Mean-field approximations of SIS epidemics on adaptive networks

Massimo Achterberg and Piet Van Mieghem

Faculty of Electrical Engineering, Mathematics and Computer Science
Delft University of Technology, P.O. Box 5031, 2600 GA Delft, The Netherlands
M.A.Achterberg@tudelft.nl

The influence of people's individual responses to the spread of contagious phenomena, like the COVID-19 pandemic, is still not well understood. We investigate the continuous-time Markovian Generalised Adaptive Susceptible-Infected-Susceptible (G-ASIS) model. The connections between nodes in the G-ASIS model change *adaptively* over time, because nodes make decisions to create or break links based on the health state of their neighbours (see Fig. 1). The G-ASIS model comprises many contagious phenomena on networks, including epidemics, information diffusion, innovation spread and human brain interactions.
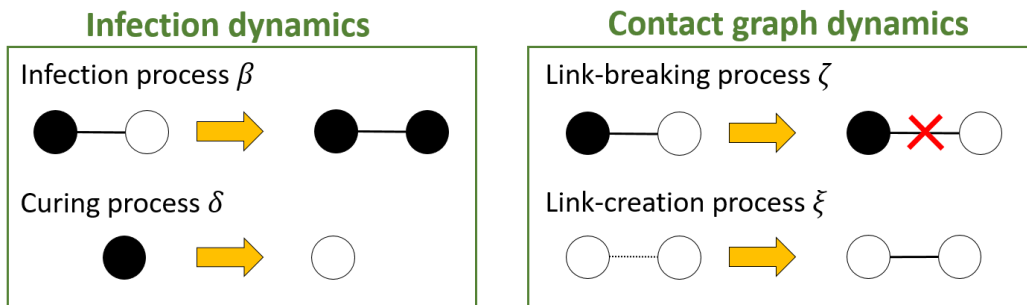

Figure 1: *All processes in the G-ASIS model. There are several choices for the link-breaking and link-creation processes.*

The analysis of the G-ASIS model is difficult, due to the exponentially large size of the corresponding Markov chain. We rigorously derived two mean-field approximations. The first-order mean-field (MF-1) approximation follows by assuming that all random variables (both nodes and links) are uncorrelated, effectively approximating the infection, link-breaking and link-creation process. The second-order mean-field approximation (MF-2) assumes that triplets of random variables are uncorrelated, effectively only approximating the infection process.

We consider two exemplary G-ASIS instances: Adaptive SIS (based on epidemic mitigation) and Adaptive Information Diffusion (based on adaptive rumour spreading). Fig. 2 shows the steady-state prevalence y_∞ versus the infection rate x. Both MF-1 and MF-2 are accurate approximations for the static Markovian SIS model. For ASIS (right) and AID (left), Fig. 2 demonstrates that MF-1 poorly resembles the Markovian steady-state prevalence whereas MF-2 is a qualitatively good approximation of the Markovian G-ASIS model.
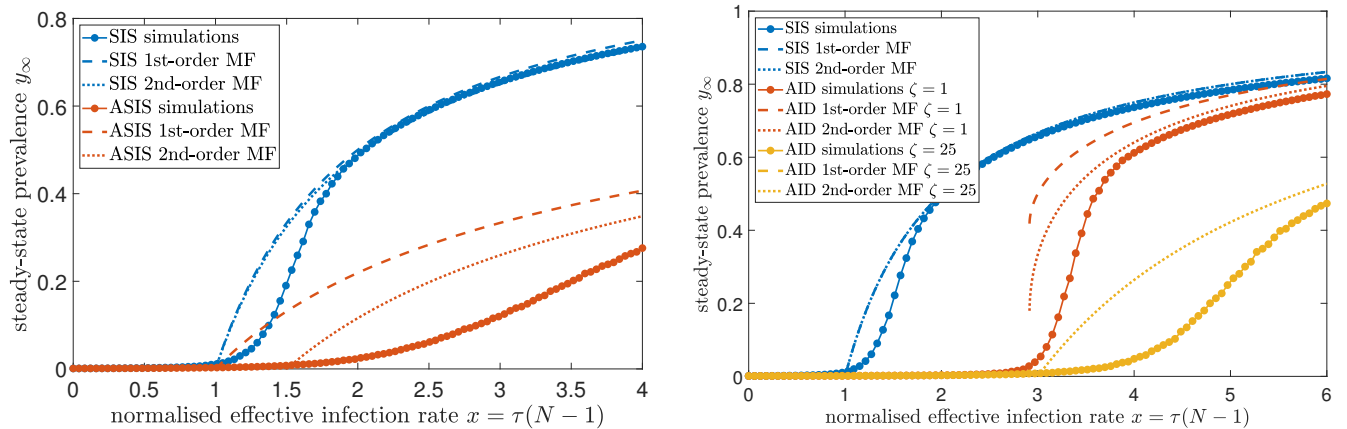

Figure 2: *A comparison for the steady-state prevalence y_∞ between the Markov model (solid), MF-1 (dashed) and MF-2 (dotted) for varying infection rates x. For the static SIS model, both approximations are rather accurate. (Left) The ASIS model increases the epidemic threshold compared to SIS, which is captured by MF-2 but not by MF-1. (Right) In the AID model, MF-1 and MF-2 are accurate for $\zeta = 1$ (red curve), but for $\zeta = 25$ (yellow curve), MF-2 correctly captures the epidemic threshold, but the MF-1 threshold is located at $x = 10$, which is far outside of the diagram.*