Dynamic models of epidemic spread on adaptive networks

Theses of Ph.D. Dissertation

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Budapest, 2016
1 Introduction

Over the last decade investigation of epidemic propagation on networks has become more and more important [3, 5, 6], and recent researches have also studied adaptive networks [1, 4, 8]. The main topic of the thesis is the stochastic, network-based SIS epidemic model. This model deals with individuals and consider the connections among the agents.

In the dissertation two major subtypes of the model are considered. The first one, when the network cannot change in time is called static SIS model and can be introduced as follows. Let us consider an undirected network with no self-loops. At any time the nodes can be susceptible (S) or infected and infectious (I). Infection is passed across an edge connecting an S and I node, or (SI) link, at rate $\tau$. Each I node recovers at rate $\gamma$, and this is independent of the network. Both infection and recovery are independent Poisson processes. It means that in a small time interval $\Delta t$ the probability of a susceptible node becomes infected is $1 - \exp(-N_I\tau \Delta t)$, where $N_I$ denotes the number of infected neighbours. Similarly, an infectious individual becomes susceptible with probability $1 - \exp(-\gamma \Delta t)$.

The other model we studied is the adaptive SIS model, when new links can be created and existing links can be terminated. This leads to an adaptive (or dynamic) model, where the network changes in time. Specifically, the model incorporates the following independent Poisson processes:

- **Infection**: Infection is transmitted across each contact between an S and an I node, or (SI) link, at rate $\tau$,
- **Recovery**: Each I node recovers at rate $\gamma$, and this is independent of the network,
- **Link activation**: A non-existing link between a node of type $A$ and another of type $B$ is activated at rate $\alpha_{AB}$, with $A, B \in \{S, I\}$,
- **Link deletion**: An existing link between a node of type $A$ and another of type $B$ is terminated at rate $\omega_{AB}$, with $A, B \in \{S, I\}$.

The master equations of the stochastic process can be formulated leading to an extremely large system of ordinary differential equations. Thus, we investigate population level quantities such as the expected number of infected nodes $[I]$. Introducing the notations $[SS], [SI], [II]$ for the expectations of (SS), (SI), (II) type links, the following system is obtained, see [7]

\[
\begin{align*}
\dot{[I]} &= \tau [SI] - \gamma [I], \\
\dot{[SI]} &= \gamma ([II] - [SI]) + \tau ([SSI] - [ISI] - [SI]) + \alpha_{SI}([S][I] - [SI]) - \omega_{SI}[SI], \\
\dot{[II]} &= -2\gamma [II] + 2\tau ([ISI] + [SI]) + \alpha_{II}([I][I] - [II]) - \omega_{II}[II], \\
\dot{[SS]} &= 2\gamma [SI] - 2\tau [SSI] + \alpha_{SS}([S]([S] - 1) - [SS]) - \omega_{SS}[SS].
\end{align*}
\]

Here $[ABC] (A, B, C \in \{S, I\})$ denotes the expected number of edge pairs, where a node of type $A$ is connected to a node of type $B$ which is connected to another node of type $C$. In order to get a self-contained system, we close the equations at the level of triples by using the well-known approximation, see [5],

\[
[ABC] \approx \frac{n - 1}{n} \frac{[AB][BC]}{[B]},
\]

1
where $n$ denotes the average degree of nodes of type $B$. Applying approximations (3) to system (1)-(4) we get a self-contained system which will be referred as the pairwise model of the process.

This summary of the dissertation is based on four papers of the author [11, 12, 13, 14]. In [14] an SIS type epidemic was studied on an artificially constructed network. In papers [11, 12] the approximating ODE model of the adaptive SIS process was investigated by bifurcation analysis. In [13] the bifurcations of the individual-based simulations were studied together with the qualitative changes of the network.

2 SIS epidemic on modified cycle graphs

In this section, we present the results of our theoretical study [14] in the case of an artificially constructed network called ‘modified cycle graph’. This network has a strong one dimensional character and can be tuned by a single parameter $d$. Following the approach developed in [9] for cyclic graphs, a new analytical model for this special network is derived. The subject of our study is the time dependence of the average number of infected nodes.

The modified cycle graph $G_{N,d}$ is constructed as follows. First, create an undirected cycle graph with $N$ nodes $C_N$, where the vertices are numbered from 1 to $N$. Second, add more edges to the graph in a systematic way, along which the degree of each node becomes three. Let us take an integer $d \geq 2$ and connect node 1 to node $1 + d$, then node 2 to node $2 + d$ and finally node $d$ to node $2d$. At this stage the degree of nodes $1, 2, \ldots, 2d$ is three. Now continue this process starting from node $2d + 1$.

A new approximating model is derived based on several observations concerning the special structure of the network. The key observation is that our graph $G_{N,d}$ consists of $N/2d$ subgraphs of size $2d$ that are lying along a circle, see e.g. $G_{24,4}$ in Figure 1a.

![Diagram of $G_{24,4}$ and a $\tilde{G}_4$ subgraph](image)

(a) $G_{24,4}$ and a $\tilde{G}_4$ subgraph denoted by bold lines and nodes.

(b) The $\tilde{G}_4$ subgraph and the shortest path (blue) along which the infection pass this subgraph.

Figure 1

The second observation is that once the nodes shown in Figure 1b are infected then the infection process runs in three separate arcs in the left, middle and right part of the subgraph. As the epidemic process evolves these arcs will finally merge and the whole subgraph will be infected. It is shown that epidemic spread in a subgraph can be approximated with the following piecewise function,

$$I_{std}(t) = \begin{cases} at & \text{if}, \quad 0 \leq t \leq t_{stat} \\ c & \text{if}, \quad t_{stat} \leq t \end{cases}$$

(6)
Here $t_{stat}$ is determined simply by the intersection point of the two lines and the parameters are $c = 2d(1 - \frac{\gamma}{3\tau})$, 

$$a = \begin{cases} 
1.5\tau - \gamma & \text{if, } d = 2 \\
2.5\tau - \gamma & \text{if, } d = 4 \\
(6\tau - 4\gamma)(1 - \frac{\gamma}{3\tau}) & \text{if, } 8 \leq d < \frac{N}{2}
\end{cases} \quad (7)$$

Then, the average time needed for the infection to spread through a $2d$ size subgraph and infect the next subgraph’s terminal node is approximated. Denoting this time with $R$ we obtain,

$$R = \begin{cases} 
R_2 & \text{if, } d = 2 \\
R_4 & \text{if, } d = 4 \\
\frac{R_2 + R_5}{2} & \text{if, } 8 \leq d 
\end{cases} \quad (8)$$

$$R_2 = \frac{260\tau^5 + 420\gamma\tau^4 + 310\gamma^2\tau^3 + 153\tau^2\gamma^3 + 6\gamma^5 + 45\tau\gamma^4}{6\tau^3(20\tau^3 + 25\tau^2\gamma + 12\tau\gamma^2 + 2\gamma^3)},$$

$$R_4 = \frac{9\tau^3 + 12\gamma\tau^2 + 8\gamma^2\tau + 2\gamma^3}{\tau^3(3\tau + 2\gamma)},$$

$$R_5 = \frac{1388\tau^3\gamma^4 + 1107\tau^6\gamma + 1900\tau^4\gamma^3 + 324\tau^7 + 1804\tau^5\gamma^2 + 24\gamma^7 + 192\tau^6\gamma + 674\tau^2\gamma^5}{\tau^8(24\gamma^4 + 216\tau^3\gamma + 120\gamma^3\tau + 81\tau^4 + 235\gamma^2\tau^2)}.$$

Using these approximation formulas for $I_{std}(t)$ and $R$ it turns out that, the number of infected nodes $I(t)$ of the whole modified cycle graph can be approximated as,

$$I(t) = 2\sum_{k=1}^{M/2} \tilde{H}(t - R(k - 1))I_{std}(t - (k - 1)R), \quad (9)$$

where $M$ is the number of subgraphs and $\tilde{H}$ is the Heaviside function whose value is zero for negative arguments and one for positive arguments. The results are shown in Figure 2 for a graph with $N = 1024$ nodes and for different values of $d$.

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Figure 2: The $I(t)$ curves for a graph with $N = 1024$ nodes and for $d = 2, 4, 8, 16, 32, 64, 512$, $\tau = 5$, $\gamma = 1$. The continuous curves are obtained by the theoretical formula (9), the circles correspond to the average of 1000 simulations (the value of $d$ is identified by the colors).
3 Bifurcations and dynamics of the pairwise approximating model

In this section, we investigate the pairwise approximating system and present a detailed bifurcation analysis based on the author’s papers [11] [12] [13]. Our main goal is to explore what kind of qualitative changes can happen and how these phenomena can be identified. We will consider three different restrictions on the parameters, but first mention a proposition concerning the disease-free steady state.

Proposition 1. The pairwise system has a trivial (disease-free) equilibrium corresponding to

\[ I = 0, \quad [SI] = 0, \quad [II] = 0, \quad [SS] = \frac{\alpha_{SS}N(N-1)}{\alpha_{SS} + \omega_{SS}}. \tag{10} \]

3.1 Detailed study of the case when \( \alpha_{II} = \omega_{II} = 0 \) and \( n \) is fixed

In [11] we considered restrictions \( \alpha_{II} = \omega_{II} = 0 \). In this case, the pairwise system takes the form,

\[ \dot{I} = \tau [SI] - \gamma [I], \tag{11} \]

\[ \dot{SI} = \gamma ([II] - [SI]) + \tau \frac{n-1}{n} \frac{[SI]([SS] - [SI])}{[S]} - \tau [SI] + \alpha_{SI} ([S][I] - [SI]) - \omega_{SI} [SI], \tag{12} \]

\[ \dot{II} = -2\gamma [II] + 2\tau \frac{n-1}{n} \frac{[SI]^2}{[S]} + 2\tau [SI], \tag{13} \]

\[ \dot{SS} = 2\gamma [SI] - 2\tau \frac{n-1}{n} \frac{[SI][SS]}{[S]} + \alpha_{SS} ([S][S] - 1) - [SS]) - \omega_{SS} [SS], \tag{14} \]

where \( n \) is considered to be fixed. We first introduce the following notations \( x = [I], q = \frac{n-1}{n}, \rho_{SS} = \alpha_{SS} + \omega_{SS} \) and determine the exact number of steady states for all possible parameter values. Since the two most important parameters are \( \tau \) and \( \omega_{SI} \) which are also used in [2], our aim is to divide the \( (\tau, \omega_{SI}) \) plane according to the number of steady states. This is done by using the parametric representation method (PRM) [10] which deals with a special curve called D-curve,

\[ D(x) = \left( \frac{f_0(x)f_2(x) - f_0(x)f'_2(x)}{f_1(x)f'_2(x) - f'_1(x)f_2(x)} \right) \frac{f_0(x)f'_1(x) - f'_0(x)f_1(x)}{f_1(x)f'_2(x) - f'_1(x)f_2(x)}, \]

where,

\[ f_0(x) = -\gamma(2\alpha_{SI}\gamma q x + (\gamma + \alpha_{SI})\rho_{SS}(N-x)), \tag{15} \]

\[ f_1(x) = (N-x)(\alpha_{SS}\gamma q(N-x-1) + \alpha_{SI}(2\gamma q x + \rho_{SS}(N-x))), \tag{16} \]

\[ f_2(x) = -\gamma(2\gamma q x + \rho_{SS}(N-x)). \tag{17} \]

The D-curve determines the saddle-node bifurcation curve and can be used to determine the number of steady states as well. These results can be summarised as follows.
Theorem 1. Let us consider the D-curve \( D(x) \) given above. Then, according to the position of the D-curve there are the following two cases.

- If the inequality
  \[
  2q^2 \alpha_{SI} \alpha_{SS}(1 - \frac{1}{N}) + (q\alpha_{SS} + \frac{\alpha_{SI}}{\gamma}\rho_{SS})(1 + \frac{\alpha_{SI}}{\gamma}\rho_{SS}) < 2q\alpha_{SI}\rho_{SS}.
  \]  
  does not hold, then the line
  \[
  \gamma(\gamma + \alpha_{SI})\rho_{SS} - \tau((N - 1)\alpha_{SS}\gamma q + N\alpha_{SI}\rho_{SS}) + \omega_{SI}\gamma\rho_{SS} = 0.
  \]  
  divides the \((\tau, \omega_{SI})\) parameter plane into two regions. If the parameter pair \((\tau, \omega_{SI})\) is in the left region, then there is only the trivial steady state given in (10). If the parameter pair \((\tau, \omega_{SI})\) is in the right region then there are two steady states (one of them is the trivial steady state).

- If the inequality (18) holds, then the D-curve and the line given in (19) divide the \((\tau, \omega_{SI})\) parameter plane into three regions. If the parameter pair \((\tau, \omega_{SI})\) is in the right region then there are two steady states (one of them is the trivial steady state). If the parameter pair \((\tau, \omega_{SI})\) is in the left region above the D-curve, then there is only the trivial steady state given in (10). If the parameter pair \((\tau, \omega_{SI})\) is in the left region below the D-curve, then there are three steady states (one of them is the trivial steady state).

For a given steady state the eigenvalues of the Jacobian matrix \( J \) have to be investigated. When \( x = 0 \), that is for the disease-free steady state, the spectrum of \( J \) can be investigated analytically leading to the following result.

Theorem 2. The disease-free steady state, given by (10), is asymptotically stable if and only if,

\[
\omega_{SI} > \tau \left( q(N - 1)\frac{\alpha_{SS}}{\rho_{SS}} + N\frac{\alpha_{SI}}{\gamma} \right) - \gamma - \alpha_{SI}
\]

holds. Moreover, in the \((\tau, \omega_{SI})\) parameter plane transcritical bifurcation occurs along the line given by (19).

For the endemic steady states the spectrum of the Jacobian can only be investigated numerically. It is shown that Hopf-bifurcation may occur and the Hopf-bifurcation is determined in a semi-numeric way. A \((\tau, \omega_{SI})\) parameter pair is said to be on the Hopf-curve, if there exists a steady state at which the Jacobian \( J \) has a pair of pure imaginary eigenvalues. Since this is only a necessary condition of the Hopf-bifurcation, we simply solve the differential equations numerically to decide whether the Hopf-bifurcation is subcritical or supercritical. The full bifurcation picture is shown in Figure 3a, and the phase portraits corresponding to the four regions in the bifurcation diagram are shown in Figure 3b.

3.2 Study of the case when \( \alpha_{SI} = \alpha_{II} = \omega_{SI} = \omega_{II} = 0 \) and \( n(t) \) is time dependent

Now we demonstrate our results from [13]. Using Proposition 1 the disease-free steady state takes the form,

\[
I = 0, \quad [SI] = 0, \quad [II] = 0, \quad [SS] = \frac{\alpha_{SS}N(N - 1)}{\alpha_{SS}} = N(N - 1).
\]
Investigating the Jacobian around the disease-free steady state leads to that the transcritical bifurcation occurs along the line

$$\omega_{SI} = \tau(N - 2) - \gamma.$$ 

**Proposition 2.** The disease-free steady state is stable if and only if $\omega_{SI} > \tau(N - 2) - \gamma$.

The endemic steady states are investigated only numerically. It turns out that Hopf-bifurcations may occur and the full bifurcation map is shown in Figure 4.
3.3 Dynamics of the link-type independent SIS model with time dependent $n(t)$

In our paper [12], the rewiring parameters are considered to be independent from the type of nodes, i.e. the following scenario is considered,

\[ \alpha_{SS} = \alpha_{SI} = \alpha_{II} = \alpha, \quad \omega_{SS} = \omega_{SI} = \omega_{II} = \omega. \quad (21) \]

Our main purpose is to prove that the link-type independent pairwise model cannot oscillate and tends to a steady state, regardless to the parameters. This has been conjectured in [7], but to our best knowledge, our study [12] is the first work proposing a proper mathematical proof of this. Using restrictions (21) in the pairwise system, we obtain the following equations,

\[ \dot{I} = \tau [SI] - \gamma I, \quad (22) \]
\[ \dot{SI} = \gamma ([II] - [SI]) + \frac{\tau}{n} \left[\frac{n - 1}{n} [SI]([SS] - [SI])}{[S]} \right] - \tau [SI] + \alpha ([S][I] - [SI]) - \omega [SI], \quad (23) \]
\[ \dot{II} = -2\gamma [II] + 2\tau \frac{n - 1}{n} \frac{[SI]^2}{[S]} + 2\tau [SI] + \alpha ([I]([I] - 1) - [II]) - \omega [II], \quad (24) \]
\[ \dot{SS} = 2\gamma [SI] - 2\tau \frac{n - 1}{n} \frac{[SI][SS]}{[S]} + \alpha ([S]([S] - 1) - [SS]) - \omega [SS]. \quad (25) \]

Using Proposition 1 the coordinates of the disease-free steady state are,

\[ [I] = 0, [SI] = 0, [II] = 0, [SS] = \frac{\alpha N(N - 1)}{\alpha + \omega}. \quad (26) \]

A two-dimensional invariant manifold in the four-dimensional state space is defined. The behaviour of the system is studied first in this manifold. The manifold is defined by conservation relations for the number of edges. We first mention that the average degree at the steady state can be determined as follows.

**Proposition 3.** Let $E(t)$ denote the number of edges at time $t$, i.e. $E(t) = [SS](t) + 2[SI](t) + [II](t)$. The average degree of the network at any steady state is

\[ k = \frac{\alpha (N - 1)}{\alpha + \omega}. \quad (27) \]

Moreover, $E(t) = (E(0) - kN)e^{-(\alpha + \omega)t} + kN$, hence if $E(0) = kN$, then $E(t) = kN$ for all $t$.

In general $k$ differs from the average degree of $S$ type nodes $n$, but if $E(0) = kN$, these two quantities are related as the following conservation relations show.

**Proposition 4.** Assuming $E(0) = kN$ where the average degree $k$ is given by (27) and $[SS](0) + [SI](0) = k[S](0)$, the solutions of (22)-(25) satisfy

\[ [SS] + [SI] = k[S], \quad [SI] + [II] = k[I]. \quad (28) \]

Summarising Proposition 3 and 4 we have the following theorem.
Theorem 3. The four-dimensional system (22)-(27) has an invariant two-dimensional manifold (in fact a plane) given by equations,

\[ SS + 2SI + II = kN, \quad SS + SI = kS. \] (29)

Applying equations (29) to system (22)-(25) the following two-dimensional system is obtained,

\[
\dot{S} = \gamma N - (\gamma + k\tau)[S] + \tau[SS], \\
\dot{SS} = 2(k[S] - [SS])\left(\gamma - \frac{\tau(k-1)[SS]}{k[S]}\right) + \alpha[S](|S| - 1) - (\alpha + \omega)[SS].
\] (30)

Based on the graphical properties of the nullclines of system (30)-(31) the direction field is investigated and the results can be summarised in the following theorem,

Theorem 4. In system (30)-(31) a transcritical bifurcation occurs at

\[ \tau_c = \frac{\gamma(2\gamma + \alpha + \omega)}{\alpha N + 2\gamma(k-1)} \] (32)

- If $\tau < \tau_c$, then there is no endemic steady state and the disease-free steady state is globally stable.
- If $\tau > \tau_c$, then the endemic steady state is globally stable and the disease-free state is unstable.

The original system (22)-(25) inherits the major properties of the reduced system (30)-(31). Introducing $A(t) = [SI](t) + [SS](t) - k[S](t)$ and without supposing $E(0) = kN$ the following system is obtained,

\[
\dot{S} = \gamma N - (\gamma + k\tau)[S] + \tau[SS] - \tau A(t), \\
\dot{SS} = 2(A(t) + k[S] - [SS])\left(\gamma - \frac{\tau(n(t)-1)[SS]}{n(t)[S]}\right) + \alpha[S](|S| - 1) - (\alpha + \omega)[SS].
\] (33)

We then prove that system (33)-(34) is asymptotically autonomous. It is known that under certain conditions the solutions of the non-autonomous system converge to the stable steady state of the autonomous system, see [15]. Using the results of [15] the behaviour of the four dimensional system (22)-(25) can be fully characterised as follows.

Theorem 5. In system (33)-(34) a transcritical bifurcation occurs at $\tau_c$ given by (32).

- If $\tau < \tau_c$, then there is no endemic steady state and the disease-free steady state is globally stable.
- If $\tau > \tau_c$, then the endemic steady state is globally stable and the disease-free state is unstable.

4 Analysis of individual-based simulations in the case when $\alpha SI = \alpha II = \omega SS = \omega II = 0$

In this section, we carry out a study of the stochastic process and analyse the agreement between simulation results and the pairwise model. Simulations show that the system
exhibits exactly those three regimes that were predicted by the pairwise model. In order to demonstrate bifurcations empirical definitions for the boundaries of the different regimes are proposed. Figure 5 shows the bifurcation diagram for the stochastic model in the \((\tau, \omega_{SI})\) parameter space.

The figure presents the bifurcation 'curves' and the domains of the three different behaviours. Identification of the oscillatory regime relies on the value of the frequency of peak power. Two potential boundaries are provided in the form of iso-lines at values 0.5 and 0.6. Peak frequency was \(\approx 0.75\) (orange colour). Near zero frequencies are shown in dark blue. These boundaries are qualitatively consistent with those observed in the theoretical model. The thick black line shows one boundary for the disease-free regime determined as the value of \(\omega_{SI}\) above which all realisations die out. The bottom boundary of the shaded area represents an alternative boundary determined as the value of \(\omega_{SI}\) under which no realisations die out. Qualitatively, the plot confirms the prediction of the theoretical model from Subsection 3.2. From a visual inspection of the two bifurcation diagrams in Figures 4 and 5 it is clear that the overall qualitative features of the model are captured well by both full stochastic and the pairwise model.

Oscillations emerge as a combination of a positive and negative feedback of \([I]\) and the average degree of the whole network \(k\) with a suitable time delay. It can be seen that the direction of change of these quantities is determined by the velocity of the following four processes: 

1. **A**: Infection with rate \(\tau [SI]\), **B**: Recovery of \(I\) nodes with rate \(\gamma [I]\), **C**: Creation of \(SS\) links with rate \(\alpha_{SS} ([S][S] - 1) - [SS]\), **D**: \(SI\) link deletion with rate \(\omega_{SI} [SI]\). There are four stages of oscillations which can be characterised as follows:
   1. **A** > **B**, **C** > **D**: \([I]\) increasing, \(k\) increasing,
   2. **A** > **B**, **C** < **D**: \([I]\) increasing, \(k\) decreasing,
   3. **A** < **B**, **C** < **D**: \([I]\) decreasing, \(k\) decreasing,
   4. **A** < **B**, **C** > **D**: \([I]\) decreasing, \(k\) increasing.

The system evolves through these stages along an oscillatory cycle.
References


