



## Simulations of Infectious Disease Propagation

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### *Author's contribution*

*The sole author designed, analyzed and interpreted and prepared the manuscript.*

### *Article Information*

DOI: 10.9734/AJRID/2020/v4i230144

#### Editor(s):

(1) Dr. Giuseppe Murdaca, University of Genoa, Italy.

#### Reviewers:

(1) Prasant Kumar Nayak, C. V. Raman Global University, India.

(2) Tatiane Rodrigues de Oliveira, Estácio Castanhal, Brazil.

(3) Angshuman Bagchi, University of Kalyani, India.

Complete Peer review History: <http://www.sdiarticle4.com/review-history/58519>

**Received 23 April 2020**

**Accepted 29 June 2020**

**Published 07 July 2020**

**Original Research Article**

### ABSTRACT

**Introduction and Objectives:** The results of two simulations of the propagation of an infectious disease are presented. The objective of this research is to track the propagation of an infectious disease as a function of particle density and time. The results are given as a percentage of the population that is infected as a function of time.

**Methods:** The method here is to use computer simulation on a particle basis to track the progress of the infection. An uninfected particle becomes infected if it is closer than the critical distance to an infected particle. The movement of the particles is force driven in the first simulation while in the second each particle executes a random walk. In the second simulation the infection rates are given for different amounts of protection in the population.

**Results and Discussion:** These simulations show the entire population is at risk if proper measures are not taken early. For 400 particles the infection rate is 100% after approximately 100,000 iterations. We give the results from one dual simulation in which protection was afforded for a significant part of the population and carried out until all of the unprotected were infected. In the second part the protection was lifted to see how fast the total population was infected. For the cases of 50% protected it took 400,000 iterations to infect the unprotected particles. After the restrictions were lifted it took 140,000 to infect the other half. The simulations here are particle based which has the advantage of seeing individual particle involvement.

**Conclusion:** The propagation of the disease can be fast and depends on particle density. Protection is vital to containing the disease. Restrictions must be lifted carefully and slowly or the total population is again at risk.

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*Keywords: Simulation; infectious disease; immunity; propagation; restrictions.*

## 1. INTRODUCTION

The work described and presented here was motivated by the current interest in disease propagation due to the coronavirus [1]. This virus is especially fast in its propagation and is lethal in many cases. It is particularly disturbing because of these propagation properties and effects of the disease. These properties have all been discussed in many places, so we will not dwell on them but proceed to describe the simulations we did. The simulations presented here were derived from simulations related to self-organization of small systems with simple dynamics [2, 3]. These will be discussed briefly later to explain what was done here. The work was performed on systems of 10,000 or fewer particles in a square 512 by 512. We realized that by adding a tag,  $z$ , to each particle and adding a rule for infection transfer we could simulate the propagation of a disease. We assigned the  $z$  tag such that if  $z=0$  the particle was uninfected, if  $z=1$  the particle was infected and if  $z=2$  the particle was immune to this disease. The rule to transfer infection between an infected particle and an uninfected particle was if the two particles were closer together than the critical distance then the uninfected particle was infected. The system is started with the layout of the particles in a square. The dynamics were applied and the particles moved accordingly. Initially two particles were chosen at random to be infected. The infection rule was applied and the next iteration taken. One such step is referred to as an iteration. This continues for a preset number of iterations. We found that the propagation of the disease is alarming and if proper steps are not taken the whole population is at risk. However, even the early on infection rate is too high to be acceptable.

We describe two different but related experiments. The simulations are at the particle level. There have been many studies of disease propagation and predictions of disease behavior based on statistical methods and analysis [2,3]. Our simulations are at the particle level so individual particles can be followed and individual particles studied. The statistical based methods have an advantage in that a large population can be modeled. Our simulations are limited in the number of particles involved because of the computer time required as the number grows. For 10,000 particles and 100,000 iterations the computer time (clock time) was 48 hours. As

stated above in all that follows the system is contained in a square of size 512 by 512. At initiation for Experiment 1 (Exp1) the particles are located by randomly placing them in the square. Exp1 has two states, entities or countries separated by a common boundary which is the vertical center line of the square. The boundary is easily crossed by a particle. Each group is contained in a rectangle of size 256 by 512. One group is on the left half of the square and the second group is contained on the right half of the square. The initial coordinates of the particles are determined by the use of a random number generator. The particles are sub-divided into strong and weak particles. The strong particles represent the elite, governance or leaders and the weak particles represent the general population. The strong particles on each side have strength of 25. The weak particles on each side have strength randomly distributed from 0 to 25. A sample distribution is shown in (Fig.1). The dynamics are governed by a set of forces between each pair of particles  $i$  and  $j$  such that  $f_{ij}=S_i*S_j/d_{ij}$  where  $S_i$  and  $S_j$  are the respective strengths of the particles and  $d_{ij}$  is the Euclidean distance between the two particles. The force of one particle on another is along the line connecting the particles and is attractive or repelling. Experiment 2 (Exp2) is similar except the dynamics are different. In Exp2 there are no internal or external forces. The movement of the particles is due to each particle executing a random walk.

Mathematical and simulation methods have been used in epidemiology in a number of cases [4, 5, 6]. Computer simulations are safe, relatively easy to implement and especially readily available due to the improved speed and memory features of computers. These approaches are especially useful in situations in which experiments on the real systems are too expensive, the system is not available for experiments or the experiment is too risky. The use of mathematics in epidemiology has been traced back to Bernoulli in 1766, [7]. Simulation of disease propagation has been in use since the 1980's. [8-13] and is now in common use.

The methods in use include Agent Based Modeling (ABM) and Susceptible Infected Recovery (SEIR) and Susceptible Infected Recovery or Dead (SEIRD) models. The ABM models are similar to the method use here [14]. The model is based on agents which have

assigned attributes and there is a set of dynamics to govern the agents travel. Some models include a variety of factors such as weather or time of the year. We have chosen a simple model in which the particles are infected based on distance to an infected particle. The SEIR and SEIRD models are based on a set of different equations and the results are given as solutions to these differential equations. One might think of our model as a macro model. That is one that is relatively simple and is perhaps aimed at a worst case scenario. The advantage of the simple model one can get a good look at the details. As mentioned the disadvantage is the limitation to using a relatively small sample size.

## 2. METHODS

The method used in this research is computer simulation. The computer code was written for this project. The code was written in the c programming language compiled with the gnu c compiler and executed on the Debian version of Linux.

### 2.1 Experiment 1

The particles interact such that every particle exerts a force on every other particle. The force is either repulsive or attractive and acts along the line between the two particles. The simulation proceeds at discrete intervals according to the dynamics equation  $d = d_0 + f \cdot \Delta t$  where  $d_0$  is the x or y coordinate before an iteration step,  $d$  is the coordinate after an iteration step,  $\Delta t$  is the size

of the iteration step and is 0.001 for all runs, and  $f$  is the force acting on the particle in x or y directions. The simulation proceeds as follows:

- n particles of each group are created and placed at random in a 512 by 512 square.
- The strength of each particle is assigned as stated above.
- Two particles on the left side are selected to be infected to start the simulation.
- The vector distance between every pair of particles is calculated.
- The net force on each particle is determined by vectorially adding all of the forces from the other particles.
- The dynamics are then applied to obtain the new position of each particle.
- The distance between each pair of particles is calculated. In a pair, if one of the particles is infected and the other is not, and they are closer than the critical distance, the uninfected particle is infected.
- With the new locations known the process starting at step d is iterated. The process is repeated for a given number of iterations so that the results can be studied.

The interactions between the strong and weak particles can be selected to be attractive or repulsive. Therefore, the interactions can be set to reflect a number of different interesting scenarios. The idea is that by modifying the type of force (attractive or repulsive), the particle strength, and the number of weak and strong particles a number of scenarios can be

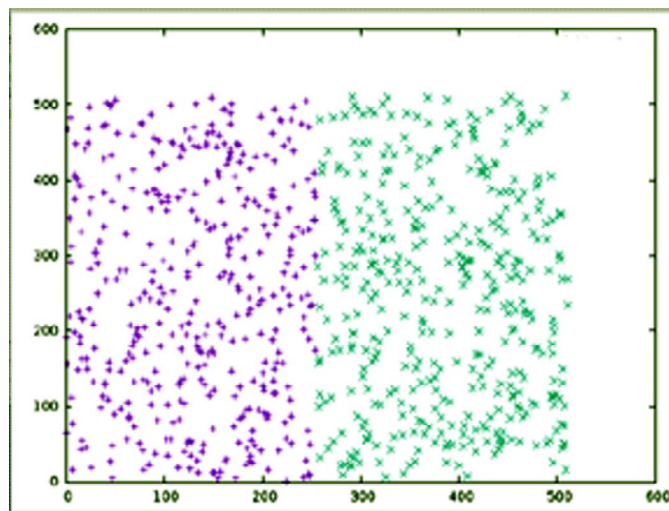


Fig. 1. An initial distribution for 400 particles on each side. X and y values are the coordinates of a particle

simulated. Consider two countries divided by a boundary. Each entity, country or state has its own government or rules and population. It is assumed on each side of the boundary strong and weak forces are attractive within the respective group. This means particles support each other within the group. It is assumed that the weak particles dislike the governance on left side of the boundary, but right side weak are favorable to the governance. Across the boundary all of the forces are repulsive except that the weak are sympathetic with their own group and with those on the opposite side. Using S to represent a strong particle and W to represent a weak particle the interactions are listed in (Table 1). This was initially designed to study migration between a “bad” country and a “good” country and the resulting self-organization.

The simulator was run for different numbers of iterations (time line). After a simulation run the infected particles were counted. The initial distributions are generated for random locations so the final infected number is dependent on these initial conditions which includes the locations of the particles and the first two chosen for infection. This accounts for the “ups” and “downs” in the plots.

**Table 1. The forces as they are for Exp1**

Force number	Force name	Type force
1	W0 to W0	A
	W1 to W1	A
2	W0 to S0	R
	W1 to S1	A
3	S0 to W0	r
	S1 to W1	A
4	S0 to S0	A
	S1 to S1	A
5	W0 to W1	R
	W1 to W0	A
6	S0 to S1	R
	S1 to S0	R
7	S1 to W0	A
	S0 to W1	R
8	W0 to S1	A

To make the nature of the forces clear let S refer to strong particle, W refer to weak particle, 0 refers to left side of the square and 1 refers to right side of the square. The sign of the each force is given in an input file. If the input is plus one the force is attractive. If the input is minus one then the force is repelling. W-W is attractive, S-W is repulsive on left and attractive on right

and across the boundary the types S-S is repulsive, S-W is repulsive W1-W0 is attractive and W0-W1 is repulsive. The strong particles are fewer in number than the weak particles. This might correspond to a situation of strong leaders but the general population is weak. Here, there are 20% strong particles and 80% weak particles on each side. Once given the initial locations the net force on each particle is calculated and the dynamics applied. The number of iterations is varied. An iteration can be considered as a time unit so we can see the propagation of the disease in time. Results of Exp1 are given and discussed in Section 3.1.

### 3. METHODS

The method used in this research is computer simulation. The computer code was written for this project. The code is written in the c programming language compiled with the gnu c compiler and compiled and executed on the Debian version of Linux.

#### 3.1 Experiment 1

The particles interact such that every particle exerts a force on every other particle. The force is either repulsive or attractive and acts along the line between the two particles. The simulation proceeds at discrete intervals according to the dynamics equation  $d = d_0 + f \cdot \Delta t$  where  $d_0$  is the x or y coordinate before an iteration step,  $d$  is the coordinate after an iteration step,  $\Delta t$  is the size of the iteration step and is 0.001 for all runs, and  $f$  is the force acting on the particle in x or y directions.

The simulation proceeds as follows:

- n particles of each group are created and placed at random in a 512 by 512 square.
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- Two particles on the left side are selected to be infected to start the simulation.
- The vector distance between every pair of particles is calculated.
- The net force on each particle is determined by vectorially adding all of the forces from the other particles.
- The dynamics are then applied to obtain the new position of each particle.
- The distance between each pair of particles is calculated. In a pair if one of the particles is infected and the other is not

- and they are closer than the critical distance the uninfected particle is infected.
- With the new locations known the process starting at step d is iterated. The process is repeated for a given number of iterations so that the results can be studied.

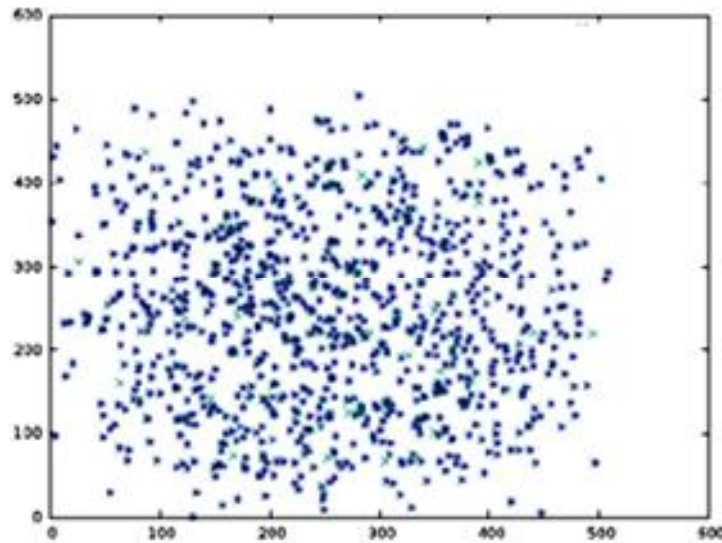
The interactions can be set between the strong and weak particles can be selected to be attractive or repulsive. Therefore, the interactions can be set to reflect a number of different interesting scenarios. The idea is that by modifying the type of force (attractive or repulsive), the particle strength, and the number of weak and strong particles a number of scenarios can be simulated. Consider two countries divided by a boundary. Each entity, country or state has its own government or rules and population. It is assumed that on each side of the boundary strong and weak forces are attractive within the respective group meaning that they support within the group. It is assumed

that the weak particles dislike the governance on left side of the boundary, but right side weak are favorable to the governance. Across the boundary all of the forces are repulsive except that the weak are sympathetic with their own group and with those on the opposite side. Using S to represent a strong particle and W to represent a weak particle the interactions are, as noted earlier, listed in (Table 1). This was initially designed to study migration between a “bad” country and a “good” country and the resulting self-organization.

The simulator was run for different numbers of iterations (time line). After an iteration run the infected particles were counted. The initial distributions are generated for random locations so the final infected number is dependent on these initial conditions which includes the locations of the particles and the first two chosen for infection. This accounts for the “ups” and “downs” in the plots.

**Table 2. Parameters used in Expl.**

Number particles	Number weak particles	Iterations	deltax	deltay	Max strength	Distance for first pair	Distance of infection
200-400	80.00%	10k-200k	0.001	0.001	25	29	0.057



**Fig. 2. Initial particle distribution Exp2 1000 particles. X and y coordinates of pa particle**

**Table 3. The parameters used in Exp2.**

Number of particles	Number of iterations	deltax	deltay	Distance of infection	Number protected
1000	20K-500K	0.001	0.001	0.057	0-90%

### 3.2 Experiment 2

Exp2 is similar to Exp1. The biggest change is in the manner in which the particles move. In Exp1 the particles move based on forces from the other particles. In Exp2 there are no forces applied. The movement of the particles is due to each particle executing a random walk. A component of the random walk occurs in the x and y directions. Of course no one person follows a random walk, but when many are observed in the aggregate this seems to be a reasonable assumption. The simulation proceeds as discussed above. Again n particles are randomly distributed in a 512 by 512 square. The parameters used in Exp2 are given in (Table 3). As before two particles are chosen to be infected. At each iteration each particle is moved and the distance between every pair of particles is calculated. The infection is transferred to the uninfected particle if the infected and uninfected particles are closer than the critical distance. The critical distance is the same as in Exp1, and is 0.057. Then the next iteration is taken. The simulation continues through a preset number of iterations. A number of different sets of iterations are taken. The number of iterations can be interpreted as a time line so we get a time analysis of how the disease progresses in time. In Exp1 there is no protections in place. The disease progresses through a vulnerable population. This is what happens if steps are not taken to halt the progress. In Exp2 there is an allowance for some protection. This is accomplished by selecting a percentage of the

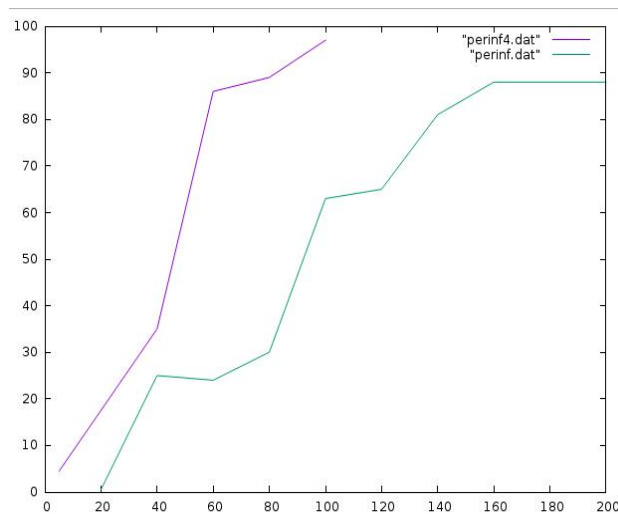
population to be unsusceptible to the disease. This would include procedures such as lock-down, natural immunity or any other reason for a particle not to get infected even if exposed. In (Fig. 2) an initial particle distribution for 1000 particles us shown. The results of the simulation are given in the Results and Discussion section.

## 4. RESULTS AND DISCUSSION

### 4.1 Experiment 1

Again referring to (Fig. 1) is a plot an initial particle distribution of 400 particles per side. (Fig. 3) is a plot of the percent of the population that is infected versus the number of iterations or the time line. It is clear that once the disease starts propagating it affects the population very quickly reaching 90 % or more of the population. Of course the rate slows down as the percent infected grows to a percentage nearing 100% because there are fewer particles to infect.

The infection transfer rate depends on the distance between particles. The commonly discussed social distance is 6 feet. We sized according to Austin, Texas. If Austin were a square it would be about 17 miles on an edge. Corresponding this to our square distance of 512 we get that 10 feet on the ground is about 0.057 units in our simulation. We use 10 feet which biases our results to infection transfer. In our simulation no particle dies or goes away. If a particle leaves the square due to the dynamics then it is reinserted at a random location in the



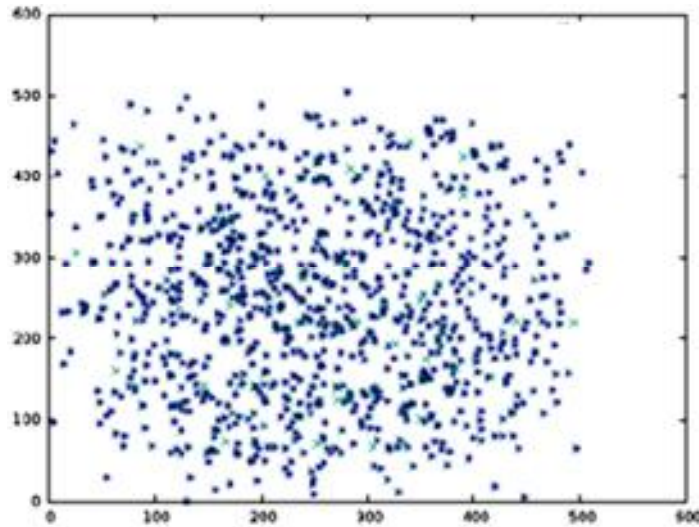
**Fig. 3. Plot of percent infected against number of iterations equivalent to a time line. Green line 200 particles per side. Purple line 400 particles per side X number of iterations. Y is the percent infected**

square. So the total number of particles remains constant. There is also no cure or recovery included. That is an infected particle remains infected for the life of the simulation. So this gives a somewhat bleak picture of what can happen if effective measures are not taken. A summary of the parameters used is given in (Table 2). As of April 24, 2020 the internet states that worldwide 2.7 million people have been infected and 195,000 have died. This yields about a 7% death rate of those infected. These

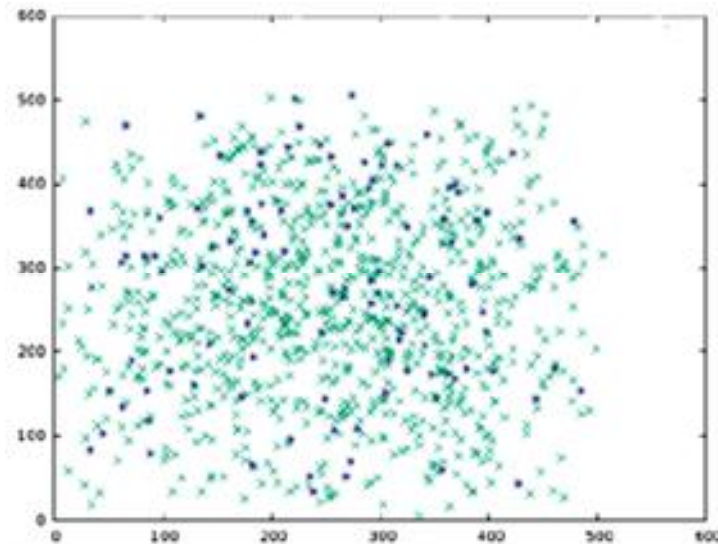
reported numbers are probably lower than the actual count. It is clear these rates are unacceptable.

#### 4.2 Experiment 2

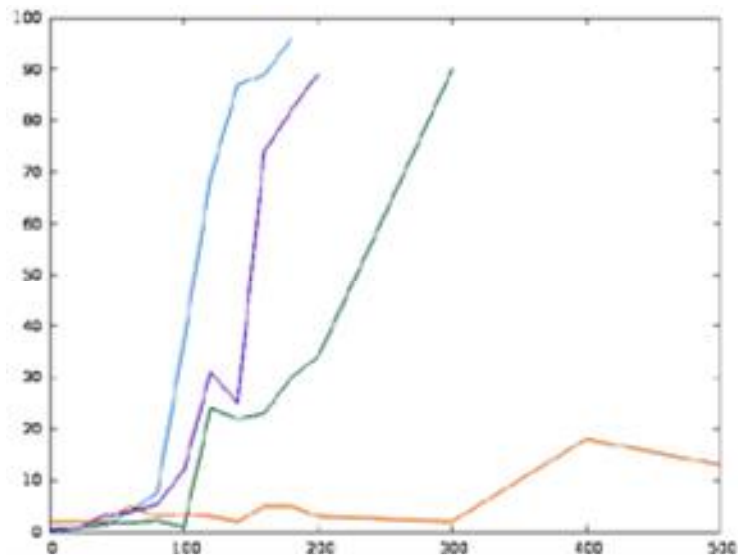
In Fig. 4 the infection rate of 96% after 180k iterations with 1000 particles and no protection is shown. In (Fig. 5) we show the infection after 140k iterations with 1000 particles 500 protected and only 22% infected. These infection percentages are the percent of the



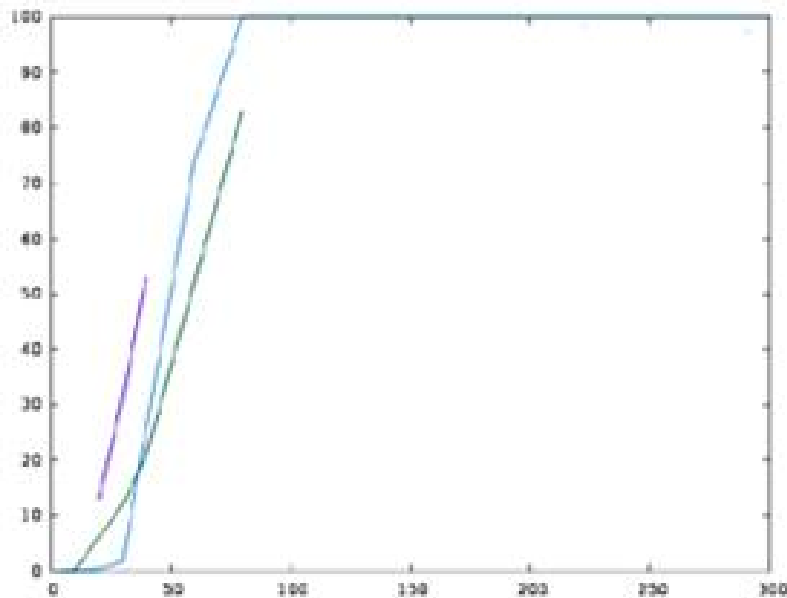
**Fig. 4. Final locations of particles. 1000 particles. No protection. 180K iterations. 962 infected. Red cross infected particles. Green x final position of the particles**



**Fig. 5. 1000 particles. 500 protected. 140K iterations 110 infected. Green x uninfected particle. Red cross infected particle X and y are coordinates of a particle**



**Fig. 6. Plots of Percent Infection of the Vulnerable Particles Versus the Number of K Iterations. Blue Zero Protected. Purple 300 Protected. Green 500 protected. Orange 900 protected. The percent is that of the vulnerable particles infected. X is the number of iterations and y is the percent infected**



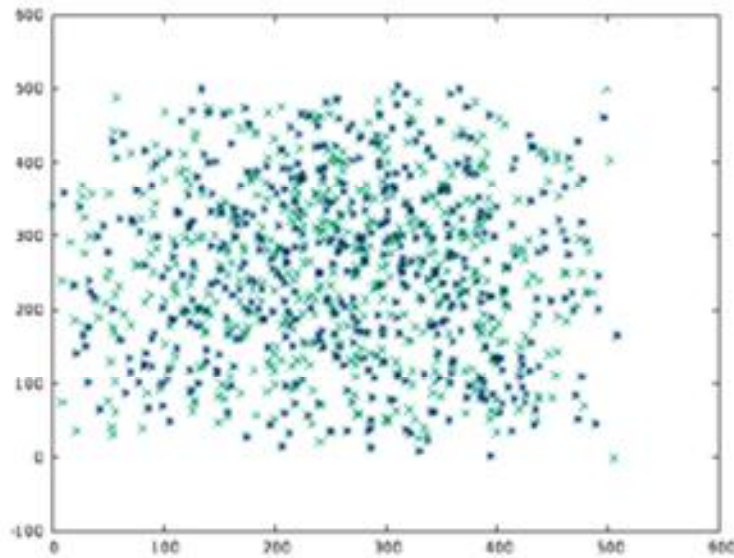
**Fig. 7. Percent infected versus number of iterations green 2,500 particles, blue 5,000 particles and purple 10,000 particles. X is the number of iterations and y is the percent infected**

vulnerable particles that are infected. It can be seen that once the disease gets started, it propagates very rapidly through the population.

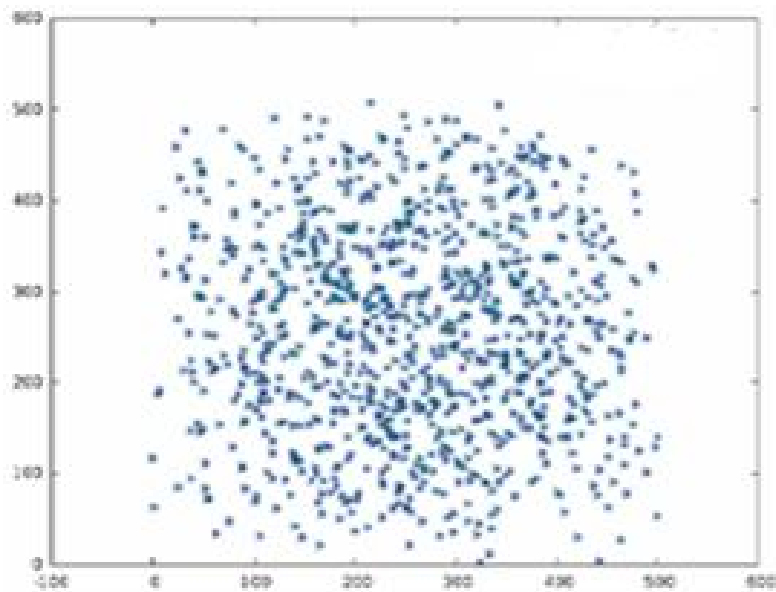
In (Fig. 6) the percent of the vulnerable particles infected particle versus the number of iterations

is given. The results are for 0 protected, 300 protected, 500 protected, and 900 protected. These data show the value of protection however it is achieved. Here the assumed protection for whatever source is lumped into one number.





**Fig. 8. 1000 particles. 500 protected. 400,000 iterations. All 500 unprotected infected. Green cross the 1000 particles. Blue the 500 unprotected and infected X an y are coordinates of a particle**



**Fig. 9. 1000 Particles 140,000 iterations after the restrictions removed. All infected after 150,000 iterations. X and y are the coordinates of a particle**

Shown in (Fig. 7) are the results for more cases of unprotected particles. The plots are for 2,500, 5,000, and 10,000 particles. In general the spread of the disease is faster with higher particle density. Only a few cases are presented due to the computer time required, but the infection rate dependency on density is clear.

For a disease with no history or prior presence the only method of protection is provided by a set of rules such as lock down, quarantine or maybe other methods as there is no natural immunity at the beginning of the disease. In the current case lock down procedures are in place nation and world-wide. There is a lot of interest in releasing the requirements for business and economic

reasons. We have carried out a simulation whereby the protection is removed after all of the unprotected are infected. For 1000 particles 500 were originally protected. The simulation was run until all of the unprotected were infected. This took approximately 400,000 iterations. The results are given in Fig. 8. The protective conditions were then removed and the simulation started using the values retained from the first part. After only 140,000 iterations all of the particles were infected. The results are given in Fig. 9. This demonstrates the hazards of

removing protection measures without adequate medical treatment or a widely available vaccine. The total population is at risk.

One of the parameters discussed in this type of research is  $R_{naught}$  or  $R_0$  which is the number of particles infected by a given particle. For the first part of the simulation this is shown in (Fig. 10) and for the second part in (Fig. 11). In (Fig. 10) the first 500 particles cannot infect others because they are protected from the disease and

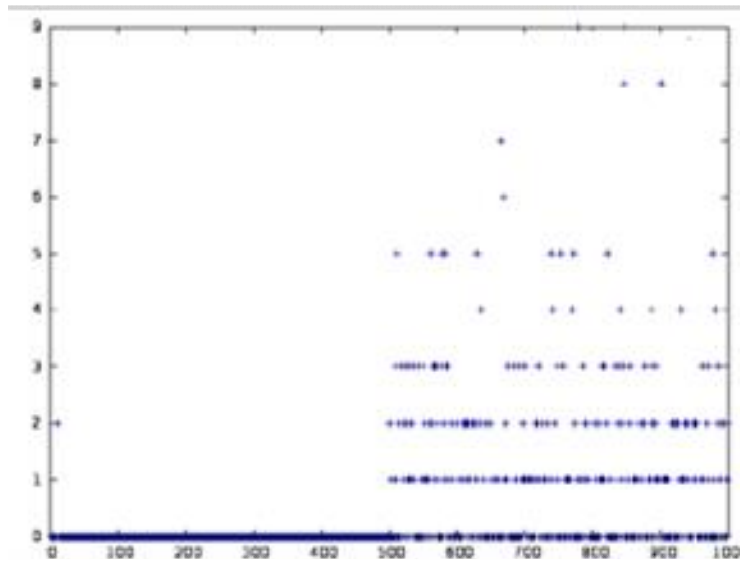


Fig. 10.  $R_0$  for the 1000 particles 400,000 iterations 500 protected. X is a particle number and y is the number of particles infected by that particle

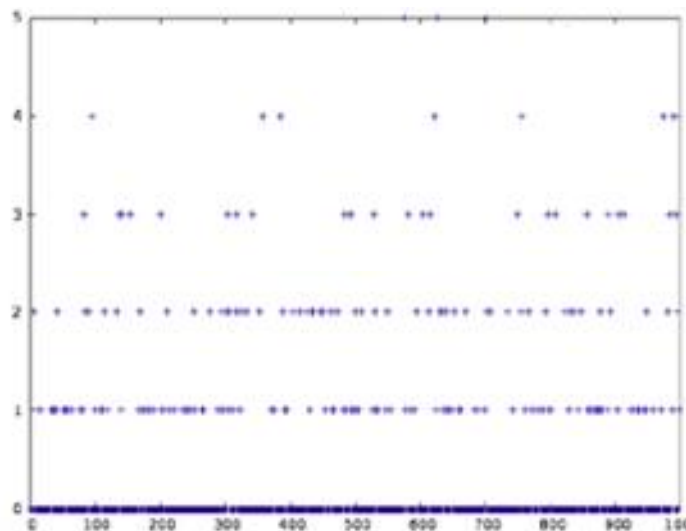


Fig. 11.  $R_0$  after restrictions removed 150,000 iterations later. All infected. X is a particle number and y is the number of particles infected by that particle

therefore cannot pass it on. However, some of the particles infect as many as 5. Report in Nature gave the result of 2.6 for Ro. [15]. It was later revised upward to 3.4.

In the second part all can infect others. The average in each case is 1 because all of the eligible particles are infected. The total number infected by a given particle is the sum from the two runs as the count is started over at the simulation start. It is clear from (Fig. 11) that the protective restrictions must be removed very carefully until there are effective measures to deal with the disease.

## 5. CONCLUSION

The conclusions are as follows:

- The two experiments reported here emphasize and underscore that which is already widely known. That is from a small sample on a vulnerable population the disease can spread rapidly, This along with the knowledge of the lethality of the disease makes early recognition and effective protective measures essential. The infection rate displays as the well-known S curve.
- Population density plays a key role in the disease's propagation. A large population density makes transfer of the disease easier because breaching the critical distance is more likely.
- Our work demonstrates and quantifies to some extent the effectiveness of protection that can be afforded through available methods. We have lumped the effect of all of the methods into one number without identifying what methods may be used. We have investigated the disease propagation with different levels of protection. As the percentage of protected particles increases the infection is slower to propagate at the start, but once it gets started the rate increases rapidly as expected from the exponential growth rate. However, in the case of 90% protected has a much slower rate and the disease is better contained. It is difficult to see how 90% protection could be achieved without an effective vaccine. The only way to stop the disease progression is an effective vaccine or restrictions on the movement of the infected particles.
- One of the primary results is that removing the protective rules too soon can lead to

rapid spread of the disease again. One of the surprising and significant results of Exp2 is the infection results for the originally protected part of the population after the restrictions are removed. What these results show is if the infected particles are free to move around then eventually all of the particles get infected.

It is inviting to compare the results of the two experiments but with different methods and parameters this is difficult. The main results from both experiments are clear and have the same trend that the disease left unaddressed would be catastrophic. Our results may be pessimistic in that there is a simple rule for transfer of the disease between a pair of particles. We could add a probability of transfer to each unprotected particle that would make it more difficult for the disease to propagate. We could also include some other attributes to each particle as the ABM models do. This could be accomplished in the same manner as adding the infection tag. However we want to get these results out so further enhancements are being put off for future investigation.

## CONSENT

It is not applicable.

## ETHICAL APPROVAL

It is not applicable.

## COMPETING INTERESTS

Author has declared that no competing interests exist.

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