

PAKISTAN INSTITUTE OF DEVELOPMENT ECONOMICS

SPECIAL COVID-19 REPORT No. 2

A NETWORKS BASED ABM TO INVESTIGATE THE EFFICACY OF LOCKDOWNS AND OTHER MITIGATION STRATEGIES

Project Lead
Amin Hussain
(Teaching Fellow)

Co-investigators
Amara Ashfaq, Aurooj Khan, Ayesha Hanif, Taha Siddique
(Students)

LAHORE UNIVERSITY OF MANAGEMENT SCIENCES (LUMS)

November 10, 2020



A Networks-based ABM to Investigate the Efficacy of Lockdowns and other Mitigation Strategies

1. Introduction

The COVID-19 pandemic is one that has left the world reeling at how it has managed to affect the entire globe and killed hundreds of thousands. The intensity with which the virus struck called for an extreme reaction to keep it from overwhelming the healthcare system. To prevent deaths from this highly contagious virus we saw countries go into lockdowns. Businesses shut down; the roads were traffic-less; entire cities became ghost-towns. As lockdowns extended, the trade-off between staying at home and being safe from the virus and going out to work to earn enough to not succumb to economic hardships became apparent; a number of lockdown strategies were proposed to keep the costs (in terms of lives lost) to a minimum. Other, significantly less drastic, measures were proposed too, with masks heading the list.

This project aims to develop an agent-based-model that allows us to simulate the real-world situation and investigate what kind of lockdown strategy is optimal, specifically in Pakistan, where a significant proportion of its population cannot adapt to a “work from home” climate, so copy-pasting strategies from more developed countries may not work. We aim to create a platform to plot the different possible courses the situation can take, and the impact of different policies in each situation. Since the situation is fluid and doesn’t seem to be ending any time soon, with fears of multiple waves, we believe this will be an important contribution to the debate surrounding policy related to Corona.

Human interactions power the economy on one hand and accelerate virus transmissions on the other. They also make the situation we are trying to study into a non-linear dynamical system which is difficult to predict and assess using traditional techniques. It can benefit a great deal from the application of techniques from Complexity Science, including network analysis, simulations and computational techniques. There exists a special relationship between complexity science, network theory and epidemiology (Danon et al. 2011). Unlike standard economics, the Complexity approach places interactions at its center and studies their impact. The complexity approach to modelling anything is to get right down to the bottom and determine how the behavior of individual parts influences the outcome for the entire system. A pandemic is the large-scale outbreak of an infectious disease over a wide geographical area. Coming up with strategies to deal with such situations is a great undertaking because there are so many variables to be considered. A strategy may look effective on paper, but the emergent aspect of changing how the agents interact could have unintended consequences that must be looked out for. Using an ABM to model the COVID-19 pandemic could prove useful in making observations about the system as a whole that might not be immediately obvious. This makes research such as this very

policy-relevant, because the course of the outbreak can be closely observed and informed decisions can be made.

Heterogenous agents are a hallmark of ABMs, and these will represent people employed in different areas of work. People form networks of interaction; the results of this interaction may have consequences that are not obvious. Networks are a collection of “nodes” and “links”, wherein the former represent the individuals in a network and the latter refers to the connection between them. Agents in our ABM can be programmed so as to simulate different types of populations and can be adapted according to the data we have on Pakistan

By introducing the virus into this Pakistan-specific network model, we shall first see how the virus behaves differently in different types of networks and then move on to simulate different lockdown strategies. In a network model, these lockdowns will be simulated by severing the links that exist between agents. The effectiveness of strategies will be judged on how many deaths occur or investigating the number of people infected.

Government actions have been shown to alter the course of outbreaks, using mathematical models. This serves as enough inducement to observe the effectiveness of different kinds of lockdowns in an environment where agents are programmed to follow simple rules and organize in network structures that can actually be seen in Pakistan, in an effort to encourage policy-making that takes the dynamics of interacting agents into account.

The model can also be extended to study the impacts of different types of medical or economic interventions. Face masks, for instance, are a factor whose effectiveness is under debate and the compulsory use of which has been debated as a possible policy intervention. This model can be used to study the effects of different levels of mask compliance on the infection rate, and the results may be used to establish confident claims to persuade the masses. Different features of the human network itself can lead to drastically different results. Thus, we also use the model to investigate results with different family sizes, etc. After our qualitative analysis is used to assess the strength of mitigation strategies, we may then go on to add real data to simulate actual situations for quantitative analysis.

2. Literature Review

When it comes to epidemics, mathematical models and simulations are great tools for assessment when results need to be obtained as quickly as possible, because the actions they influence must also be taken swiftly. There is a significant amount of literature on studying epidemics through mathematical models. The seminal work of Kermack and McKendrick (1927) founded the deterministic compartmental epidemic modelling. In three papers, they introduced the SIR (Susceptible, Infected, Recovered) Model for the number of people infected with a contagious

illness in a closed population over time.¹ It was proposed to explain the rapid rise and fall in the number of infected patients observed in epidemics such as the plague (London 1665-1666, Bombay 1906) and cholera (London 1865). It assumes that the population size is fixed (no births, deaths due to disease, or deaths by natural causes), incubation period of the infectious agent is instantaneous, and duration of infectivity is same as length of the disease. It also assumes a completely homogeneous population with no age, spatial, or social structure. Traditional models of epidemics such as this one assumes that the contact between individuals remains fixed over the course of an outbreak, but this may not be true. The number of contacts an individual has may remain the same, but the identities of these contacts may change. Erik Volz and Lauren Ancel Meyers (2007)² worked dynamic contact networks into the existing SIR model to counter the homogenous mixing assumption.

There is a growing body of work done on Network Theory, which is what our ABM will simulate. A network consists of a set of actors or nodes along with a set of ties of a specified type (such as friendship) that link them. The ties interconnect through shared end points to form paths that indirectly link nodes that are not directly tied (Borgatti and Halgin, 2011).³ Bougheas (2017) investigates contagion in stable networks by studying how agents derive benefits from other agents they are linked to and suffer losses when any agent connected to the same path as them is hit by a shock.⁴ There is an important interplay between network theory and epidemiology; Keeling et al. (2011) and House (2011) look into the spread of infectious diseases on networks, and the types of network structures that are relevant to epidemiology. As the COVID-19 pandemic runs its course, new studies lend importance to network theory in trying to understand the new containment regime. Hanel et al. (2020)⁵ show how assuming realistic contact networks can explain this better than traditional models of epidemics, which do not explain the growth patterns with prolonged linear regions. If prominent features of contact networks are taken into account, the course of this novel pandemic can be more precisely illustrated.

For the highly infectious COVID-19, lockdowns have been the dominant response to controlling the pandemic. However, it has quickly been realized that a complete uniform lockdown cannot be sustained for long periods of time because there are economic costs to consider. The working paper *Optimal Targeted Lockdowns in a Multi-Group SIR Model* by Acemoglu et al. (2020)⁶

¹ A contribution to the mathematical theory of epidemics. (1927). Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character, 115(772), 700-721. doi:10.1098/rspa.1927.0118

² Volz, Erik & Meyers, Lauren. (2008). Epidemic threshold in dynamic contact networks. Journal of the Royal Society, Interface / the Royal Society. 6. 233-41. 10.1098/rsif.2008.0218.

³ Borgatti, S., & Halgin, D. (2011). On Network Theory. SSRN Electronic Journal. doi:10.2139/ssrn.2260993

⁴ Bougheas, S. (2017). Contagion in Stable Networks. SSRN Electronic Journal. doi:10.2139/ssrn.3039414

⁵ Thurner, S., Klimek, P., & Hanel, R. (2020). Why are most COVID-19 infection curves linear? doi:10.1101/2020.05.22.20110403

⁶ Acemoglu, D., Chernozhukov, V., Werning, I., & Whinston, M. (2020). Optimal Targeted Lockdowns in a Multi-Group SIR Model. doi:10.3386/w27102

looks into implementing different lockdown policies for different age-groups and finds that these differential optimal policies surpass uniform optimal policies. They also found that enforcing stricter lockdowns for the oldest and, therefore, most at-risk groups produces the most gains and also makes it possible for less strict lockdowns for groups that are not as vulnerable.

Our study also looks into lockdowns, but instead of focusing on implementing the same kind of lockdown differentially over risk-groups, we look into differential lockdown strategies. These include hotspot lockdowns, which are lockdowns within a certain radius that reports a higher number of cases; cyclical lockdowns, where a period of lockdown is alternated with a period in which economic and other activities are allowed, and a cycle is created; and others. In addition, with the primary network in place, other mitigation strategies can be easily incorporated, and their effectiveness tested out. The standard SIR model ignores network effects, which we account for by building our model around networks themselves. Our study is also unique in that it focuses on Pakistan, by building an ABM that is Pakistan-specific, which can then yield vital pieces of information about what lockdown (and other mitigation) strategy will work best here. It can also be used to critically observe the course the virus outbreak will follow in Pakistan, allowing the government to be better equipped to dealing with it.

3. Research Methodology

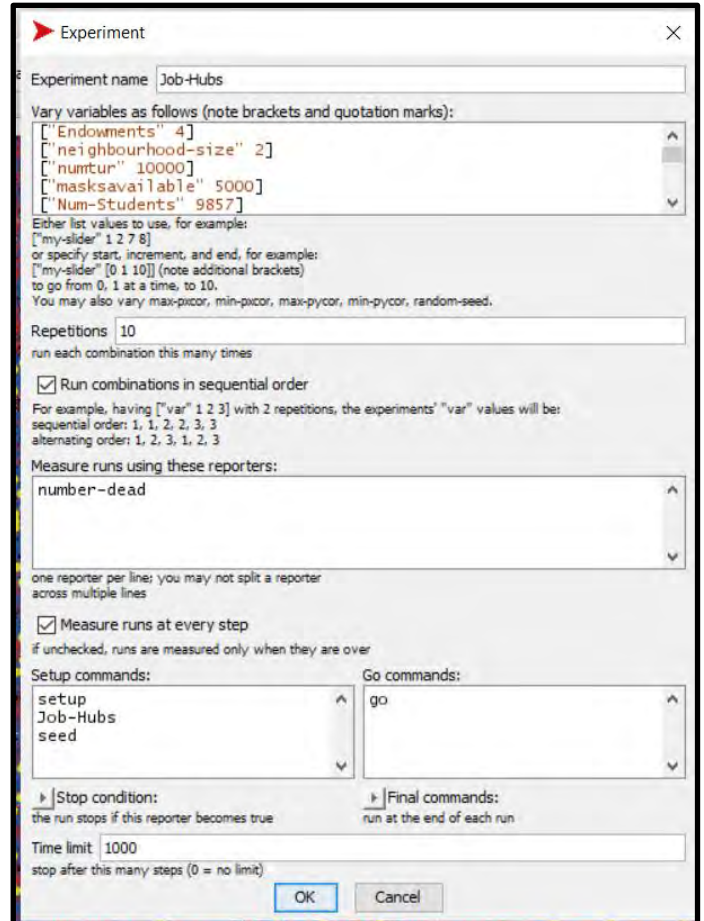
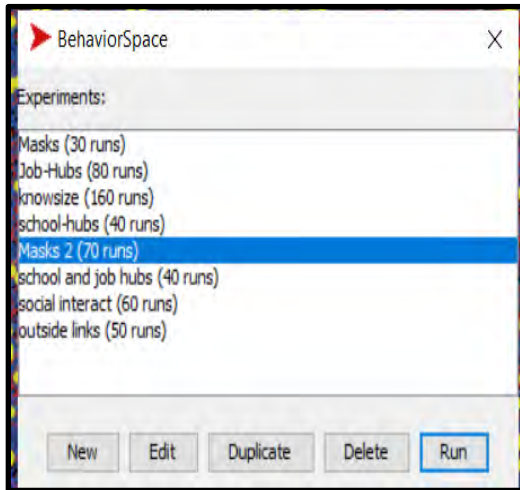
We employ Agent Based Models (ABMs) in which autonomous decision-making entities called agents individually assess their situation and make decisions based on a set of rules, and we observe the system as a whole. The agents can be made heterogeneous by programming a different set of rules for a particular group. The agents (people) move about and form secondary-links, which can be in a job or school context, in our model. Restrictions on forming secondary links come about due to different kinds of lockdowns. All agents are initially given a certain amount of endowment, which serves as their savings during the lockdown. The fact that human movement and interaction cannot be strict and may vary is explored through the concept of networks, in which humans encounter each other in varying frequencies and intensity. We use the Netlogo programming language and Integrated Development Environment (IDE) to explore the emergent phenomena that arise. The user manual in the **Appendix** can be referred to for a detailed explanation of the model, and how to use it.

The variables in the model pertain to:

- I. Virus Characteristics: transmission rate, recovery rate, etc;
- II. Disease Characteristics: percentage-symptomatic, sympto-infected, etc;
- III. Human and Network Characteristics: employed, outside links, know size, etc;
- IV. Economic: endowments.

Properties of the virus (transmission rate, recovery rate, etc) and variables influenced by human behaviour can be adjusted in the model in order to achieve realistic results, depending on the context. This is done because human behaviour varies greatly and also to cater to the fact that the current information available about the workings of the virus itself is contested.

Due to the complex nature of the variables involved, the research in question is non-linear which is why the focus is not merely on driving the



Reproductive Rate (R_0) below 1. In addition to this, calculating R_0 is a difficult task in the middle of a pandemic.⁷ Instead, we employ BehaviorSpace (a software tool integrated with Netlogo) to derive optimum results, keeping health and economic factors in mind. BehaviorSpace is a powerful tool for “parameter sweeping”.

Because our model contains a variety of parameters that can take a range of values, in order to best understand the behaviours the model is capable of producing, we run ten iterations of specific scenarios in order to find optimum results. In a parameter space such as ours, running the model with different configurations of variables can produce substantially different results. BehaviorSpace streamlines this experimentation and saves time. Each experiment is run ten times and the averages are calculated and reported.

⁷ Hussain, A. (2020). Explaining the R_0 in the COVID-19 Projections. Pakistan Institute of Development Economics.

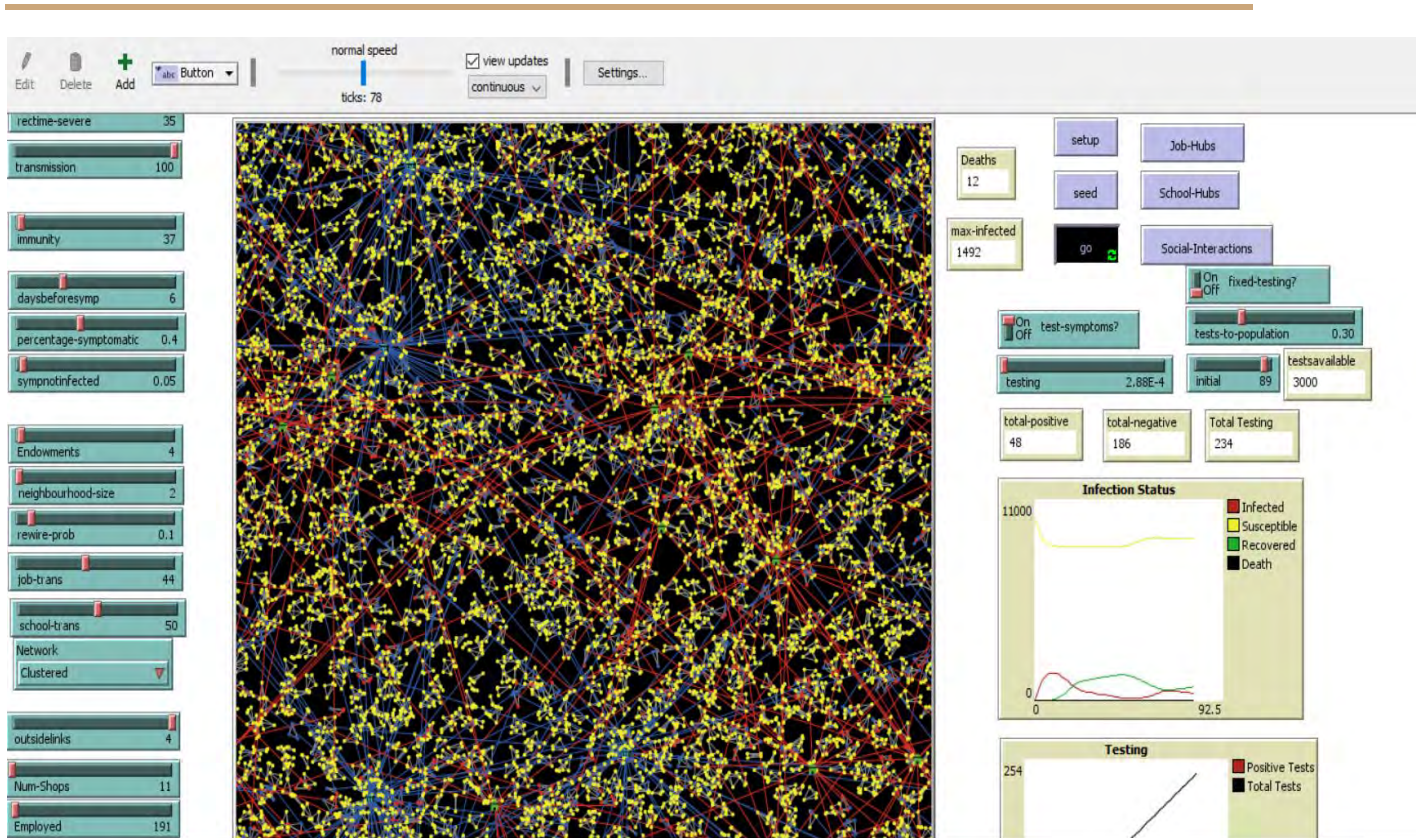


Figure: The running model.

4. Results and Discussions⁸

Our ABM consists of a vast parameter space, which allows for exploration of a host of scenarios. The parameter settings can be changed to keep in line with any new virus related research that surfaces, in addition to investigating the efficacy of policies created to deal with the pandemic.

We have created a variation of links to represent different scenarios. Primary links (Plinks) focus on showing interactions inside one’s home; Secondary links (Slinks) represent connections through schools and jobs which are individually colored blue and red, respectively. Lastly, we introduced social interactions outside an individual's house using tertiary links (Tlinks), shown as yellow links connecting nodes to each other. To differentiate each link we allowed it to be fully customizable by allowing the user to set different transmission rates and spawn rates for every form. Furthermore, the density of each variable within the model is customizable so long as it remains below the maximum population. Each variation of links adds greater depth to the model by accounting for numerous factors that occur in our daily lives.

⁸ All results have been obtained by running ten iterations of a particular scenario in Netlogo’s integrated software tool BehaviorSpace.

Unless otherwise stated, the experiments are run with a population of ten thousand. The immunity period following recovery from infection is set to one hundred days, which is in line with research that claims immunity lasts around three months.⁹ The experiments are run for a certain number of ticks, where one tick corresponds to one day, and the network type is Clustered. The Clustered Network resembles a real world world network, wherein we find clusters of families and friends connected through primary links, and then some secondary links exist which form links between individual clusters.

4.1 Masks

Face masks were one of the earliest responses to curtail the spread of COVID-19. The virus spreads when a susceptible person either comes into close contact with an infected person, or a surface that has been touched, coughed, or sneezed on by an infected person. Because the virus is contained in an infected person's nose and throat, it was hypothesized that masks that effectively covered the mouth and nose would prove monumental in lowering virus transmissions. There has been a lot of debate centered around whether wearing masks should be made compulsory. A lot of campaigning has been required to send the message that masks may be the best defense against contracting the virus, in the absence of a vaccine.

The model we have built allows for control over how many people wear masks in the population. By adjusting the slider, we ran the model for different levels of mask compliance. Because masks are expected to slow down transmissions, we expected that this would lead to a fewer number of infected people in the short run.

4.11 Masks and the maximum number of infected people

This experiment was run to study the effects of different levels of mask compliance on the maximum number of people infected in the population. If mask compliance really did slow down the transmission of the virus, this would allow for an inversely proportional relationship between mask compliance and max-infected, in the short run.

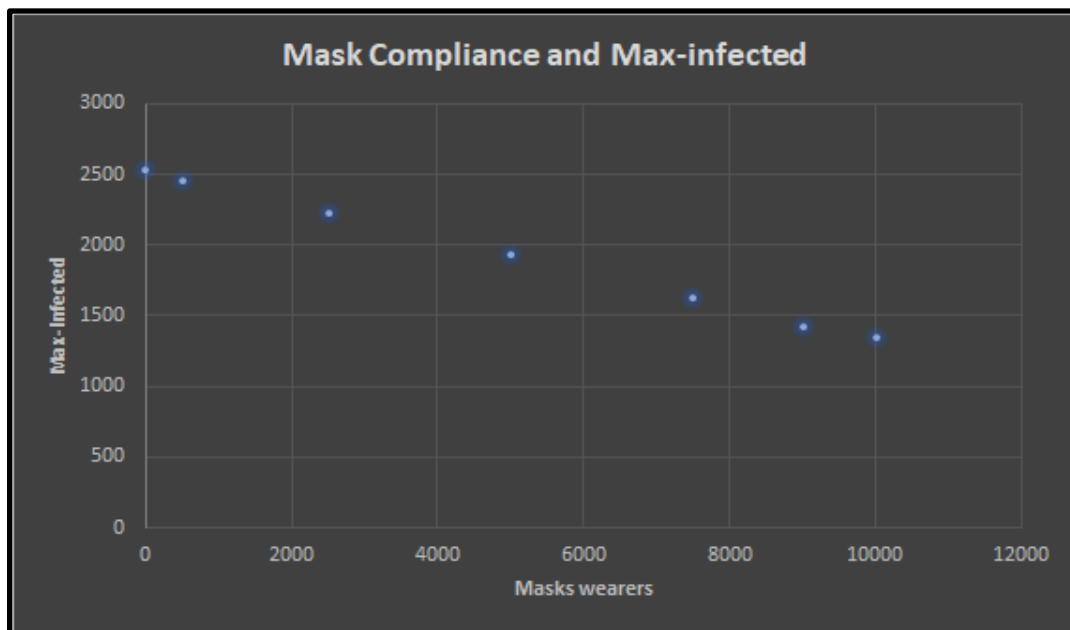
The levels of mask compliance are calculated via the number of mask wearers in the population (which is set to ten thousand). Thus, 10,000 mask wearers imply full mask compliance, while 0 mask wearers imply complete non-compliance. When the experiment is run for 500 ticks, the following results are obtained.

⁹ Healthline, How Long Immunity Lasts After COVID-19. <https://www.healthline.com/health-news/how-long-does-immunity-last-after-covid-19-what-we-know>. Accessed 10 Sept. 2020

Table 4.11.

Mask Wearers	Max-infected
0	2527
500	2459.6
2,500	2222.7
5,000	1930.2
7,500	1622
9,000	1420.5
10,000	1344.4

Figure 4.11A

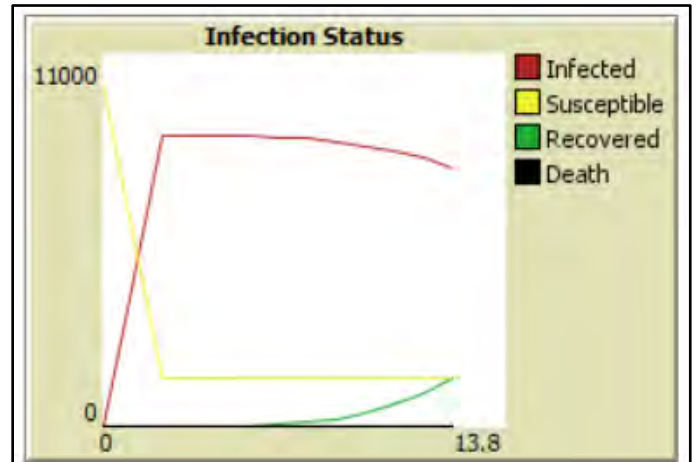
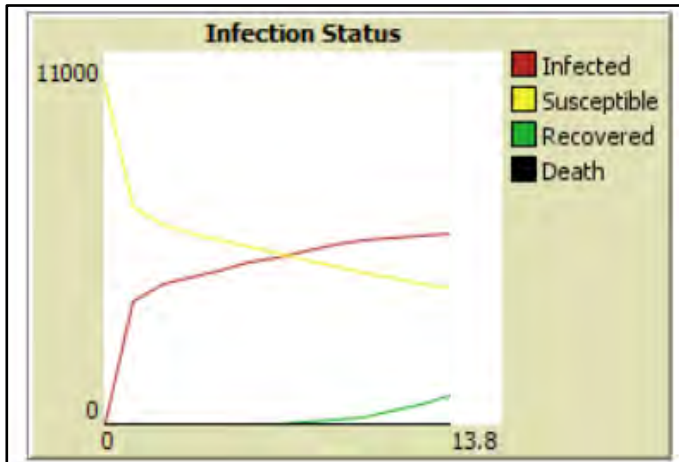


As evident from **Fig. 4.11A**, higher mask compliance does lead to a fewer number of people that are infected over the course of 500 ticks. It must be noted that max-infected value reflects all the infected people over the course of the pandemic. That is, infected people are included even if they eventually died or recovered.

This result is an encouraging one and supports the use of face masks, because they are shown to slow down infections. Over a thousand infections are delayed when most of the population wears masks, relative to when none do. More than five hundred infections are prevented when half the population complies, compared to when no one does. The graph depicts a decreasing linear function, which is what we expected.

Fig. 4.11B: 50% Mask Compliance

Fig. 4.11C: Zero Mask Compliance



A comparison of **Fig. 4.11B** and **Fig. 4.11C** makes it fairly obvious that the spread of infection is very quick in **4.11C**, where there is zero mask compliance as compared to **4.11B**, where the infection spreads more slowly because there is some level of mask compliance. The peak of the infection is reached a lot more quickly in **C** than in **B**.

4.12 Masks and the number of infected people

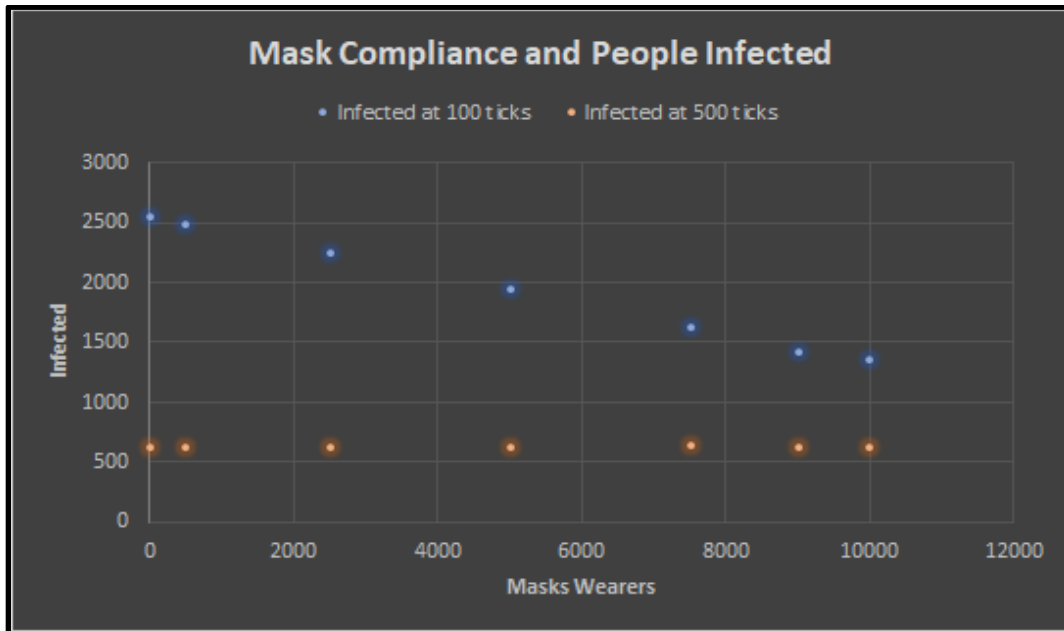
This experiment was run to observe the effect of different levels of mask compliance on the number of people infected at a certain point in time. Since masks decrease the chances of successful virus transmission, we expected a higher number of mask wearers to lower the infected population in the short term.

We observed the effects of masks at 500 ticks and 100 ticks.

Table 4.12.

Mask Wearers	Number Infected at 100 ticks	Number Infected at 500 ticks
0	2547.3	619.3
500	2477.5	627.9
2,500	2243.8	629
5,000	1950.9	630.8
7,500	1621.9	636.3
9,000	1427.5	625.1
10,000	1361.1	623.6

Fig. 4.12.



An observation evident from both **Fig. 4.12** and **Table 4.12** is that the number of infected people at 100 ticks, regardless of the level of mask compliance, is always greater than the number of infected people at 500 ticks. This has to do with the characteristics of the clustered network, where the infection spreads quickly in its early stages. Moreover, by the 500th tick, a lot more people have either recovered or died, thus decreasing the number of people infected at that point in time.

It is also evident that masks do decrease the number of infections in the short run (100 ticks). Full compliance reports more than a thousand fewer infections than when there is no compliance. It is also clear that further along the line, at the 500th tick (more than a year), the number of infections are more or less the same, regardless of mask compliance. Together, these two results serve to show that masks are indeed efficacious in slowing down the spread of the virus.

4.2 Testing



After a surge of daily cases, Pakistan seemed to have reached its peak of the pandemic during June. However, soon afterward, there was an evident decline in the cases, and that downward trajectory has continued to the present day (September 16). While many celebrated this as a victory, others quickly pointed out systematic flaws that might give us misleading results. According to Our World in Data, the estimate of Pakistan's daily tests per thousand people was 0.1 as of July 16, a rather sharp decline from 0.13 tests in June.

To this effect, we introduced two features in our model; fixed daily testing and a fixed number of tests that must be carried out on the population (by placing a cap on the total number of tests available). By doing so, we kept the number of tests conducted daily constant. We analyzed the results at different levels of daily testing. The results were as follows.

Positive Tests	Daily Tests
1	8
0	8
2	8
2	8
1	9
1	8
1	8

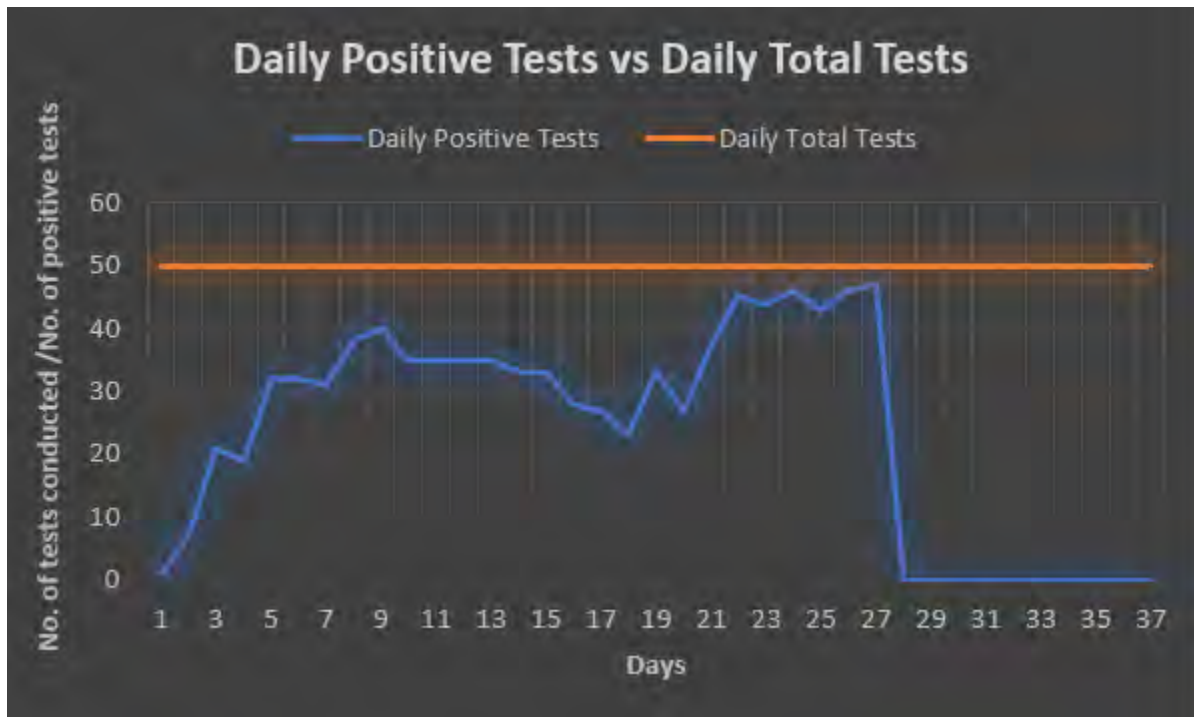
8 tests per day

Positive Tests	Daily Tests
0	20
2	20
5	20
7	
5	20
4	20
3	20

20 tests per day

Positive Tests	Daily Tests
2	50
8	50
11	50
19	50
23	50
16	50
5	50

50 tests per day



Our results clearly indicate that given a fixed number of tests daily, after a certain time period there seems to be a decrease in the number of positive results. From the graph above, we can see that 50 tests were carried out daily. Initially, we saw a rise in the number of positive results (a peak of 47 positive tests in a day) but with time the number of positives test results started to decline. This points to the fact that less people are getting infected over time thus our model predicts that the decline in the cases is not a function of decreased testing rather it is a result of a lower infection rate.

In our model, we included two graph plotters to observe patterns in testing: one which depicts the total number of tests conducted and positive test results on a cumulative basis since the start of the model, and one which depicts the *daily* statistics for total tests conducted and positive test results. The latter of these plots- depicting daily testing statistics- in the context of our model's fixed number of tests conducted daily, provides valuable insights to the nature of the spread of infection, depending on what the value the immunity slider is set at.

Figure 4.2A: Immunity at 100 Days

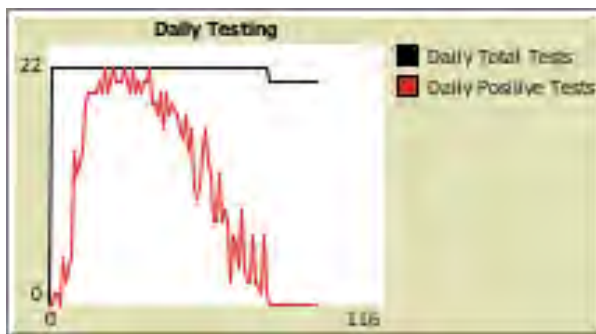


Figure 4.2B: Immunity at 30 days



The graph plots above depicting the trends in daily testing show us an interesting parallel. In **Figure 4.2A**, the period of immunity following recovery from infection is set at approximately 100 days (approximately 3 months), and the initial spike and gradual subsequent decline of the infection is clear by the red plot for positive tests. By day 116, there are no more infected members of the population, so as a natural result of infection declining, positive tests reach a value of zero. On the contrary, in **Figure 4.2B**, immunity is set at approximately 30 days. As re-infections are common and frequent, we don't see the infection dying out completely, but we do see periodic fluctuation in the number of daily positive test results. Note that daily total tests conducted are constant- acting as a controlled factor in our model, so that trends in positive test results can be observed objectively.

Note: In order to simulate the real life scarcity of tests available- which was a notable problem in some countries during the peak of the global pandemic in March- we introduced an adjustable cap on the total number of tests available, along with an option to enforce this cap, or discard it altogether and run unlimited testing.

4.3 Lockdowns

Lockdown strategies in a network based ABM, where agents do not move around but are connected to each other through links, revolve around the idea of severing links. However, it is not as simple as looking at the total number of links in the network and severing a percentage of them. It is important to realise that a linear relationship between severed links and infections may not exist, and certainly not a one-to-one relationship.

In fact, lockdown strategies have a lot to do with the type of network that is present. Smart lockdown strategies should be investigating potential tipping points to see how most deaths can be prevented while still making sure essential activities can take place. The focus should also be on which links to sever, instead of how many links to sever.

4.31 Complete Lockdown

The complete lockdown is labeled in our network based model as lockdown type 1 where all secondary and tertiary links to the nodes are deactivated. Two parameters are set, Complete-Threshold-1 and Complete-Threshold-2, which determine the number of people infected to start a complete lockdown and the number of people infected at which lockdown is eased respectively.

To determine the effectiveness of complete lockdowns we ran BehaviourSpace at 100 ticks and results were as follows.

Table 4.31A

threshold1-threshold2	Max-Infected	Deaths
150-0	832.4	6.6
15-0	800	5.6
150-50	787.8	11.8

Table 4.31B

Lockdown Type	No Lockdown	Complete (150-0)	Complete(15-0)
Max-Infected	1318	832.4	800
Deaths	14.5	6.6	5.6

The effectiveness of complete lockdowns is fairly visible with a drastic drop of maximum infections and total deaths. Node clusters of our network model are limited to their primary links during the time of the lockdown, which allows the infection to be contained within close parameters. Therefore, at an upper threshold of 150, as soon 150 people were infected, lockdown was imposed and as a result, nearly 500 fewer infections were observed. Furthermore, a lower upper threshold leads to an even smaller amount of maximum infections.

It is interesting to note however, that the smallest number of infections were observed with a lower threshold in place, this can be explained by the immunity of those that were infected to spread the disease further. This points towards the importance of easing lockdowns when they are no longer necessary.

4.32 Cyclical Lockdown

The cyclical lockdown model corresponds to lockdown type 2, where all secondary and tertiary links to the nodes are deactivated periodically for a predetermined amount of time and then eased, in a cycle. Two parameters are set, Cyclical-Count-Up and Cyclical-Count-Down, count-down is the time for which lockdown is in place and count-up is when it is eased.

Running BehaviourSpace with similar parameters to the complete lockdown, that is, 100 ticks averaged over 10 runs with a population of 10000 nodes. The results were as follows.

Table 4.32A

Cyclical (down, up)	Max-infected	Deaths
4, 10	1561.6	11.6
10,4	1144.6	11.6
15,10	980	12.6

Table 4.32B

Lockdown Type	No Lockdown	Cyclical (4-10)	Cyclical (10-4)	Cyclical (15, 10)
Max-Infected	1318	1561.6	1144.6	980
Deaths	14.5	11.6	11.6	12.6

Cyclical lockdowns demonstrate a similar result to the complete lockdown where the longer a lockdown is in place, the lower the maximum number of people infected. This can be seen as longer count-down times (the amount of time lockdowns are in place) and show a decrease in maximum infections.

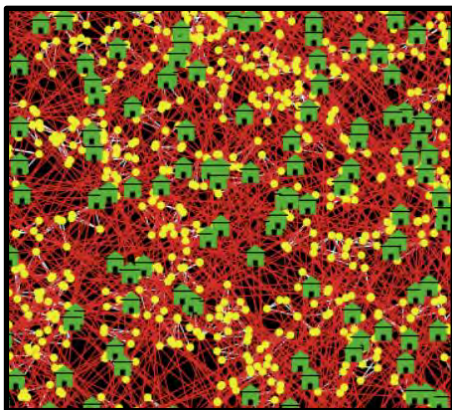
It is surprising to see, however, that having (4-10) as the configuration for cyclical lockdowns resulted in higher maximum infections than having no lockdowns. This can be helpful in understanding which forms are optimal and which are not. It also demonstrates how agent-interactions can lead to results that are not easily explained.

4.4 Hubs

We introduce another type of node in the model called hubs. These are places that are frequented by many people, so they are linked to a lot of the people nodes in the clusters. Our model includes two types of these hubs: Job-hubs and School-Hubs. Employed people in a family are connected to a job-hub, and school going children are connected to a shop-hub.

4.41 Job-Hubs

A job-hub represents a specific type of job in the model. So, one job-hub would mean only one type of job is available in the model. The number of job-hubs can be controlled through the slider labelled “Num-Shops”.



The greater the number of job-hubs, the more the variety of jobs available in the economy. The number of people employed (can be adjusted through the “Employed” slider) are each connected to a specific hub; if there is only one job-hub, all employed nodes will be linked to that hub. As with everything else, it would be intuitive to expect that a greater number of job-hubs would be associated with a rapidly spreading infection rate, and a greater death toll. Below are the results of the experiment. It was run with half the population wearing masks.

Fig 4.41A: with 11 job-hubs.

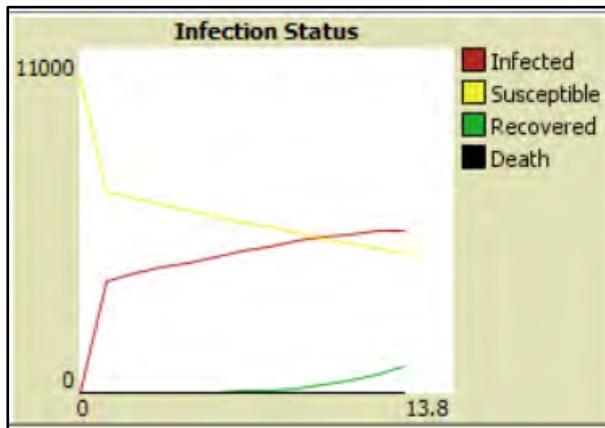
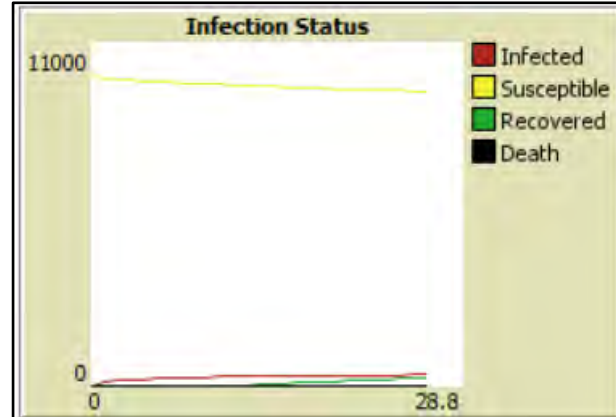


Fig 4.41B: with 800 job-hubs.



From figures 4.41A and 4.41B, we observe what is really happening is not as straightforward as one would expect, and would be especially counter-intuitive to those not familiar with network theory. We see that when there are fewer types of jobs available, the infection rises very suddenly and only goes higher. However, when there are a great number of different job-hubs, the spread of the infection is slow and very low.

The reason for this becomes clear when we picture a situation where the employed nodes are all connected to, for example, one job-hub. If any of these people are initially seeded with the infection, then all those other people that they are linked to, via the job-hub, have a high chance of contracting the virus. All those infected through that one job-hub will then infect their individual family clusters, and this will lead to the situation described by Fig.4.41A, where there is a higher spread rate due to there being a lower number of hubs. Conversely, if there are a lot of job-hubs, then it is entirely possible that many hubs may be connected to individuals that were not initially seeded with the infection at all. And individuals who were initially seeded, and do spread the infection through their place of employment, will spread it to a fewer number of people (because there are a fewer number of people who work there). Thus, the infection spreads more slowly, and there are fewer deaths, as a result. A higher number of job-hubs means that employed people (and, therefore, their families) are not connected in one big star network. A greater number of types of jobs can lead to lesser connectivity in the network, which is very attractive in a pandemic.

Upon closer inspection, we can detect how many job-hubs should be allowed to operate, in order to keep the spread of the infection, and the death count low. These are the results:

Table 4.41.

Job-Hubs	Deaths (5k masks)
1	248.4
2	246.4
4	246.6
6	253.3
8	248.9
10	245
15	249
30	240
60	165.8
75	132.8
100	90.7
200	45.4
300	24.4
400	18.6
500	15.5
1,000	5.3
3,000	4.2
5,000	3.2
10,000	2.9

Fig. 4.41C: General view

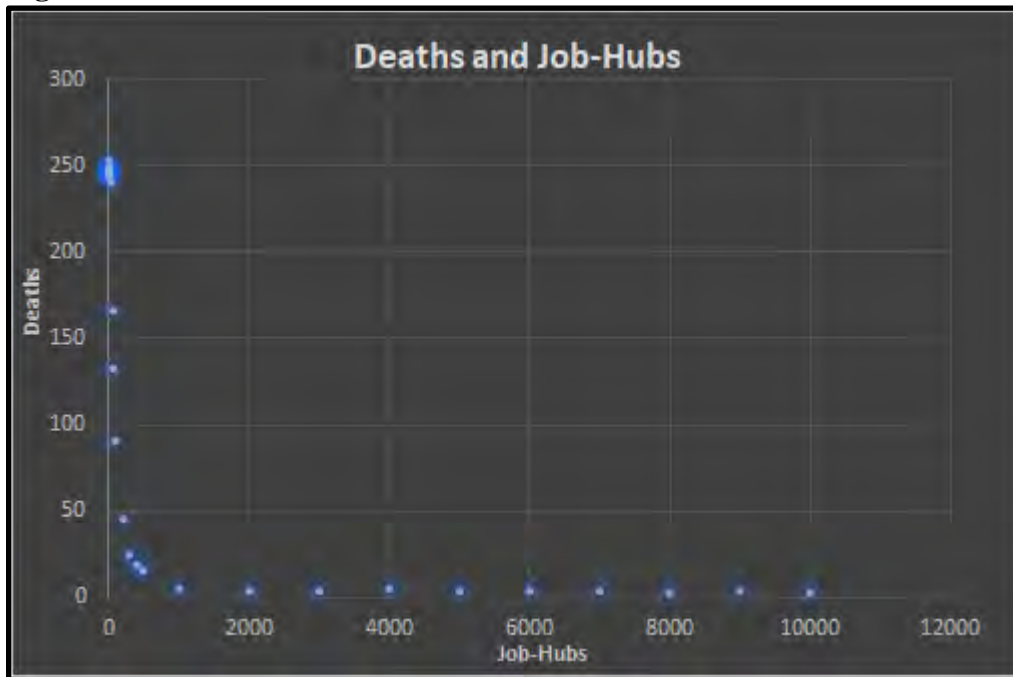
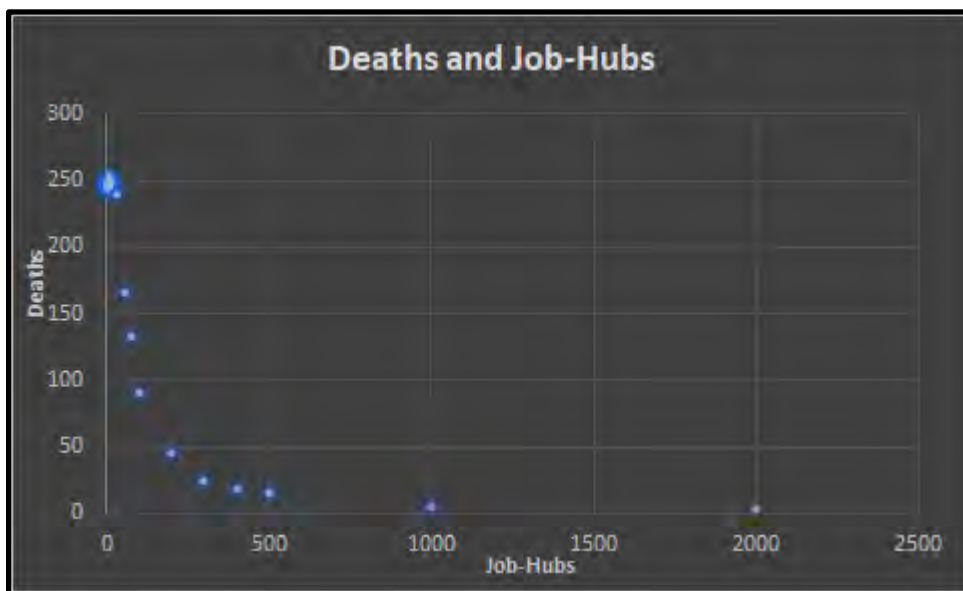


Fig. 4.41D: Closer inspection

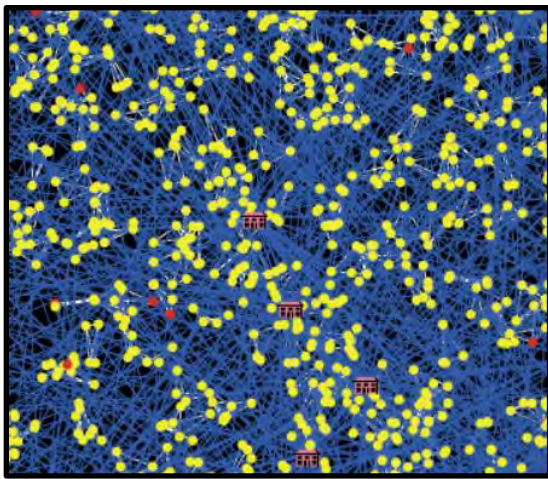


The table and figures make it very clear that the higher the number of job-hubs that are present, the lesser the associated death count. The highest death toll is observed when there is only one type of job available in the model, and after the 1000 threshold is crossed, the death toll is very small and, more or less, constant. The figures exhibit a relationship that resembles the power law graph.

From **Table 4.41**, it is very obvious to note the dramatic drops in the death toll in the first hundred job-hubs. There is a huge drop of almost a hundred deaths when the types of jobs are increased from thirty to sixty. There is also a pronounced drop in the death count when there is a jump in job-hubs from seventy-five to one hundred. This result highlights how important it is to not expect policies to affect the environment in a predictable, linear fashion. Our ABM demonstrates how nonlinearity is pre-dominant.

4.42 School-Hubs

The other type of hub we incorporated in the model was the school-hub. This works in a similar way to the job-hub.



A school-hub represents a specific type of job in the model. So, one school-hub would mean only one school is available in the model. The number of school-hubs can be controlled through the slider labelled “Num-Schools”. The number of students (can be adjusted through the “Num-Students” slider) are each connected to a specific hub; if there is only one school-hub, all students attend that school.

A similar result to job-hubs is seen in this case. Fewer school-hubs mean a lot of students are connected to one school, and if any student is infected, the virus will travel quickly via the hub

and infect other students and their families in the clusters.

Table 4.42.

School-Hubs	Deaths
1	247.7
10	243.3
50	193.7
60	160.7

70	140
80	113.1
90	103
100	95.8
200	34.9
300	18.8
400	14.7
500	9.9
1,000	6.5
2,000	4.1
3,000	4.3
5,000	3

It is evident that the greater the number of schools, the fewer the associated deaths (because of the slower spreading infection). However, the relationship is certainly not linear. Closer inspection can reveal exactly where the greatest leaps occur. For example, there is a significant decrease in deaths when the number of schools is increased from seventy to eighty.

Fig. 4.42A: General View

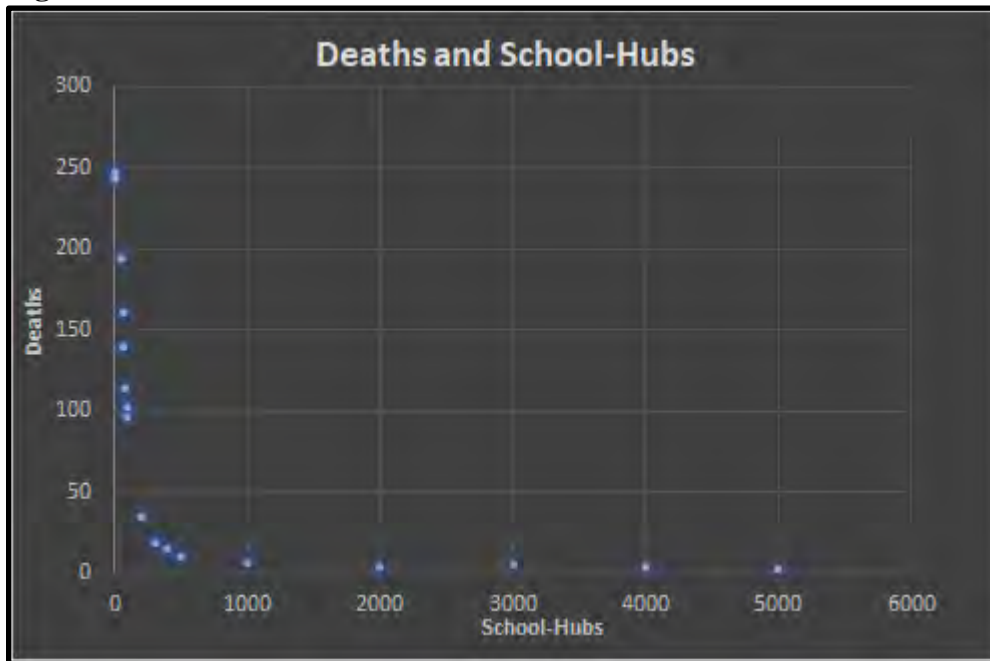
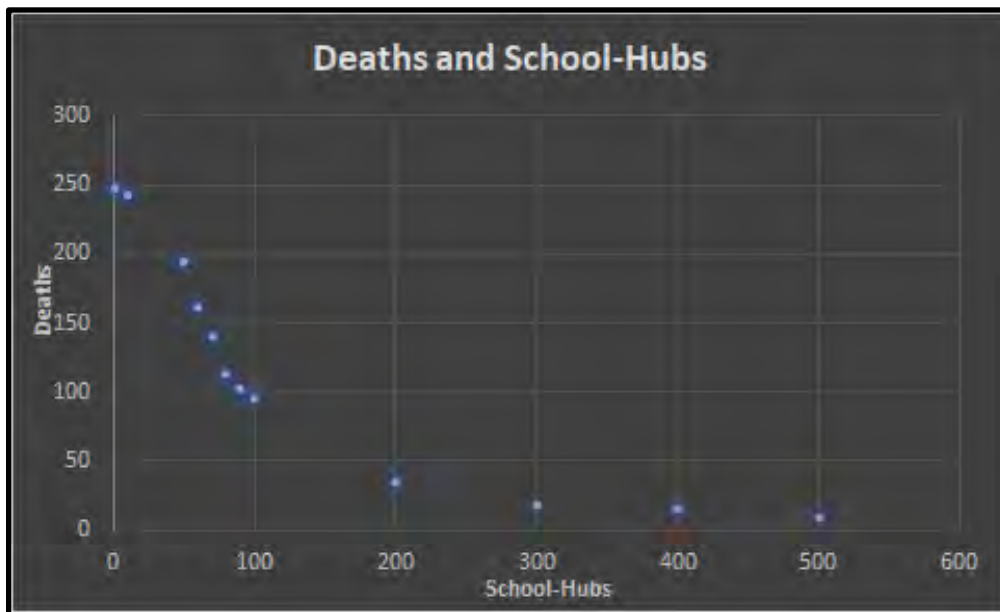


Fig. 4.42B: Closer Inspection



4.5 Employed

This experiment was run to investigate the relationship between the number of people employed in the model (which can be adjusted through a slider) and the deaths. Would a greater number of people working and interacting with each other lead to more cases, and, ergo, more deaths? The

experiment was run keeping the number of job-hubs (that is, the number of types of jobs available) fixed at 11. It was also run for 2000 ticks. The results are displayed below.

Fig. 4.5A: 7000 employed

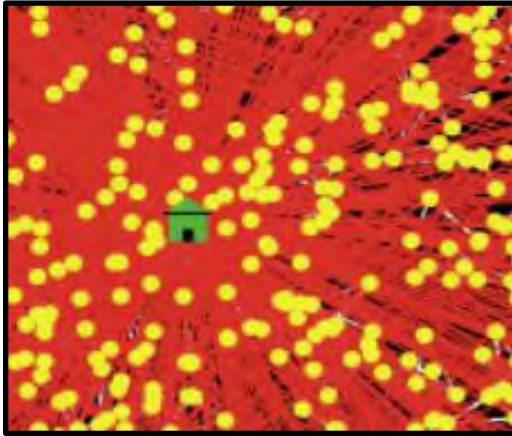


Fig. 4.5B: 250 employed

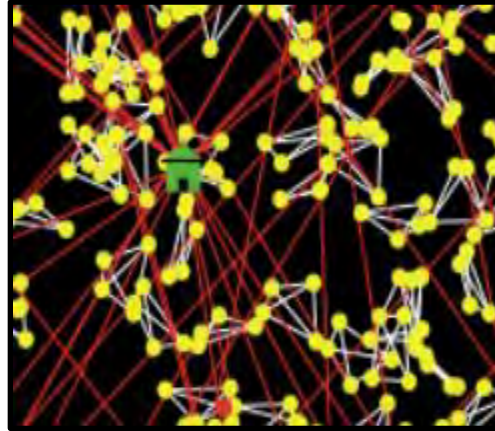
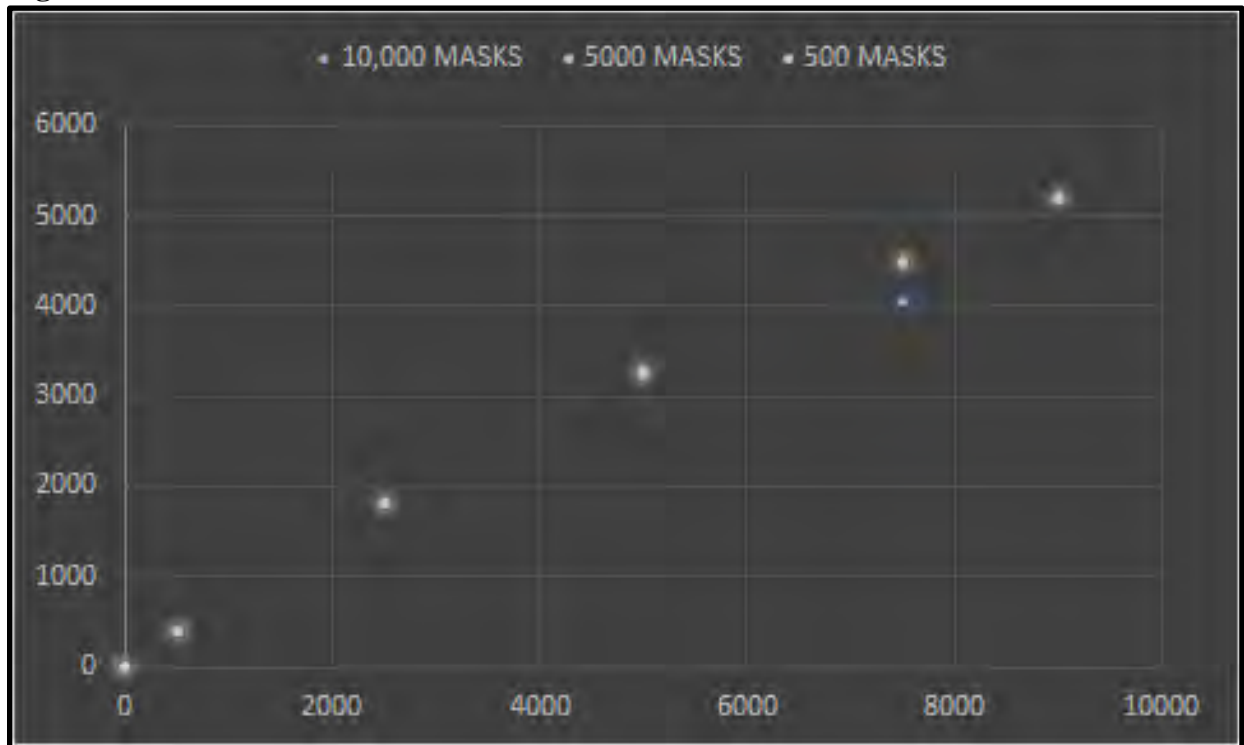


Table 4.5.

Employed	Deaths with 10,000 Masks	Deaths with 5,000 Masks	Deaths with 500 Masks
0	3.2	1.8	3.3
500	399.1	396	400.2
2,500	1820.4	1813.1	1801.7
5,000	3241.7	3287	3267
7,500	4044.6	4503.7	4481.5
9,000	5179.2	5200.5	5176.9

Fig. 4.5C.



Two observations are prominent from **Fig. 4.5C** and **Table 4.5**. Firstly, an increasing linear trend is observed. This means that an increase in the number of people employed, keeping the types of jobs available constant, is associated with an almost constant increase in deaths.. This result is one that we would also expect intuitively.

The second observation is that different levels of mask compliance do not seem to have any effect on the total death count. This is only because the experiment was run for 2000 ticks, which is more than five years. Masks, as has been discussed, only slow down the infection, so results are obvious in the short run.

4.6 Family Size

Knowsize is a feature specific to the Clustered Network, and refers to the number of people in one cluster, so it can be used as a measure for family size. Lockdowns only deal with severing secondary links, so it was interesting to see how family size could affect the death toll. Because large families and joint families are common in Pakistan, this experiment works with knowsize upto 20, and investigates whether it might have anything to do with deaths.

Fig. 4.6A: Family size= 3

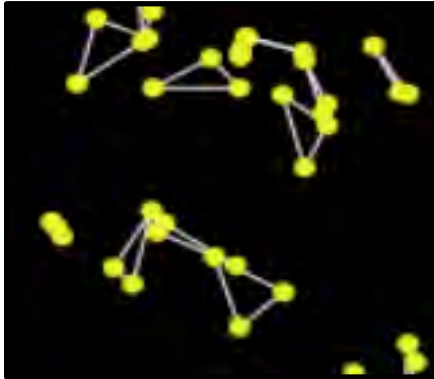


Fig. 4.6C: Family size= 8

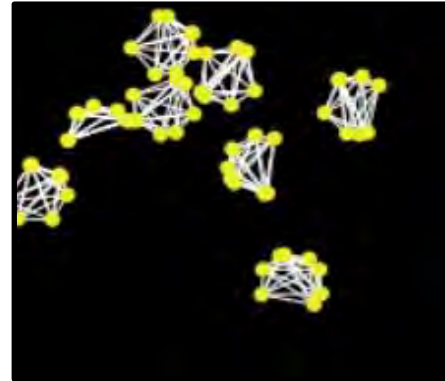
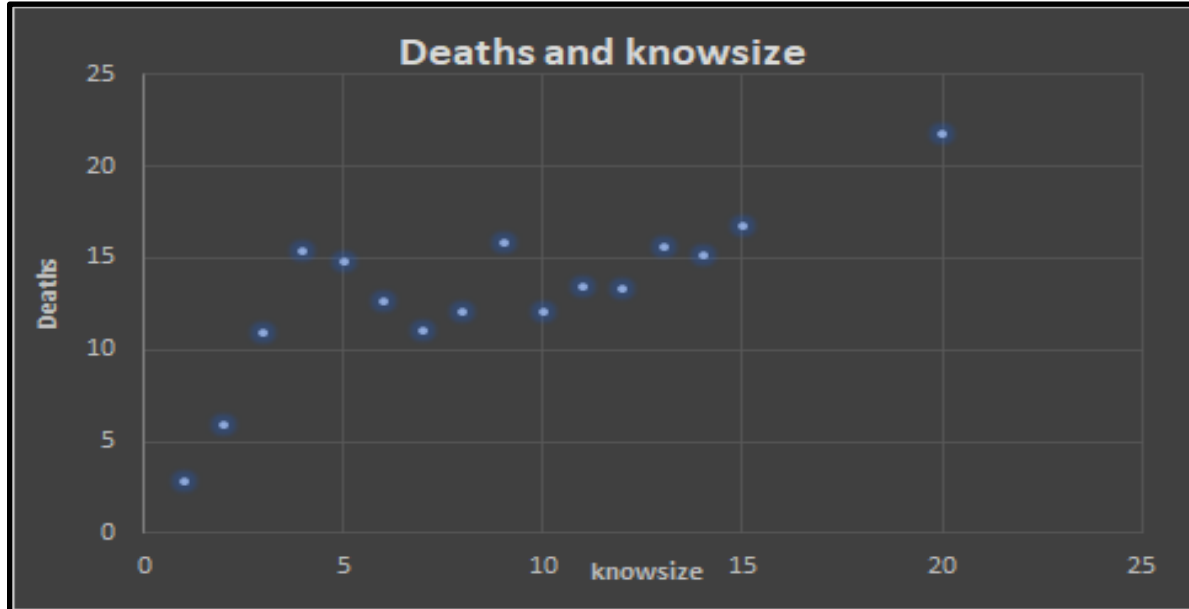


Table 5.6.

Knowsize	Deaths
1	2.8
2	5.9
3	10.9
4	15.4
5	14.8
6	12.6
7	11.1
8	12.1
9	15.8
10	12.1
11	13.4
12	13.3
13	15.6
14	15.1
15	16.8
20	21.8

Fig. 4.6C.



While a general increasing trend is observed, it is certainly not a constant increase. It is an example of a nonlinear result, where we would expect a simple linear result. This serves to show that autonomous interacting agents lead to results that may not be as obvious as we would expect them to be. However, we can conclude that, on average, a greater knowsize is associated with higher deaths.

4.7 Wealth and endowments

Our model includes an economic dimension, which we have added through including endowments in the model. The economics of the country can be mimicked by adjusting each person's endowment. A lack of quantitative data meant we could not derive any results on the economic aspect, but if a researcher wished to use our model to come up with the economic tradeoffs that lockdowns would lead to, or any other policy related to the economic situation, it could be easily incorporated into the ABM.

5. Conclusions

We have established that ABMs can lead to counter-intuitive results; results that may not be easily predicted unless they are modelled. There are numerous parameters to be considered, and the adjustment of any one can lead to drastically different results. Government policies affect the entire country, which is why any decisions about policy must be made extremely carefully. Our ABM provides an exciting platform that can be used to set the correct context, and then study the effects of a policy. Before any policy regarding the pandemic is authorized, a trial run can be

done on our model, and tweaks to the policy can also be tested out, to gain comprehensive understanding of the policy and understand which one would be optimal for a particular context. In a situation such as that of a global pandemic, a hastily implemented, bad policy will not just result in the loss of precious resources, but also human lives. Now that there is a platform that allows for test runs, it would be irresponsible of policy-makers to not avail themselves of it.

Our results and other research have now established that the COVID-19 pandemic is the perfect example of a rare event that can be explained by Complexity Theory. We employed our ABM to make observations about the situation, which led to results that may not be obvious to everyone. Our findings include many examples of nonlinear results.

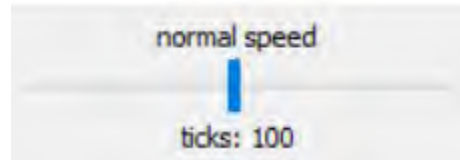
We now have evidence to support full mask compliance. Our findings illustrate the efficacy of wearing masks, which can be used to deter any backlash that masks may still face. Our nonlinear findings associated with hubs and family size serve as a reinforcement of the fact that interacting agents can lead to unpredictable results. There is a reason why so many traditional predictions regarding how COVID-19 deaths in Pakistan would pan were all proved wrong. There is a reason why the world failed to predict the pandemic in the first place. Linearity in results is what we may be used to, but that does not mean it is what we should always expect.

These results were all derived without the support of any data. Our ABM can be enriched with quantitative data and the results have the potential to become very specific, if data is applied. As stated, information about the local context is especially crucial in models such as ours. If the needed data is applied, this ABM will become a power-house on which to do trial runs for policy. If Pakistani data is applied, the model will mimic the Pakistani context, and become a guide for the government as well as a means of explaining certain policy decisions to the public.

APPENDIX

Instruction Manual

4.0 Ticks

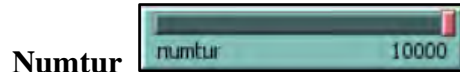


In most NetLogo models, time passes in discrete steps called “ticks”. In our model, time is measured in days, so

1 tick = 1 day.

NetLogo includes a built-in tick counter so we can keep track of how many ticks have passed. The current value of the tick counter is shown above the view.

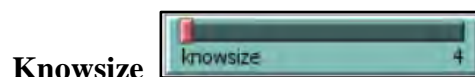
4.1 Sliders



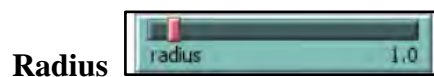
The total population of individuals at the start of the model.



The number of infected people on the grid when the infection is planted (and before the model is run). For example, a value of 4 on this slider will mean that 4 random people on the grid are planted with the infection before running the model. To plant this initial infection, click on the button titled “Seed”.



The number of people that each individual is in contact with. This is specific towards the clustered network model where the links between people can be manually adjusted.



In the lattice network, this slider determines how far a link can extend. For example, a value of 1 on the radius slider implies that links in the lattice network will only extend to neighbors in the immediate vicinity (within a radius of 1 from any given person).

Masksavailable 


The number of mask-wearing individuals on the grid.

Comorbidities 

The percentage of individuals in the population who have comorbidities, such as heart conditions, breathing problems, diabetes, etc. A slider value of 0.25 implies that 25% of the total starting population are diagnosed with comorbidities.

Death-probability 

The average probability of dying from the infection for an individual without comorbidities, and not elderly (above 65 years of age). In the code, this probability is multiplied by 2 for individuals with either comorbidities or old age (above 65 years), and multiplied by 4 for individuals with both these characteristics.

Rectime-mild 

The average number of days it takes to recover from the virus after contracting the infection (for **mild** cases wherein the individual has no comorbidities and is not elderly). This is based on a normal distribution with the slider value representing the mean number of days that a person remains infected.

Rectime-severe 

The average number of days it takes to recover from the virus after contracting the infection (for **severe** cases wherein the individual is diagnosed with comorbidities, is elderly, or both). This is based on a normal distribution with the slider value representing the mean number of days that a person remains infected.

Transmission 

The rate of transmission as a percentage. For example, a slider value of 100 implies that all people in the model have a 100% chance of being infected upon coming into contact with an infected individual.



The average number of days after recovering from the virus that an individual remains immune to reinfection. For example, a slider value of 30 implies that a person, after recovering from infection, stays immune to reinfection for the next 30 days. Once this period is over, they become susceptible to catching the virus again.



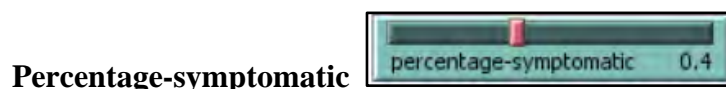
The percentage of the population that undergoes testing for the infection every day. A slider value of 0.000138 for a population of 10,000 implies that, on average, 1.38 tests are conducted per day.



In the case of a limited number of tests available, (see “**fixed-testing?**” below), this slider sets the number of tests available as a percentage of the initial population. For example, a slider value of 0.4 for an initial population of 10,000, implies that there are 4000 tests available for use, and after they are used up, testing will stop altogether. Hence, exactly 40% of the initial population will undergo testing- no more, no less. For this slider to have effect, the **fixed-testing?** switch needs to be turned “ON”.



The average number of days it takes for symptoms to appear in an infected individual. This is based on a normal distribution with the slider value representing the mean number of days until symptoms become apparent in infected individuals. Individuals can only be labelled symptomatic or asymptomatic once this ‘incubation period’ is over.



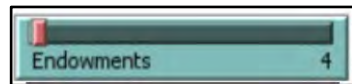
The percentage of the infected population that shows symptoms, as opposed to being asymptomatic. For example, a slider value of 0.4 implies that approximately 40% of the infected population is symptomatic (when infected), while the remaining 60% are asymptomatic (when infected).

Symptoinfected



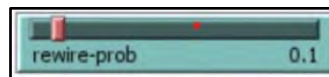
The percentage of the non-infected population that show symptoms, but do not have the virus. These individuals, when tested for their symptoms, test negative for the virus. For example, a slider value of 0.05 implies that approximately 5% of the **non-infected** population are showing symptoms, while the remaining 95% are not showing symptoms.

Endowments



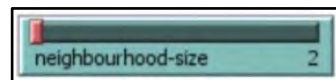
The initial range of income that every individual receives, the amount of wealth however varies slightly between each individual as to demonstrate a variety of individuals in the model.

Rewire-prob



Relevant to the Watts and Strogatz Network. The probability of rewiring each link so that there is a link between a pair of nodes that are chosen uniformly at random. This creates the links that span across the ring. A rewiring probability of zero creates a regular circle network. A rewiring probability of one creates an Erdős–Rényi random graph.

Neighbourhood-size



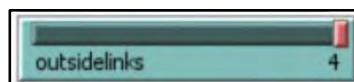
Relevant to the Watts and Strogatz Network. The number of links connected to each node in the original ring network.

Job-trans



The rate of transmission as a percentage. Job-Trans differs from the transmission slider by being specific to the links created by Jobs and not affecting the transmission rate of primary links.

Outsidelinks



The amount of people in the same place who frequently go outside their homes. This slider is specific to the clustered network model.

Employed



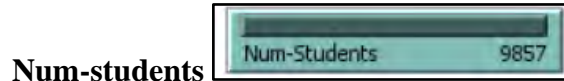
The number of people in the model who have jobs. If the value is higher than the total population, then the model considers everyone to be employed.



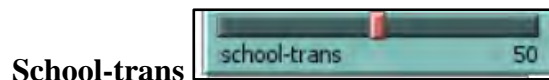
The number of different jobs available in the model. This is specific to the clustered format where jobs are illustrated using a green shop icon and allows secondary links for anyone who is employed.



The number of schools available in the model. This is specific to the clustered format where schools are illustrated using a pink shop icon and allows secondary links for students.



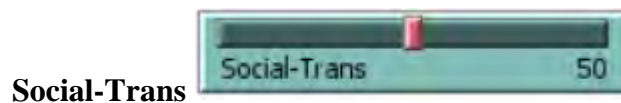
The number of people in the model who are school-going students. If the value is higher than the total population, then the model considers everyone to be students.



The transmission rate of schools and students. This affects secondary links that are colored blue and are activated by the button “School-Hubs”.



The number of people who will have social interactions with people beyond their homes in circumstances other than jobs and schools.

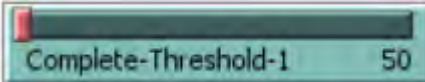


The transmission rate of social interactions. This affects tertiary links which are colored yellow and are activated by the button “Social-Interactions”.



This defines what type of a lockdown is implemented.

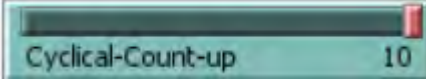
Lockdown-Type	Slider Value
No Lockdown	0
Complete Lockdown	1
Cyclical Lockdown	2

Complete-Threshold-1 

The number of people infected in order to start a complete lockdown.

Complete-Threshold-2 

The number of people infected at which the complete lockdown is eased.

Cyclical-Count-up 

Count-up defines the number of days (or ticks) for which the cyclical lockdown is eased.

Cyclical-Count-Down 

Count-down is the number of days for which lockdown is implemented

4.2 Choosers

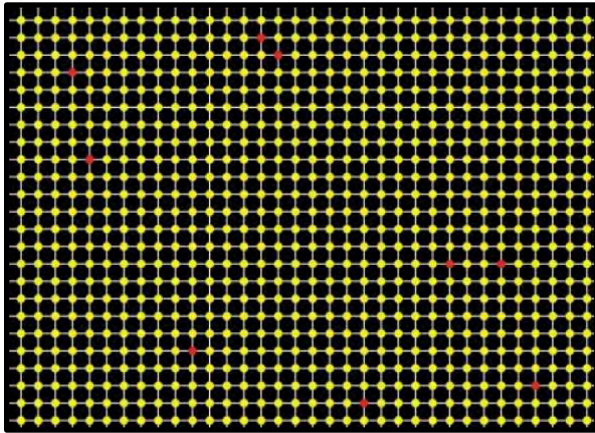
Network

Allows the user to select the type of network of links on which the model will run. The options are a Lattice Network, a Clustered Network, and a Newman-Watts variant of the Watts-Strogatz “small-world” Network.

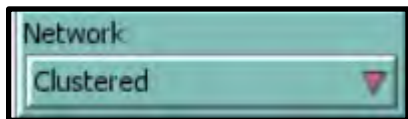
-Lattice



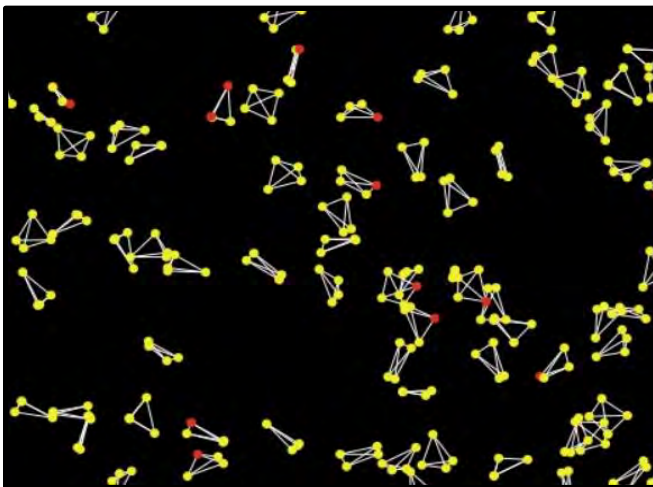
Nodes are arranged in a grid-like structure. This creates a network that exhibits a high degree of clustering, and long average path lengths.

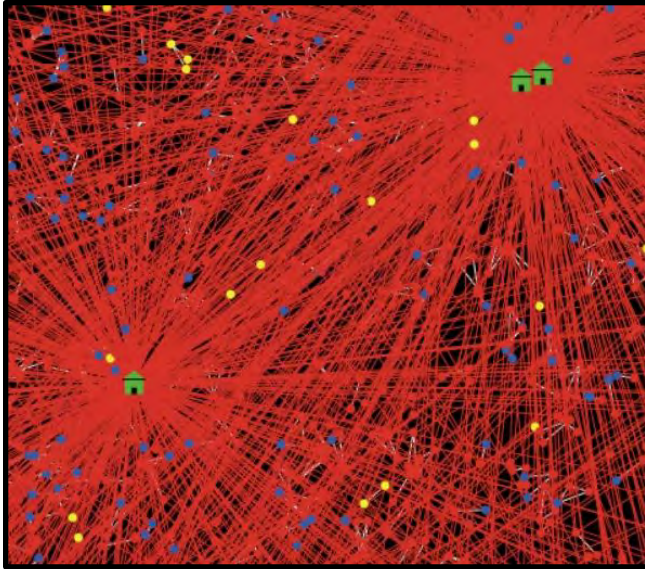


-Clustered

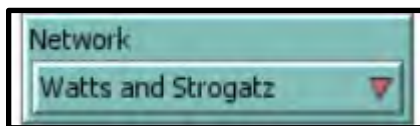


Clusters of nodes exist that are assumed to have some primary link between them. These may be connected to other clusters through the secondary links.

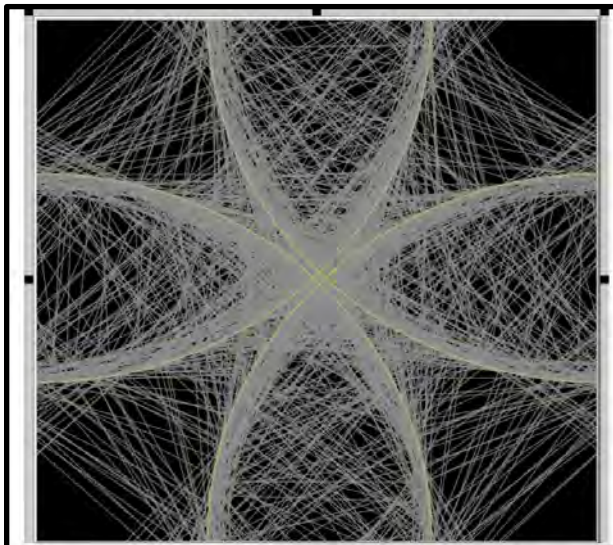




-Watts and Strogatz

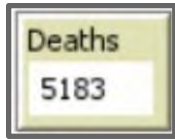


This is a network that exhibits high clustering and short average path lengths and is created by starting with a ring model in which every node has a degree of **neighbourhood size**. We go through each of the edges and rewire it with some probability so that we pick two nodes uniformly at random and connect them with a new link. This allows for “short-cuts” between some nodes. The Newman-Watts variant allows for no links to be severed when rewiring. So, some nodes will have a greater degree than others.



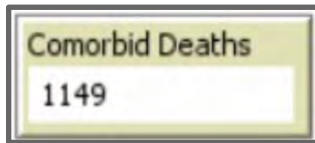
4.3 Monitors

Deaths



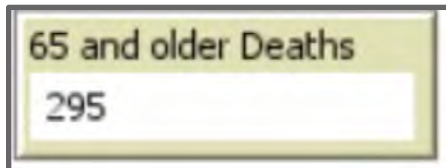
This monitor counts the total number of deaths that occurred since the model started running.

Comorbid Deaths



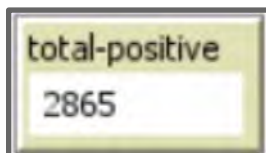
This monitor counts the total number of deaths for people with comorbidities since the model started running.

65 and Older Deaths



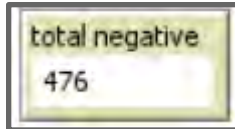
This monitor counts the total number of deaths for people above 65 years of age since the model started running.

Total-positive



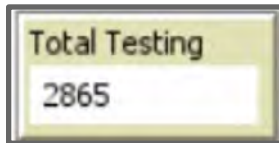
The total number of positive test results since the model started running.

Total-negative



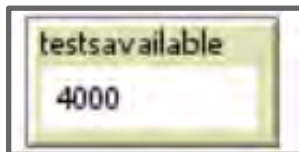
The total number of negative test results since the model started running.

Total-testing



The total number of tests that have been administered since the model started running.

Tests-available



In the case of a limited number of tests available (see “**fixed-testing?**” below), this monitor tracks the real time number of tests available, and as they are used up, while the model is running.

Max-Infected



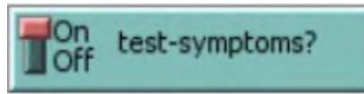
The maximum number of people that have been infected in the population.

4.4 Switches



If this switch is turned on, only a fixed and limited number of tests (as a proportion of the initial population) will be carried out, after which testing will stop. Use the slider “**tests-to-population**” to fix the number of tests available (as a percentage of the initial population). The monitor

“**testsavailable**” will track the real time number of tests available as the model is being run. If this switch is turned off, testing will occur unlimitedly (no scarcity of tests available).



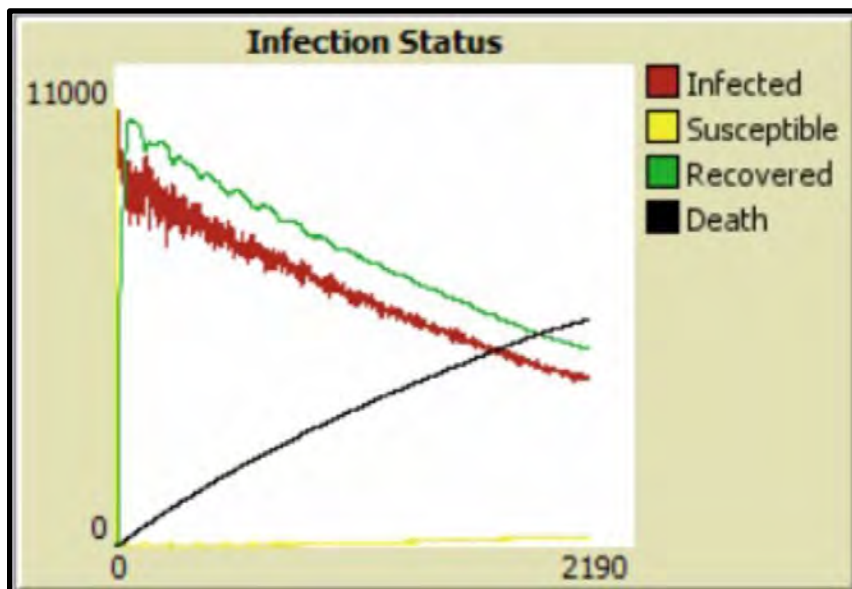
Test-symptoms?

In the case of unlimited testing, if this switch is turned on, only testing for symptom showing individuals will occur. If it is turned off, testing can occur for individuals who show no symptoms.

4.5 Plots

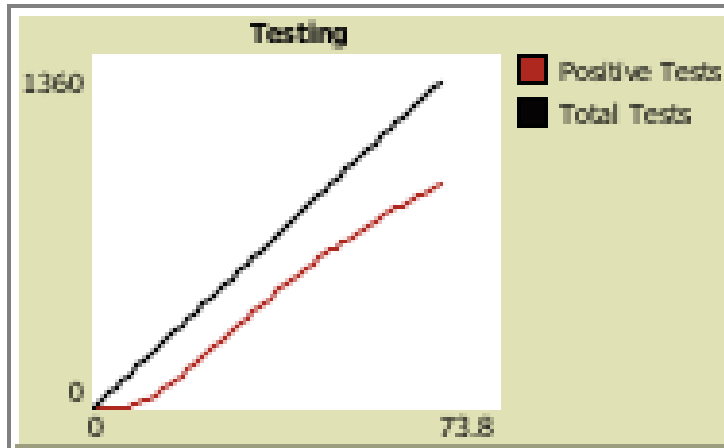
Infection Status

Plots a graph of the total number of infected, susceptible, and recovered populations, as well as the total number of deaths that have occurred, against the time in days that has passed since the model started running.



Testing

Plots a graph of the total number of positive tests, negative tests, and total tests against the time in days that has passed since the model started running.



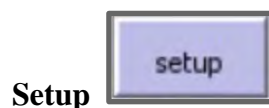
Daily Testing

Plots the daily statistics for total tests conducted (per day), and positive test results (per day). Our model assumes that a fixed number of tests is carried out per day (as per the value of the “testing” slider).



4.6 How to Run the Model

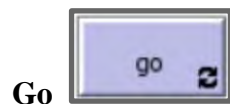
Set all parameters using the sliders and choose the type of network to be displayed on the interface. Once these are set, follow these steps in the order that they are listed:



After setting all parameters using the sliders, and choosing the type of network to be displayed, click on this button to set up (or reset) the model with your chosen parameters.



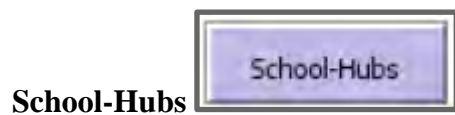
This button plants the initial infection into the model. Depending on the value of the “initial” slider, clicking on Seed will infect randomly selected “initial” individuals on the grid with the virus.



This button runs the model. It will continue running infinitely until the user clicks on this button again to stop or pause the running of the model.



This button sets up the shops and its links to the people that are employed. The links that people have with these jobs are illustrated by the green lines which connect employed people to their jobs.



This button sets up schools and their links to students. These links will be secondary and are colored blue in order to show all students that are connected to their respective schools. The schools have their own icon which is colored cyan.



Social-Interactions is a button which creates tertiary links for people. These links are colored yellow and signify social interactions amongst people beyond their homes.