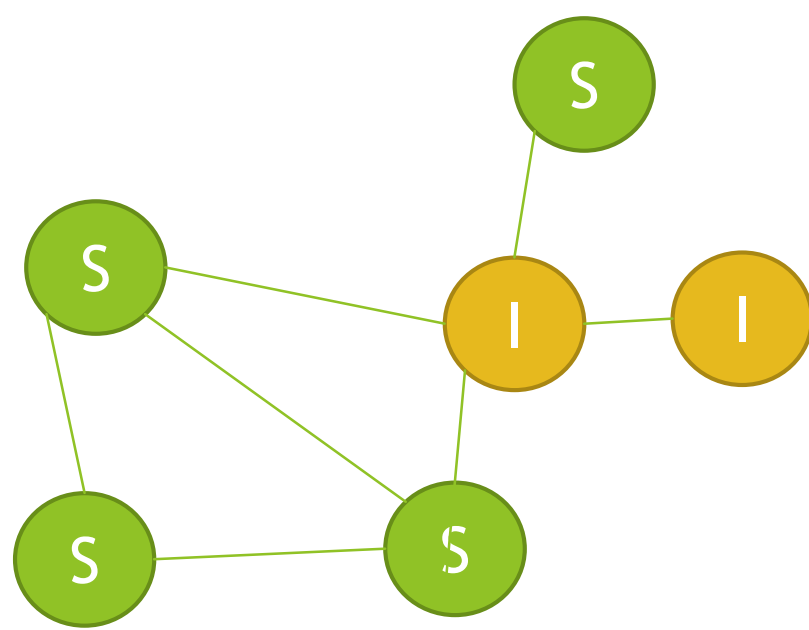


Winning the competition: enhancing counter-contagion in SIS-like Markov processes

Model & Open questions

N-intertwined SIS

The Susceptible-Infected-Susceptible (SIS) model represents the spreading of an infection in a network.



The network is characterized by the adjacency matrix A . Each node can be infected ($X=1$) or susceptible ($X=0$), and the state evolves according to:

$$X_i(t) : \begin{cases} 0 \rightarrow 1 & \text{with probability rate } \beta \sum_j A_{ji} X_j \\ 1 \rightarrow 0 & \text{with probability rate } \delta \end{cases}$$

where β and δ are the infection parameters.

Treatments-Allocation problem

Consider the possibility to heal a limited amount of nodes by rising the recovery probability by a parameter, ρ , that quantifies the strength of the cure.

What is the best way to allocate the cures?

Two-States Continuous-Time Markov process

$$X_i(t) : \begin{cases} 0 \rightarrow 1 & \text{with probability rate } \mathcal{I}_i(\underline{X}(t)) \\ 1 \rightarrow 0 & \text{with probability rate } \mathcal{H}_i(\underline{X}(t)) \end{cases}$$

where the functions are different in each node and depend on the whole network state.

We recover the SIS-scenario and the following assumptions:

- **Locality:** The probability rates depend only on the nodes neighbours;
- **Exchangeability:** The probability does not depend on the order in which we consider its neighbours;
- **Node invariance:** The probability rate functions are the same for every node.

Analysis

Nodes scores

Define a cost function that penalizes the total amount of infected in the period and apply a greedy minimization:

$$S_i \doteq - \left[(\mathcal{H}_i + \mathcal{I}_i) + \sum_{j \neq i} \left[X_j (\mathcal{H}_j - \mathcal{H}_j^-) - (1 - X_j) (\mathcal{I}_j - \mathcal{I}_j^-) \right] \right]$$

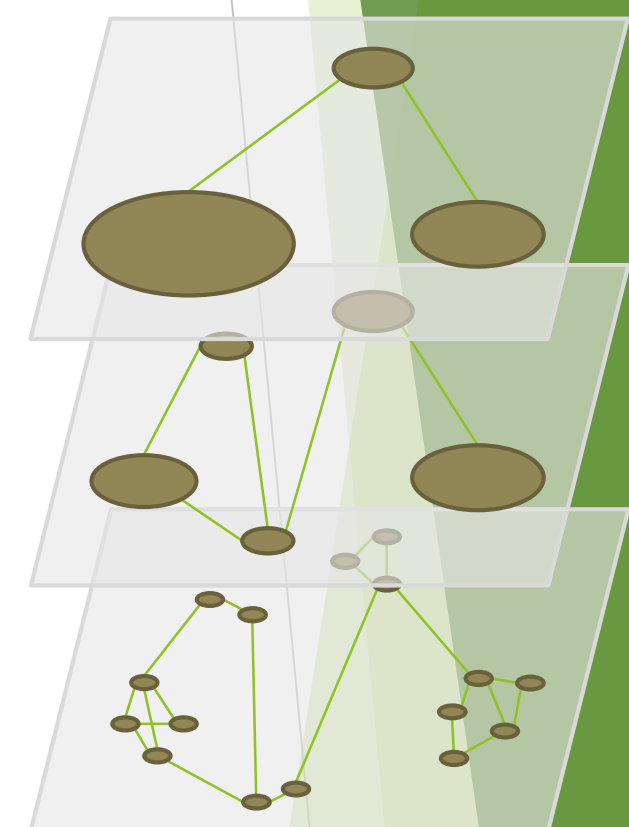
Under the SIS-assumptions, it simplifies:

$$S_i \doteq - \left[(\mathcal{H}_i + \mathcal{I}_i) + \sum_j A_{ij} \left[X_j (\mathcal{H}_j - \mathcal{H}_j^-) - (1 - X_j) (\mathcal{I}_j - \mathcal{I}_j^-) \right] \right]$$

Hierarchical score

In order to take advantage of the network structure, we generalize the score to the clusters and propose a hierarchical ordering of the nodes according to the scores.

The main issue in dealing with real situations concerns the possibility to obtain detailed information about the network in real time. Often we do not know exactly the state of each node, but we can only access averages about the infections. The proposed approach can also cover such situations.



Results

Simulation settings

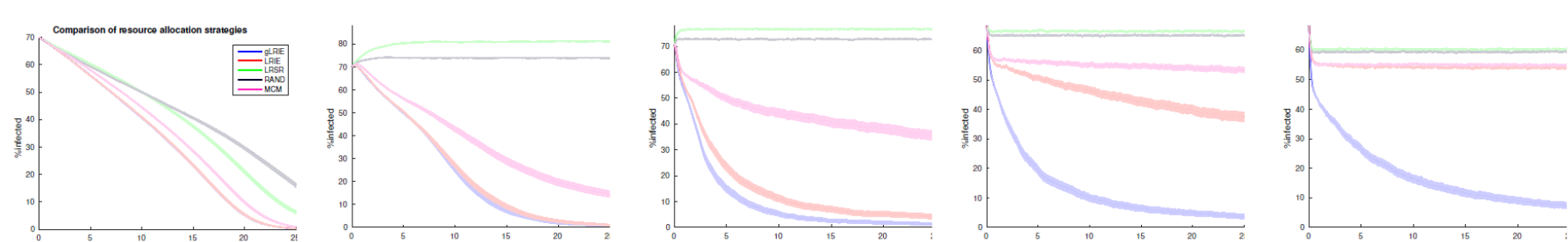
The simulations were performed, on real and random networks, in the SIS-assumptions. The probability rates evolve according to sigmoid functions that depend on parameters, that controlled slope and saturation level. We selected competitors that make use of different approaches to the problem:

- **Random (RAND):** select infected nodes at random;
- **Largest Reduction in Spectral Radius (LRSR):** select the nodes that maximize the reduction of the spectral radius;
- **Maxcut Minimization (MCM):** proceed according to the ordering that minimize the cutwidth;
- **Largest Reduction in Infectious Edges (LRIE):** focus on the safest and most diffusive nodes.

The plots represent the evolution of the infection percentage in time in random networks. In the heatmap, we defined a metric to evaluate the performance and we show the ratio between our algorithm and the competitors (LRIE, MCM) in the (α, β) -space. Finally, the gray-map is the convergence region.

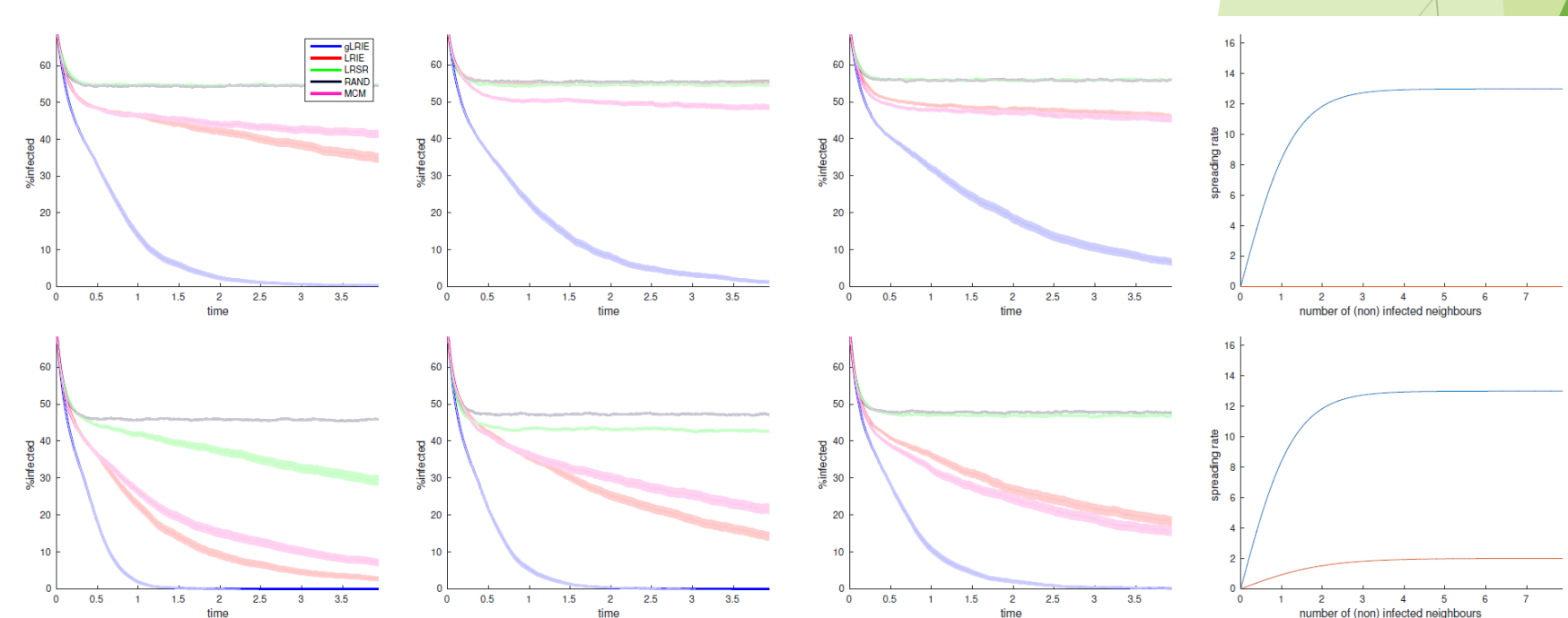
From linear to non-linear

Tuning the parameter, we obtain "almost"-linear spreading functions. Here we show the difference moving from linear to non-linear diffusion.



The effects of healthy diffusion

In these plots we show the effects of tuning the healthy diffusion. The first row does not present healthy diffusion, while the second does.



Exploring the parameter space space in Gnutella

In the heatmap, we defined a metric to evaluate the performance and we show the ratio between our algorithm and the competitors (LRIE, MCM) in the (α, β) -space. Finally, the gray-map is the convergence region.

