Epidemic propagation on networks: a differential equation approach

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S/S EPIDEMIC ON A NETWORK

A graph with N nodes is given

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

SIS EPIDEMIC ON A NETWORK

A graph with N nodes is given

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Transitions:

- $S \to I$, rate: $k\tau$, k is the number of I neighbours.
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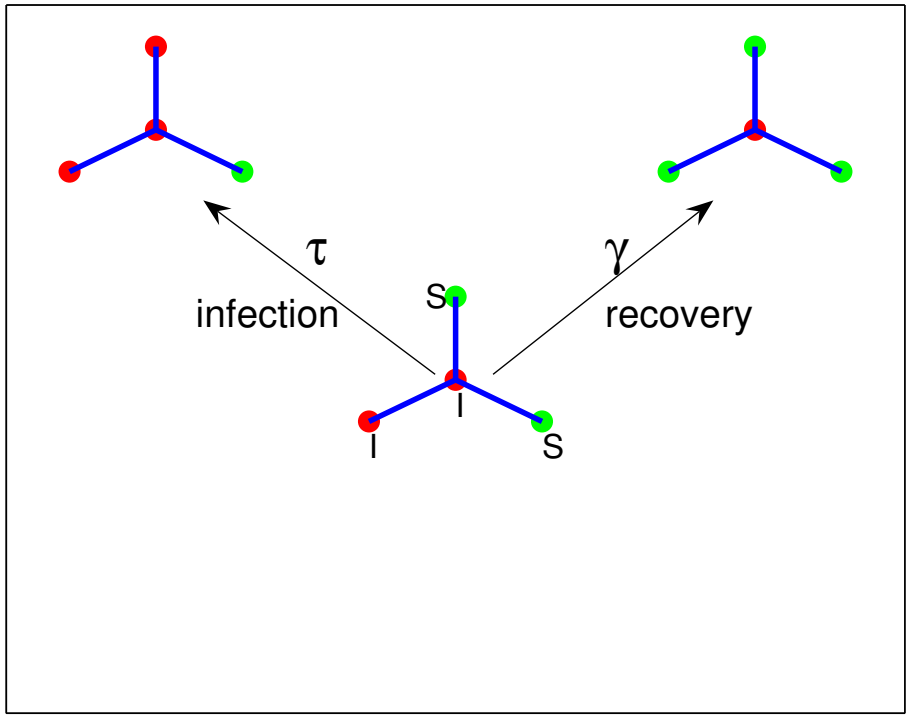

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Known models:

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

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(R has no effect on the propagation)

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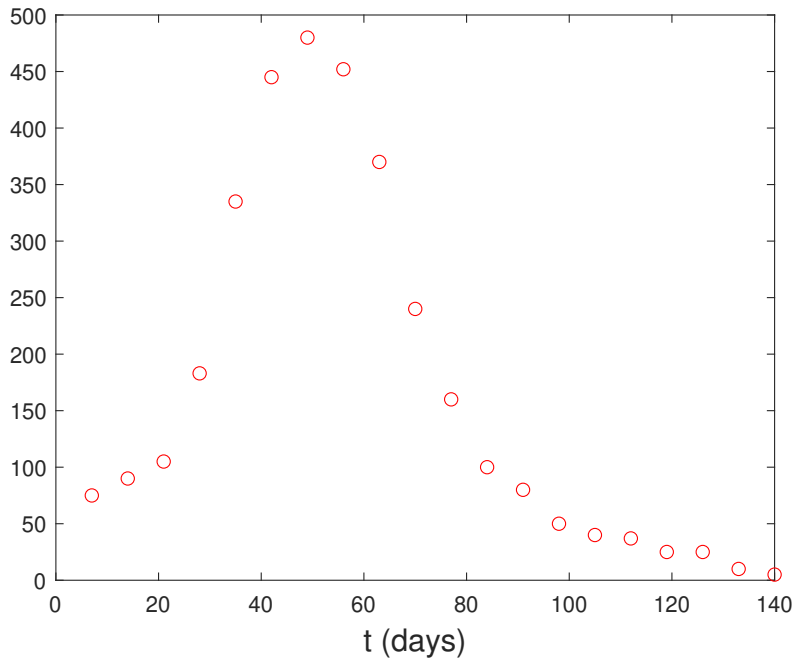
Example: Influenza in Hungary in 2016.
Weekly number of new reported cases for 100,000 persons.



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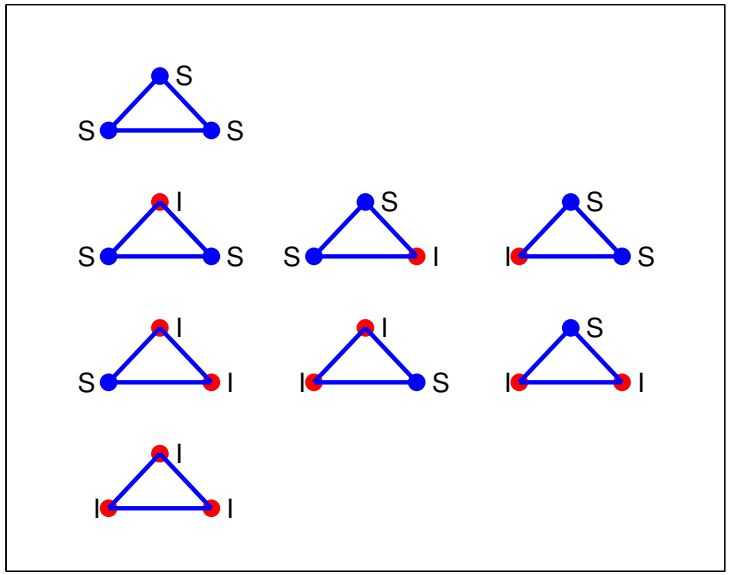
For simplicity, we present the theory for the SIS.

State space for a triangle graph



Master equations for *SIS* epidemic

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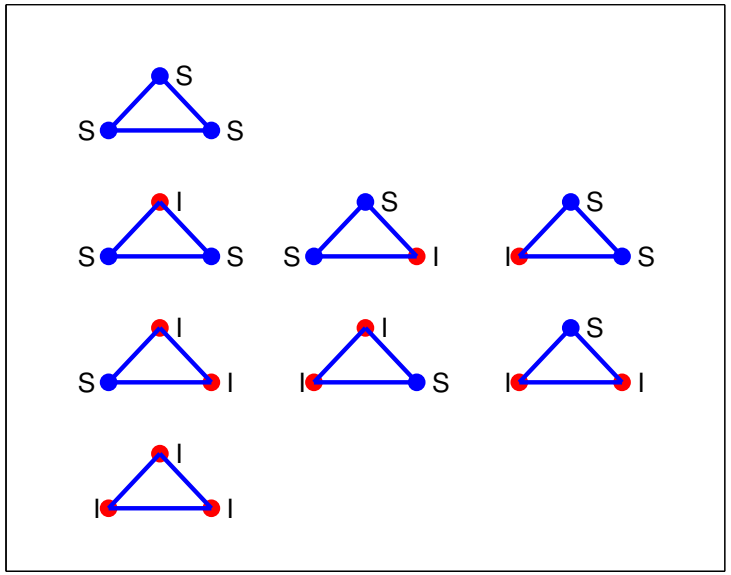

- Infection: $SIS \rightarrow IIS$
- Recovery: $SIS \rightarrow SSS$

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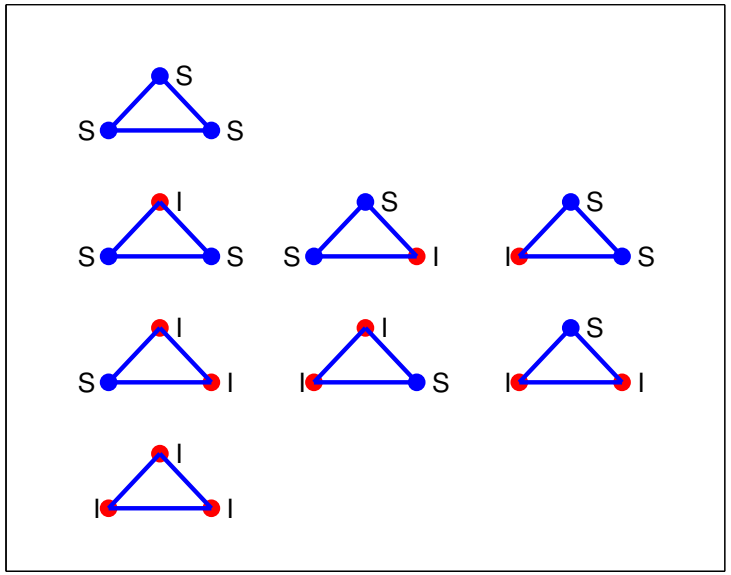

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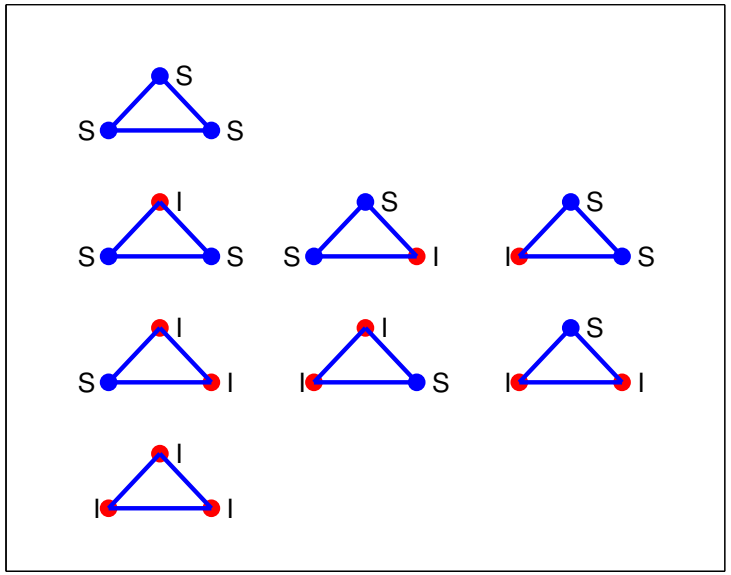

- Infection: $SIS \rightarrow IIS$
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Master equations are formulated for the probabilities of states.

$X_{SIS}(t)$ is the probability of state SIS at time t.

Master equations

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\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}, \\
\dot{X}_{III} &= -3\gamma X_{III} + 2\tau(X_{SII} + X_{ISI} + X_{IIS}),
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2^N equations for a graph with N nodes

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\end{aligned}
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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).

Population level quantities

$[I](t)$ and $[SI](t)$: expected values of I nodes and SI edges at time t

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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.

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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.

Comparison of ODE models to simulation

Regular random graph with $N = 1000$ nodes, average degree $n = 20$, $\gamma = 1$, critical value of τ from compartmental model: $\tau_{cr} = \gamma/n$

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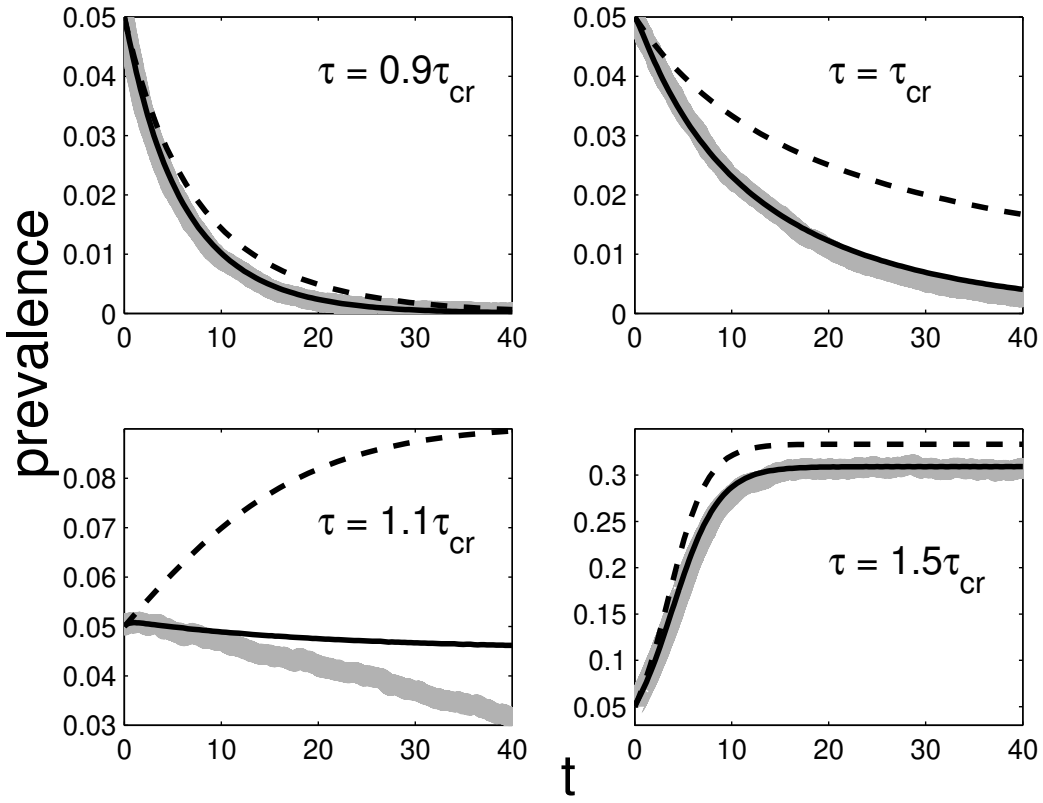

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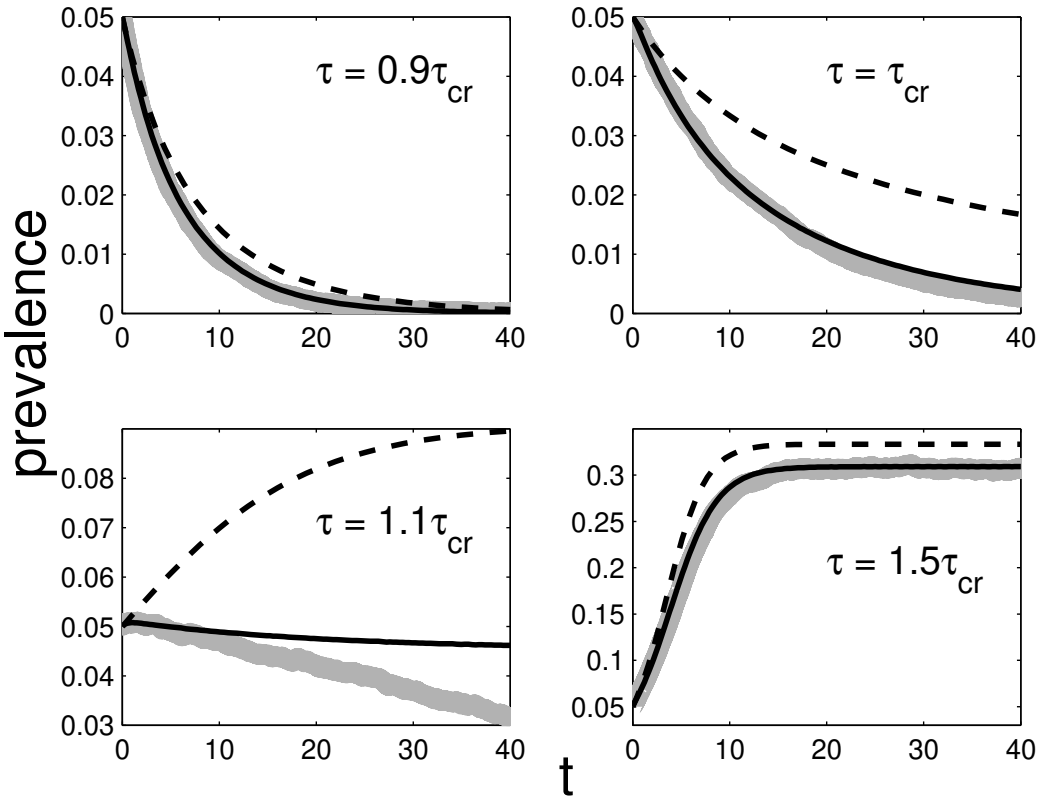

Mean-field: dashed, Pairwise: continuous
Simulation (average of 200 runs): grey thick curve

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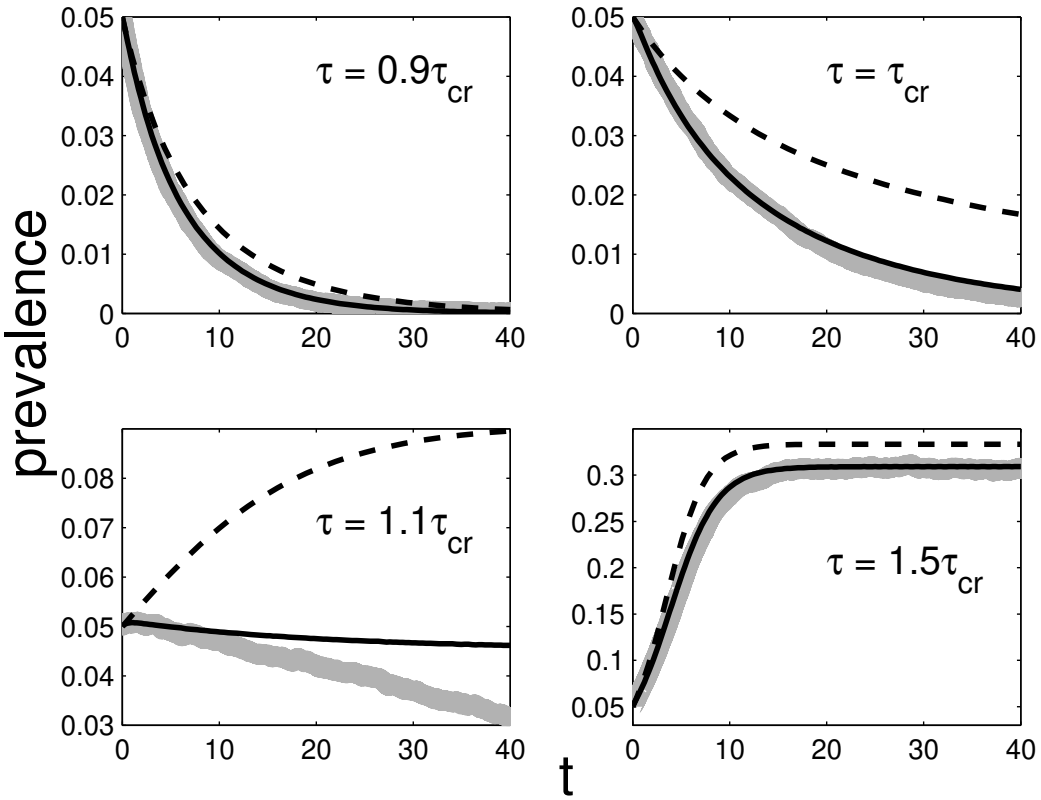

$\tau = \tau_{cr} \Leftrightarrow$ basic reproduction number $R_0 = 1$.

Comparison of ODE models to simulation

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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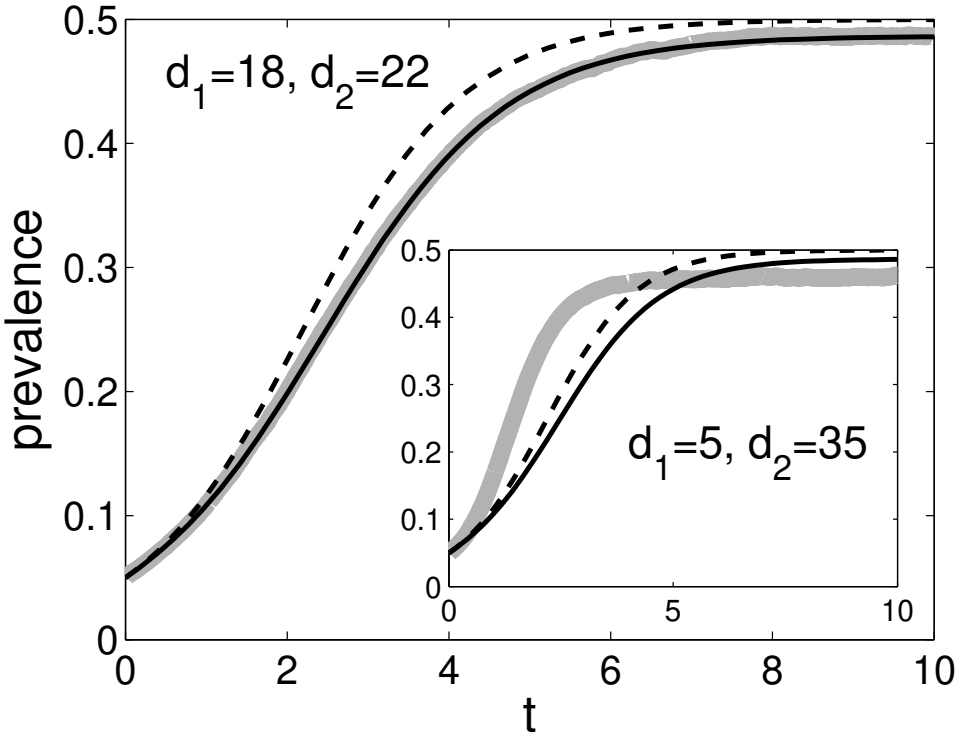

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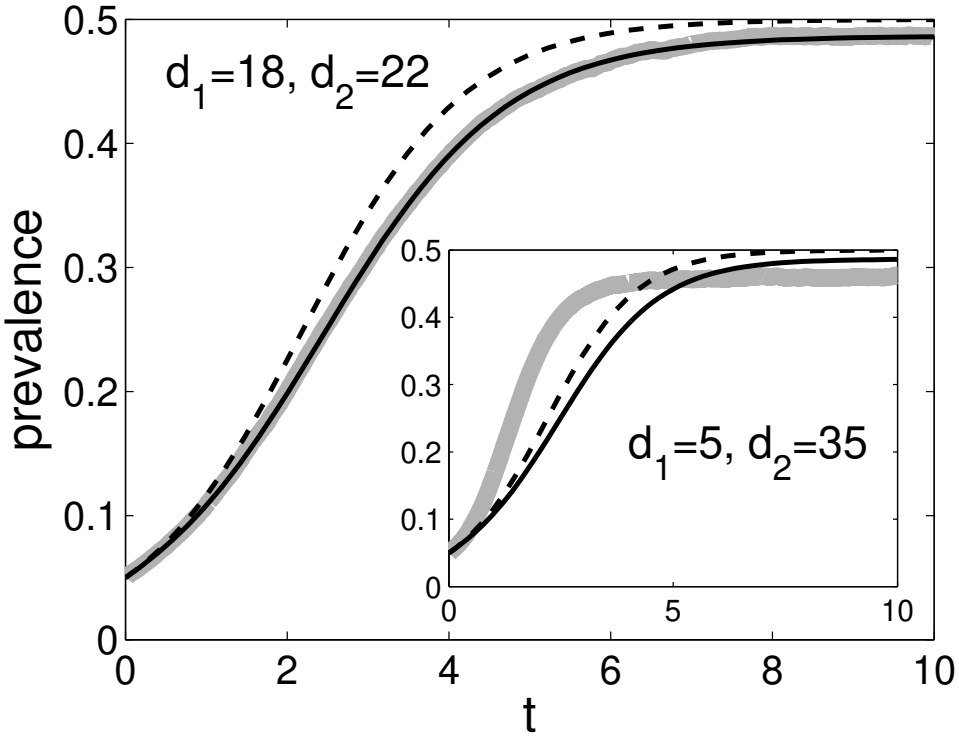

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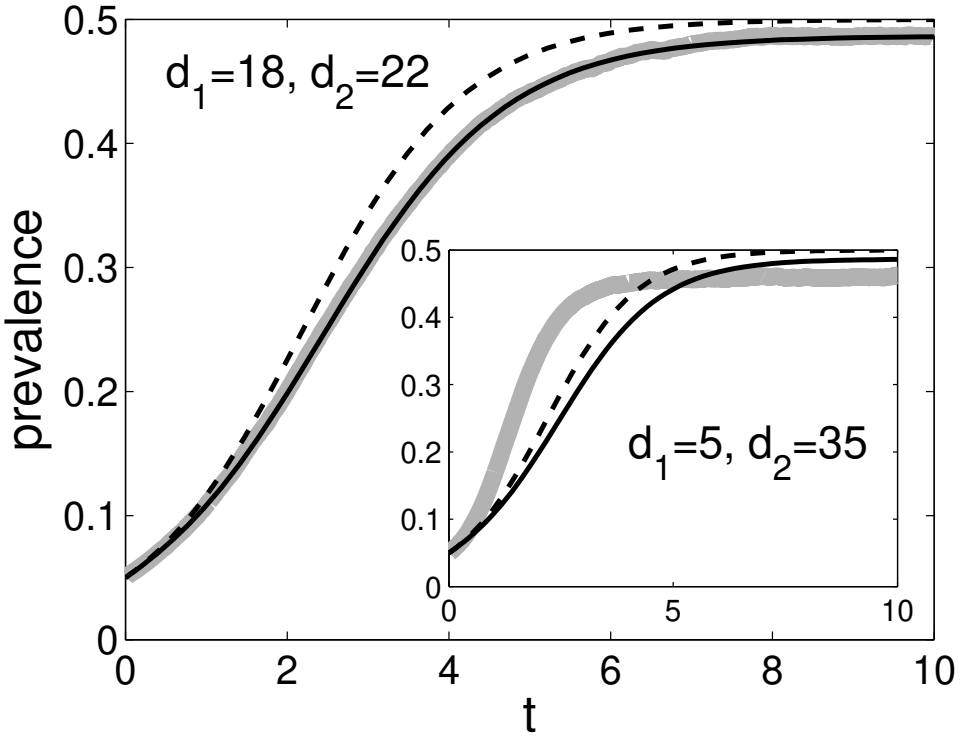

Reason of inaccuracy: in the closure $[ABC] \approx \frac{n-1}{n}\frac{[AB][BC]}{[B]}$ it is assumed that each node has the same degree n.

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Mean-field model at the level of singles:

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Closure: $[S_k I]$ can be expressed in terms of singles, $[S_k]$,

or in terms of pairs, $[SI]$, and singles.

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Compact pairwise model: $K + 3$ equations

Comparison of ODE models to simulation

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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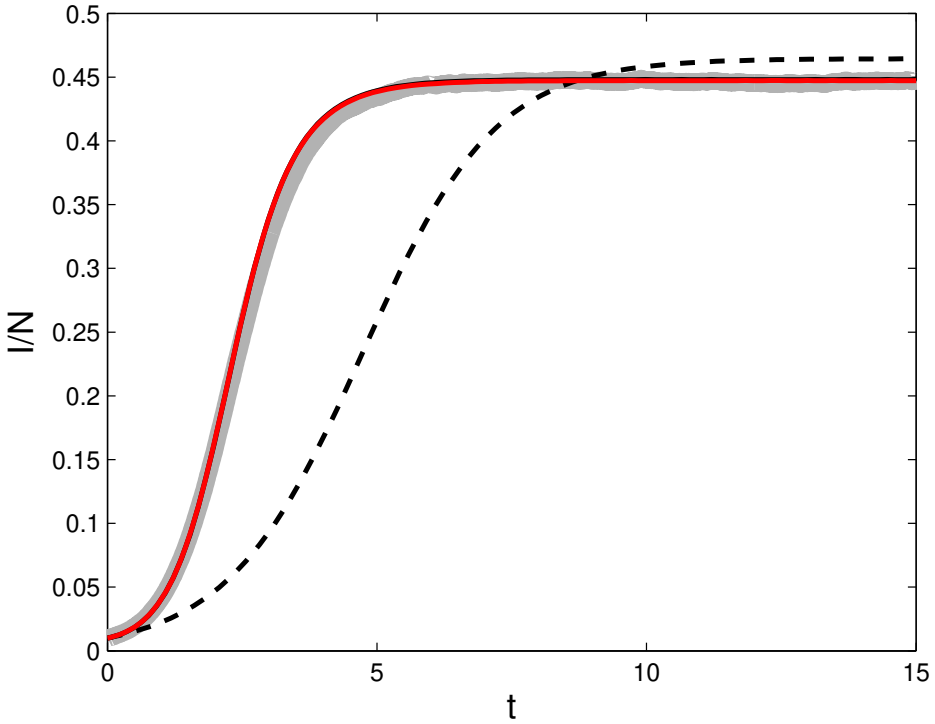

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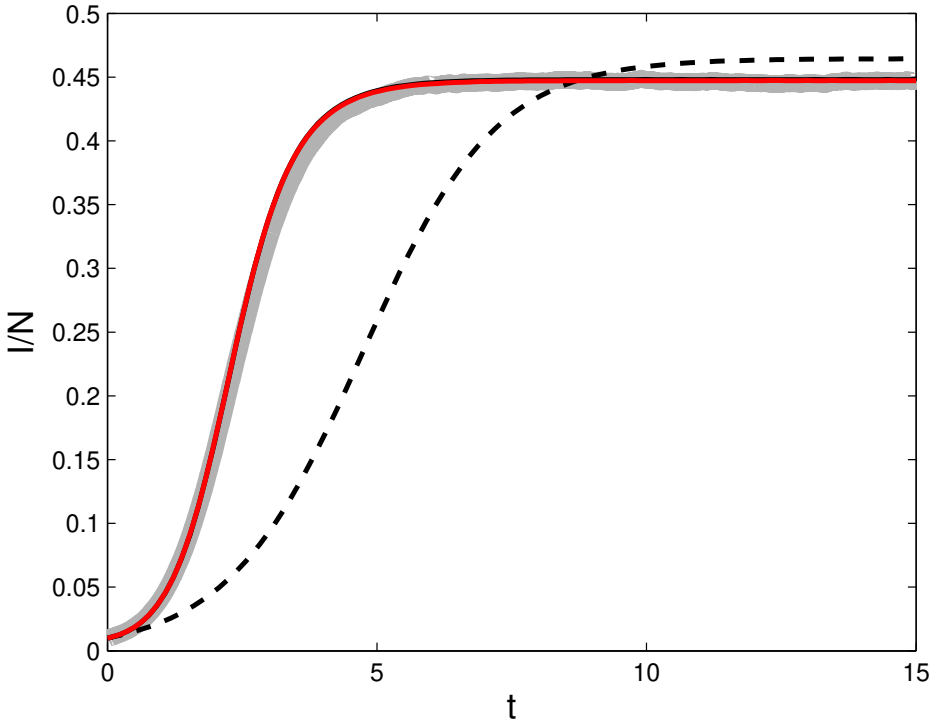

Pairwise: dashed, Compact pairwise: continuous red,
Simulation (average of 200 runs): grey thick curve

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AIM: Derive a simple system of differential equations for the expected number of infected nodes $[I](t)$.

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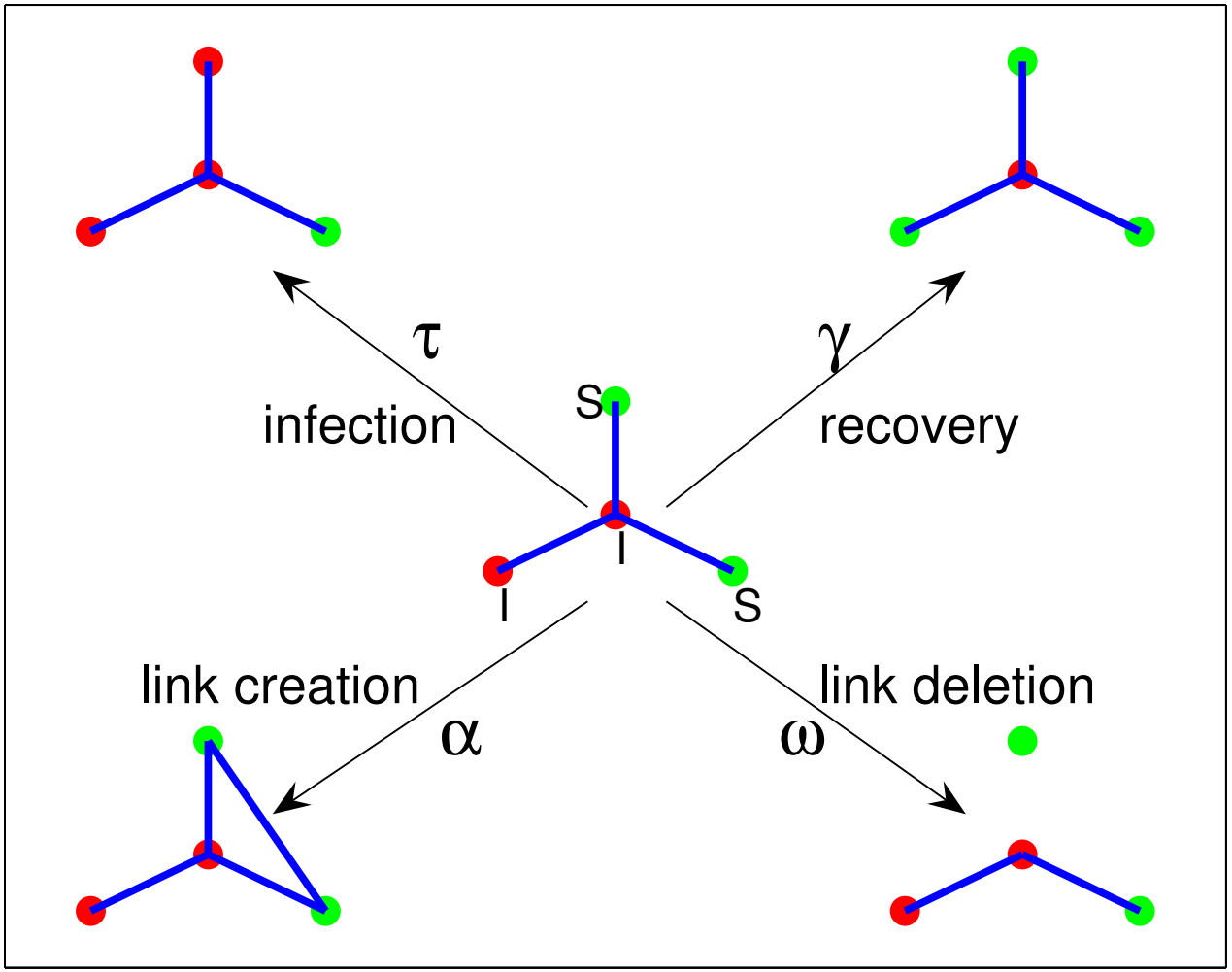
S/S EPIDEMIC ON AN ADAPTIVE NETWORK



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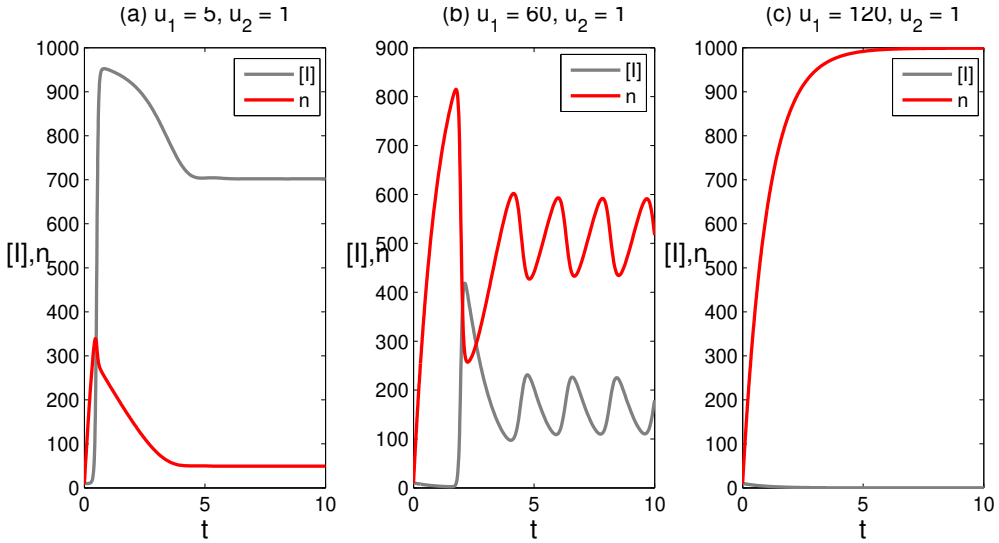

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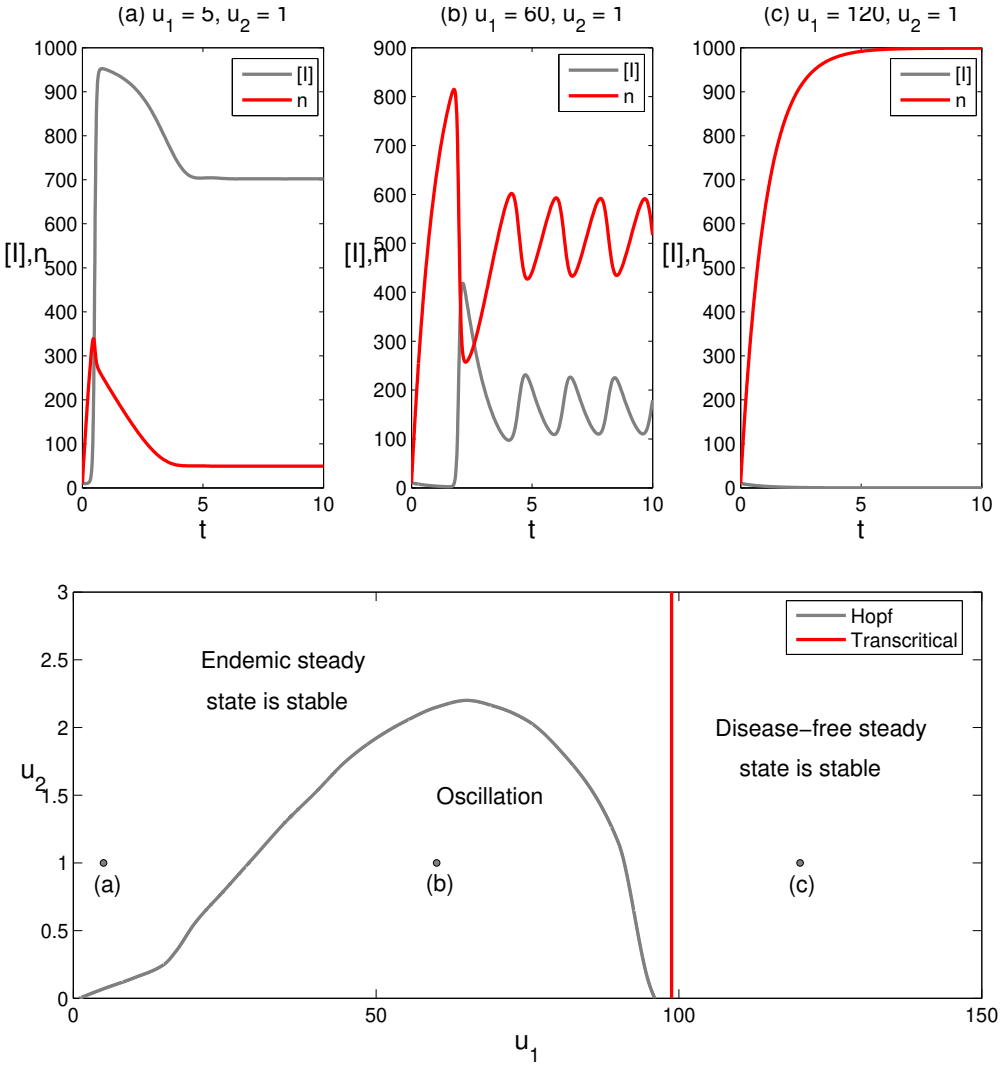

$\tau = 0.1$, $\gamma = 1$, $N = 1000$

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Total population $N = 10000$, is divided into households of different sizes.

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Geometry: adjacency matrix of the households.

Work places and schools: complete graphs with given sizes and randomly chosen members.

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The network is not a random graph, hence ODE approximations are more difficult to derive.

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This is a joint work with Ágnes Backhausz and Bence Bolgár.

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Results of a Gillespie simulation on the above network with open (red) and closed (black) schools.

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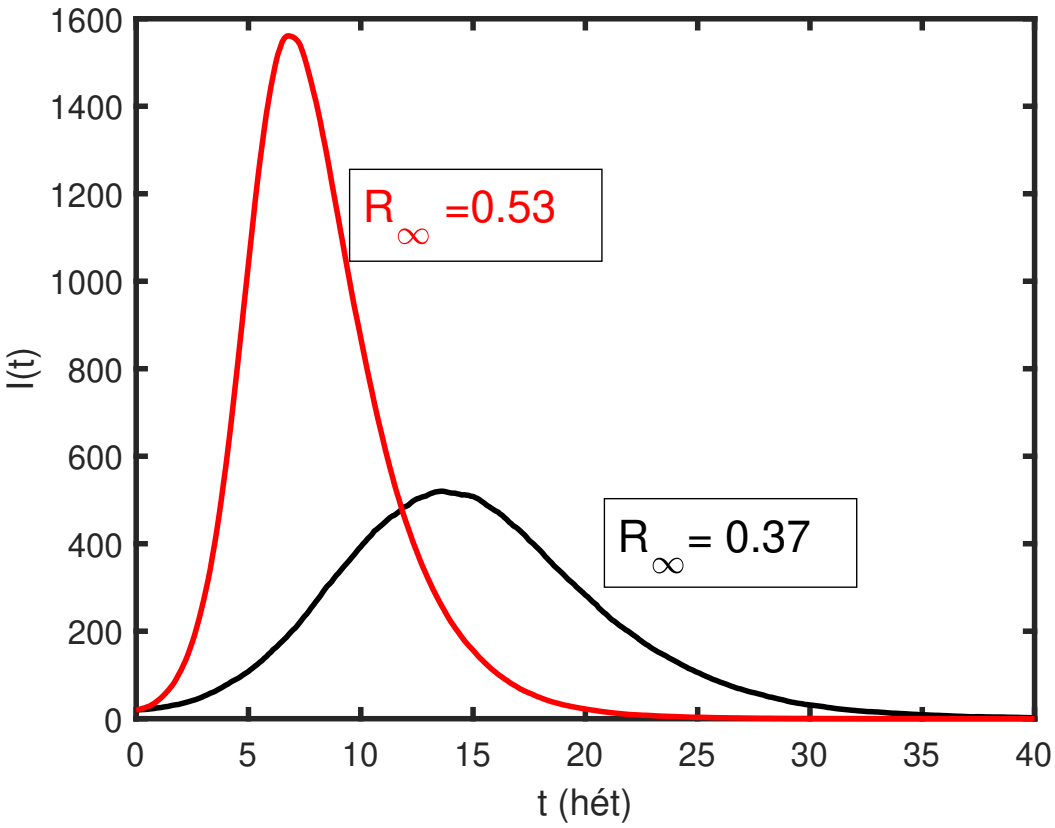

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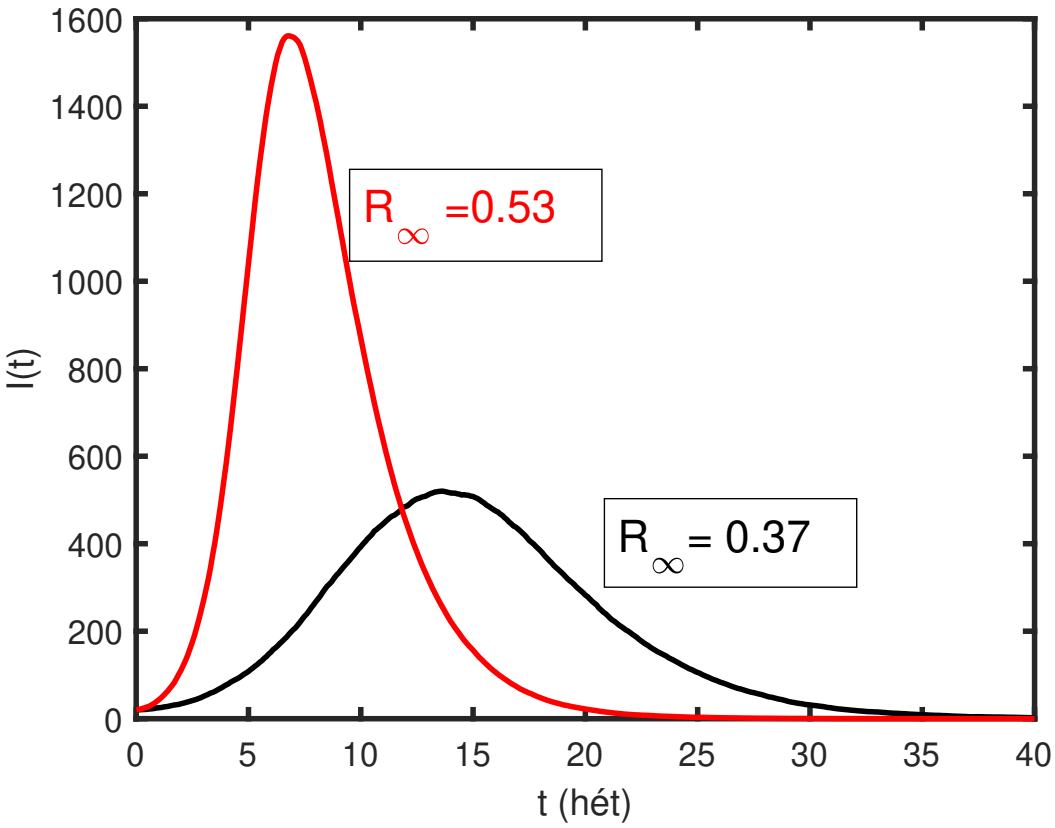

R_∞: final epidemic size, i.e. proportion of the population having immunity when the epidemic is over. ($N = 10000$, $R_0 \approx 2$.)

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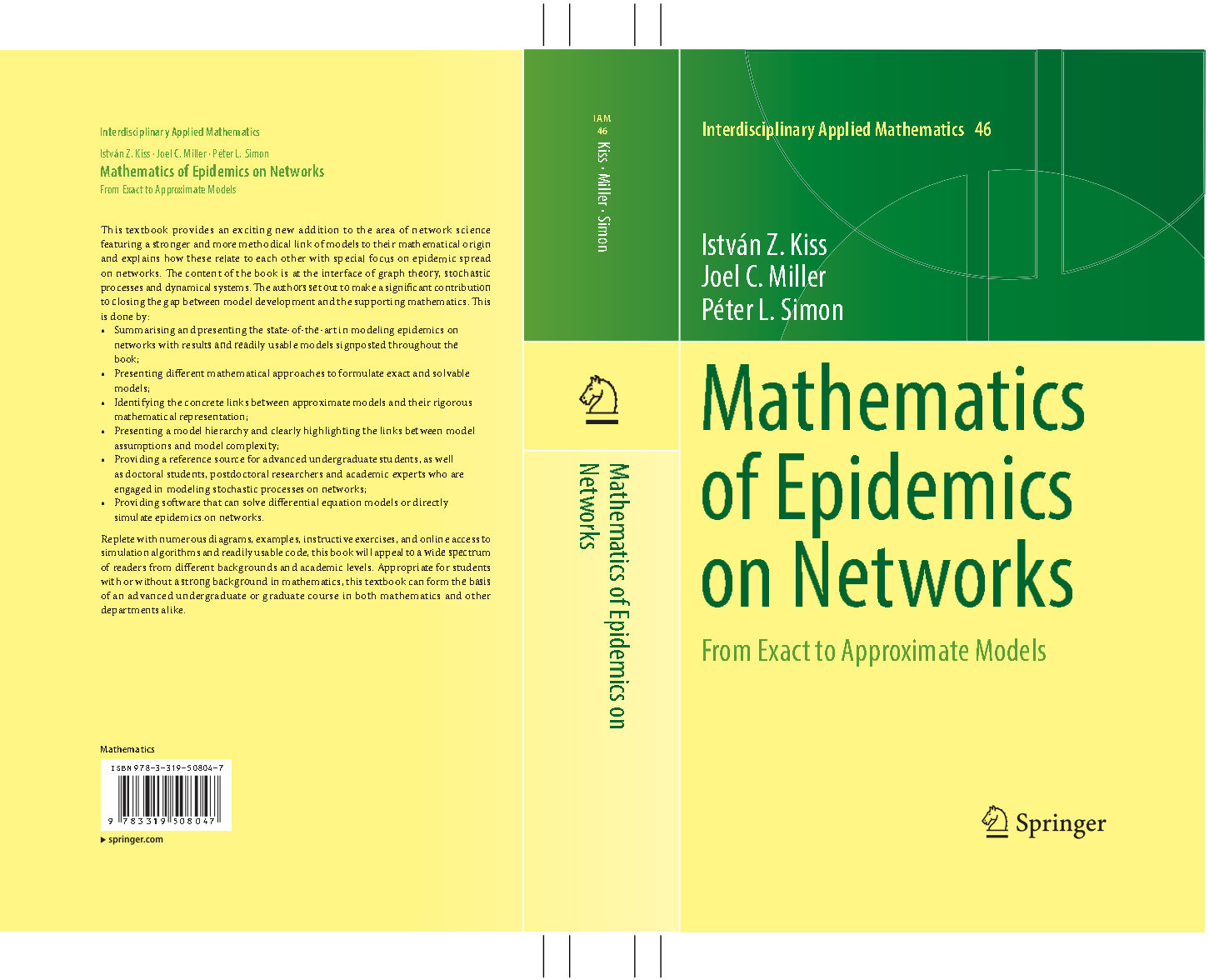

Thank you for your attention!