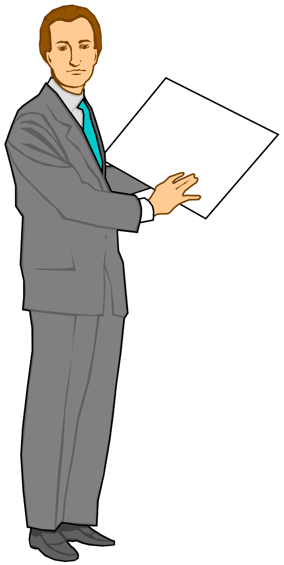
Graph Spectra & the N-intertwined Mean-field SIS approximation on Networks

Piet Van Mieghem

work in collaboration with Eric Cator, Huijuan Wang, Rob Kooij

Outline



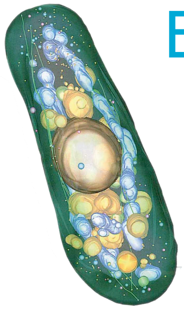
Introduction & Definitions

Exact SIS model

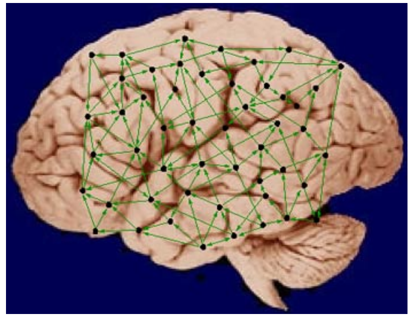
The N-intertwined MF approximation

Extensions

Summary



Effect of Network on Function



Biology

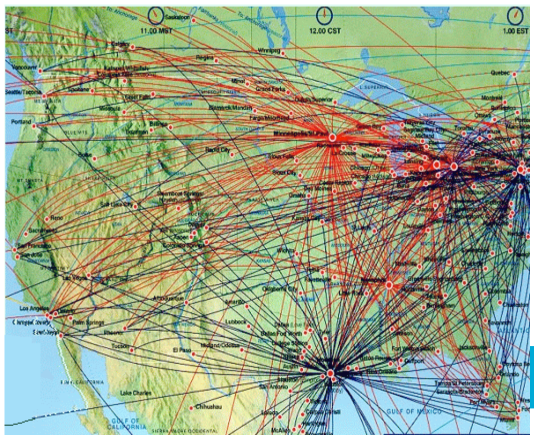
Brain

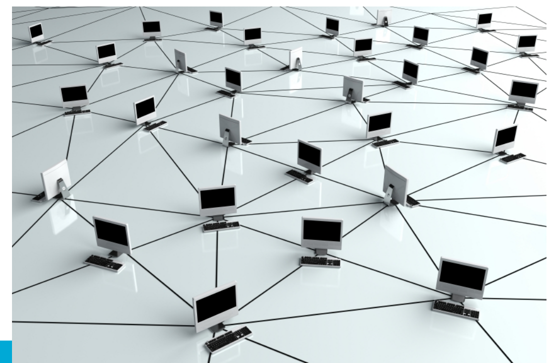
Economy

Network Science

Social

networking





Man-made Infrastructures
Internet, power-grid

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

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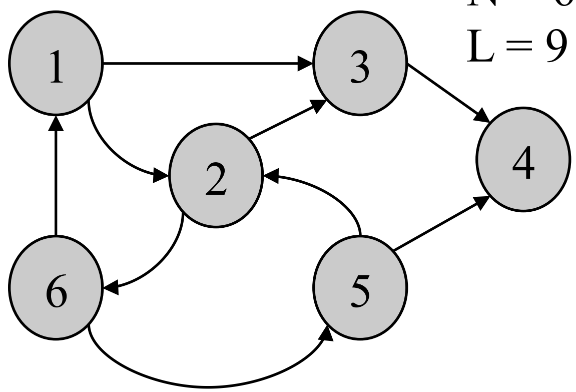
Motivation for virus spread in networks

- **Digital world:**
  - Information spread in on-line social networks
  - security threat to Internet (Code Red worm: several billion $ $ in damage)
- **Real world: Biological epidemics** (e.g. Mexican flue)

- **Why do we care**?
  - Understanding the spread of a virus is the first step in prevention
  - How fast do we need to disinfect nodes so that the virus dies quickly? Which nodes?

Algebraic graph theory

Any graph G can be represented by an adjacency matrix A and an incidence matrix B, and a Laplacian Q



N = 6
L = 9

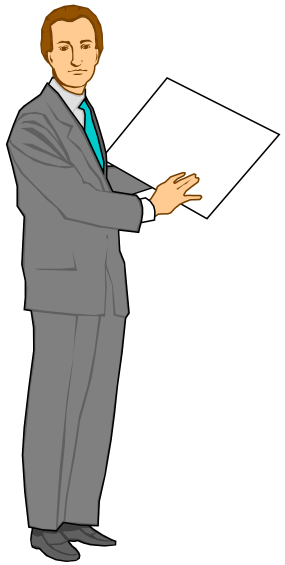
$$A_{N\times N} = \begin{bmatrix} 0 & 1 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 & 1 & 0 \end{bmatrix} = A^T$$

$$B_{N\times L} = \begin{bmatrix} 1 & 1 & -1 & \cdots & 0 \\ -1 & 0 & 0 & & 0 \\ 0 & -1 & 0 & & 0 \\ 0 & 0 & 0 & & 0 \\ 0 & 0 & 0 & & -1 \\ 0 & 0 & 1 & & 1 \end{bmatrix}$$

$$Q = BB^T = \Delta - A$$

$$\Delta = diag(d_1 \quad d_2 \quad \ldots \quad d_N)$$

Outline



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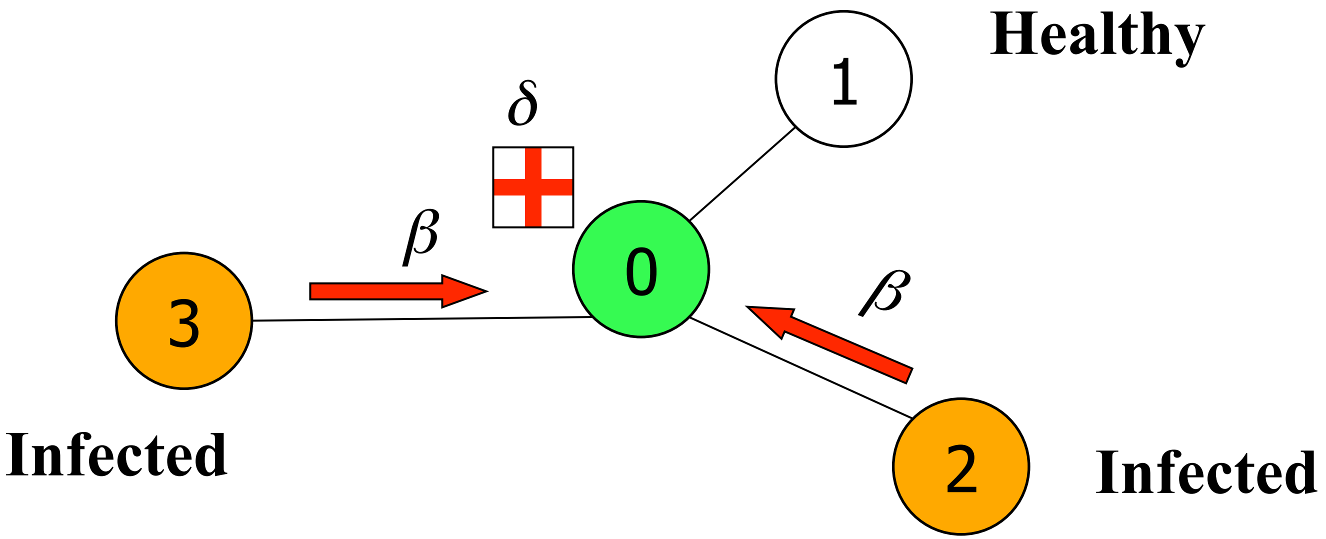
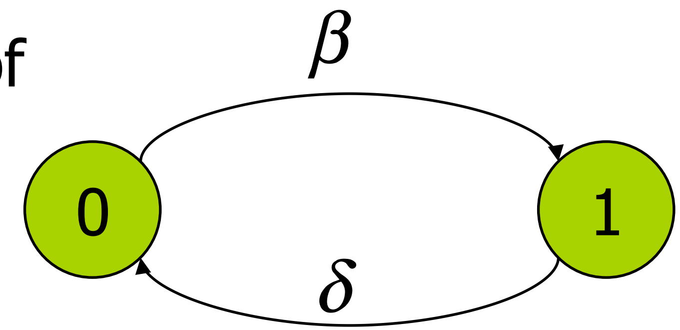
Simple SIS model

- 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



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 $Q_j(t) = \begin{vmatrix} -q_{1j} & q_{1j} \\ q_{2j} & -q_{2j} \end{vmatrix} = \begin{bmatrix} -q_{1j} & q_{1j} \\ \delta & -\delta \end{bmatrix}$

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

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

Joint probabilities

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

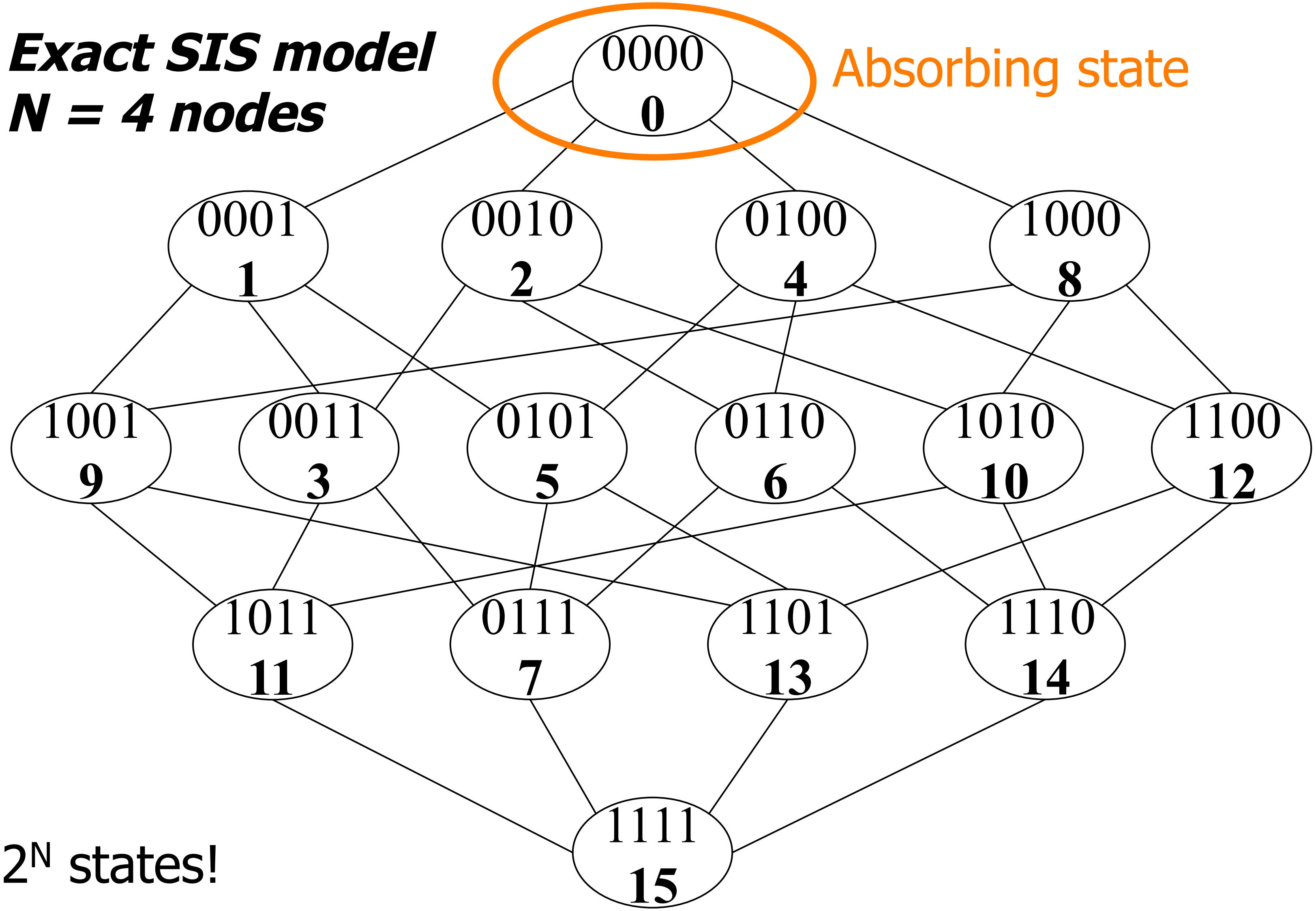
$$= -2\delta E\left[X_iX_j\right] + \beta\sum_{k=1}^{N} a_{ik}E\left[X_jX_k\right] + \beta\sum_{k=1}^{N} a_{jk}E\left[X_iX_k\right] - \beta\sum_{k=1}^{N}\left(a_{jk}+a_{ik}\right)E\left[X_iX_jX_k\right]$$

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

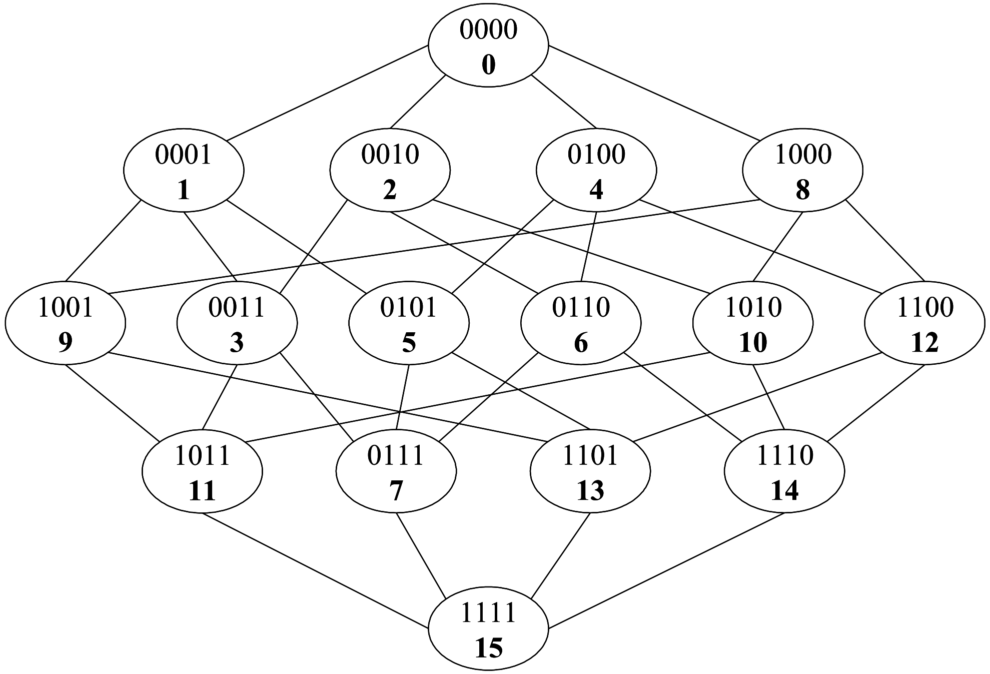
E. Cator and P. Van Mieghem, 2012, "Second-order mean-field susceptible -infected-susceptible epidemic threshold", Physical Review E, vol. 85, No. 5, May, p. 056111.

Exact SIS model
N = 4 nodes

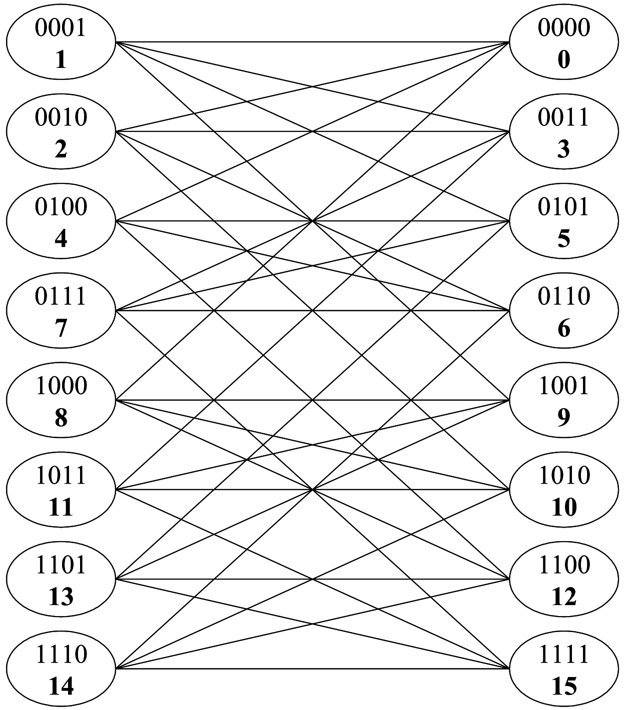


2^N states!

Markov theory



bi-partite Markov graph



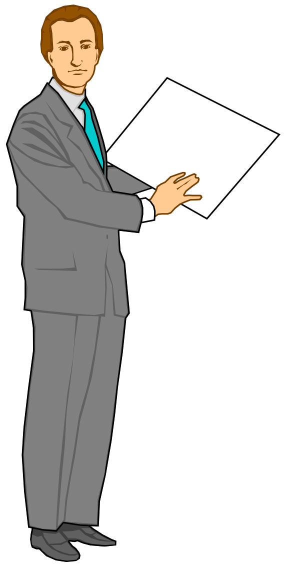
Recursive structure of infinitesimal general Q_N

Van Mieghem, P. and E. Cator, ε-SIS epidemics and the epidemic threshold,
Physical Review E, to appear 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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TUDelft

N-intertwined mean-field approximation

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

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

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

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

N-intertwined mean-field approx. (= equality above)
upper bounds the probability 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.

N-intertwined non-linear equations

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

where the viral probability of infection is

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

In matrix form:

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

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

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

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

Is the point V = 0 stable?
For a very few infected nodes, we can ignore the quadratic terms

$$\frac{dV(t)}{dt} = \left(-\delta I + \beta A\right) V(t)$$

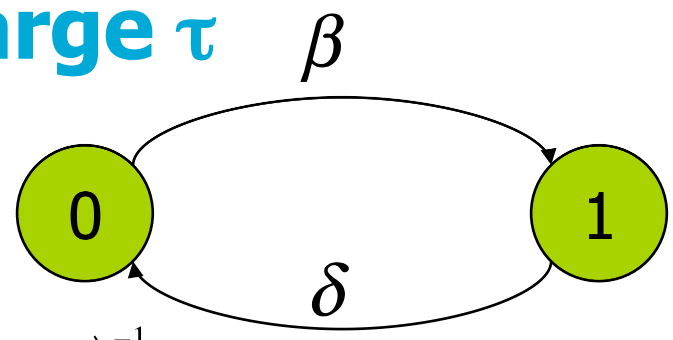
The origin V=0 is stable attractor if all eigenvalues of $\beta A - \delta I$ are negative (v_j tends exponentially fast to zero with *t*). Hence, if

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

The N-intertwined mean-field epidemic threshold is precisely

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

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 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: $$\left.\frac{dy_\infty(s)}{ds}\right|_{s=0} = \frac{1}{N}\sum_{j=1}^{N}\frac{1}{d_j} = E\left[\frac{1}{D}\right]$$

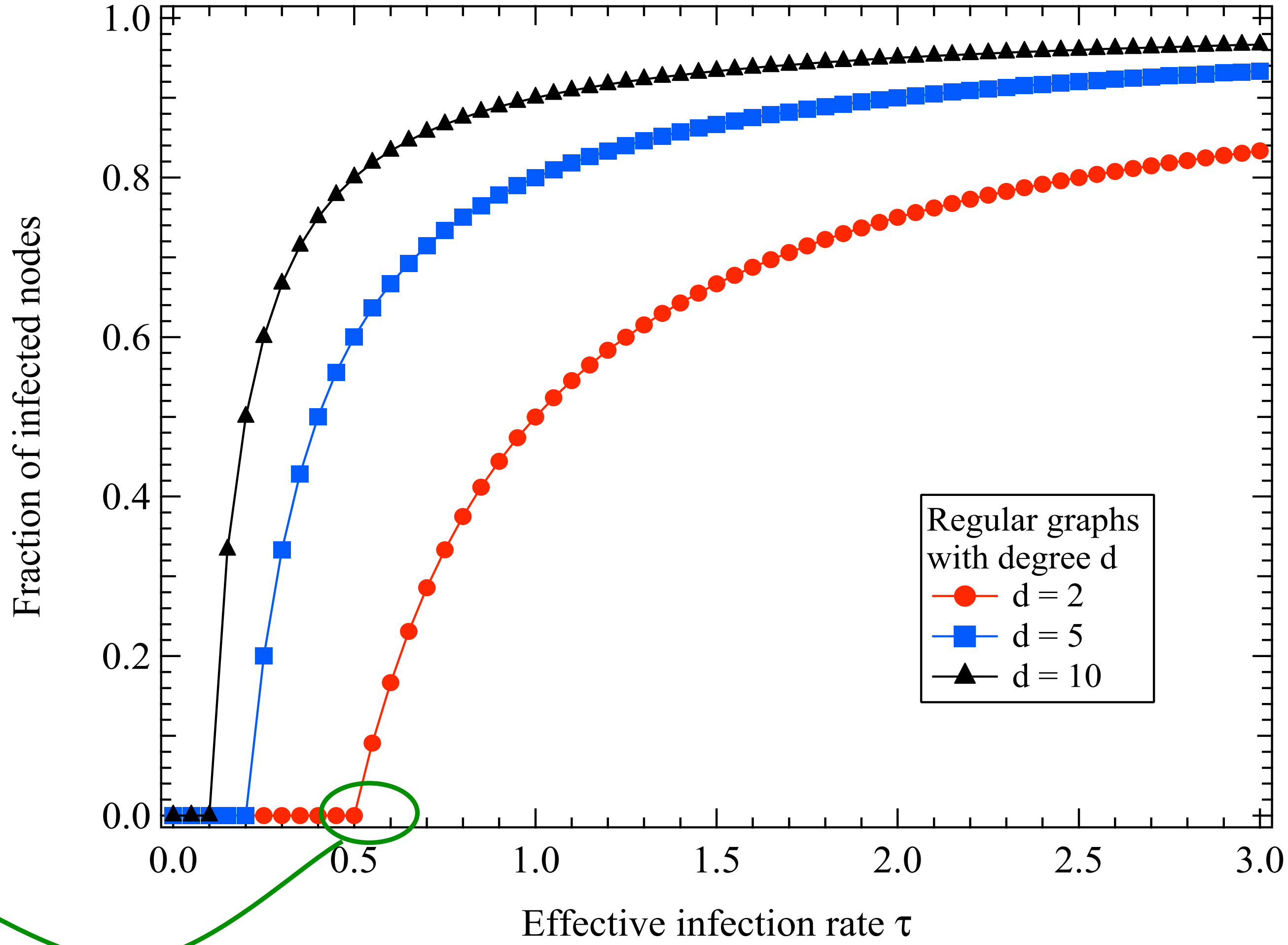
P. Van Mieghem, 2012, “The Viral Conductance in Networks”, Computer Communications, Vol 35, No. 12, pp. 1494-1509.

What is so interesting about epidemics?

β : infection rate per link

δ : curing rate per node

τ= β/ δ : effective spreading rate



- **Final epidemic state**
- **Rate of propagation**
- **Epidemic threshold**

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

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

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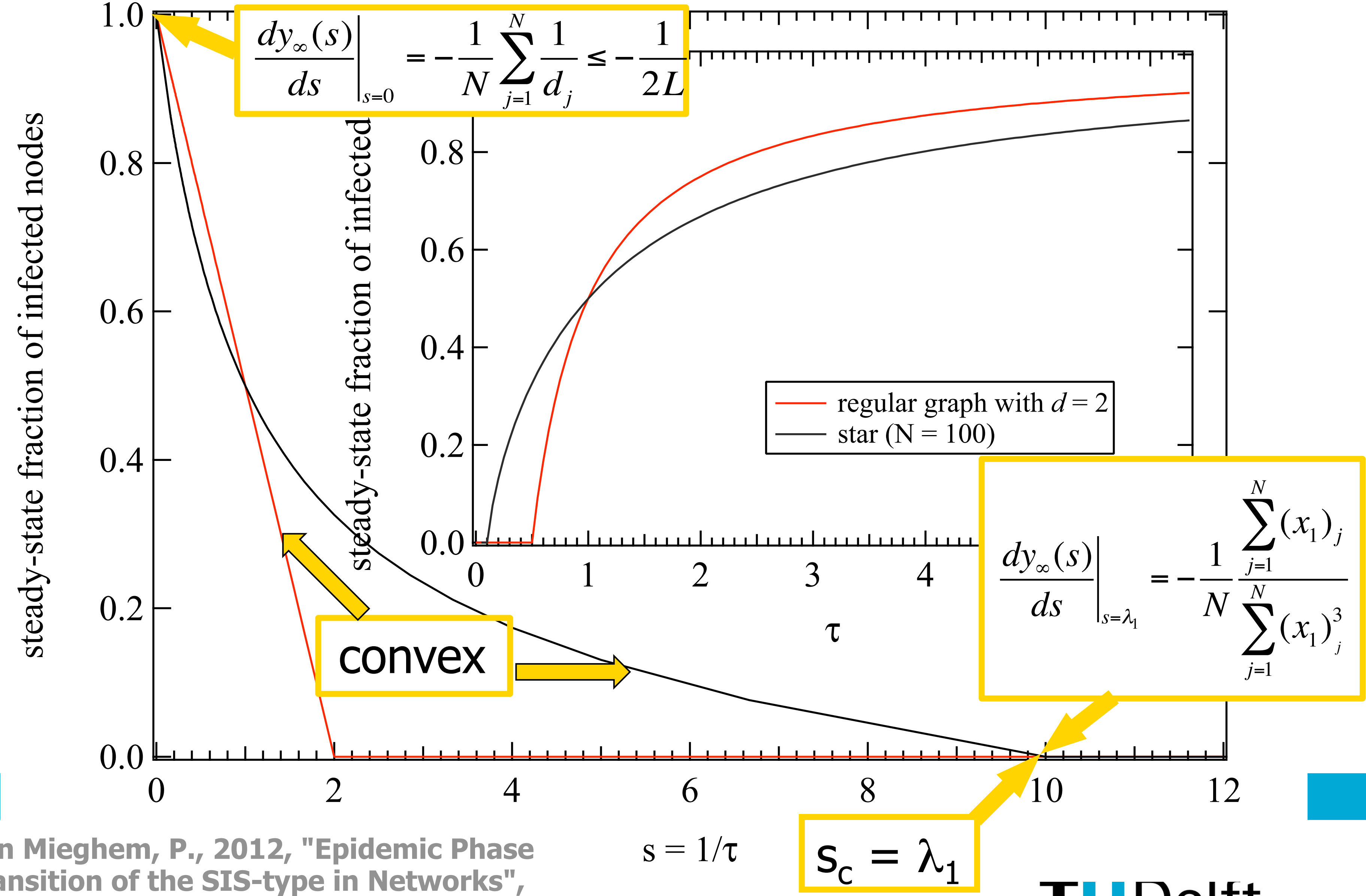
Transformation $s = \dfrac{1}{\tau}$ & principal eigenvector



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

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

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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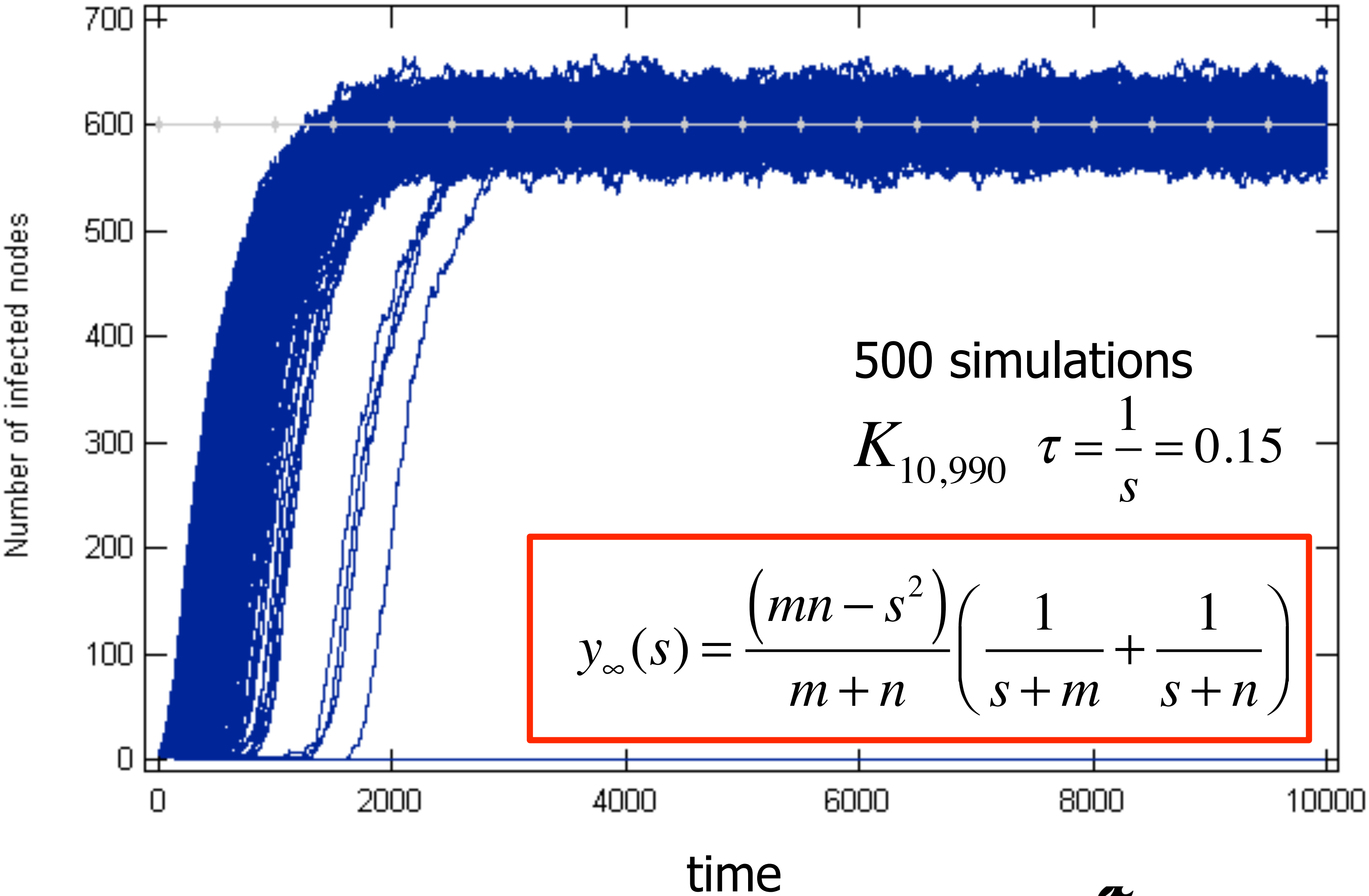
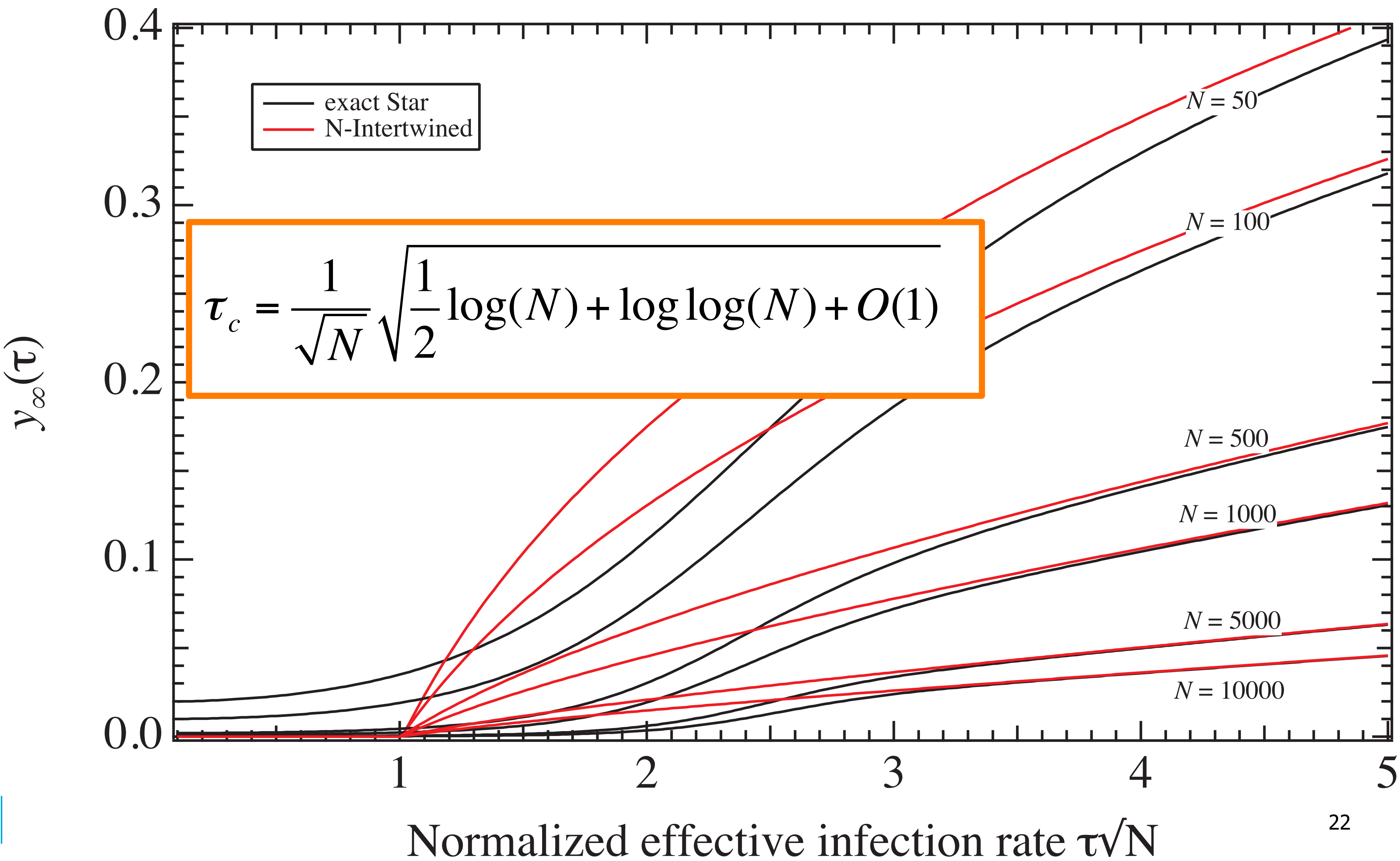
Simulations



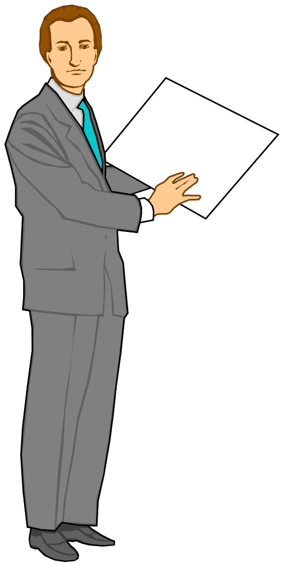
Star graph



$$\tau_c = \frac{1}{\sqrt{N}}\sqrt{\frac{1}{2}\log(N) + \log\log(N) + O(1)}$$

E. Cator and P. Van Mieghem, 2012, **"SIS epidemics on the complete graph and the star graph: exact analysis"**, unpublished.

Outline



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Heterogeneous virus spread

- The N-intertwined model is extended to a hetergeneous setting:

$$\boxed{\frac{dV(t)}{dt} = A\,diag(\beta_i)V(t) - diag(v_i(t))\left(A\,diag(\beta_i)V(t) + C\right)}$$

where the curing rate vector $C^T = [\delta_1\ \delta_2 \ldots \delta_N]$

- *Results:*
  - Extended multi-dim. threshold for virus spread
  - Generalized Laplacian that extends the classical Laplacian of a graph: $\boxed{Q(q_k) = diag(q_k) - A}$
  - Strong convexity v_k with respect to δ_k, concave with respect to others δ_j (j different from k).
  - Choose C vector in network protection via game theory

- J. Omic, P. Van Mieghem, and A. Orda, "Game Theory and Computer Viruses", *IEEE Infocom09.*
- P. Van Mieghem and J. Omic, "In-homogeneous Virus Spread in Networks", TUDelft report (see my website)

Extensions of the N-intertwined model

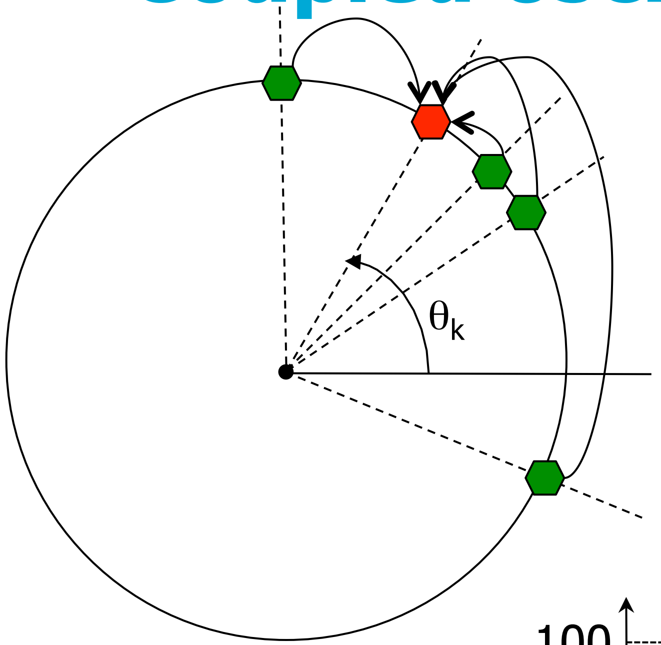
- SAIS instead of SIS:
  - From 2 states (Infected and Susceptible) to a 3-states (Infected, Susceptible, Alert)
  - "Epidemic Spread in Human Networks", F. Darabi Sahneh and C. Scoglio, 50th IEEE Conf. Decision and Contol, Orlando, Florida (2011)
- SIR instead of SIS:
  - "An individual-based approach 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, submitted IEEE/ACM Transactions on Networking

Affecting the epidemic threshold

- Degree-preserving rewiring (assortativity of the graph)
  - Van Mieghem, P., H. Wang, X. Ge, S. Tang and F. A. Kuipers, 2010, "Influence of Assortativity and Degree-preserving Rewiring on the Spectra of Networks", The European Physical Journal B, vol. 76, No. 4, pp. 643-652.
  - Van Mieghem, P., X. Ge, P. Schumm, S. Trajanovski and H. Wang, 2010, "Spectral Graph Analysis of Modularity and Assortativity", Physical Review E, Vol. 82, November, p. 056113.
  - Li, C., H. Wang and P. Van Mieghem, 2012, "Degree and Principal Eigenvectors in Complex Networks", IFIP Networking 2012, May 21-25, Prague, Czech Republic.
- Removing links/nodes (optimal way is NP-complete)
  - Van Mieghem, P., D. Stevanovic, F. A. Kuipers, C. Li, R. van de Bovenkamp, D. Liu and H. Wang, 2011,"Decreasing the spectral radius of a graph by link removals", Physical Review E, Vol. 84, No. 1, July, p. 016101.
- Quarantining and network protection
  - Omic, J., J. Martin Hernandez and P. Van Mieghem, 2010, "Network protection against worms and cascading failures using modularity partitioning", 22nd International Teletraffic Congress (ITC 22), September 7-9, Amsterdam, Netherlands.
  - Gourdin, E., J. Omic and P. Van Mieghem, 2011, "Optimization of network protection against virus spread", 8th International Workshop on Design of Reliable Communication Networks (DRCN 2011), October 10-12, Krakow, Poland.

E.R. van Dam, R.E. Kooij, The minimal spectral radius of graphs with a given diameter, *Linear Algebra and its Applications,* 423, 2007, pp. 408-419.

Coupled oscillators (Kuramoto model)

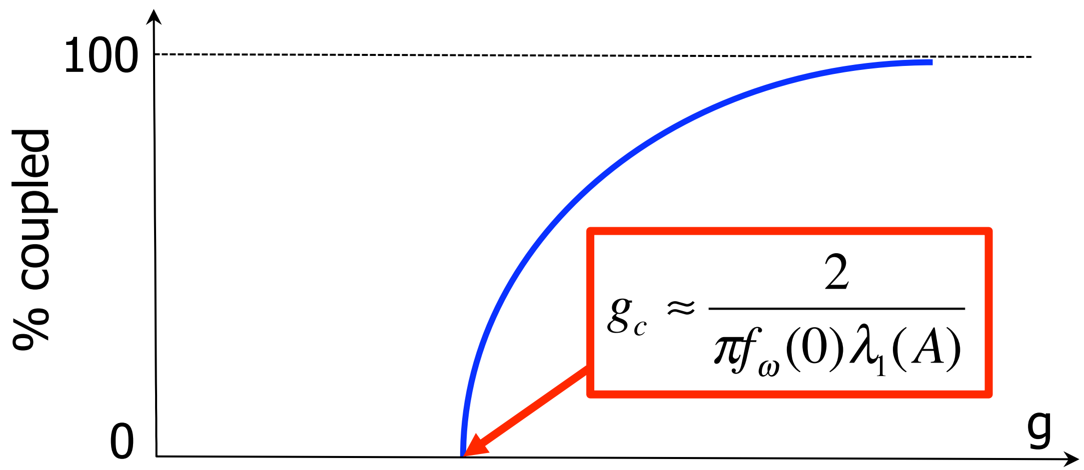


Interaction equals sums of sinus of phase difference of each neighbor:

$$\dot{\theta}_k = \omega_k + g\sum_{j=1}^{N} a_{kj} \sin\left(\theta_j - \theta_k\right)$$

coupling strength

natural frequency



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

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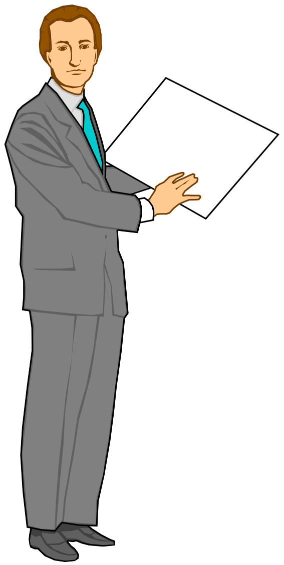

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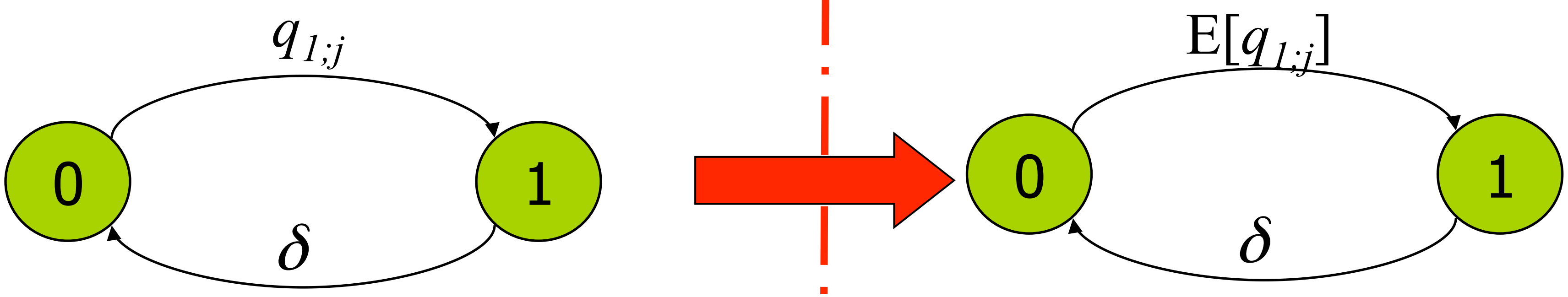
Mean-field approximation



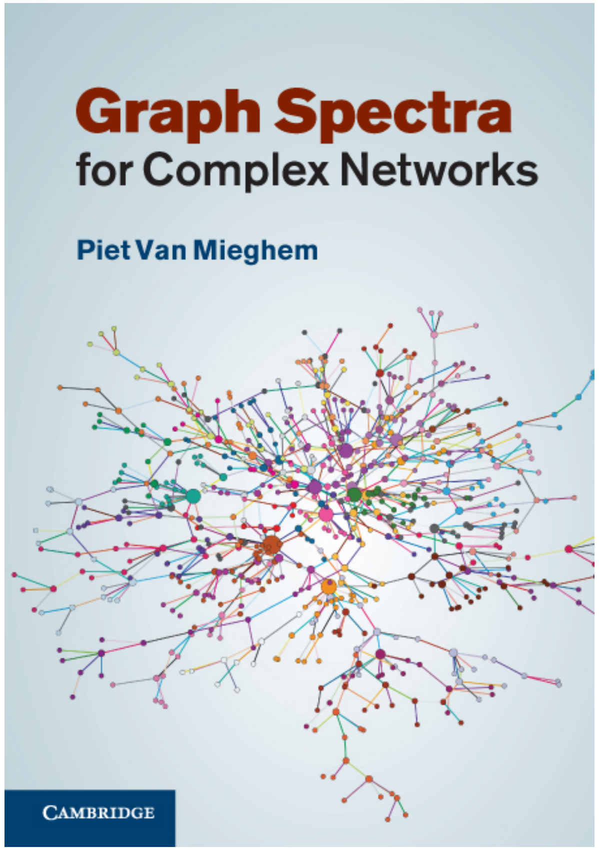
- 2^N linear equations
- Steady-state
  - absorbing (healthy) state
  - reached after unrealistically long time
- difficult to analyze

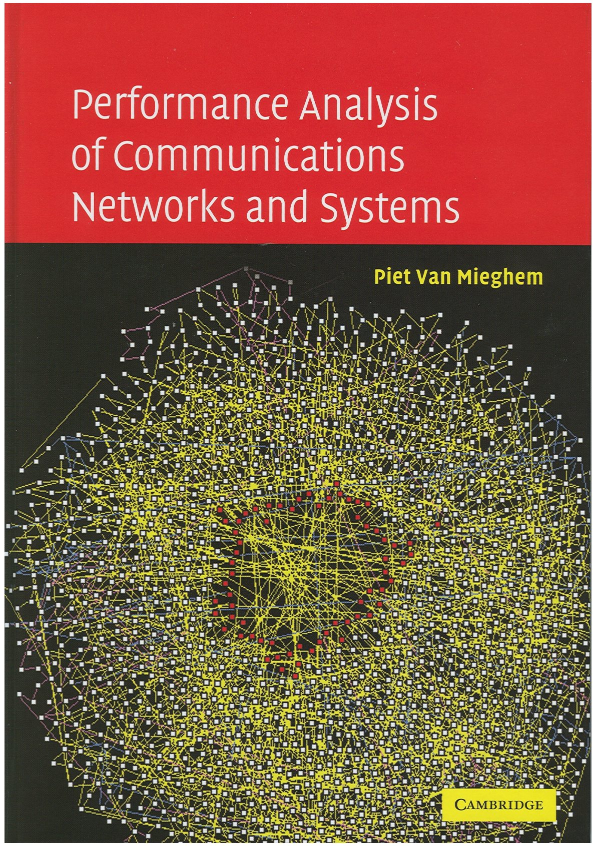
- *N* non-linear equations
- Meta-stable state:
  - phase-transition
  - epidemic threshold
  - realistic
- analytically tractable

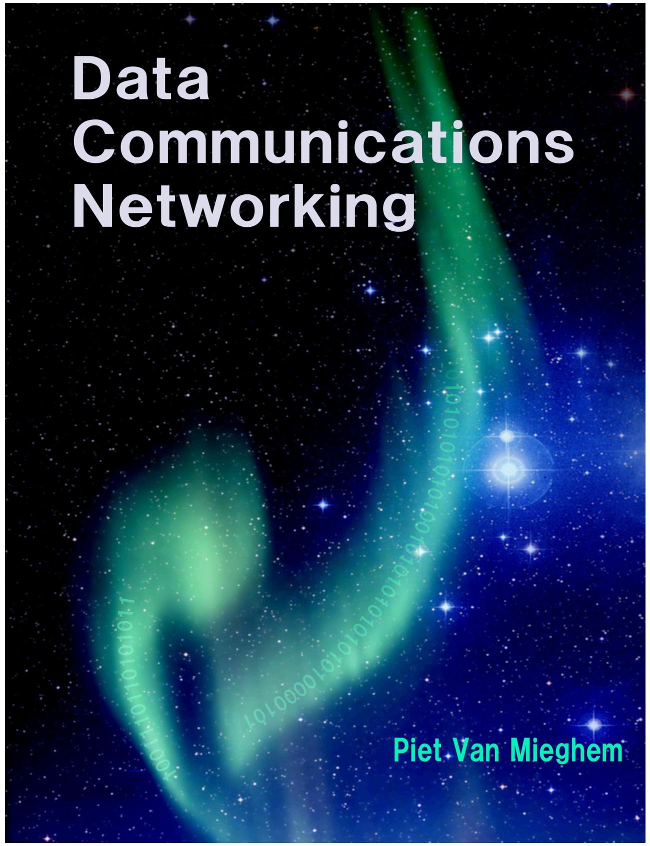
Agenda for future research

- Accuracy of *N*-intertwined mean-field approximation
- Exact computations for graphs beside the complete graph and the star
- Coupling of the virus spread process and the underlying topology (adaptive networks)
- Multiple, simultaneous viruses on a network
- Eigenvectors and eigenvalues of a graph: what do they "physically" mean?

Books







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

Thank You

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