

LUND UNIVERSITY  
FACULTY OF ENGINEERING (LTH)

FRTN 30

NETWORK DYNAMICS

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# The Influenza H1N1 2009 Pandemic in Sweden, Hand-In 4

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# 1 Preliminary parts

First we will run a simulation on a given graph, secondly we will generate a random graph with preferential attachment.

## Epidemic on a known graph

We will simulate an epidemic on a  $k$ -regular graph with  $n = 500$  nodes. An example of a  $k$ -regular graph with 8 nodes and  $k = 4$  can be seen in figure 1.

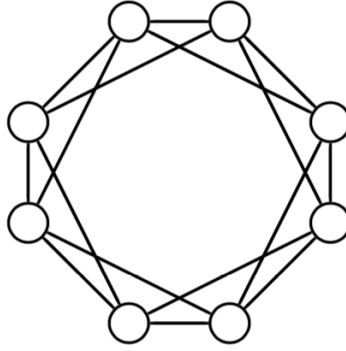


Figure 1: Example of a  $k$ -regular graph with 8 nodes.

In our model, a node (person) can either be infected I, susceptible S, or recovered R. The nodes are therefore in a state  $X_i(t) \in \{S, I, R\}$  at any time  $t$ . The probability of getting infected by one of its neighbors is  $1 - (1 - \beta)^m$  where  $m$  is the number of infected neighbors. A node will recover with a probability  $\rho$ .

**Problem 1.1:** You should simulate an epidemic on a symmetric  $k$ -regular graph  $\mathcal{G} = (\mathcal{V}, \mathcal{E})$  with  $|\mathcal{V}| = 500$  nodes and  $k = 4$ . See Figure 1 for an example with  $n = 8$  nodes. Let  $\beta = 0.3$  and  $\rho = 0.7$ . With one week being one unit of time, simulate the epidemic for 15 weeks. You can choose an initial configuration with 10 infected nodes selected at random from the node set  $\mathcal{V}$ , or make a different choice of initial configuration (in the latter case, please briefly discuss your motivation).

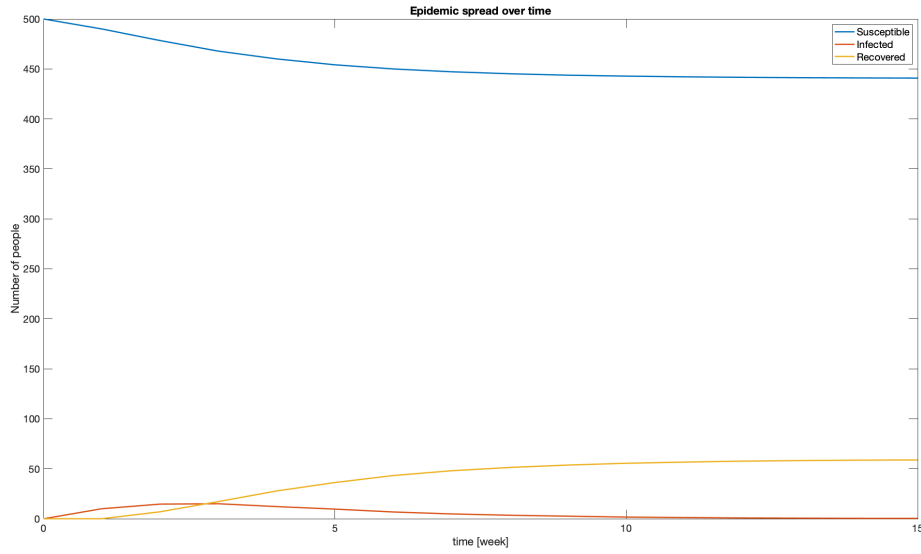


Figure 2: The average total number of susceptible, infected, and recovered individuals at each week for the given graph. The initially infected people are chosen randomly.

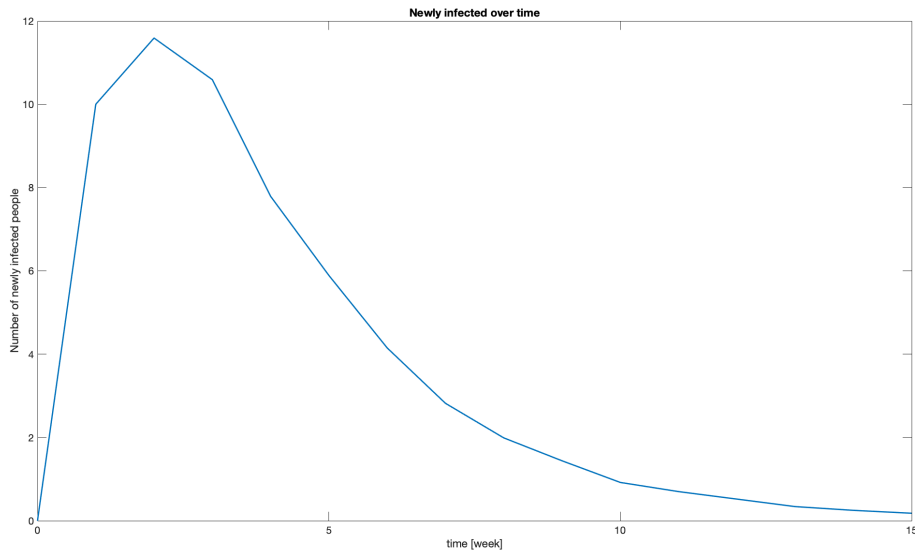


Figure 3: The average number of newly infected individuals each week for the given graph. The initially infected people are chosen randomly.

The peak in figure 3 make sense since there are 10 infected week 1, they have 40 neighbors in total and they each spread their virus with a  $\beta = 0.3$  probability, therefore the expected value of people getting infected in week 2 is  $40 * 0.3 = 12$  which is close to the empirical data in figure 3.

## Generate a random graph

**Problem 1.2:** Your goal is to, by using preferential attachment, generate a random graph of a large size (at least 900 nodes) with average degree  $k \in \mathbb{Z}^+$ . Let the initial graph  $\mathcal{G}_\infty = (\mathcal{V}_\infty, \mathcal{E}_\infty)$  be a complete graph with  $|\mathcal{V}_1| = k_0 = k + 1$  nodes. Note that the goal here is to implement a fairly general algorithm where it is very easy to change the average degree. It should be possible to change the average degree by only changing the value of  $k$  in your algorithm. This algorithm will then be used in Section 4.

See attached code for implementation.

## 2 Simulate a pandemic without vaccination

In this part we will use the graph generated in Problem 1.2 and use the method developed in Problem 1.1.

**Problem 2:** Using the methods developed in Section 1, generate a preferential attachment random graph  $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ , with  $|\mathcal{V}| = 500$  nodes. The average degree should be  $k = 6$ . Let  $\beta = 0.3$  and  $\rho = 0.7$ . With one week being one unit of time, simulate the epidemic for 15 weeks.

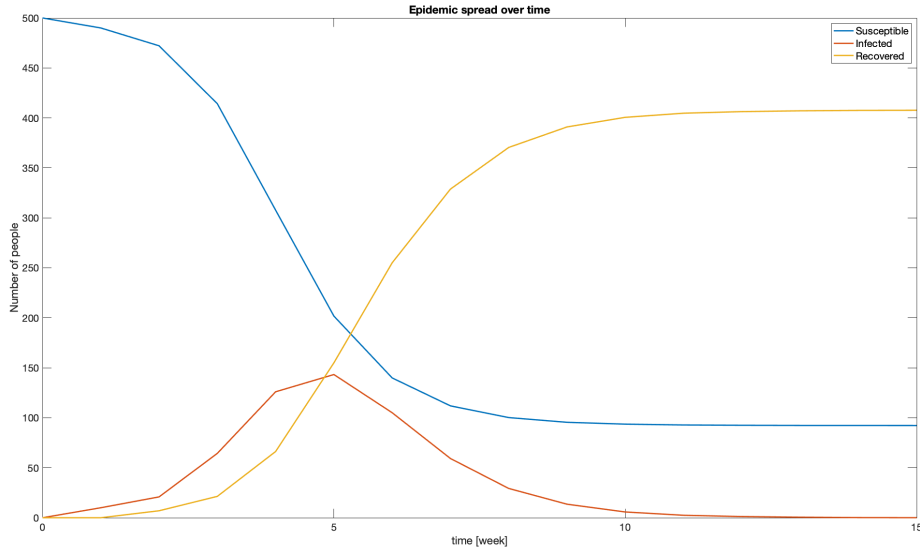


Figure 4: The average total number of susceptible, infected, and recovered individuals at each week for a random graph generated by preferential attachment. The initially infected people are chosen randomly.

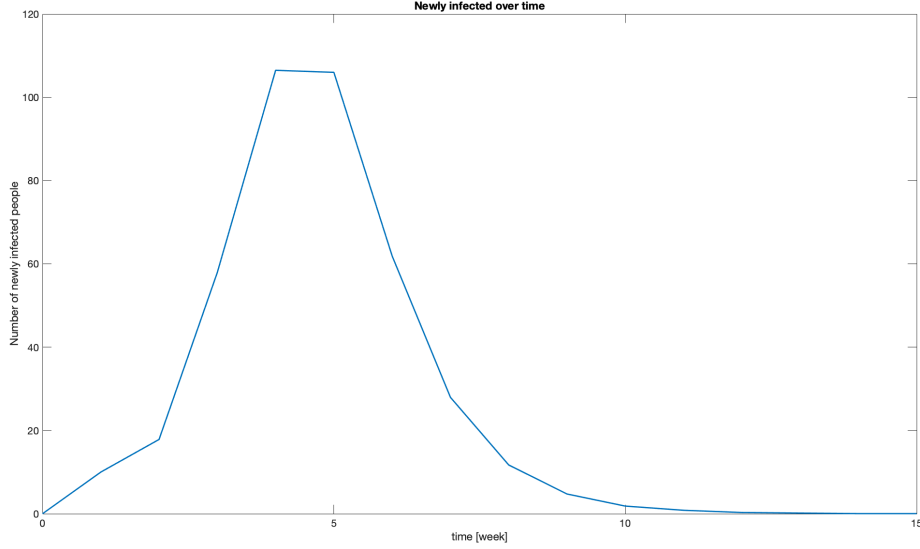


Figure 5: The average number of newly infected individuals each week for a random graph generated by preferential attachment. The initially infected people are chosen randomly.

Here we see that the number of infected people have increased a lot, this is because the average degree  $k$  has increased from 4 to 6 and the graph is randomly generated. The expected number of newly infected people week 2 is,  $10 * 6 * 0.3 = 18$  which seem to correspond well to figure 5. Also, because the infections are much higher the amount of people that are recovered will increase drastically, which can be seen in figure 4.

### 3 Simulate a pandemic with vaccination

We now introduce a new class of people, vaccinated people. The vaccination is distributed to the people according to the following vector

$$Vacc(t) = [0, 5, 15, 25, 35, 45, 55, 60, 60, 60, 60, 60, 60, 60, 60] \quad (1)$$

**Problem 3:** Using the method developed in the previous section, generate a random graph  $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ , with  $|\mathcal{V}| = 500$  nodes. The average degree should be  $k = 6$ . Let  $\beta = 0.3$  and  $\rho = 0.7$ . With one week being one unit of time, simulate the epidemic with vaccination for 15 weeks, using the vaccination scheme  $Vacc(t)$  above. You can choose an initial configuration with 10 infected nodes selected at random from the node set  $\mathcal{V}$ , or make a different choice of initial configuration (in the latter case, please briefly discuss your motivation).

See attached code for implementation.

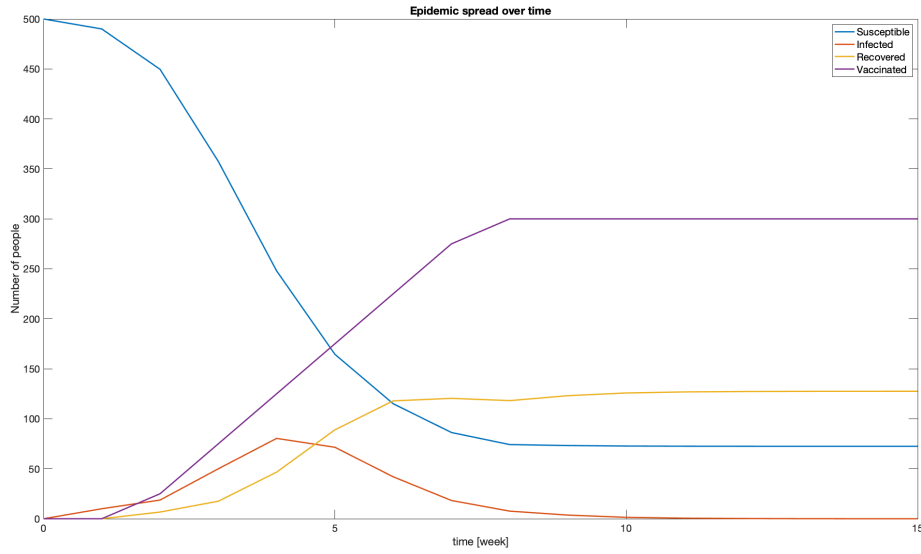


Figure 6: The average total number of susceptible, infected, recovered and vaccinated individuals at each week for a random graph generated by preferential attachment. The initially infected people are chosen randomly.

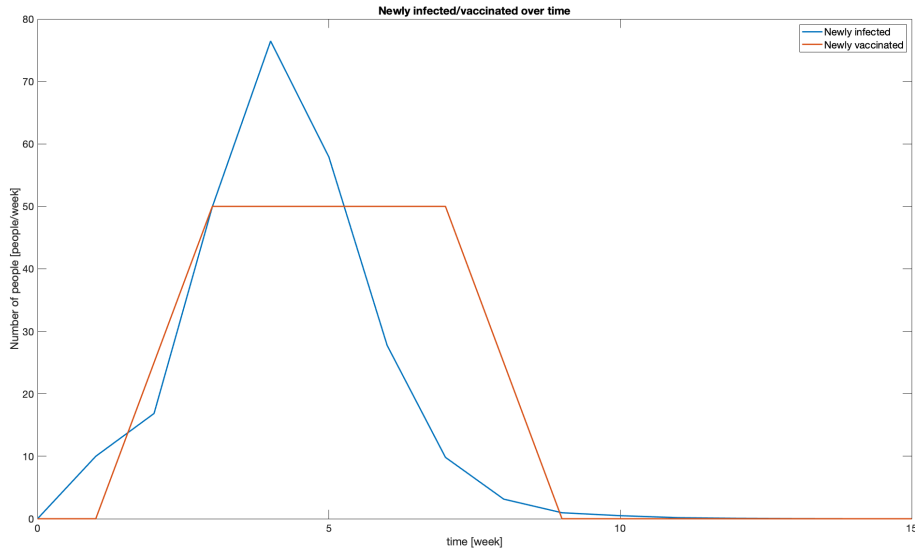


Figure 7: The average number of newly infected and vaccinated individuals each week for a random graph generated by preferential attachment. The initially infected people are chosen randomly.

In figure 8 a new function has been added, the vaccinated people. As we can see after a couple of weeks the amount of vaccinated people is constant but the infection has already reached its peak by that point. Since we introduced this new class the amount of recovered people has decrease a lot, this is in part because recovered

people can also be vaccinated.

The peak of newly infected people in 9 is lower than in figure 5, i.e. the infection doesn't spread as fast now that the vaccination is introduced.

## 4 The H1N1 pandemic in Sweden 2009

We are now ready for the modeling of the H1N1 pandemic in Sweden 2009. We want to fit the function

$$I_0(t) = [1, 1, 3, 5, 9, 17, 32, 32, 17, 5, 2, 1, 0, 0, 0, 0] \quad (2)$$

where  $I_0(t)$  is the number of newly infected people each week  $t$ . We improve our fit by changing the parameters  $k, \beta$  and  $\rho$ . The fraction of people who had received vaccination was

$$\text{Vacc}(t) = [5, 9, 16, 24, 32, 40, 47, 54, 59, 60, 60, 60, 60, 60, 60, 60] \quad (3)$$

In order to quantify the fit we use the Root-Mean-Square-Error, RMSE.

$$\text{RMSE} = \sqrt{\frac{1}{15} \sum_{t=1}^{15} (I(t) - I_0(t))^2} \quad (4)$$

The combination of parameters who give the smallest RMSE will be used to model the problem.

**Problem 4:** Using the algorithm above, estimate the average degree  $k$  and the disease-spread parameters  $\beta$  and  $\rho$  for the pandemic.

I cooperated with Gustav Östgren and Ian Thorslund on this task. Modification to the previous code was made, mainly adding the RMSE and creating for-loops for the different parameters. See attached code for implementation.

The best parameters that the model was able to produce was

$k$	$\beta$	$\rho$
8	0.3	0.1

Using these yielded the following result

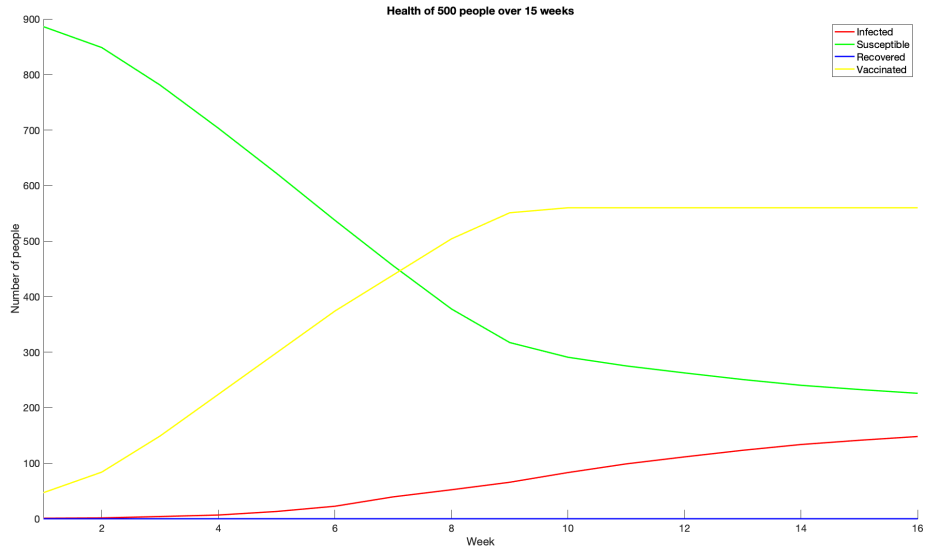


Figure 8: The average total number of susceptible, infected, recovered and vaccinated individuals at each week for a random graph generated by preferential attachment. The initially infected people is just one and is chosen randomly.

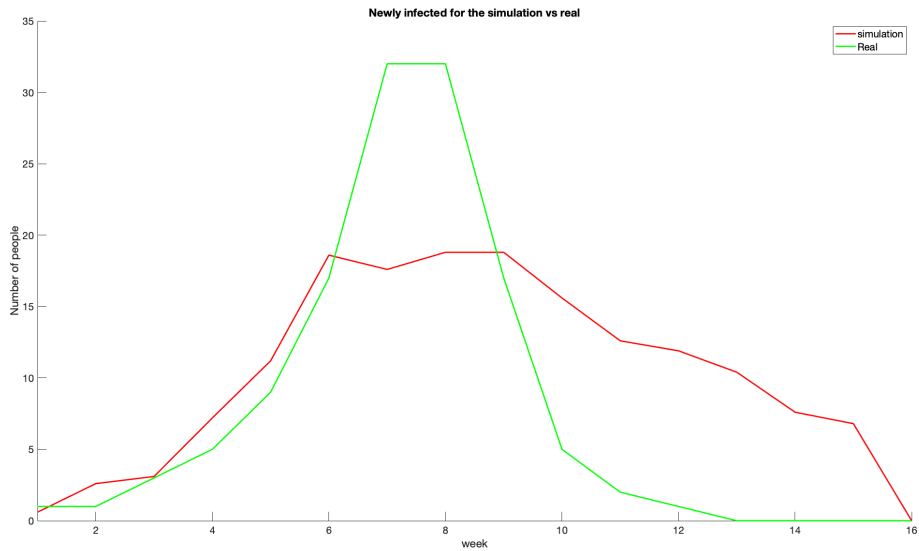


Figure 9: The average number of newly infected and vaccinated individuals each week for a random graph generated by preferential attachment. The initially infected people is just one and is chosen randomly. The fit isn't super good but decent. It is hard for the model to create the tall peak, it "wants" to spread out more.