

# Viral Spreading Covid-19 in a Small-World Network

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November 16, 2020

## Abstract

In this paper we will be doing an in depth study of the Covid-19 pandemic modeled as a small-world network and how changes to this network (such as closing borders by removing nodes) affect the spread of the disease throughout the world. We start by investigating a model for the dynamics of the disease and its spread, then compare our model with real life data, then implement our model into a Small world network.

## 1 Introduction

A small world network is a system of nodes connected via edges in such a way that to get from one node to any other node, only a small number of edges need to be traversed.

The popular "6 degrees of separation" theory is a type of small world in which you and any other person in the world are connected via, on average, a maximum of 6 acquaintances.

The model is a combination of the regular lattice network and the random connection network, all of which are shown below:

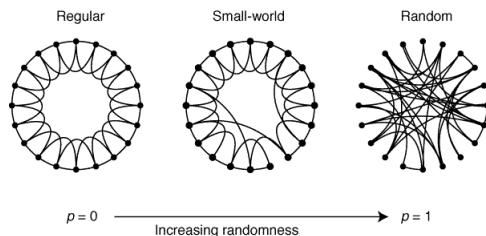


Figure 1: The 3 types of networks[1]

Where  $\rho$  is the random chance that an edge will swap nodes. A perfectly optimised value for  $\rho$  will yield a network with a very low average path length from one node to another. The regular graph will have a low path length to nodes in close proximity while a very long path length to nodes far away. On the other hand, a random graph will have completely random path lengths, sometimes a path may be really short and sometimes a path may be really long. A small word is an ideal network where there is just enough randomness so that a node can take a series of "shortcuts" to a far away node.

We will model the world's airports as a small world network. We will allow people to travel between nodes (i.e. fly from one country to another) via the small world network, with each person on a plane having a chance of being infected based on the number of infected people in the country they are leaving.

Before we start simulating disease spread in a small world network, we need to find a model that can relatively accurately represent the spread of a disease in a closed system.

To model the spread of covid, we will be using a variation of the SIR model, which we will touch on shortly, called the SEIRD model. We will attach this SEIRD model to each country, tracking the spread of Covid-19 in each country.

We will then attempt to simulate the Covid-19 pandemic and monitor its spread when different preventative measures are in place. Such measures include closing borders, implementing lockdowns, distributing masks, social distancing

and more. We will also monitor how lifting these preventative measures too early or implementing them too late causes a resurgence and/or fails to prevent covid's spread.

We will also attempt to simulate outrage/unrest in a country as people start becoming fed up with lockdown and start gradually decreasing their preventative measures and/or completely stop preventative measures.

## 2 The SIR Model

The very basic model for disease spread in a closed system is the SIR model. It stands for "Susceptible, Infectious and Recovered". It models a population into 3 categories, as shown below:

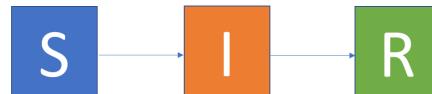


Figure 2: The SIR model in a closed system

In this model, a person starts out as being susceptible (i.e. able to contract the disease). When they contract the disease they become "infectious" and are able to spread the disease to others. After some time (the recovery time for that disease) they recover and are no longer able to spread the disease.

Initially in a disease outbreak for a population of  $N$  people, the number of infectious individuals is 1 and thus the number of people susceptible is  $(N - 1)$ .

The number of infectious people will grow exponentially based on the total number of susceptible people. However, since infectious people are no longer susceptible, the number of infectious people will stop growing exponentially after a certain period of time.

In conjunction with this, after a period of time infectious people will recover and no longer be able to spread or catch the disease.

We write this out as a system of ordinary differential equations:

$$\begin{cases} \frac{dS}{dt} = -\gamma \frac{S}{N} I \\ \frac{dI}{dt} = \gamma \frac{S}{N} I - \psi I \\ \frac{dR}{dt} = \psi I \end{cases}$$

Where  $\gamma$  and  $\psi$  are defined below:

$$\begin{cases} \psi = \frac{1}{T_R} \\ \gamma = R_0 \psi \end{cases}$$

Where  $T_R$  is the total time taken for a person to recover from the disease and  $R_0$  is a measure of the average number of people the initial infectious individual will directly infect over the course of their infection.

We can then show that this system is closed (i.e. that at any point in time the the total number of  $S$ ,  $I$  and  $R$  added together is constant).

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

$$\int \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} dt = \int 0 dt$$

$$S + I + R = C, \text{ where } C \text{ is a constant.}$$

Substituting in initials values for  $S$ ,  $I$  and  $R$ , we see that, intuitively, at any point in time the total number of  $S$ ,  $I$  and  $R$  is equal to the total population.

Since this system of ODE's is closed, we can represent it as a system of iterative equations:

$$\begin{cases} S_{i+1} = S_i - (\gamma \frac{S_i}{N} I_i) \Delta t \\ I_{i+1} = I_i + (\gamma \frac{S_i}{N} I_i - \psi I_i) \Delta t \\ R_{i+1} = R_i + \psi I_i \Delta t \end{cases}$$

Where each population group at  $i + 1$  is calculated using the population at  $i$ . Also,  $\Delta t$  is the change in time between  $i + 1$  and  $i$ . Note that the values for  $\gamma$  and  $\psi$  depend on the unit of time being used. If  $\Delta t$  is 1 **day**, then  $\psi$  should be calculated using the number of **days** a person takes to recover.

We see this system of iterative equations graphically below:

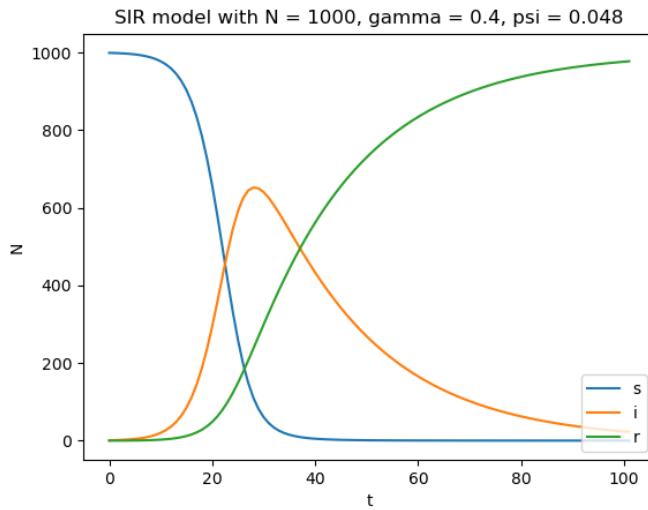


Figure 3: Graphical representation of the SIR model

### 3 Problems with the SIR model

Unfortunately, the SIR model is not a perfect model for disease spread, especially with Covid-19. There are many reasons on why we cannot use it as our model, which we will now touch on.

#### 3.1 Incubation period

In many diseases, there is a period of time in which an infected individual cannot transmit (or has very little chance of transmitting) the disease to others, because the pathogen is still reproducing/incubating in the individual and (thus) no symptoms have developed. This is the case with Covid-19. According to the WHO, Covid-19 has an incubation period of 5-6 days [2]. Which means that for the first 5-6 days a person is infected, they have an extremely low chance (a fraction of the original chance) to infect others. Thus, we cannot call these people infectious and have to separate them from  $I$ . This necessitates the creation of a third group of the population. The number of people carrying the virus who have not yet developed symptoms.

### 3.2 Importance of the incubation period and lockdowns

The incubation period is especially important to modeling the Covid-19 pandemic due to its importance regarding a lockdown. During a complete lockdown, we can assume that there is zero chance of an individual spreading Covid-19 to another individual and thus the number of infected individuals should suddenly stop increasing as soon as the lockdown is in place and then start gradually decreasing as people recover. Such a scenario would look like so:

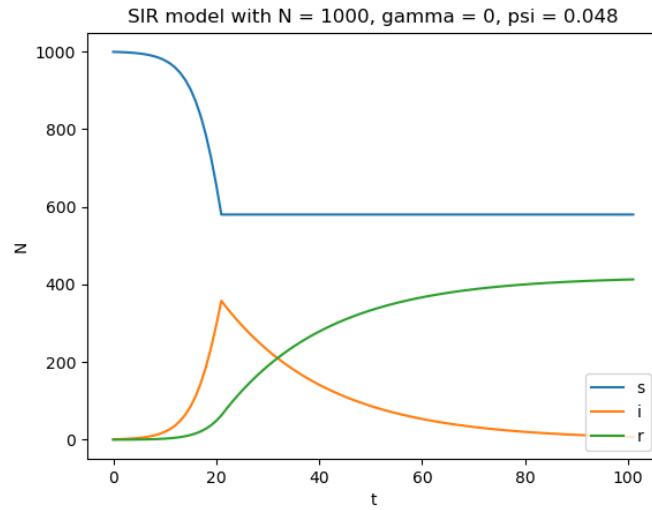


Figure 4: Graphical representation of the SIR model

At  $t = 20$  we introduce a lockdown, and as we expected from our SIR model, the number of infected individuals suddenly stopped increasing and started decreasing as people started to recover.

Let us compare this graph to real life data. The graph below shows the Covid-19 pandemic in Italy:

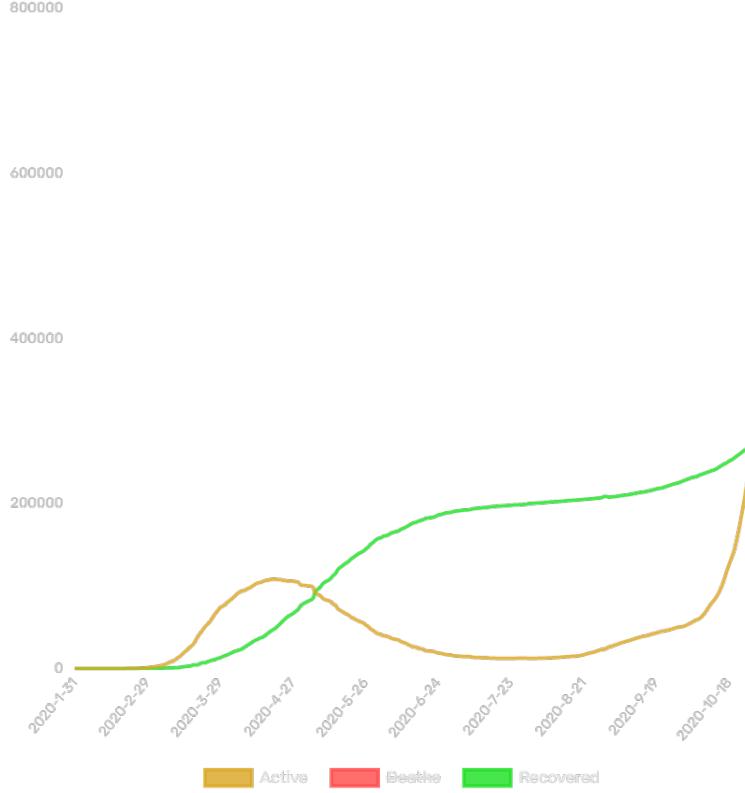


Figure 5: Covid-19 pandemic in Italy, taken from CovidVisualiser[3]

As we can see, the SIR model looks nothing alike when compared with the real life results. Lockdown commenced in Italy 37 days after the first case was recorded, yet the number of cases continued to increase. On the 9th of May (when lockdown started) there were 7,985 recorded cases, yet the number of cases increased more than 10-fold to a peak of 108,257 cases on the 19th of April. This is due to several factors. The main factor being that:

Infected people who had no symptoms (i.e. Covid-19 is still incubating) at the start of lock down, are now starting to develop symptoms and are then being tested. Thus there is a delay between the starting time of lockdown and the time where active cases ( $I$ ) starts decreasing, which we see in the real life example. As a side note, this stresses the importance of early testing since the lockdown date was started based on the number of symptomatic people, not the number of actual people infected. If people were tested early (i.e. a day or two after contracting the virus, during the incubation period) then Italy would have realised that the number of people with the virus in them is drastically more than the number of people showing symptoms.

This further necessitates the creation and tracking of a 4th group of the population, the number of people infected with the virus but not yet showing symptoms. We call this population the "exposed" population,  $E$ .

### 3.3 Mortality of Covid

Another problem with the SIR model is that there is only one group that people join after being infectious. It either assumes that every infectious person recovers, every infectious person dies, or lumps the number of dead and recovered people into one group called "removed". This is a problem for two reasons: 1) We want to show record the number of deaths the pandemic will cause and show how preventative measures directly impact the number of deaths in a country. 2) Not taking the death rate into account would make the model less accurate as people die and recover at different rates. Death rates are also different for each country due to many factors, some of which we will touch on later.

## 4 Developing a new Model

We will now begin my developing a new model by combining two popular models together.

## 4.1 The SEIR model

The first alternative to the SIR model, is the SEIR model. We touched on how the Covid-19 pandemic needs to be modeled by a system that tracks the exposed population,  $E$ .

This model does just that.



Figure 6: SEIR model diagram

Here we see the SEIR model, similar to the SIR model, except infected individuals are first considered "exposed" and then after an incubation time they are considered "infectious". Our system of ordinary differential equations from the SIR model is now modified to following:

$$\left\{ \begin{array}{l} \frac{dS}{dt} = -\gamma \frac{S}{N} I \\ \frac{dE}{dt} = \gamma \frac{S}{N} I - \epsilon E \\ \frac{dI}{dt} = \epsilon E - \psi I \\ \frac{dR}{dt} = \psi I \end{array} \right.$$

Notice that the number of susceptible individuals still decreases at a rate proportional to  $I$  because only infectious individuals can spread the disease. It also follows that the number of exposed individuals increases proportional to the number of infectious individuals as an individual must first be exposed before they can become infectious.

Similar to the SIR model, this system is closed. Which means that at any time  $t$ :

$$S + E + I + R = N$$

We can then write this model as an system of iterative equations.

$$\begin{cases} S_{i+1} = S_i - (\gamma \frac{S_i}{N} I_i) \Delta t \\ E_{i+1} = E_i + (\gamma \frac{S_i}{N} I_i - \epsilon E_i) \Delta t \\ I_{i+1} = I_i + (\epsilon E_i - \psi I_i) \Delta t \\ R_{i+1} = R_i + (\psi I_i) \Delta t \end{cases}$$

Where  $\gamma$  and  $\psi$  and  $\epsilon$  are defined below:

$$\begin{cases} \psi = \frac{1}{T_{inf}} \\ \gamma = R_0 \psi \\ \epsilon = \frac{1}{T_{inc}} \end{cases}$$

Where  $R_0$  is the same as the  $R_0$  used in the SIR model,  $T_{inc}$  is the incubation time in days and  $T_{inf}$  is the time a person is infectious for, also in days.

We can now represent this system graphically:

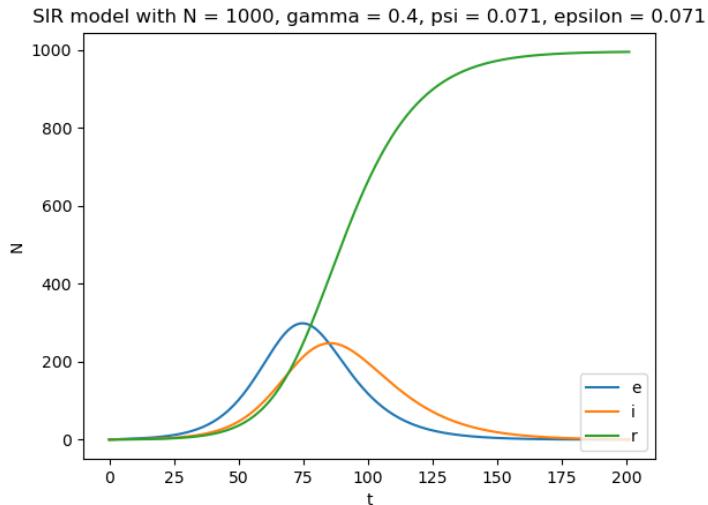


Figure 7: Graph showing the SEIR model in action

Now, lets implement a lock down at  $t = 20$ .

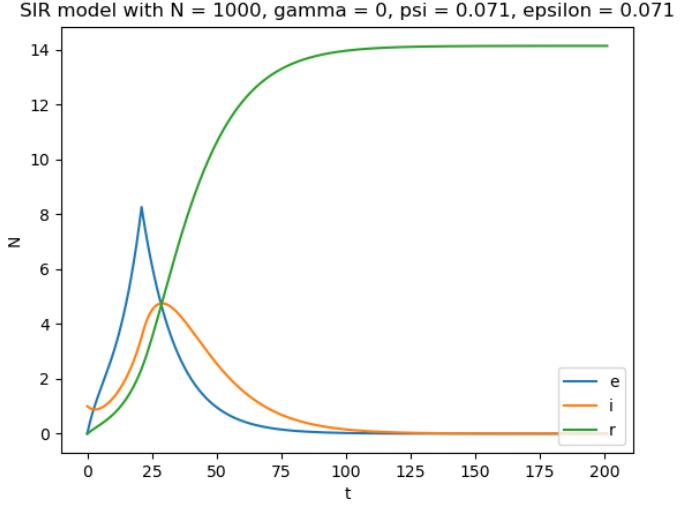


Figure 8: The SEIR graph, but with a lockdown occurring at  $t = 20$

We see the peak number of infectious cases, 5, in the SEIR graph with lockdown at  $t = 20$  drops significantly from the peak number of infectious cases, around 250, in the graph with no lock down.

We more importantly see that while the number of exposed individuals suddenly stops increasing and starts decreasing, the number of infectious individuals continues to rise for some time after lock down starts. The graph of infectious individuals in the SEIR model with lockdown is also a lot smoother of a curve than the graph of infectious individuals for the SIR model with lock down, fitting a curve similar to that of real life.

## 4.2 The SIRD model

Another variation of the SIR model is the SIRD model. In this model, infectious individuals either die or they recover. We may represent this with the following diagram:

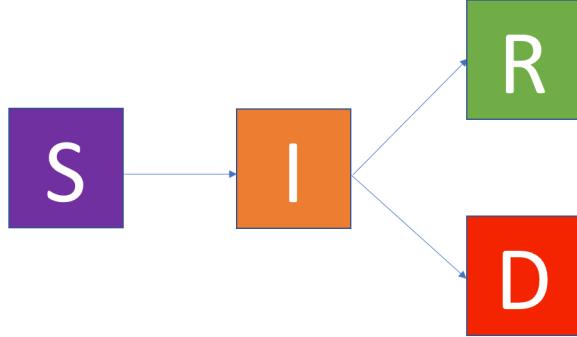


Figure 9: A model of the SIRD system

This can be shown as the following system of ordinary differential equations:

$$\begin{cases} \frac{dS}{dt} = -\gamma \frac{S}{N} I \\ \frac{dI}{dt} = \gamma \frac{S}{N} I - \psi I - \lambda I \\ \frac{dR}{dt} = \psi I \\ \frac{dD}{dt} = \lambda I \end{cases}$$

Where  $\gamma$  and  $\psi$  and  $\lambda$  are defined below:

$$\begin{cases} \psi = \frac{1}{T_{inf}} \\ \gamma = R_0 \psi \\ \lambda = M \psi \end{cases}$$

Where  $M$  is the mortality rate of the disease (i.e. the chance that the average person will die from the disease).

This model is often used to model diseases with no/low incubation time. It takes into account and tracks the number of deceased individuals,  $D$ , which is something we want our model to do as well. It is also a closed system and be shown as a system of iterative equations.

### 4.3 Our Covid-19 SEIRD model

Finally, combining the SIRD model with the SEIR model, we arrive at our new model, the SEIRD model.

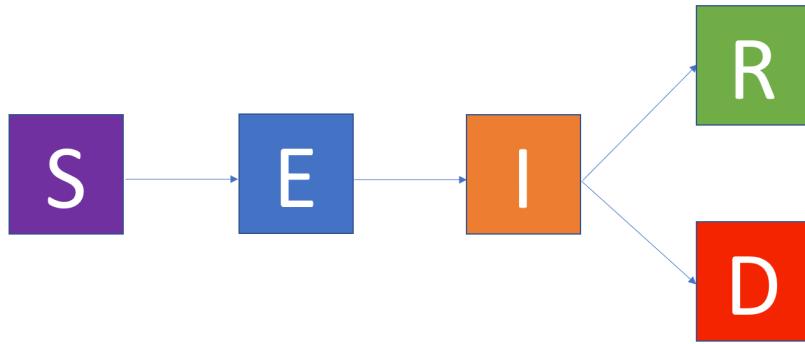


Figure 10: A model of the SEIRD system

In this system, a non-infected individual starts out as being susceptible  $S$ . After coming into contact with the virus, they then become exposed  $E$ . After the disease has incubated for a period of time,  $T_{inc}$ , they become infectious  $I$  and can spread the disease to others. After a period of time, they either die  $D$  or they recover  $R$ . This is the bare minimum model needed to accurately describe the Covid-19 pandemic.

The system can be represented as the following system of ordinary differential equations:

$$\left\{ \begin{array}{l} \frac{dS}{dt} = -\gamma \frac{S}{N} I \\ \frac{dE}{dt} = \gamma \frac{S}{N} I - \epsilon E \\ \frac{dI}{dt} = \epsilon E - \psi I - \lambda I \\ \frac{dR}{dt} = \psi I \\ \frac{dD}{dt} = \lambda I \end{array} \right.$$

Where  $\gamma$  and  $\psi$ ,  $\lambda$  and  $\epsilon$  are defined below:

$$\left\{ \begin{array}{l} \psi = \frac{1}{T_{inf}} \\ \epsilon = \frac{1}{T_{inc}} \\ \gamma = R_0 \psi \\ \lambda = M \psi \end{array} \right.$$

The death rate of Covid-19 depends largely on a single factor: The age distribution of a country (since Covid-19 kills at much higher rate for older populations). While there are many other factors that may affect the mortality rate of Covid-19 in a country (such as the country's access to healthcare), we will only consider this factor for simplicity.

We then say that the mortality constant,  $\lambda$ , is defined as:

$$\lambda = \alpha \psi$$

Where  $\alpha$  is calculated as the percentage chance the average person with Covid-19 will die in that country, based on age distribution. We take the average death chance of Covid in Italy for each age group as our baseline. For ages 0-14, 15 - 64 and 65+ the death chances are 0%, 1.14% and 17.25%. We then multiply each death chance by the respective % of the population that group represents in that country. For Italy, it is 13.5 %, 63.5 % and 23.0% then add that together to get a final value for  $\alpha$ .

Once again, the system is closed and can be expressed as a system of iterative equations.

$$\left\{ \begin{array}{l} S_{i+1} = S_i - (\gamma \frac{S_i}{N} I_i) \Delta t \\ E_{i+1} = E_i + (\gamma \frac{S_i}{N} I_i - \epsilon E_i) \Delta t \\ I_{i+1} = I_i + (\epsilon E_i - \psi I_i - \lambda I_i) \Delta t \\ R_{i+1} = R_i + (\psi I_i) \Delta t \\ D_{i+1} = D_i + (\lambda I_i) \Delta t \end{array} \right.$$

Finally, we can visualise our model graphically.

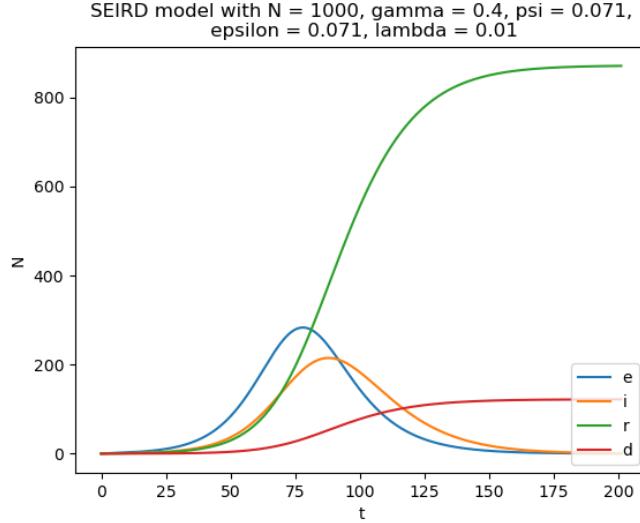


Figure 11: Graphical representation of our SEIRD model

From the graph above we see a system that accurately describes a pandemic where no preventative measures are taken to stop the spread of the disease.

## 5 Perfecting the SEIRD model

### 5.1 Implementing a lock down

We will now implement a lockdown, just like we did for the SIR and the SEIR model and compare it to that of real life.

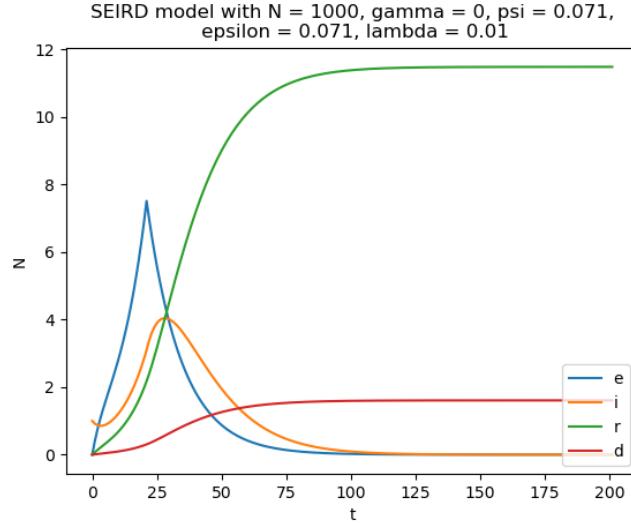


Figure 12: Graphical representation of our SEIRD model with lockdown at  $t = 20$

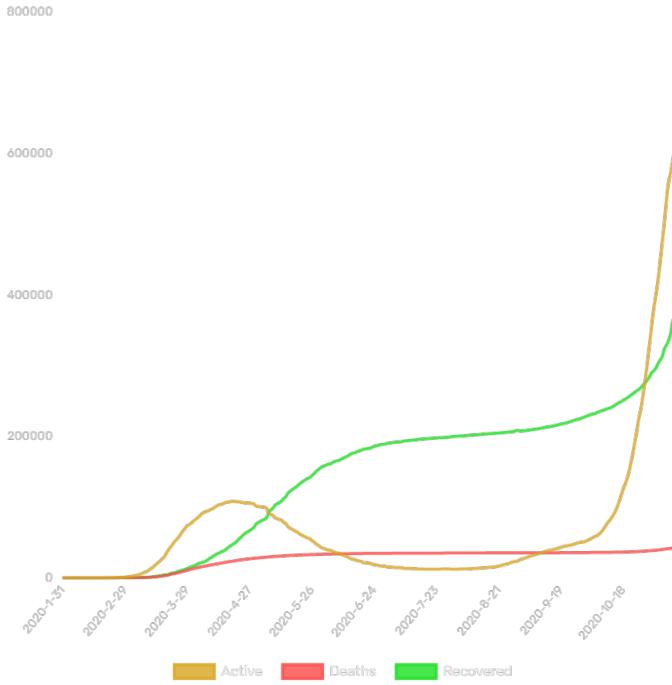


Figure 13: Graph showing real life data of the Covid-19 pandemic in Italy

As we can see, the two graphs are very similar in shape. There is, however one crucial difference. Italy has a massive resurgence of Covid-19 a few months after lockdown ended on the 18th of May. After the first initial peak of 108,257 cases on the 19th of April, there is a steady decrease in cases all the way until a local minimum of 12,248 cases on the 21st of July. After this local minimum, the number of covid cases start to steadily, but exponentially, increase until suddenly, on the 5th of October, the number of cases starts to rapidly increase to an amount of 635,054 on the 12th of November, which is almost 6 times more than the previous max on the 19th of April.

We shall attempt to describe this profound behaviour.

## 5.2 A Premature Celebration

Never count your chickens before they hatch. On the 18th of May, lockdown in Italy was suspended. This date was far too early for lockdown to end and as a result the number of infected individuals was never reduced to zero, resulting in a second wave of the Covid-19 pandemic. This time with a much larger initial number of infected individuals. However, this not the full story.

## 5.3 Preventative measures

While a second wave took place, it occurred quite long after the end of lockdown. This is most likely due to several preventative measures being put into place to prevent further spread. These preventative measures include, but are not limited to:

1) Social distancing (physically).

This includes keeping a physical distance from people we interact with, such as standing 1 meter apart in the queue at a store.

2) Wearing Masks

3) Social distancing (socially, i.e seeing less people per day)

Lockdown ended and the gradient of the active cases starts to increase. Looking at the graph for Covid-19 in Italy, we can assume that after lockdown ended,  $\gamma$  was changed from 0 to some small positive fraction. Gamma must have been initially quite small as the number of active cases took a long time to start increasing again.

We can represent  $\gamma$  as a product of all the factors affecting the spread of Covid-19 and some constant,  $C_1$ .

Let the percentage of the population practicing social distancing be  $\sigma$ . We also let the percentage of the population wearing masks be  $\mu$ .

We can then say that:

$$\gamma = C_1(1 - \mu)(1 - \sigma)$$

This assumes that if every person practiced social distancing or if every person wore a mask at all times, then there would be no new infections as  $\gamma = 0$ . However, this is not the case as we know that Masks and social distancing are only so effective.

According to the world health organisation, social distancing of 1m apart from others can reduce Covid spread [4] by 82%. We can then say that if the entire population practiced social distancing, the maximum amount that gamma would be reduced by is 82%. Similarly, the WHO has also stated that wearing masks can reduce Covid spread by 85%. We then say that:

$$\gamma = C_1(1 - 0.85\mu)(1 - 0.82\sigma)$$

Here,  $C_1$  is actually just  $R_0\psi$  since  $R_0$  is the number of people an infectious person will infect over their infectious period, which suggests we must divide by the number of days someone is infectious for.

$$\gamma = R_0\psi(1 - 0.85\mu)(1 - 0.82\sigma)$$

$R_0$  will be different for each country. Some countries have extremely high interaction with others (like Italy) and an infectious person may infect several people per day and have a relatively high  $R_0$ , whereas some countries will have very little interaction with others (such as Finland) and will have a relatively low  $R_0$ .

For simplicity however, we shall use Italy as a baseline with  $R_0 = 9$  and assume that other countries had preventative measures put into place once they noticed the severity of Covid-19 but it got out of control.

Another important thing to note is that  $\gamma$  may or may not be a constant. If more people over time get access to masks, then  $\mu$  is an increasing function over time. Similarly, if more people start practicing social distancing over time due to increased public awareness, then  $\sigma$  is also an increasing function over time.

On the other hand, if more people become fed up with the pressures/stress of quarantine, the number of people wearing masks or practicing social distancing may reduce over time.

## 5.4 Stress and Tensions rise

Many countries who had their first Covid-19 patient early in the year have had drastic resurgences in active cases recently. Protests are taking place all over the world against the measures put in place by quarantine. During this period of chaos, very few people are social distancing or wearing masks, causing the number of active cases to increase dramatically.

Our model will then have to take into account that after a certain period of time after the number of active cases has reached a minimum, a period of "chaos" will begin and people will stop wearing masks and stop social distancing.

## 5.5 Phases to a lockdown

Another important factor to take into account is that a lockdown will have phases/level's to its "strictness". A lockdown may start out at level 5 and have zero people making contact with others but then after a few weeks lower a level or two, allowing people to make infrequent contact with others.

## 5.6 Implementing all the factors graphically

Now that we have discussed what factors increase and decrease the rate of spread of Covid-19 during a pandemic, let us take a look at how these contribute to the shape of our SEIRD graph.

Let us assume that Covid-19 was introduced into a population of  $N = 10000$  with an infection constant  $\gamma = 1$ . We assume that the spread of Covid-19 follows the standard SEIRD model we have defined with the following exceptions:

- 1) A lock down takes place at  $t = 30$ . Here the lockdown is at a maximum level and  $\gamma = 0$ .

- 2) After  $t = 40$  the lockdown is put into a less strict level where  $\gamma = 0.1$ .
- 3) After  $t = 50$  the lockdown is put into a slightly more strict level where  $\gamma = 0.09$ .
- 4) After  $t = 60$  the lockdown is put back into a maximum,  $\gamma = 0$ .
- 5) After  $t = 100$  the lockdown is lifted, but masks are being worn and preventative measures are in place,  $\gamma = 0.1$ .
- 6) Finally, after  $t = 170$  tensions rise and people have started protesting and/or have stopped most of their preventative measures,  $\gamma = 0.4$ .

Plotting this we have the following graph:

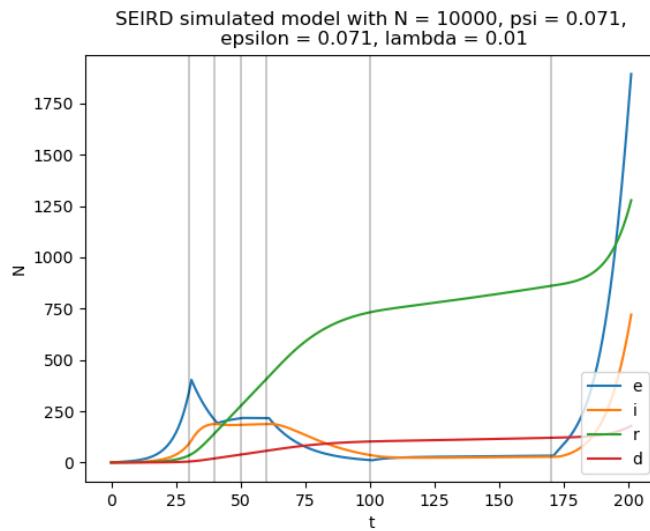


Figure 14: A graph showing our simulated pandemic

We can see from the graph that the number of exposed individuals,  $E$ , follows the behaviour we would expect. After the first lockdown phase, there are no new infections and  $E$  starts decreasing. After the second phase,  $E$  starts to increase slightly due to the lowered strictness of lockdown and then starts to flatten a little more as the third phase takes place. Then after the fourth phase occurs,  $E$  starts to decrease once again. Lockdown is ended at  $t = 100$ , a time where the number of active cases has yet to be reduced to zero. But since preventative measures are in place, the number of exposed only gradually increases. Then at  $t = 170$  when the chaos period begins the number of exposed individuals rapidly increases.

Let us now look at the number of infectious individuals,  $I$  and the number of deceased individuals,  $D$ .

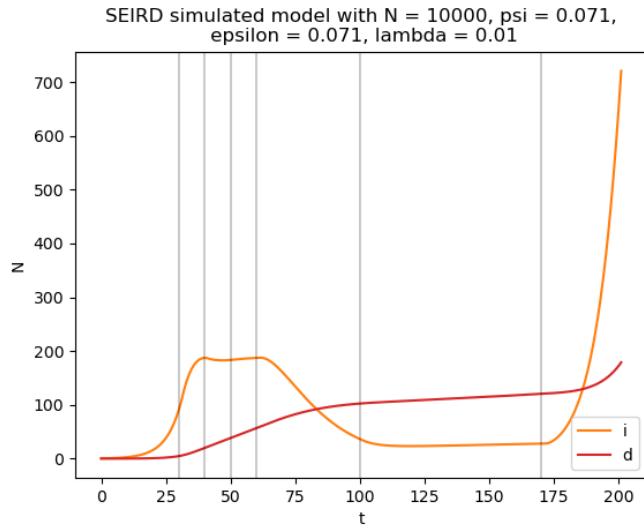


Figure 15: A graph showing our simulated pandemic, but only showing E and D

This graph has an almost identical shape to the pandemic in Italy, shown below:

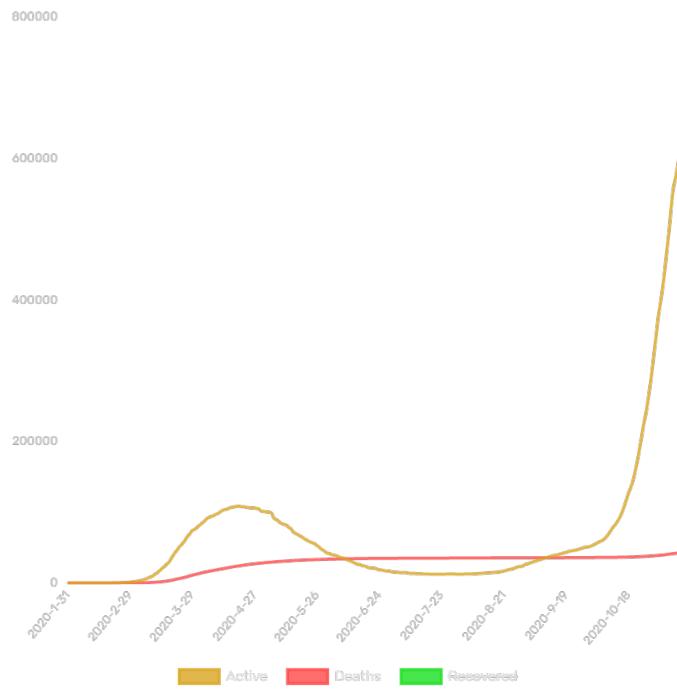


Figure 16: Real life statistics for the pandemic in Italy, CovidVisualiser

We have proven that our model can yield results similar to real life statistics, including the implementation of lock downs. All that is left for our model is to find the values for the different constants.

## 5.7 Constant values for our simulation

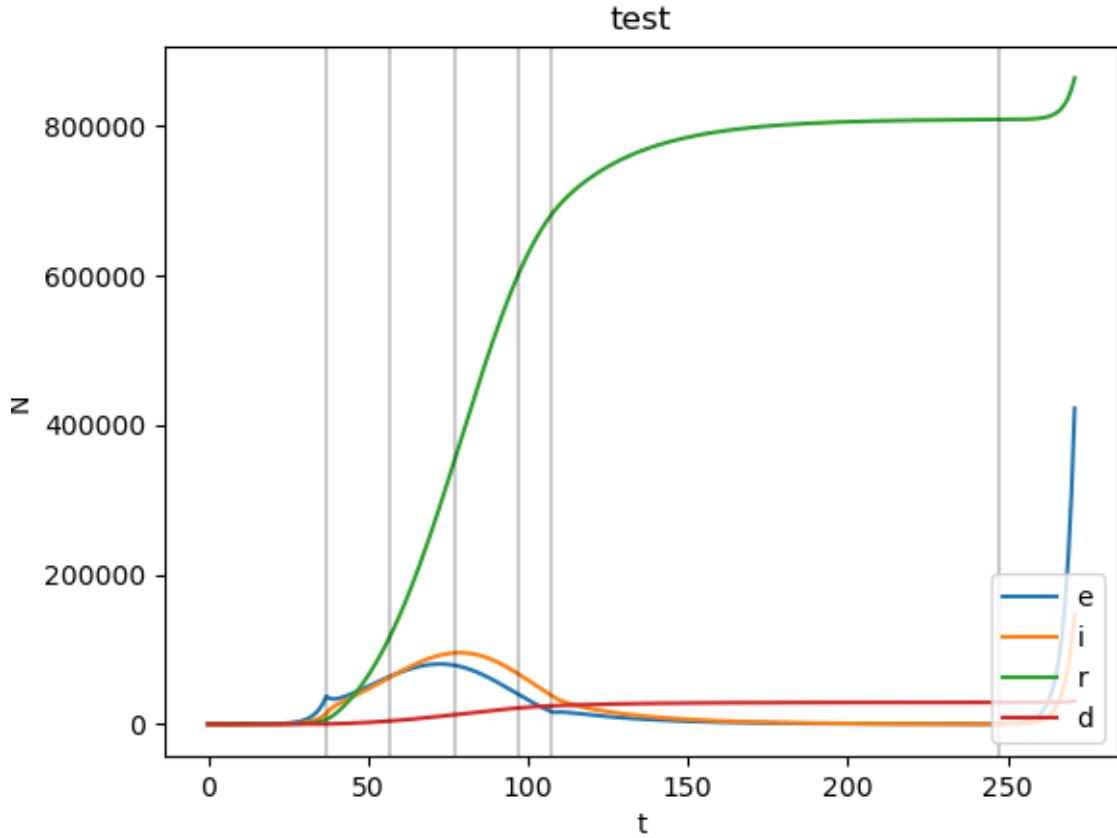


Figure 17: Our "close enough" model for Italy

In this graph, we have defined the following constants for our model:

$$\begin{cases} \psi = \frac{1}{7} \\ \epsilon = \frac{1}{5.5} \\ \gamma = 9(\psi) \\ \lambda = \alpha\psi \end{cases}$$

Using a text file filled with Countries and their associated population, we fill out the values for  $N$  for each country. We also use a text file filled with population distributions for each country, which was taken from wikipedia[5], to compute  $\alpha$ . Using data from Italy [6], we define the Mortality rate  $\xi$  by age group to be:

$$\begin{cases} \xi = 0\% & \text{for ages}[0, 14] \\ \xi = 1.14\% & \text{for ages}[15, 64] \\ \xi = 17.25\% & \text{for ages}[65, \infty) \end{cases}$$

Now, it is finally time to attach our model to countries in a small world network.

## 6 The Small World Network

### 6.1 Setting up a basic Small World

Let us begin by generating, and then analysing, some basic small world networks.

```
public void populateSmallWorld(double beta, int K, int N)
{
    //creating regular lattice
    this.N = N;
    for(int i = 0; i < N; i++)
    {
        //nodes.add(new Node(i));
        for(int j = i+1; j < N; j++)
        {
            if(Math.abs(i-j)%(N - K/2) <= K/2 && i!=j)
            {
                edges.add(new Edge(new Node(i), new Node(j)));
            }
        }
    }
    //rewiring according to beta
    for(int i = 0; i < N; i++)
    {
        for(int j = i + 1; j < i + K/2 + 1; j++)
        {
            if(Math.random() < beta)
            {
                int k = (int)(Math.random() * (N+1));
                replaceEdge(new Edge(new Node(i), new Node(j%N)), new Edge(new Node(i), new Node(k)));
            }
        }
    }
}
```

Figure 18: Code I created to generate a small world

In the above code, edges are added to the graph in the shape of a regular lattice. Then, once the regular lattice has been generated, we iterate through the number of edges again, but this time at each edge, there is a chance for the edge to be replaced with another, swapping nodes. This chance is dependent on the values of  $\beta$ , with 0 being no chance of a edge being swapped and 1 being a guaranteed chance that an edge will be replaced with another. Here,  $K$  is the number of edges stemming from each node, and  $N$  is just the number of nodes in the network.

We may vary these values to suit our needs.

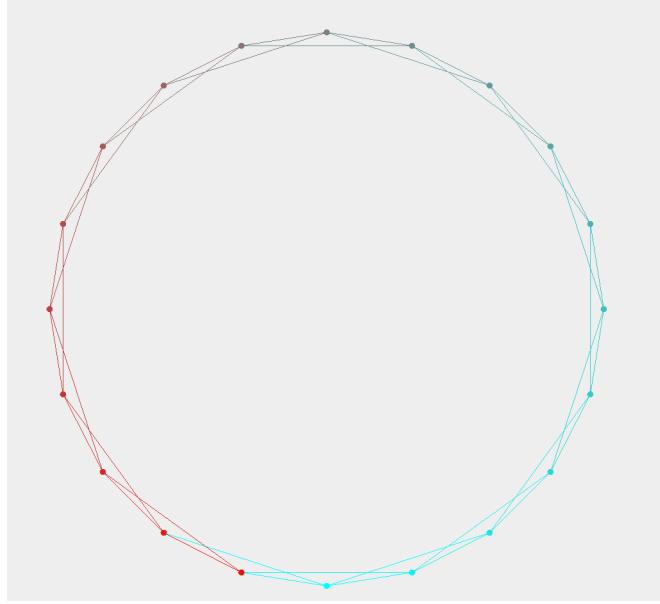


Figure 19: Network generated from  $\beta = 0$ ,  $k=4$  and  $n=20$

Here we see a regular lattice is generated, since  $\beta = 0$ , therefore zero chance of edge replacement. We note that each node is connected to 4 others directly. Let us take a look at varying our values for  $\beta$ .

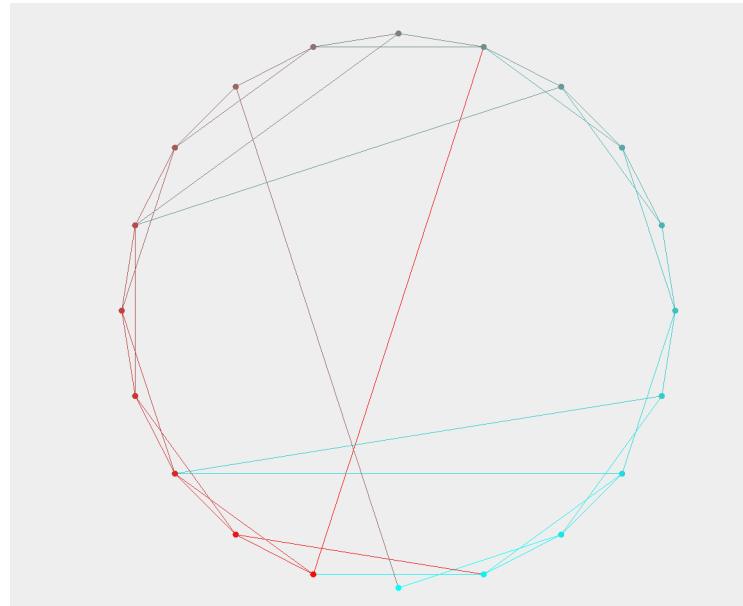


Figure 20: Network generated from  $\beta = 0.2$ ,  $k=4$  and  $n=20$

Here we see that a few edges have been randomly replaced with others, allowing for a few "short cuts" to appear.

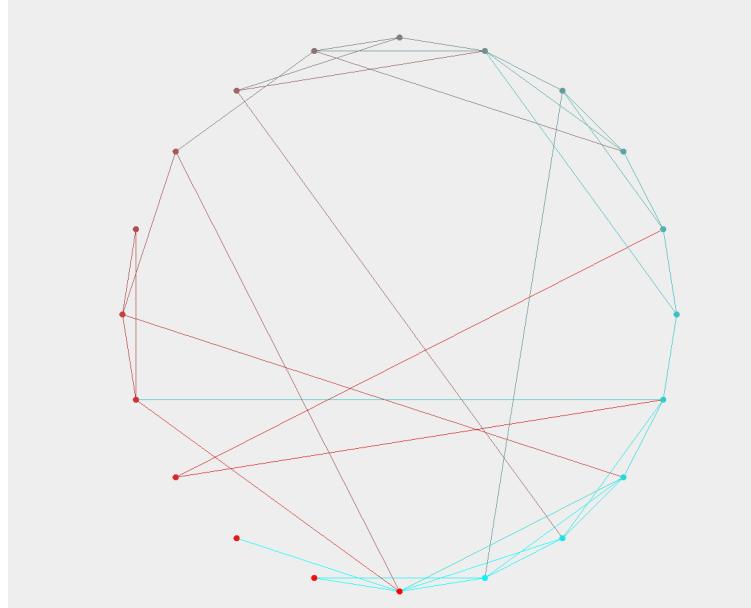


Figure 21: Network generated from  $\beta = 0.4$ ,  $k=4$  and  $n=20$

We see that with an even higher value of  $\beta$  there are more edges that were randomly replaced.

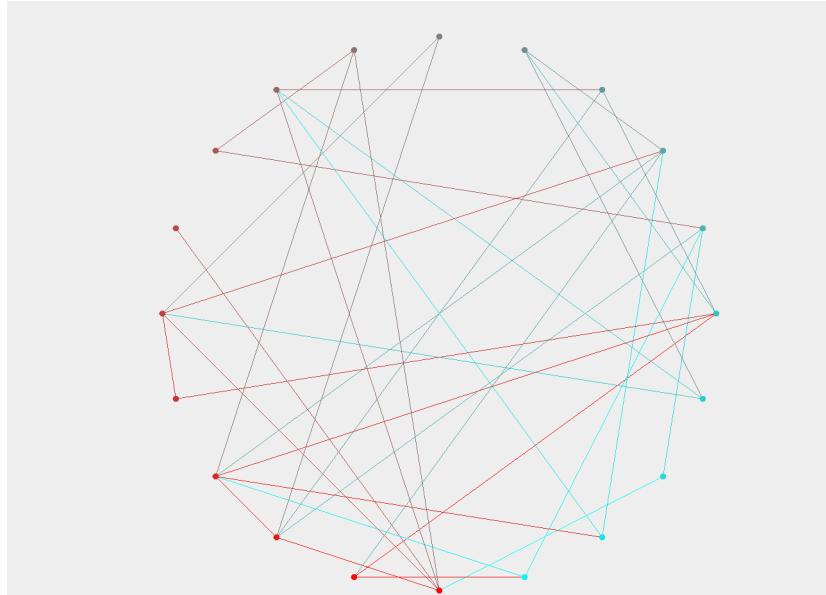


Figure 22: Network generated from  $\beta = 1$ ,  $k=4$  and  $n=20$

Finally, when we let  $\beta = 1$ , we see that our network is completely random.

## 6.2 Largely populated networks

Since we have a solid foundation for disease spread, our SEIRD model, we may conduct some experiments on how varying the values for  $k$  and  $\beta$  affect the spread of Covid-19 throughout the world. But first, let us take a look at how a largely populated network reacts to changes in  $k$  and  $\beta$ .

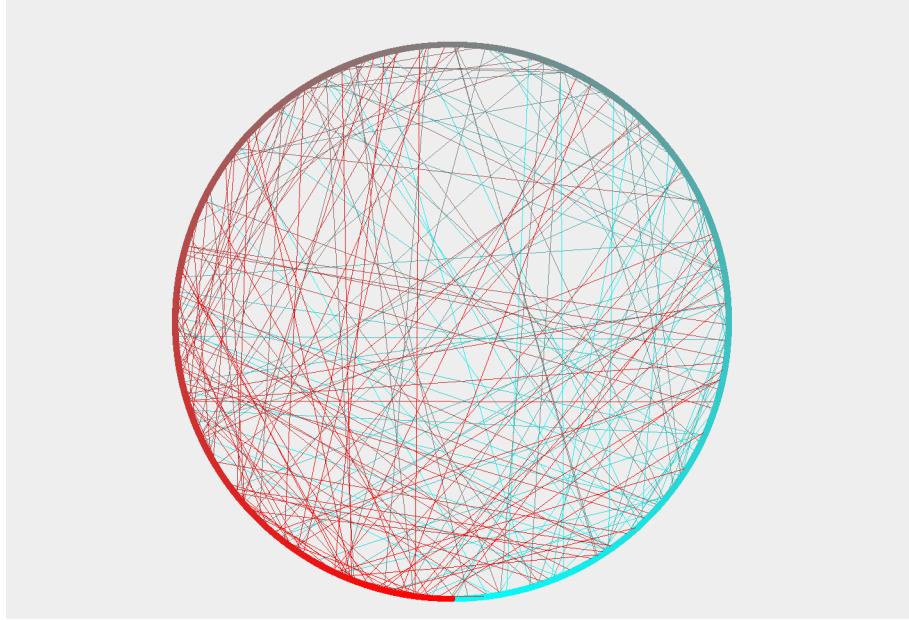


Figure 23: Network generated from  $\beta = 0.01$ ,  $k=4$  and  $n=10000$

We see in the above network, that even a really small value of  $\beta$  results in a relatively large amount of random connections. This is intuitive of course, the more nodes, the more chances an edge can be replaced. But it goes to show that the slightest variations can yield drastic changes to the results in our network.

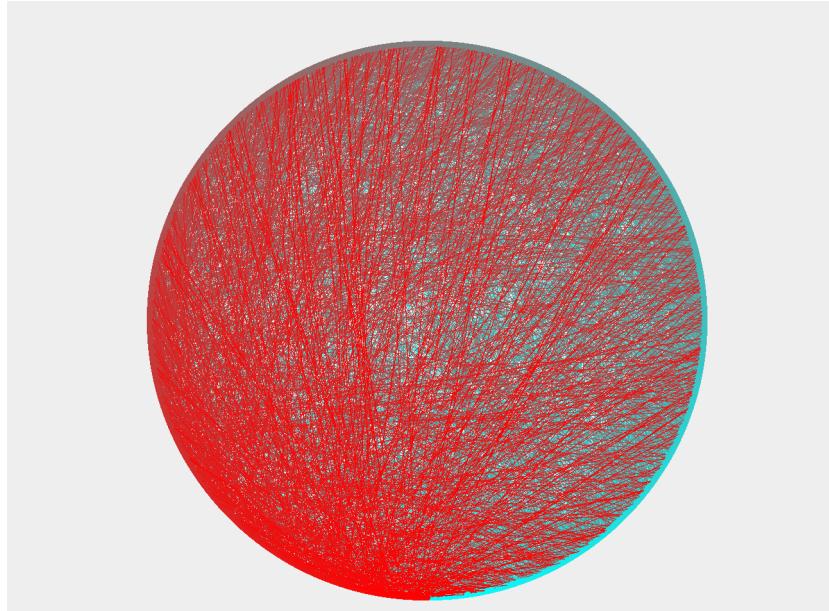


Figure 24: Network generated from  $\beta = 0.2$ ,  $k=4$  and  $n=10000$

We see here that with a 20% chance of edge replacement, the network is a thick mesh.

Let us halve the number of direct connections and see what happens.

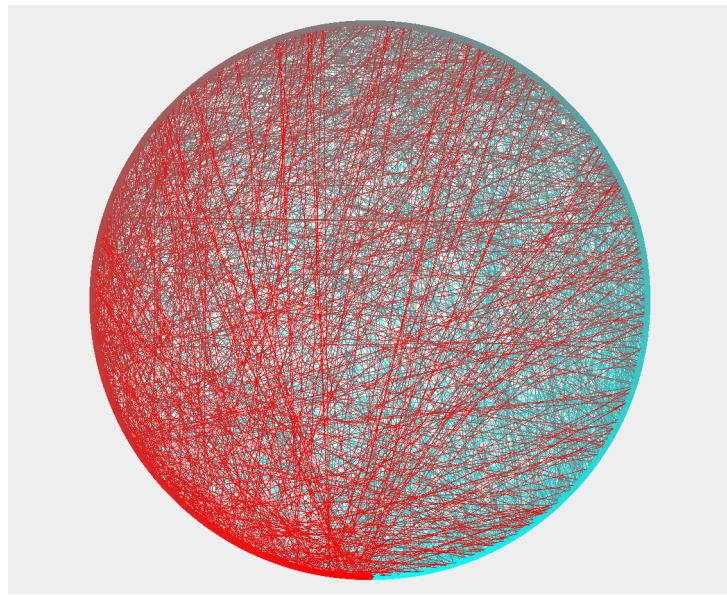


Figure 25: Network generated from  $\beta = 0.2$ ,  $k=2$  and  $n=10000$

We see here that the "thickness" of the mesh is a lot lower.

### 6.3 Fitting the airports in our small world network

After iterating through a text file[7] and discarding outliers (we don't care about airports in Antarctica or other remote regions), we generate a list of airports with x and y coordinates as well as the countries they belong to.

We assign airports to nodes and plot them in their real life coordinates. This looks like the following:

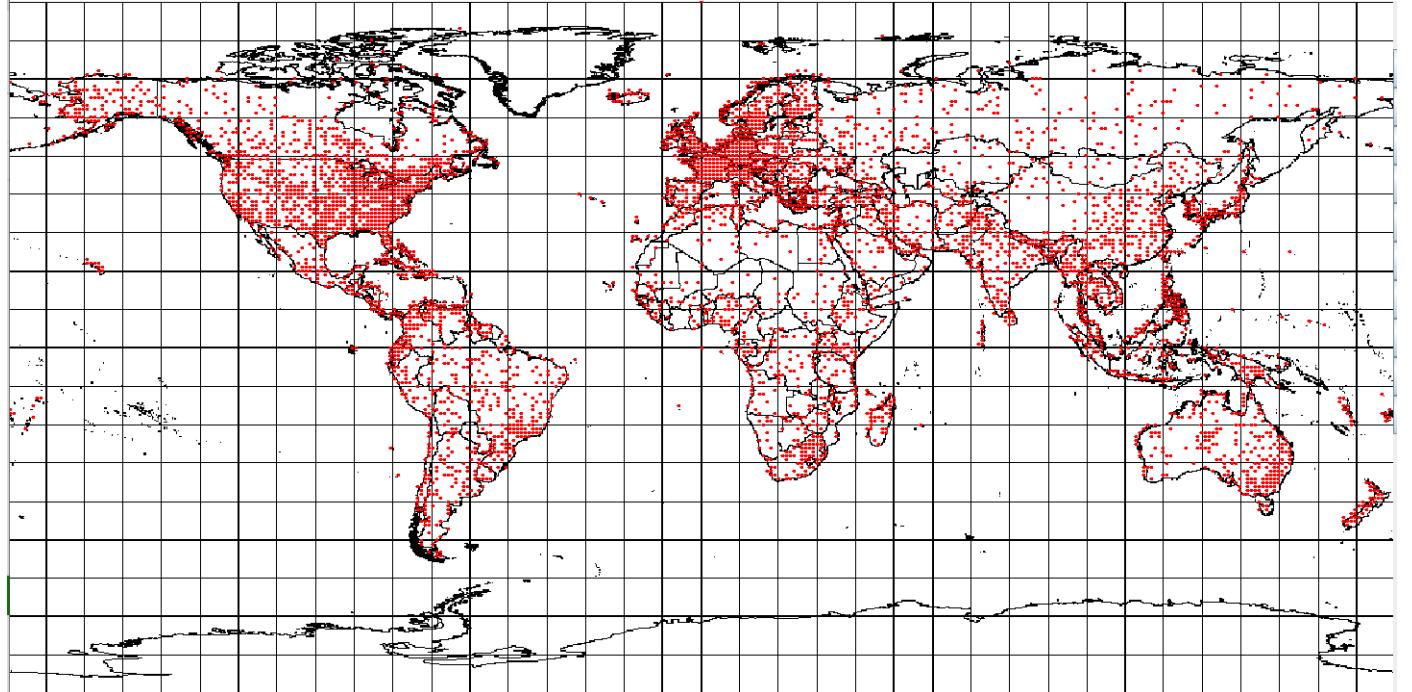


Figure 26: Airports drawn at their real life coordinates

Here the total number of nodes,  $N$  is 7215.

We then set the x and y coordinates of the countries the airports belong to as the average x value of all airports in that country and the average y value of all airports in that country. We display this like so:

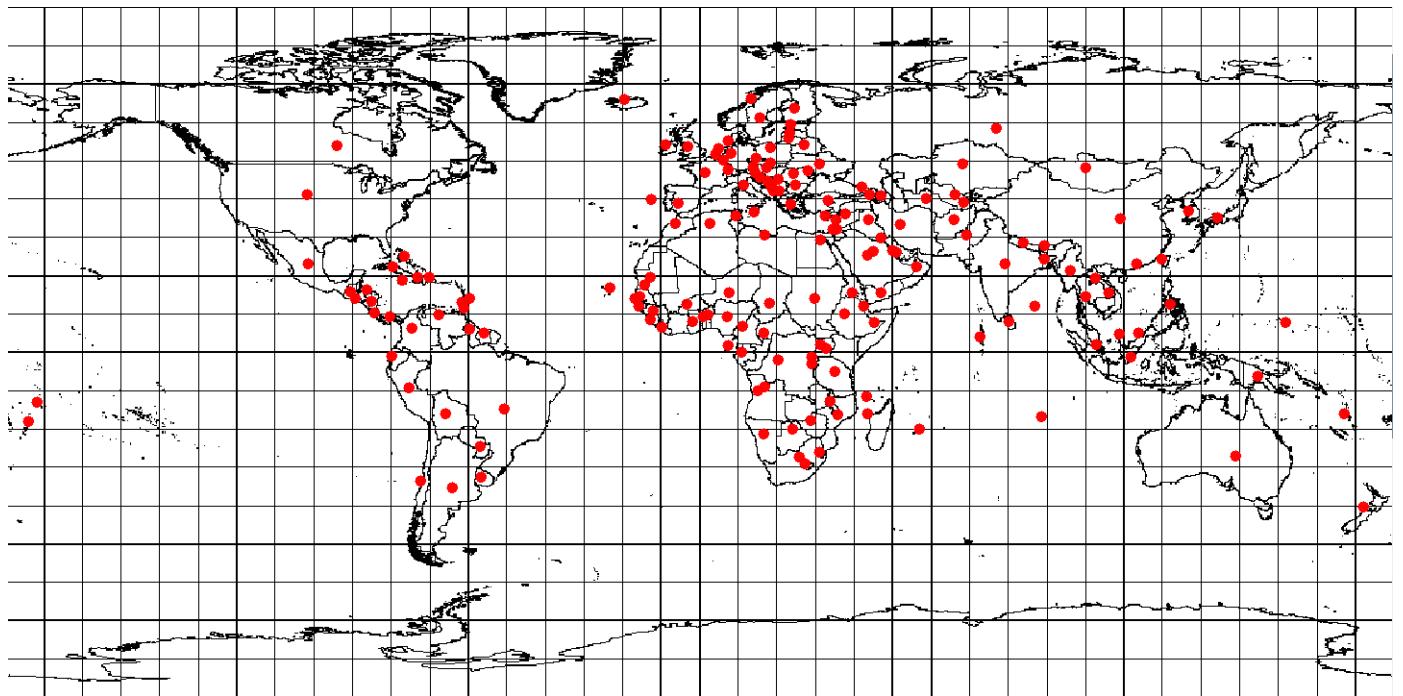


Figure 27: A map of the world with each country represented as a red circle

We let our network of airports be our "small world", but we keep track of pandemics in each Country.  
Let us now take a look at some varying values of  $\beta$  and  $k$ .

## 6.4 Varying constant values and their effects on the small world network

Let us start out by letting  $k = 2$  and  $\beta = 0$ .

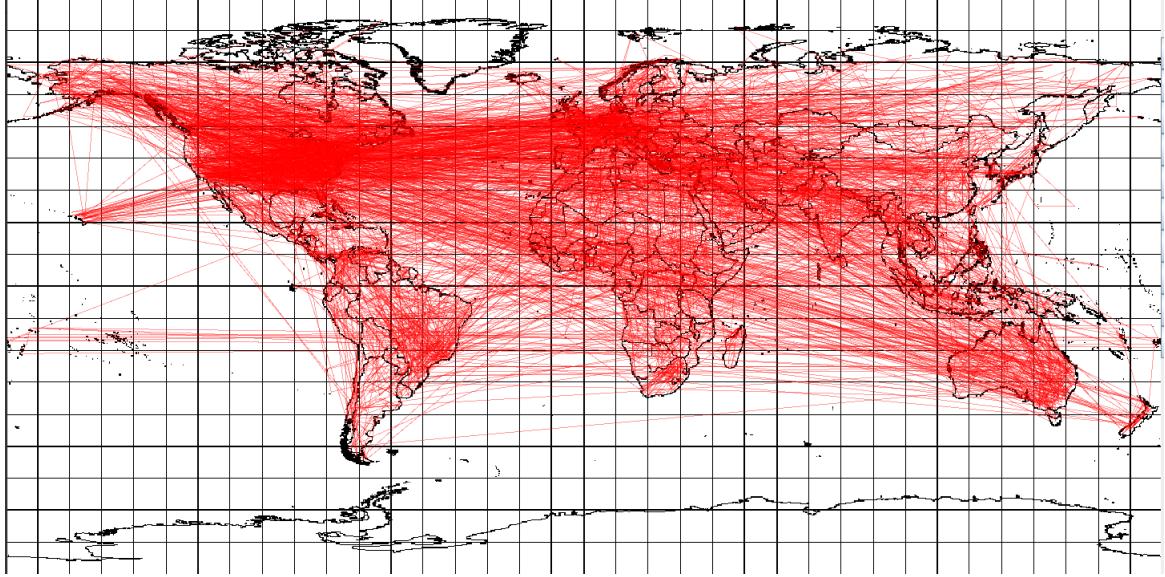


Figure 28: Our small world network, depicting all edges/flight paths

Here we see our network in the flesh. We see that countries with lots of airports have a high density of red over them (from all the connections). What we also note is that, due to the text file being ordered by country/location, that there are lots of airports connected to airports in the same country, much like how a regular lattice is connected to its closest neighbours. If this is correct, then by increasing the value of  $\beta$ , we should see flight paths that are more spread out, covering most of the map. Let us test this by increasing  $\beta$  to 0.2.

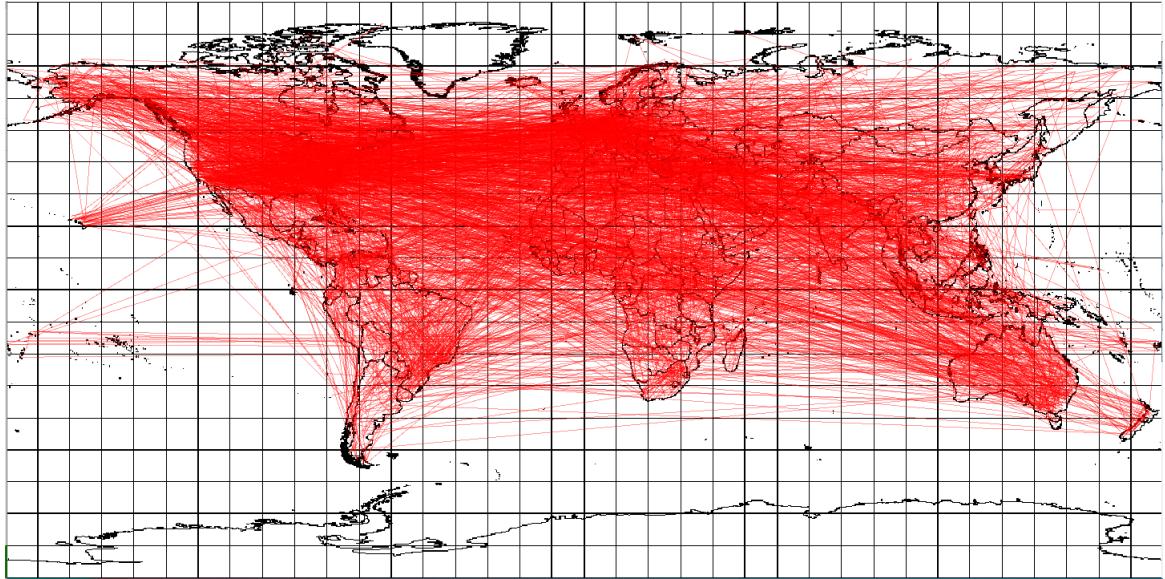


Figure 29: Our small world network, depicting all edges/flight paths, but with random replacement at  $\beta = 0.2$

We see, just like we suspected, that the clustering is reduced and flights are more spread out. What if we increase  $\beta$  all the way to 1?

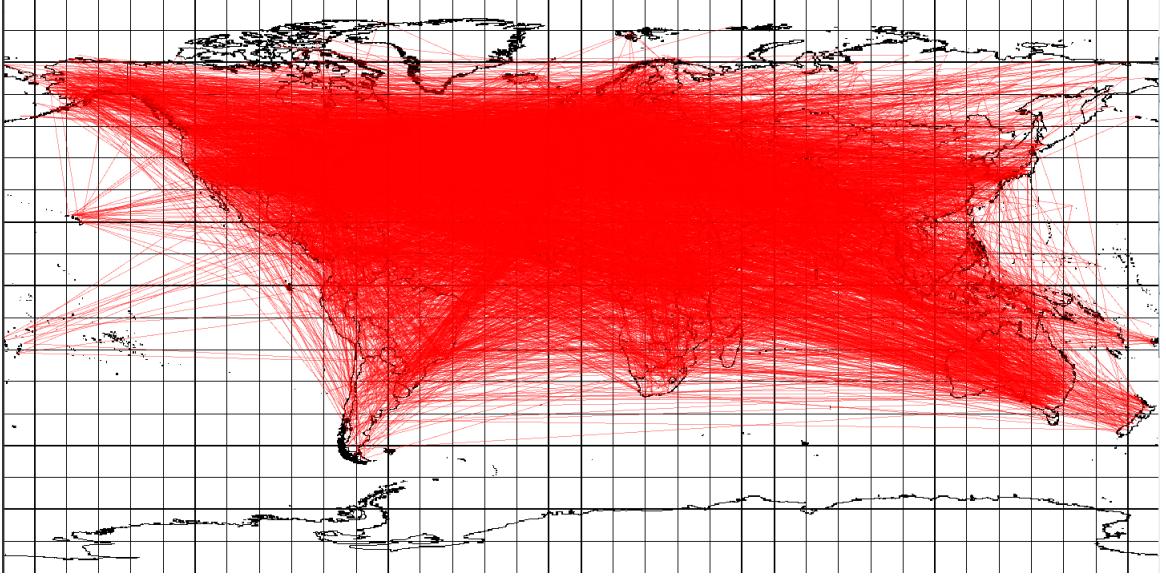


Figure 30: Our small world network, depicting all edges/flight paths, but with random replacement at  $\beta = 1$

We see here that flights are spread out all over the place, with any clustering taking place being by pure chance. Now that we have established the fact that the airports make up a pseudo small world and are affected by  $\beta$  similarly to a standard small world, we may now begin testing disease spread across the world.

## 7 The simulation Begins

### 7.1 Simulating without lockdown

Let us first start out by simulating the spread of Covid-19 under the assumption that the world's governments provide zero solutions or preventative measures to stop the spread of Covid-19. We will watch as a country's number of infectious individuals grows exponentially until the ratio between Susceptible and infectious individuals causes the number of cases to decline. We expect that a huge portion of each Country will very quickly become infected and then very quickly recover (a tall spire of infections in comparison to the gradual slope that arises due to preventative measures and lockdown). We will compare the amount of time (days) it takes for the last country to fully recover, for each value of  $\beta$ . In theory, the value of  $\beta$  that yields the quickest time for the world to fully recover should be the most efficient small world. Let us begin testing.

#### 7.1.1 $\beta = 0$

We begin by testing the pseudo-regular-lattice scenario where  $\beta = 0$ . We of course let the starting country be China. We say that every ten days, a flight of 39 passengers (which is the average number of passengers an international plane carries [8]) occurs for each flight path. Each of those 39 passengers is equally likely to carry Covid-19 from their point of infection to the country they visit.

We also assume that once an infectious person has traveled from one country to another, they cannot go back and no further infectious individuals may take that flight path. We set the radius of the circle (just for visual purposes) representing the country's infectious population (in red) to increase up to and based off of a fraction of their population. We similarly set the radius of the circle (in gray) the number of deaths in a country to increase up to and based off of a fraction of their population. I will now run the simulation and show key times where large changes occur.

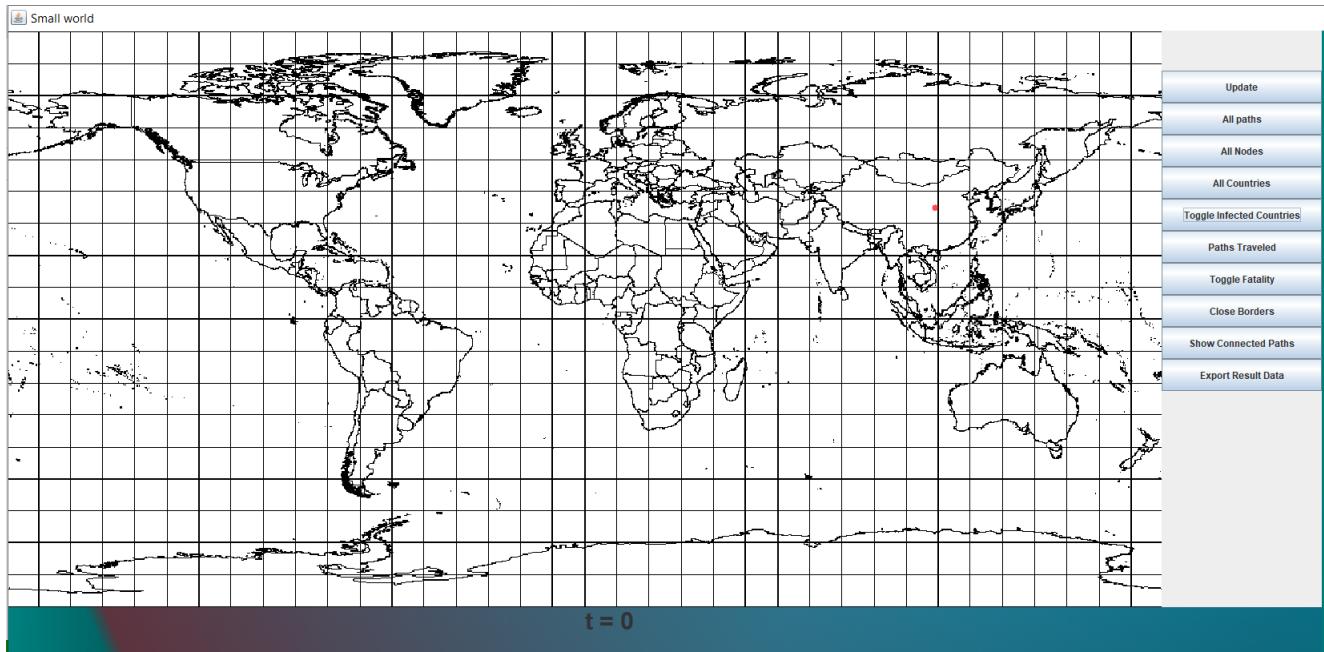


Figure 31: Our Covid-19 pandemic simulation begins in China at  $t = 0$

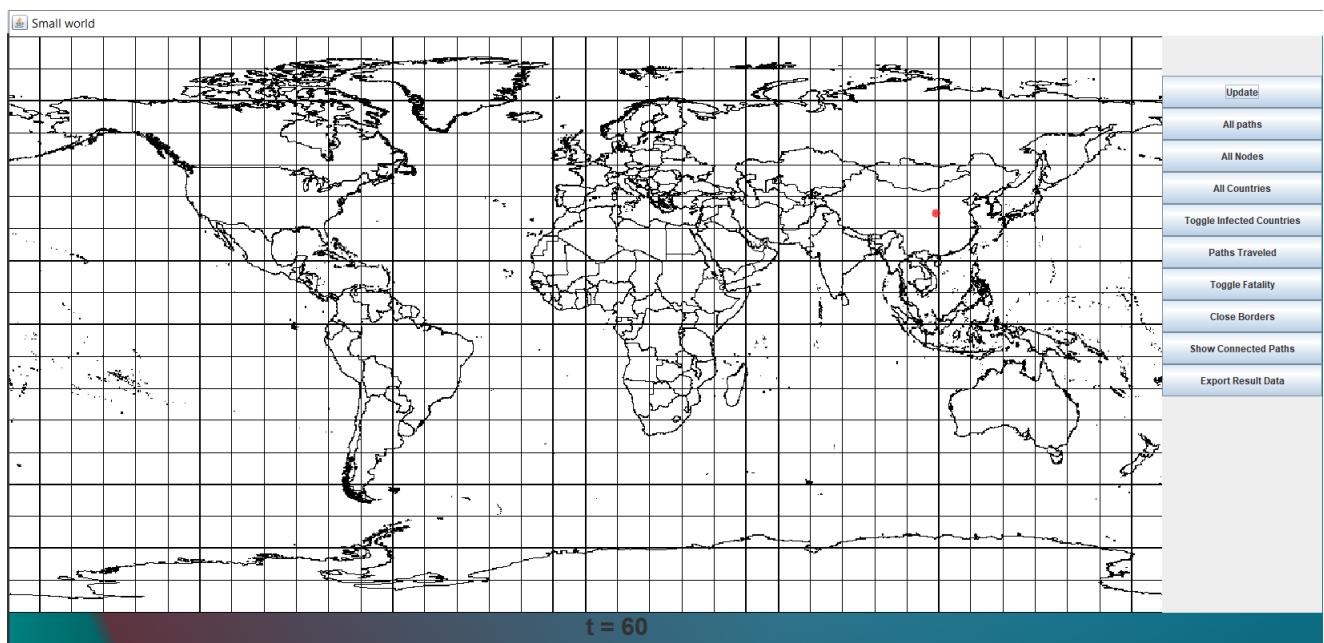


Figure 32: Our Covid-19 pandemic simulation at  $t = 60$

After 60 days, the number of infectious individuals has started to increase dramatically (while it is hard to see, the radius of the circle is about double that of  $t = 0$ ).

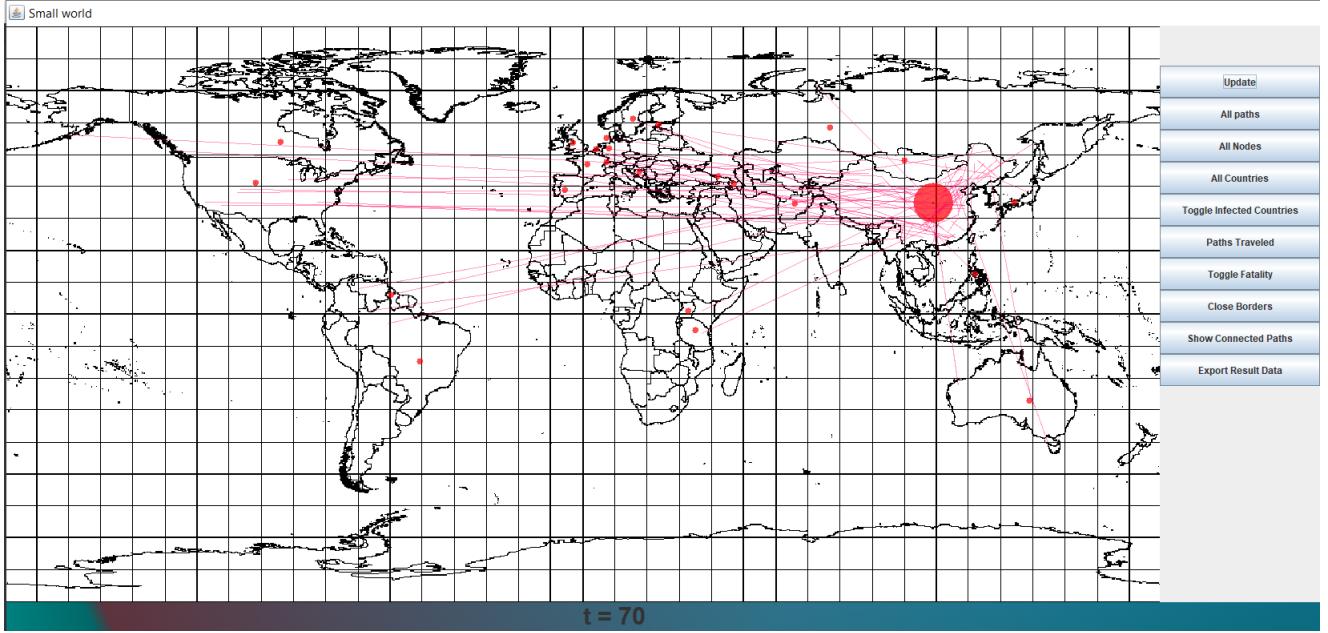


Figure 33: Our Covid-19 pandemic simulation at  $t = 70$

After a further 10 days, the number of infectious individuals in China has drastically increased and as a result many other countries have received an infectious individual on a plane trip from China. We see several lines coming out from China, starting many new outbreaks.

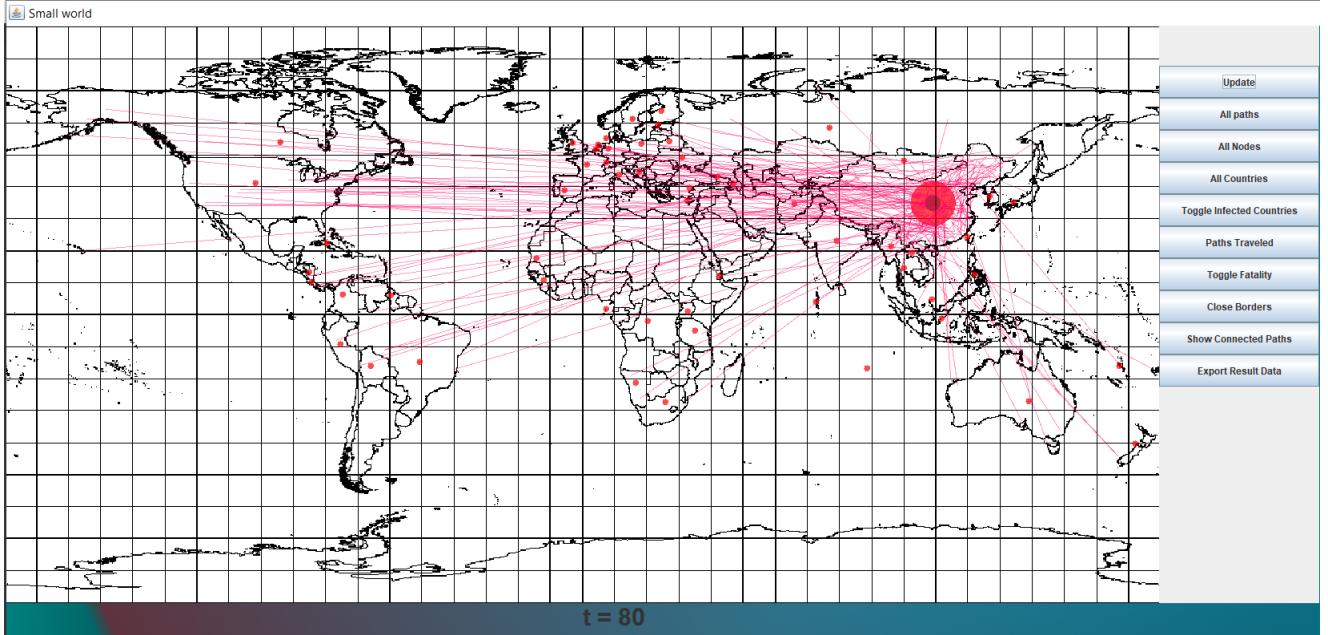


Figure 34: Our Covid-19 pandemic simulation at  $t = 80$

At  $t = 80$ , we see a large number of deaths has started to occur in China. We also see that many more countries connected to China's airports have had an outbreak begin. However, these countries are still in the early days of their outbreak and we can only reasonably expect them to grow rapidly after another 20 to 30 days.

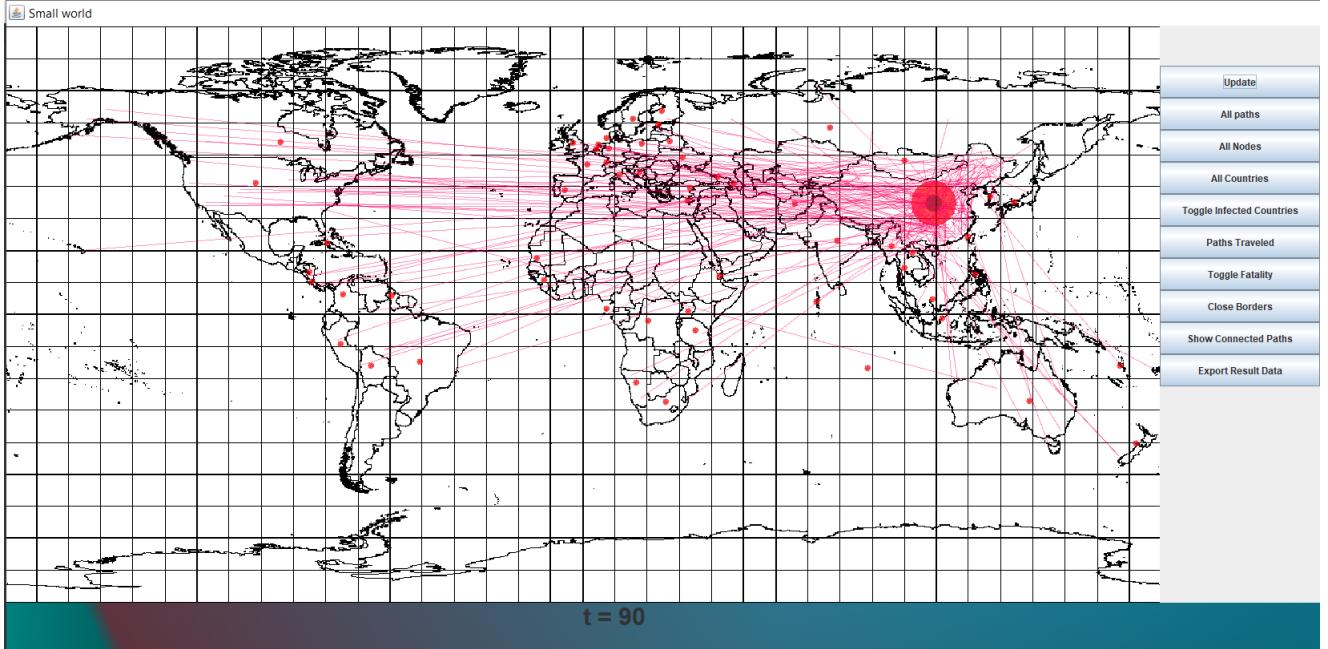


Figure 35: Our Covid-19 pandemic simulation at  $t = 90$

Here we see China's Infectious population is starting to go down. We do however note that there are lines of infection coming from countries other than china (if we look at Australia, we see a line branches out towards Africa).

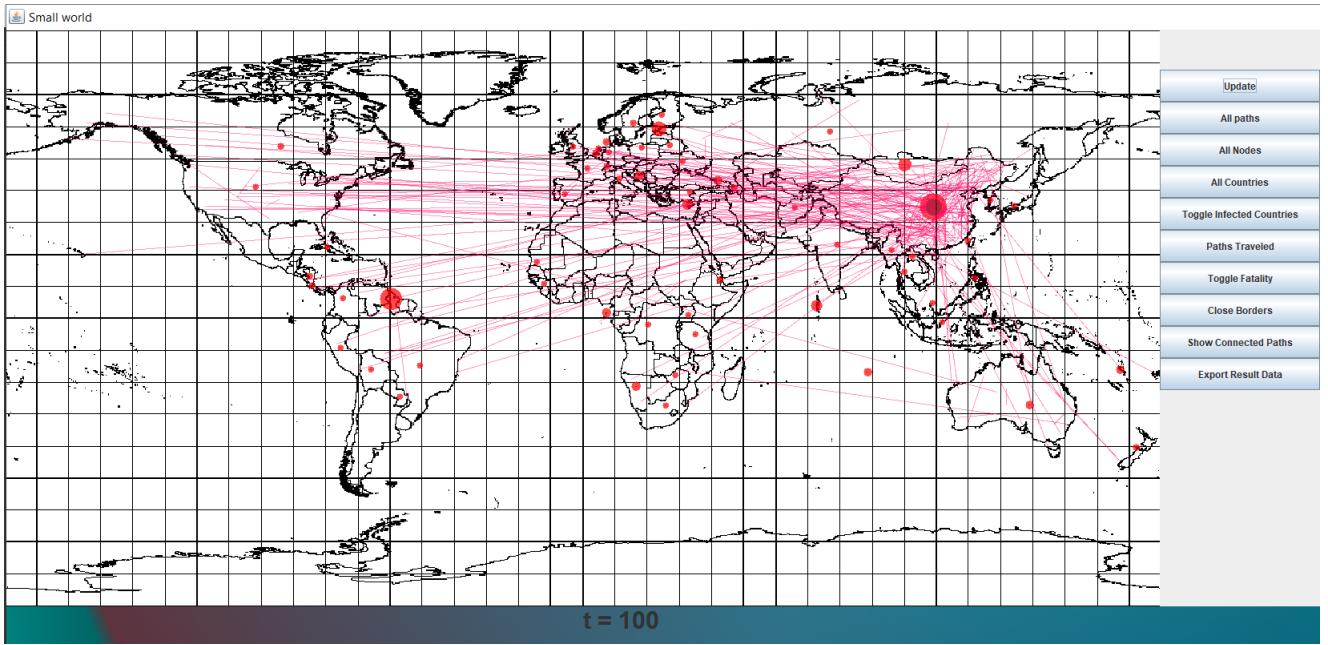


Figure 36: Our Covid-19 pandemic simulation at  $t = 100$

Here we see China's infectious population has started to rapidly decrease, while other countries (including Venezuela, Mongolia and Finland) have started to rapidly increase in numbers. We expect to see these countries rapidly increase and start to infect many other countries, then start to rapidly decrease. The chain will continue until the last infected individual recovers.

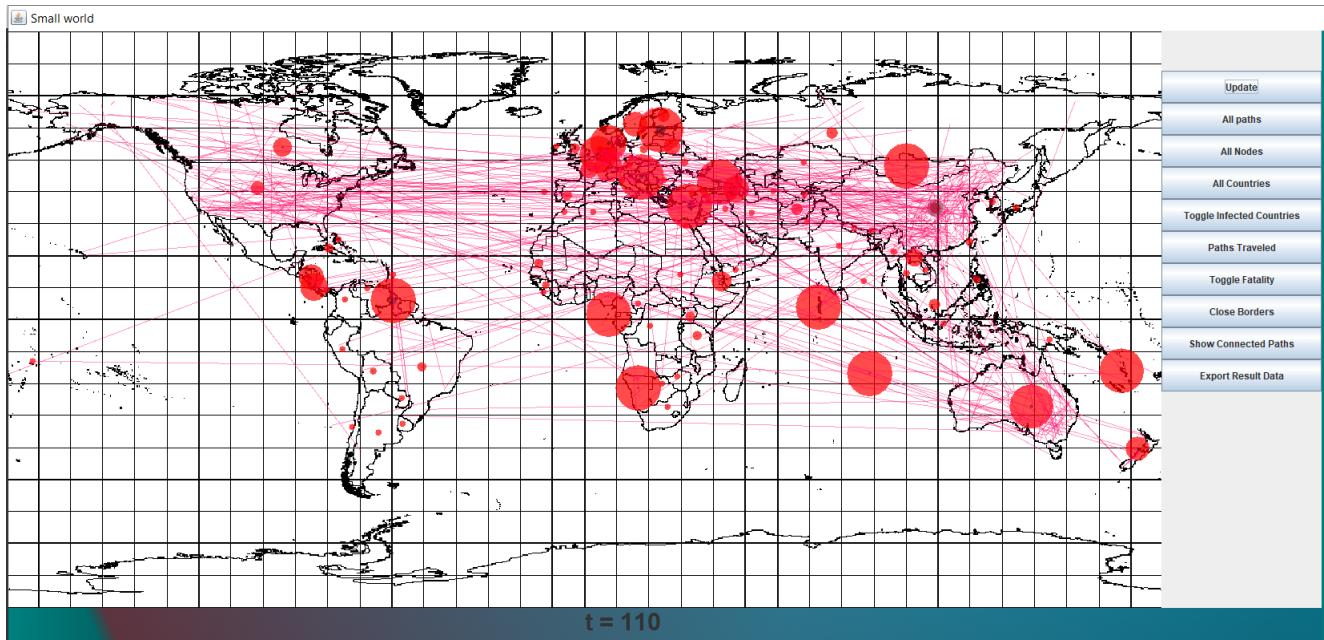


Figure 37: Our Covid-19 pandemic simulation at  $t = 110$

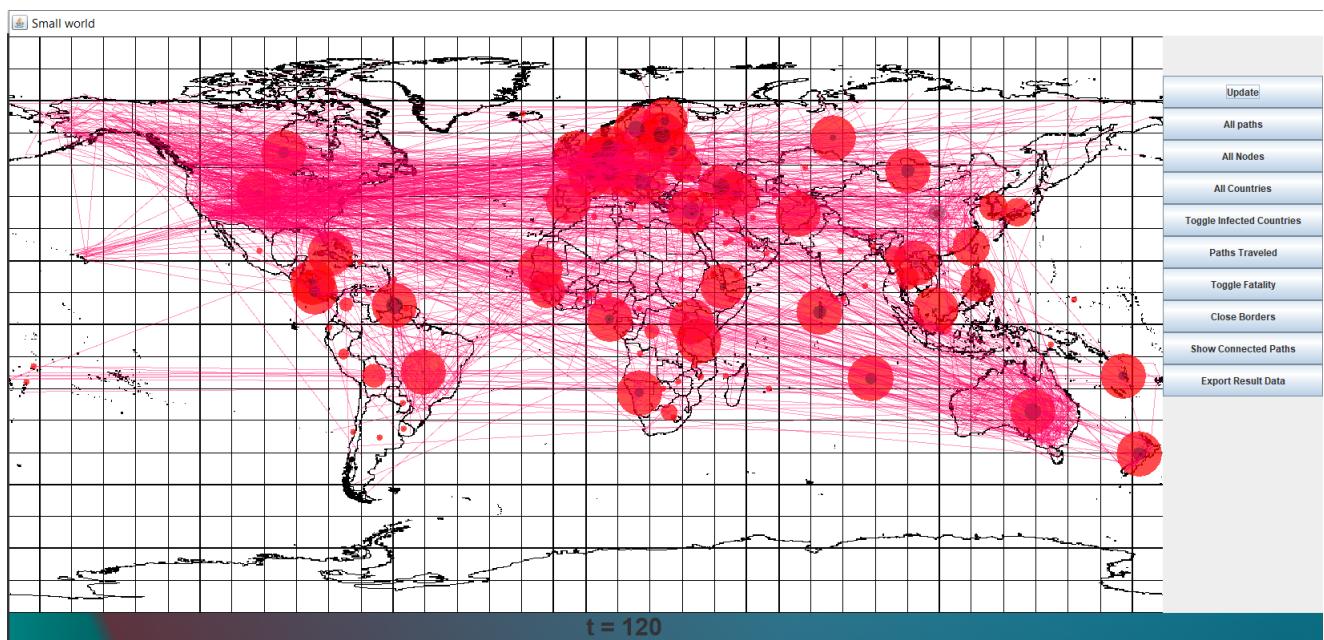


Figure 38: Our Covid-19 pandemic simulation at  $t = 120$

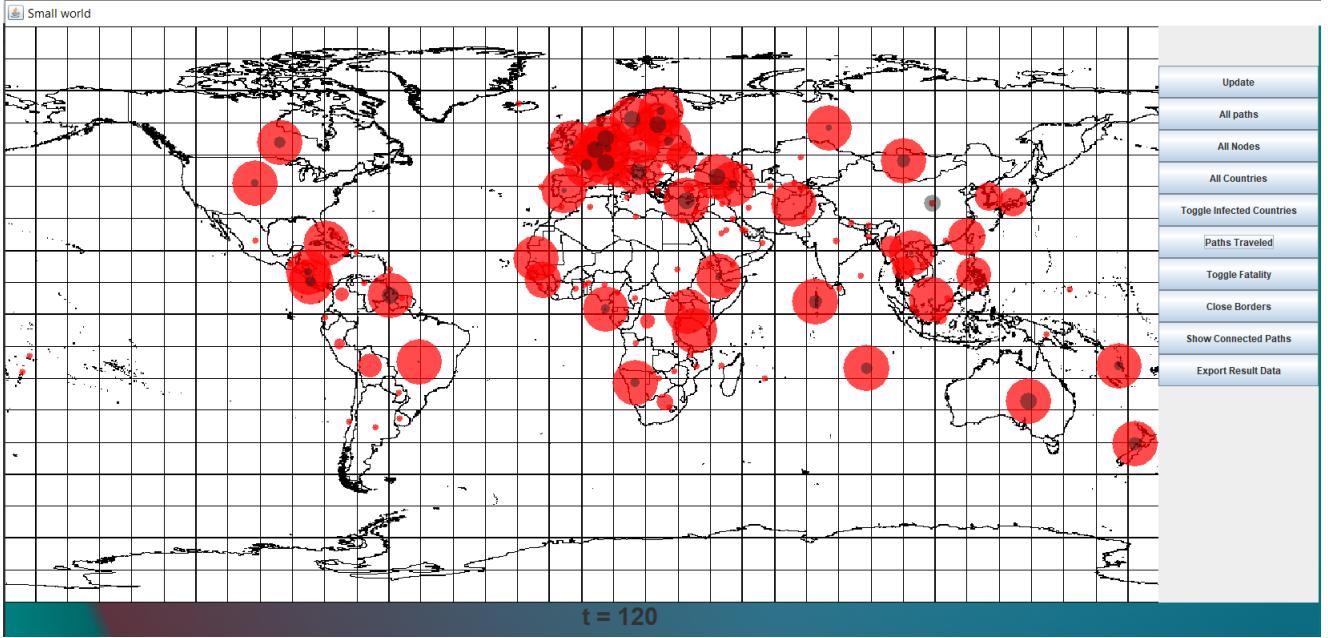


Figure 39: Our Covid-19 pandemic simulation at  $t = 120$

We remove the lines of infection so that we may better see the severity of the pandemic (via infection circles).

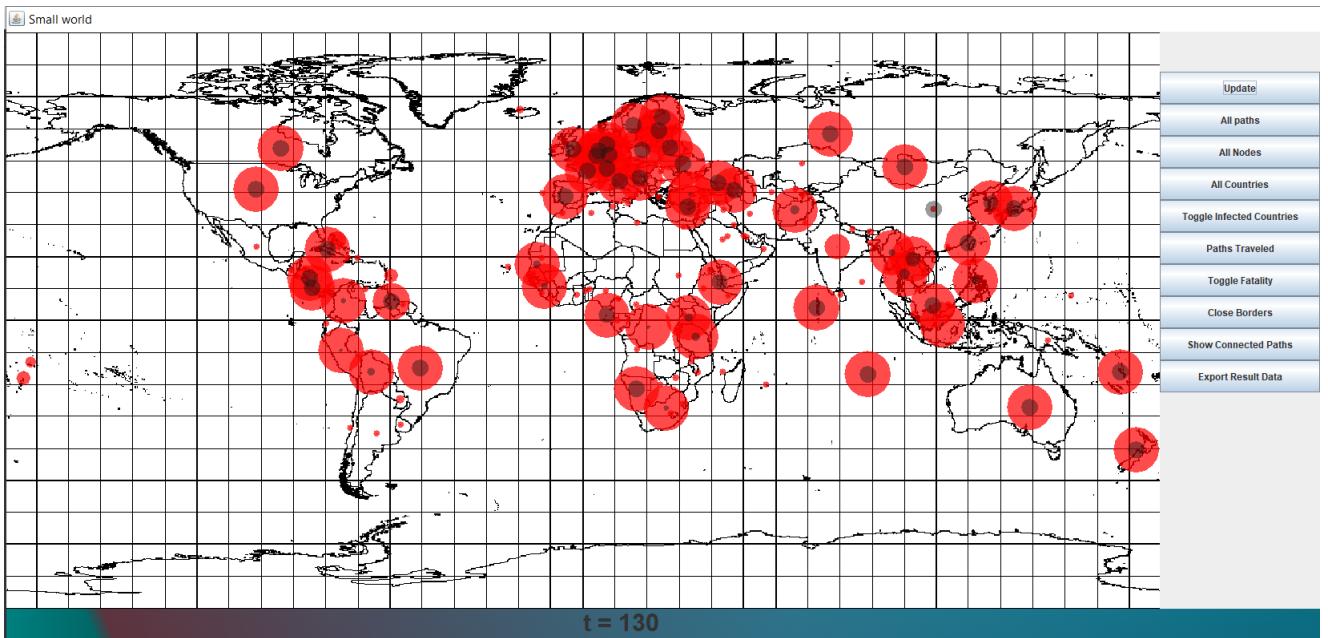


Figure 40: Our Covid-19 pandemic simulation at  $t = 130$

We see that mass world-wide death is occurring. The dark circles reach their max radius at the point where 1% of the country's population is dead, this number may increase but it is not reflected on the radius of the circles.

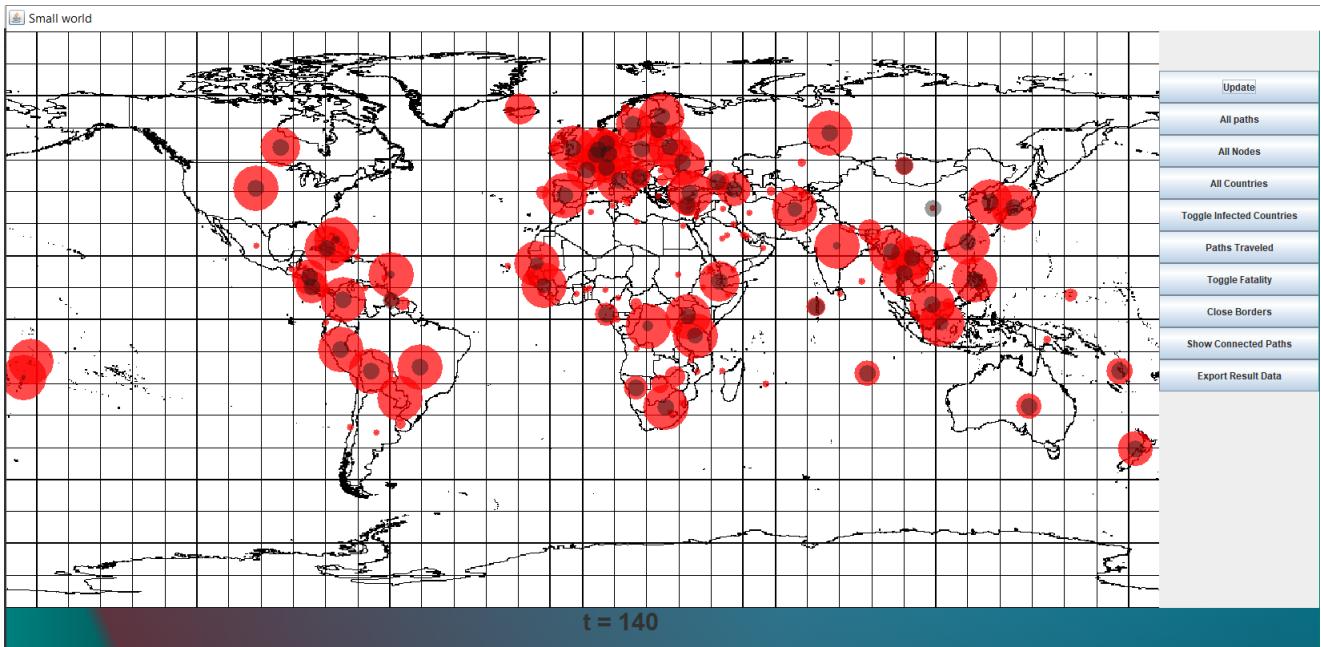


Figure 41: Our Covid-19 pandemic simulation at  $t = 140$

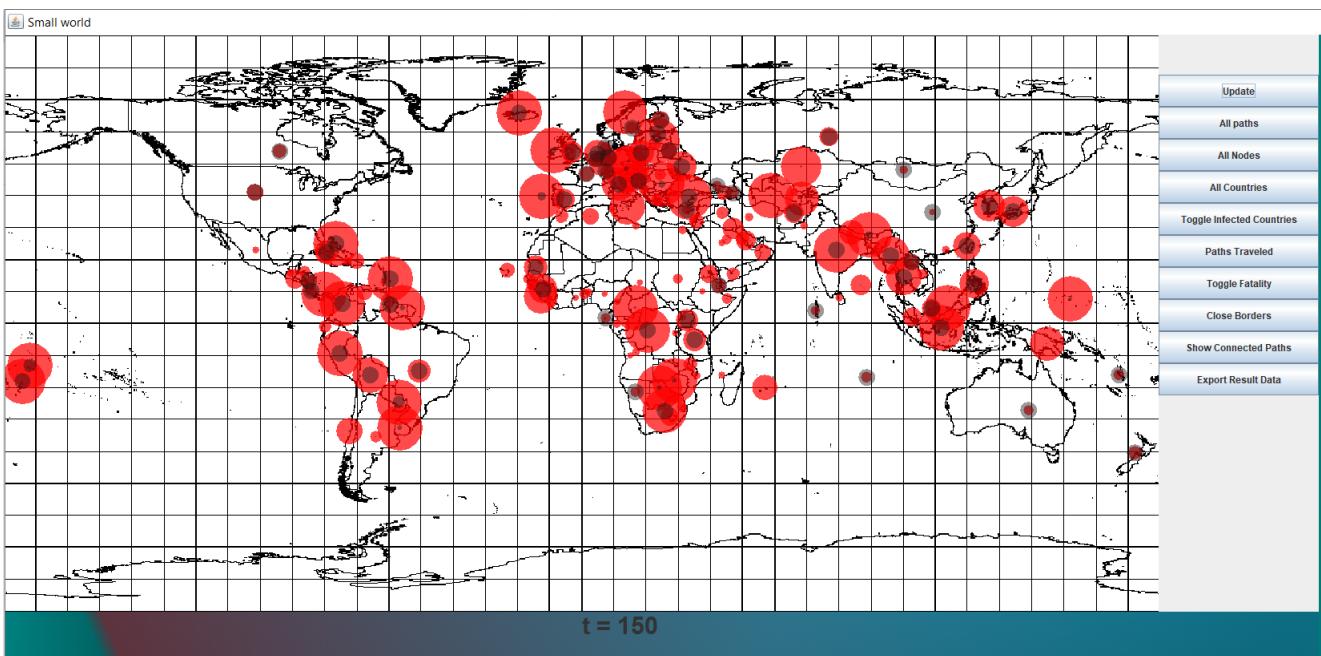


Figure 42: Our Covid-19 pandemic simulation at  $t = 150$

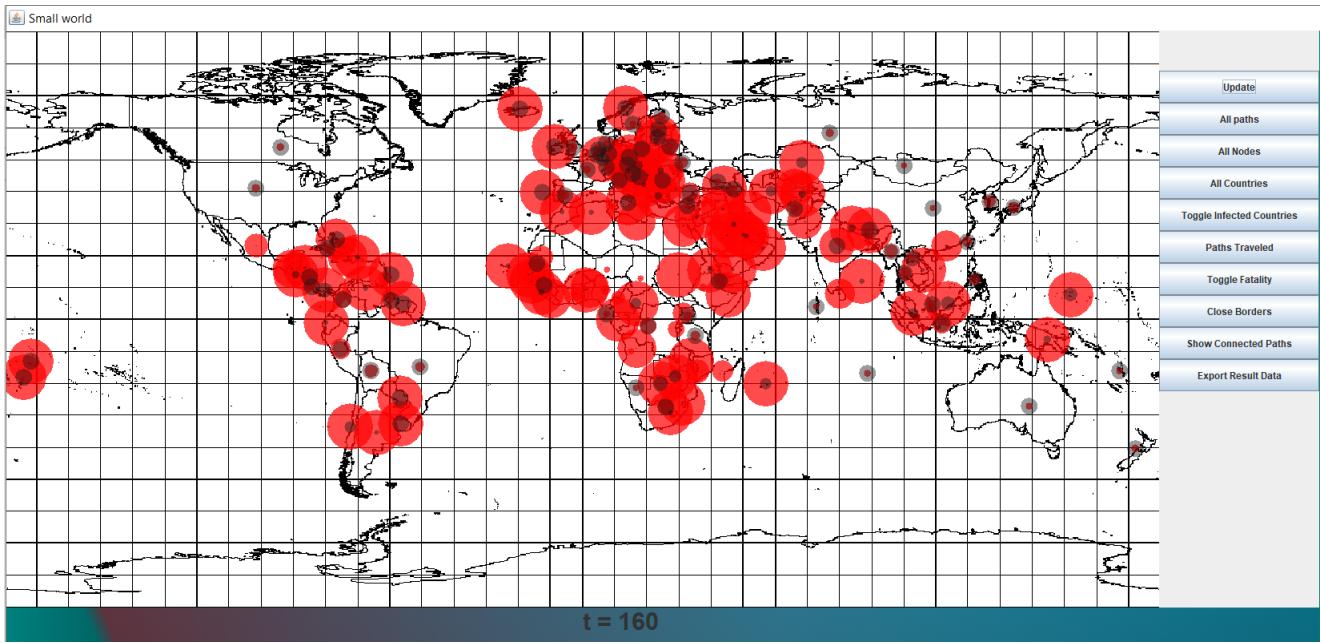


Figure 43: Our Covid-19 pandemic simulation at  $t = 160$

It would appear that the number of Infectious individuals peaks between the graph above and the graph below.

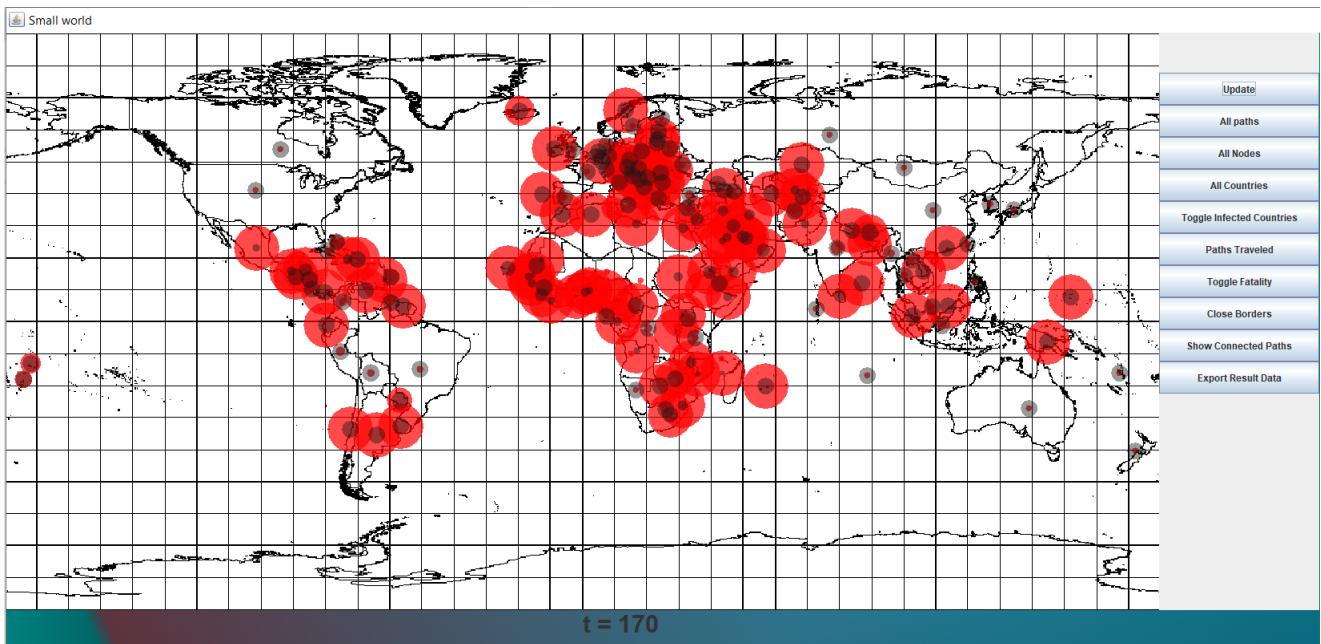


Figure 44: Our Covid-19 pandemic simulation at  $t = 170$

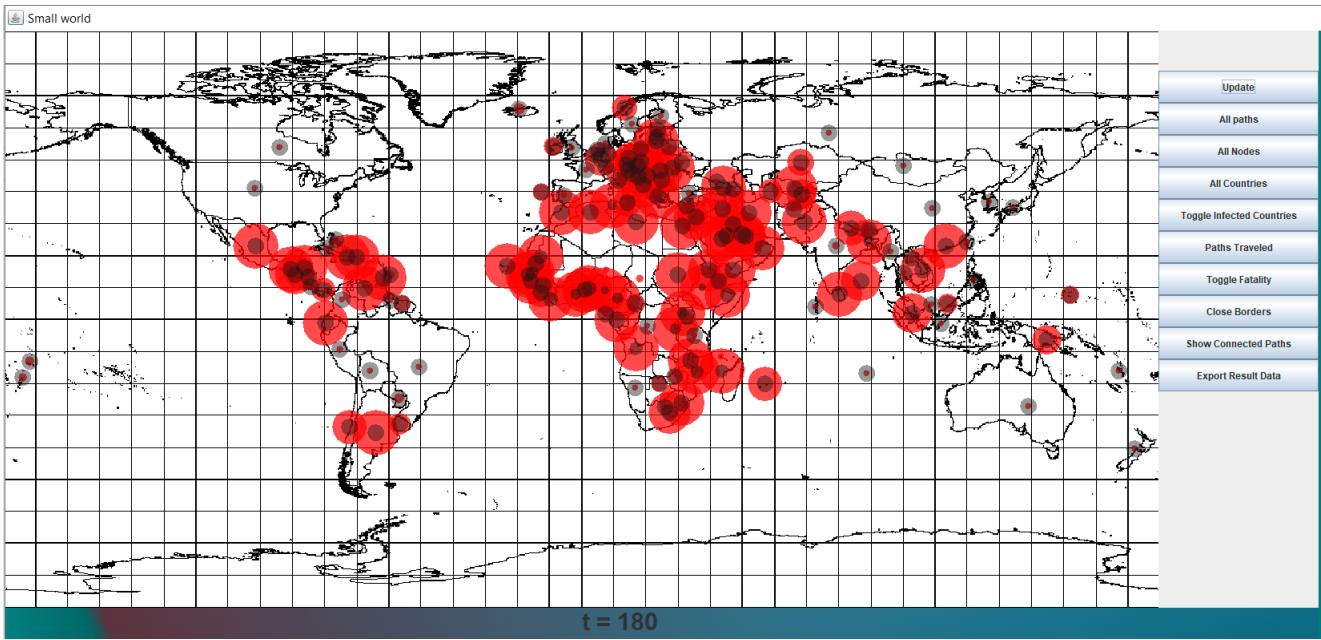


Figure 45: Our Covid-19 pandemic simulation at  $t = 180$

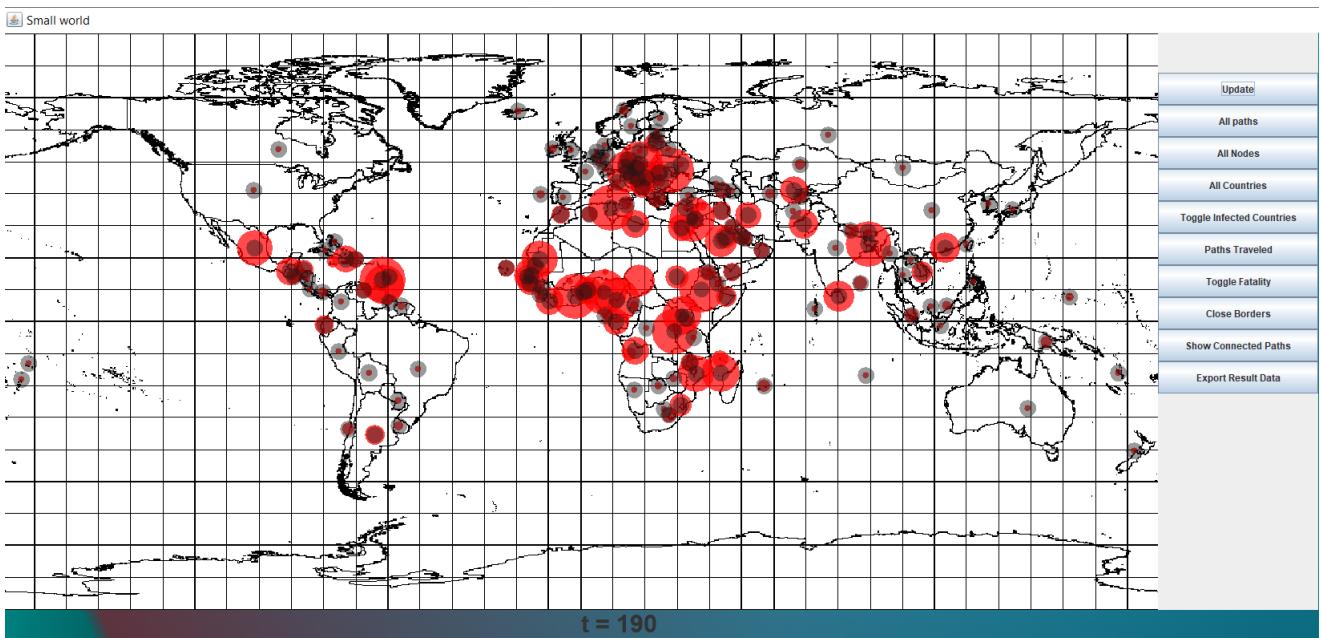


Figure 46: Our Covid-19 pandemic simulation at  $t = 190$

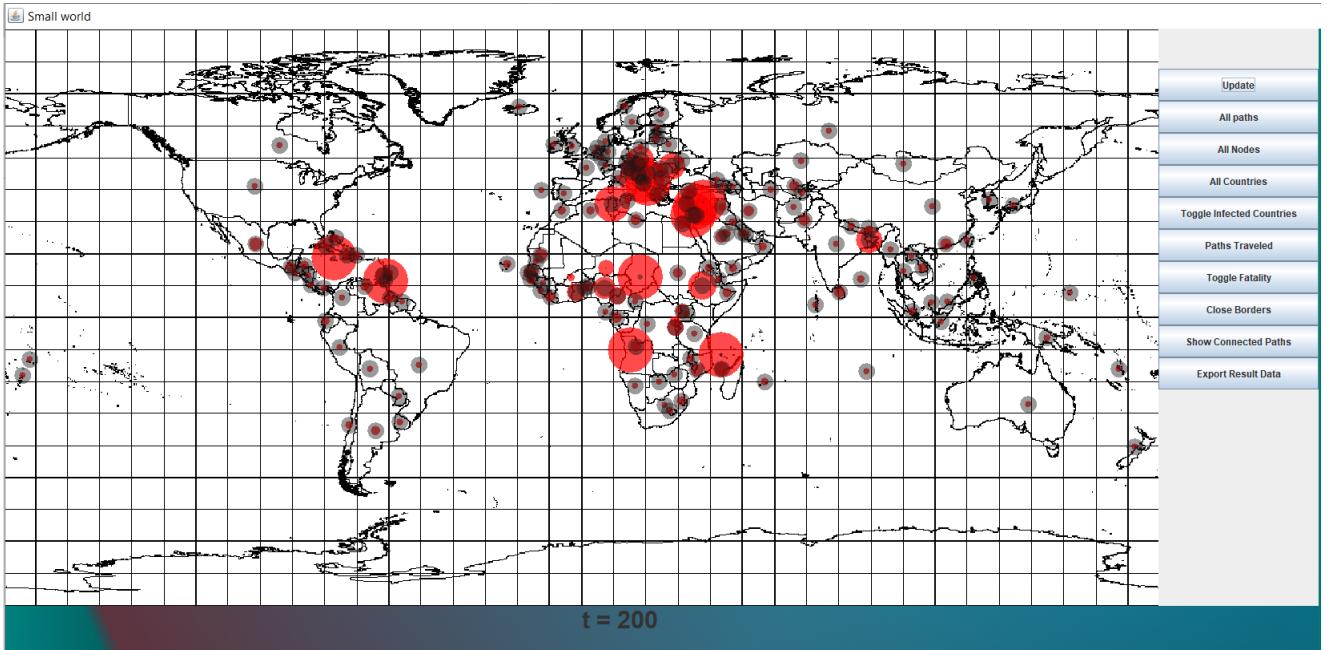


Figure 47: Our Covid-19 pandemic simulation at  $t = 200$

Here we see the last few countries (central/western Africa), that had their outbreak occur the latest, exhibit a rapid growth in Infectious individuals, while the rest of the world is recovering.

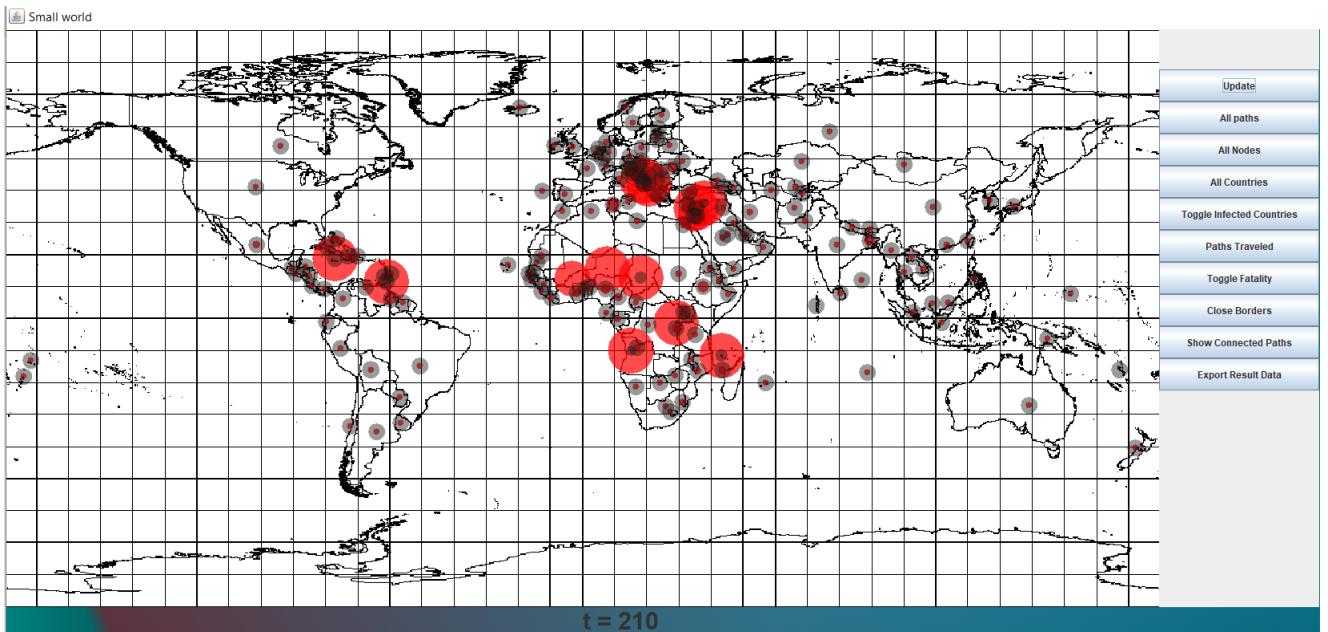


Figure 48: Our Covid-19 pandemic simulation at  $t = 210$

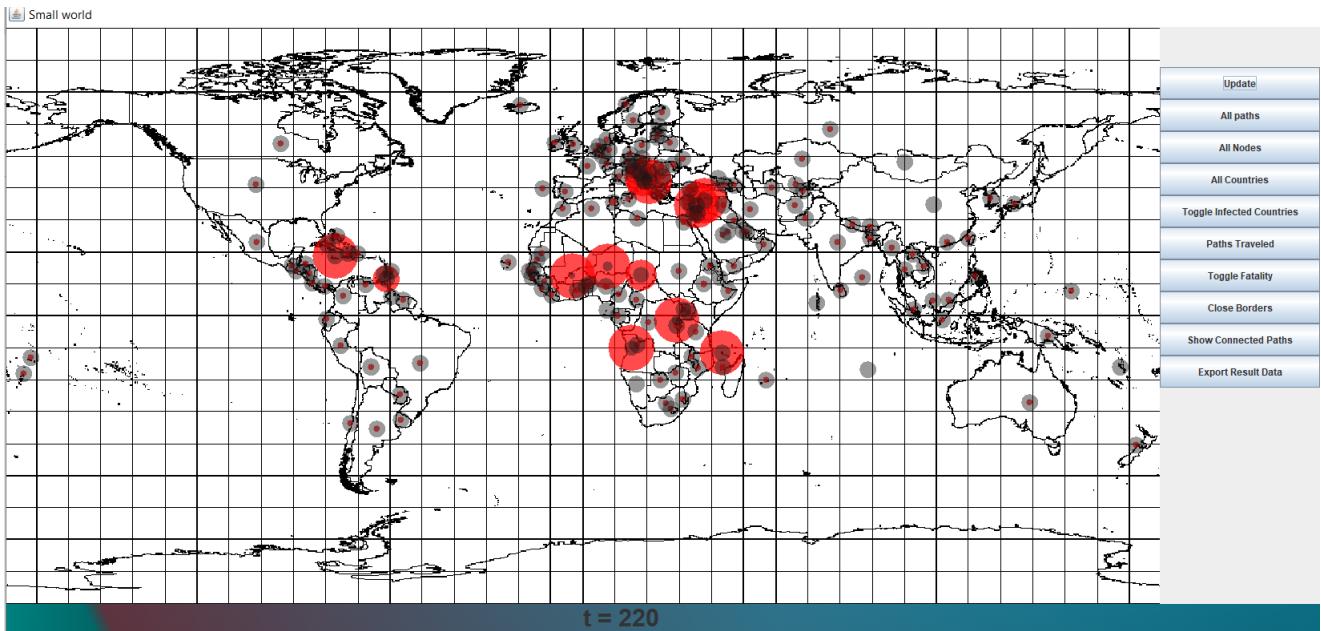


Figure 49: Our Covid-19 pandemic simulation at  $t = 220$

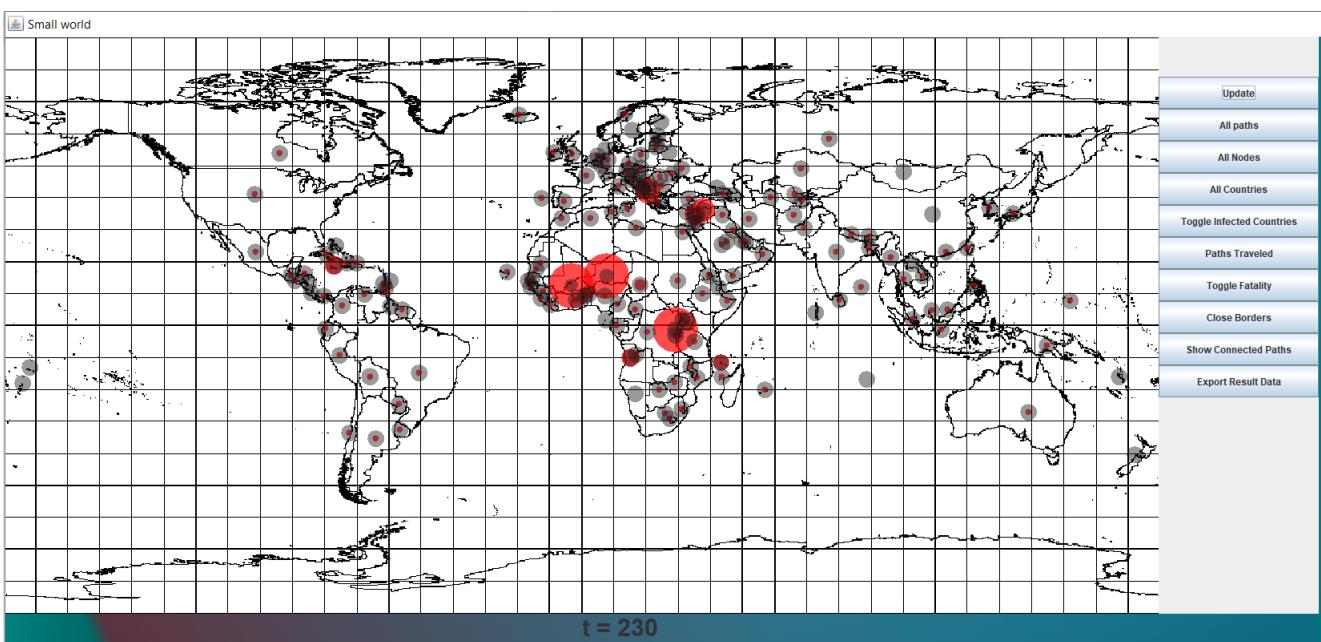


Figure 50: Our Covid-19 pandemic simulation at  $t = 230$

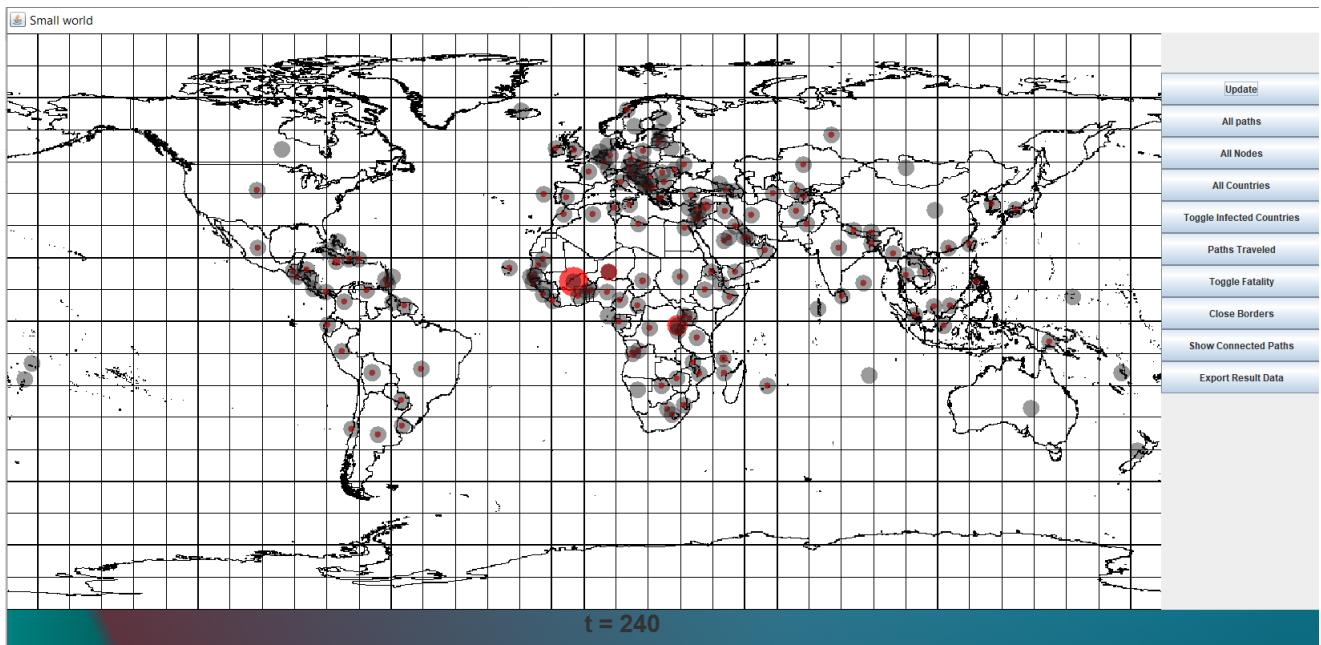


Figure 51: Our Covid-19 pandemic simulation at  $t = 240$

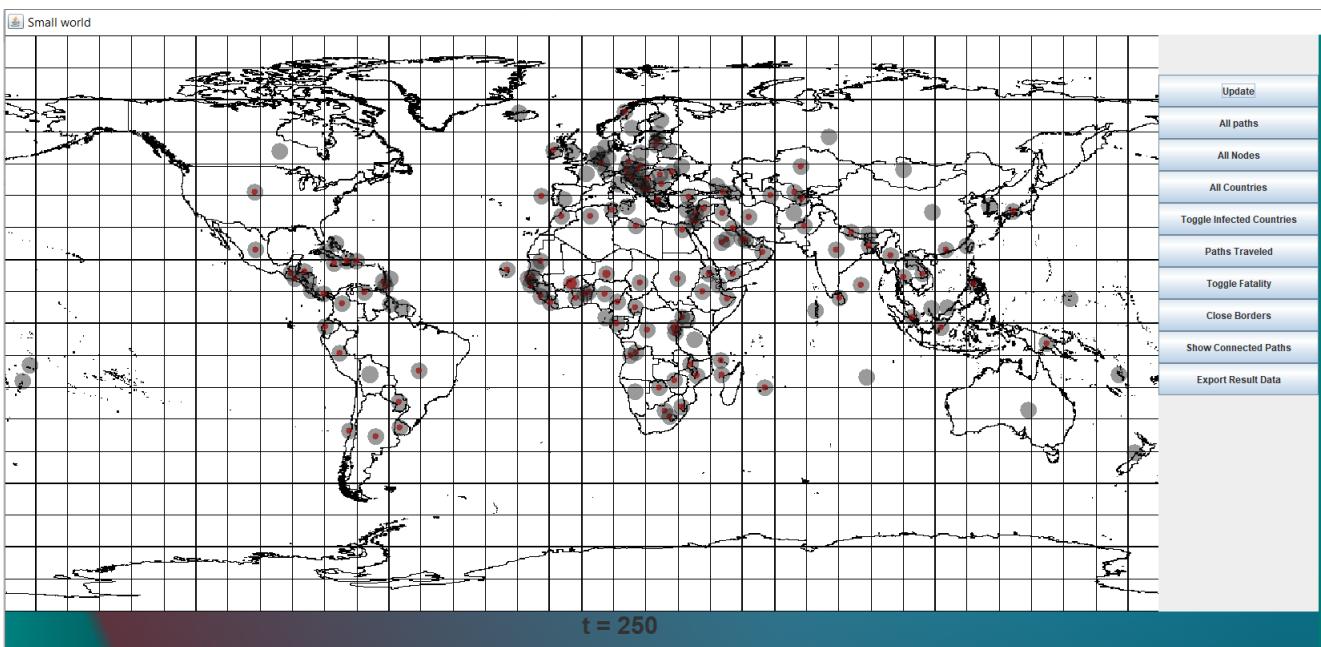


Figure 52: Our Covid-19 pandemic simulation at  $t = 250$

Almost all countries have recovered at this point, but there are still some dark red blips on the map where the number of infectious individuals is probably around 100 - 1000, and steadily decreasing

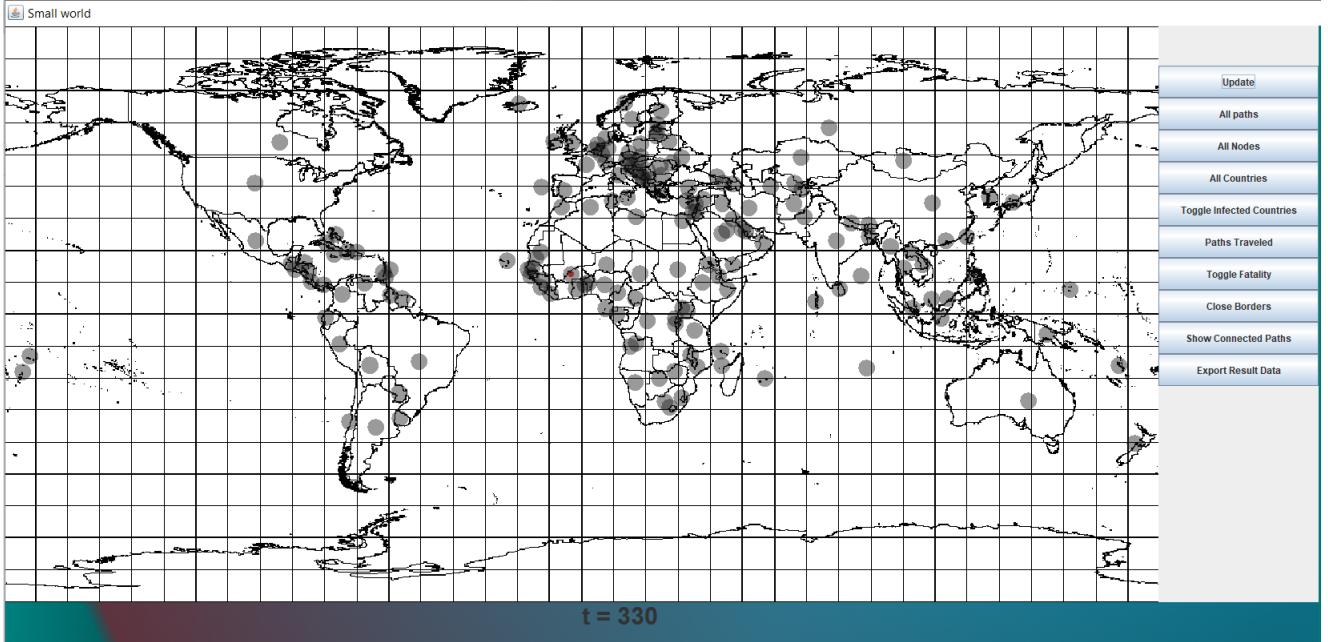


Figure 53: Our Covid-19 pandemic simulation at  $t = 330$

We see the last country to recover in western Africa finally recovers after 340 days (from the graph above to the graph below).

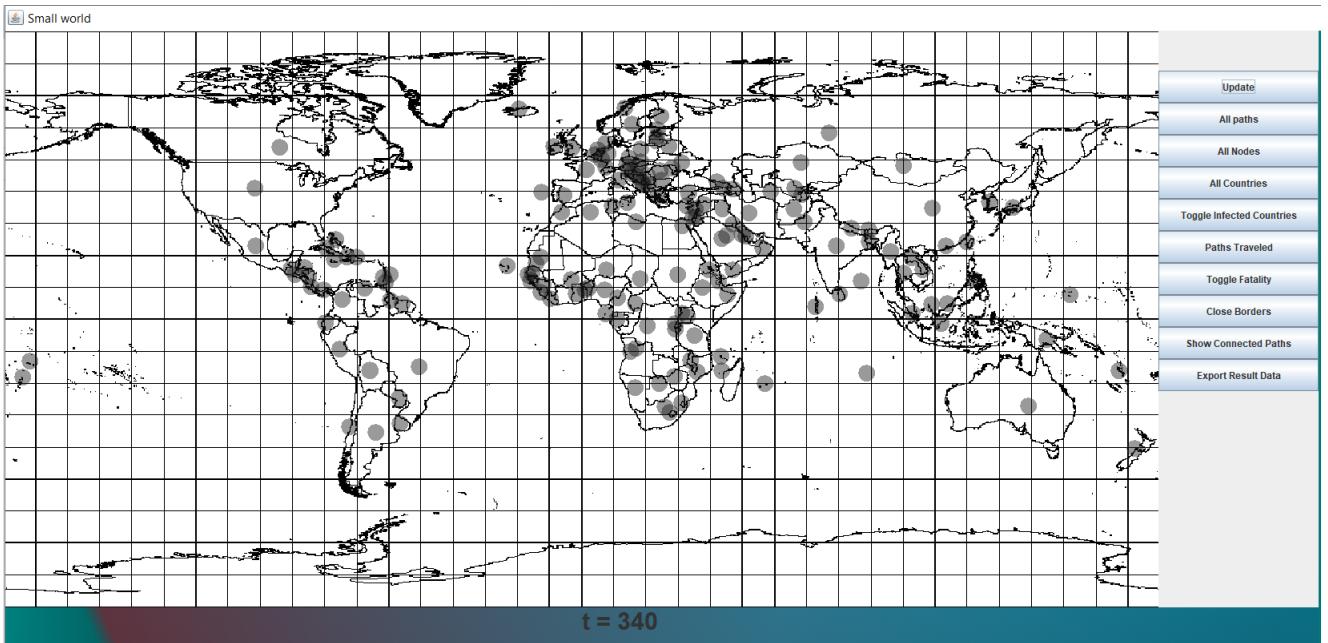


Figure 54: Our Covid-19 pandemic simulation at  $t = 340$

The model behaved pretty much exactly as expected, however the amount of time for the last country to recover feels rather long. Without showing all the time stages to the simulation, I will run it again for  $\beta = 0.3$ ,  $\beta = 0.5$  and  $\beta = 1$ .

## 7.2 Expectations and results

After running the simulation 4 times for each value of  $\beta$ , I have found some rather unexpected results.

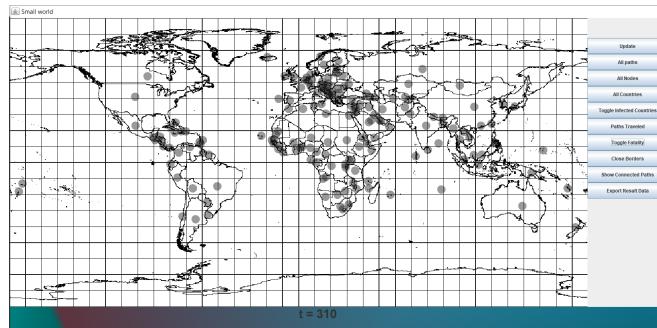


Figure 55:  $\beta = 0.3$ ,  $t_{\text{Final}} = 310$

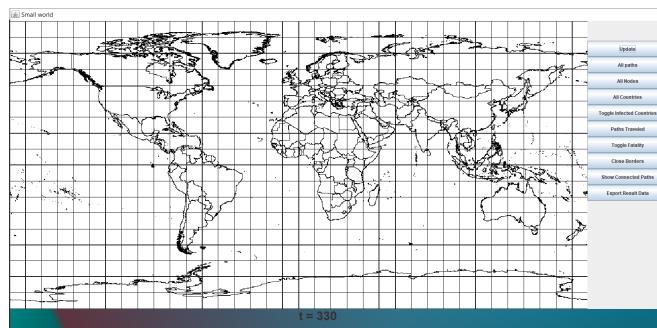


Figure 56:  $\beta = 0.3$ ,  $t_{\text{Final}} = 320$

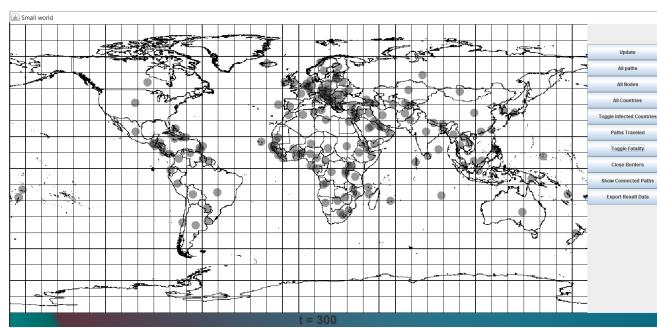


Figure 57:  $\beta = 0.3$ ,  $t_{\text{Final}} = 300$

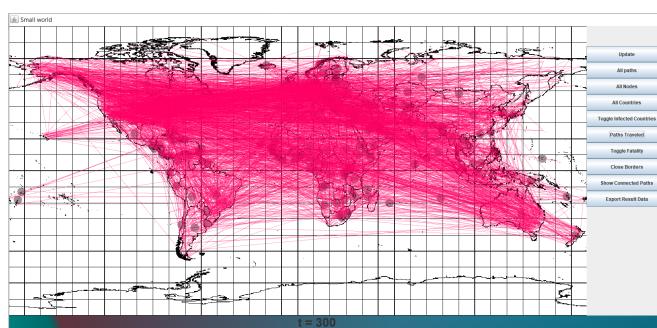


Figure 58:  $\beta = 0.3$ ,  $t_{\text{Final}} = 300$

We expected to see this from our first value of  $\beta$ . With a little randomness comes more "shortcuts" and a lower average path length. We test  $\beta = 0.5$  to see if there is an even more efficient value for our small world.

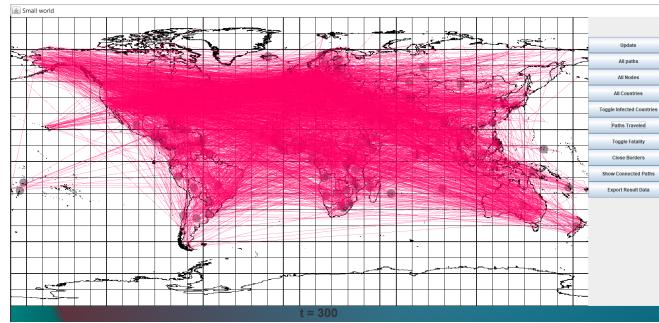


Figure 59:  $\beta = 0.5$ , tFinal = 300

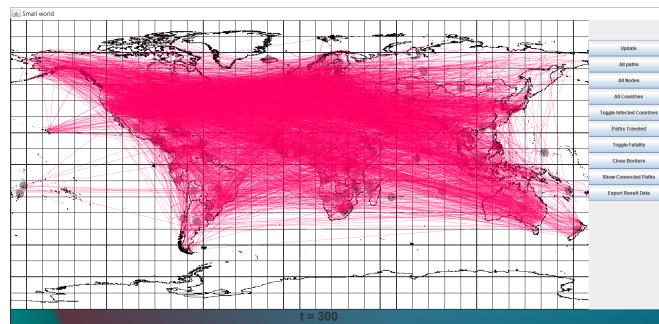


Figure 60:  $\beta = 0.5$ , tFinal = 300

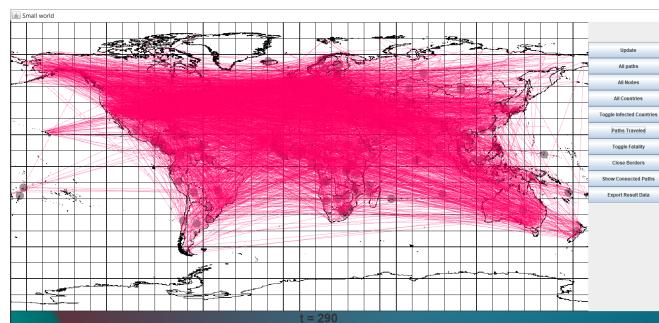


Figure 61:  $\beta = 0.5$ , tFinal = 290

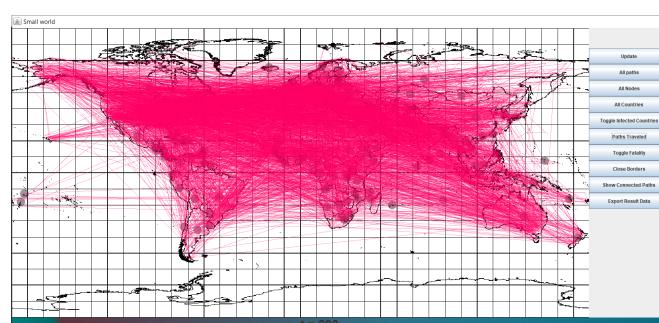


Figure 62:  $\beta = 0.5$ , tFinal = 290

These results are even better than the previous, but this is a little suspicious. What happens if we set the randomness to a max, which we know will not yield a small world network.

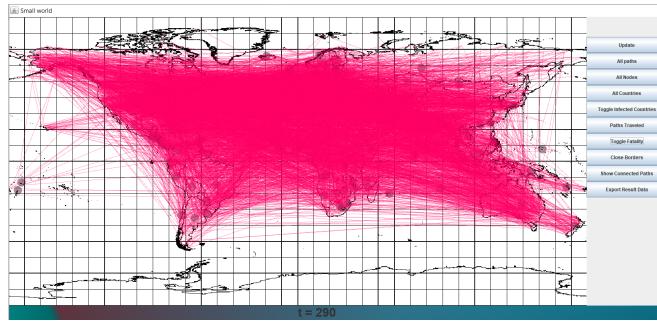


Figure 63:  $\beta = 1$ ,  $t_{\text{Final}} = 290$

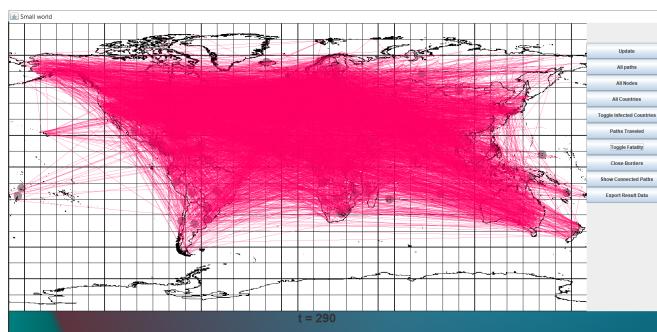


Figure 64:  $\beta = 1$ ,  $t_{\text{Final}} = 290$

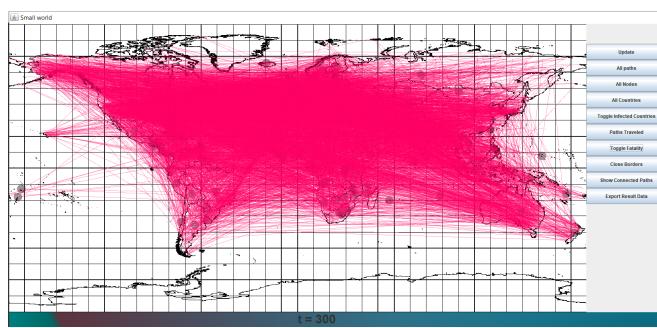


Figure 65:  $\beta = 1$ ,  $t_{\text{Final}} = 300$

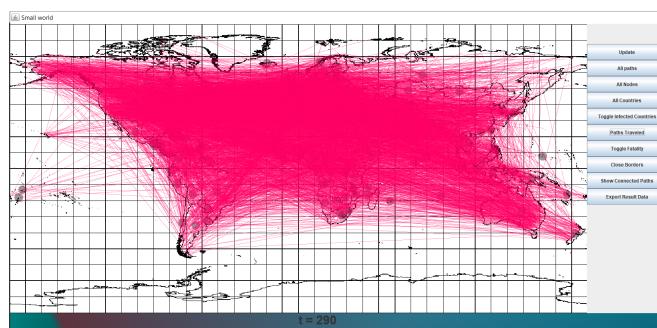


Figure 66:  $\beta = 0.5$ ,  $t_{\text{Final}} = 290$

These results are the most shocking. The shortest time for the world to recover is when  $\beta = 1$ . This suggests that our network cannot be optimised as a small world.

Now while this may seem strange, the reason behind it is that when  $\beta$  is higher, less flight paths are national. i.e. Since the data is clustered within close proximity, many of the flights don't actually leave the country. Many of the flight paths are national as opposed to international. This means that when  $\beta = 1$ , the chance that a flight path is national is much lower than the chance that a flight is international (since the number of nodes in the country is much less than the total number of nodes in the world). The more flight paths being international, the faster the spread of the disease across the world.

### 7.3 Realism

Now while this may seem upsetting, we take reassurance from the fact that it is much more realistic for a country to have a few national flight paths than for it to have only international. We can then assume that our ideal but realistic value for  $\beta$  must be somewhere between 0.3 and 0.5.

## 8 Implementing Border shutdowns

We may now test out the effects of closing a countries borders. i.e. preventing all entering and leaving of infectious individuals from and to a country.

Lets run a simulation where **some** countries close their borders quickly after noticing the outbreak. We assume  $\beta = 0.4$ , which we know will yield a time of around 290-300 total days for total recovery.

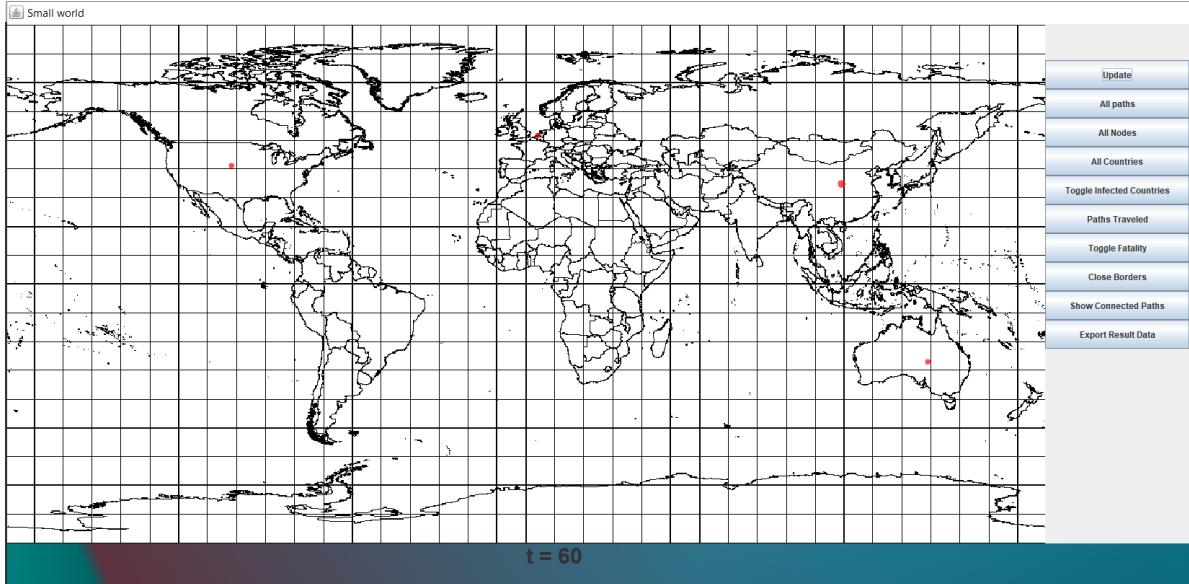


Figure 67:  $\beta = 0.4$ ,  $t = 60$

Here we have a point in time where China's infectious individuals are starting to rapidly increase and have infected Australia, the USA and the Netherlands. Lets assume that to prevent further infection and spread of Covid-19, China has closed off its borders, preventing its massively increasing population of infectious individuals from spreading to other countries.

Here we see in green, the countries with closed border's and in yellow the countries with open borders.

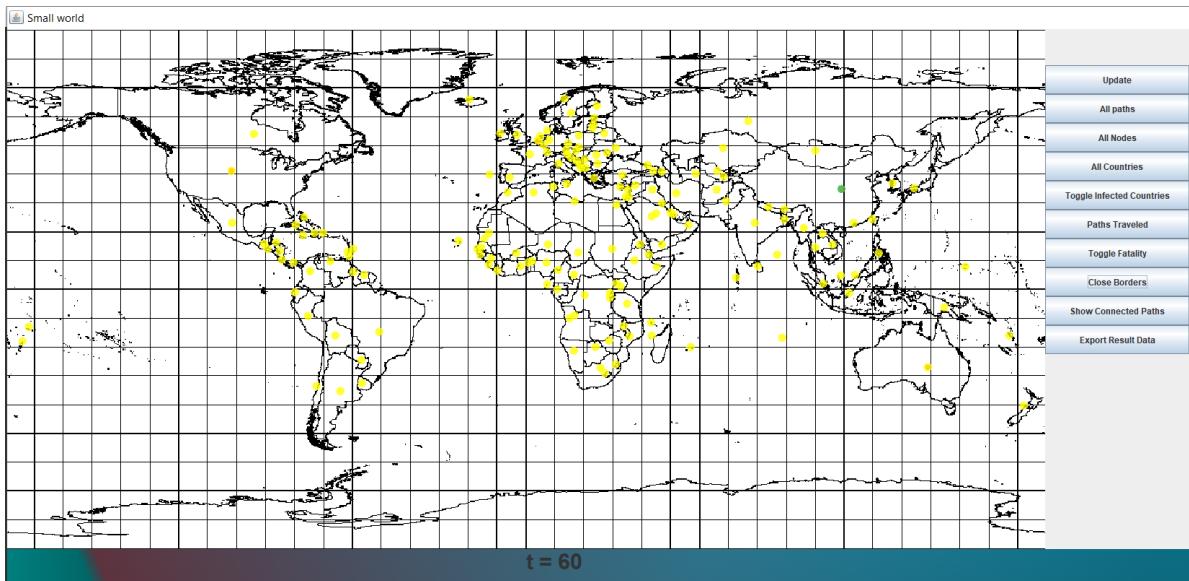


Figure 68:  $\beta = 0.4$ ,  $t = 60$

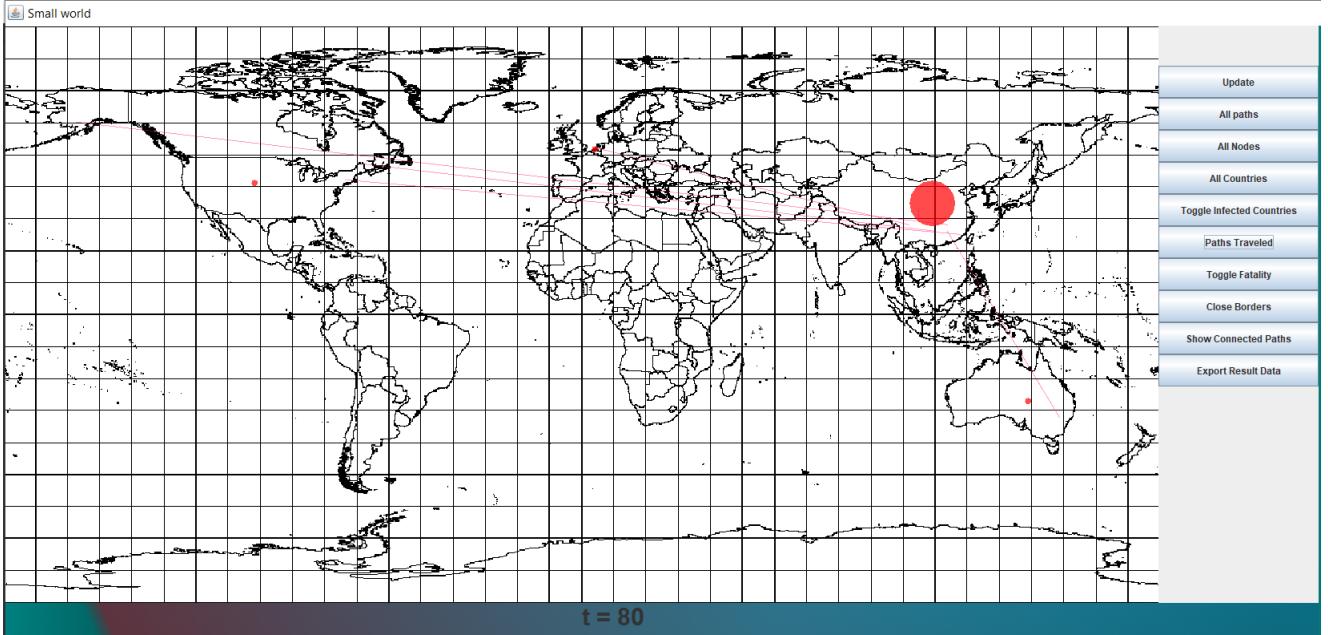


Figure 69:  $\beta = 0.4$ ,  $t = 80$

Here we see that while China's infectious population is rising exponentially, the number of new countries infected since its border lockdown is zero, since the number of infectious individuals in Australia and America are not yet high enough for them to spread to other countries.

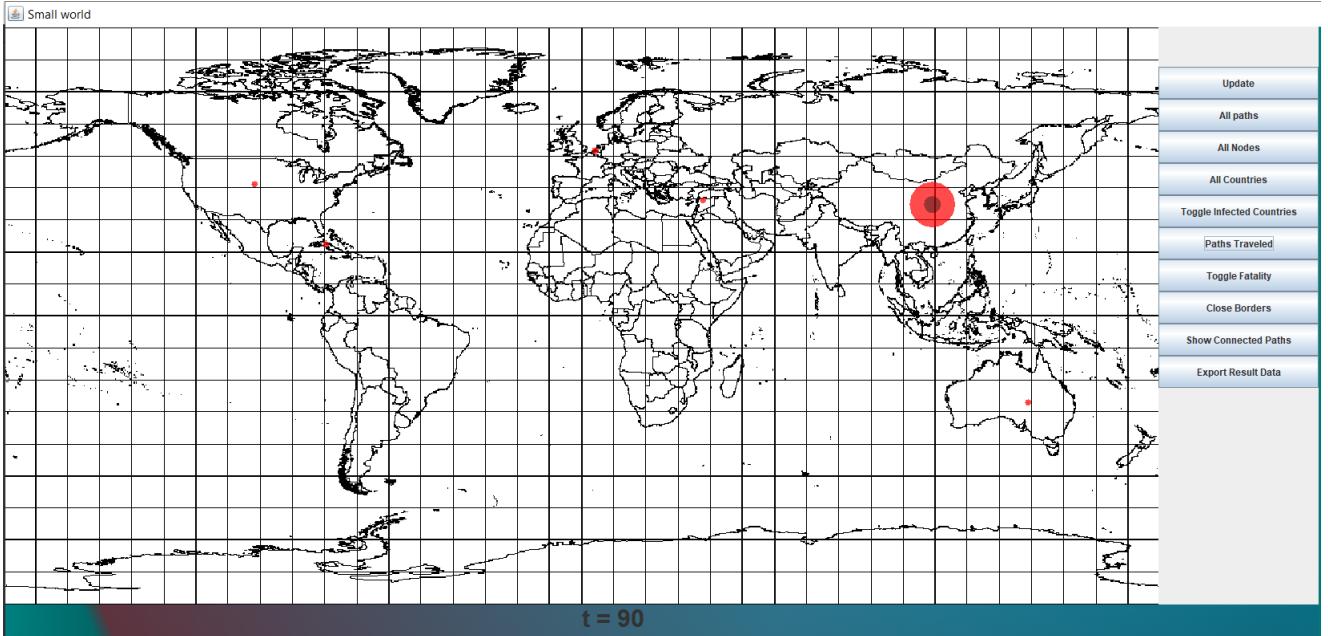


Figure 70:  $\beta = 0.4$ ,  $t = 90$

However, after a further 10 days, 2 new breakouts have occurred due to Australia, America and the Netherlands.

Let us assume that at this point, Australia, the Netherlands and the newly infected Caribbean all decide to close their borders to prevent a further outbreak, but America and the middle east refuse to comply.

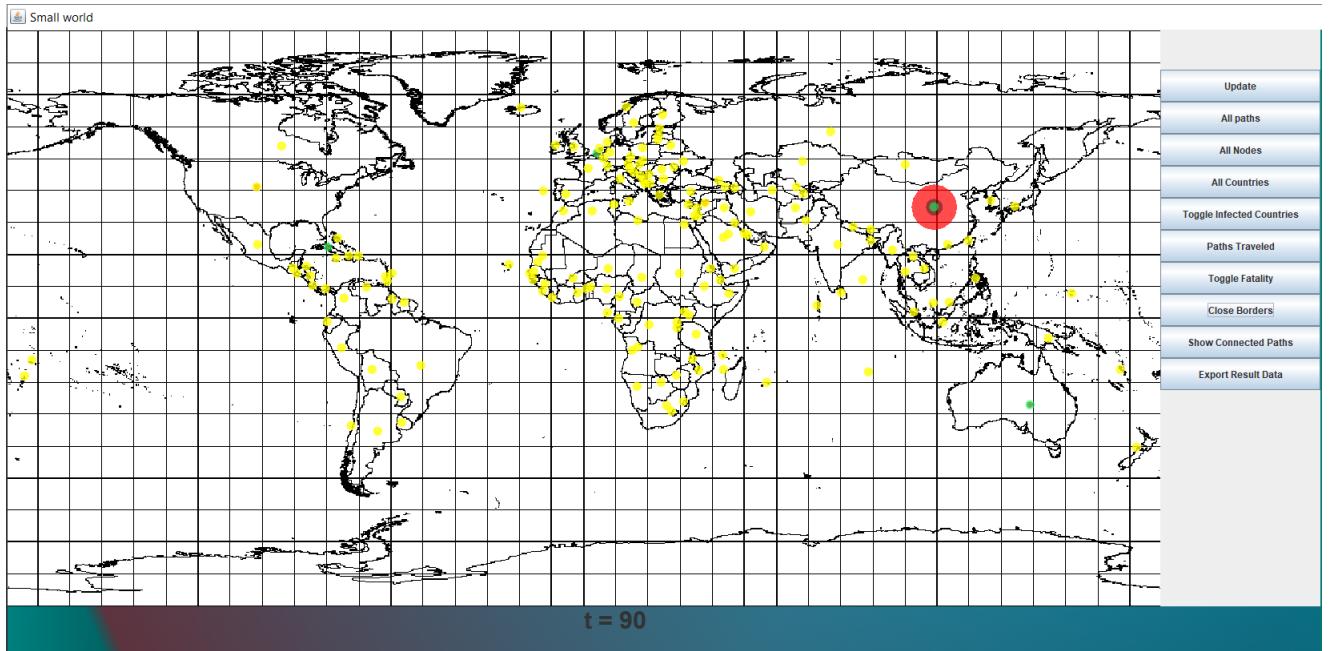


Figure 71:  $\beta = 0.4$ ,  $t = 90$

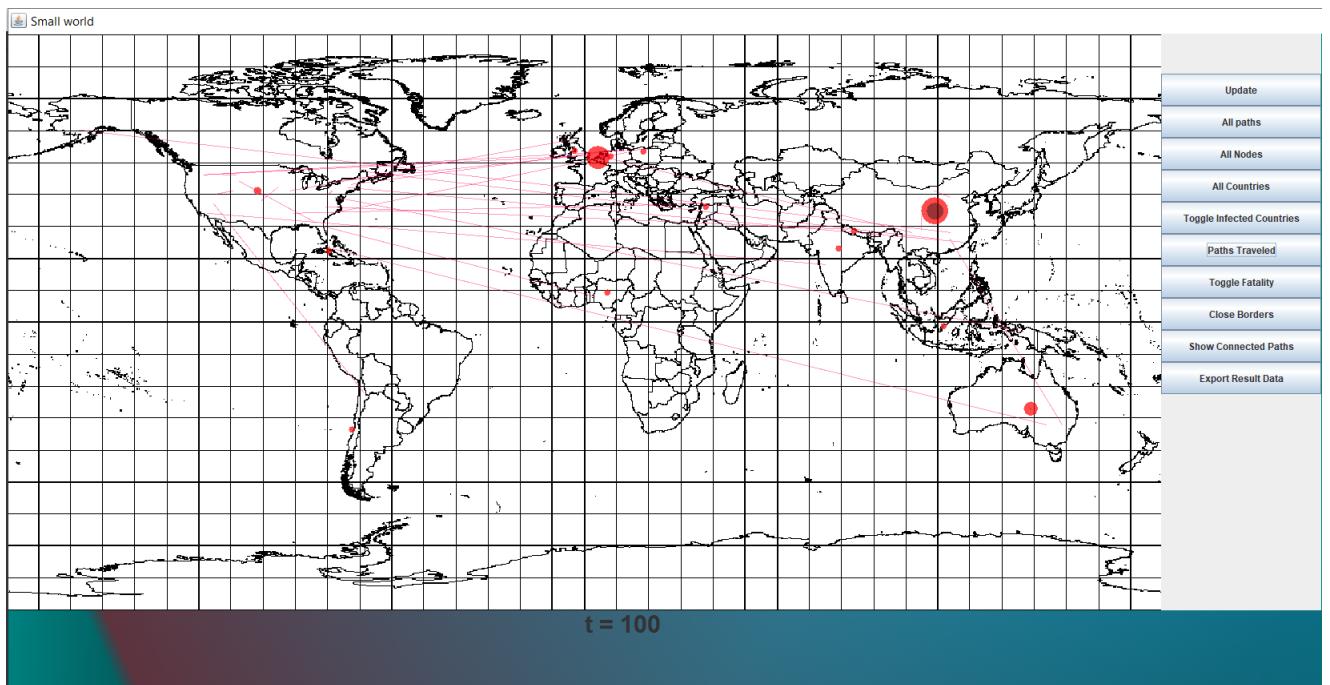


Figure 72:  $\beta = 0.4$ ,  $t = 100$

We see America quickly starts to infect many countries, including India and Nigeria. China's population starts recovering. If we compare this to  $t = 100$  for our simulation without lockdown, we see that despite  $\beta$  being a less optimal value for spreading, the simulation without locking down borders had far more infected countries at  $t = 100$ , primarily because of China.

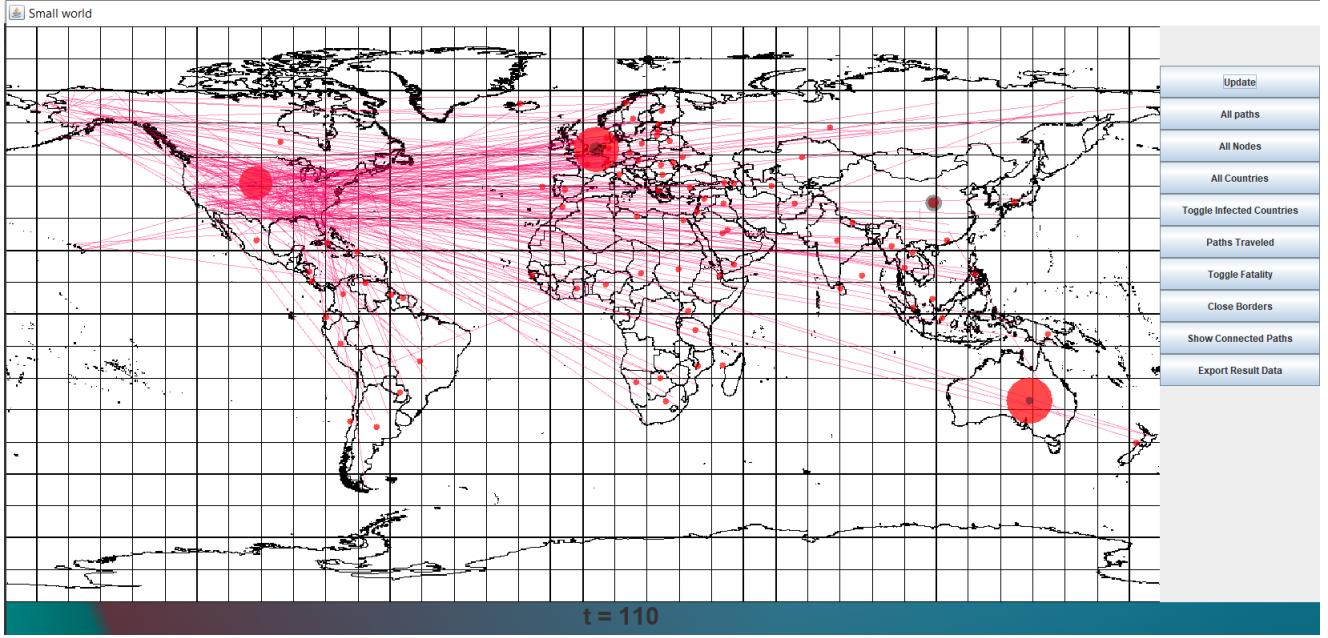


Figure 73:  $\beta = 0.4$ ,  $t = 110$

Although China locking down borders was a great success, since the USA did not follow through, the outbreak has spread to far too many countries for it to be controlled. We see that all it takes is one Country to not follow through with Lockdown, for the disease to rapidly become a problem once again. Below we see the shear number of infection lines coming from America.

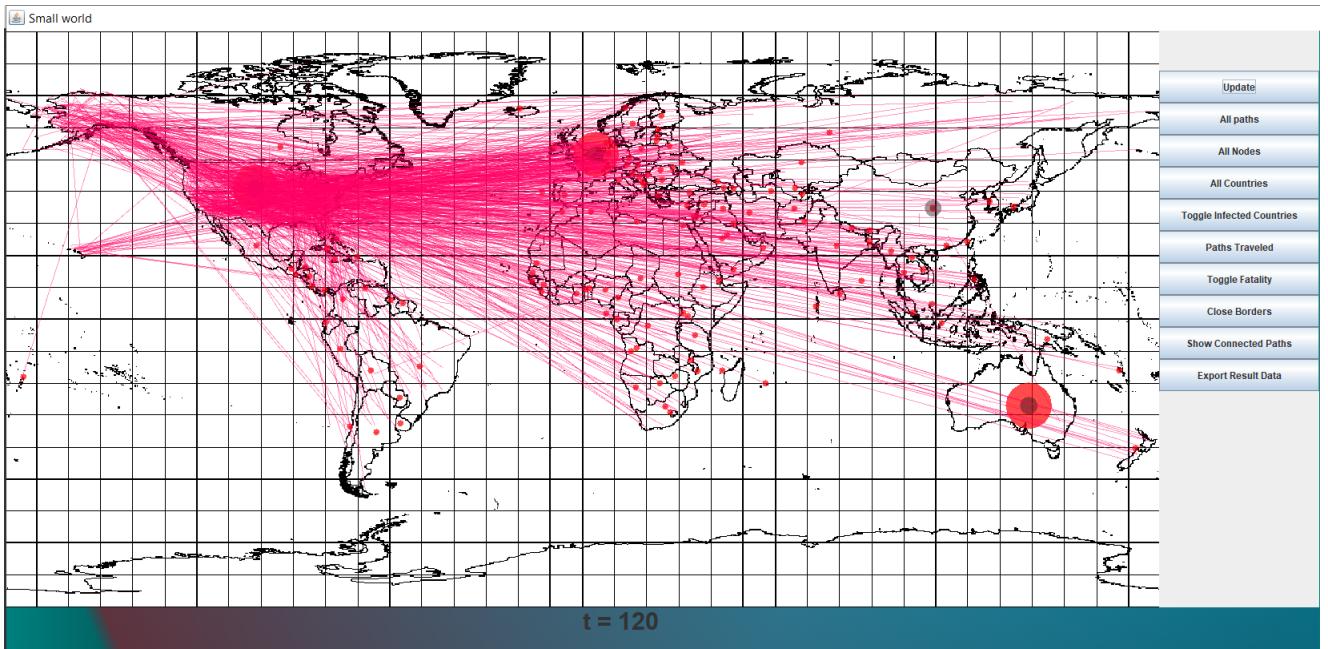


Figure 74:  $\beta = 0.4$ ,  $t = 120$

At this point the pandemic should progress how we would normally expect it to, just delayed by a month or two.

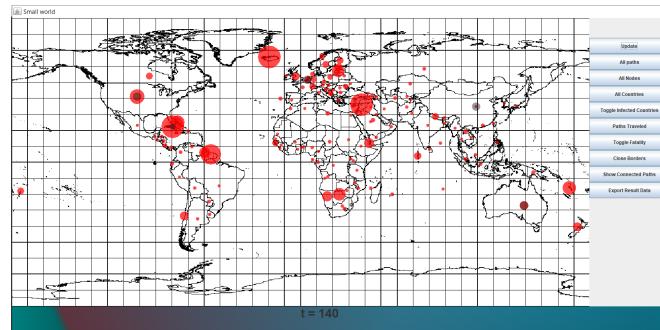


Figure 75:  $\beta = 0.4$ ,  $t = 140$

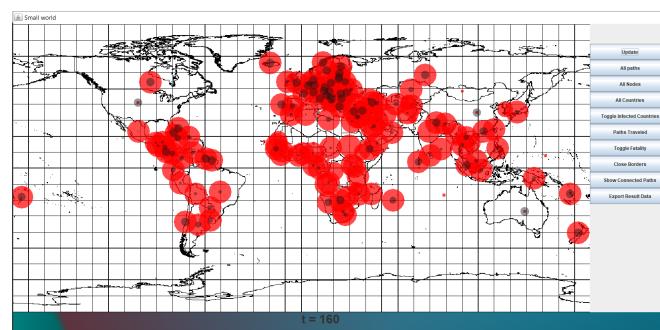


Figure 76:  $\beta = 0.4$ ,  $t = 160$

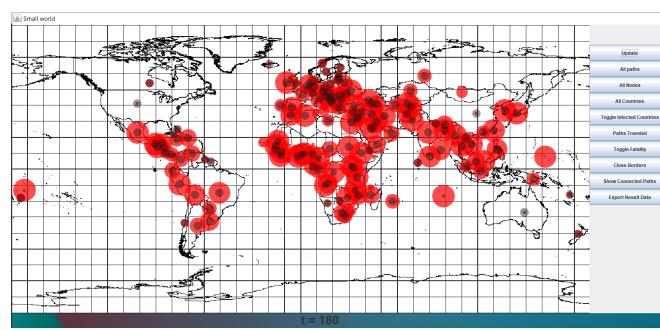


Figure 77:  $\beta = 0.4$ ,  $t = 180$

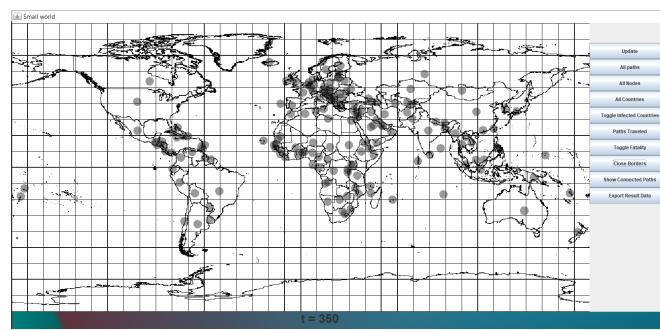


Figure 78:  $\beta = 0.4$ ,  $t = 350$

## 9 Implementing a national lock down

We now implement a national lockdown in conjunction with an international border closure. This should cause the number of infectious individuals to start decreasing inside the country shortly after lockdown is put in place.

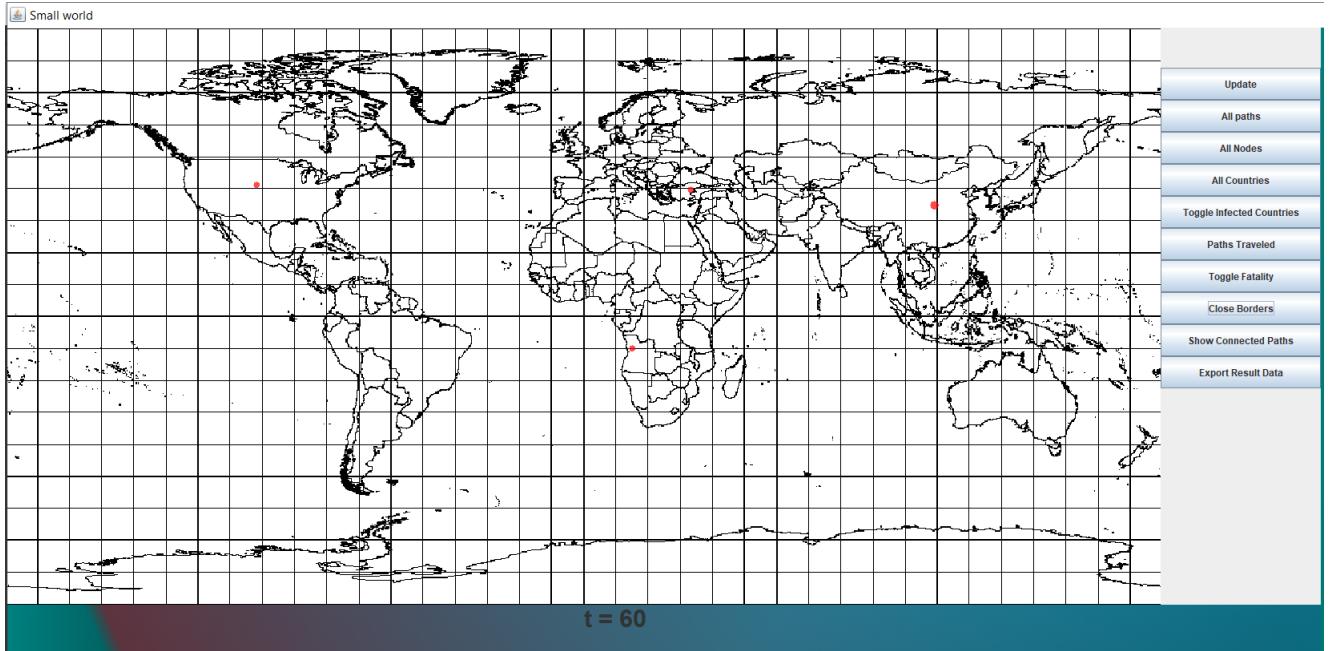


Figure 79:  $\beta = 0.4$ ,  $t = 60$

We lockdown the countries in green.

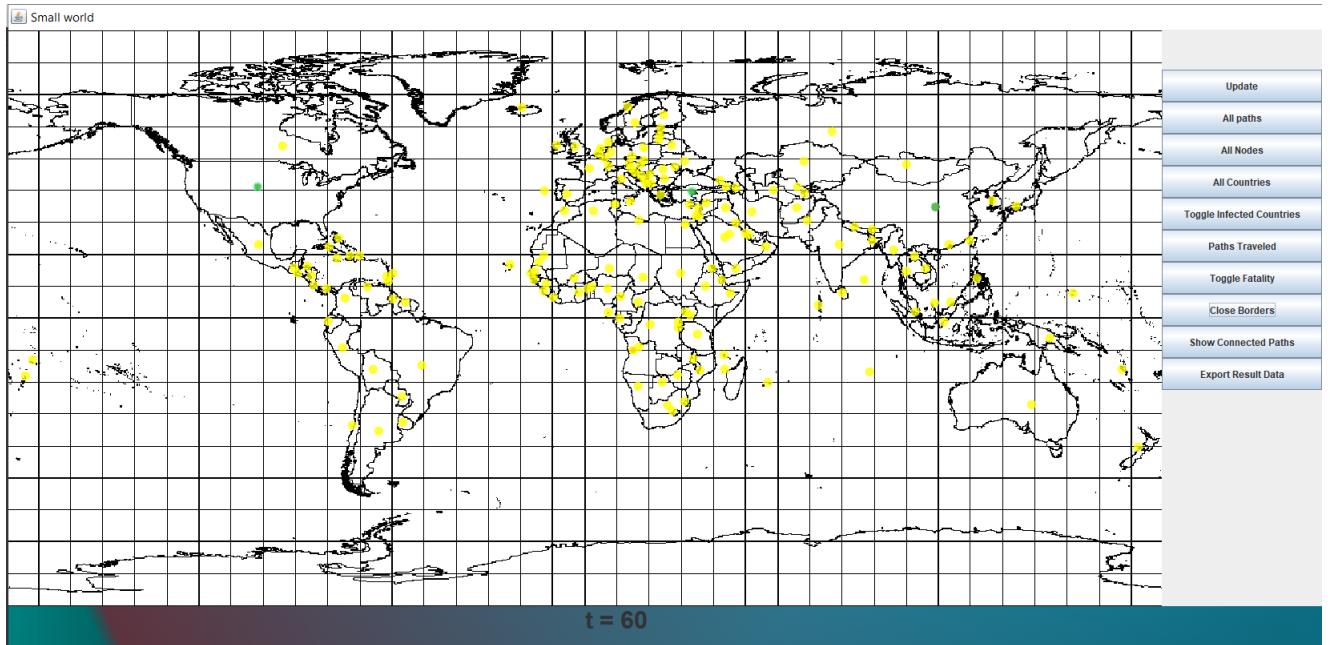


Figure 80:  $\beta = 0.4$ ,  $t = 60$

Here we see China reaches its peak number of cases, but its really low compared to normal.

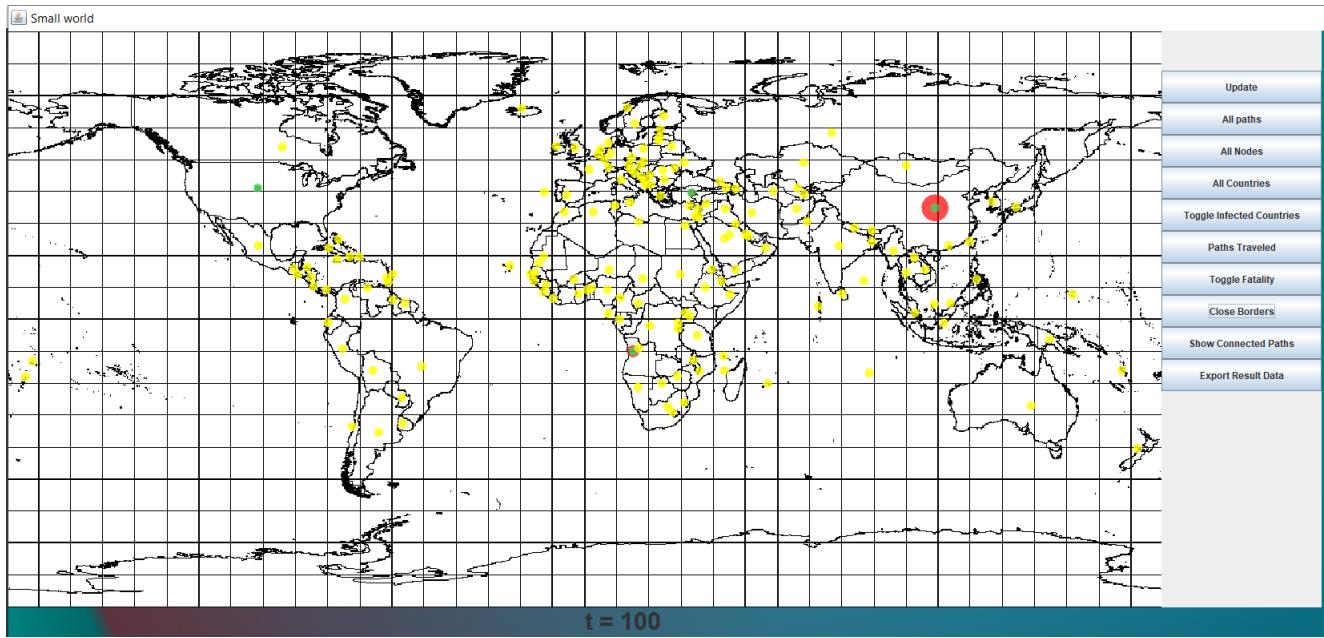


Figure 81:  $\beta = 0.4$ ,  $t = 100$

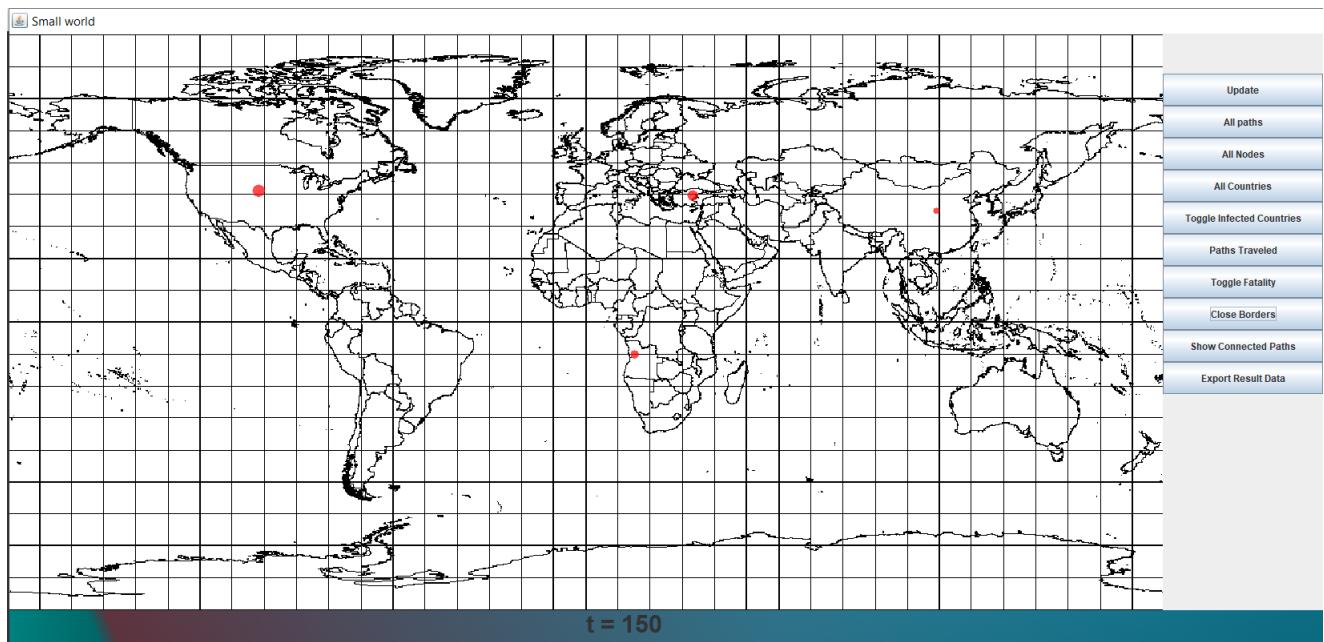


Figure 82:  $\beta = 0.4$ ,  $t = 150$

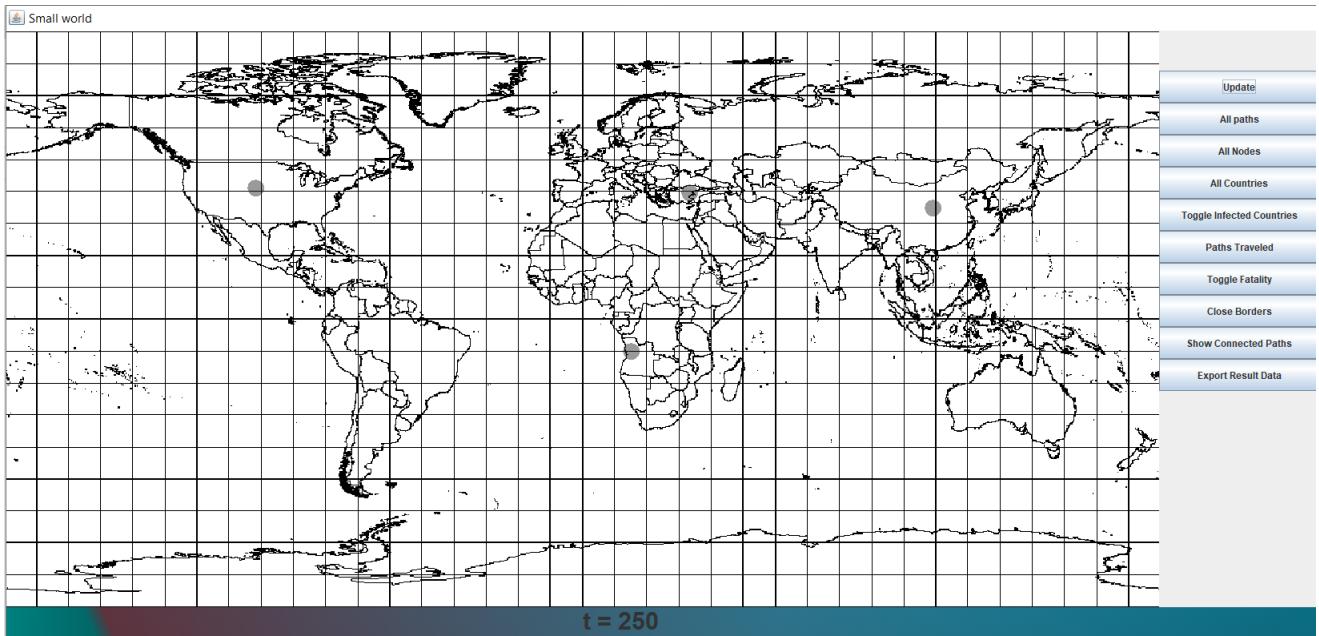


Figure 83:  $\beta = 0.4$ ,  $t = 250$

## 10 Discussion and Future Work

### Acknowledgments:

I would like to thank APMonitor.com for an introduction into modeling a disease as an SEIR model. I will include a video tutorial that helped me in the references.[9]

CovidVisualizer was an essential website I used frequently for real life statistics to help build an accurate SEIRD model. Most real-life graphs used were taken from the official website.

A paper [10] written by Prerana Laddha on the degree of separation in a small world network was extremely helpful with gaining an understanding of the mathematics behind a small world as well as understanding the logic so that I could translate the system into code.

### Additional Notes:

My code fills out text files with # delimited values for S, E, I, R and D for each country (about 12MB of data). I would have liked to plot each country and compare them to each other and real life data, but I became short on time.

## References

- [1] Duncan J. Watts Steven H. Strogatz  
*Collective dynamics of ‘small-world’ networks.*  
<https://www.nature.com/articles/30918>
- [2] Transmission of SARS-CoV-2: implications for infection prevention precautions  
<https://www.who.int/news-room/commentaries/detail/transmission-of-sars-cov-2-implications-for-infection-prevention-precautions>
- [3] Covid-19 in Italy  
<https://covidvisualizer.com/country?iso=IT>
- [4] Face masks may reduce COVID-19 spread by 85%, WHO-backed study suggests  
<https://www.livescience.com/face-masks-eye-protection-covid-19-prevention.html>
- [5] List of countries by age structure  
[https://en.wikipedia.org/wiki/List\\_of\\_countries\\_by\\_age\\_structure](https://en.wikipedia.org/wiki/List_of_countries_by_age_structure)
- [6] Coronavirus (COVID-19) death rate in Italy  
<https://www.statista.com/statistics/1106372/coronavirus-death-rate-by-age-group-italy>
- [7] Airport, airline and route data  
<https://openflights.org/data.html>
- [8] Though far from the norm, nearly 500 US flights per day depart more than 70% full  
<https://edition.cnn.com/travel/article/flight-capacity-united-states-coronavirus/index.html>
- [9] Solve ODEs in SEIR COVID-19 Model, APMonitor.com  
<https://www.youtube.com/watch?v=Tb1ktCtTMB4>
- [10] Prerana Laddha  
*Degree of Separation in Social Networks.*  
<https://arxiv.org/ftp/arxiv/papers/1007/1007.5476.pdf>