Network Dynamics IV

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1 Preliminary parts

1.1 Epidemic on a known graph

The task is to simulate an epidemic using the SI-model for a known k-regular graph. In the SIR-model on a graph, each node X_i can either be susceptible S, infected I or recovered R. For a time-discrete model with $t = 0, 1, 2, ...$ we can model the spread of the epidemic for each time-step by the following equations

$$P(X_i(t+1) = I | X_i(t) = S, \sum_{j \in \mathcal{V}} W_{ij} \delta^I_{X_j(t)} = m) = 1 - (1-\beta)^m, \tag{1}$$

$$P(X_i(t+1) = R | X_i(t) = I) = \rho. \tag{2}$$

W is the weight matrix of the graph and $\delta^I_{X_j(t)}$ is an indicator function which takes the value 1 if $X_j(t)$ is in state I and 0 otherwise, which means that $\sum_{j \in \mathcal{V}} W_{ij} \delta^I_{X_j(t)}$ is the number of infected neighbours of $X_i(t)$. The parameter $\beta \in [0, 1]$ is the probability of infection from an infected node connected to susceptible one, and $\rho \in [0, 1]$ is the probability that an infected node will recover. Once a node has recovered in state R, it cannot change state.

I simulate this epidemic on a $k = 4$ regular undirected graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ which is a graph where every node in $\mathcal{V}$ is directly connected to k neighbours whose index is their closest modulo $n = |\mathcal{V}|$. Here we use $n = 500$ nodes.

I simulate the epidemic according to instructions and the results have been plotted in Figure 1. One can notice the typical behaviour of epidemics, a huge spike in newly infected until the infection dies out with exponential functions for the number of susceptible and recovered.

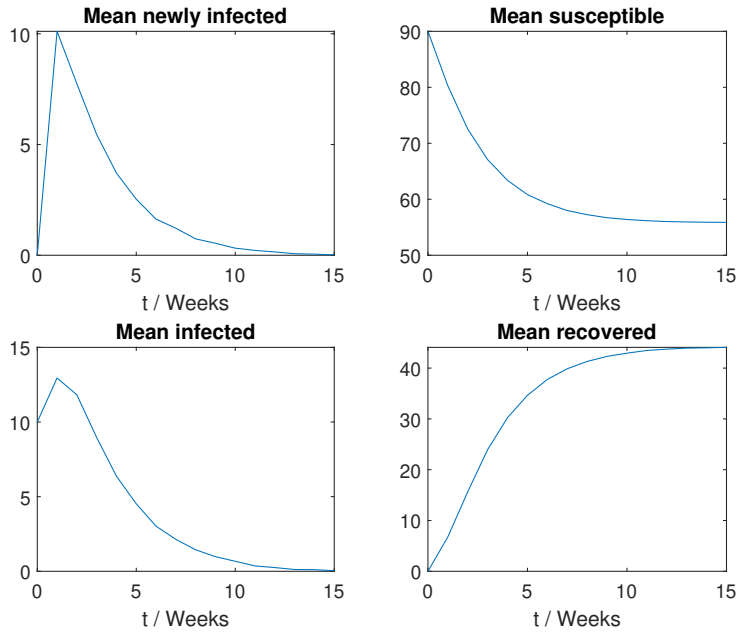

Figure 1: Mean newly infected, mean susceptible, mean infected and mean recovered for an SIR-epidemic on $k = 4$ regular graph with $n = 500$ nodes, $\beta = 0.3$ and $\rho = 0.7$. Initial number of infected is 10. Simulated $N = 100$ times.

1.2 Generate a random graph

In this section we will generate a graph with random degree k according to the preferential attachment rule. In simple terms we start out with a complete graph (simple and undirected where all vertices are connected to each other) $\mathcal{G}_1$ with $k_0 = k + 1$ nodes. Then at every time step $t \geq 2$ we add a new node n_t to $\mathcal{G}_{t-1}$ and connect it some of the existing nodes.

For attaching the node to the old graph we use preferential attachment rule: The probability of there being a link between node n_t and a node $i \in \mathcal{V}_{t-1}$ in the old graph is given by

$$P(W_{n_t,i}(t) = W_{i,n_t}(t) = 1 | \mathcal{G}_{t-1} = (\mathcal{V}_{t-1}, \mathcal{E}_{t-1})) = \frac{w_i(t-1)}{\sum_{j \in \mathcal{V}_{t-1}} w_j(t-1)}, \tag{3}$$

where $w_i(t-1)$ is the prior degree of the node i before adding a new node. This means that this is essentially a "rich get richer" type of scheme, where nodes that are already highly connected have a higher probability of adding a new node.

At every time step we want to add c new links to the new node. If k is an even integer then $c = k/2$. To generate a general graph with average degree $k \geq 2$ you can use the following algorithm:

$c \leftarrow \lfloor k/2 \rfloor$
if $\text{mod}(k/2, 1) \geq u \sim U(0,1)$ **then**
$c \leftarrow c + 1$
end if

For example if $k = 2.6$ then at each time step $c = 1$, and with probability 0.3 $c = 2$, so $\mathbb{E}[c] = 0.7 \cdot 1 + 0.3 \cdot 2 = 1.3 = k/2$. This algorithm works better the more nodes you have since you'll decrease the variance of c.

In Figure 2 below I've plotted a random graph with $n = 900$ nodes with average degree 2.3.

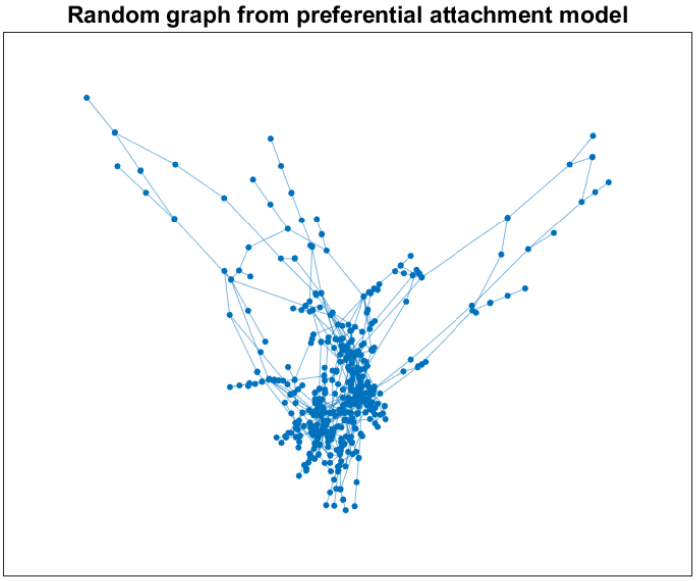

Figure 2: Random graph generated using preferential attachment model with $n = 900$ nodes with average degree 2.3.

2 Simulate a pandemic without vaccination

Using the methods from the previous section, we will simulate an epidemic using an SIR-model on a randomly generated graph created using preferential attachment.

I simulate the model according to the instructions. The results have been plotted in Figure 3.

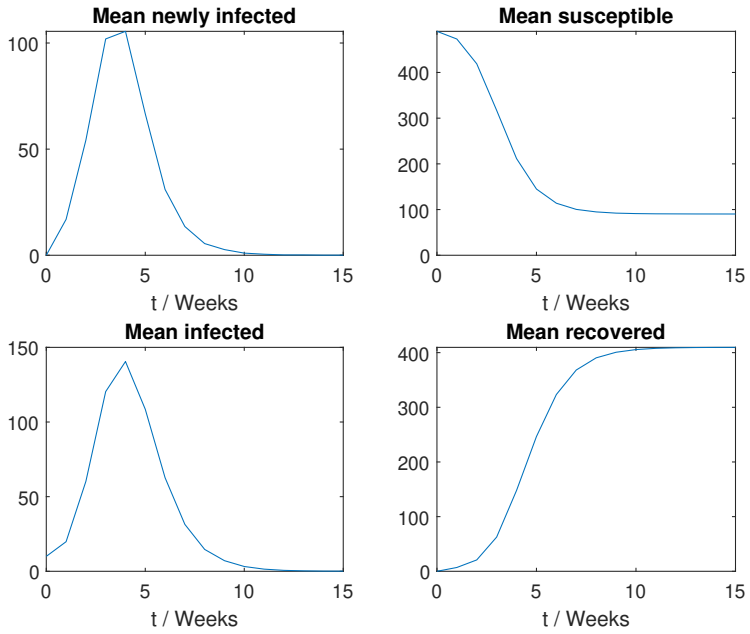

Figure 3: Mean newly infected, mean susceptible, mean infected and mean recovered for an SIR-epidemic on a preferential attachment graph with $n = 500$ nodes, average degree 6, $\beta = 0.3$ and $\rho = 0.7$. Initial number of infected is 10. Simulated $N = 100$ times.

3 Simulate a pandemic with vaccination

I simulate an SIR-model on a preferential attachment graph this time with vaccines. I simulate it according to instructions. The results have been plotted in Figure 4.

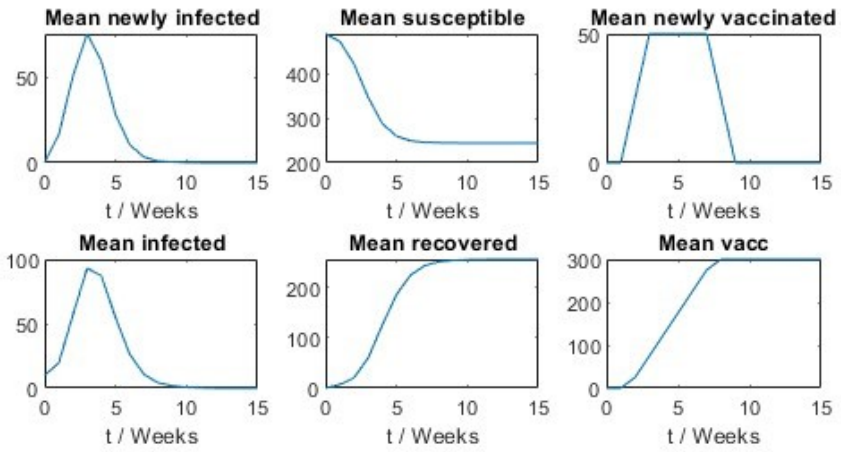

Figure 4: Mean newly infected, mean susceptible, mean infected and mean recovered, mean vaccinated and mean newly vaccinated for an SIR-epidemic on a preferential attachment graph with $n = 500$ nodes, average degree 6, $\beta = 0.3$ and $\rho = 0.7$. Initial number of infected is 10. Simulated $N = 100$ times.

4 The H1N1 pandemic in Sweden 2009

I use optimization algorithm described in instructions and find an estimation of the variables. The estimated variables are $k = 11.5$, $\beta = 0.17$, and $\rho = 0.55$ with an RMSE = 9.2587.

The results have been plotted in Figure 5 and 6. One can surely make better estimates than this but halfway through writing this rapport I realized that there was an error in my code so I had to redo all my experiments last minute.

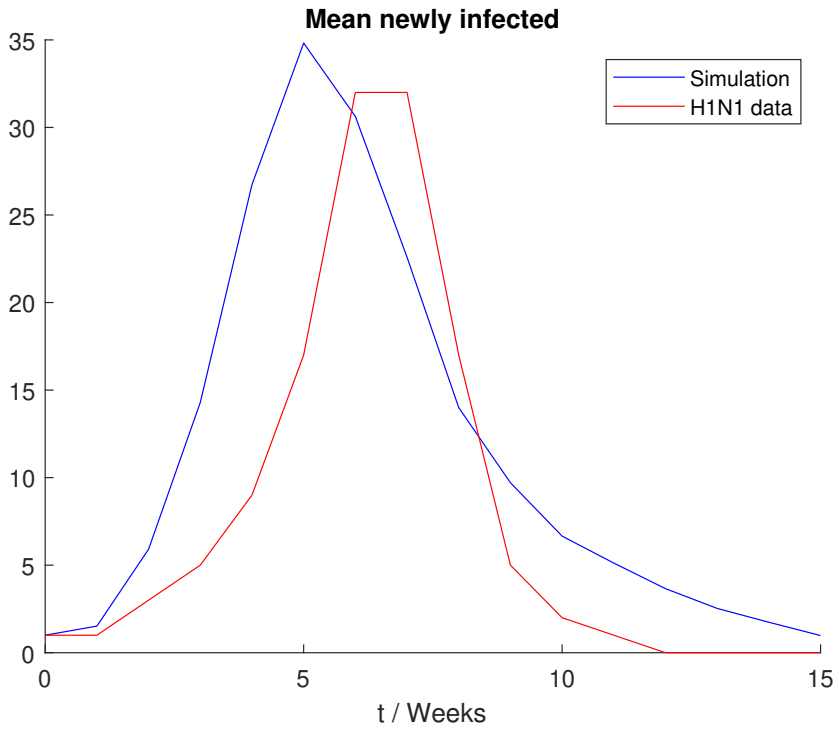

Figure 5: Mean newly infected with data from H1N1 (red) and simulated SIR-model with vaccines (blue). The simulation was on a preferential attachment graph with $n = 934$ nodes, average degree $k = 11.5$, $\beta = 0.17$ and $\rho = 0.55$. Initial number of infected is 10. Simulated $N = 100$ times.

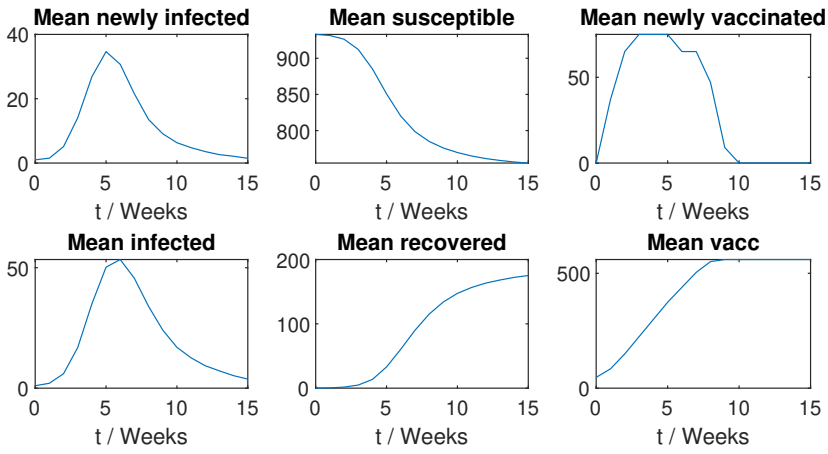

Figure 6: Mean newly infected, mean susceptible, mean infected and mean recovered, mean vaccinated and mean newly vaccinated for an SIR-epidemic on a preferential attachment graph with $n = 934$ nodes, average degree $k = 11.5$, $\beta = 0.17$ and $\rho = 0.55$. Initial number of infected is 1. Simulated $N = 100$ times.

5 Challenge

For the challenge I tried to model the graph using an Erdős-Rényi graph with clusters. It works like this: Choose a number of clusters. Each node *within* a cluster has a probability p of being connected. Then select random nodes between clusters and connect them with edges. Nodes of *different* clusters have a probability of being connected q.

I create a new model using this graph and optimize it with line search. The results have been plotted in Figure 7. The estimated variables were $p = 0.01$, $q = 0.02$, $\beta = 0.175$ and $\rho = 0.95$ with an RMSE $= 5.7232$. Again this can surely be improved but I won't due to lack of time.

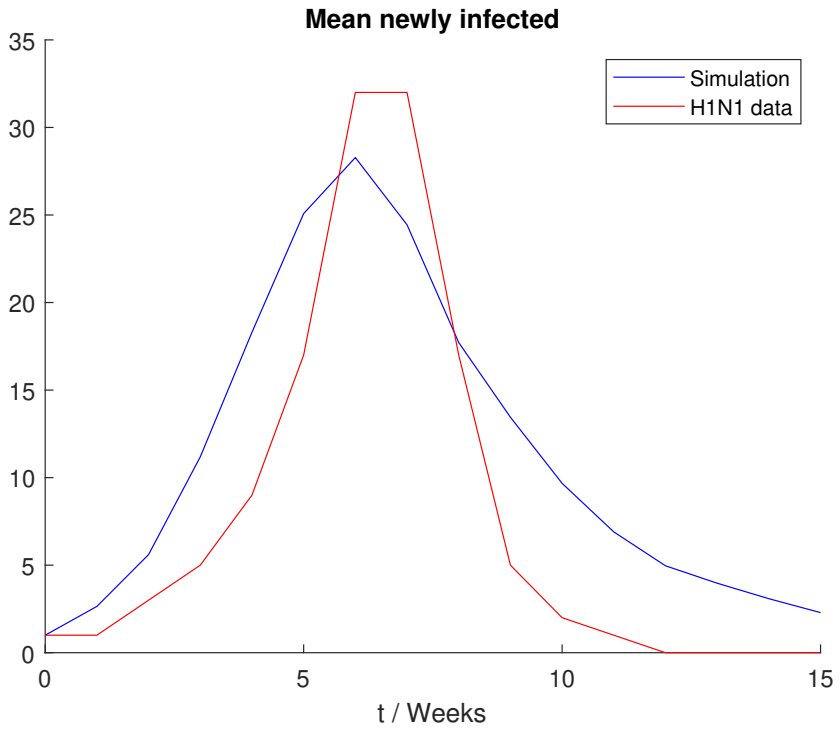

Figure 7: Mean newly infected with data from H1N1 (red) and simulated SIR-model with vaccines (blue). The simulation was on an Erdős-Rényi graph with clusters graph with $n = 934$ nodes, $p = 0.01$, $q = 0.02$, $\beta = 0.175$ and $\rho = 0.95$. Initial number of infected is 10. Simulated $N = 200$ times.

I also tried changing the optimization algorithm to the Genetic Algorithm in MATLAB. In simple terms it's based on natural selection: Fit individuals survive and cross with each other to create new and improved offspring. You can read more about it here: https://se.mathworks.com/help/gads/what-is-the-genetic-algorithm.html

I used the hyperparameters `PopulationSize` $= 25$, `MaxGenerations` $= 15$, `CrossoverFraction` $= 0.8$, `EliteCount` $= 2$, `MutationFcn` $=$ @mutationadaptfeasible.

I get the estimates $p = 0.0061525$, $q = 0.0054639$, $\beta = 0.49186$, $\rho = 0.5804$ with an RMSE $= 6.8955$. The results have been plotted in Figure 8. Again this can surely be improved but I won't due to lack of time.

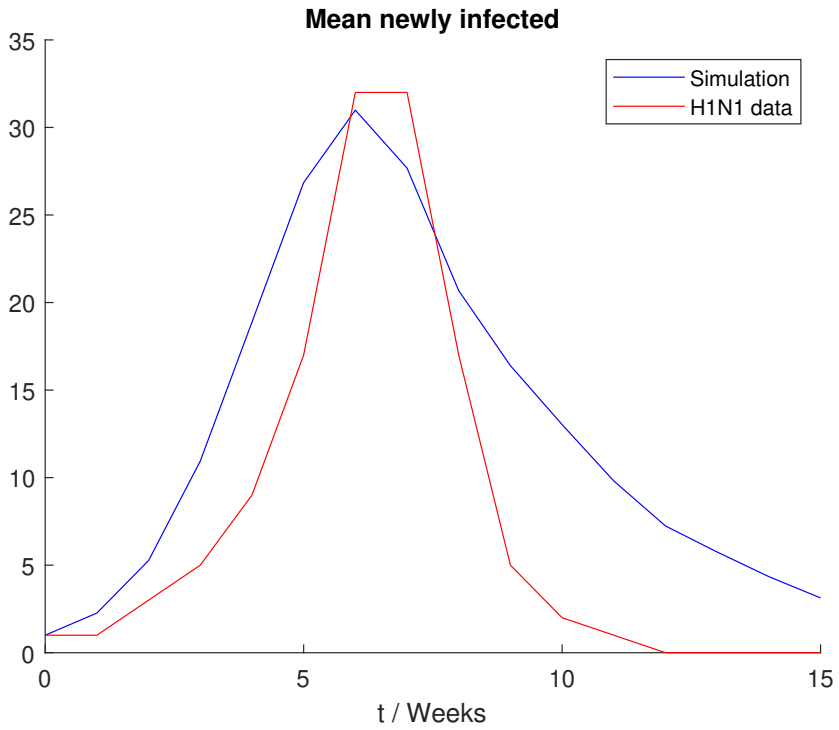

Figure 8: Mean newly infected with data from H1N1 (red) and simulated SIR-model with vaccines (blue). The simulation was on an Erdős-Rényi graph with clusters graph with $n = 934$ nodes, $p = 0.0061525$, $q = 0.0054639$, $\beta = 0.49186$ and $\rho = 0.5804$. Initial number of infected is 10. Simulated $N = 200$ times.