Network Dynamics and Learning
Homework 3 - Report

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Aim

The aim of this laboratory is to model the H1N1 2009 pandemic in Sweden, studying both population and epidemic characteristics.

1 Preliminary parts

1.1 Epidemic on a known graph

The first part of this laboratory consists of simulating an epidemic on a known graph through a discrete-time SIR model.
The possible node states are:

- S: susceptible

- I: infected

- R: recovered

Assuming that

$$\beta = P\left[X_i(t+1) = I \mid N_i = \{j\} \wedge X_i(t) = S \wedge X_j(t) = I\right] \tag{1}$$

and that node i can be indepenently infected by its different neighbors, transition probabilities are:

$$P\left[X_i(t+1) = I \mid X_i(t) = S \wedge \sum_{j \in \mathcal{V}} W_{ij}\delta^I_{X_j(t)} = m\right] = 1 - (1-\beta)^m \tag{2}$$

$$P\left[X_i(t+1) = R \mid X_i(t) = I\right] = \rho \tag{3}$$

i.e. the probability of a susceptible node to get infected in one week with m infected neighbors and the probability of an infected node to recover in one week.
The first simulation is run over a k-regular graph (Fig. 1) with:

- $|\mathcal{V}| = 500$ nodes

- $k = 4$

- time unit: 1 week

- simulation time: 15 weeks

- $\beta = 0.3$

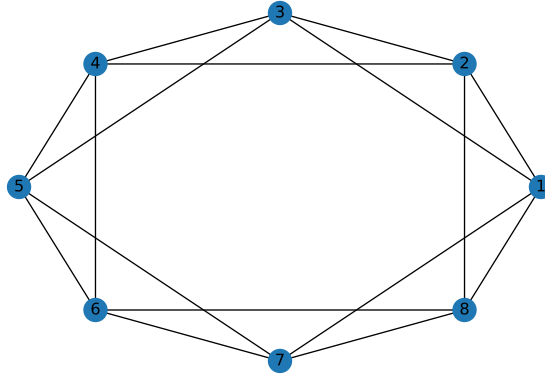- $\rho = 0.7$

- 10 initial random infected nodes

Figure 1: Example of a 4-regular graph with 8 nodes (each node has 4 neighbors).

We want to esimate:

- the number of newly infected people each week (Fig. 2)

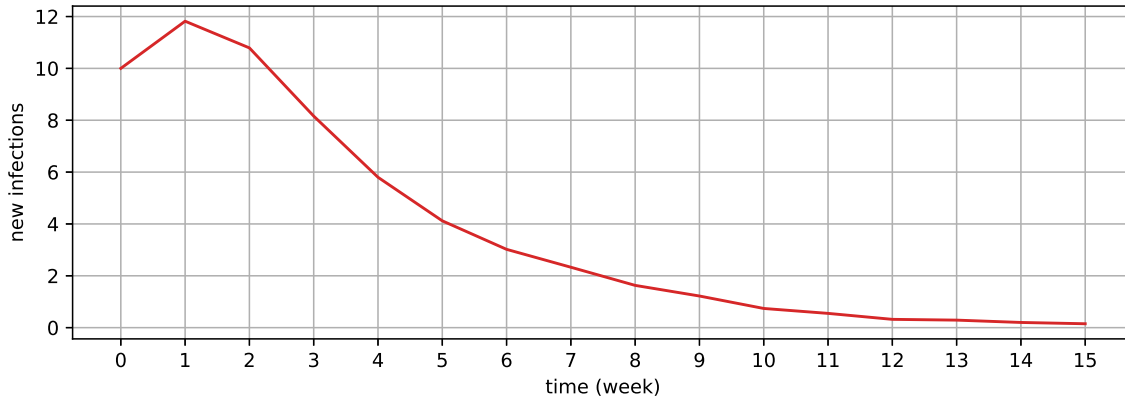- the number of people in each state (S, I, R) each week (Fig. 3)
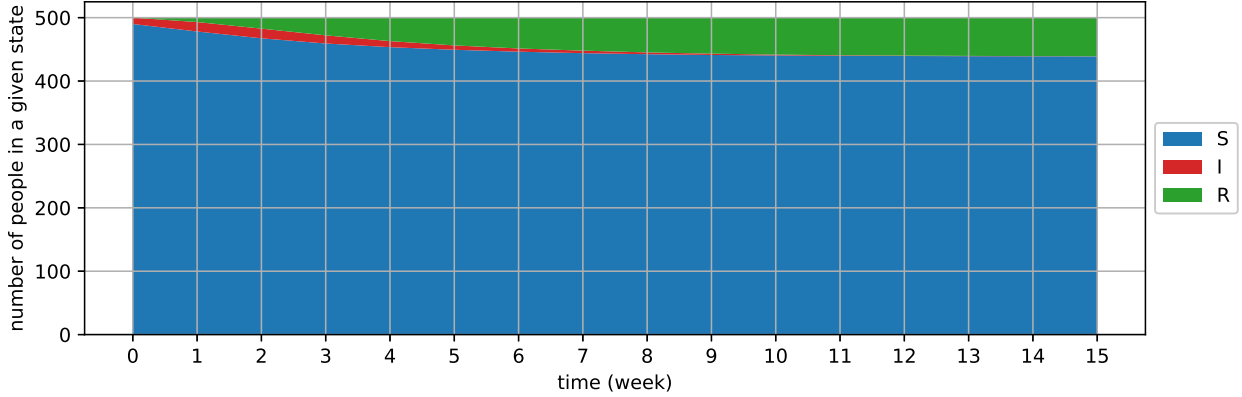

Figure 2: New infections per week

Figure 3: State distribution per week

1.2 Generate a random graph

Next step is the generation of a random graph: we will use the *preferential attachment model* (Fig. 4) with (approximate) average degree k.

This consists of:

- generating a complete graph with $k + 1$ nodes

- adding one node at a time with $\frac{k}{2}$ links to other nodes each, chosen with probability proportional to their degrees (thus the name *preferential*)

    - if k is odd, we can alternate $\left\lfloor \frac{k}{2} \right\rfloor$ and $\left\lceil \frac{k}{2} \right\rceil$
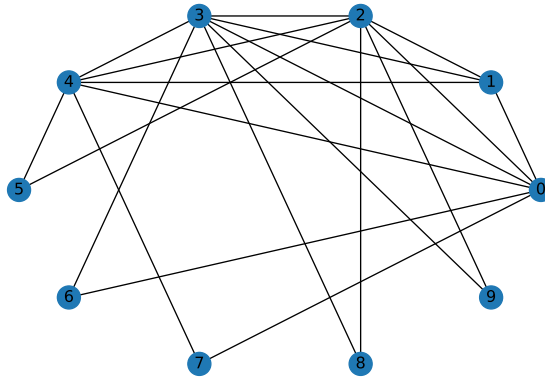

Figure 4: Example of a preferential attachment random graph with 10 nodes and average degree 4, we can note that nodes $\{0, 1, 2, 3, 4\}$ constitute a clique

2 Simulate a pandemic without vaccination

The first simulation on a random graph is done using the same epidemic model used in section 1.1.
The simulation runs on a preferential attachment random graph with:

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- $|\mathcal{V}| = 500$ nodes

- $k = 6$

- time unit: 1 week

- simulation time: 15 weeks

- $\beta = 0.3$

- $\rho = 0.7$

- 10 initial random infected nodes

We want to esimate:

- the number of newly infected people each week (Fig. 5)

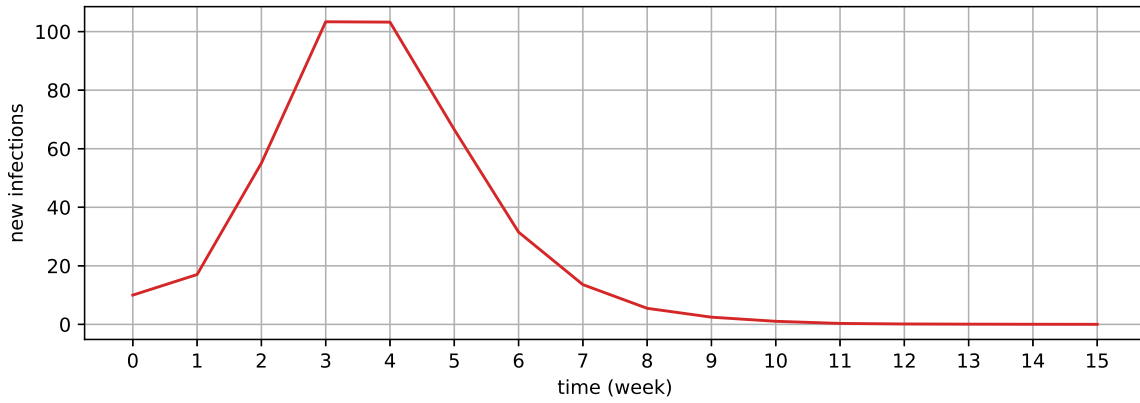- the number of people in each state (S, I, R) each week (Fig. 6)
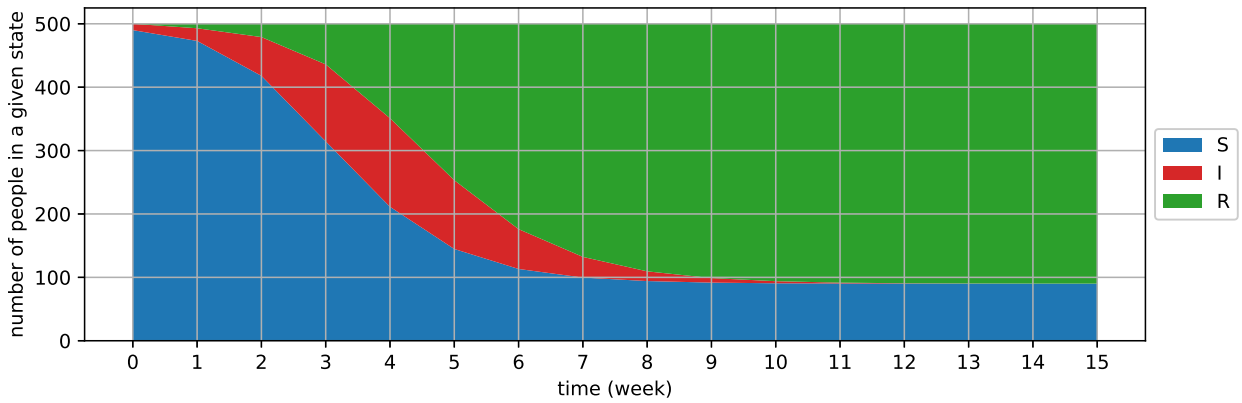
Figure 5: New infections per week

Figure 6: State distribution per week

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3 Simulate a pandemic with vaccination

The next simulation is done using an epidemic model similar to the one used in section 1.1, but with a new class V (Vaccinated).

Each week a portion of the non-vaccinated population is randomly chosen and vaccinated. We assume that a person who receives the vaccine becomes immediately not infected (even if infected at vaccination time) and not able to infect other people.

The simulation runs on a preferential attachment random graph with:

- $|\mathcal{V}| = 500$ nodes

- $k = 6$

- time unit: 1 week

- simulation time: 15 weeks

- $\beta = 0.3$

- $\rho = 0.7$

- 10 initial random infected nodes

- $\text{Vacc}(t) = [0, 5, 15, 25, 35, 45, 55, 60, 60, 60, 60, 60, 60, 60, 60]$

    - percentage of vaccinated population (with respect to the total population) each week

We want to esimate:

- the number of newly infected people each week with respect to the number of newly vaccinated people (Fig. 7)

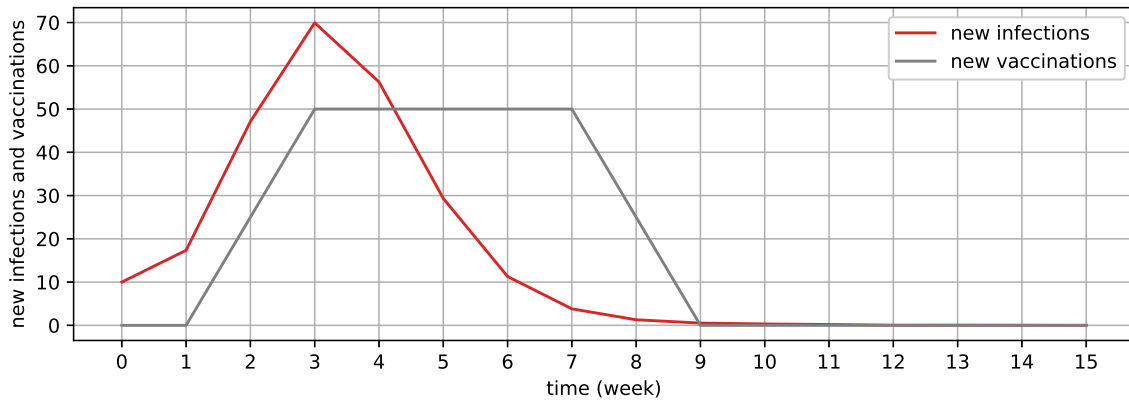- the number of people in each state (S, I, R, V) each week (Fig. 8)

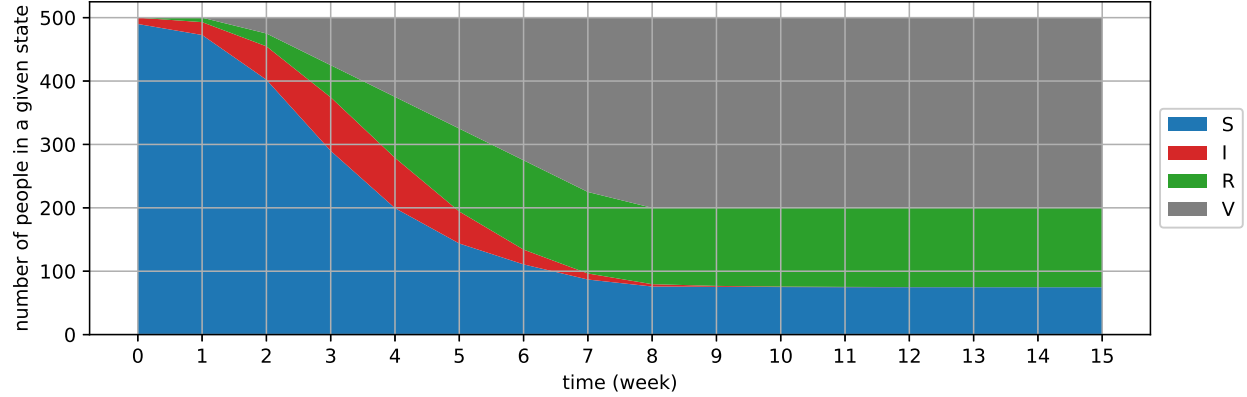Figure 7: New infections and new vaccination per week

Figure 8: State distribution per week

4 The H1N1 pandemic in Sweden 2009

Now we can use the method developed in section 3 to estimate some parameters of the H1N1 pandemic in Sweden.

Scaling down the population by a factor 10^4, the parameters of graph and simulation are:

- $|\mathcal{V}| = 934$ nodes

- k: unknown

- time unit: 1 week

- simulation time: 15 weeks (from week 42, 2009 to week 5, 2010)

- β: unknown

- ρ: unknown

- 1 initial random infected node

- $\text{Vacc}(t) = [5, 9, 16, 24, 32, 40, 47, 54, 59, 60, 60, 60, 60, 60, 60, 60]$[1]

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

    - (scaled) number of newly infected people each week[1]

To find the best-fitting values of k, β and ρ, we will use a gradient-based search starting with:

- $k_0 = 10$

- $\beta_0 = 0.3$

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[1]as reported by the Swedish Civil Contingencies Agency and the Swedish Institute for Communicable Disease Control

- $\rho_0 = 0.6$

and moving each time by:

- $\Delta k = 1$

- $\Delta \beta = 0.1$

- $\Delta \rho = 0.1$

For each parameter set, the number of newly infected people each week (I) is estimated, and to choose the best-fitting parameters the formula (4) is used.

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

The parameters' values found are:

- $k = 8$

- $\beta = 0.2$

- $\rho = 0.7$

With an RMSE of 7.29.
Finally, we want to esimate:

- the number of newly infected people each week with respect to the actual number of newly infected people (Fig. 9)

- the number of people in each state (S, I, R, V) each week (Fig. 10)
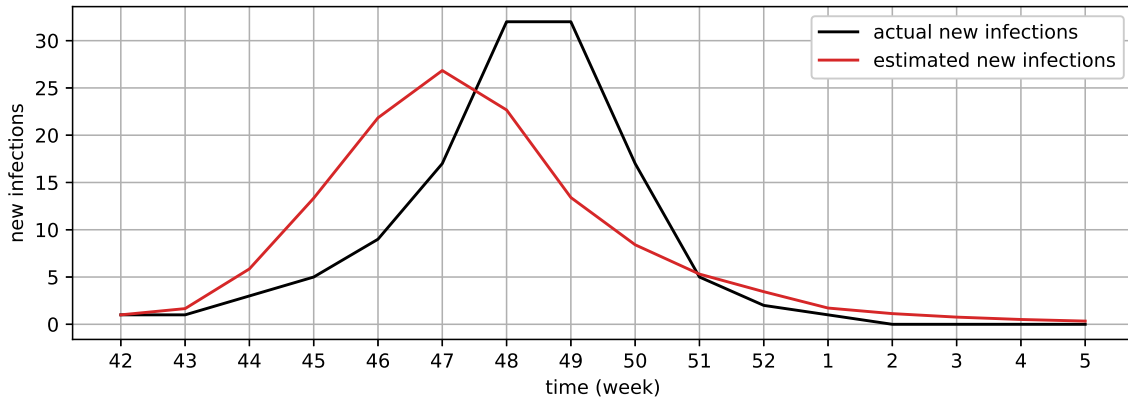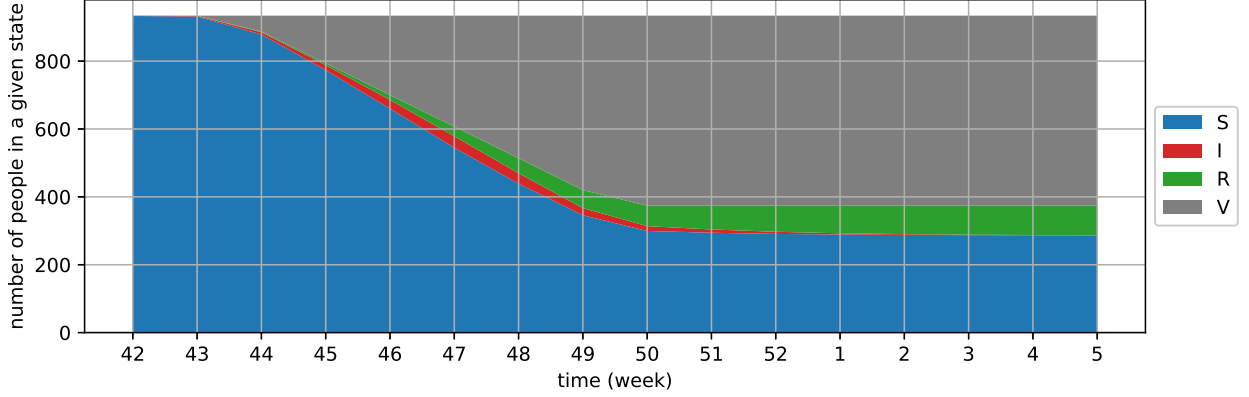

Figure 9: New infections per week

Figure 10: State distribution per week

5 Different graph approaches

Now we try to model Swedish population using different random graph models, and evaluating them as done in section 4.

This time we will use two different parameter discretization levels: we will lower deltas after a first convergence and rerun the simulation using the first result as starting point.

Also, now every epidemic run is simulated on a different graph (each one created with current given parameters).

We will use the following graph models:

- Preferential attachment (the same used earlier)

- Small world

- Erdős-Rényi

- Configuration

with initial paramters:

- $k_0 = 10$

- $\beta_0 = 0.3$

- $\rho_0 = 0.6$

- $p_0 = 0.002$ (Small world)

- $p_0 = 0.01$ (Erdős-Rényi)

and deltas:

- $\Delta k = \frac{2}{n_{it}}$

- $\Delta\beta = \frac{0.1}{n_{it}}$

- $\Delta\rho = \frac{0.1}{n_{it}}$

- $\Delta p = \frac{0.001}{n_{it}}$ (Small world)

- $\Delta p = \frac{0.002}{n_{it}}$ (Erdős-Rényi)

where n_{it} is the iteration number $\in \{1, 2\}$.

The parameters obtained are showed in Table 1.

Table 1: Parameters obtained from simulations

	β	ρ	k	p	RMSE
Preferential attachment	0.20	0.45	7		6.42
Small world	0.75	0.55	11	0.0120	8.72
Erdős-Rényi	0.20	0.70		0.0120	6.59
Configuration model	0.30	0.85	8		6.10

We can see from the results (Fig. 11), according to RMSEs (Fig. 12), that *Configuration* is the graph model that better approximates the Swedish population during the H1N1 pandemic.
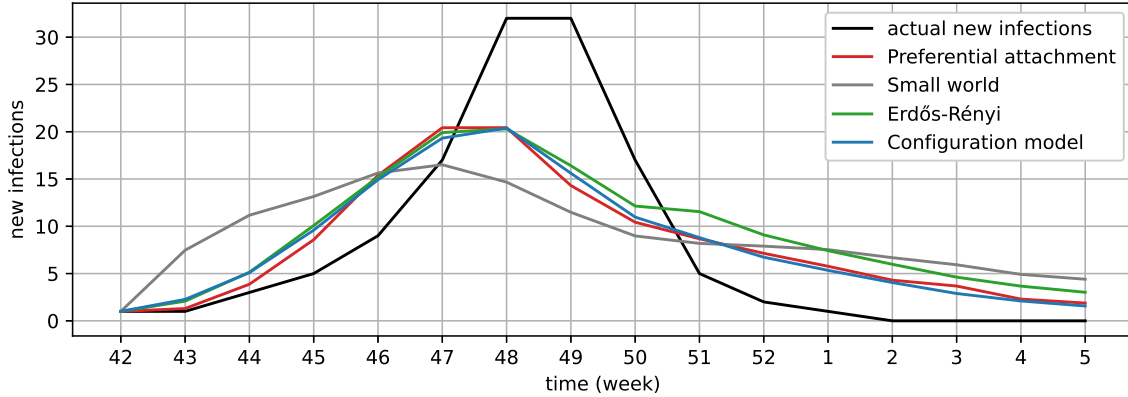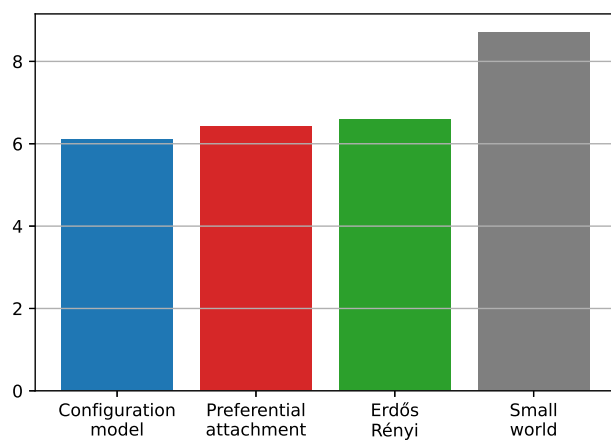

Figure 11: New infections per week

Figure 12: RMSEs of estimations of weekly infections