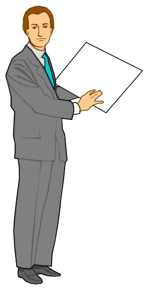
Virus Spread in Networks

Piet Van Mieghem

work in collaboration with Jasmina Omic, Huijuan Wang, Rob Kooij, Mina Youssef and Caterina Scoglio

Outline



Introduction & Definitions

The N-intertwined model for virus spread

Extensions

Viral Conductance

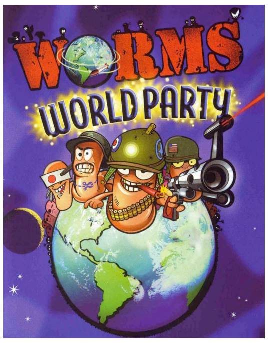
Modifying the epidemic threshold

Summary

Motivation for virus spread in networks

- Computer viruses
  - security threat to Internet
  - annoyance
  - very costly
    - Code Red worm: several billion $$ in damage
- Why do we care?
  - Understanding the spread of a virus is the first step in preventing it
  - How fast do we need to disinfect nodes so that the virus dies quickly? Which nodes?

Applications of virus spread models



- **Computer virus and worms modelling**
- **Epidemic algorithms**
- **Error propagation in networks**
- **Any self-replicating object on a dynamic network**
- **Emotions as infectious diseases in social networks**

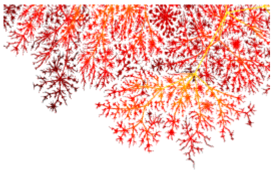
History*

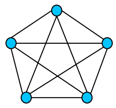
First epidemic model by Bernoulli (1760)

Homogeneous mixing model (biology)

Epidemic on a graph (Kephart and White)

Power-law graphs (Pastor-Satorras and Vespignani)





* “Epidemic modelling – an introduction” – D. J. Daley and J. Gani

State of the art of epidemic modeling

- Timing parameters modelling.
  - “Modelling the Effects of Timing Parameters on Virus Propagation” (Y. Wang and C. Wang)
- Topology influence on epidemic.
  - “The Effect on Network Topology on the Spread of Epidemic” (Ganesh, Massoulie, Towsley)
  - “Threshold for Virus Spread on Networks” (Draief, Ganesh, Massoulie)
- Percolation and generating function approach.
  - “The spread of epidemic disease on networks” (Newman)
- Contact Processes (mathematical theory)
  - Branch of continuous-time Markov theory (book by Liggett)

Spreading process

- *States in which a node can be*:
  - susceptible (S)
  - infected (I)
  - incubating
  - alert
  - removed (either cured or death)
- *Time description of the model*:
  - continuous-time
  - discrete-time

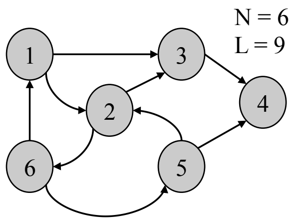
- *Focus here is a simple model*:
  - a SIS model in continuous time applicable to **any network**

A few graph metrics…

- Number of **nodes** N and **links** L in a graph G
- **Degree** d_i of a node i: number of directly linked neighbors
  - degree distribution of all your first hop neighbors, all second hop neighbors, etc…
- **Hopcount** (number of links) of a shortest path between two nodes
  - **Diameter:** largest possible hopcount (distance)
  - ***k*-th level set**: number of nodes at hop k in the shortest path tree rooted at a node (also called the **expansion** of G)
- **Connectivity** and number of **components (clusters)**
  - strongly connected components
  - number of **cliques** (= complete subgraphs K_m with $m < N$)
  - **edge/vertex connectivity**: minimum number of links/node whose removal disconnects G
- **Betweenness** of a link/node: number of shortest paths between all pair of nodes in G that traverses the link/node
- **… and many more**…

Algebraic graph theory

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



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

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

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

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

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A wealth of relations…

Degree law: $\sum_{j=1}^{N} d_j = 2L$

Number of k-hop walks between node i and j: $(A^k)_{ij}$

Any **real symmetric matrix S** can be written as $S = X \Lambda X^T$, where X is the orthog. matrix with real eigenvectors in the columns and $\Lambda = diag(\lambda_1,\ldots,\lambda_N)$, where λ_j is the j-th real eigenvalue. Eigenvalues can be ordered as $\boxed{\lambda_N \le \lambda_{N-1} \le \cdots \le \lambda_2 \le \lambda_1}$

Spectrum of A: 1) all eigenvalues lie in the interval $(-d_{max}, d_{max}]$

2) $\sum_{j=1}^{N} \lambda_j = 0 \qquad \sum_{j=1}^{N} \lambda_j^2 = 2L \qquad \sum_{j=1}^{N} \lambda_j^k = Trace(A^k) = \sum_{j=1}^{N} (A^k)_{jj}$

Spectrum of Q: 1) any eigenvalue μ_k is non-negative and smallest $\mu_N = 0$.

2) complexity (number of spanning trees) is $\xi(G) = \frac{1}{N}\prod_{k=1}^{N-1} \mu_k$

3) the second smallest eigenvalue (**algebraic connectivity μ_{N-1}**) is related to how strongly a graph is connected

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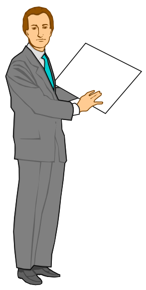
Outline



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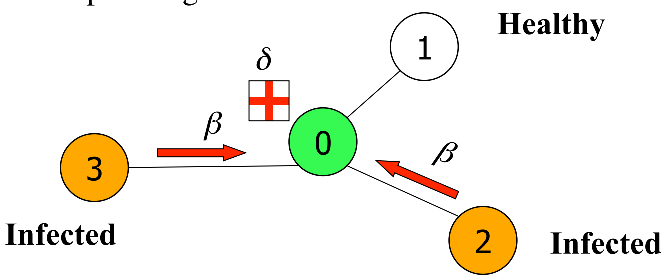
Simple SIS model (1)

- 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



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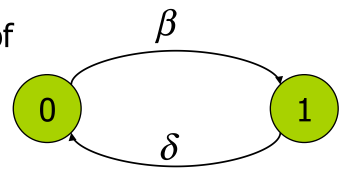
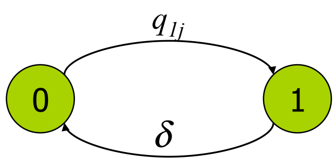
Simple SIS model (2)

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



Simple SIS model (3)

- Nodes are interconnected in graph:
  $$Q_j(t) = \begin{bmatrix} -q_{1j} & q_{1j} \\ \delta & -\delta \end{bmatrix}$$



where the infection rate is due all infected neighbors of node *j:*

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

and where the adjacency matrix of the graph is

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

Simple SIS model (4)

- 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:

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

- 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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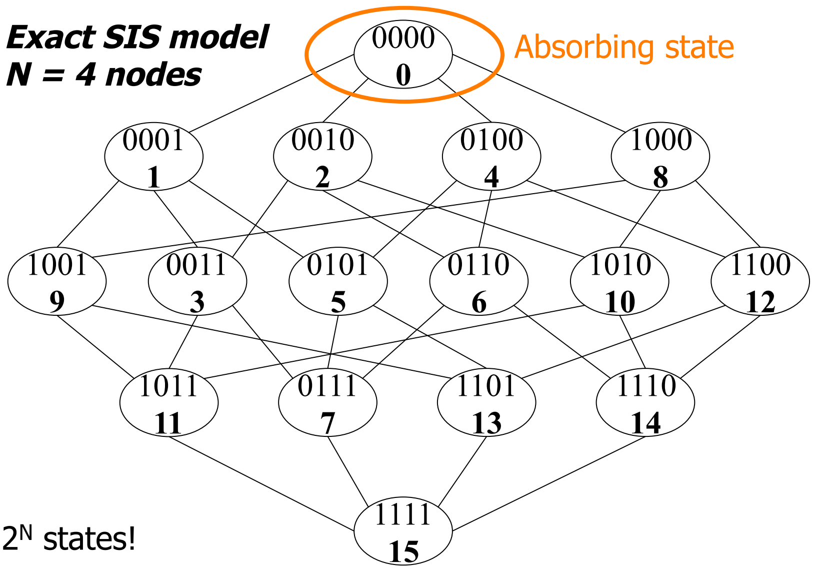
Exact SIS model
N = 4 nodes



2^N states!

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Simple SIS model (5): mean field

- The infinitesimal generator

$$Q_j(t) = \begin{bmatrix} -q_{1j} & q_{1j} \\ \delta & -\delta \end{bmatrix} \qquad \boxed{q_{1j}(t) = \beta \sum_{k=1}^{N} a_{jk} 1_{\{X_k(t)=1\}}}$$

is replaced by its mean (***the only approximation***!)

$$Q_j = \begin{bmatrix} -E[q_{1j}] & E[q_{1j}] \\ \delta & -\delta \end{bmatrix} \qquad \boxed{E[q_{1j}(t)] = \beta \sum_{k=1}^{N} a_{jk} \Pr[\{X_k(t)=1\}]}$$

- Being able now to apply ordinary Markov theory, we arrive at our **_N_-intertwined model for virus spread**

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

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

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N-intertwined virus spread model

- Non-linear matrix equation:

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

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

- *Results:*
  - Probability of infection v_k for each node k separately
  - Number of infected nodes in the steady state
  - Phase transition phenomena for any network (largest eigenvalue of the adjacency matrix A)
  - Analytic computations feasible:
    - expansions of v_k as a function of the effective infection rate around the epidemic threshold and around infinity

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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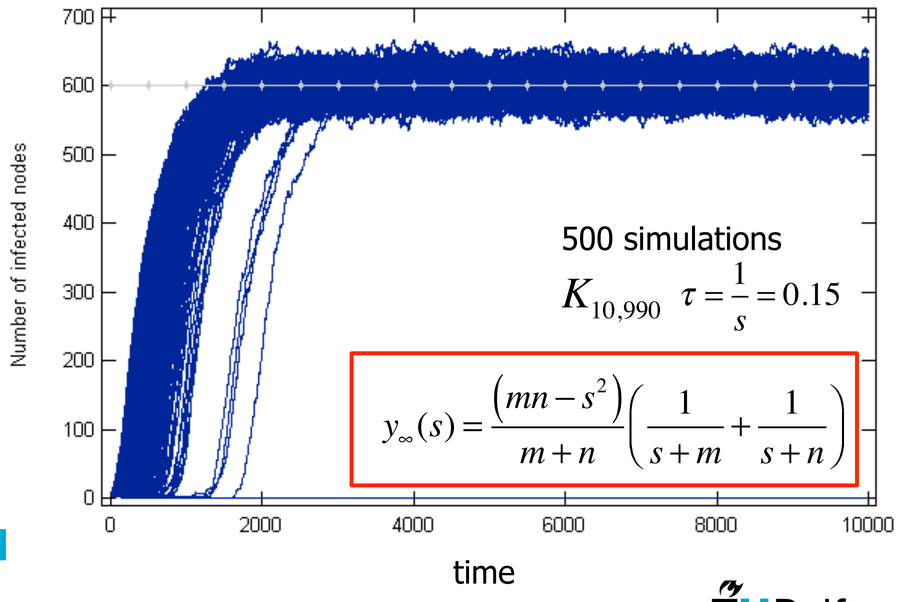
Simulations



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Kephart-White model

Assume perfect homogeneity & symmetry: a graph of degree *r*

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

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

steady-state

$$v = 1 - \frac{1}{r\tau} \quad \text{where} \quad \tau = \frac{\beta}{\delta}$$

threshold

$$\tau \geq \tau_c = \frac{1}{r} \quad \text{then} \quad v \geq 0$$

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J. O. Kephart and S. R. White, "Directed-graph epidemiological models of computer viruses," *Proc. IEEE Comput. Soc. Symp. Research in Security and Privacy*, May 1991, pp. 343–359.

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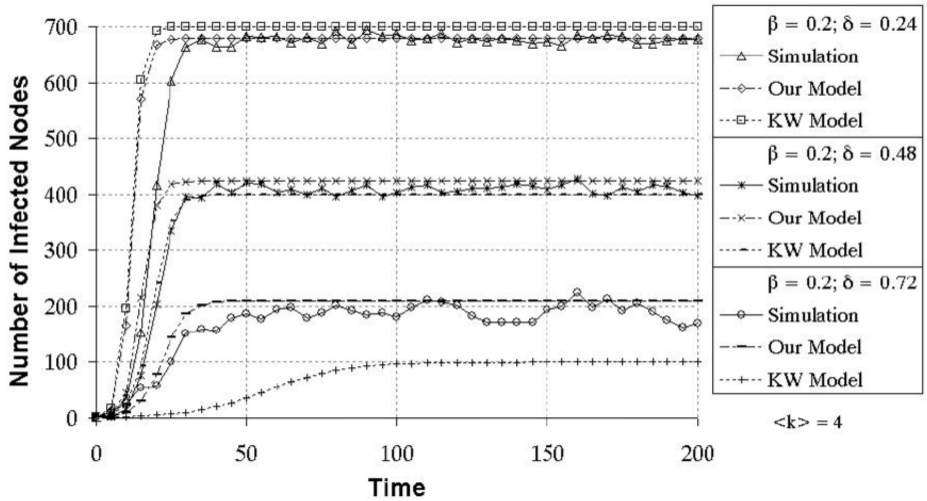
Comparison with simulation



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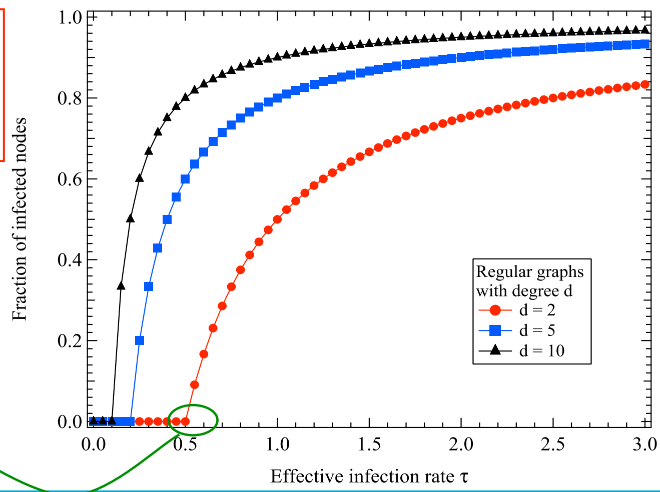
What is so interesting about epidemics?

β : infection rate per link
δ : curing rate per node
τ= β/ δ : effective spreading rate



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

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

$$E[D] = \frac{2L}{N} \le \lambda_1(A) \le d_{\max}$$

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Application example: distributed storage

- each network node reserves memory space for other nodes
- each node spreads own files with rate β
- each node deletes files from neighbors with rate δ

$$\tau = \frac{\beta}{\delta} > \tau_c = \frac{1}{\lambda_1(A)}$$

Then your file is stored at node *j* in the network with probability $v_j > 0$

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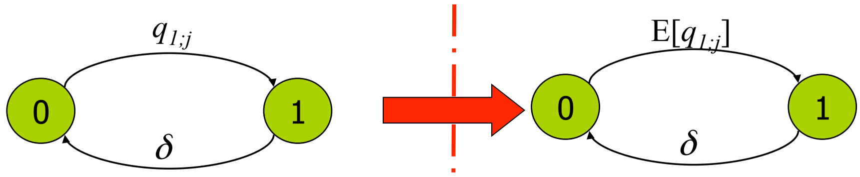
Mean-field approximation



- 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

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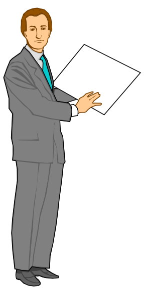
Open question

- What is the accuracy of the *N*-intertwined model?
  - due to single approximation of a mean-field type
- Why is this a difficult to determine:
  - exact Markov chain cannot be compute for $N > 20$
  - simulations have own "accuracy limits"
  - mathematical derivation (contact networks)
    - assume asymptotic analyses ($N \rightarrow$ infinity)
    - absorbing state is reached with almost zero probability
    - only very few results exist (for specific graphs)

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

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- 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)

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Extension 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:
  - "R" state for "removed"
  - "An individual-based approach to SIR epidemics in contact networks", M. Youssef and C. Scoglio, Journal of Theoretical Biology 283, pp. 136-144, (2011).

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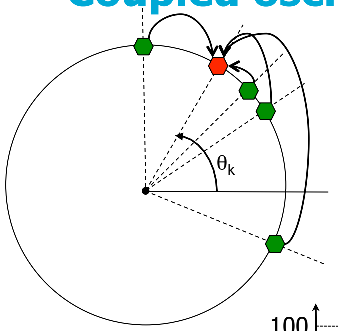
Coupled oscillators (Kuramoto model)

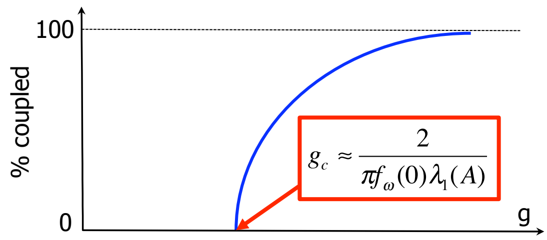


Interaction equals sums of sinus of phase difference of each neighbor:

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

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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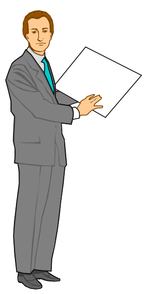
Outline



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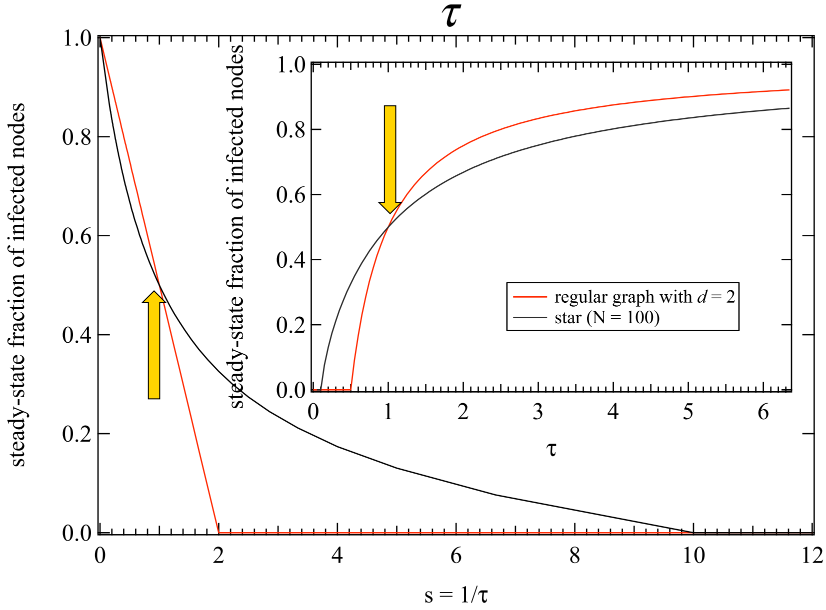
Transformation $s = \frac{1}{\tau}$



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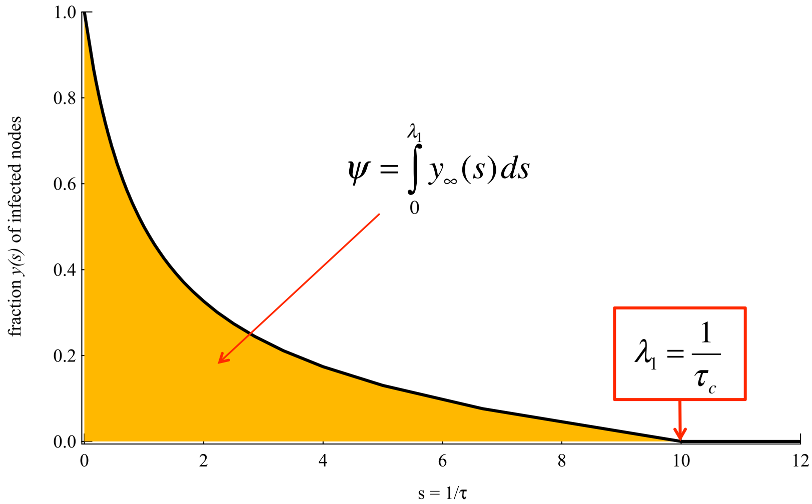
Viral Conductance: definition



$$\psi = \int_0^{\lambda_1} y_\infty(s)\,ds$$

$$\boxed{\lambda_1 = \frac{1}{\tau_c}}$$

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R. E. Kooij, P. Schumm, C. Scoglio and M. Youssef, "A new metric for robustness of networks with respect to virus spread", IFIP Networking 2009

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Viral Conductance: properties

$$\psi = \int_0^{\lambda_1} y_\infty(s)\,ds$$

Bounds: $\frac{1}{2} d_{\min} \le \psi \le \frac{1}{2}\lambda_1$

Viral Robustness metrics: (τ_c, ψ)

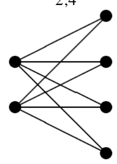
What are the graphs with maximum and minimum ψ ?

Some analytic evaluations:

$$\psi_{regular} = \frac{d}{2}$$

$$\psi_{K_{m,n}} = \sqrt{mn} - \frac{mn}{m+n} + \frac{(n-m)}{m+n}\log\frac{\left(1+\sqrt{n/m}\right)^m}{\left(1+\sqrt{m/n}\right)^n}$$

$K_{2,4}$



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M. Youssef, R. E. Kooij and C. Scoglio, "Viral conductance: Quantifying the robustness of networks with respect to spread of epidemics", Journal of computational science, to appear 2011

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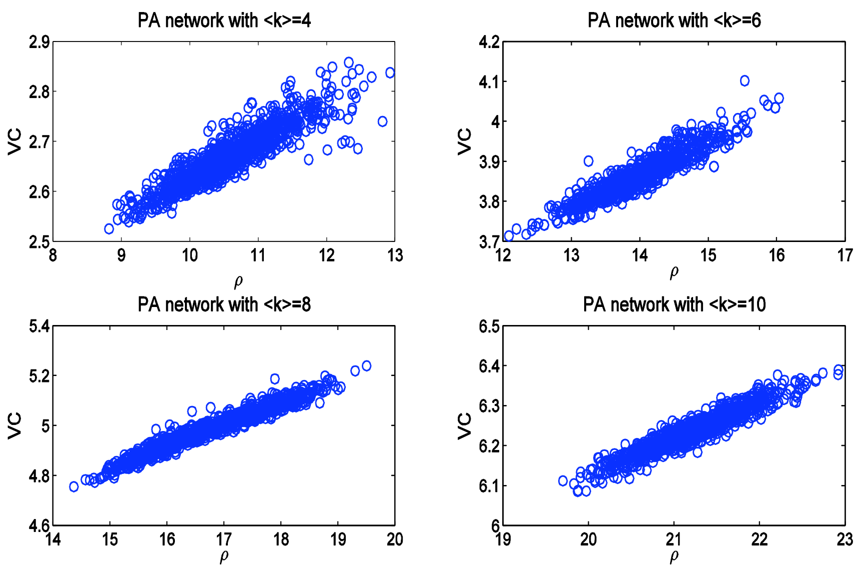
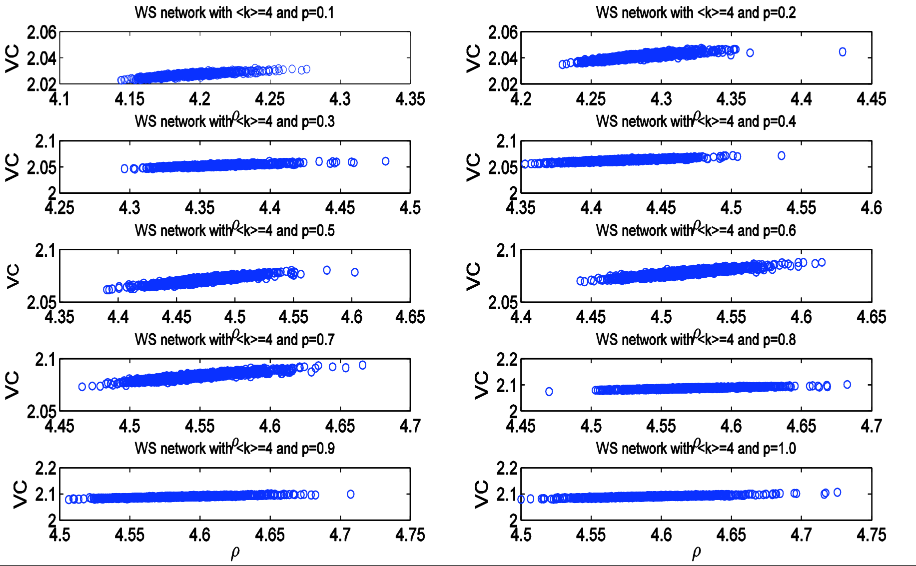
Preferential Attachment nets with E[D]=<k>= 4, 6, 8, and 10



Watts-Strogatz nets with <k>=4 and $0 \le p \le 1$



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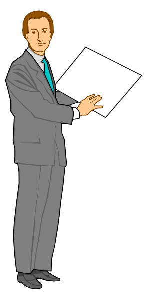

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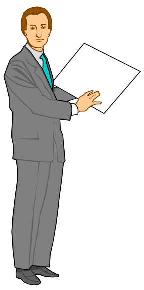
Affecting the epidemic threshold

- Degree-preserving rewiring
  - Changing the 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.
- 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: Removing inter-module links
  - 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.

Outline



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Summary (1)

- Epidemic theory can model many processes: information spread, real viruses, storage, emotions in social nets, ...
- Real epidemics: phase transition at $\tau_c = 1/\lambda_1$
- The topology plays an important role in spreading
- Networks can be designed to protect individual nodes via its curing strength δ (virus software, fire-wall, etc...). Protection, however, does cost money...
- Epidemic threshold engineering:
  - Degree-preserving *assortative* rewiring increases λ_1, while degree-preserving *disassortative* rewiring decreases λ_1.
  - Removing links/nodes to maximally decrease λ_1 is NP-hard.

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Summary (2)

- *Agenda for future research:*
  - accuracy of *N*-intertwined model, i.e. of the mean-field approximation
  - coupling of the virus spread process and the underlying topology
  - most general extensions of the *N*-intertwined model (to $m > 2$ states per node)
  - Multiple, simultaneous viruses on a network

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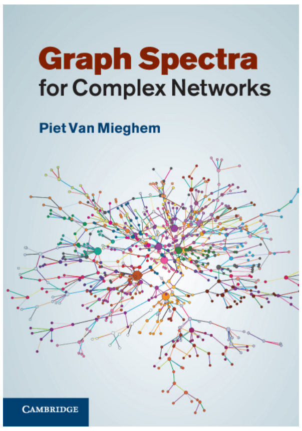
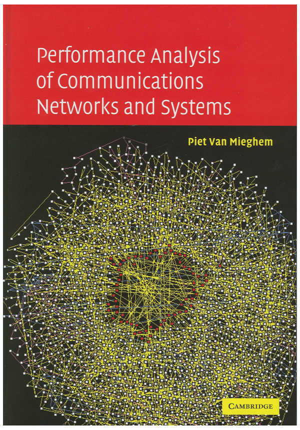
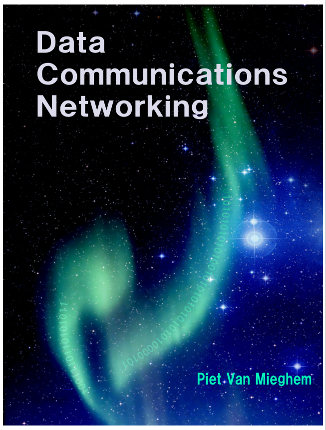
Books







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

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Thank You

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