Modelling and Analysis of Complex Networks

Exercise 7

Due: 13:00 on Nov. 15, 2024

The maximum score of this assignment is: **16 points**. Please submit the assignment in any readable data format (.txt, .doc, .pdf, .md ...) and submit the assignment before the deadline. If you have additional information concerning your answers, please also upload the document to the Moodle, or include the link to the document in your answers (e.g., link to your Github repository). Please indicate your team number in your submission.

The goal of this lab is to introduce the basic models used to simulate epidemics in networks, experiment with them, and compare them. We will explore both types of diffusion models, decision-based and epidemic ones. As a use case, we are going to use the coauthorship network of network scientists, which you can load with the function read gml from networkx library.

The following questions can be answered with the help of networkx and NDlib and the accompanying notebook. You may also use other packages to deal with the problem. Please answer the following questions and submit your executable code.

(a) The Sznajd model is a variant of spin model based on social impact, which takes into account the fact that a group of individuals with the same opinion can influence their neighbours more than one single individual. Please use the Sznajd model to simulate the cascade of misinformation between the network of network scientists for 100 steps with different initial "infected" numbers: 100, 300, and 700. Please visualize the results and output a prevalence plot. (May refer to NDlib.)

(b) Although the interaction networks in real-life are different from the social networks we have, it is still meaningful to simulate the epidemics cascade with our dataset. The SIR model was introduced in 1927 by Kermack. In this model, during the course of an epidemic, a node is allowed to change its status from Susceptible (S) to Infected (I), then to Removed (R). Please use the SIR model to simulate for 100 iterations the cascade of the epidemic with the following three sets of infection/removal probabilities: (0.5, 0.2), (0.3, 0.3), (0.4, 0.5) on the network science dataset, and visualize the results.