MODELING PROPAGATION PROCESSES ON NETWORKS BY USING DIFFERENTIAL EQUATIONS

Peter L. Simon

Department of Applied Analysis and Computational Mathematics,
Institute of Mathematics, Eötvös Loránd University Budapest, and
Numerical Analysis and Large Networks Research Group, Hungarian Academy of Sciences,
Hungary

SIS EPIDEMIC ON A NETWORK

A graph with N nodes is given

The nodes can be susceptible (S) or infected (I)

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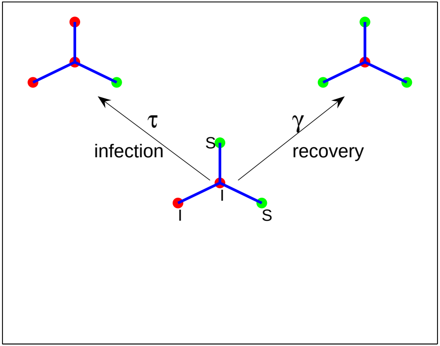

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Known models:

- Master equation
- Mean-field equation
- Pairwise model
- Compact pairwise model
- ...

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The transitions between different states can be described by a Poisson process

Probability of a transition from state a_i to state a_j in a time interval of length Δt is:

$$1 - \exp(-\lambda_{ij}\Delta t).$$

SIS epidemic

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States of the nodes: $\{S, I\}$.

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Transitions and their rates

- $S \to I$, $\lambda = k\tau$, k is the number of I neighbours.
- $I \to S$, $\lambda = \gamma$

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- $S \rightarrow I$, $\lambda = k\tau$, k is the number of I neighbours.
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States of the nodes: $\{X, Y, Z\}$ (ignorant, spreader, stifler).

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Transitions and their rates

- $X \to Y$, $\lambda = k\tau$, k is the number of Y neighbours.
- $Y \to Z$, $\lambda = \gamma + jp$, j is the number of Y and Z neighbours.

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Transitions and their rates

- $E_+ \to E_-$, $\lambda = \alpha$.
- $E_- \to E_+$, $\lambda = \tanh(iw_E - jw_I + h_E)$, i, j is the number of E_+ and I_+ neighbours.
- $I_+ \to I_-$, $\lambda = \alpha$.
- $I_- \to I_+$, $\lambda = \tanh(iw_E - jw_I + h_I)$, i, j is the number of E_+ and I_+ neighbours.

AIM OF THE RESEARCH

Derive differential equations for different processes and for different types of graphs.

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Frequently used random graphs:

- Erdős-Rényi
- Configuration model (Bollobás)
- Small-world (Watts-Strogatz)
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Examples for network processes:

- Epidemic propagation
- Rumour spreading
- Propagation of neuronal activity

Markov chain for *SIS* epidemic

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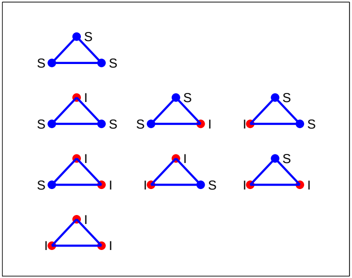
State space for a triangle



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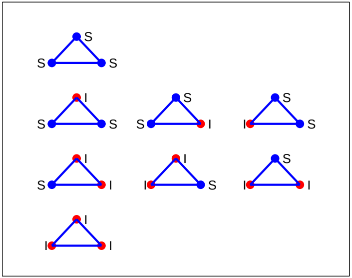

- Infection: $SIS \to SII$, IIS
- Recovery: $SIS \to SSS$

Master equations

$$
\begin{aligned}
\dot{X}_{SSS} &= \gamma(X_{SSI} + X_{SIS} + X_{ISS}),\\
\dot{X}_{SSI} &= \gamma(X_{SII} + X_{ISI}) - (2\tau + \gamma)X_{SSI},\\
\dot{X}_{SIS} &= \gamma(X_{SII} + X_{IIS}) - (2\tau + \gamma)X_{SIS},\\
\dot{X}_{ISS} &= \gamma(X_{ISI} + X_{IIS}) - (2\tau + \gamma)X_{ISS},\\
\dot{X}_{SII} &= \gamma X_{III} + \tau(X_{SSI} + X_{SIS}) - 2(\tau + \gamma)X_{SII},\\
\dot{X}_{ISI} &= \gamma X_{III} + \tau(X_{SSI} + X_{ISS}) - 2(\tau + \gamma)X_{ISI},\\
\dot{X}_{IIS} &= \gamma X_{III} + \tau(X_{SIS} + X_{ISS}) - 2(\tau + \gamma)X_{IIS},\\
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\dot{X}_{ISS} &= \gamma(X_{ISI} + X_{IIS}) - (2\tau + \gamma)X_{ISS},\\
\dot{X}_{SII} &= \gamma X_{III} + \tau(X_{SSI} + X_{SIS}) - 2(\tau + \gamma)X_{SII},\\
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2^N equations for a graph with N nodes

Master equations

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\dot{X}_{SII} &= \gamma X_{III} + \tau(X_{SSI} + X_{SIS}) - 2(\tau + \gamma)X_{SII}, \\
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The size of the system can be reduced by using the automorphisms of the graph:

Simon, P.L., Taylor, M., Kiss., I.Z., Exact epidemic models on graphs using graph-automorphism driven lumping, J. Math. Biol., 62 (2011).

Exact equation: $[\dot{I}] = \tau[SI] - \gamma[I]$

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$[SI](t)$: expected number of SI edges

This differential equation holds for any graph

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Approximating differential equation for $[I]$

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MEAN-FIELD APPROXIMATION FOR SIS EPIDEMIC

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Reason: the approximation assumes random distribution of infected nodes.

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Better idea: derive a differential equation for $[SI]$, this leaded to the pairwise model.

Keeling, M.J., The effects of local spatial structure on epidemiological invasions, *Proc. R. Soc. Lond. B* **266** (1999), 859-867.

Pairwise approximation

Keep the exact equation $\quad \dot{[I]} = \tau[SI] - \gamma[I]$

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\dot{[I]} &= \tau[SI] - \gamma[I], \\
\dot{[SI]} &= \gamma([II] - [SI]) + \tau([SSI] - [ISI] - [SI]), \\
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\dot{[SS]} &= 2\gamma[SI] - 2\tau[SSI].
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Approximation:

$$[ABC] \approx \frac{n-1}{n}\frac{[AB][BC]}{[B]}, \quad n \text{ average degree}$$

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M. Taylor, P. L. Simon, D. M. Green, T. House, I. Z. Kiss, From Markovian to pairwise epidemic models and the performance of moment closure approximations, *J. Math. Biol.* **64** (2012), 1021-1042.

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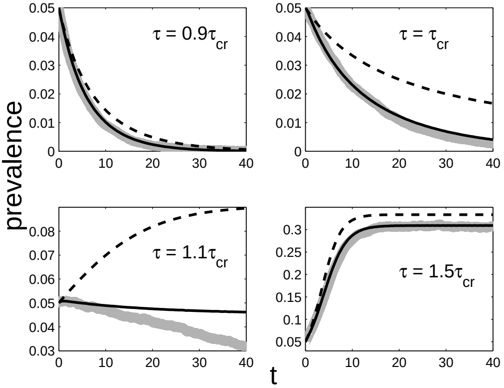

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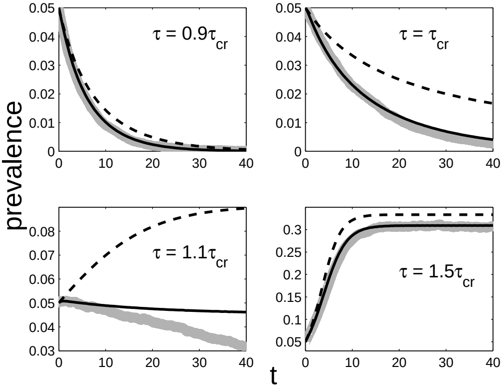

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Simulation (average of 200 runs): grey thick curve

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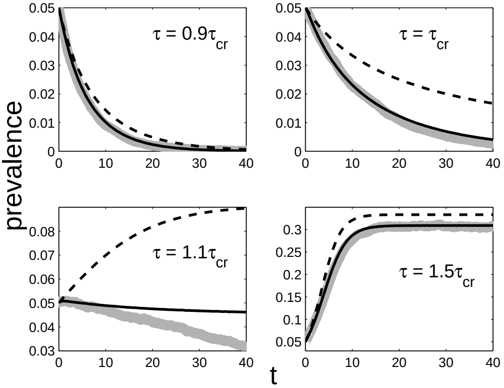

$\tau = \tau_{cr} \Leftrightarrow$ basic reproduction number $R_0 = 1$.

Bimodal random graph with $N = 1000$ nodes, average degree $n = 20$, $\gamma = 1$, $\tau = 2\tau_{cr} = 2\gamma/n$
$N/2$ nodes have degree d_1, $N/2$ nodes have degree d_2.

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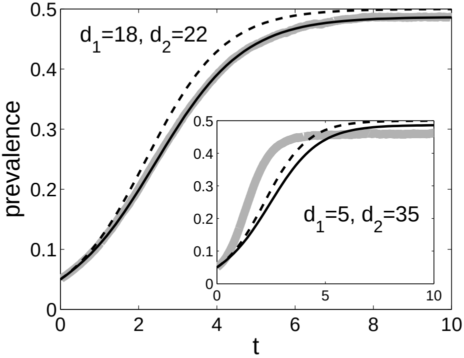

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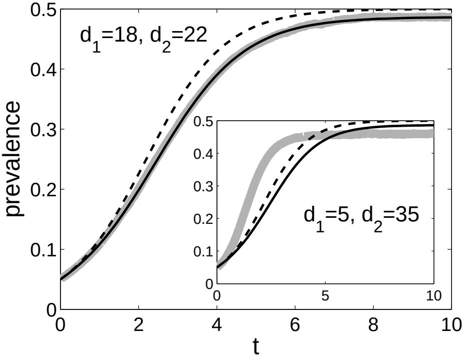

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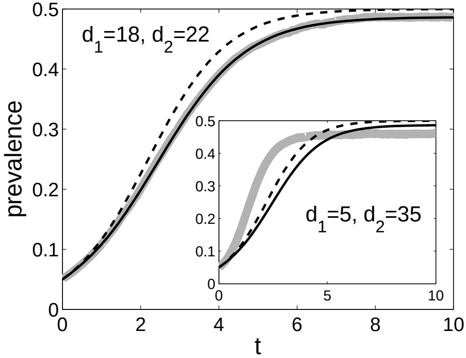

Reason of inaccuracy: in the closure $[ABC] \approx \frac{n-1}{n} \frac{[AB][BC]}{[B]}$ it is assumed that each node has the same degree n.

There are N_k nodes with degree d_k for $k = 1, 2, \ldots, K$.

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$$[ASI] = \sum_{k=1}^{K} [AS_k I], \qquad [AS_k I] \approx \frac{d_k - 1}{d_k} \frac{[AS_k][S_k I]}{[S_k]}$$

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$[S_k]$: expected number of susceptible nodes of degree d_k,
$[S_k I]$: expected number of edges connecting an infected node to a susceptible node of degree d_k

Compact pairwise approximation

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Differential equations are needed for the new unknowns.

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$$[S_kA] \approx [SA] \frac{d_k[S_k]}{\sum_{l=1}^{K} d_l[S_l]}$$

$$[AS_kI] \approx \frac{[AS][SI]d_k(d_k - 1)[S_k]}{S_1^2} \Rightarrow [ASI] \approx [AS][SI] \frac{S_2 - S_1}{S_1^2}$$

$$S_1 = \sum_{k=1}^{N} d_k[S_k], \qquad S_2 = \sum_{k=1}^{K} d_k^2[S_k].$$

Compact pairwise model

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\begin{aligned}
\dot{[S_k]}_c &= \gamma[I_k]_c - \tau d_k [S_k]_c \frac{[SI]_c}{S_s}, \\
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with $S_s = \sum_{k=1}^{K} d_k [S_k]_c$ and $P = \frac{1}{S_s^2} \sum_{k=1}^{K} (d_k - 1) d_k [S_k]_c$.

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Compact pairwise model: $K+3$ equations

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More complex and accurate models:

Pre-compact pairwise model: $5K$ equations

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More complex and accurate models:

Pre-compact pairwise model: $5K$ equations

Heterogeneous pairwise model: $2K^2+K$ equations

Bimodal random graph with $N = 1000$ nodes, average degree
$n_1 = 20$, $\gamma = 1$, $\tau = 3\gamma n_1/n_2$, $\quad n_i = \sum d_k^i p_k$
$N/2$ nodes have degree $d_1 = 5$, $N/2$ nodes have degree $d_2 = 35$.

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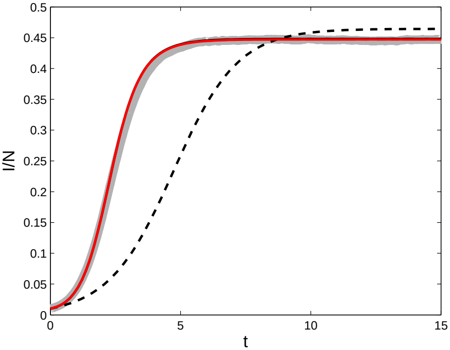

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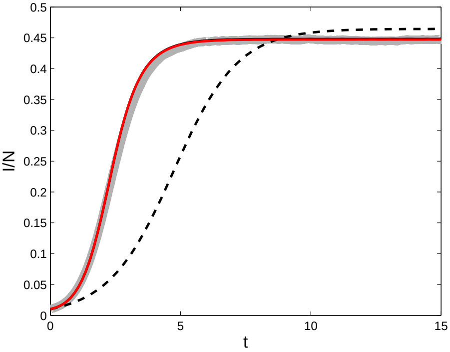

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Global behaviour for $\gamma < n\tau$: all solutions converge to the endemic steady state $I^{e} = N(1 - \frac{\gamma}{n\tau})$.

Exact differential equations:

$$
\begin{aligned}
[\dot{I}] &= \tau[SI] - \gamma[I], \\
[\dot{S}] &= \gamma[I] - \tau[SI], \\
[\dot{SI}] &= \gamma([II] - [SI]) + \tau([SSI] - [ISI] - [SI]), \\
[\dot{II}] &= -2\gamma[II] + 2\tau([ISI] + [SI]), \\
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Approximation:

$$
[ABC] \approx \frac{n-1}{n} \frac{[AB][BC]}{[B]}, \quad n \text{ average degree}
$$

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\end{aligned}
$$

Conservation relations:

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[I] + [S] = N, \quad 2[SI] + [II] + [SS] = nN, \quad [SI] + [SS] = n[S]
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Reduced system

$$\begin{aligned}
\dot{[S]} &= \gamma N - (\gamma + n\tau)[S] + \tau[SS], \\
\dot{[SS]} &= 2(n[S] - [SS])\left(\gamma - \tau(n-1)\frac{[SS]}{n[S]}\right).
\end{aligned}$$

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\end{aligned}$$

Steady states and their stability

- If $\tau(n-1) < \gamma$, then there is no endemic steady state and the disease-free steady state is asymptotically stable.
- If $\tau(n-1) > \gamma$, then the endemic steady state is asymptotically stable and the disease-free steady state is unstable.

Reduced system

$$
\begin{aligned}
\dot{[S]} &= \gamma N - (\gamma + n\tau)[S] + \tau[SS], \\
\dot{[SS]} &= 2(n[S] - [SS])\left(\gamma - \tau(n-1)\frac{[SS]}{n[S]}\right).
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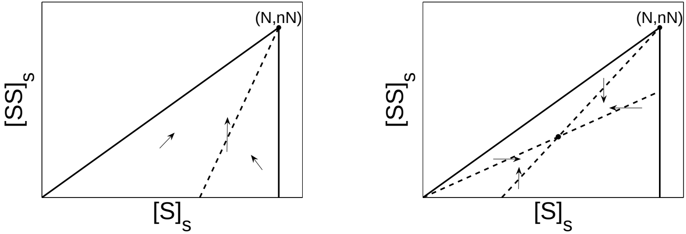
\end{aligned}$$

Phase plane analysis



Direction field: $\tau(n-1) < \gamma$ (left panel), $\tau(n-1) > \gamma$ (right panel).

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Köszönöm a figyelmet!

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