



# Estimating the state probability distribution for epidemic spreading in complex networks



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## ABSTRACT

The problem of state estimation of spreading phenomena in complex networks is considered on the basis of a detectability-based approach. Using a simple, reduced model based state distribution estimator, where the monitored nodes are driven directly by the measured data, asymptotic convergence conditions are provided in terms of the number and location of the required sensors on the basis of the network topology. The convergence of the estimator is established in terms of the largest eigenvalue of a reduced connectivity matrix which stems from removing the monitored nodes and their connections from the original graph. In the case of unit weights, this condition corresponds to measuring the nodes with highest degree. Numerical simulations for a complete and a scale-free network each of 500 nodes and randomly distributed and unit weights, respectively, illustrate the estimator functioning with 20 sensors for the complete, and 38 sensors for the scale-free network.

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## 1. Introduction

Epidemic spreading has become a subject of increasing attention during the last years, with fundamental and important breakthroughs in modeling and simulation [1–9] as well as in control or immunization perspectives [10–13]. The considered spreading phenomena may include classical virus outbreaks [6,12,14], computer viruses [15,16] or even tobacco epidemics [17]. State estimation in complex networks in general and for spreading dynamics in particular has in turn achieved less attention. Having a reliable estimate of the state probability distribution for a spreading process in a complex network is of great benefit for the monitoring of epidemics and the determination of corresponding vaccination policies and implementation of adequate control strategies. One major burden relies in the complex evaluation of observability properties and the question on how to exploit them for adequate estimation algorithms is by no means a trivial one. In particular, this involves a good model of the process dynamics and the decision on which states in the network have to be measured or monitored.

Particular studies and methods for the sensor location problem (and the dual problem of network controllability) have been provided for linear network dynamics in [18–20] on the basis of the system observability, a property which allows for the determination of the complete state on the basis of the knowledge of the measurement data over some arbitrary time interval. These approaches involve complex graph-theoretic algorithms for the determination of the underlying matchings

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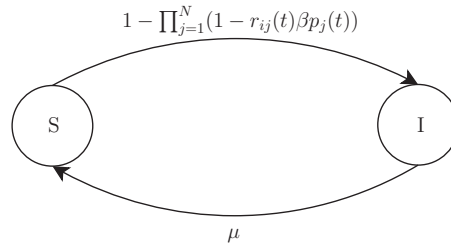


Fig. 1. State automaton for the SIS dynamics of a single node  $i$ .

in the graph. The observability of the system dynamics opens the way for several well-studied observer design approaches. Nevertheless, most of these approaches break down in absence of system observability.

Considering nonlinear spreading dynamics with changing interactions and unknown interaction weights in complex networks [1–4] implies that these approaches cannot be applied directly to the problem of interest but require some crucial simplifications. In particular, it is necessary to linearize the system dynamics around some equilibrium point, but this make it impossible to determine the exact domain of stability for the observer (i.e. the region in state space over which the state can be reconstructed) and completely breaks down when complex attractors, like limit cycles or higher order periodic or non-periodic attractor sets are present.

On the other hand, it is known from state estimation theory that a fundamental property underlying any state estimator (or observer) is the detectability property [21–23], i.e. the possibility of uniquely determining (maybe asymptotically) the state of a system on the basis of the measured output (and input) data over a sufficiently long (maybe infinite) time interval. Some observer design approaches, like the dissipativity-based observer [24–26], do not require the observability of the system, but involve calculations of an adequate model-dependent prediction–correction mechanism, which is hard to achieve if unknown interaction structures are at play. A possible modification consists in considering these interactions as completely unknown and employ the robust extensions of these approaches called unknown-input observers [26–28].

Another approach used in the context of distillation columns [29,30] and systems described by semi-linear parabolic partial differential equations [31] consists in restricting the possible solution space for the observer by directly imposing the measurement data in form of algebraic constraints. This approach has turned out to have a good performance when the system is detectable.

These considerations motivate the present study dealing with the observer design for a class of epidemic spreading models in complex networks based on the detectability properties of the system. For this purpose, first the Markov-chain based model for a Susceptible-Infectious-Susceptible (SIS) dynamics over complex networks is recalled [1,4,10] and conditions for detectability under time-varying and partially unknown interaction weights are derived. Based on these conditions, an observer design is proposed which takes into account only structural and statistical information about the interconnection structure and can deal with partially unknown network topologies (up to the degree of each node). The proposed design method is illustrated for a scale-free network with unit weights and a complete network with randomly time-varying connection weights, each with 500 nodes.

## 2. Problem formulation

Consider a network of  $N$  nodes distributed along a graph  $\Gamma = (\mathcal{E}, \mathcal{V})$  with edge set  $\mathcal{E}$  and vertex set  $\mathcal{V} = \{v_1, \dots, v_N\}$ , where each node represents an agent which can be either susceptible to infection or infectious itself. Each node  $v_i$ ,  $i = 1, \dots, N$  is connected with  $\kappa_i$  neighbors. Self-loops are excluded from the network. The underlying state automaton for a single agent is shown in Fig. 1. Note that the transition probability from susceptible to infectious depends on the actual probabilities of all neighbors.

These dynamics have been modeled using discrete-time Markov-chain-based dynamical systems in [1,4] and here a continuous-time equivalent is considered. The modeling equations are

$$\dot{p}_i(t) = -\mu p_i(t) + (1 - p_i(t)) \left( 1 - \prod_{j=1}^N (1 - r_{ij}(t)\beta p_j(t)) \right), \quad i = 1, \dots, N \tag{1a}$$

$$y_k(t) = p_{i_k}(t), \quad i_k \in \mathcal{M}, \quad k = 1, \dots, m. \tag{1b}$$

Here,  $p_i \in [0, 1]$  is the probability of node  $i$  to be infected,  $\mu > 0$  is the recovery rate from infection,  $r_{ij} \in [0, 1]$  is the connectivity weight of node  $i$  with node  $j$ ,  $r_{ii} = 0$ ,  $\beta \in [0, 1]$  is the infection probability, i.e. the probability that a contact of an infected agent with a susceptible one yields infection, and  $y_k$  is the  $k$ th measurement, which is given by the probability of agent  $k_l$  to be infectious, where the  $k_l$  are the monitored nodes (to be identified). The set of all monitored nodes is given by  $\mathcal{M}$ .

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