

Boğaziçi University

# IE 588 – Term Project Report

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10-1-2019

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## *1.Problem Description*

Diseases, especially infectious diseases, cause an enormous economic burden on the shoulders of both individuals and societies. When individuals are ill, they are required to take necessary drugs and medications to get recovered. Obviously, it will cost them some money. Moreover, diseases cause a loss of social-welfare either by decreasing the work-efficiencies of employees or hindering them from attending their job.

The cost of preventing a disease from spreading is considerably less than treating it. Therefore, public health services establish policies that aiming the prevention of the mass-spread diseases before they occur. Although vaccines do not provide hundred per cent protection against contagious diseases, they increase the immunization of individuals. Hence, the studies related to vaccines have a key role to maintain the public health. Thanks to the vaccines, people are not vulnerable anymore to the diseases that cause deadly catastrophic events in the past.

To be able to hold the number of incidents under control, public health services develop various vaccination strategies, and apply them even if the infection is not a threat currently. However, there are some rumors claiming vaccinations may have some serious side-effects on the health of people. Some people prefer not being vaccinated due to these rumors, and they stay vulnerable against these diseases.

At first glance it can be thought that unless a disease exists in a society, to choose not to be vaccinated will not cause any problem. However, nowadays, we are living in a global world, and contagious diseases are easily carried from one society to another. Moreover, since the spread rate of these diseases is excessively high among vulnerable people, it is likely to be infected for any vulnerable people in case of encountering disease causing factor. Due to this reason, when the number of vulnerable people exceeds a critical level, the spread of the disease may become unavoidable, and the disease starts spreading even among vaccinated people. After this point, the effects become irreversible rapidly, and it is required to be dealt with harsh consequences as a society. In order to avoid such a situation, it is vital to keep track of the number of vulnerable people in the society. In this way, how the number

of vulnerable people may affect the whole society can be foreseen, and necessary steps can be taken on time.

Measles, is one of the contagious diseases, of which some outbreaks were observed during the history. According to the available statistics, before the vaccine for the disease is developed, three to four million people were infected in the US annually. Moreover, even after the invention of the vaccine, the death rates connected to measles disease are around 5 per cent in some parts of the world where there is no available medical care. (“Measles History”) Additionally, there is no treatment for this disease, infected people remain sick for more than a week. Therefore, lack of work-force is an inevitable outcome of this disease in case of a new outbreak which in the end cause huge amount of loss of money. Due to the reasons mentioned above, for a society, it is good to know when a threat of measles outbreak would be on the table. Therefore, we present a perspective on how spread occurs and try to analyze the effect of initially vaccinated percentage on the final infected ratios. Meanwhile, we investigate the conditions allowing a possible intervention to stop or limit the outbreak.

## *2.Methodology*

Contagious diseases is hard to tackle with in that their speed of spread is proportional with the number of sick people in turn causing exponentially growing spread rate. Thus, anticipating the behavior of a contagious disease is especially crucial for both taking precautions and creating crisis scenarios.

To model spread of a disease, there are lots of tools that can be utilized. Systems modelling is commonly used in disease spread models. However, definition of stock variables requires homogeneity assumption. For example, system models assume that every individual in the susceptible stock has equal risk to catch the disease. In the case of highly contagious diseases, we know that close circle of the sick person is especially at high risk which is overlooked in the systems modelling. Moreover, people differ in their social nature. Number of people interacted during a day and number of close relationships for a person highly differ among population. Corresponding infection probabilities are also different for these two types of interactions. Thus, both probabilistic nature and heterogeneity of human social networks makes it harder to come up with an analytical solution without making further simplifications or assumptions.

Above mentioned reasons makes simulation a better option in that it is easy to implement this probabilistic nature to a simulation model. It allows to conduct different scenario analyses such as changing the initially vaccinated percentage to foresee the effect on total percentage of infected people in the end.

Among the simulation methodologies, agent based modeling is advantageous in that the interaction between the sick, susceptible and vaccinated people can easily be captured and reflected by its object oriented nature. It allows us to consider both random interactions among the people and close relations of people. This spread in two layers (one in a social network and the other is random between the people) can be observed and analyzed in ABM which also allows us to extend our model to include vaccine preferences of people depending on the total sick percentage in the population and the number of sick close relations. This type of extensions require decision making within an agent and suitable for ABM.

### *3. Model Description*

Initially, a representative network consisting of a thousand people is constructed.. Each individual in the society is connected to a definite number of other people, and a link between two people represents that these two people are in close relation. Random network is constructed to represent this social connections. Additionally, at each round, people get into interaction with random people. For each person in the society, the number of people randomly interacted is a normally distributed random variable. The disease spreads via both close relations but also random interactions between people. Obviously, the spread rate via close relations is considerably higher.

Before starting the simulation, specific percentage of the society is vaccinated, and one person is randomly selected to be infected. All of the infected people remain sick until the end of recovery period, and during the recovery period, they spread the disease as already explained above. Vaccine gives immunization to people during their life-time, so when they encounter with an infected person, they are less likely to get sick. On the other hand, once patients are recovered from the disease, they gain lifetime protection against the disease. At

this point, in order to avoid notion confusion, let us clarify that immune-vaccinated and susceptible-vulnerable word pairs are used interchangeably in the rest of the report.

In the simulation model, time ticks represents days. In any typical day in the simulation, first of all, it is decided which people will be infected in the next day by considering the current situation of the whole society. Then, following three steps are applied for each person sequentially:

- 1) If the person is sick, remaining days to be recovered is updated.
- 2) If it is decided that the person will be infected in the next day, the health condition of the person is altered to infected at the end of the day.
- 3) If the patient remained sick for average duration of disease, the sick person will recover from the disease and gains life-time protection.

The code performing the operations described above can be found in Appendix A.

In order to conduct the spreading process of the disease some parameters such as infection rate of the disease via close relation and random interaction, the effectiveness of the vaccine and the average recovery duration must be provided.

First of all, the studies of **Centers for Disease Control and Prevention(CDC)** declares that susceptible people will be infected with probability 90% in case of close relation with any infected person. (“Transmission of Measles”) Secondly, according to the **World Health Organization(WHO)**, “[t]he virus remains active and contagious in the air or on infected surfaces for up to 2 hours.” (“Measles”, WHO) Since time ticks represent days in the simulation, susceptible people will be infected in next day with probability  $0.0833$  ( $2 \text{ hours} / 24 \text{ hours}$ ).

According to the CDC, the vaccine provides 97% protection against the infection. Hence, for immune people, while the chance of being infected through close relations decreases to 2.7%, it decreases to 0.25% via random interactions. (“Measles Vaccination”)

Finally, CDC denotes that the average recovery period for the disease is 8 days. (“Transmission of Measles”) The first 4 days of the disease can be considered incubation period. During this period, although infected people can spread the disease, they do not show

any specific sign of sickness. In the other 4 days, the indications of the sickness appears. For such a contagious disease, it is reasonable to decrease the spreading chance during the second half of the disease. However, since this change did not cause any significant change in the behaviour of the original model, analyses are conducted via utilizing the original model in order to simplify the processes. The updated version of the code can be found in Appendix B-1.

#### 4. Validation & Verification

To verify our model we followed a systematic approach. First, we conducted tests with one or two nodes to verify the agent procedures. Secondly, we tried to find the intervals for the parameters chosen with which the model still works. Average node degree represents the average number of close relations of a person. Below table shows how the initially %96 vaccinated population behaves under different average node degrees. It is clear that after 12 the model converges to having almost 100% sick. However, it is not reasonable to assume an average person have more than eight close relations, thus we assumed average node degree of 3. Note that model still gives different results between [2,12] however we recommend to use this parameter within the ranges of [2,8] to get reasonable results.

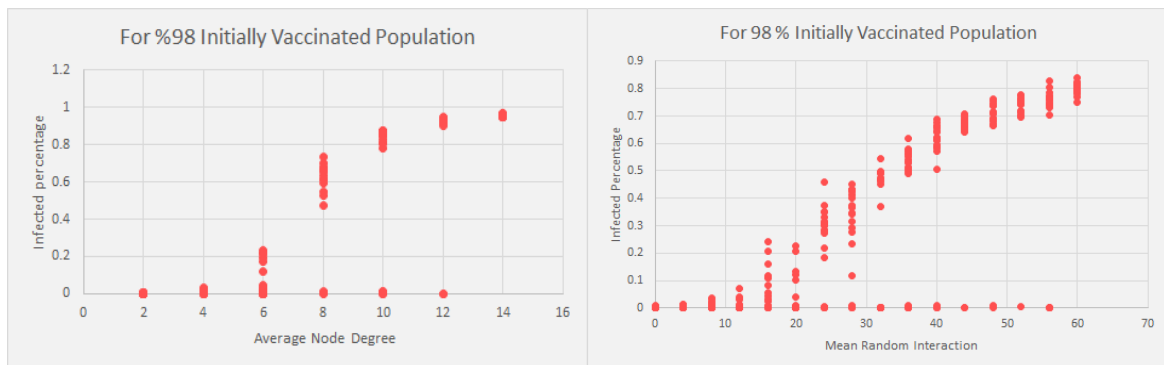


Figure 1 : Sensitivity analysis for average node degree and mean random interactions.

Number of random interactions that one person have is a normally distributed random variable with provided mean and standard deviation parameters. For the mean random interaction parameter model still gives different results but since it is not reasonable to end up with more than 30% sick people for such high vaccinated rate we recommend the use of this parameter within the range of [5,25]. Having less than 5 random interaction still gives results but it overlooks the two level spread nature that we build. Thus for this model it is better to use the mean parameter more than 5. Standard deviation parameter seems like having no

effect provided that it is less than the mean parameter. Further investigation of the parameter effects can be found in the global sensitivity analysis in the Experimental Results section.

If we compare the behavioral results of the model with the real life data from the previous measles epidemics, we see that spread rate of the disease and effectiveness of the vaccine matches with real life data. (İrsoy, Özcan 2019) Moreover, we chose the infectiousness rates from the reliable sources such as Centers for Disease Control and Prevention(CDC) and World Health Organization (WHO). This gives us confident to play with the model and do some deductions in that even if the quantitative predictions lack the precision, the behavior of the model seems valid for the real life.

## *5. Experimental Results & Discussion*

For the first part, local sensitivity analysis of the initially vaccinated percentage parameter is conducted. Initially vaccinated percentage ranging from 9.9 to 99.9 following parameters collected to conduct the analysis;

- Infected percentage among susceptible population
- Infected percentage among immune population
- Infected percentage among whole population
- Time passed until infection stops
- Maximum percentage of the sick people

Note that mean random interaction is 5, standard deviation of random interaction number is 2 and average node degree is 5 for all of these runs.

Scatter plots for the first three outputs are as follows;



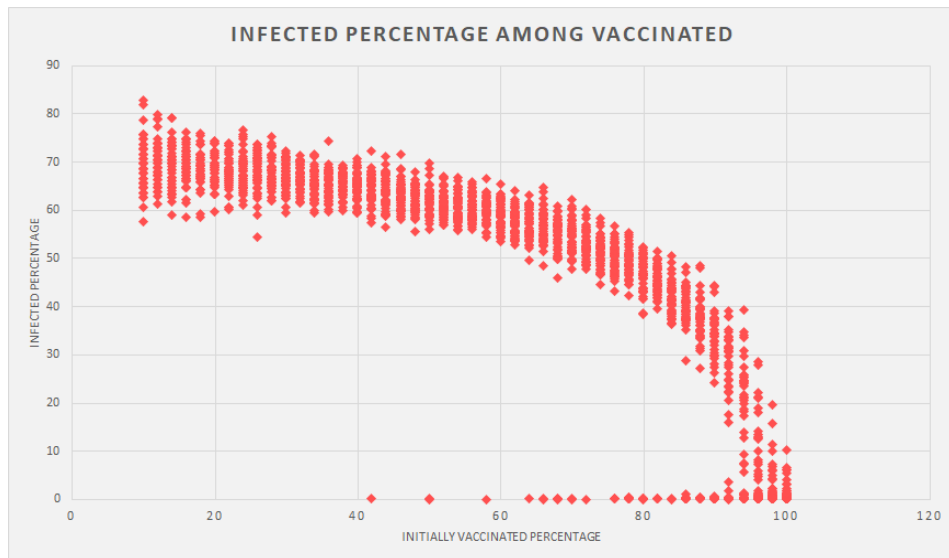


Figure 2 : Scatterplot of infected ratio among immune population.

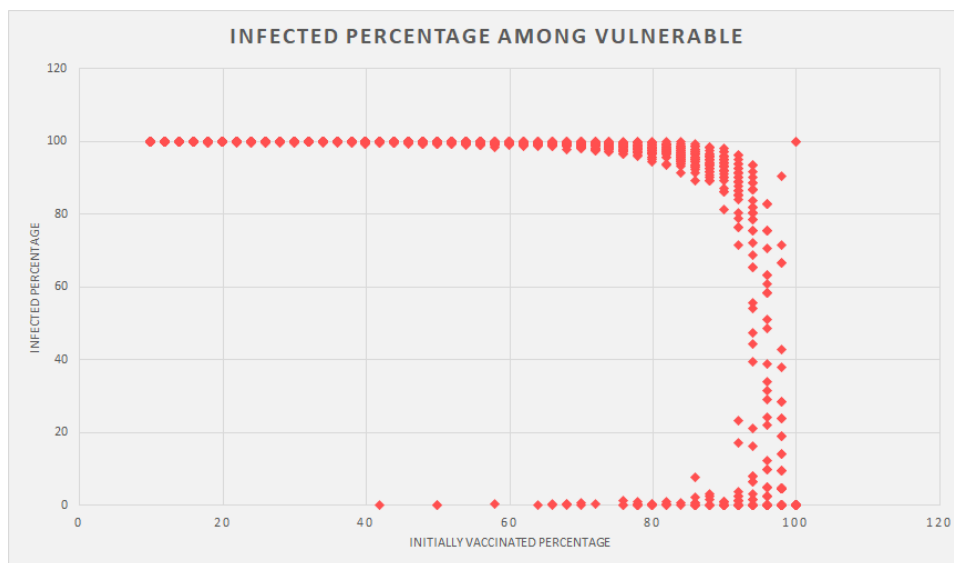


Figure 3 : Scatterplot of infected ratio among susceptible population.

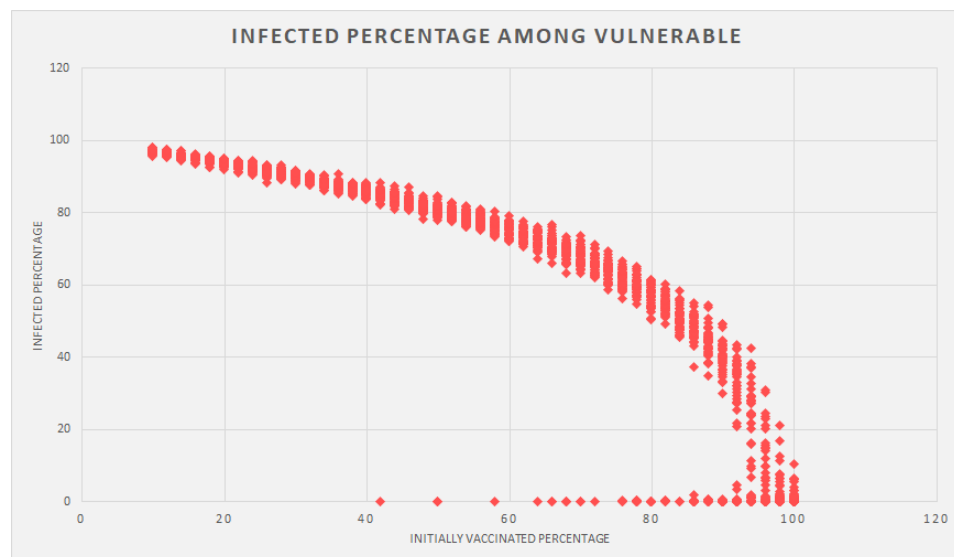


Figure 4 : Scatterplot of infected ratio among mixed population

Looking at the scatter plots we see a clear bifurcation as initially vaccinated percentage decreases. This shows that for the medium levels of initially vaccinated percentage, we have two possible scenarios i.e. spread either starts and dominates after one person or it stops before jumping to other people. This pattern observed is also a validation of the current model for measles since it is consistent with the other agent-based infection spread models. This bifurcation can also be observed in the density graphs in Appendix C-1. Although for the higher vaccinated percentages there are more than two peaks, densities converge to double peak which represents the before mentioned two scenarios.

When we compare the spread of the disease among vaccinated and vulnerable populations we can see that disease spread in the vulnerable population more easily. Although it is a trivial result below the 80% vaccination almost every vulnerable person seems to get infected in case of a spread which shows that susceptibles are the main target of the contagion. Moreover, when the initially vaccinated percentage drops we see that infected percentage among immune population also increases significantly. Remember that we built this model assuming that vaccine provides 97% protection while as the initially vaccinated population decreases the effectiveness of the vaccine is badly affected.

A non-linear relationship between initially vaccinated percentage and infected percentage is observed for all graphs. This non-linear nature can be clearly observed from the graphs and boxplots comparing the mean infected rates for the specific initially vaccinated percentages in the Appendix C-2.

The percentage changes of the infected ratio among all three populations depending on the percentage change in the initially vaccinated percentage are given as a table in the Appendix C-3. These tables also represent the non-linear spread nature of the disease. Notice that base value is taken as 99.9% initially vaccinated population and percentage changes are calculated from that base value.

By analyzing the maximum number of people who are sick at the same time in Figure 5, we can make some inferences about what percentage of the society will be infected eventually. When we analyze the graph below it can be observed that when max sick

percentage is between 0% and 10%, the increase in the infected percentage for whole population is drastic. When the spread rate is at these levels, taking the necessary precautions becomes vital to decrease the spreading rate of the disease. Moreover, applying preventions to oncoming measles outbreak will be easier at these levels. In Appendix D, it can be seen how the relation between max sick percentage and infected percentage changes for different percentages of vaccinated people.

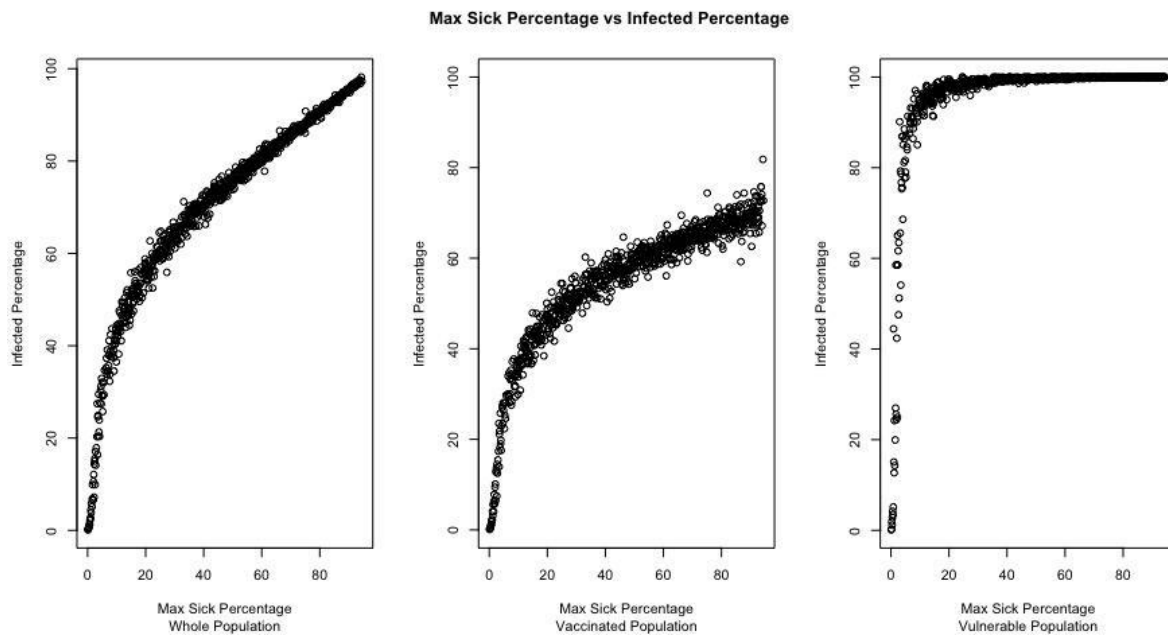


Figure 5 : Scatterplots of reached maximum sick person percentage vs infected percentage.

Analyzing passing average time until infection stops allowed us to make further inferences. When majority of the society is vaccinated, most of the time, disease can not spread. Therefore, infection disappears in a short time period. If the percentage of vaccinated people is decreased gradually, infection can obtain the chance of spreading. However, in the beginning, since significant proportion of the society is still vaccinated, the spread speed of the infection is considerably less. Thus, it can be concluded that there is still chance to interfere with the infection. On the contrary, if the percentage of vaccinated people is less than a certain level, the infection pops in a short time interval, and it turns into an outbreak. For such cases, the chance of stopping the infection can become very low. The related graphs indicating this relation can be seen in Appendix E.

For the second part we conducted a global sensitivity analysis. Initially vaccinated percentage is taken as policies with 10 different levels. For the scenarios, two different levels for mean and standard deviation of random interactions and three levels for average node degree are chosen which constitutes 12 different scenarios. Infected percentage of the whole population is taken as a performance measure. Corresponding levels for the parameters as follows;

- Initially infected percentage [65, 75, 80, 85, 87.5, 90, 92.5, 95, 97, 99.6]
- Mean of random interactions [5, 7]
- Sd. of random interactions [2, 4]
- Average node degree [3, 5, 7]

Three dimensional graph of the infected percentage on different scenarios and policies is provided below.

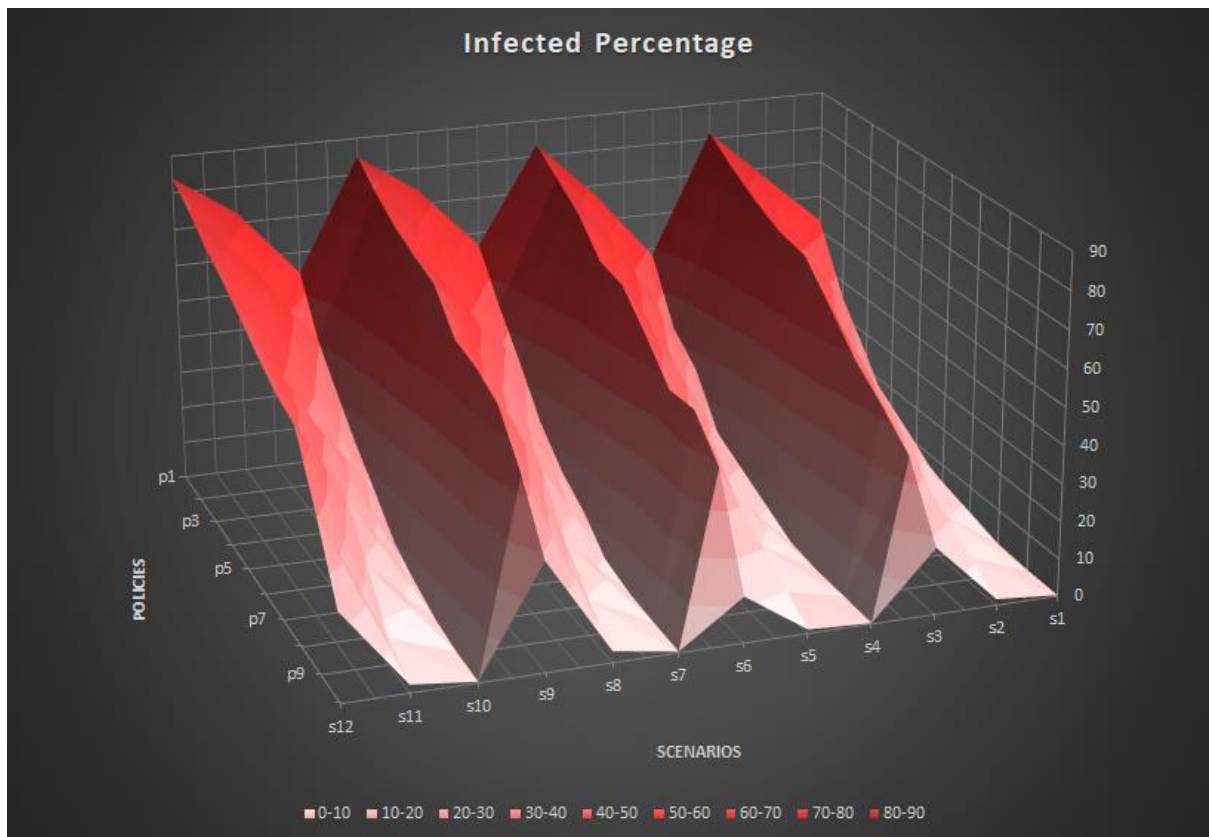


Figure 6 : Infected ratios in different scenarios and policies.

From the Figure 6 it is easy to say that policies seem to have a constant effect which is the ratio of infected people decreases as the initially vaccinated percentage increase which is a trivial observation. The graph can be converted in the Table 1 form below which allows to observe the cause of peaks in the scenario parameters.

	Rand-mean	5	5	5	5	5	5	7	7	7	7	7	7
	Rand-sd	2	2	2	4	4	4	2	2	2	4	4	4
	Close links	3	5	7	3	5	7	3	5	7	3	5	7
Initially vac.		s1	s2	s3	s4	s5	s6	s7	s8	s9	s10	s11	s12
65	p1	52.864	67.13	81.676	48.208	67.332	83.176	56.528	73.716	84.832	54.274	72.812	84.07
75	p2	35.44	53.948	76.342	32.306	58.186	78.428	44.588	65.756	79.662	40.486	62.396	80.17
80	p3	24.048	50.19	71.816	25.866	51.472	73.496	34.382	53.918	75.31	31.844	58.446	75.38
85	p4	11.722	41.692	68.304	12.932	43.226	65.564	23.094	51.56	72.52	23.644	49.734	71.942
87.5	p5	9.902	34.364	66.894	5.456	36.176	64.202	15.466	41.418	70.318	16.726	39.548	67.642
90	p6	3.78	27.55	58.316	4.056	32.232	56.304	10.602	34.63	61.086	9.11	39.194	63.08
92.5	p7	1.63	22.9	49.264	1.638	17.466	47.506	3.54	30.386	59.428	5.352	29.974	59.04
95	p8	0.894	11.78	42.88	0.622	10.538	48.204	1.718	18.124	55.622	2.364	18.684	56.83
97	p9	0.354	5.978	35.482	0.548	4.13	39.138	0.894	9.484	44.044	0.792	7.052	40.984
99.6	p10	0.272	1.644	17.698	0.242	1.044	12.202	0.346	3	28.672	0.308	2.188	23.242

Table 1 : Table is colored according to infection rate values, all values are considered together.

From the Table 1 it seems that average node degree (i.e. number of close links) dominates among the scenario parameters. To illustrate further we can arrange the table in increasing average node degree and observe each row separately.

	Rand-mean	5	7	5	7	5	7	5	7	5	7	5	7
	Rand-sd	2	2	4	4	2	2	4	4	2	2	4	4
	Close links	3	3	3	3	5	5	5	5	7	7	7	7
Initially vac.		s1	s7	s4	s10	s2	s8	s5	s11	s3	s9	s6	s12
65	p1	52.864	56.528	48.208	54.274	67.13	73.716	67.332	72.812	81.676	84.832	83.176	84.07
75	p2	35.44	44.588	32.306	40.486	53.948	65.756	58.186	62.396	76.342	79.662	78.428	80.17
80	p3	24.048	34.382	25.866	31.844	50.19	53.918	51.472	58.446	71.816	75.31	73.496	75.38
85	p4	11.722	23.094	12.932	23.644	41.692	51.56	43.226	49.734	68.304	72.52	65.564	71.942
87.5	p5	9.902	15.466	5.456	16.726	34.364	41.418	36.176	39.548	66.894	70.318	64.202	67.642
90	p6	3.78	10.602	4.056	9.11	27.55	34.63	32.232	39.194	58.316	61.086	56.304	63.08
92.5	p7	1.63	3.54	1.638	5.352	22.9	30.386	17.466	29.974	49.264	59.428	47.506	59.04
95	p8	0.894	1.718	0.622	2.364	11.78	18.124	10.538	18.684	42.88	55.622	48.204	56.83
97	p9	0.354	0.894	0.548	0.792	5.978	9.484	4.13	7.052	35.482	44.044	39.138	40.984
99.6	p10	0.272	0.346	0.242	0.308	1.644	3	1.044	2.188	17.698	28.672	12.202	23.242

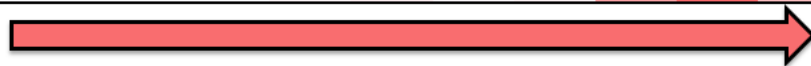


Table 2 : Table is colored for each row.

From the Table 2 we can conclude that number of close links is the most effective parameter compared to the random mean and random sd. Same procedure might be followed for each column. Looking at the Table 3 we can safely conclude that effect of initially vaccinated percentage is robust to changes in other parameters.

		Rand-mean	5	5	5	5	5	5	7	7	7	7	7	7
		Rand-sd	2	2	2	4	4	4	2	2	2	4	4	4
		Close links	3	5	7	3	5	7	3	5	7	3	5	7
Initially vac			s1	s2	s3	s4	s5	s6	s7	s8	s9	s10	s11	s12
65	p1		52.864	67.13	81.676	48.208	67.332	83.176	56.528	73.716	84.832	54.274	72.812	84.07
75	p2		35.44	53.948	76.342	32.306	58.186	78.428	44.588	65.756	79.662	40.486	62.396	80.17
80	p3		24.048	50.19	71.816	25.866	51.472	73.496	34.382	53.918	75.31	31.844	58.446	75.38
85	p4		11.722	41.692	68.304	12.932	43.226	65.564	23.094	51.56	72.52	23.644	49.734	71.942
87.5	p5		9.902	34.364	66.894	5.456	36.176	64.202	15.466	41.418	70.318	16.726	39.548	67.642
90	p6		3.78	27.55	58.316	4.056	32.232	56.304	10.602	34.63	61.086	9.11	39.194	63.08
92.5	p7		1.63	22.9	49.264	1.638	17.466	47.506	3.54	30.386	59.428	5.352	29.974	59.04
95	p8		0.894	11.78	42.88	0.622	10.538	48.204	1.718	18.124	55.622	2.364	18.684	56.83
97	p9		0.354	5.978	35.482	0.548	4.13	39.138	0.894	9.484	44.044	0.792	7.052	40.984
99.6	p10		0.272	1.644	17.698	0.242	1.044	12.202	0.346	3	28.672	0.308	2.188	23.242

Table 3: Table is colored for each column.

To observe the average node degree effect separately we can form groups of three cells and consider the effects. Although in general higher number of close links indicates high infection rates, difference between 3 and 5 seems insignificant when the initially vaccinated percentage is high (around 99%).

		Rand-mean	5	5	5	5	5	5	7	7	7	7	7	7
		Rand-sd	2	2	2	4	4	4	2	2	2	4	4	4
		Close links	3	5	7	3	5	7	3	5	7	3	5	7
Initially vac.			s1	s2	s3	s4	s5	s6	s7	s8	s9	s10	s11	s12
65	p1		52.9	67.1	81.7	48.2	67.3	83.2	56.5	73.7	84.8	54.3	72.8	84.1
75	p2		35.4	53.9	76.3	32.3	58.2	78.4	44.6	65.8	79.7	40.5	62.4	80.2
80	p3		24.0	50.2	71.8	25.9	51.5	73.5	34.4	53.9	75.3	31.8	58.4	75.4
85	p4		11.7	41.7	68.3	12.9	43.2	65.6	23.1	51.6	72.5	23.6	49.7	71.9
87.5	p5		9.9	34.4	66.9	5.5	36.2	64.2	15.5	41.4	70.3	16.7	39.5	67.6
90	p6		3.8	27.6	58.3	4.1	32.2	56.3	10.6	34.6	61.1	9.1	39.2	63.1
92.5	p7		1.6	22.9	49.3	1.6	17.5	47.5	3.5	30.4	59.4	5.4	30.0	59.0
95	p8		0.9	11.8	42.9	0.6	10.5	48.2	1.7	18.1	55.6	2.4	18.7	56.8
97	p9		0.4	6.0	35.5	0.5	4.1	39.1	0.9	9.5	44.0	0.8	7.1	41.0
99.6	p10		0.3	1.6	17.7	0.2	1.0	12.2	0.3	3.0	28.7	0.3	2.2	23.2

Table 4: Table is colored for groups of three cells, isolating the effect of average node degree.

To isolate the mean random interaction effect, groups containing two cells are formed in the Table 5. Usually, increase in the mean random interactions followed by increased infected percentage. However, in the presence of other dominating parameter such as high vaccinated percentage and low close link number or vice versa (left bottom or upper right corners), difference becomes insignificant.

	Rand-mean	5	7	5	7	5	7	5	7	5	7	5	7
	Rand-sd	2	2	4	4	2	2	4	4	2	2	4	4
	Close links	3	3	3	3	5	5	5	5	7	7	7	7
Initially vac.		s1	s7	s4	s10	s2	s8	s5	s11	s3	s9	s6	s12
65	p1	52.9	56.5	48.2	54.3	67.1	73.7	67.3	72.8	81.7	84.8	83.2	84.1
75	p2	35.4	44.6	32.3	40.5	53.9	65.8	58.2	62.4	76.3	79.7	78.4	80.2
80	p3	24.0	34.4	25.9	31.8	50.2	53.9	51.5	58.4	71.8	75.3	73.5	75.4
85	p4	11.7	23.1	12.9	23.6	41.7	51.6	43.2	49.7	68.3	72.5	65.6	71.9
87.5	p5	9.9	15.5	5.5	16.7	34.4	41.4	36.2	39.5	66.9	70.3	64.2	67.6
90	p6	3.8	10.6	4.1	9.1	27.6	34.6	32.2	39.2	58.3	61.1	56.3	63.1
92.5	p7	1.6	3.5	1.6	5.4	22.9	30.4	17.5	30.0	49.3	59.4	47.5	59.0
95	p8	0.9	1.7	0.6	2.4	11.8	18.1	10.5	18.7	42.9	55.6	48.2	56.8
97	p9	0.4	0.9	0.5	0.8	6.0	9.5	4.1	7.1	35.5	44.0	39.1	41.0
99.6	p10	0.3	0.3	0.2	0.3	1.6	3.0	1.0	2.2	17.7	28.7	12.2	23.2




Table 5 : Table is colored for groups of two cells, isolating the effect of mean random interaction.

Lastly, for standard deviation we see that there is no clear pattern. For some values it is increasing the infected ratio and for some other it is the opposite. Thus we conclude no significant effect of standard deviation of random interactions. Correlations between the infected ratio and other parameters in Figure 7 also sums up our analysis.

	Rand-mean	5	5	7	7	5	5	7	7	5	5	7	7
	Rand-sd	2	4	2	4	2	4	2	4	2	4	2	4
	Close links	3	3	3	3	5	5	5	5	7	7	7	7
Initially vac.		s1	s4	s7	s10	s2	s5	s8	s11	s3	s6	s9	s12
65	p1	52.9	48.2	56.5	54.3	67.1	67.3	73.7	72.8	81.7	83.2	84.8	84.1
75	p2	35.4	32.3	44.6	40.5	53.9	58.2	65.8	62.4	76.3	78.4	79.7	80.2
80	p3	24.0	25.9	34.4	31.8	50.2	51.5	53.9	58.4	71.8	73.5	75.3	75.4
85	p4	11.7	12.9	23.1	23.6	41.7	43.2	51.6	49.7	68.3	65.6	72.5	71.9
87.5	p5	9.9	5.5	15.5	16.7	34.4	36.2	41.4	39.5	66.9	64.2	70.3	67.6
90	p6	3.8	4.1	10.6	9.1	27.6	32.2	34.6	39.2	58.3	56.3	61.1	63.1
92.5	p7	1.6	1.6	3.5	5.4	22.9	17.5	30.4	30.0	49.3	47.5	59.4	59.0
95	p8	0.9	0.6	1.7	2.4	11.8	10.5	18.1	18.7	42.9	48.2	55.6	56.8
97	p9	0.4	0.5	0.9	0.8	6.0	4.1	9.5	7.1	35.5	39.1	44.0	41.0
99.6	p10	0.3	0.2	0.3	0.3	1.6	1.0	3.0	2.2	17.7	12.2	28.7	23.2

Table 6 : Table is colored for groups of two cells, isolating the effect of sd of random interaction.

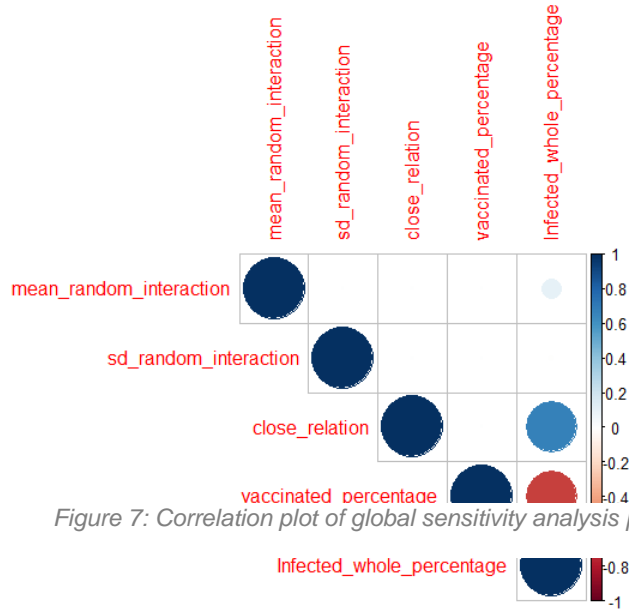


Figure 7: Correlation plot of global sensitivity analysis parameters.

## 6. Conclusion

In conclusion, by conducting this simulation study, we gained huge insights on the spread of the measles. Firstly, since it is a highly contagious disease and the vaccine is effective, vaccination should be done by the authorities in order to prevent a possible outbreak. Moreover, depending on how many people is currently sick, some deductions might be made such as estimation of the final infected ratio. As an another aspect, from the global sensitivity analysis we concluded that average node degree is one of the significant parameters that affect infected ratio in the end. Thus, adding a network and assigning different probabilities looks like a better option than just random interactions.

Additional to the first extension in Appendix B-1, as a further research we suggest adding vaccination diffusion model in which people decide to get vaccinated or not depending on their inclination, currently sick person percentage and number of close links that are sick. Although this extension in Appendix B-2 doesn't cause any behavioral change for our model, we think that this perspective might construct a better understanding for some other diseases that vaccination is not mandatory.



## 7. APPENDICES

### Appendix A Original NetLogo Code

```
globals [ spread-in-network-v ;; infection rate in network for vaccinated people
  spread-random-v ;; spread rate in random interactions for vaccinated people
  spread-in-network ;; infection rate in network
  spread-random ;; spread rate in random interactions
  mean-of-random-interactions ;; mean of random interaction number
  sd-of-random-interactions ;; sd of random interaction number
  recovery-time ;; how long does it takes to recover from infection]

turtles-own[ sick? ;; true if the turtle is infected, false otherwise
  sick-time ;; Time passed since the turtle is infected
  vaccinated? ;; true if the turtle is vaccinated
  recovered? ;; true if a turtle has recovered from the disease
  random-interaction-number ;; with how many people the turtle interacts per tick (normally distributed among turtles with
  mean and sd)
  next-step-sick? ;; true if turtle infected in that tick]

to setup
  clear-all
  reset-ticks
  ask patches [set pcolor 86]

  set mean-of-random-interactions mean-random-interaction-number
  set sd-of-random-interactions sd-of-random-interaction-number
  set recovery-time 8
  set spread-in-network-v 0.9 * (1 - 0.97)
  set spread-random-v 0.083 * 0.03
  set spread-in-network 0.9
  set spread-random 0.083

  setup-nodes
  setup-network

  ask links
    [ set color white]
end

to setup-nodes
  set-default-shape turtles "circle"
  crt number-of-nodes
  [
    setxy (random-xcor * 0.9) (random-ycor * 0.9)
    set sick? false
    set vaccinated? false
    set recovered? false
    set sick-time 0
    set next-step-sick? false
    set random-interaction-number round (random-normal mean-of-random-interactions sd-of-random-interactions)
    if random-interaction-number < 0 [ set random-interaction-number 0]
    if random-interaction-number > number-of-nodes [set random-interaction-number number-of-nodes]
    set color red
    set size 3
  ]
  ask n-of round ((vaccinated-percentage / 100) * number-of-nodes) turtles [set vaccinated? true
    set size 5]
```

```

ask n-of 1 turtles
[set sick? true
 set color green
]

end

to setup-network
let num-links (average-node-degree * number-of-nodes) / 2
while [count links < num-links ]
[
  ask one-of turtles
  [
    let choice (min-one-of (other turtles with [not link-neighbor? myself])
      [distance myself])
    if choice != nobody [ create-link-with choice ]
  ]
]
; make the network look a little prettier
repeat 10
[
  layout-spring turtles links 0.3 (world-width / (sqrt number-of-nodes)) 1
]
end

to go
ask turtles [update-info]
ask turtles [update-wellbeing]
tick
if (ticks > RunLength) [stop]
end

to update-info
let sick-link count link-neighbors with [sick? = true]
let possible n-of random-interaction-number turtles
let possible-sick count possible with [sick? = true]

if (sick? = false) and (recovered? = false) [
  ifelse (vaccinated? = true)
  [ repeat sick-link [ if random-float 1 < spread-in-network-v [set next-step-sick? true]]
    repeat possible-sick [ if random-float 1 < spread-random-v [set next-step-sick? true]]
  ]
  [ repeat sick-link [ if random-float 1 < spread-in-network [set next-step-sick? true]]
    repeat possible-sick [ if random-float 1 < spread-random [set next-step-sick? true]]
  ]
]

]
end

to update-wellbeing
if (sick? = true) [ set sick-time sick-time + 1]

if (next-step-sick? = true) [set sick? true
  set color green
  set next-step-sick? false]

if sick-time > recovery-time [set sick? false
  set recovered? true
  set color yellow
  set sick-time 0]
end

```

## Appendix B-1 Extension of code regarding the incubation period

```
to update-info
  let sick-link-known count link-neighbors with [sick? = true and sick-time >= 4]
  let sick-link-unknown count link-neighbors with [sick? = true and sick-time < 4]
  let possible n-of random-interaction-number turtles
  let possible-sick count possible with [sick? = true]

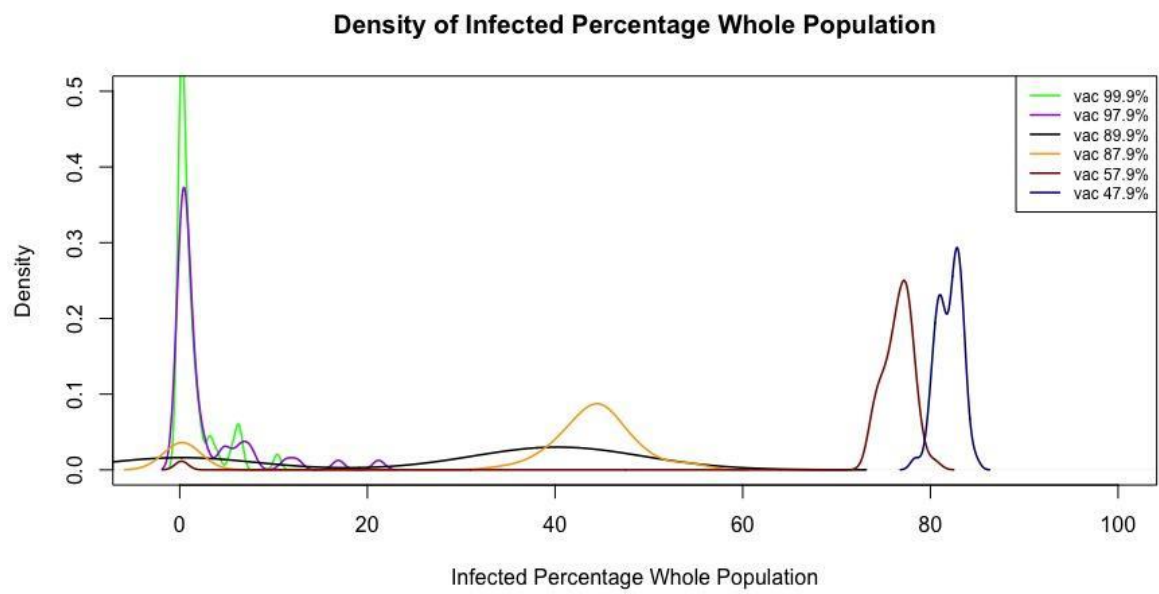
  if (sick? = false) and (recovered? = false) [
    ifelse (vaccinated? = true)
      [ repeat sick-link-known [ if random-float 1 < spread-in-network-v / 2 [set next-step-sick? true]]
        repeat sick-link-unknown [ if random-float 1 < spread-in-network-v [set next-step-sick? true]]
        repeat possible-sick [ if random-float 1 < spread-random-v [set next-step-sick? true]]]
      [ repeat sick-link-known [ if random-float 1 < spread-in-network / 2 [set next-step-sick? true]]
        repeat sick-link-unknown [ if random-float 1 < spread-in-network [set next-step-sick? true]]
        repeat possible-sick [ if random-float 1 < spread-random [set next-step-sick? true]]]
    ]
  end
```

## Appendix B-2 Extension of code regarding vaccine preferences

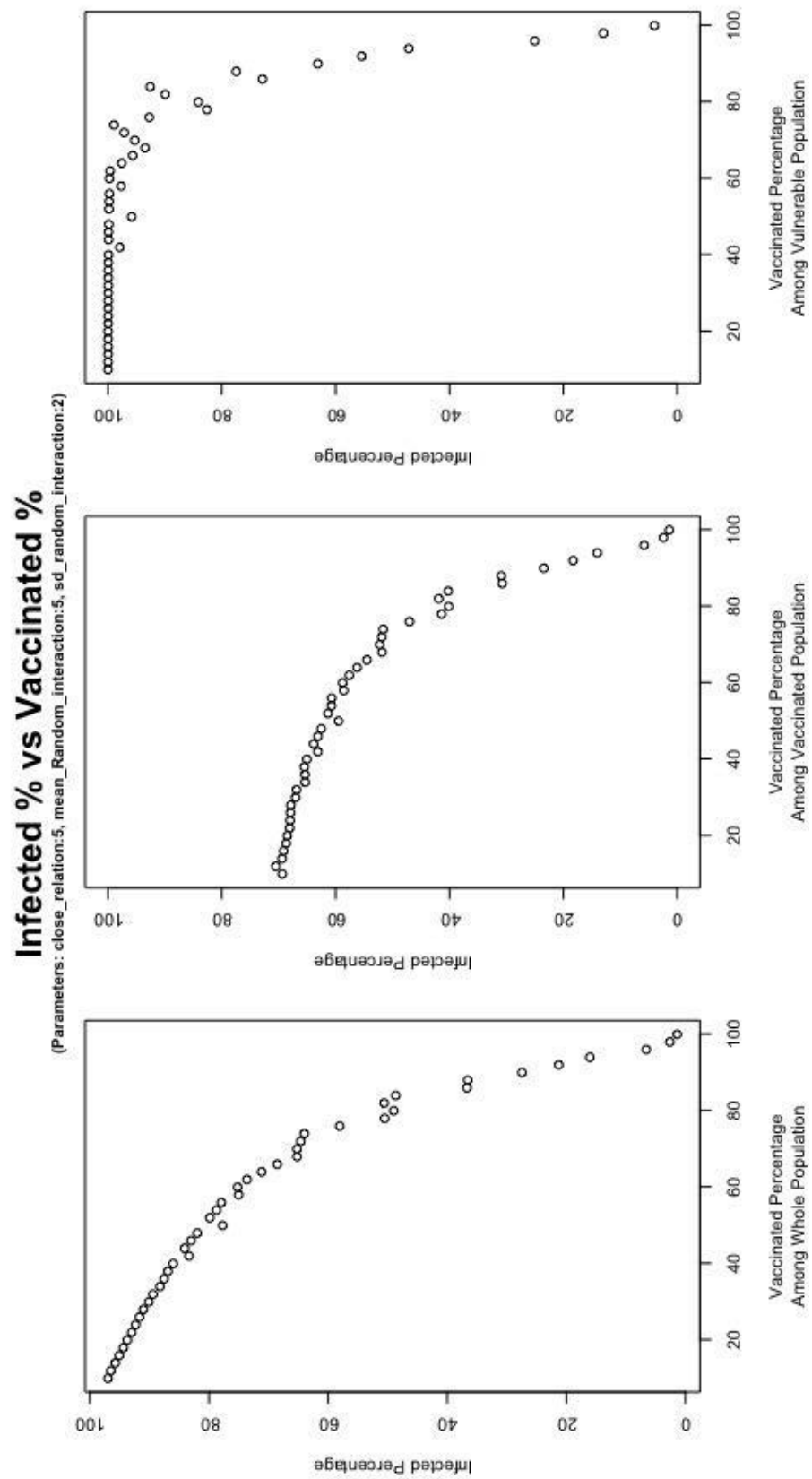
```
turtles-own[ vac-opinion ;; 0 is the ones who are up for that while 1 represents the ones that don't want to use
vaccination]
```

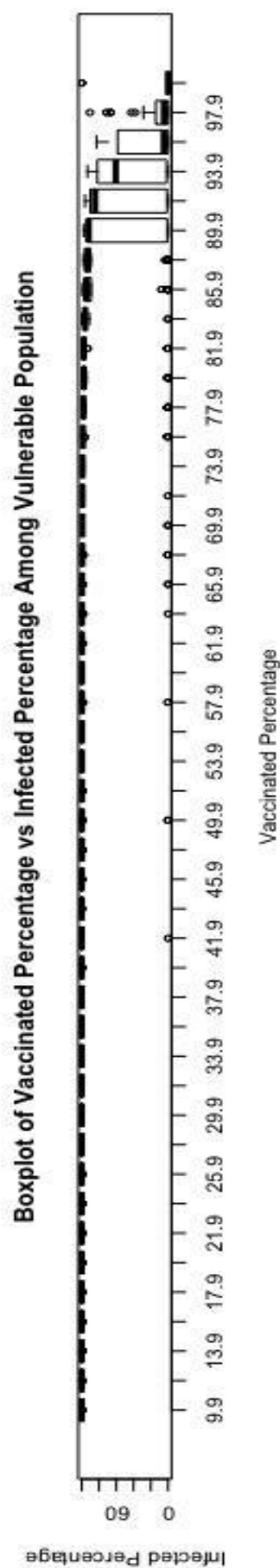
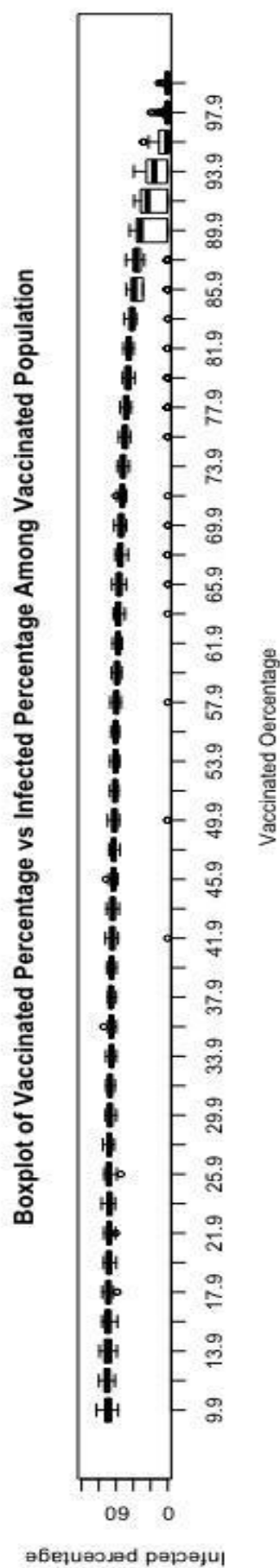
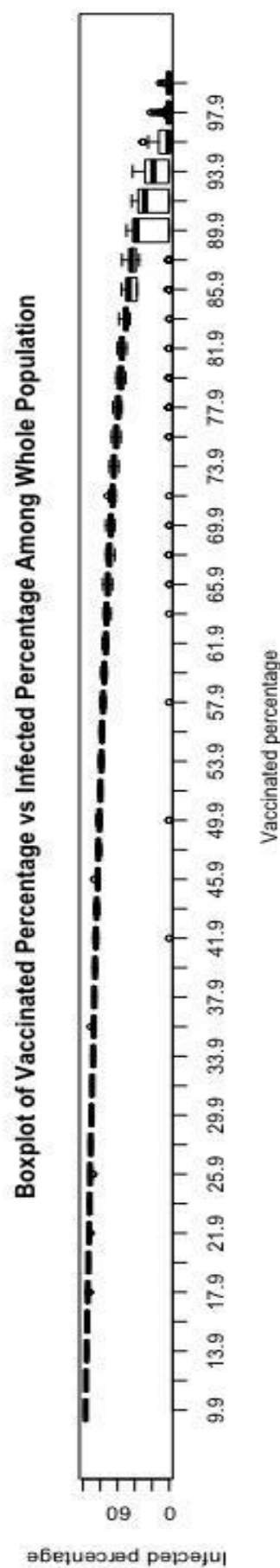
```
to consider-vaccination
  let sick-link-known count link-neighbors with [sick? = true]
  if vac-opinion < (sick-link-known * (count turtles with [sick? = true] / count turtles))
    [set vaccinated? true]
```

## Appendix C-1 Density Graphs



## Appendix C-2 Mean Values and Boxplots for Different Initially Vaccinated Percentages

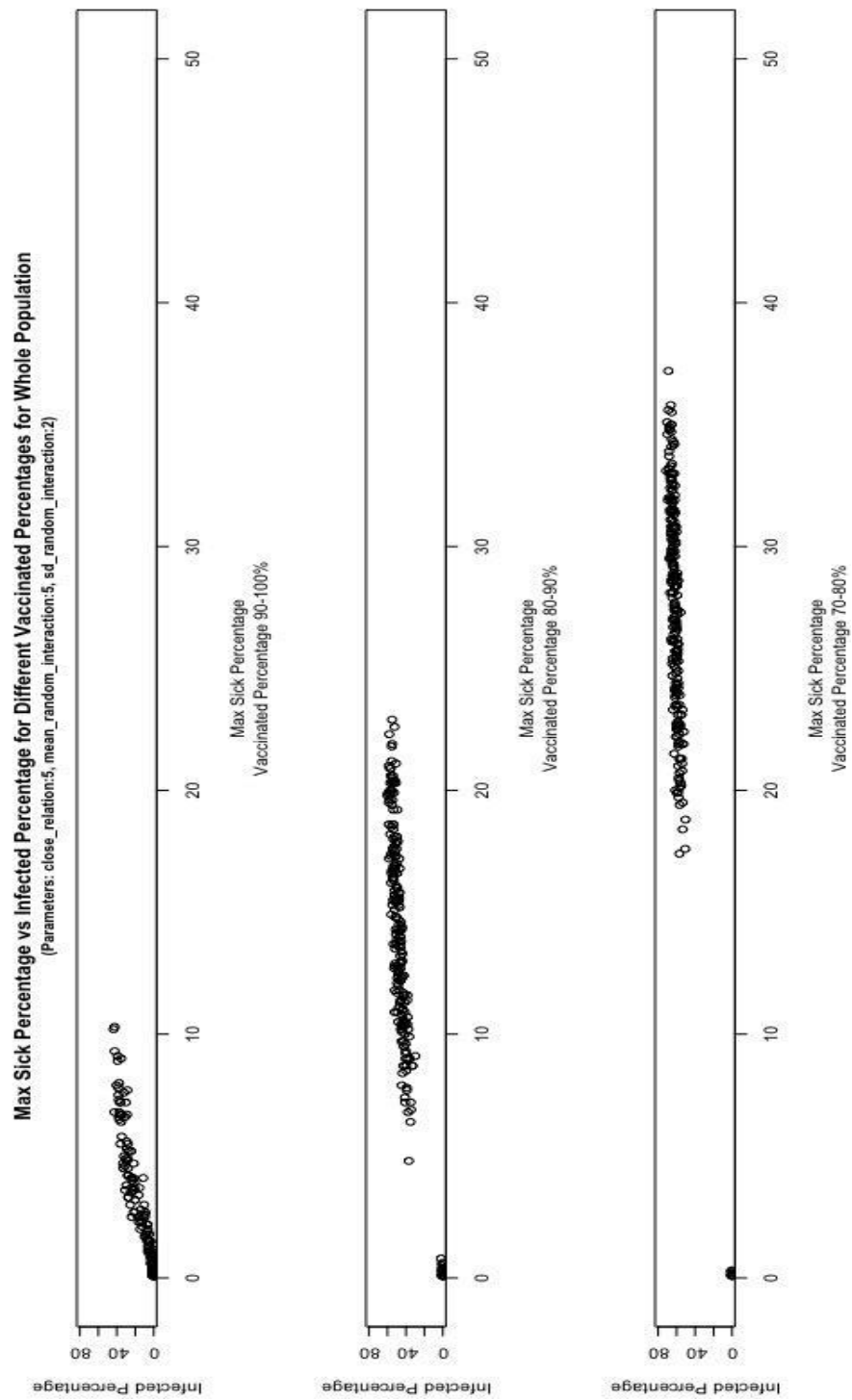




### Appendix C-3 Percentage changes in infection ratios among different populations

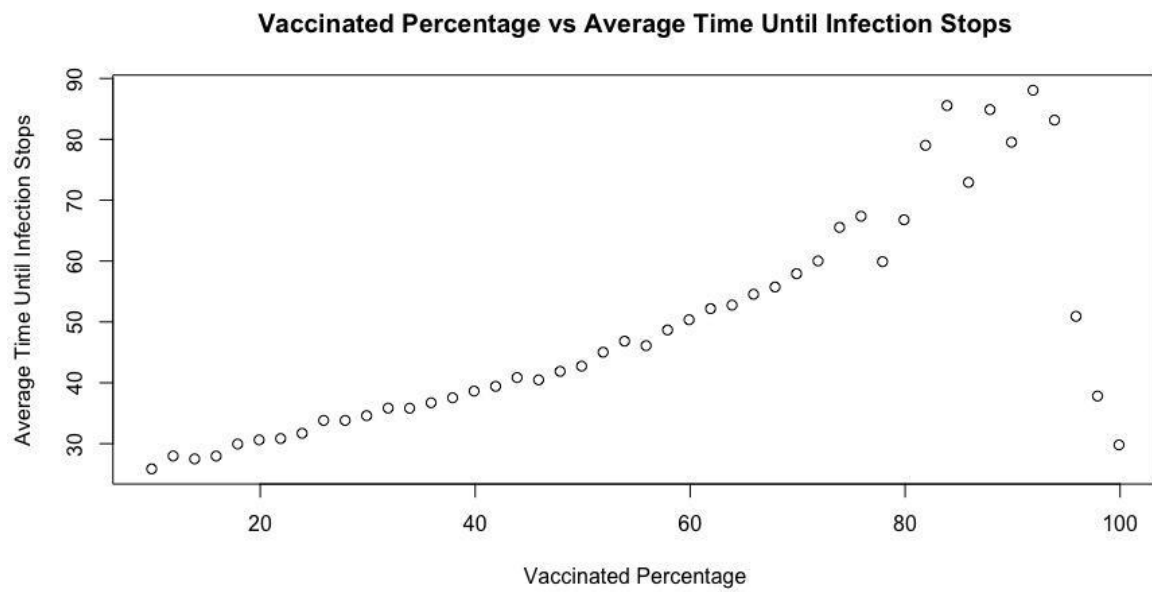
% Change in Vaccinated Percentage	% Change in Infected Ratio		
	Vulnerable Population	Whole Pop.	Vaccinated Pop.
-90.09	2399.78	6865.52	4893.11
-88.09	2399.55	6830.60	4974.47
-86.09	2399.36	6776.87	4895.72
-84.08	2399.52	6730.32	4876.62
-82.08	2399.51	6680.03	4843.29
-80.08	2399.63	6632.61	4829.68
-78.08	2399.17	6579.89	4800.15
-76.08	2399.08	6532.47	4794.24
-74.07	2399.12	6485.49	4789.79
-72.07	2398.89	6437.93	4785.98
-70.07	2398.64	6372.99	4724.43
-68.07	2398.90	6322.56	4713.01
-66.07	2398.64	6237.79	4604.43
-64.06	2398.75	6188.65	4605.38
-62.06	2398.55	6142.10	4614.59
-60.06	2397.92	6078.88	4582.82
-58.06	2348.36	5887.50	4442.78
-56.06	2397.42	5940.09	4496.50
-54.05	2397.78	5863.94	4442.05
-52.05	2396.16	5788.94	4400.86
-50.05	2295.91	5481.75	4181.52
-48.05	2395.53	5636.78	4315.80
-46.05	2394.79	5556.32	4270.79
-44.04	2393.88	5497.99	4268.92
-42.04	2342.40	5290.52	4114.77
-40.04	2393.39	5302.16	4130.01
-38.04	2390.81	5188.51	4045.89
-36.04	2339.75	5012.21	3947.22
-34.03	2291.06	4822.99	3822.42
-32.03	2236.92	4584.34	3631.20
-30.03	2282.06	4585.06	3662.01
-28.03	2328.65	4540.66	3633.84
-26.03	2373.56	4497.13	3617.33
-24.02	2218.26	4069.97	3285.15
-22.02	1965.61	3528.02	2878.93
-20.02	2003.23	3418.68	2788.87
-18.02	2148.62	3533.76	2914.47
-16.02	2214.60	3395.11	2794.92
-14.01	1721.63	2534.63	2112.01
-12.01	1836.78	2525.14	2124.56
-10.01	1478.22	1871.98	1587.19
-8.01	1285.80	1428.74	1214.96
-6.01	1078.69	1053.16	909.94
-4.00	525.61	373.71	317.88
-2.00	223.81	88.51	72.91
0	0	0	0

## Appendix D Max. Sick Percentage vs Infection Rate

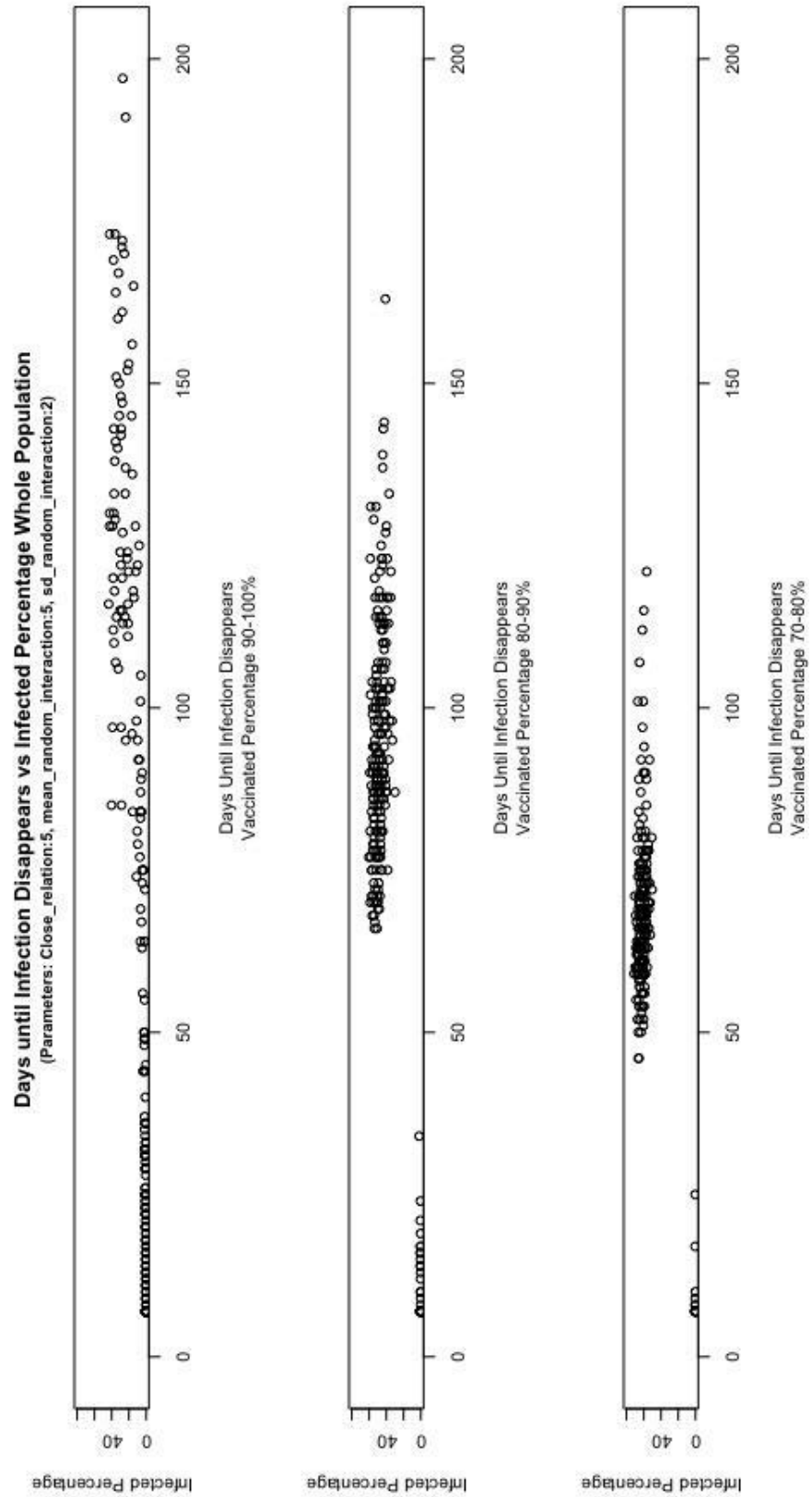




## Appendix E-1 Average Time Until Infection Stops



## Appendix E-2 Days Until Infection Disappears



## 8. References

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