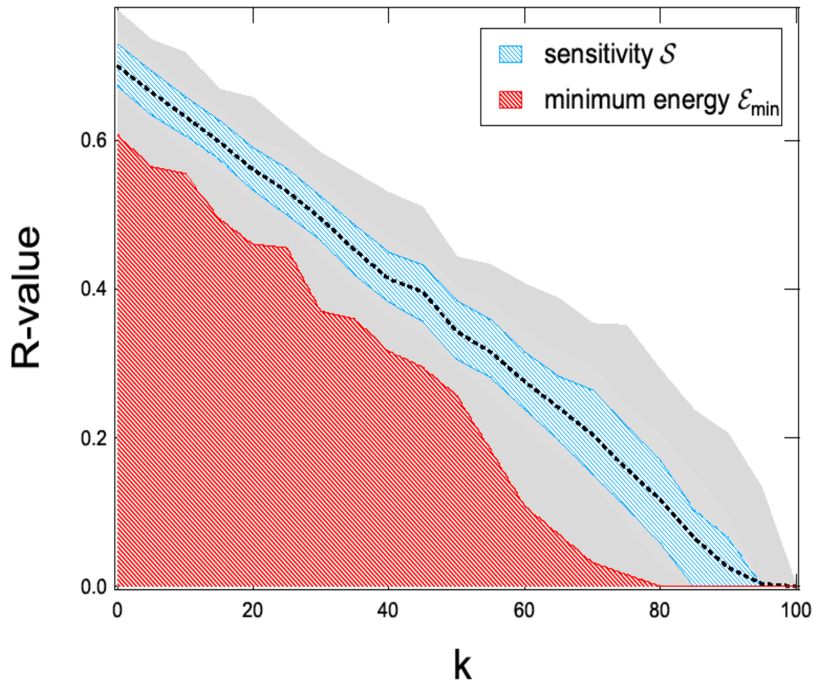
Robustness of Networks





R-value: network robustness metric
R = 0: no robustness
R = 1: ideal

Higher **sensitivity** results in better stability.

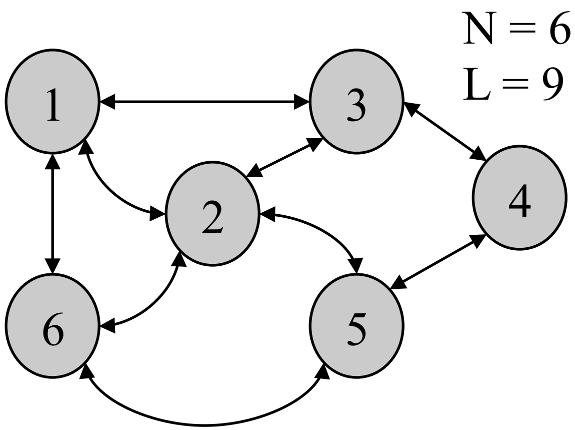
Higher **energy** results in better average R-value.

S. Trajanovski, J. Martin-Hernandez, W. Winterbach and P. Van Mieghem, 2013, "Robustness Envelopes of networks", Journal of Complex Networks, vol 1., p. 44-62

P. Van Mieghem, C. Doerr, H. Wang, J. Martin Hernandez, D. Hutchison, M. Karaliopoulos and R. E. Kooij, 2010, "A Framework for Computing Topological Network Robustness", Delft University of Technology, report20101218

Graph theory

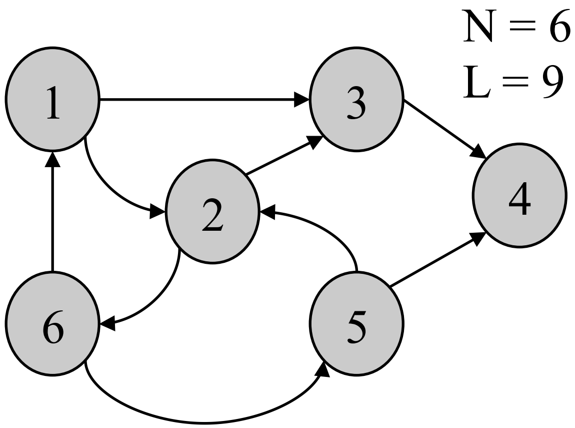
Any graph G can be represented by an adjacency matrix A (and other graph related matrices such as the incidence matrix B and the Laplacian Q



$$A_{N\times N} = \begin{bmatrix} 0 & 1 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 & 1 & 0 \end{bmatrix} = A^T$$

Graph metrics: degree, clustering, path length, modularity, …

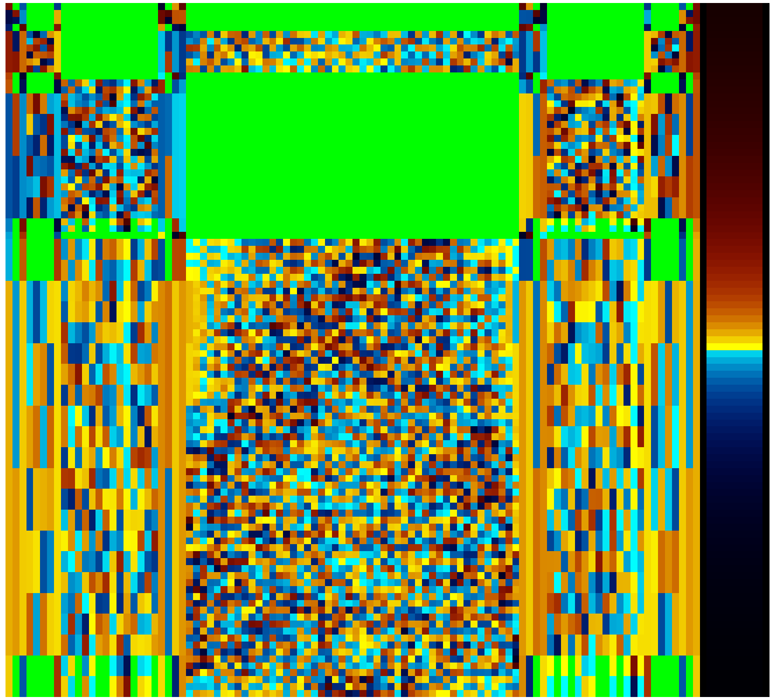
Topology domain



Most network problems:
- shortest path
- graph metrics
- network algorithms

Spectral domain

$$A = X \Lambda X^T$$

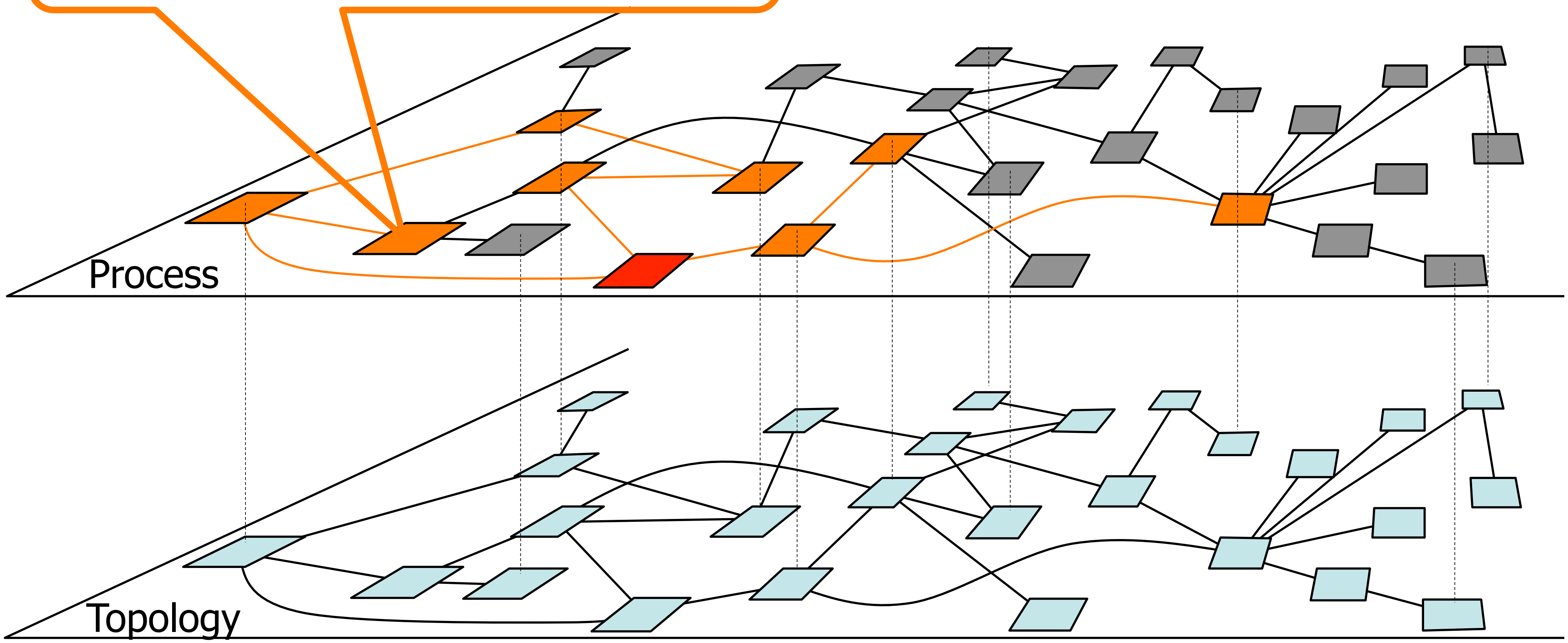


$X_{\text{3-ary tree}}$: green = 0

What is the physical interpretation of eigenvalues and of eigenvectors of A?

Local Rule – Global emergent property

If orange, then infect a neigbor;
after some time, become grey.



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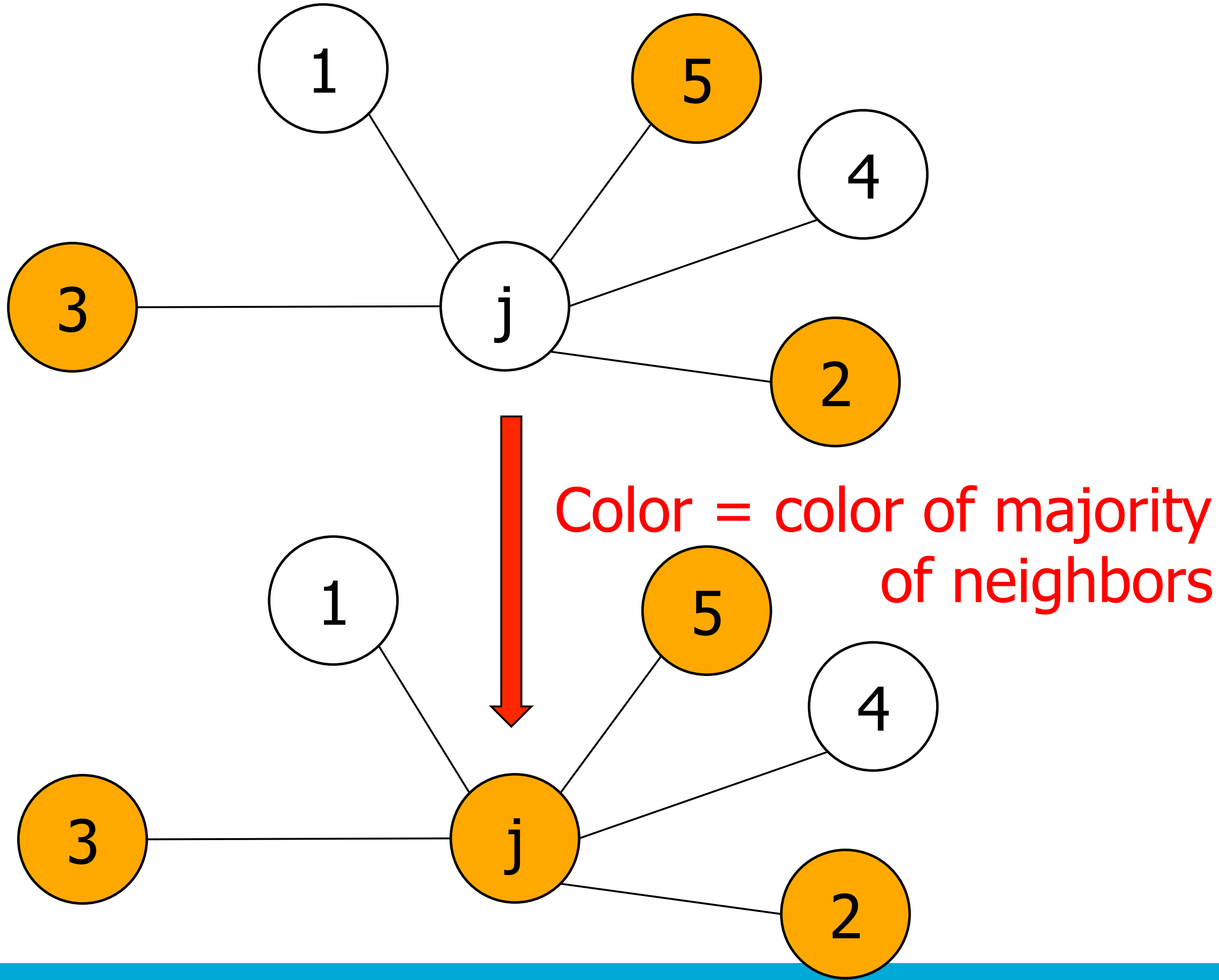
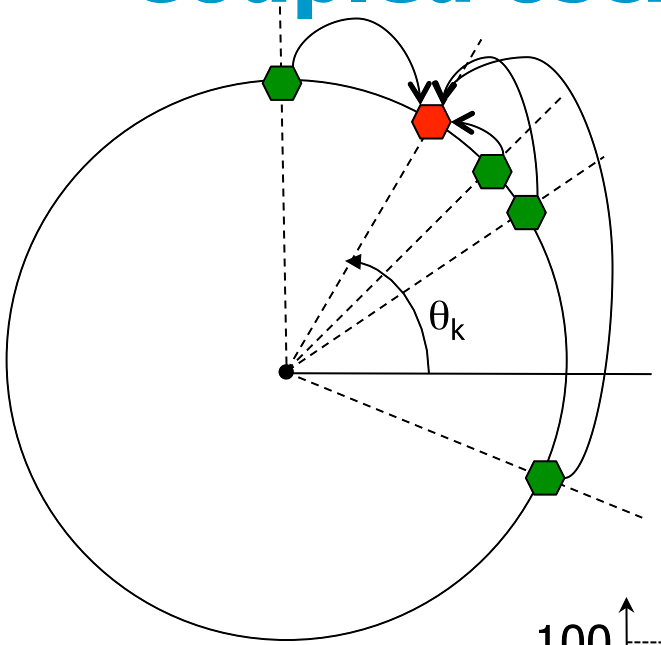
Opinion model(s)

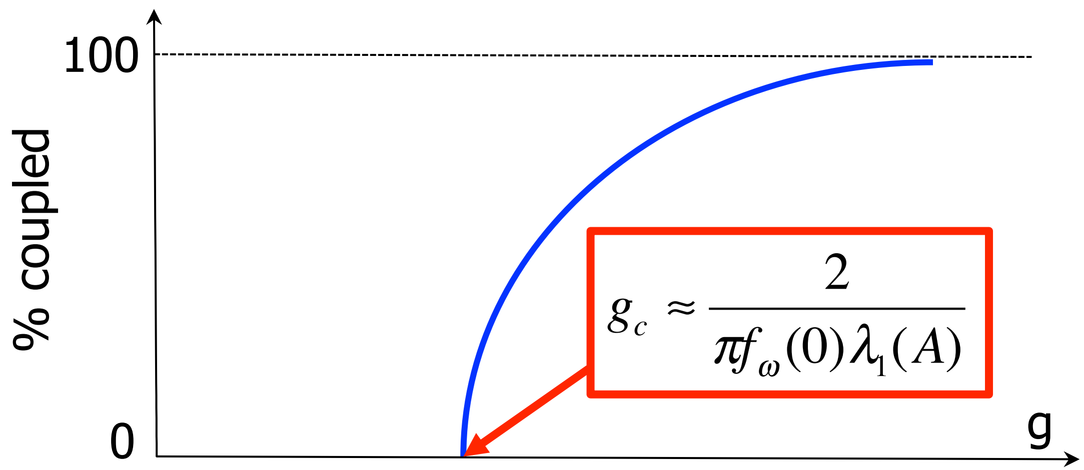


Coupled oscillators (Kuramoto model)



Interaction equals sums of sinus of phase difference of each neighbor:

$$\dot{\theta}_k = \underset{\text{natural frequency}}{\uparrow}\!\!\omega_k + \underset{\text{coupling strength}}{\uparrow}\!\! g \sum_{j=1}^{N} a_{kj} \sin\left(\theta_j - \theta_k\right)$$



J. G. Restrepo, E. Ott, and B. R. Hunt. Onset of synchronization in large networks of coupled oscillators, Phys. Rev. E, vol. 71, 036151, 2005

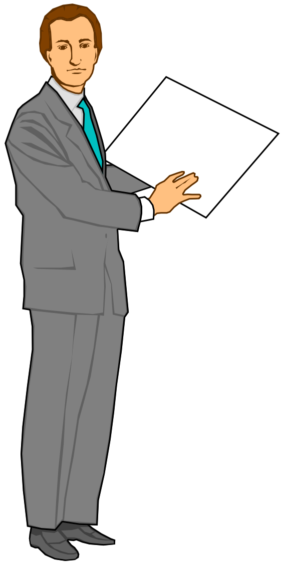
Local rule – Global emergent property models on networks

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

Many feature a phase transition

All crucially depend on the graph

Outline



Network Science in brief

Exact SIS model

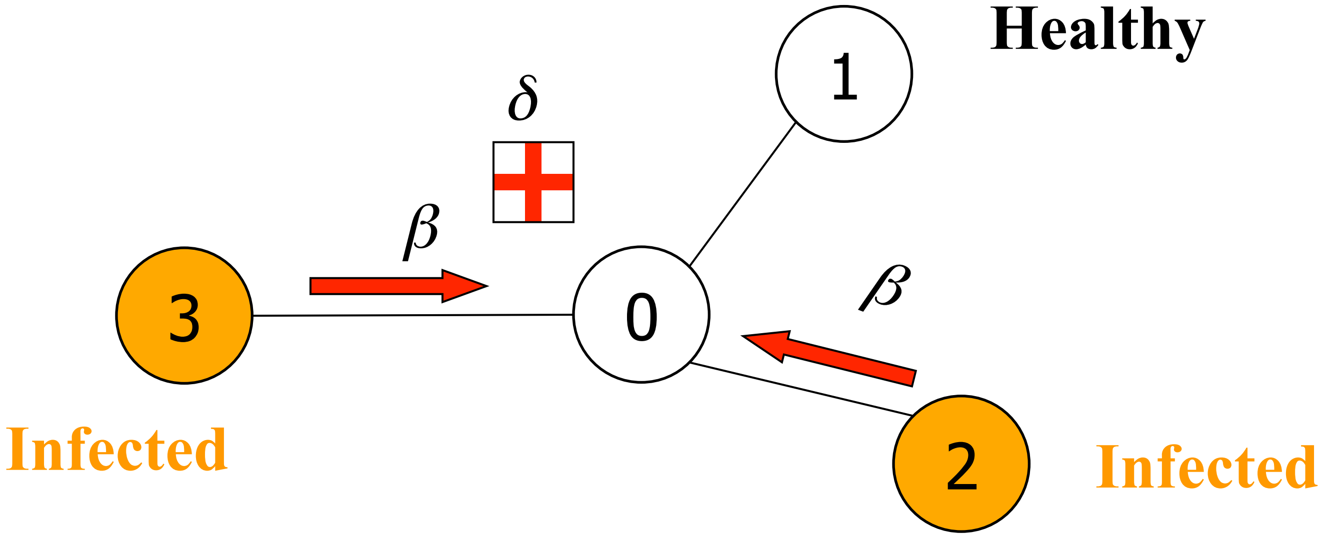
NIMFA: N-intertwined MF approximation

Recent developments

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

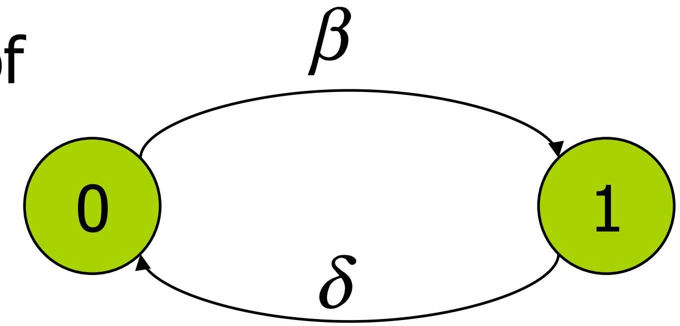
$\tau = \beta / \delta$: effective spreading rate



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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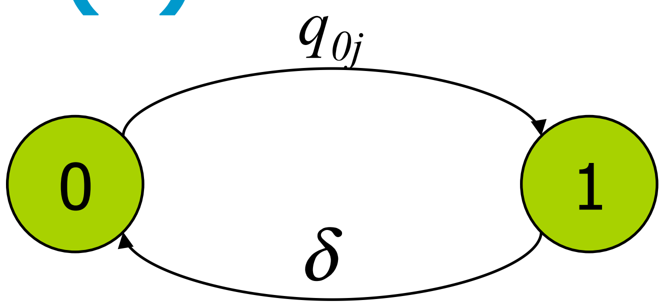
SIS model on networks (2)



- 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:*

$$\boxed{q_{0j}(t) = \beta \sum_{k=1}^{N} a_{jk} X_k(t)}$$

and where the adjacency matrix of the graph is

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

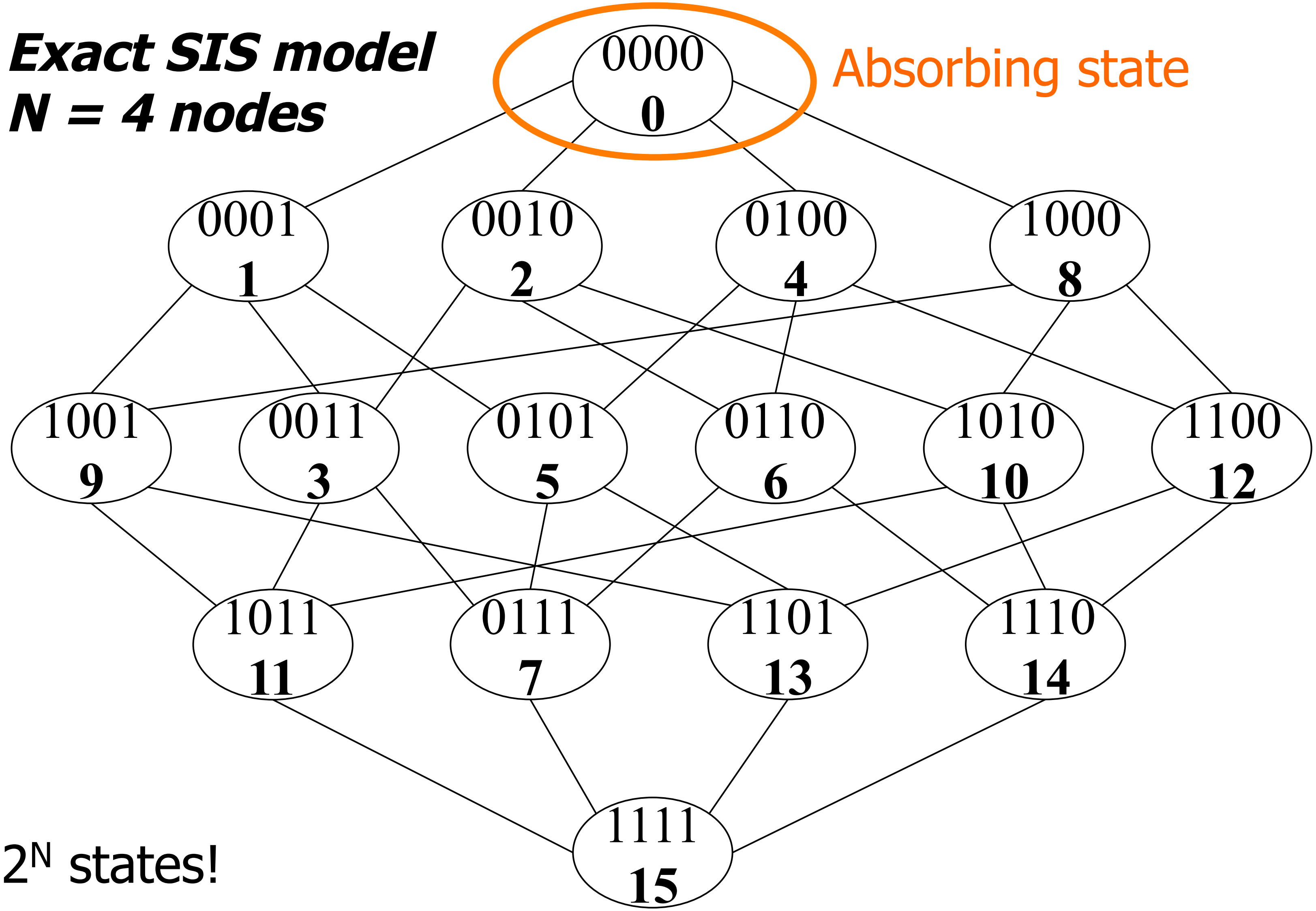
SIS model on networks (3)

- 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:

$$q_{0j}(t) = \beta \sum_{k=1}^{N} a_{jk} X_k(t)$$

- 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, 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 susceptible -infected-susceptible epidemic threshold", Physical Review E, vol. 85, No. 5, May, p. 056111.

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...

Outline

Network Science in brief

Exact SIS model

NIMFA: N-intertwined MF approximation

Recent developments

NIMFA: N-intertwined mean-field approxim.

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

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

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.

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

P. Van Mieghem, 2014, "Accuracy criterion for the mean-field approximation in SIS epidemics on networks," unpublished.

Lower bound for the epidemic threshold

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

Ignoring the correlation terms

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

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

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

What is so interesting about epidemics?

network protection

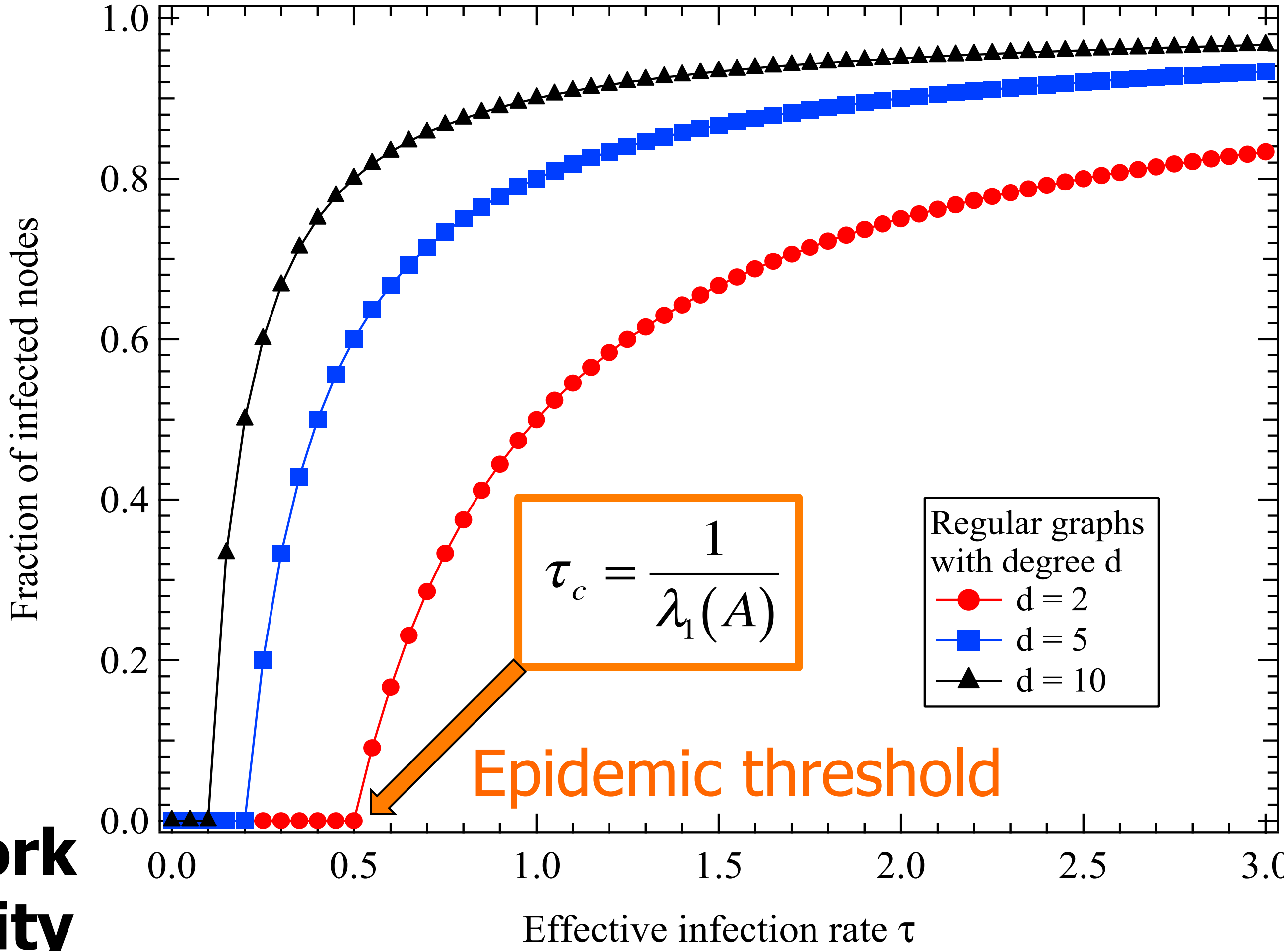
self-replicating objects (worms)

propagation errors

rumors (social nets)

epidemic algorithms (gossiping)

cybercrime : network robustnes & security



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

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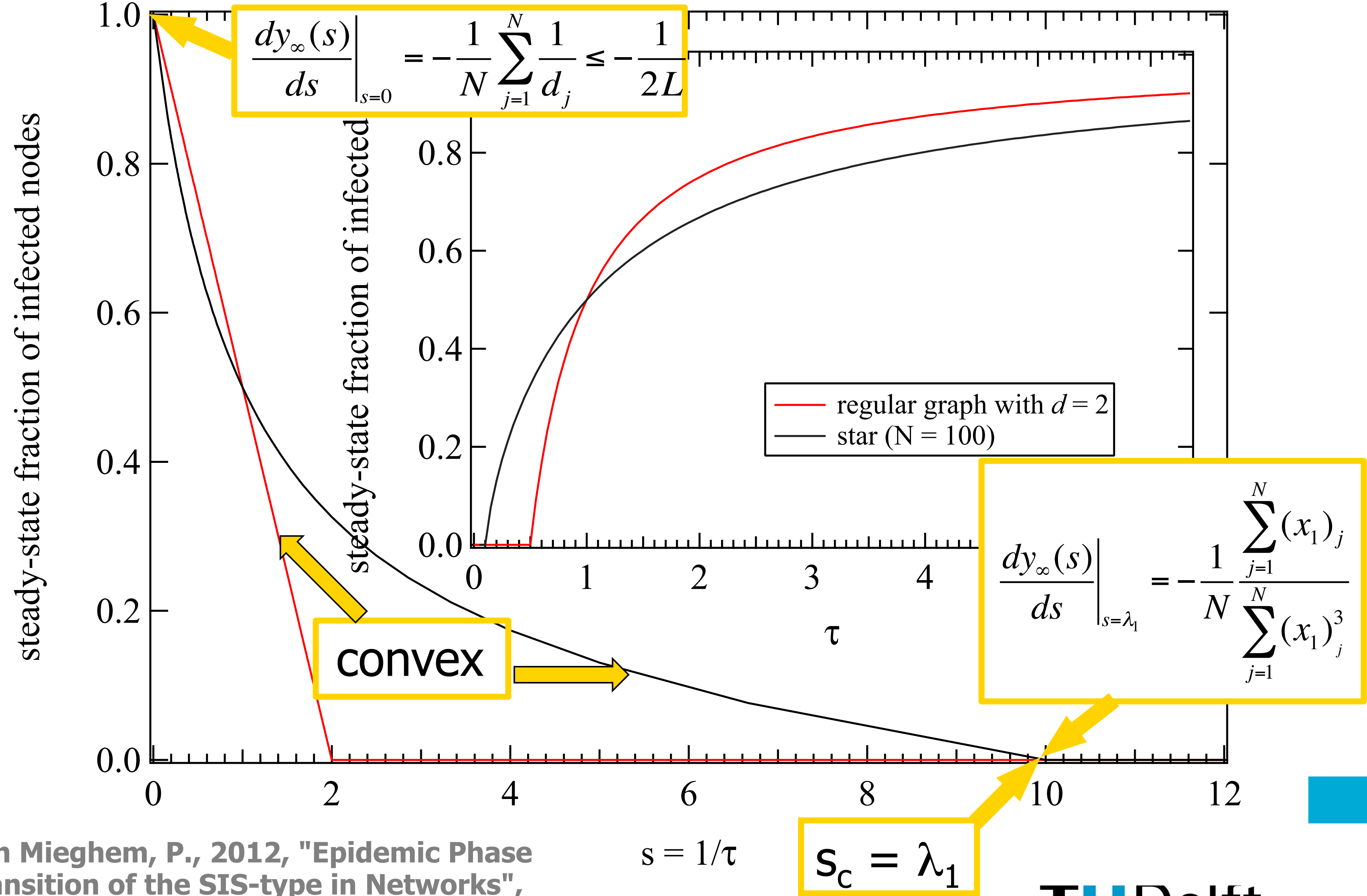
Transformation $s = \frac{1}{\tau}$ & principal eigenvector



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

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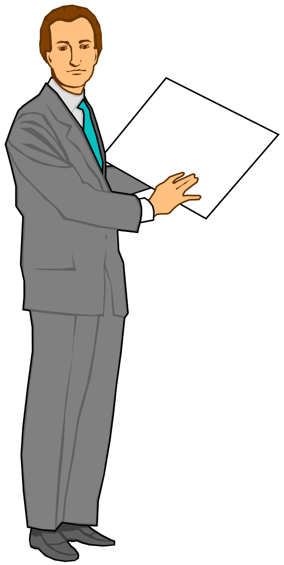
Extensions of the NIMFA

- **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



Network Science in brief

Exact SIS model

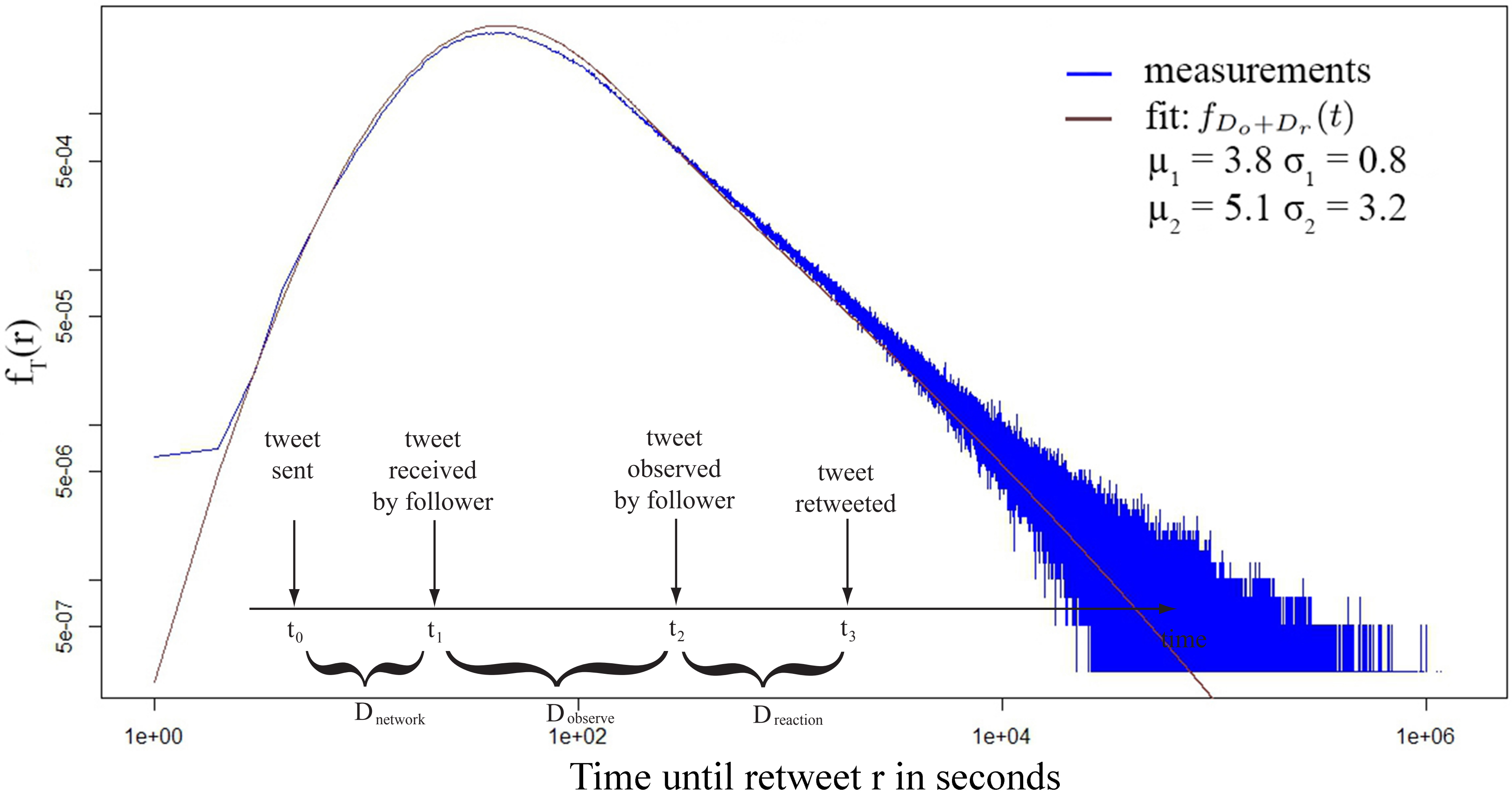
NIMFA: N-intertwined MF approximation

Recent developments

- Non-Markovian epidemics

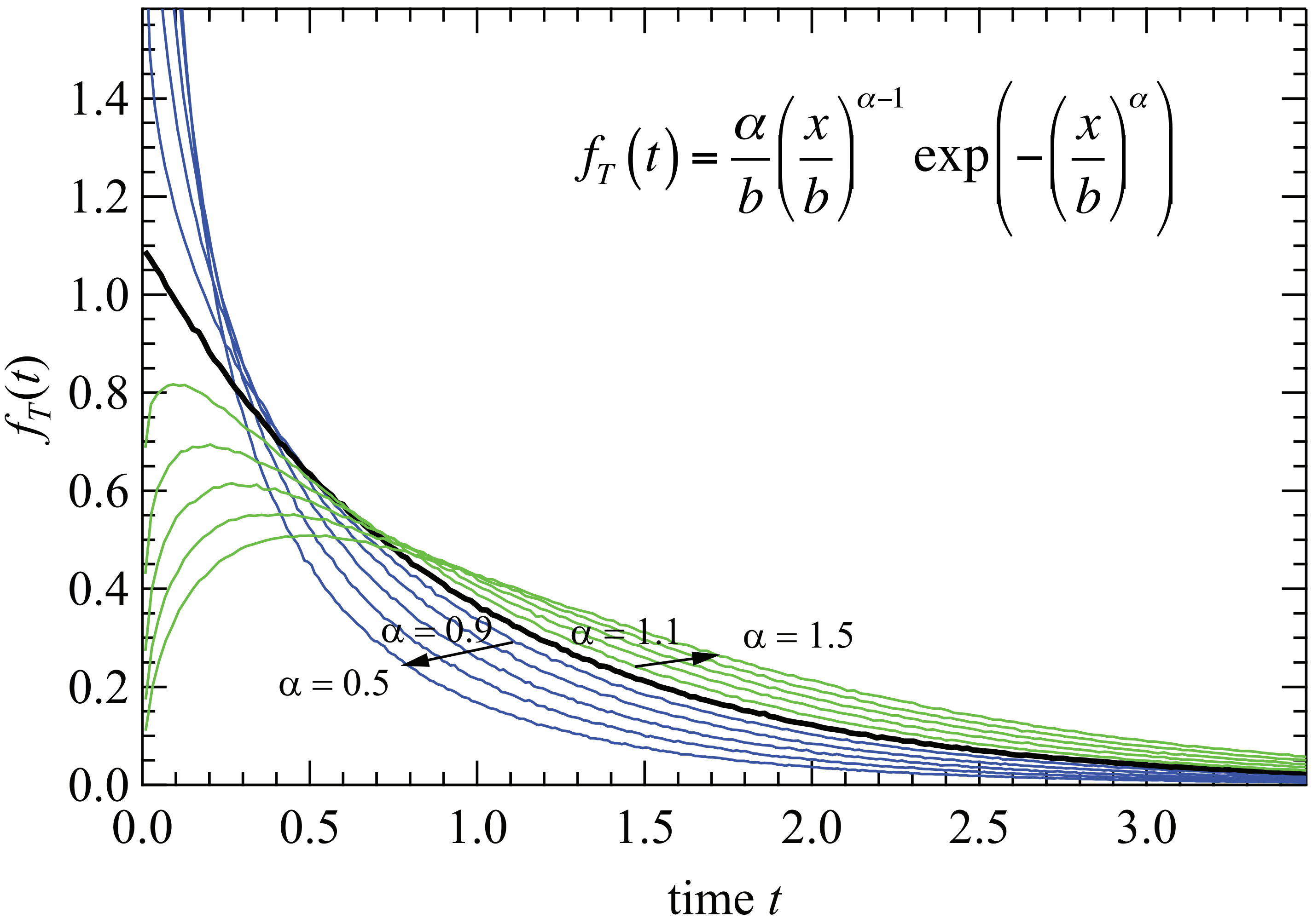
- Time-dependent rates
- Survival time

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

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

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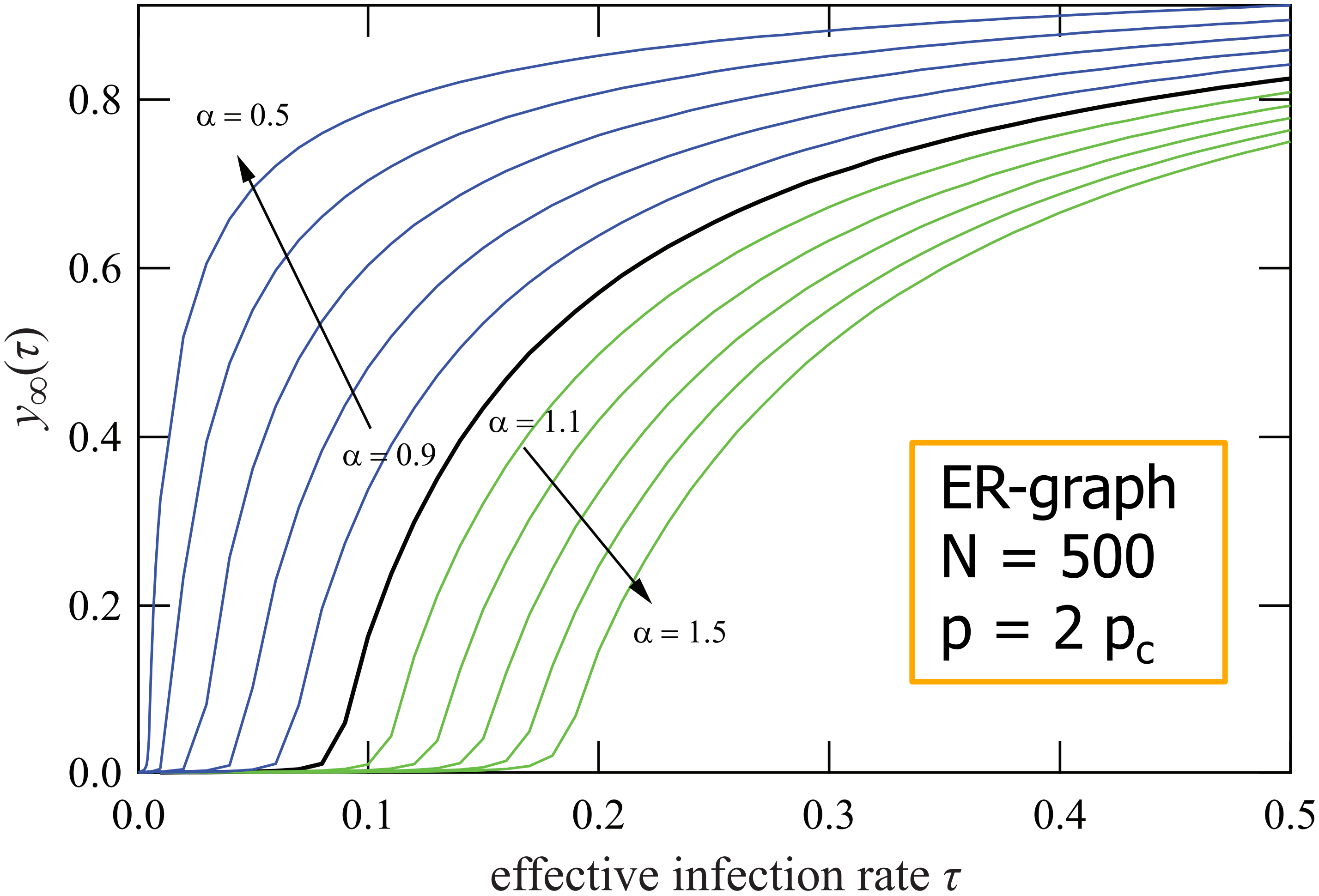
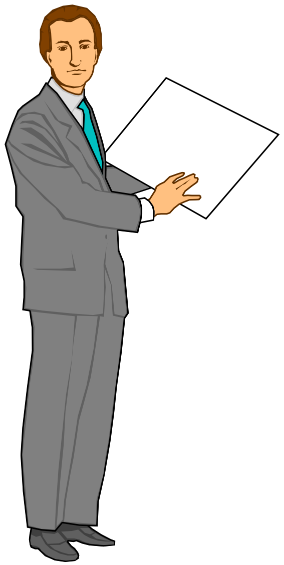
Non-Markovian epidemic threshold



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.

Outline



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- Non-Markovian epidemics
- **Time-dependent rates**
- Survival time

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Time-dependent rates in NIMFA for regular graphs

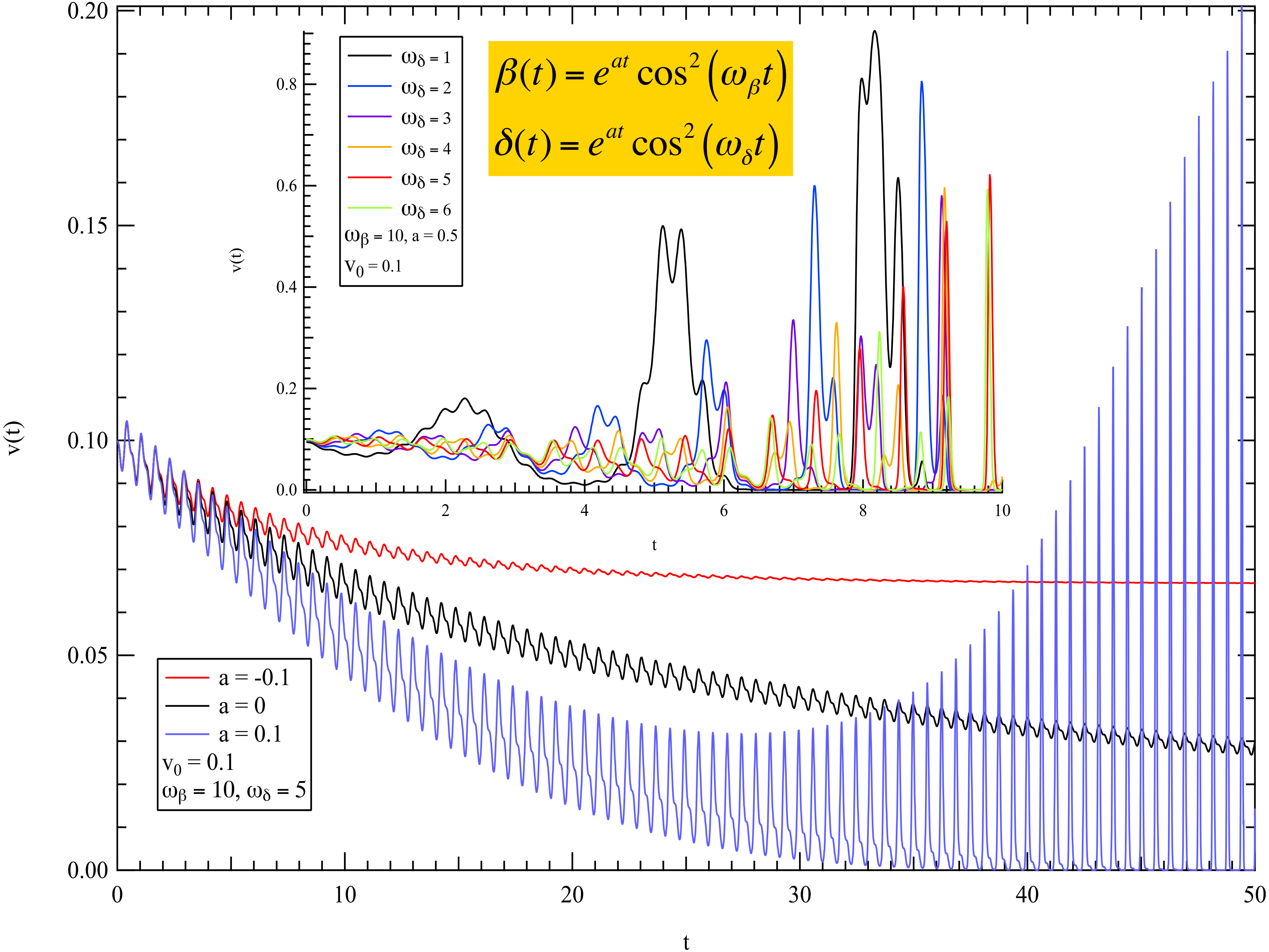
$$\frac{dv(t)}{dt} = r\beta(t)v(t)\left(1-v(t)\right)-\delta(t)v(t)$$

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

Reduces to the classical case (constant rates): Kephart & White (1992)

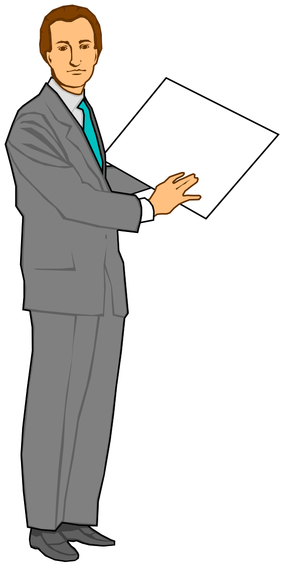
$$v(t)=\left(\frac{1}{v(0)}\exp\left(\left\{\left\{\delta-r\beta\right\}\right\}t\right)+\left(1-\frac{1}{r\tau}\right)^{-1}\left(1-\exp\left(\left\{\delta-r\beta\right\}t\right)\right)\right)^{-1}$$

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



v(t)
t
0.00
0.05
0.10
0.15
0.20
0
10
20
30
40
50
a = -0.1
a = 0
a = 0.1
$v_0 = 0.1$
$\omega_\beta = 10$, $\omega_\delta = 5$
$\omega_\delta = 1$
$\omega_\delta = 2$
$\omega_\delta = 3$
$\omega_\delta = 4$
$\omega_\delta = 5$
$\omega_\delta = 6$
$\omega_\beta = 10$, a = 0.5
$v_0 = 0.1$
0.0
0.2
0.4
0.6
0.8
2
4
6
8
$\beta(t) = e^{at}\cos^2(\omega_\beta t)$
$\delta(t) = e^{at}\cos^2(\omega_\delta t)$

Outline



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- Time-dependent rates
- **Survival time**

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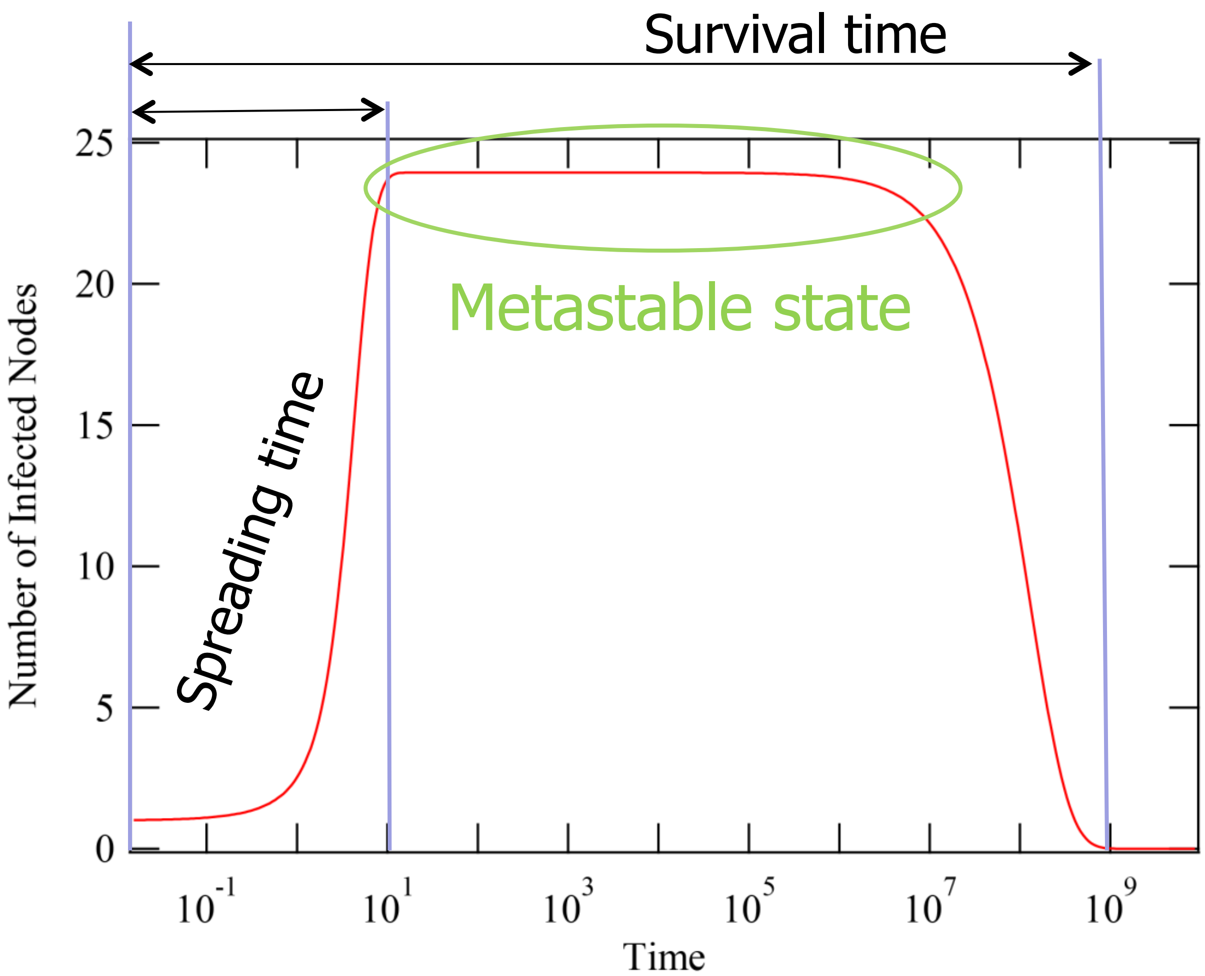
Spreading and survival time



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)

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

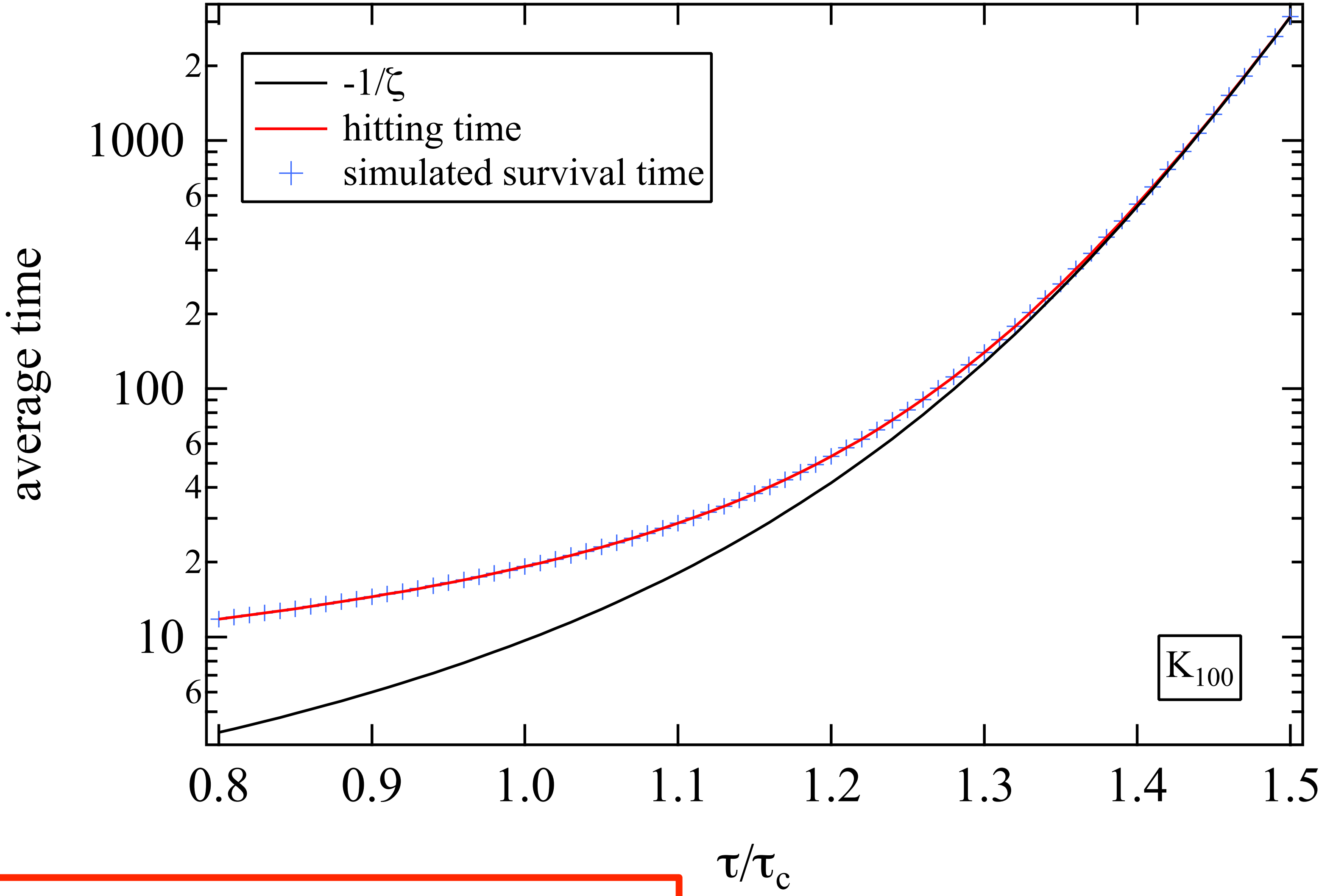
Complete graph K_N:

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

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

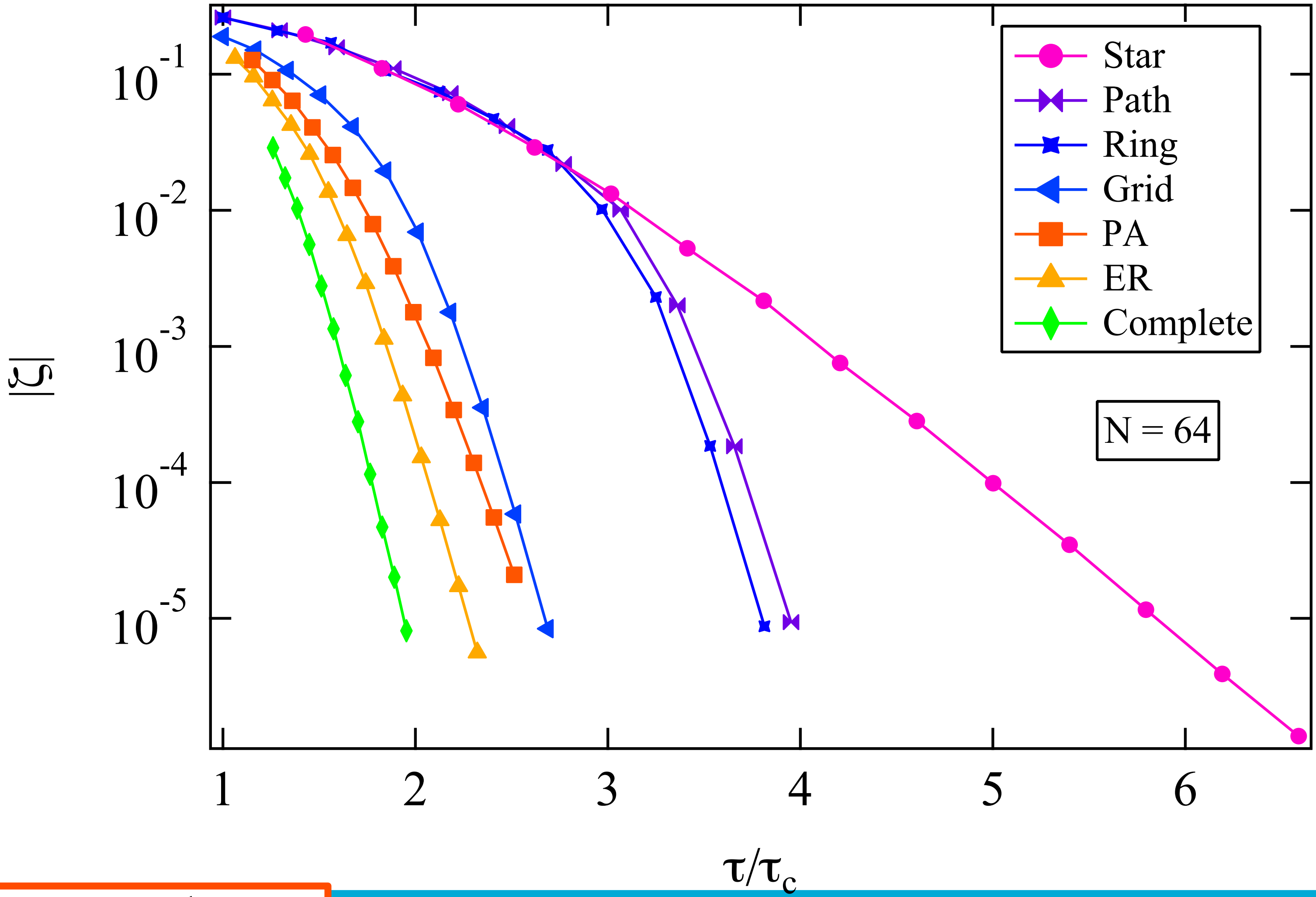
P. Van Mieghem, "Decay towards the overall-healthy state in SIS epidemics on networks", arxiv1310.3980 (2013).
R. van de Bovenkamp and P. Van Mieghem, "Survival time of the SIS infection process on a graph", unpublished (2014).

Average survival time in K_N



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

Second smallest eigenvalue Q in graphs



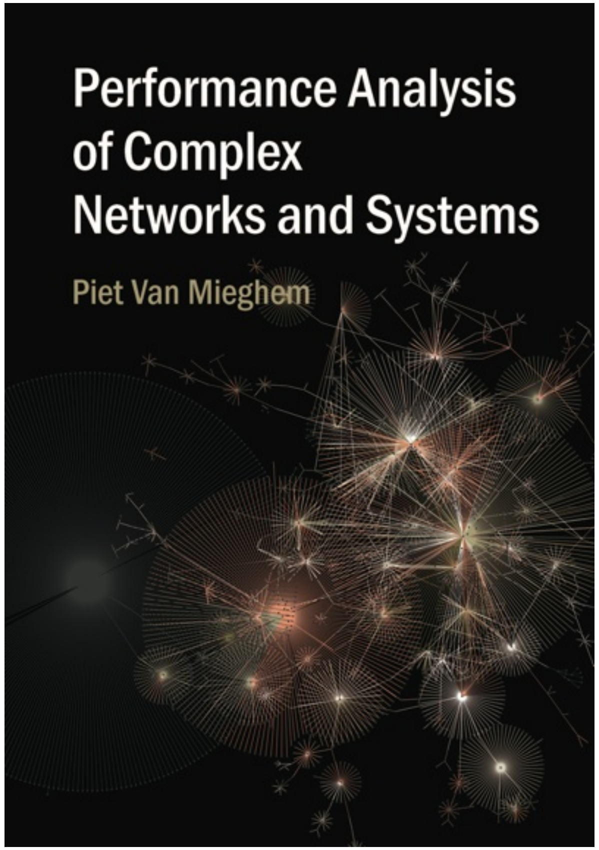
$$\boxed{|\zeta| \approx \frac{1}{E[T]}}$$

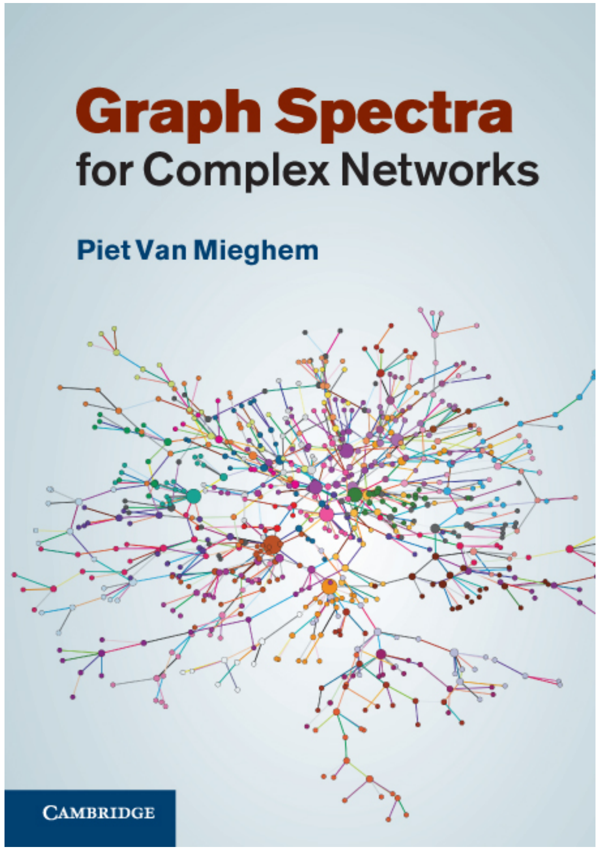
TU Delft

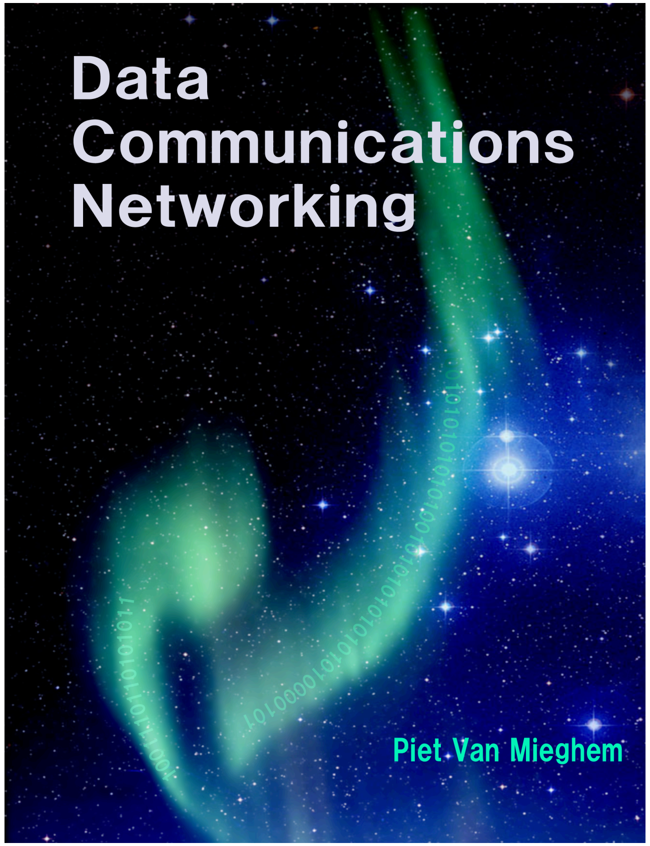
Challenges for SIS epidemics on nets

- Tight upper bound of the epidemic threshold (for any graph), or near to exact determination of τ_c
- A general mean-field criterion that specifies the graphs for which NIMFA is accurate
- Time-dependent analysis of SIS epidemics
- Non-Markovian epidemics
- Epidemics on *evolving* and *adaptive* networks
- Competing and mutating viruses on networks
- Modeling of social contagion
- **Measurements** of epidemics (e.g. fraction of infected nodes) in real-world networks are scarce

Books







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

Thank You

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