Simulation Paper

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Abstract. In this paper we will examine the Stride tool and discover its functionalities. We will discuss some findings about the use of different parameters, populations and more. In the end there is a briefly discussion of the performance of the program, a very important topic within computer related problems.

1 Simulation

1.1 Stochastic variation

We use the Stan (STochatsic ANalysis) controller to examine the influence of stochasticity on the results obtained from the simulation.
In Figure 1 the number of cummulatice cases per time-step is plotted. Here we can observe an exponantial grow of the number of cases througout time. This is not surprisingly because it can be deducted from common reason. If per time more people are affected, a larger contactpool is possibly infected. These people who are now new carriers of the disease will enter their personal contactpool and again more people will be reached.
Towards the end a flattening of the curve occurs. This can be explained because the population is obviously not infinite. At one point anyone who can be infected will effectively become a carrier of the disease.
The same explanation can explain the curve in Figure 2. Now the cases are not the cummulative ones but the number of new cases in each time-step. A similar course of the curve can be observed.

1.2 Determining an extinction threshold

In the previous section 1.1 (Stochastic variation) we found that extinction will influence the outcome. It is neccessary to be able to exclusively look at outbreaks. If we can find some threshold where there is a clear difference between large outbreaks and extinctions we can seperate the two scenarios. After creating a number (50 - KAN NOG WORDEN AANGEPAST) of simulations we can plot the total number of infected cases and their occurences. We used the file "stochastic_analysis.xml" for the simulations. After running the simulator the

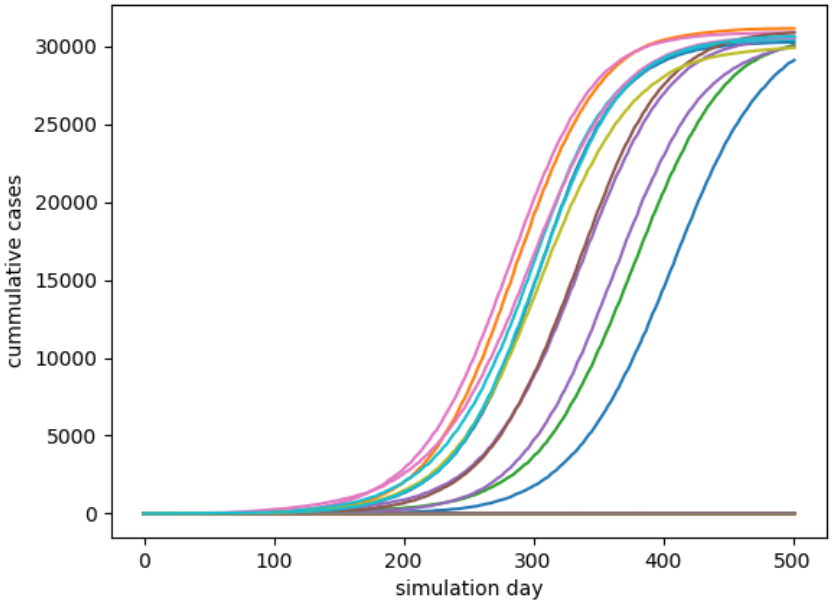


Fig. 1. Result of a number of stochastic runs. The figure displays the distribution of the number of cummulative cases per time-step.

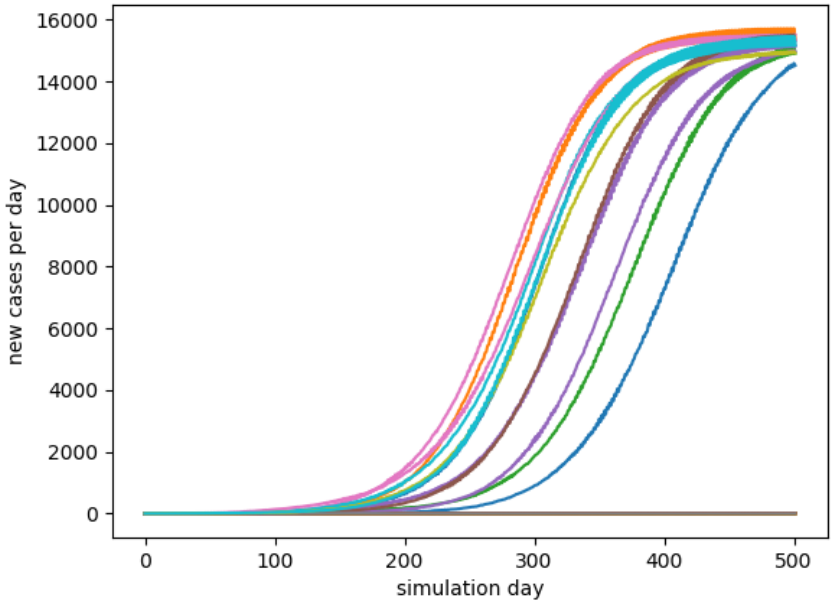
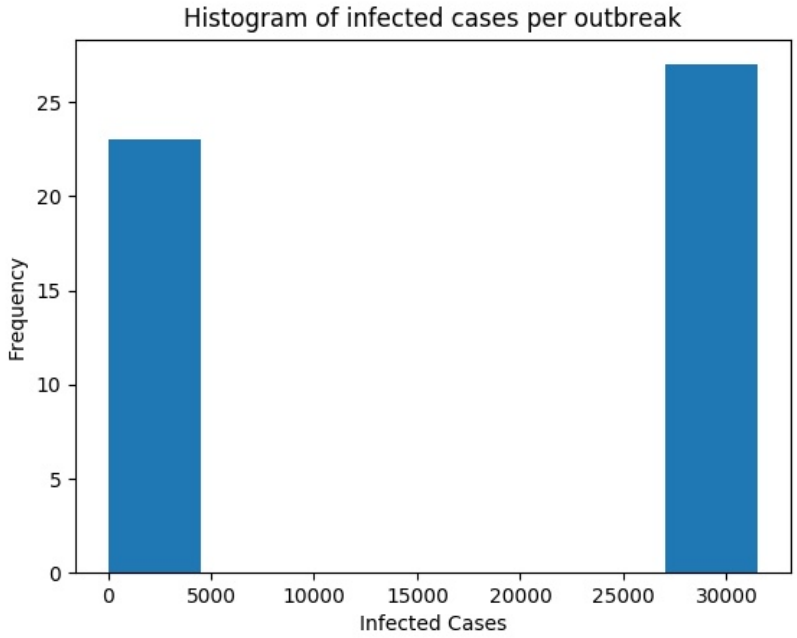
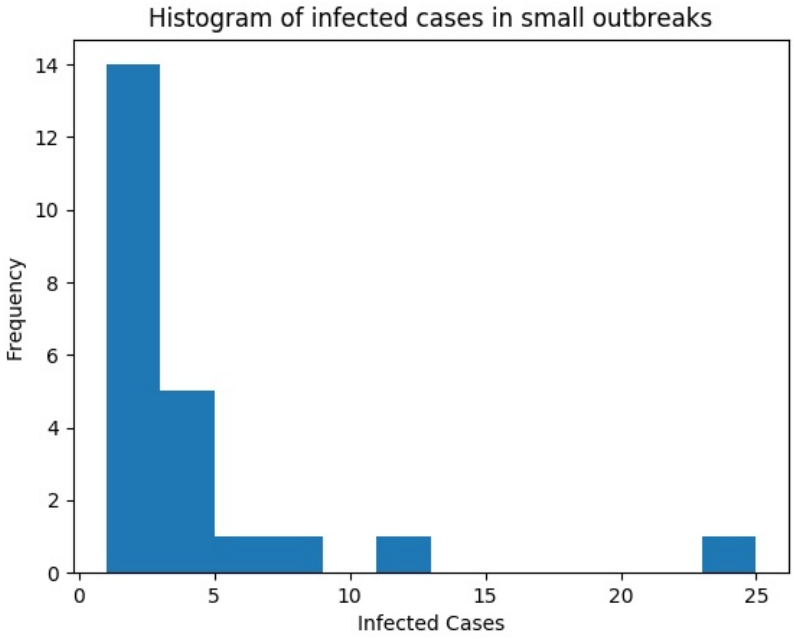


Fig. 2. Result of a number of stochastic runs. The figure displays the distribution of the number of new cases per time-step.

outcome is plotted in the histogram "extinction_all.jpg" where the frequency of the amount of infected cases is plotted.
There is a clear distinction between large outbreaks and smaller ones. The smaller ones are again plotted in the second histogram "extinction_small.jpg". There it can be noticed that small outbreaks are really small (25 maximum). Which can be called an extinction after 500 days. The threshold can be set between than 50 and 25 000. Either of those thresholds should eliminate all extinctions in this case.
A very low threshold might allow some extinctions to be passed while a high threshold might eliminate an outbreak. What can be noticed is the total lack of simulations between 100 and 25000 infected cases. But there can still be exceptions in the infected cases. A threshold of 1000 would be more than adequate. It will eliminate all extinctions while keeping the outbreaks.
It should be noted that this threshold will change for al lot of variables. Variables like time and population will affect the threshold. A new threshold should be determined for each simulation.





1.3 Estimating the immunity level

1.4 Estimating R_0

2 Population generation

2.1 Investigating the influence of demography on epidemics

2.2 Vaccinating on campus

2.3 Is commuting to work important for disease spread?

3 Performance profiling of sequential code

To study the performance of the code we will discuss a few parameters.
First we will choose a random number of days to run a simulation and look at the time needed to complete the algorithm.

Number of days	Time needed
10	00:00:03:192:028
50	00:00:04:827:135
150	00:00:09:313:779
500	00:00:22:090:867
1000	00:00:39:660:327

As could be expected, there is an increase in execution time when we take a larger amount of days. But surprisingly enough is the simulation even with 1000 days rapidly. This is because after a period of time everyone will be infected and thus no further computation is necessary for the remaining amount of days. Only increasing the number of days will not make a difference in the performance of the simulation.

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(days = 50)

Immunity rate	Time needed
0.2	00:00:04:869:367
0.4	00:00:04:873:811
0.6	00:00:04:966:409
0.8	00:00:05:035:361
0.99	00:00:04:921:399

Varying the immunity rate, there is not a significant difference in runtime for different configurations.

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