

# EPIDEMIC SPREADING IN ADAPTIVE MULTILAYER NETWORKS

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## Summary

Adaptive networks, which combine topological evolution of the network with dynamics on the network, are ubiquitous across disciplines. Examples include technical distribution networks such as road networks and the internet, natural and biological networks, and social science networks. These networks often interact with or depend upon other networks, resulting in multilayer adaptive networks. We study susceptible-infected-susceptible (SIS) epidemic dynamics on such networks revealing a new stable state which only emerges in the case of weakly coupled networks [5]. In this state, the disease is endemic in one network but neither becomes endemic nor dies out in the other. Instead, it persists only at the interconnected nodes and does not break out into the wider network.

## Additional details

We consider two networks A and B with the same number of nodes  $N_A = N_B = N$ , where a randomly chosen fraction of nodes  $p_{\text{coup}}$  from each network are connected through inter-network connections to nodes in the other network [2, 1], see Fig. 1.

We extend Gross *et al.*'s model of SIS epidemic dynamics on adaptive networks [4] from a single to multilayer networks. Nodes in both networks can be in either one of two states – susceptible or infected – where susceptible nodes can get infected from their intra- and inter-network neighbors and infected nodes can recover and become susceptible again. In addition, each network is independently adaptive in the sense that susceptible nodes can rewire their intra-network edges from infected neighbors to randomly selected susceptible ones.

However, the inter-links connecting between networks are permanent (nonadaptive). This limits an individual network's ability to adapt in the face of challenges, since it can change its own topology but not its dependence on other networks. In geographically distant social networks, for example, long-distance links are often family links which are not subject to rewiring compared to short-distance friend and acquaintance links.

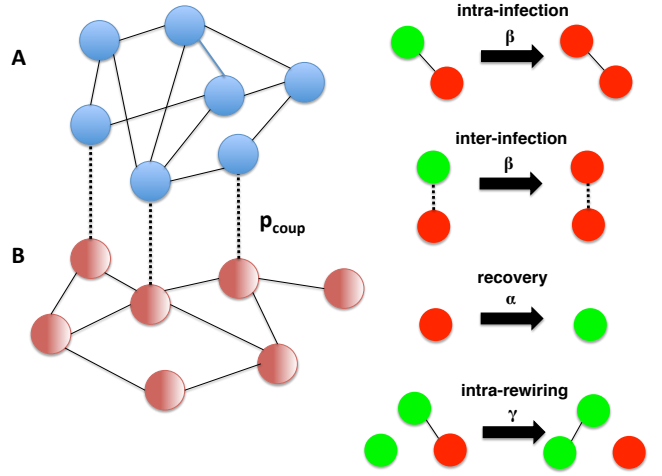


Figure 1: Illustration of adaptive SIS dynamics consisting of four local transformation rules on two interconnected networks of the same size.

## Results

We develop an analytical formalism consisting of 9 nonlinear ODEs and 10 pair approximations, and confirm it with an explicit simulation of the dynamics over a system of two interconnected adaptive networks using the LARGENET2 C++ library [6]. We analyze the stability of stationary disease prevalences using the dynamical systems analysis software XPPAUT [3], see Fig. 2. For  $p_{\text{coup}} = 0$  (i.e. two disconnected networks), our model recovers previous results for single adaptive networks [4] where the system two stable branches corresponding to lower and upper transition depending on the initial number of infected nodes.

For  $p_{\text{coup}} = 0.01, 0.1$ , both the results obtained analytically and numerically (shown more obviously in the inset) show a new stable state of intermediate  $I_B^*$  values, where the epidemic does not spread to all nodes in network B, but does not die out either. This state is obtained by starting the numerical simulation with no infected nodes in network B and significant number of infected nodes in

network A. As a result, the disease is quickly becoming an endemic in network A but only spreads to the interconnected nodes in network B and does not break out into the wider network. This is the reason for the quantitative disagreement between the analytical solution and the numerical simulation observed for this state – in a partially invaded network correlations exist that are not captured by the pair approximation.

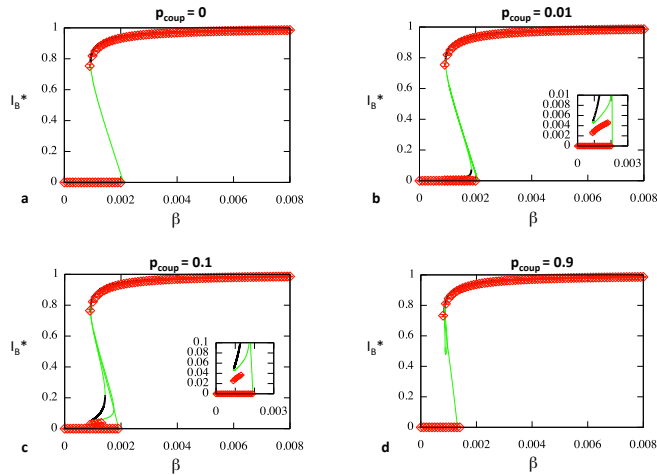


Figure 2: Bifurcation diagram of the stationary disease prevalence in network B,  $I_B^*$  as a function of the infection rate,  $\beta$ . To compare results with those obtained for single networks, we consider two ER networks of size  $N_A = N_B = 100\,000$  nodes with similar properties to the ones considered by Gross *et al.* [4], i.e. average connectivity 20, recovery rate  $\alpha = 0.002$  and rewiring rate  $\gamma = 0.04$ .

The third stable state observed for  $p_{\text{coup}} = 0.01, 0.1$  becomes unstable again for strongly coupled networks, see Fig. 2d. This is since for larger  $p_{\text{coup}}$  there exists a larger number of interconnected nodes that can not protect themselves from infection due to inter-network links even at small infection rates. Therefore, any epidemic persisting in one network, will eventually spread and persist in the other network as well.

Finally, we note that the width of the multistability area becomes smaller as  $p_{\text{coup}}$  increases. In other words, the range of  $\beta$  values for which more than one stable state is reachable depending on the initial conditions becomes smaller with more inter-network links meaning that a system of tightly coupled networks is more stable and depends less on the initial conditions.

## Discussion

We have examined the stationary states of adaptive SIS dynamics on a multilayer network consisting of two randomly interconnected networks. Our analytical model provides the exact number of nodes that, if their state were synchronized across two networks (i.e. if they were coupled), a process spreading in one network would spread to the other. This approach could be used to determine optimum firewall placement to resist cyber attacks and to determine the maximum number of people that can travel between two countries such that an epidemic spreading in one will not spread to the other.

Perhaps more importantly, our work is also providing an important insight into the future efforts needed to take place in order to analytically describe the behavior of multilayer networks. While the pair approximation approach works well for single random networks, it fails to describe the new stable state observed for weakly coupled networks.

## References

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