

Assignment 4

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1 Random network

I generate a Erdős-Renyi random graph with $N = 5000$ vertices by creating a $N \times N$ triangular matrix with entries sampled from a uniform distribution on $[0, 1]$ and forming the adjacency matrix from that by selecting those entries which are less than or equal to 0.0016. The degree distribution of the resulting network is show in fig. 1. This is a binomial distribution, and the average degree is 7.999.

1.1 Epidemic simulation

I have implemented the model as follows:

1. Each node makes at most one state transition per time step
2. An infectious node that recovers does not contribute to the spread at that time step

A node v that is connected to n infectious nodes becomes infected if $X = -\ln(U)p^{-1} \leq n$, where U is sampled from a uniform distribution on $[0, 1]$. That is, X is exponentially distributed $\implies P(X \leq n) = 1 - e^{-np} = P_I(n)$.

Fig. 2 and fig. 3 show the evolution over 1000 time steps for $p \in \{0.001, 0.002, \dots, 0.01\}$. The final state as a function of rp^{-1} is shown in fig. 4, and fig. 5 shows the evolution over all time steps against rp^{-1} . We see that when $p \leq 0.004 \iff rp^{-1} \geq 7.5$, there is no epidemic.

Also worth noting it that our link density $0.0016 < N^{-1}\ln(N) = 0.0017$ in this case, so the network is almost certainly disconnected. Thus we would almost certainly never see 100% of the population infected.

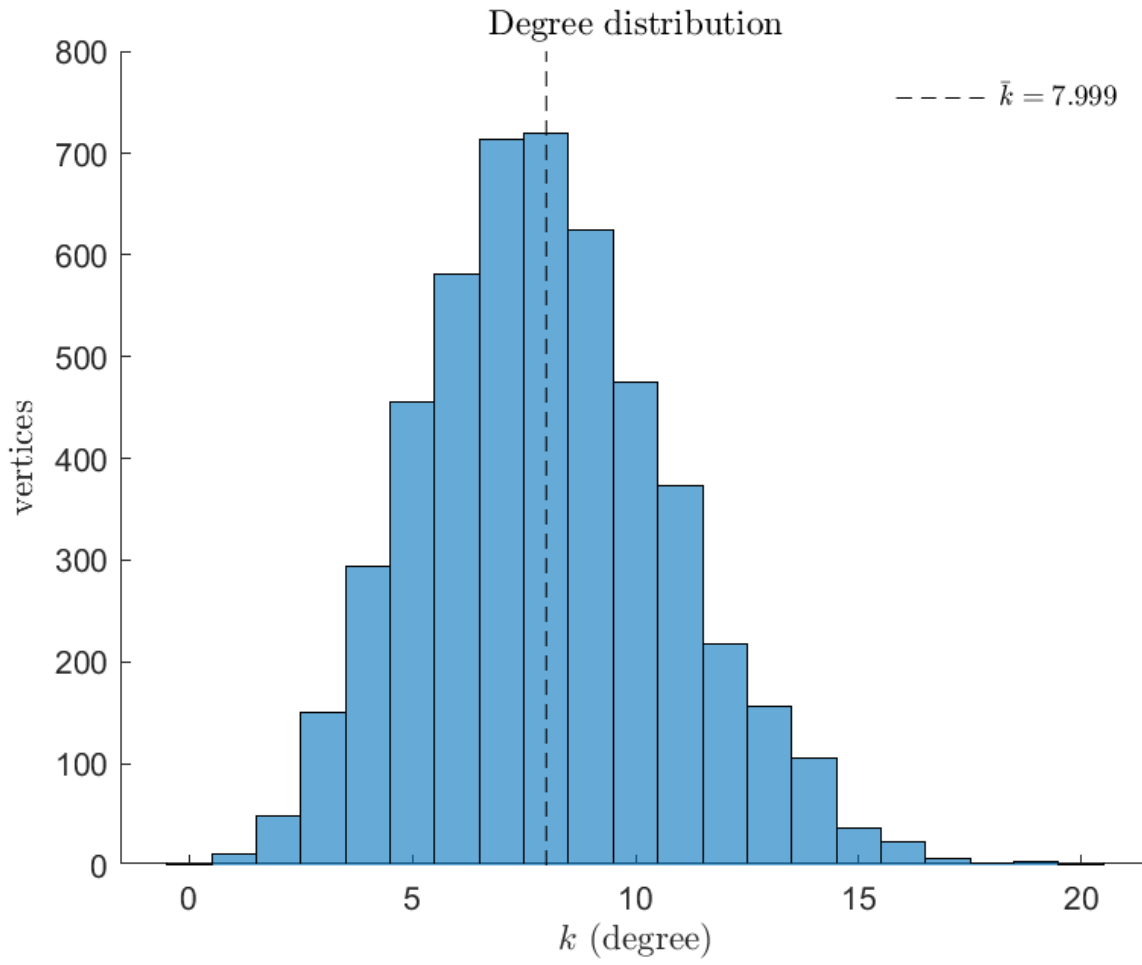


Figure 1: Erdős-Renyi random graph with link density 0.0016 and 5000 vertices

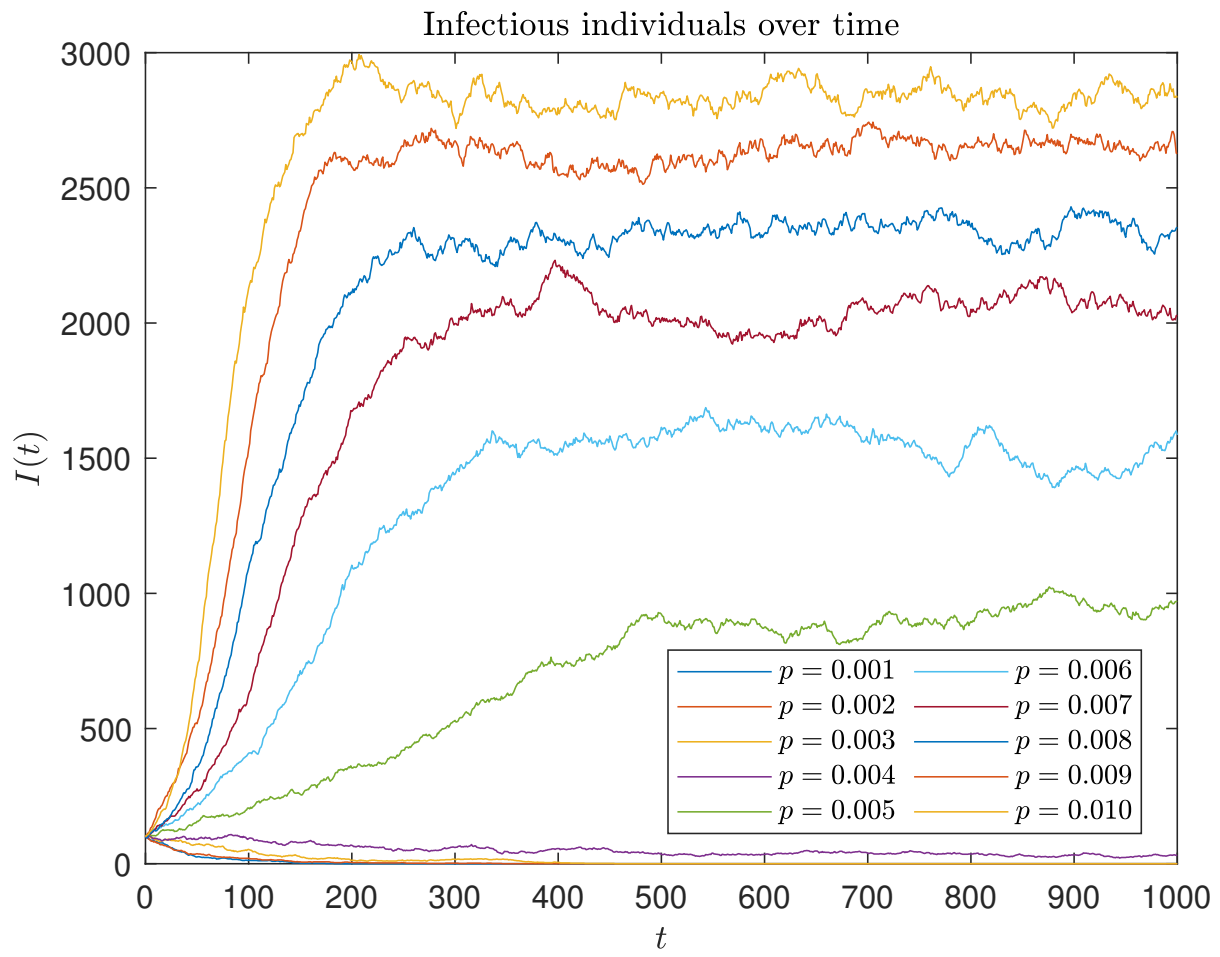


Figure 2: Epidemic on Erdős-Renyi random graph with 5000 vertices

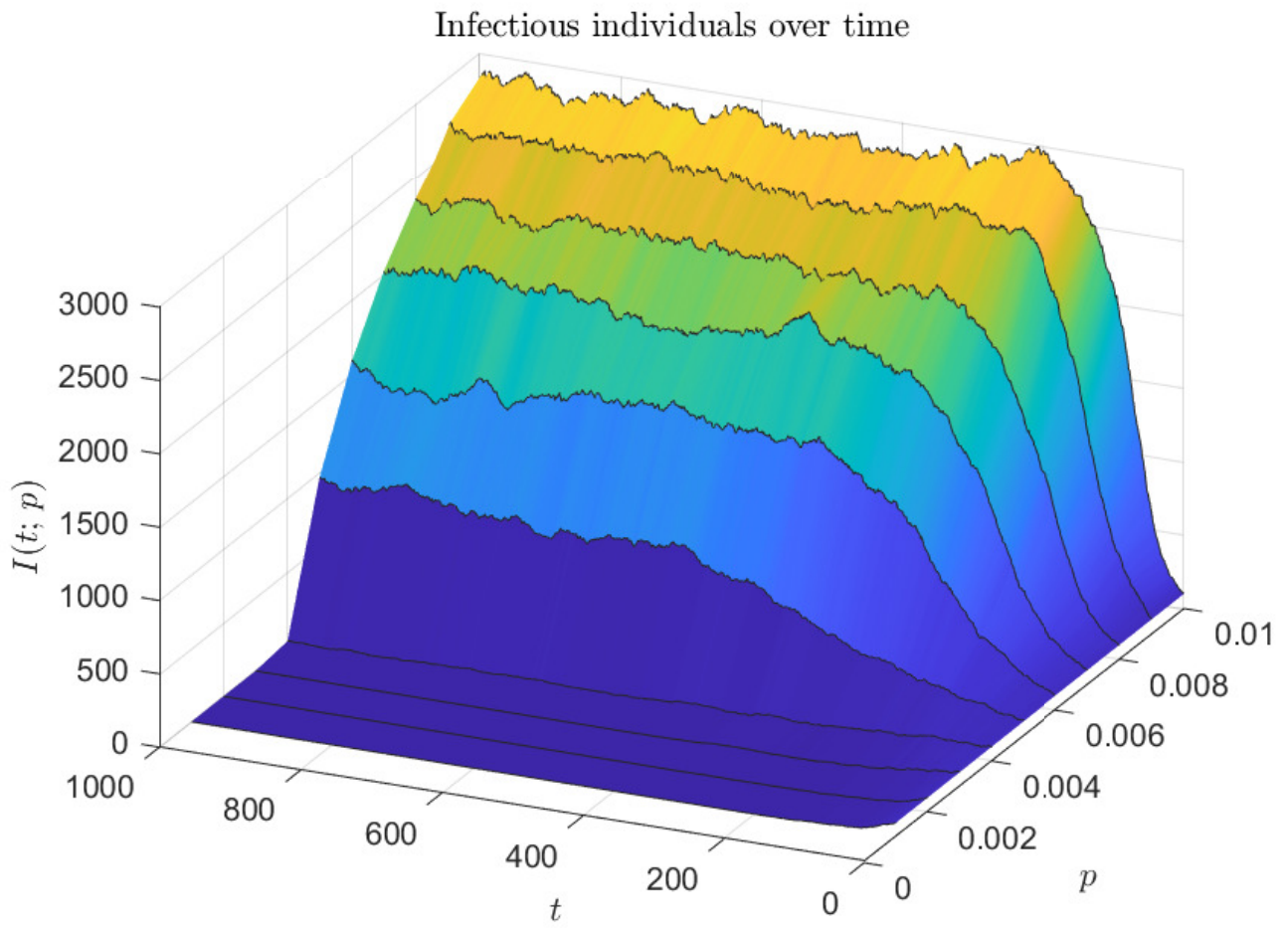


Figure 3: Epidemic on Erdős-Renyi random graph with 5000 vertices

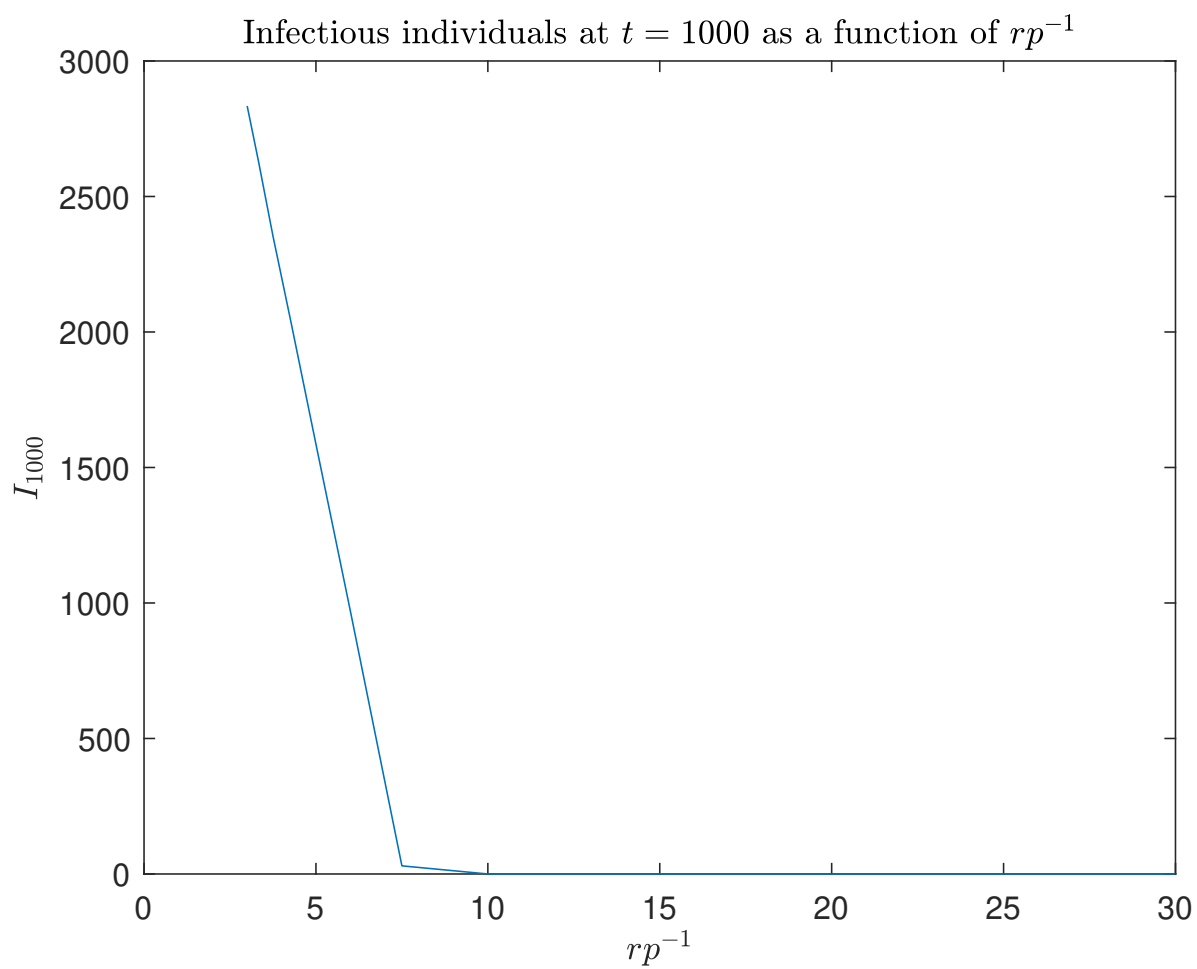


Figure 4: Epidemic on Erdős-Renyi random graph with 5000 vertices

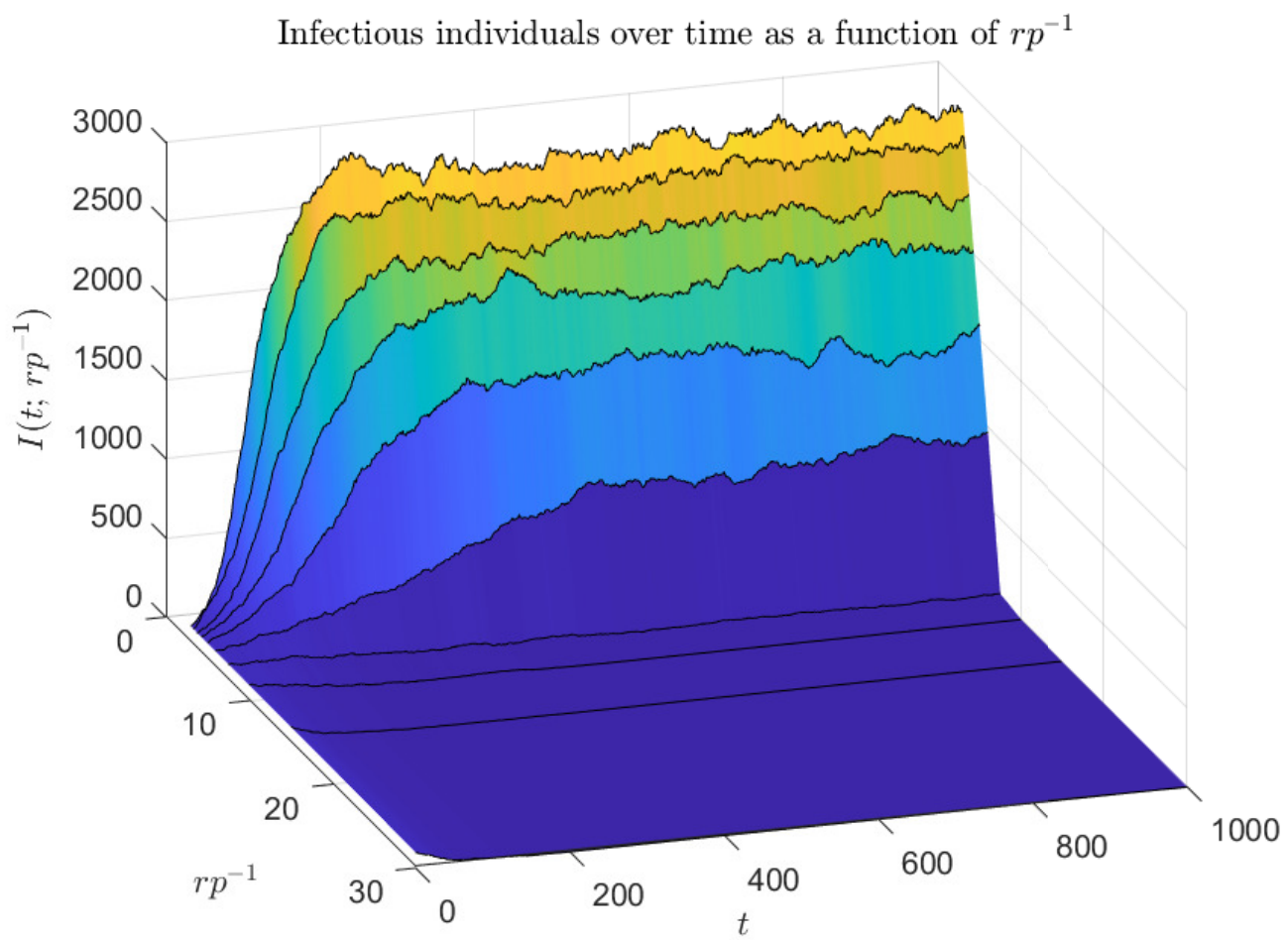


Figure 5: Epidemic on Erdős-Renyi random graph with 5000 vertices

2 Preferential attachment

I generate a graph with preferential attachment based on the Barabási-Albert model. Each new vertex connects to m existing vertices, and the process starts with $n_0 = m + 1$ vertices that are cyclically connected by a total of n_0 edges. In this case we use $m = 1$.

At each step, a set $\{x_1, \dots, x_n\}$ of random numbers are sampled from a uniform distribution on $[0, 1]$, and an existing vertex v_i is considered if $x_i \leq k_i(2E)^{-1}$, where E is the total number of edges currently in the graph and k denotes degree. The new vertex v_{n+1} connects to a uniform random m -permutation of the set of considered vertices.

The degree distribution is shown in fig. 6. It is a power-law distribution, and the average degree is 2.

2.1 Epidemic simulation take 2

This time, there is a lot more diversity among the results for different values of p , and a lot less monotonicity. fig. 7 and fig. 8 show the evolution over 1000 time steps. Since this network is scale free and contains a small number of highly connected vertices, the evolution of the epidemic is highly affected by which individuals are infected. Contrary to the first simulations, we see cases where the number of infectious individuals initially decline, but then rise sharply. The equilibrium also appears much less stable, and the dependency on p is less obvious.

In fig. 9 and fig. 10, we see something similar to the first simulations, with a sharp cut-off point at $p = 0.005 \iff rp^{-1} = 6$.

I would say that this type of network makes for a better model than the Erdős-Renyi graph since it captures the importance of highly connected nodes that are key in spreading the disease. However, it is (at least in this case) far from a good fit to real-world examples of social networks. For example, a network generated with $m = 1$ always has zero clustering coefficient.

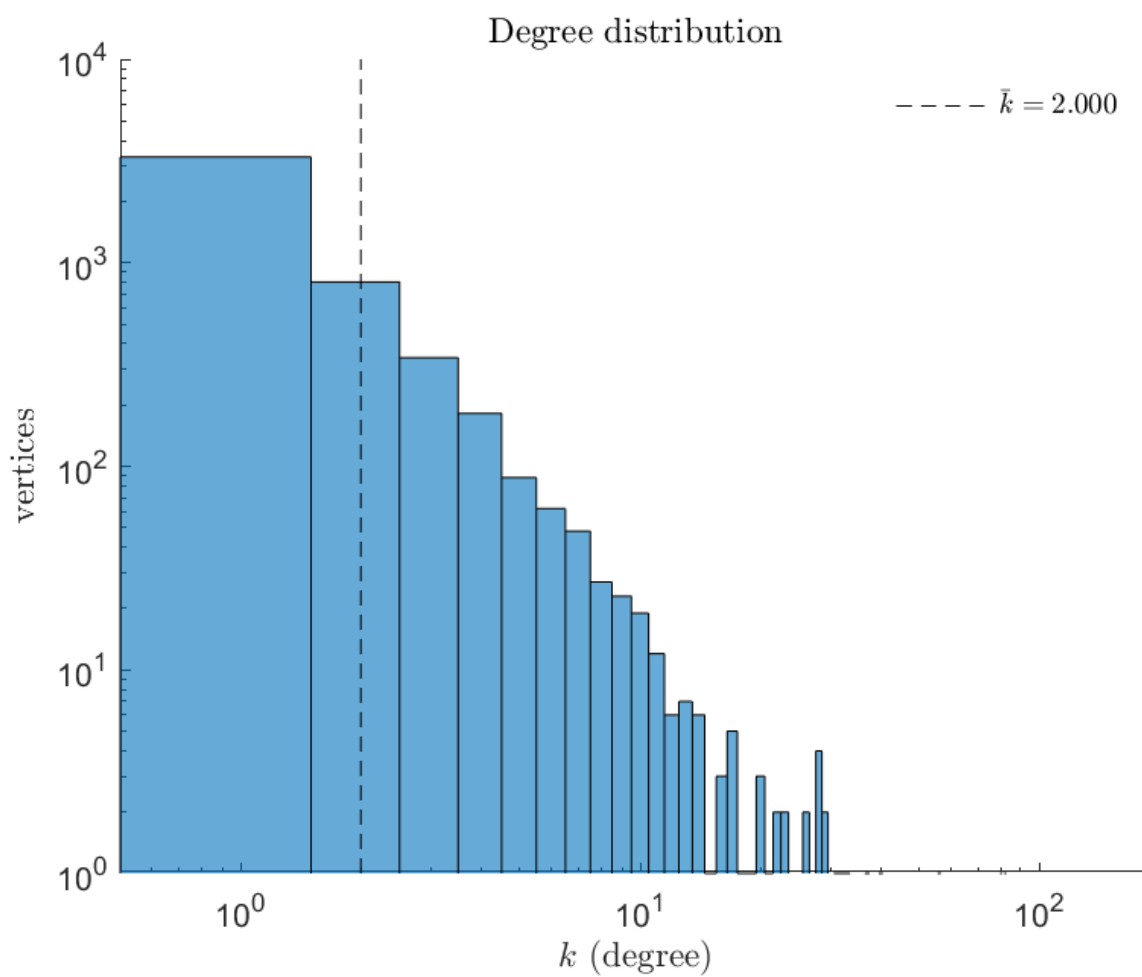


Figure 6: Barabási-Albert graph with $n_0 = 2, m = 1$ and 5000 vertices

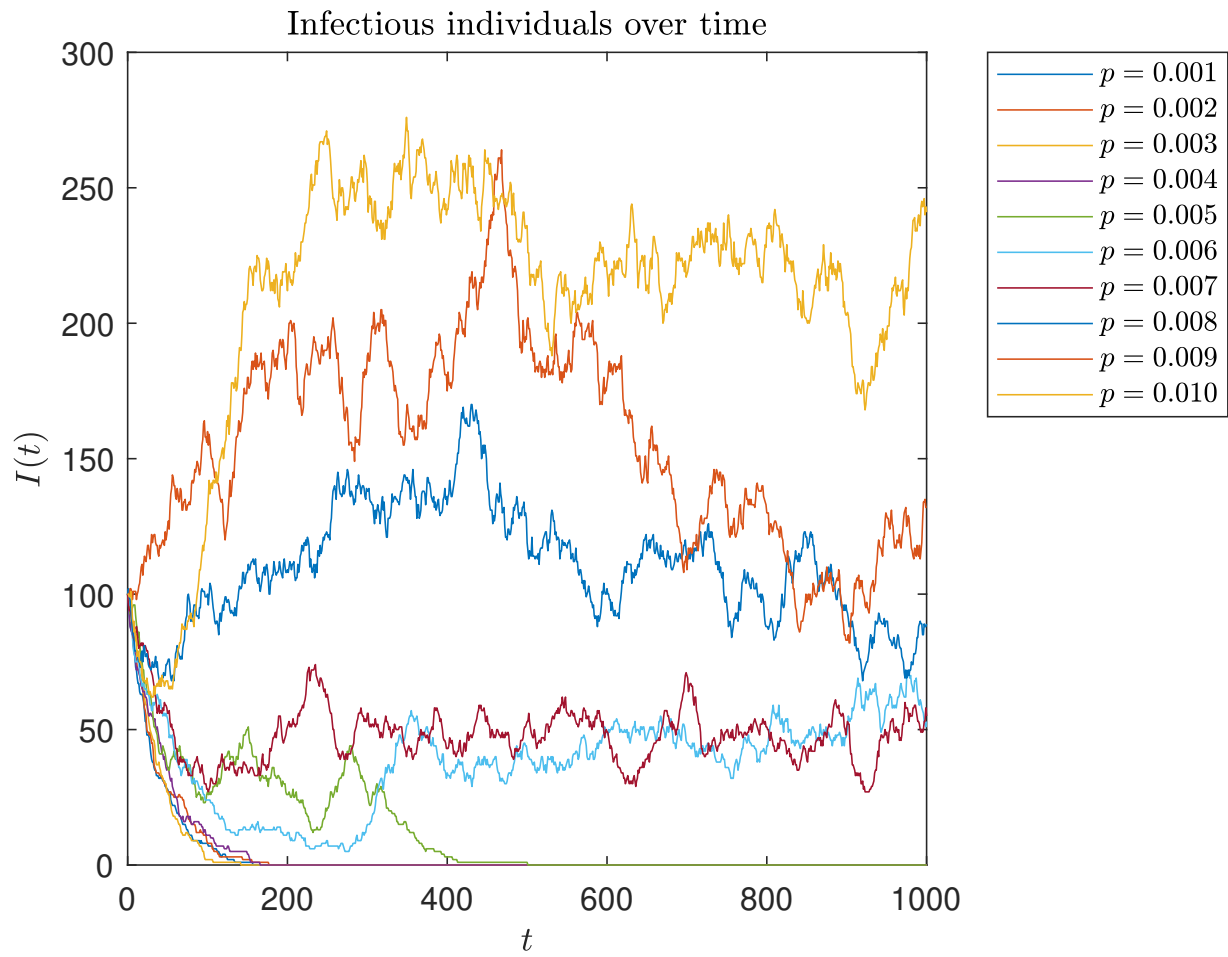


Figure 7: Epidemic on Barabási-Albert graph with 5000 vertices

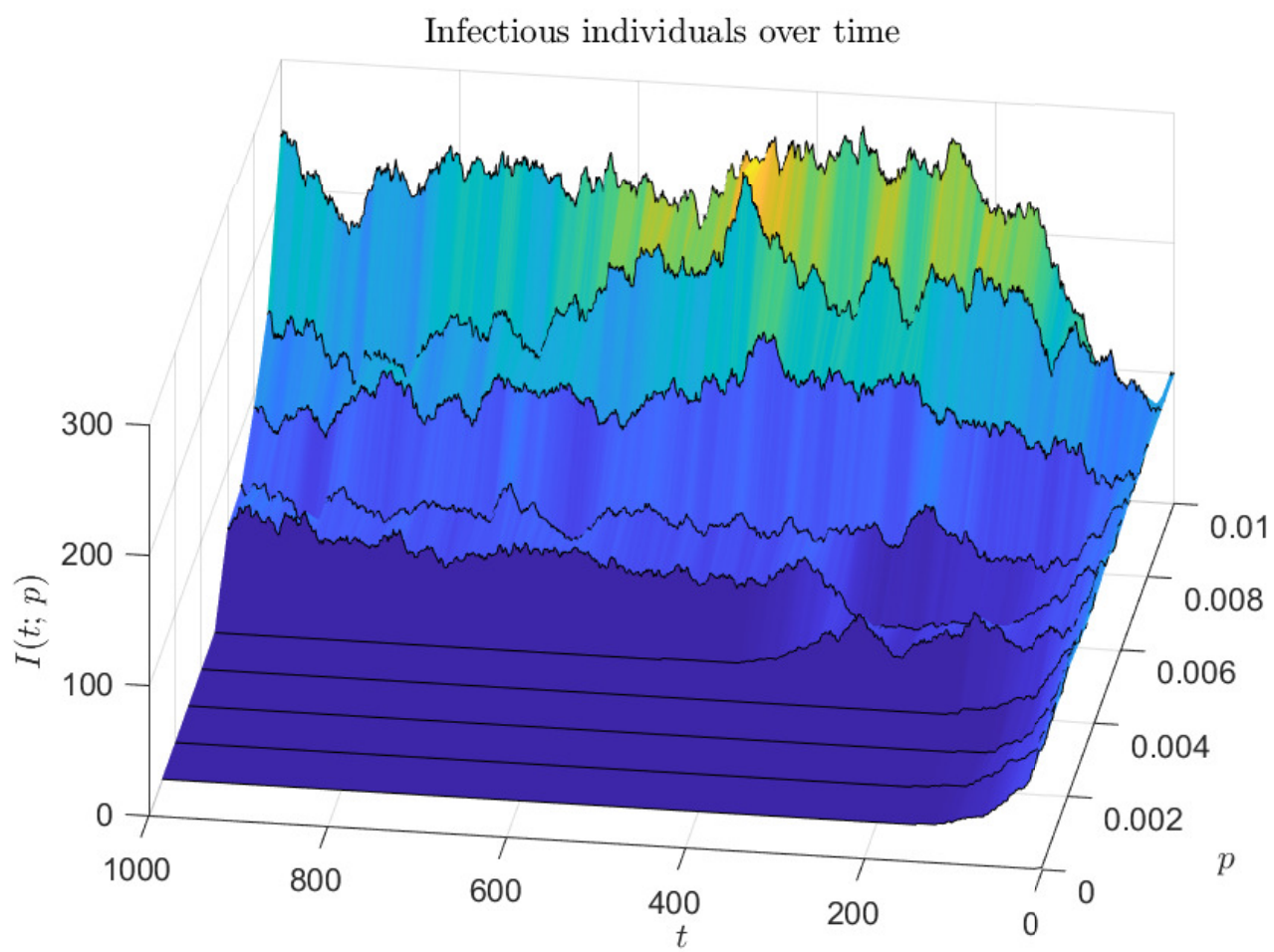


Figure 8: Epidemic on Barabási-Albert graph with 5000 vertices

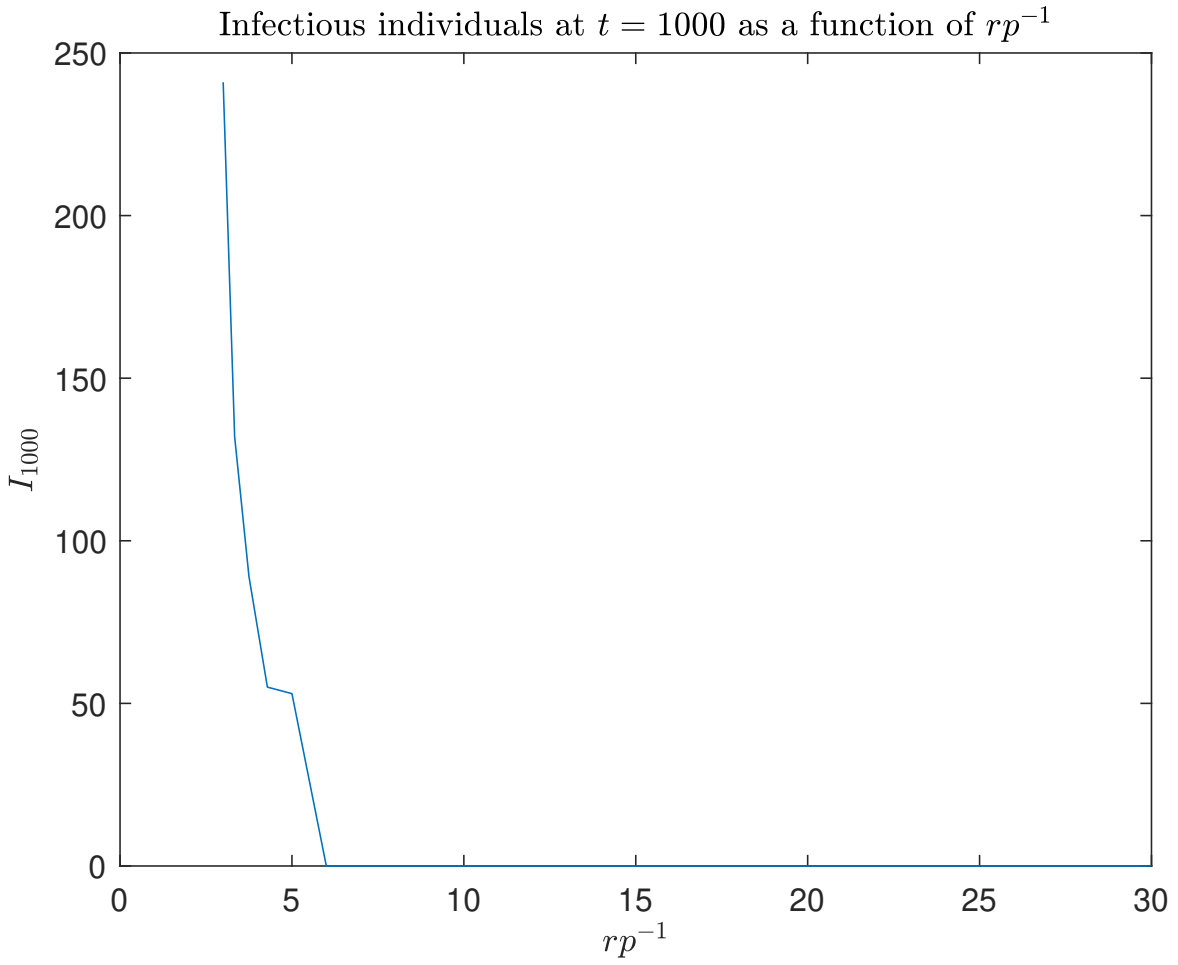


Figure 9: Epidemic on Barabási-Albert graph with 5000 vertices

Infectious individuals over time as a function of rp^{-1}

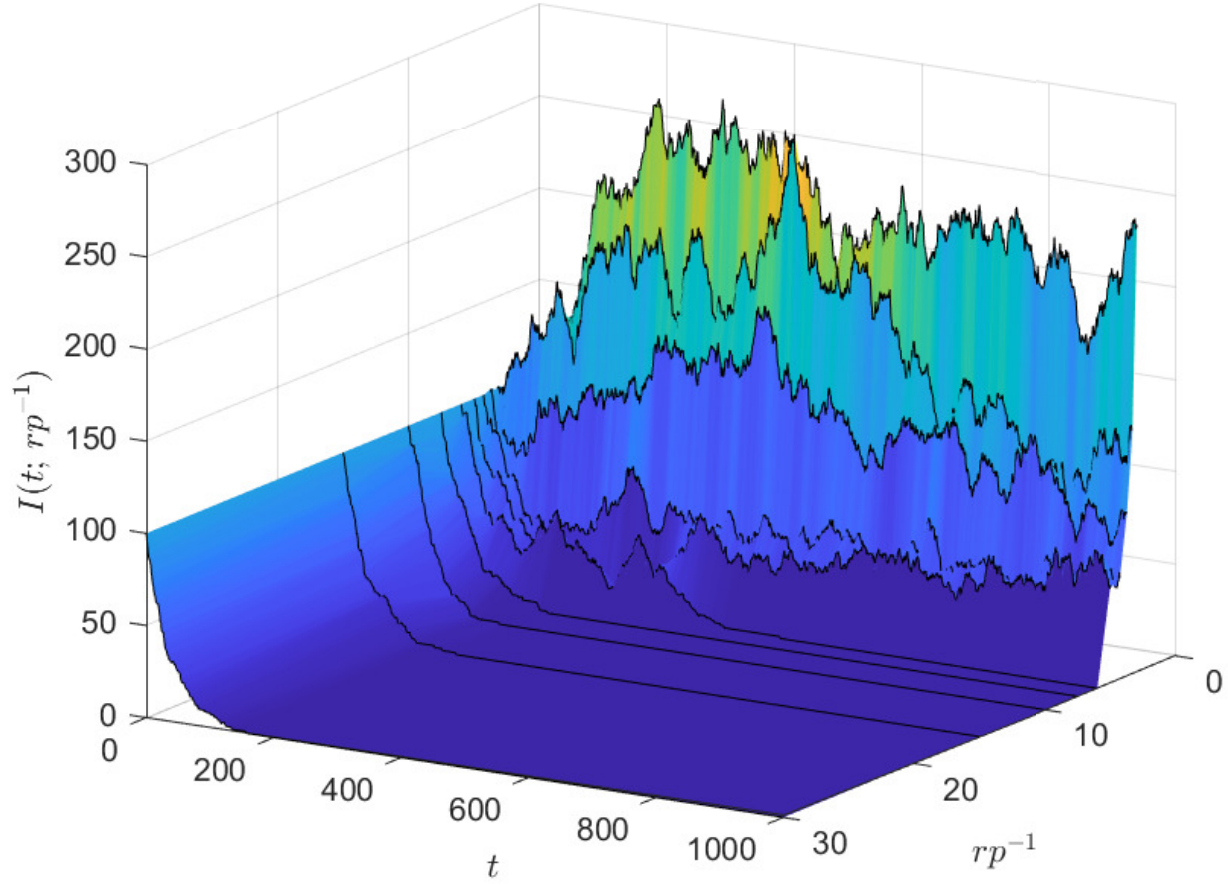


Figure 10: Epidemic on Barabási-Albert graph with 5000 vertices

A Code

All the code can be checked out at

<https://github.com/Fredrik-M/BERV-MCS/tree/master/MCS/lab4>

The implementation of the epidemic model is found in

<https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab4/step.m>

and https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab4/inf_exp.m

The graphs were generated with

https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab4/graph_er.m

and https://github.com/Fredrik-M/BERV-MCS/blob/master/MCS/lab4/graph_pa.m