Stride*

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Abstract. A summary of explanations why some variables have influence on the results of simulations run with Stride and if they have an impact on the performance.

Keywords: Stride · Epidemiology · Simulations.

1 Simulations

This section contains the results of the simulation exercises using Stride and our interpretation of these results. Simulations were run using the STAN and pyStride controllers.

1.1 Stochastic variation

After running multiple simulations, using 10 and 100 seeds, it seems that the chance has a big influence over the results. The graph in figure 1 shows the two possible outcomes:

- Outbreak: The amount of infected people starts small but quickly starts to grow. Around 30000 people will be infected at the end.
- Extinction: A few people get infected (a maximum around 35) and the amount stays constant throughout the remaining time. Which is noticeable on figure 2.

Meaning it really depends on the first infected people. No other situations where, for example, only 10000 people were infected are present. With this configuration there's a $\pm$ 50% chance for an outbreak or extinction with this configuration.

Plotting the number of new cases per day, as seen in figure 3, shows us that in case of an outbreak the number of new cases per day has a distribution that can be approximated by a binomial distribution. It seems that the reason for this is the fact that at the beginning of an outbreak there are few infected people that can infect others. As time passes more people get infected and the number of new cases per day will thus increase as well, until a point is reached where there are more people left with a lower chance of getting infected, thus resulting in a lower number of new cases per day.

* Supported by organization COMP.

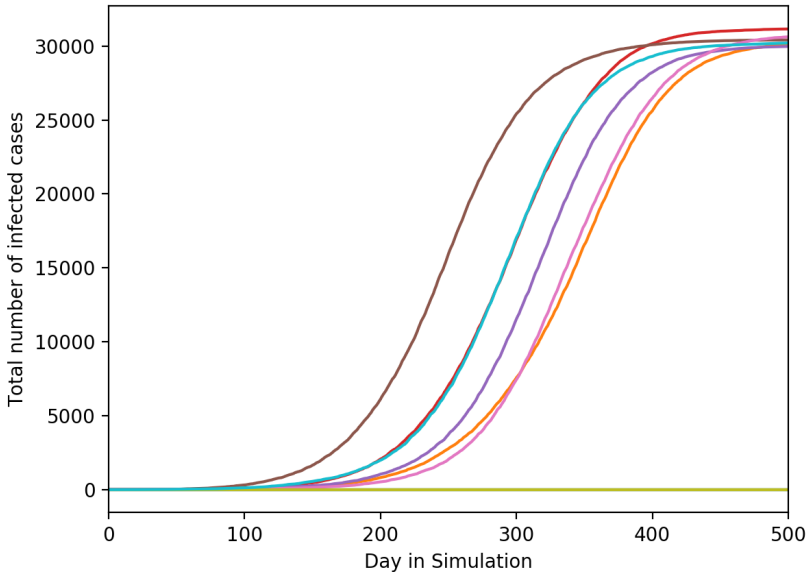

Fig. 1. Cumulative plot of 10 simulations using 10 random seeds

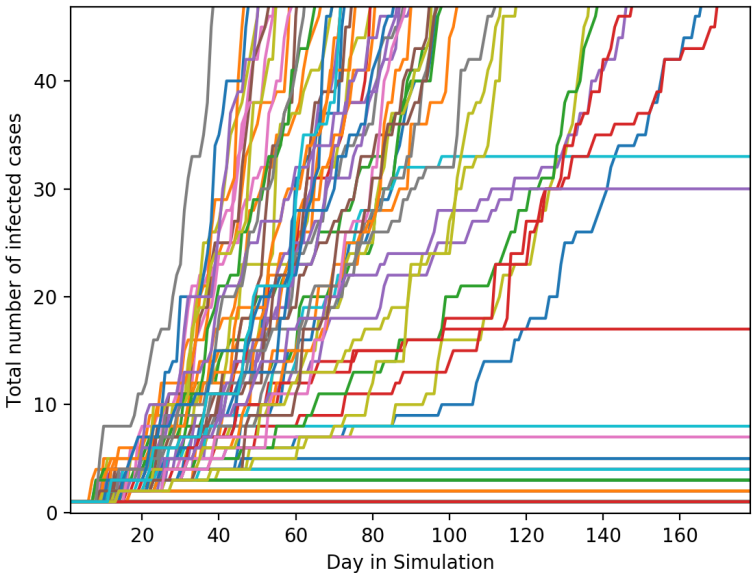

Fig. 2. Zoomed cumulative plot of 100 simulations using 100 random seeds

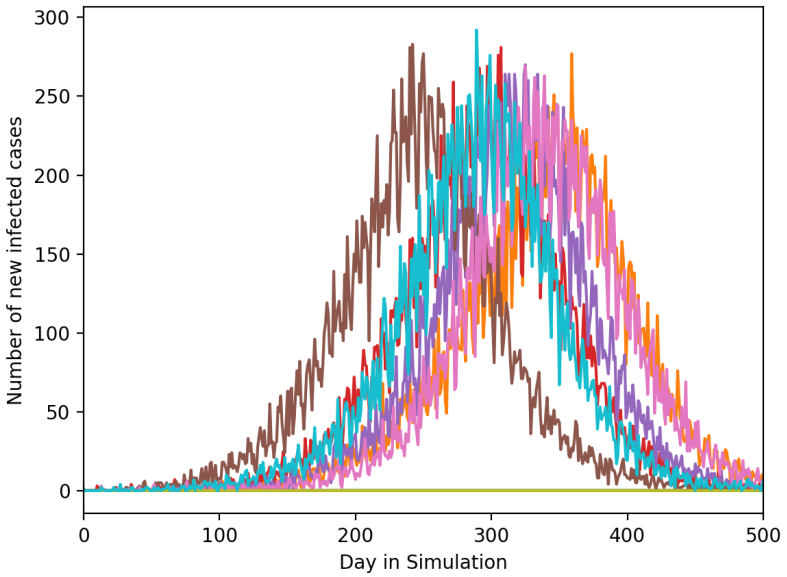

Fig. 3. Plot of amount of new cases per day in 10 simulations using 10 random seeds

1.2 Determining an extinction threshold

Plotting the final number of infected cases from the previous section in a histogram, results in figure 4. The two possible outcomes that could be seen in the previous section, can be seen here as well. Either the final frequency remains very low or it becomes very high. A very rough estimate of 2500 can be made for the extinction threshold based on this plot; however, a better estimate can be made using a different kind of plot.

Figure 5 shows a bar plot of the final number of cases for all of the simulations. When first presented with this plot, not much useful information can be derived from it; however, if the simulations are sorted based on their value and the plot is zoomed in, so the smaller values are visible, figure 6 is produced. Based on this graph a much better estimate can be made for the extinction threshold. In the middle of the plot there is a big difference in value between two simulations where a possible approximation of the threshold can be found. The simulations on the left side, which all have a frequency below $\pm$ 35 (which is a possible threshold), are the extinctions and the ones on the right are the outbreaks. For estimating an extinction threshold it is possible to use many different plots like for example the cumulative plot in figure 2. The possible threshold of $\pm$ 35 estimated earlier can also be seen there.

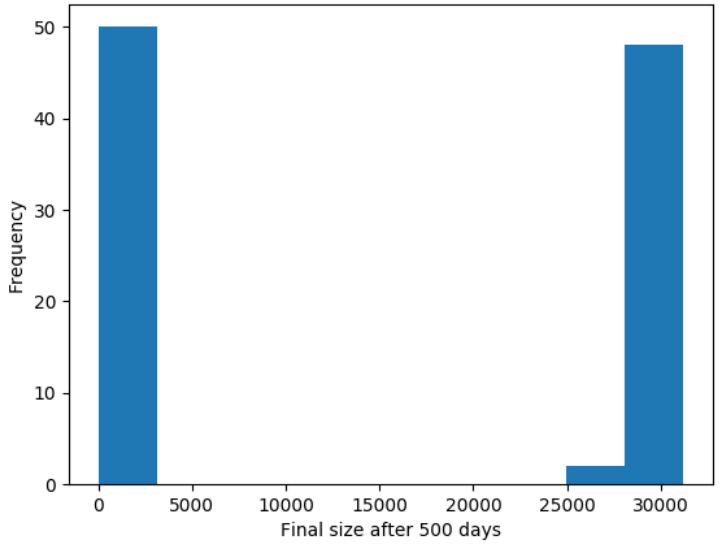

Fig. 4. Histogram

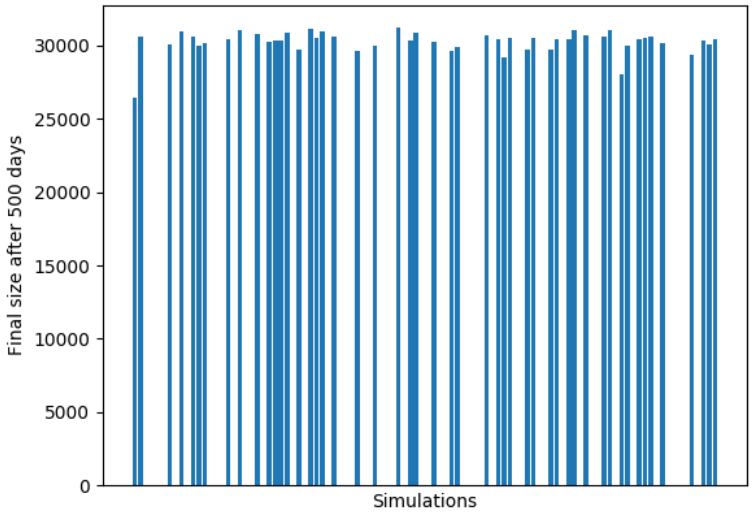

Fig. 5. Final numbers of infected cases of 100 simulations using 100 random seeds

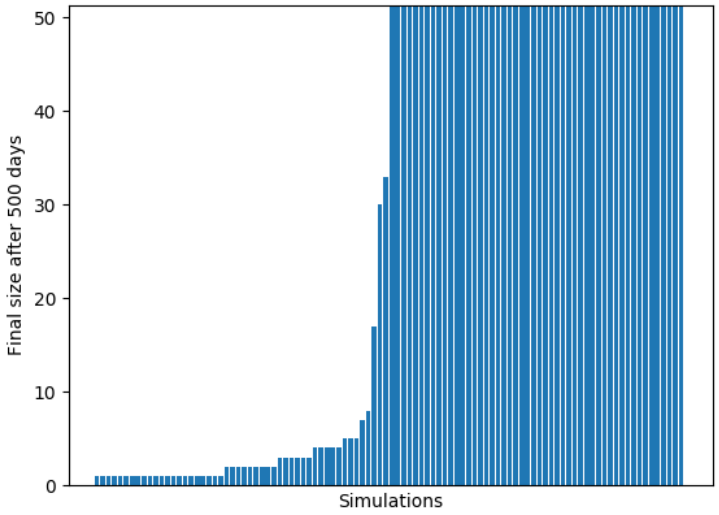

Fig. 6. Zoomed and sorted barplot of the final numbers of infected cases of 100 simulations using 100 random seeds

1.3 Estimating the immunity level

To find the best estimate for the immunity level of the population the vaccination profile was set to *None* and the immunity profile to *Random*. Then for each immunity level, ranging from 60% to 80%, 10 simulations were run using different seeds, and the average was then plotted to compare with the given plot. Immunity levels of 70% and 71%, figures 7 and 8 respectively, bore the most resemblance to the given plot.

Since these plots still differed quite a bit from the given plot, more simulations were run, this time for every 10th of a percentage between 70% and 71%, which can be seen plotted in figure 9. Several of these plots, like for example figure 10, looked like a good approximation. So taking into account the stochasticity of the simulations it is quite safe to say that the the immunity level of the given population is somewhere between 70% and 71%.

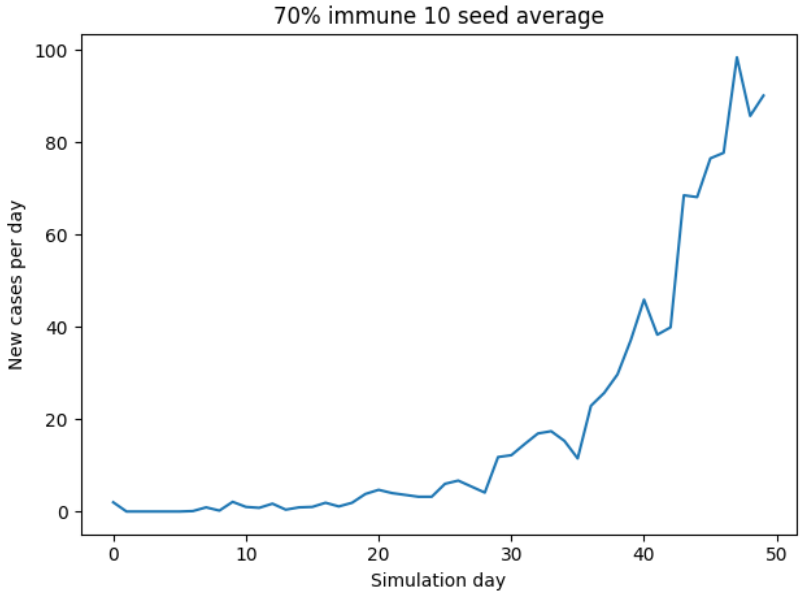

Fig. 7. New cases per day for 70% immunity level

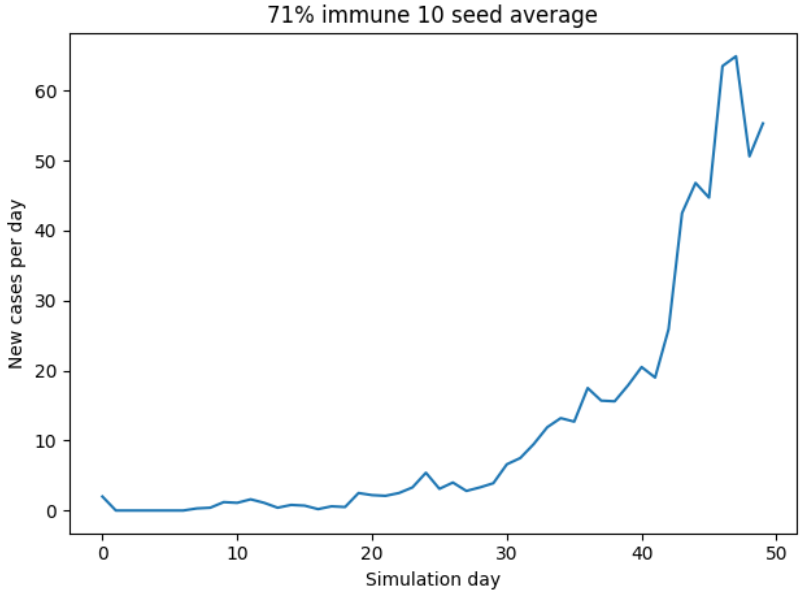

Fig. 8. New cases per day for 71% immunity level

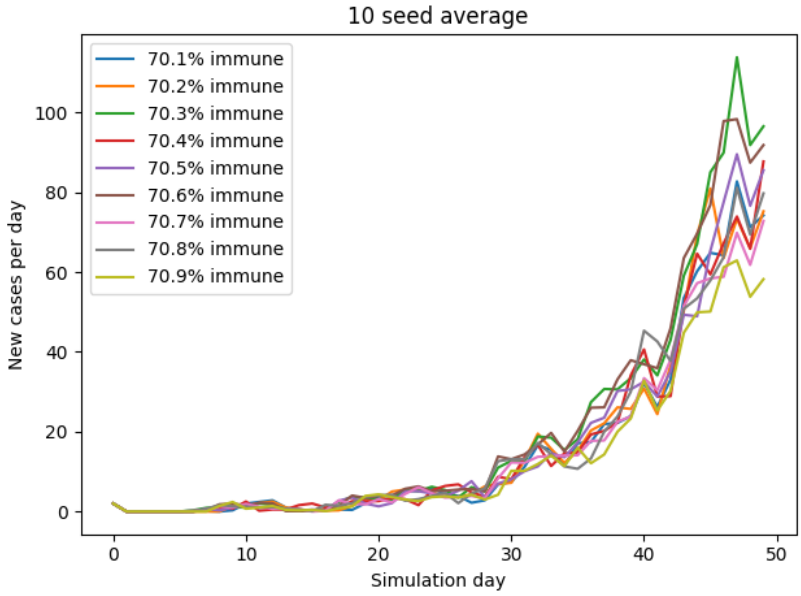

Fig. 9. New cases per day for immunity levels of 70.1% to 70.9%

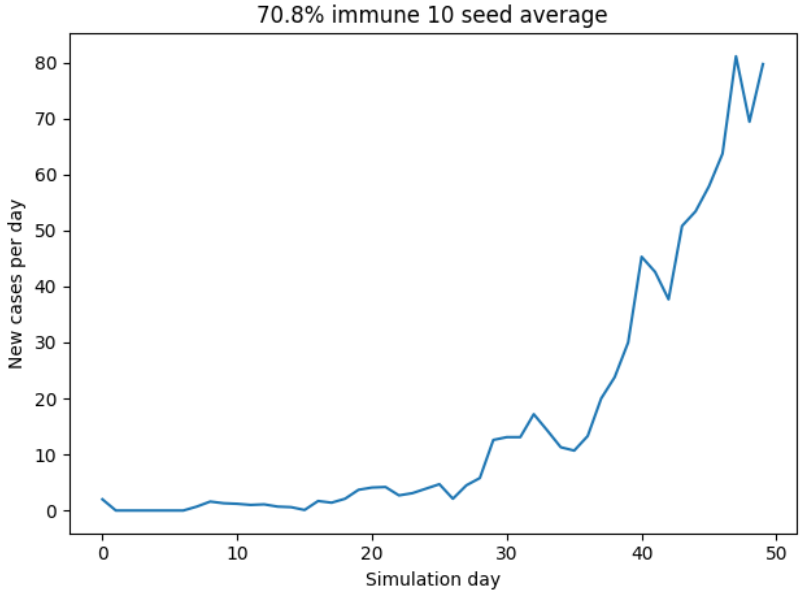

Fig. 10. New cases per day for 70.8% immunity level

1.4 Estimating R_0

During the simulations in the previous section a fixed value of 15 was used for the basic reproduction number, R_0. To see whether or not the conclusion of that section is dependant upon this value, the immunity level was fixed at a good approximation, i.e. 70,8% (figure 10), and simulations were run for R_0 ranging from 12 to 18, a range used for the basic reproduction number of measles.

Plotting the results of those simulations in one graph resulted in figure 11, which clearly shows that the results of the simulations and thus the conclusion of the previous section are indeed dependant upon the value for R_0. It is, however, noticeable that all the plots have similar oscillations, with the main difference being that plots of simulations with a higher R_0 value grow quicker.

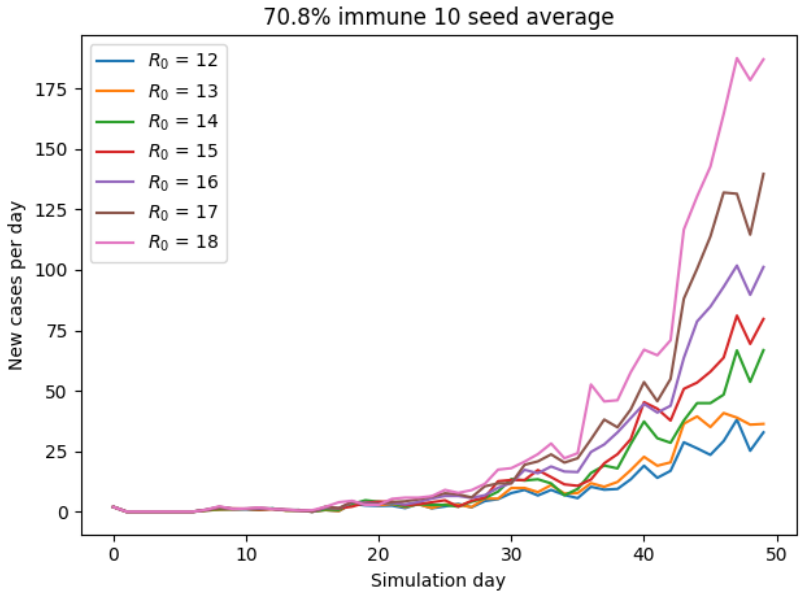

Fig. 11. New cases per day for 70.8% immunity level for several R_0

2 Population generation

Simulation results can also depend on the population in which a simulation is run. The following sections describe how they do that.

2.1 The influence of demography on epidemics

Two populations were created, named Region A and Region B. Both are quite similar, but what is important to notice is the difference in age. The people in Region A are much younger than those in Region B. The results from running simulations on both populations show that in 95% of the cases, an outbreak is present for Region A while Region B only shows outbreaks in 89% of the cases. So the chance for an outbreak is bigger in Region A with more younger people. Younger people are going out much more and to more different places which causes them to meet much more people than older people. This way the sickness can be spread more easily and that explains why the chance is higher in Region A.

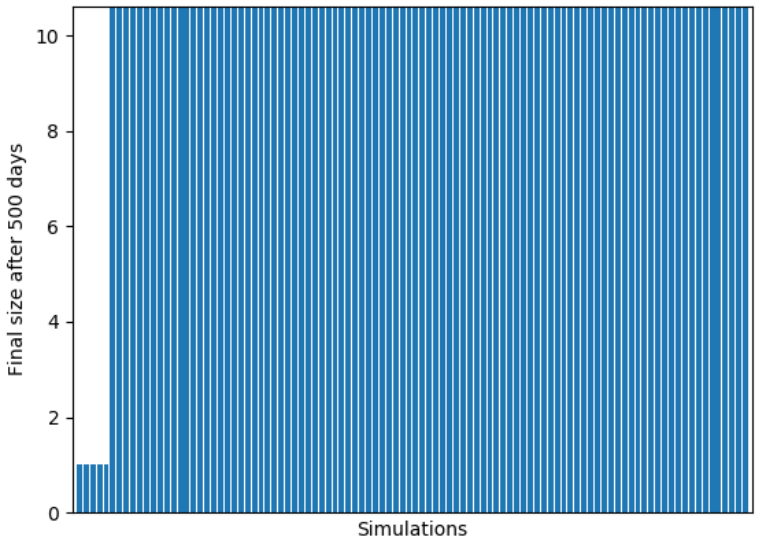

Fig. 12. Zoomed plot of final infected cases of Region A of 100 simulations using 100 random seeds

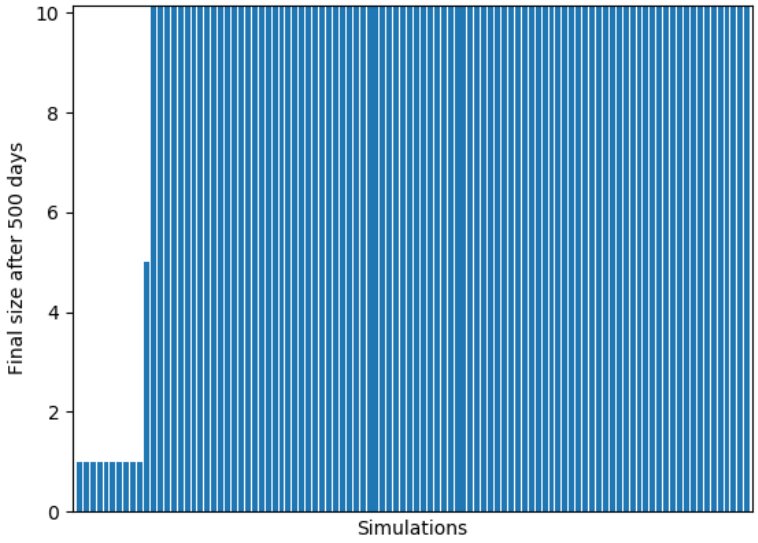

Fig. 13. Zoomed plot of final infected cases of Region B of 100 simulations using 100 random seeds

2.2 Vaccinating on campus

When students get vaccinated, the amount of new cases per day is more often 0 then when they aren't vaccinated. The line which represents the simulation with vaccination doesn't only have less spikes, the spikes it has, are also lower. That vaccination will cause the spread to go slower.

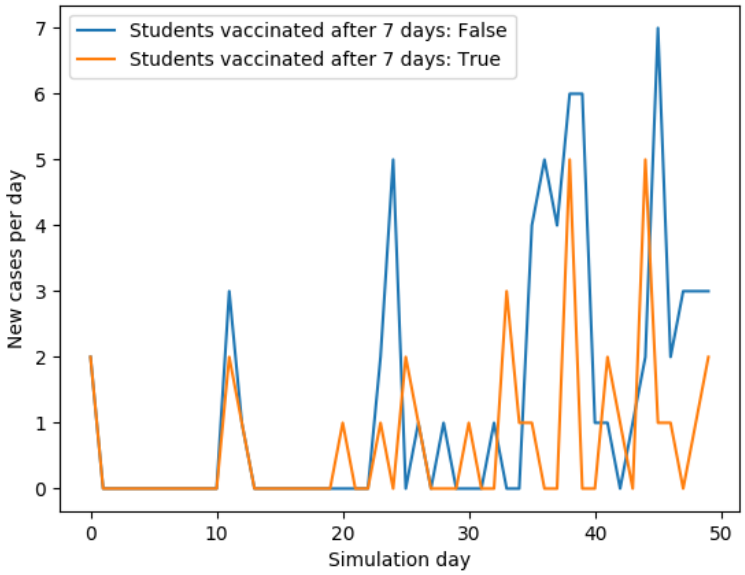

Fig. 14. New cases per day plot of 2 simulations with the same seed and one where students are vaccinated after 7 days

2.3 Commuting to work

The more people that have to commute to work, the more people they meet, the faster the disease will spread. This is visible in figure 15. If nobody has to go to their work space, so assuming they stay in the same city, the new cases will rise slow. If you don't meet a lot of new people, then passing the disease to someone new is much more difficult. The higher the amount of people that have to commute to work, the faster pikes of new cases for a day will appear. The peak stays the same, which is visible in figure 16. Eventually the same amount of people will get infected.

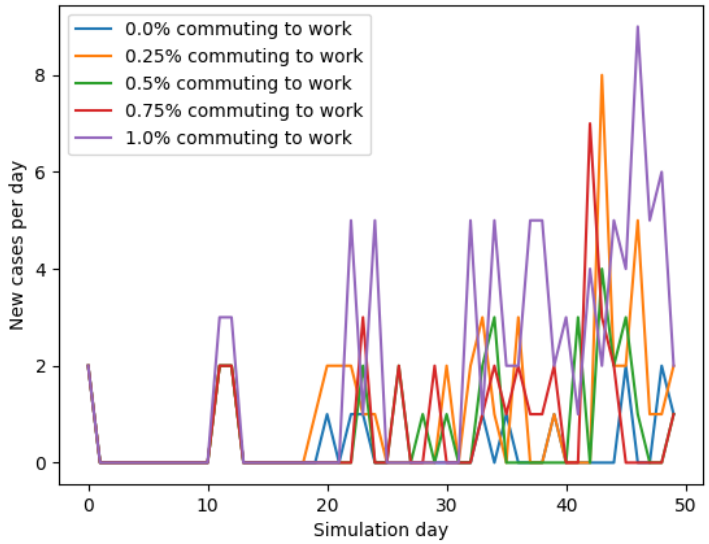

Fig. 15. Plots of new cases per day of 5 simulations with the same seed but different commuting percentage over 50 days

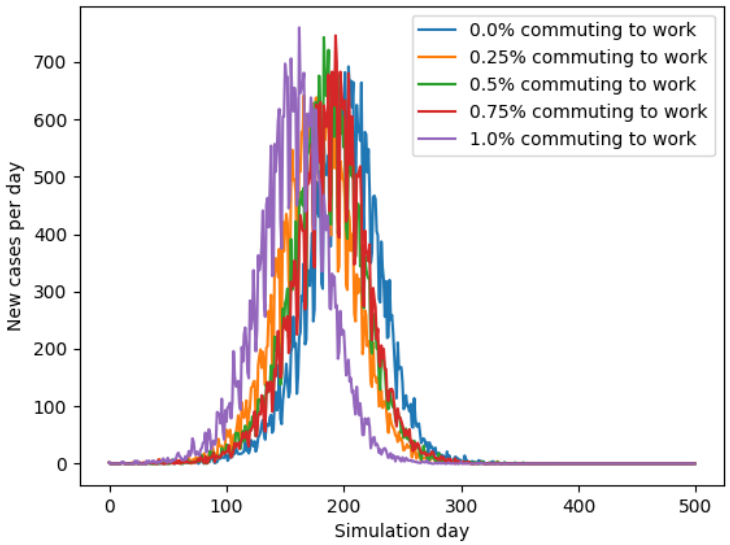

Fig. 16. Plots of new cases per day of 5 simulations with the same seed but different commuting percentage over 500 days

3 Performance profiling of sequential code

In this section we will discuss the results from the performance profiling with different parameters. For the profiling we disabled OpenMP to get the performance of the sequential code. We run the default configuration and change only the parameter and measure the wall clock time. We don't evaluate absolute measurements. The results shown are averages from 3 tests so that they are not interfered with other processes on the computer.

3.1 Simulated Days

In figure 17 we see that the amount of days is linearly proportional to execution time.

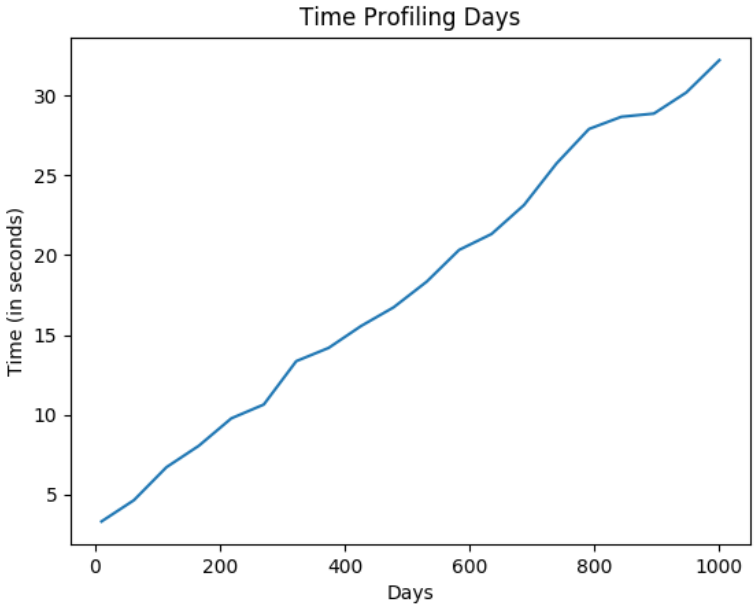

Fig. 17. Profiling plot days versus time

3.2 Population size

In figure 18 it also appears to be a linearly proportionality between the population size and time.

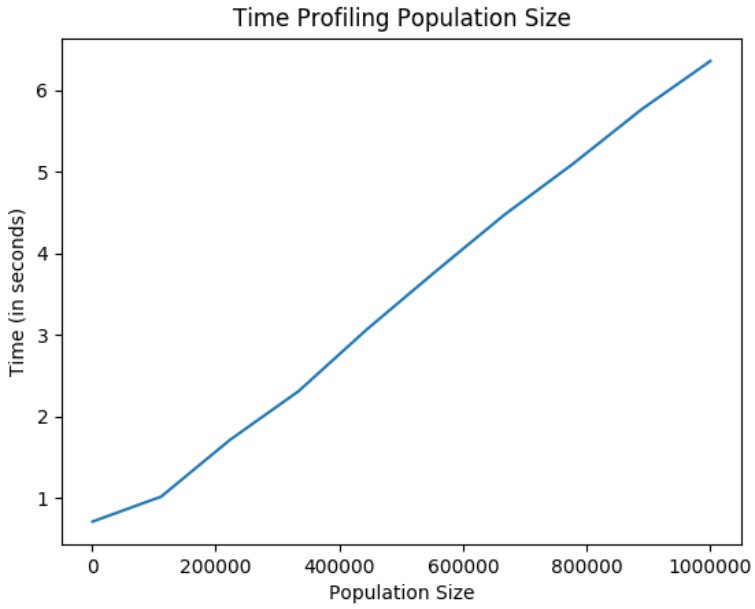

Fig. 18. Profiling plot population size versus time

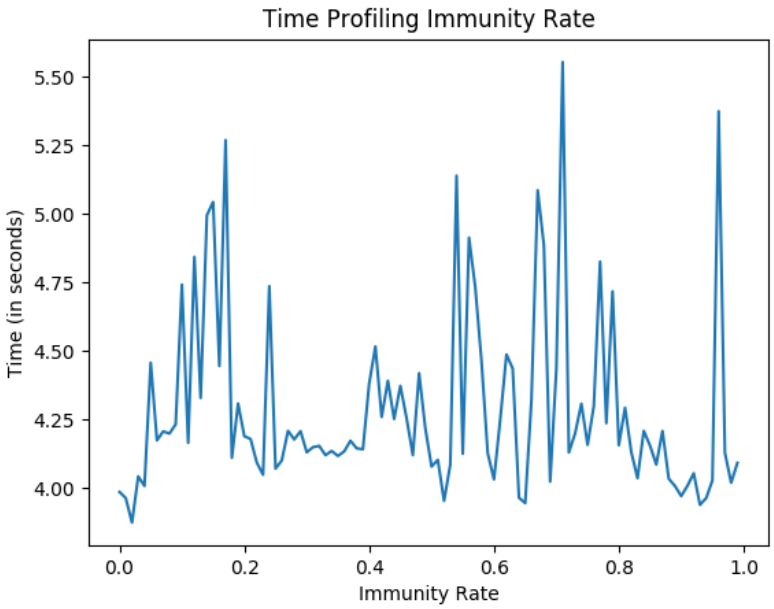

Fig. 19. Profiling plot immunity rate versus time

3.3 Immunity rate

In figure 19 we see that the differences with all immunity rates are minimal and not significant. Thus, the immunity rate doesn't affect the wall clock time of the simulation.

3.4 Seeding rate

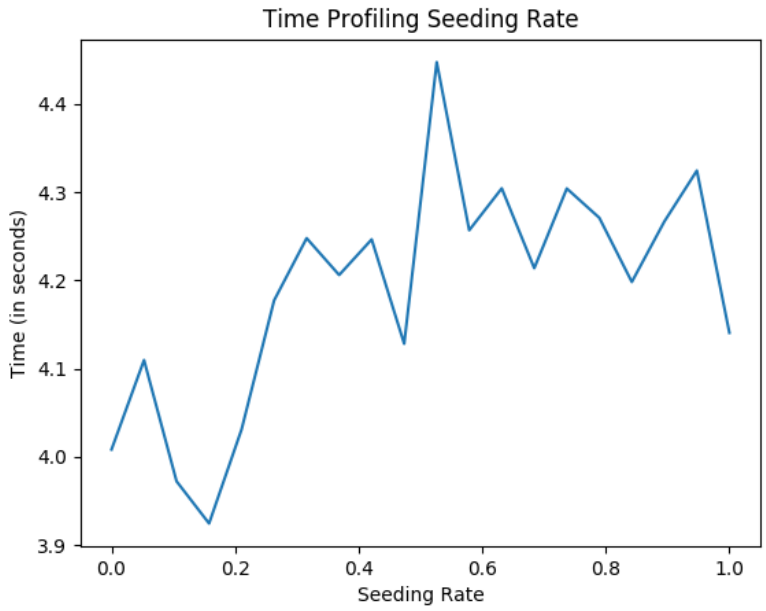

Fig. 20. Profiling plot seeding rate versus time

In figure 20 we see little differences between the execution times so we can conclude that the seeding rate solely has no direct influence to the execution time.

3.5 Contact log mode

Here we going to monitor the time that is needed for different levels of contact log. In figure 21 we see that 'All' and 'Susceptibles' require more time for simulations.

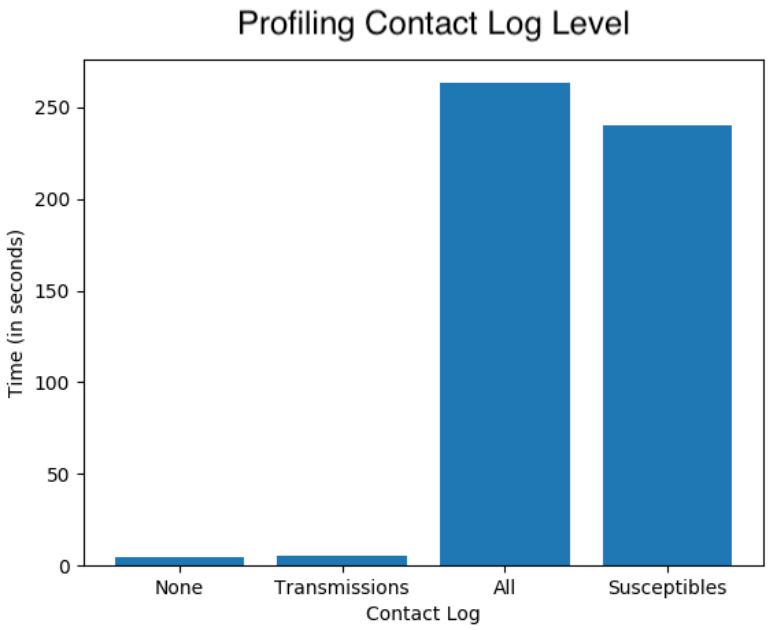

Fig. 21. Profiling plot time per type of contact log level