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# Simulations of Infectious Disease Propagation II, Focusing on Herd Immunity

**William J. B. Oldham[1*]**

*[1]Texas Tech University, 3877 Royal Troon Dr. Round Rock, Texas 78664, USA.*

***Author's contribution***

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

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## ABSTRACT

**Introduction and Objectives:** The results of simulations of the propagation of an infectious disease are presented. In managing and controlling the spread of an infectious disease, such as Covid-19, the concept of Herd Immunity (HI) is often invoked as to when the disease's propagation will dwindle to acceptable levels. We have extended a previous work with explicit attention on the usefulness of this concept. The objectives of this research was to track the propagation of an infectious disease as a function of population density, time, and to evaluate HI. The population was divided into two groups. One group was protected from the infection. The second group was unprotected. The results are given as a percentage of the unprotected population that is infected as a function of time.

**Methods:** The method used here was to use computer simulation on a person level to follow the progress of the diseases infection across the population. In the beginning, the people are uniformly distributed in a square. Each person performed a random walk, which simulated the movement of the people. Infection rates are given for the unprotected portion of the population as a function of time. The disease was transferred from an infected person to an uninfected person if the two people are closer together than a given distance.

**Results and Discussion:** These simulations show the unprotected portion of the population was at total risk if proper measures are not taken early. For 400 unprotected people 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

**Corresponding author: E-mail: oldhamwj@yahoo.com;*

unprotected were infected. In the second part the protection was lifted to see how fast the total population was infected. For the case of 50% protected it took 400,000 iterations to infect the unprotected people. After the restrictions were lifted it took 150,000 to infect the other half. The simulations here were people based which has the advantage of seeing individual personal involvement. Results of infection rates were calculated for 1,000, 2,500, 5,000, and 10,000 people.
**Conclusions:** The propagation of the disease can be fast and depends on population density. Protection is vital to containing the disease. Restrictions must be lifted carefully and slowly or the total population is again at risk. According to the results obtained here the concept of HI is not a viable concept in controlling or managing the spread of the disease.

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

## 1. INTRODUCTION

The work described and presented here and in PI [1] was motivated by the current interest in disease propagation due to the coronavirus [2,3]. In PI our focus was on the propagation of the disease. In PII our attention was on the Herd Immunity (HI) concept. The HI concept says that if the percentage of the population that has been infected has passed a certain level then the propagation of the disease will be at an acceptable level. 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 work related to self-organization of small systems with simple dynamics [4,5]. These will be discussed briefly later to explain what was done here. Portions of the previous works are repeated here so that this paper is as clear and complete as possible. The work was performed on systems of 10,000 or fewer people in a square 512 by 512. A tag, z, was assigned to each person and we added a rule for infection transfer. We could then simulate the propagation of a disease. We assigned the z tag such that if z=0 the person was uninfected, if z=1 the person was infected, and if z=2 the person was immune to this disease. The rule to transfer infection between an infected person and an uninfected person was if the two people were closer together than the critical distance then the uninfected person was infected.. The system is started with the layout of the people in a square. The dynamics were applied and the people moved accordingly. Initially, two people were chosen at random and were infected. The infection rule was applied and the next iteration taken. One such step is referred to as an iteration. This continued for a preset number of iterations. We found that the propagation of the disease is alarming and if proper steps were not taken the whole unprotected population was at risk. However, even the early on infection rate is too high to be acceptable.

Mathematical and simulation methods have been used in epidemiology studies [6,7,8]. 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, [9]. Simulation of disease propagation has been in use since the 1980s [10-15] and is now in common use. The methods in use include Agent Based Modeling (ABM), Susceptible Infected Recovery (SEIR), and Susceptible Infected Recovery or Dead (SEIRD) models. The ABM models are similar to the method use here [16]. The model is based on agents which have assigned attributes. 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 people are infected based on distance to an infected person. The SEIR and SEIRD models are based on a set of differential equations. 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 was that one could get a good look at the details. The disadvantage was the limitation due to using a relatively small sample size. Our focus here was on the HI concept. This concept is that if the percentage of the population infected is greater than some specified amount then the rate of infection dwindles to an acceptable level. Our

results show that in managing and handling the spread of the disease HI is not a useful concept. The disease continues to propagate until all are infected. It is just a matter of time until all are infected.

## 2. METHODS

The method used in this research was computer simulation. The computer code was written for this project and was used for PI. The code was written in the c programming language, compiled with the gnu c compiler, and executed on the Debian version of Linux. There were no forces applied. The movement of the people was due to each person executing a random walk. Components of the random walk occurred 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 as follows:

1. n people were randomly distributed in a 512 by 512 square.
2. The distance between every pair of people was calculated.
3. The infection rule was applied.
4. The movement of the people was done, and the next iteration starting at 2 was done.

The parameters used are given in Table 1. In the beginning, two people were chosen to be infected. At each iteration each person was moved, and the distance between every pair of peoples was calculated. The infection was transferred to the uninfected person if the infected and uninfected people are closer than the critical distance. The critical distance was the equivalent of 10 feet on the ground. Then the next iteration was taken. The simulation continued through a preset number of iterations. A number of different sets of iterations were taken. The number of iterations can be interpreted as a time line so we could get a time analysis of how the disease progresses in time. The doubling time refers to the time it takes for the number of infections to double. The doubling times are a function of geography. A summary of doubling times are given in [17]. If we use two weeks as the doubling time we can get a time per iteration in our simulation. From one of the curves we got a doubling from 30,000 infections to 60,000 infections in 10,000 iterations. This equates to about 2 min/iteration. For 100,000 iterations this is about 20 weeks. For 500,000 iterations this is about 100 weeks, close to two years. This is about where we are with covid-19. If no protection was in place, the disease progressed through a vulnerable population. This is what happens if steps are not taken to halt the progress. Later we made an allowance for some protection. This was 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 person not to get infected even if exposed. In Fig.1 an initial person distribution for 1000 people is shown. The results of the simulation are given in the Results and Discussion Section. The simulator was run for the number of people starting at 1,000, then for 2,500, 5,000, and 10,000.

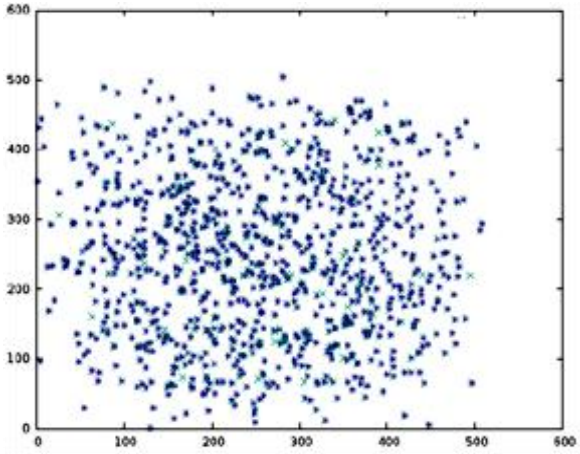


**Fig. 1. Initial person distribution 1000 people. x and y coordinates of a person**

## 3. RESULTS AND DISCUSSION

The infection transfer depends on the distance between people. 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 was about 0.057 units in our simulation. We used 10 feet that biases our results to favor infection transfer. In our simulation no person died or went away. If a person left the square due to the dynamics then that person was reinserted at a random location in the square. The total number of people remained constant. There was also no cure or recovery included. That is, an infected person remained infected for the duration of the simulation. This gives a somewhat bleak picture of what can happen if effective measures are not taken.

**Table 1. The parameters used**

| Number of People | Number of Iterations | deltax | deltay | Distance of Infection | Number Protected |
|---|---|---|---|---|---|
| 1000 | 20K-500K | 0.001 | 0.001 | 0.057 | 0-90% |

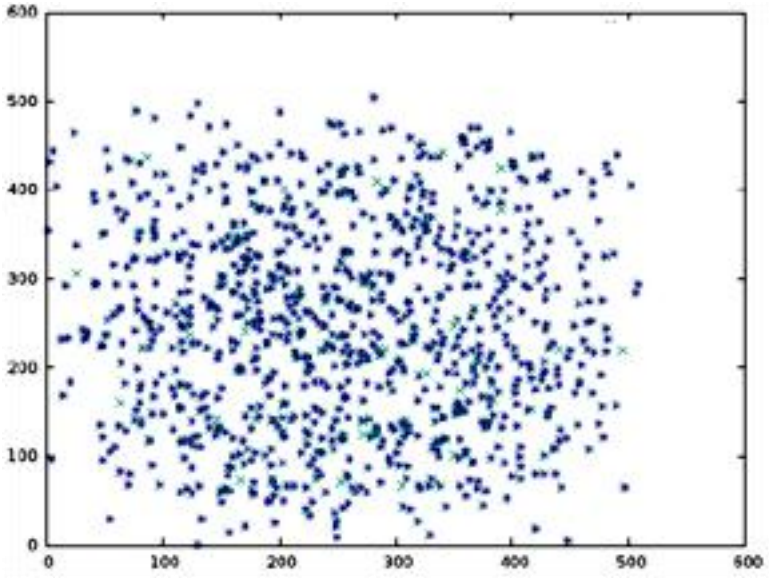


**Fig. 2. Final locations of people. 1000 people**
*No protection. 180K iterations. 962 infected.*
*Red cross infected people. Green x final position of the people.*

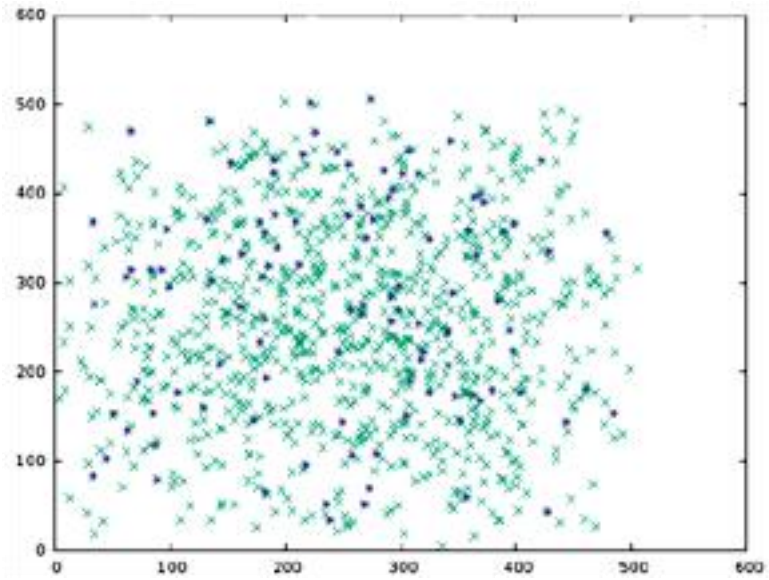


**Fig. 3. 1000 people. 500 protected. 140K iterations 110 infected. Green x uninfected people. Red cross infected people. x and y are coordinates of a person**

A summary of the parameters used is given in Table 1. As of August 26, 2021 the Internet states that worldwide 4,494,905 people have died, 191,692,845 have recovered, and there are now 20,110,545 active cases [18]. These reported numbers are probably lower than the actual count. It is clear these rates are unacceptable. To get started we show in Fig. 2

an infection rate of 96% after 180k iterations with 1000 people and no protection. In general the spread of the disease is faster with higher population density. Only a few cases are presented in PI due to the computer time required, but the infection rate dependency on population density is clear. It is interesting to note all of the curves have the same slope in the linear region. In Fig. 3 we show the infection after 140k iterations with 1000 people 500 protected and only 22% infected. These infection percentages are the percent of the vulnerable people that are infected. It can be seen that once the disease gets started, it propagates very rapidly through the population.

In Fig. 4 the percent of the vulnerable people infected versus the number of iterations is given. The results are for 0 protected, 200 protected, 300 protected, 400 protected, 500 protected, and 900 protected. These data show the value of protection however it was achieved. Again looking at Fig.4, it can be seen that these curves resemble the S shaped curve. Early on there were few carriers so the curve is flat. Later on there were more carriers and most of the population uninfected so the rate of infection increases. Even later there were many carriers, but few people to infect so the curve flattens.

In PI, we gave the same data but for 500,000 iterations. From that data it appeared that a 90% protected portion of the population would be safe. However, we ran more iterations and more cases. The results of these runs is also shown in Fig. 4. It takes longer for the 90% case to get moving, but once it does it infects the population rapidly. Then HI has no relevance.

Table2 shows results for a number of people, a large number of iterations, and a given protection percentage of 90 percent. Results are given for 1,000, 1,500, 2,500 and 5,000 people. The infection rate is very high. From our time line analysis 500,000 iterations corresponds to about 2 years. Hence, given enough time all of the unprotected will be infected. . These data show that HI is not a useful concept in managing or handling the disease. The goal was to include results for 10,000 people. The computer program had completed a small fraction of the iterations after nearly a week. A rough estimate showed it would take on the order of 50-60 days to complete. This job was halted.

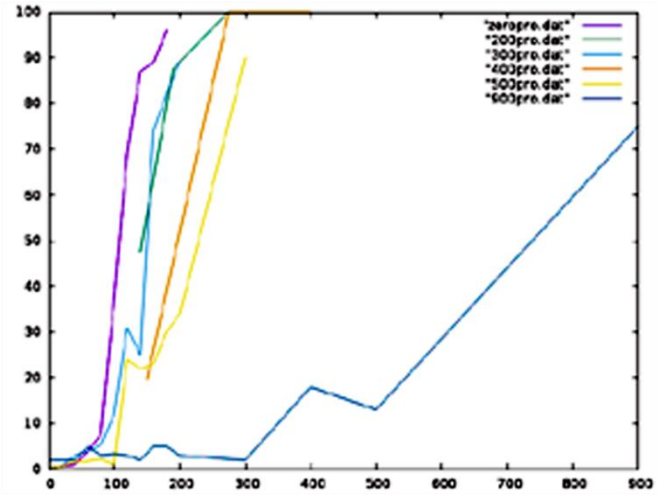


**Fig. 4 Plot of number of infections versus number of k iterations**

*See the legend in the upper right hand corner. xxxpro.dat means that xxx of the 1000 people were unprotected against the disease. The data is for 0 protected, 200 protected, 300 protected, 400 protected, 500 protected and 900 protected.*

**Table 2. The percent of the number of originally unprotected people infected after the given number of iterations.**

| # people | # protected | # unprotected | # iterations | # unprotected infected |
|---|---|---|---|---|
| 1000 | 900 | 100 | 400k | 98 |
| 1500 | 1350 | 150 | 500k | 26 |
| 2500 | 2250 | 250 | 450k | 48 |
| 5000 | 4500 | 500 | 500k | 96 |

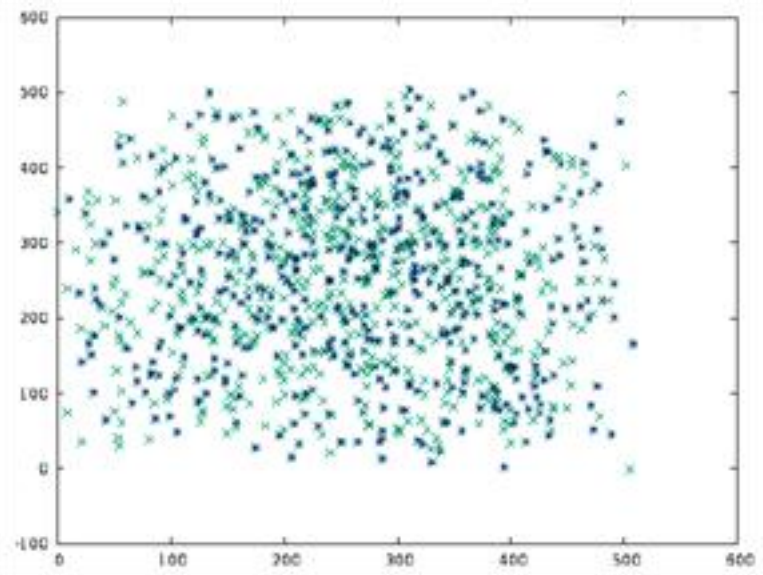

**Fig. 5. 1000 people. 500 protected. 400,000 iterations. All 500 unprotected infected. Green cross the 1000 people. Blue the 500 unprotected and infected. x an y are coordinates of a person**

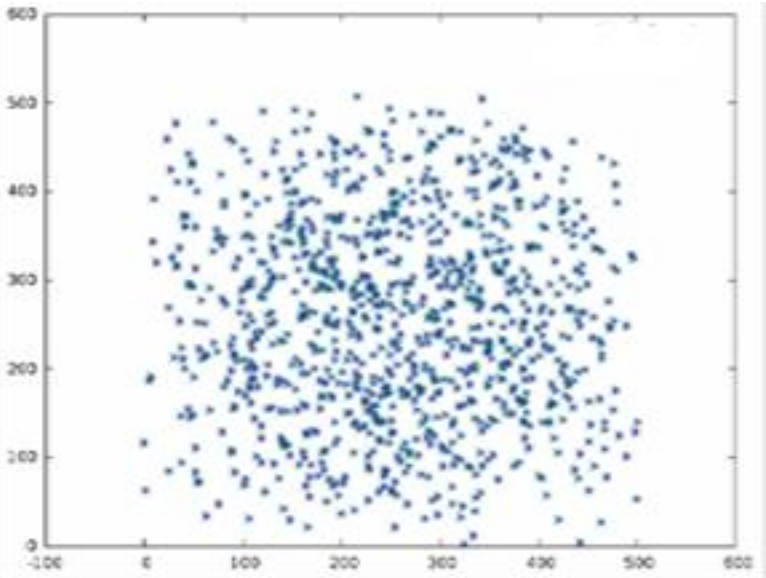

**Fig. 6. 1000 People 140,000 iterations after the restrictions removed. All infected after 150,000 iterations. x and y are the coordinates of a person.**

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 was no natural immunity at the beginning of the disease. In the current case lock down procedures were in place nationwide and worldwide. There was a lot of interest in releasing the requirements for business and economic reasons. We carried out a simulation whereby the protection is removed after all of the unprotected were infected. For 1000 people, 500 were originally protected. The simulation was run until all of the unprotected were infected. This took 400,000 iterations. The protective conditions were then removed and the simulation started using the people coordinates retained from the first part. After only 150,000 iterations all of the people were infected. The results are given in Figs.5,6. This demonstrates the hazards of removing protection measures

without adequate medical treatment or a widely available vaccine. The total population is at risk. From the view point of HI it is clear that it has no usefulness here.

## 4. CONCLUSIONS

The conclusions are as follows:

1. The concept of HI is of no value in fighting, managing, and handling the propagation of the disease.
2. From a small sample on a vulnerable population the disease spreads rapidly. The lethality of the disease makes early recognition and effective protective measures essential. The infection rate displays as the well-known S curve.
3. A larger population density makes transfer of the disease easier because breaching the critical distance is more likely. Our results are optimistic because people live in locations with high population density. We used a random distribution. This does not reflect the higher population density of big cities.
4. 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 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 people 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 the progression of the disease has a much slower rate at the start. The disease is better contained early on. However, without proper measures in place even 90% protected is not enough. Every unprotected person will get infected. The only way to stop the disease progression is an effective vaccine or restrictions on the movement of the infected people. A secondary issue is to get people to accept and take the vaccination injection.
5. One of the primary results was that removing the protective rules too soon leads to
   rapid spread of the disease. One of the surprising and significant results was the infection results for the originally protected part of the population after the restrictions were removed. What these results show is if the infected people are free to move around then eventually all of the people get infected.

Our results may be pessimistic in that there is a simple rule for transfer of the disease between a pair of people. On the other hand our results may be too optimistic. We started the simulation with the people randomly located in the square. We know that population density is a key factor in the propagation of the disease. In a city people live in much denser locales than a random distribution. We could add a probability of transfer to each unprotected person that would make it more difficult for the disease to propagate. We could also include some other attributes to each person 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

As per international standard or university standard written ethical approval has been collected and preserved by the author(s).

## COMPETING INTERESTS

Author has declared that no competing interests exist.

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