

Lab7: Simulation of SIS model over networks

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1 Introduction

We will simulate a SIS epidemic model on networks. We will use a binary tree, a scalefree graph, an Erdos-Renyi graph, a complete graph and a star graph. We will also look at their thresholds (the inverse of the highest eigenvalue of the graph) and try to see how they influence the epidemic behaviour.

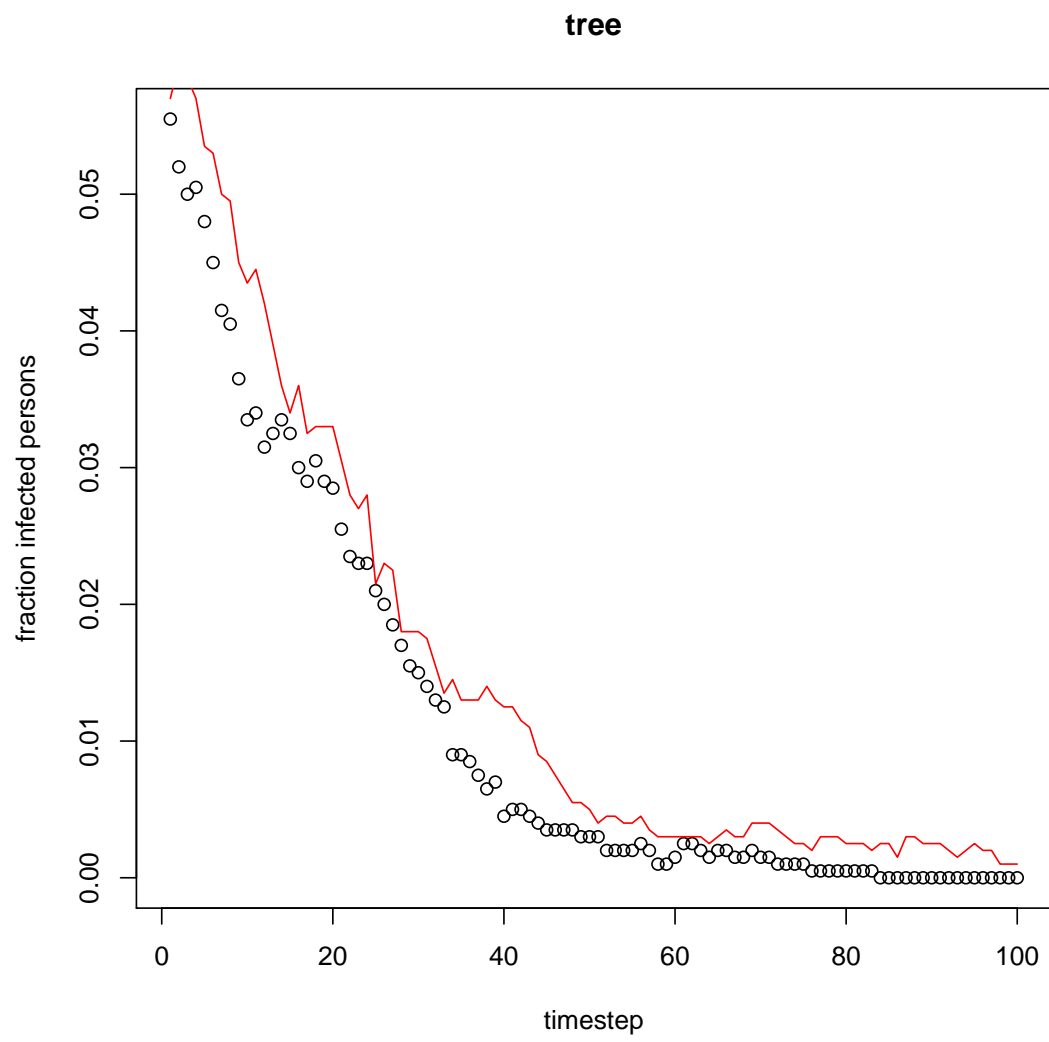
2 Results

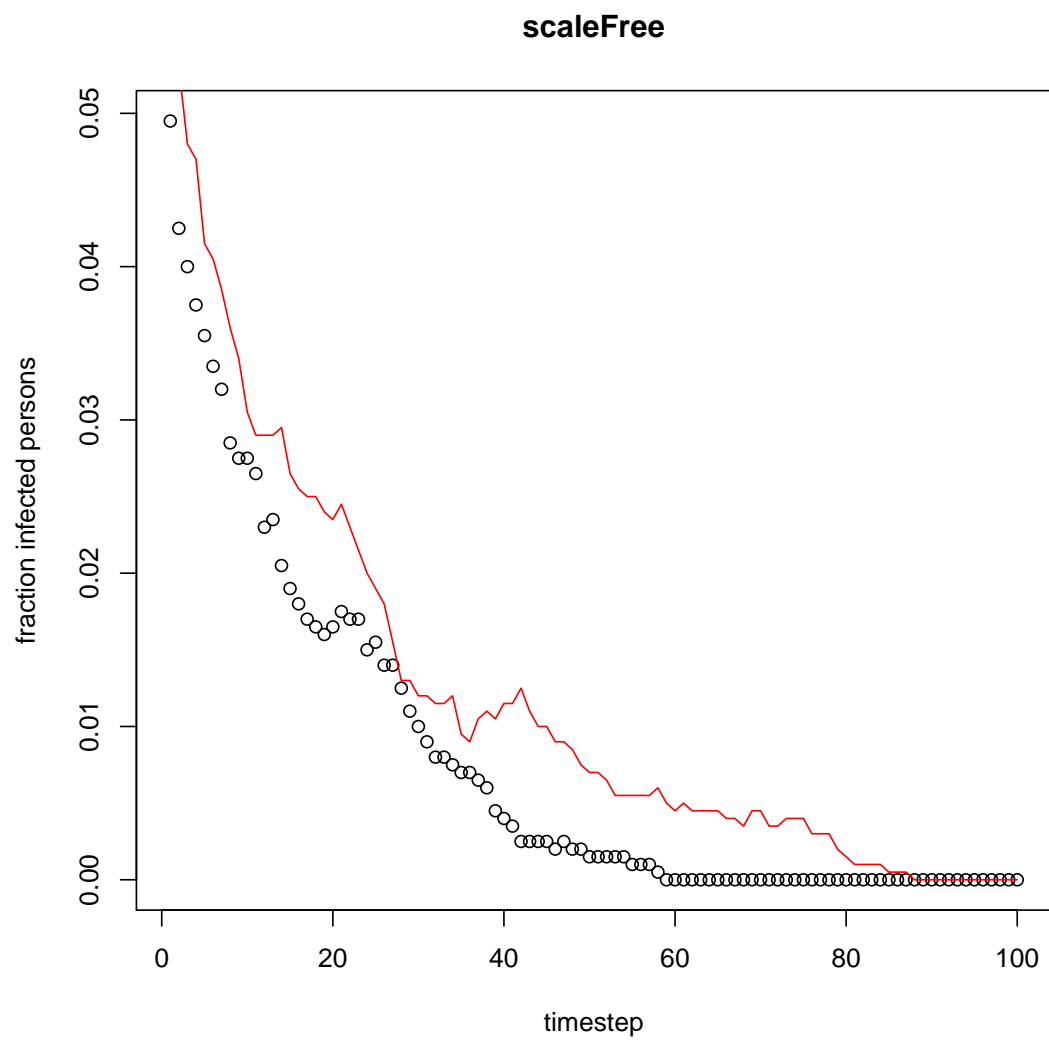
The following graphs are the result of a simulation on 5 different graphs with 100 timesteps. For every graph we took $\gamma = .1$, then we calculated the thresholdvalue for β . We increased β by 10% (plotted dots) and decreased β by 10% (plotted red line). We started with 5% infected

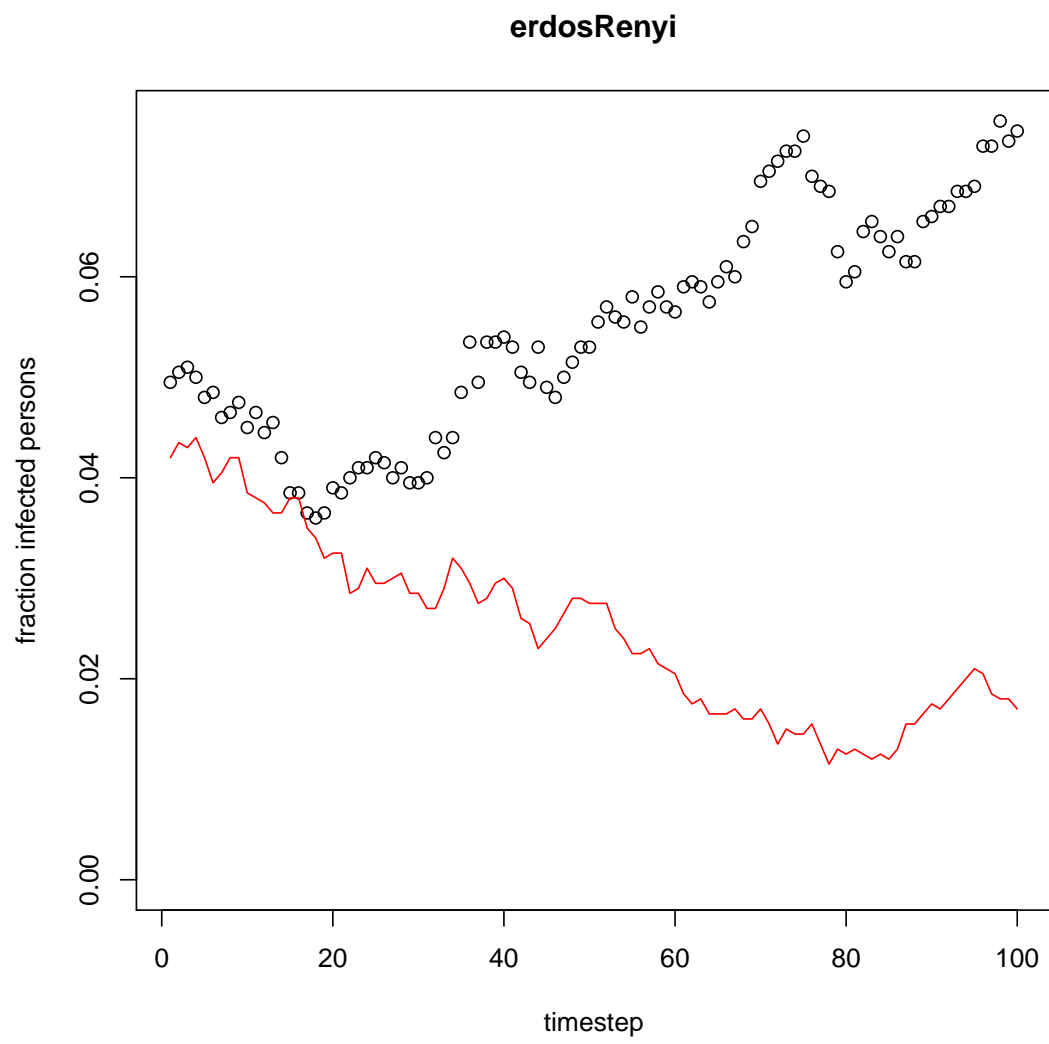
3 Discussion

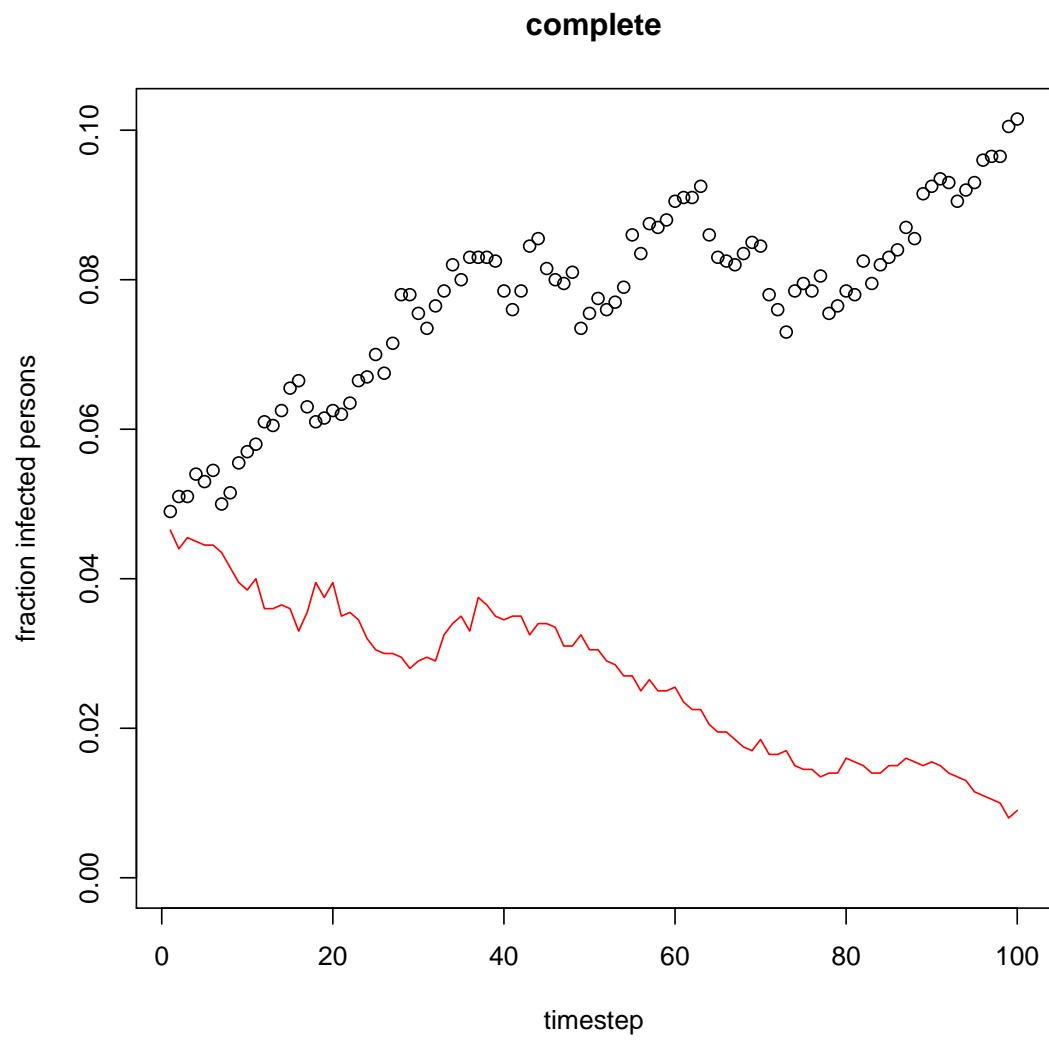
We notice that we see we crossed a threshold value for the complete and the Erdos-Renyi graph. The star graph, tree and scalefree graph, however, do not seem to have crossed any threshold. If we would

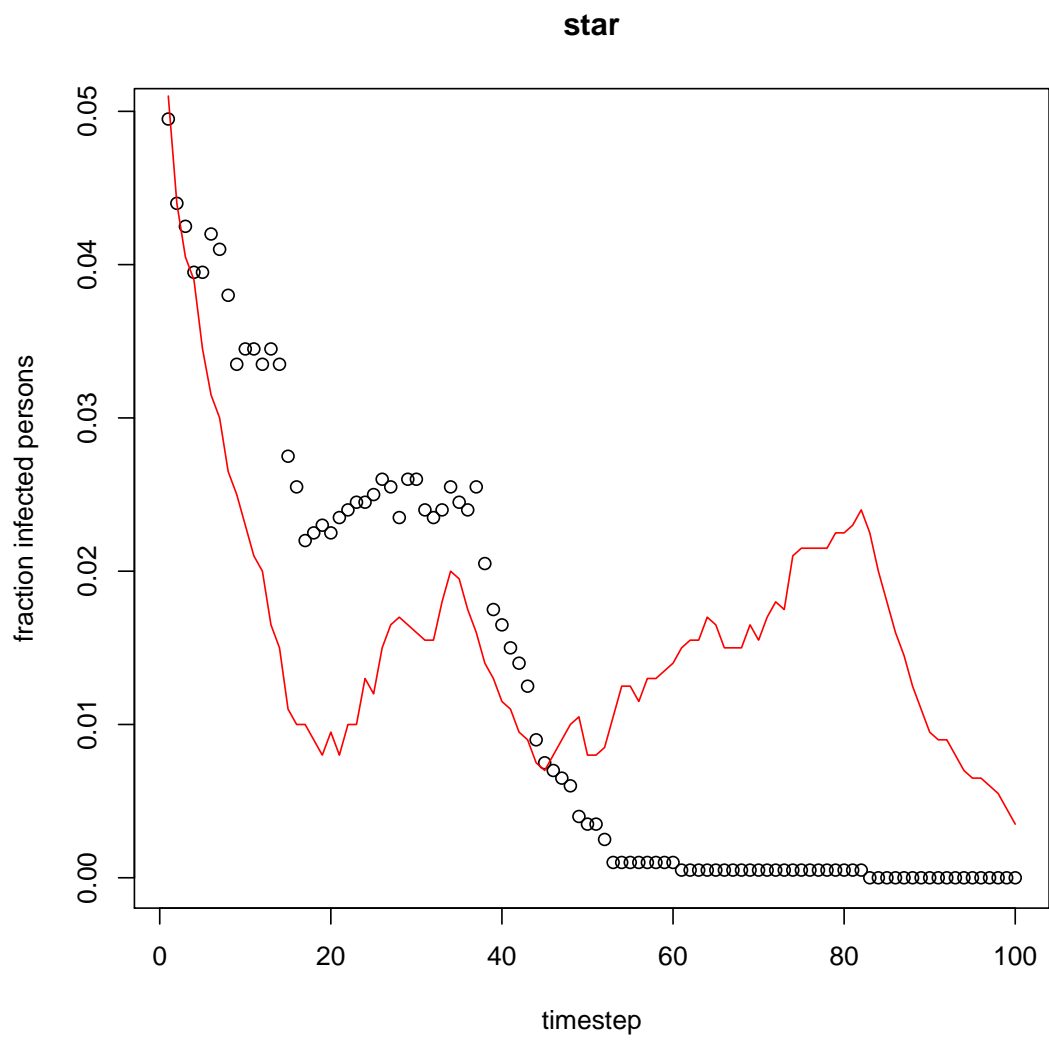
From this, we can conclude that the theory doesn't hold for some graphs. To be sure it does hold for the complete and Erdos-Renyi graph, we would have to do some more tests (values closer to the threshold, different numbers of vertices, run the simulation longer), but we are confident there is a clear threshold here.











4 Methods

To find the thresholds we used ARPACK, a package partially built in in igraph. It has fast methods for calculating the largest eigenvalue of a graph. Calculating the 5 eigenvalues of the 5 graphs with 2000 vertices only takes seconds.

For generating the graphs and plots we set a seed so it can be easily replicated.