

# Analysis of Simulated Covid 19 Infection Patterns

Harshith Nadiga Prakashreddy, Manan Shah, Aashima Bassi, and Sounak Ghosh

Trier University Behringstr.21, 54296 Trier, Germany

{s4hanadi, s4mashah, s4aabass, s4soghos}@uni-trier.de

## Abstract

The SARS-CoV-2 virus, which causes the infectious disease commonly referred to as COVID-19, has subsequently been responsible for its rapid global spread. In order to identify social patterns, significant variables, and correlations that influence the spread of the disease along the typical infection chains, the output data from the DFKI's (German Research Centre for Artificial Intelligence) social simulation of Covid 19 infection dynamics have been analyzed in this paper. The goal of the paper is to identify the cause of the super spread of this disease, as well as which locations are the most infected, by comparing various datasets to determine where and how exactly Covid 19 spread. To do this, analysis is performed, and the data is then displayed with the aid of graphs.

## 1 Introduction

Most infected individuals often suffer from mild to severe respiratory illnesses and then get better without requiring extra care. Elderly adults and those with underlying medical illnesses including cardiovascular disease, diabetes, chronic lung disease, or cancer were among those who were critically unwell and needed medical attention. In December 2019, the COVID-19 coronavirus was initially discovered in the Wuhan region of China. The large COVID-19 outbreak started in Italy, spread to Iran and South Korea, and was then declared a pandemic by the World Health Organization on March 11, 2020.

We are well aware that COVID-19 spreads through respiratory droplets, such as coughing, sneezing, or even speaking, which essentially just means coming in touch with an individual who has the virus. But the reason for its rapid global expansion remains a mystery. What could be our next steps to prevent such situations as we are still seeing a few examples every now and again despite taking so many precautions, even when there is a small gathering. We lost more lives than we anticipated last year as a result of the proliferation of Covid 19 cases, which was significantly influenced by social patterns. As soon as the lockdown ended, folks were able to resume their normal lives. The unexpected rise in instances was brought on by weddings, parties, concerts, and, primarily, the reopening of schools[14].

A superspreading event is when an infectious disease spreads more widely than usual, and a superspreader is an unusually contagious organism that is infected with a disease. A superspreader is a person who, relative to the average afflicted person, is more likely to spread a human-borne illness to others. In epidemiology, these superspreaders are very concerning.

Consider what this number implies for a moment even if you may have seen it before. Imagine if a single unlucky individual in a crowded restaurant who has the novel coronavirus but isn't yet showing symptoms that would cause her to notice it infects 10 additional people. Her 10 coworkers, who all caught the illness at the same time as her, do not at all pass it to anybody else. This kind of dispersal—what epidemiologists refer to as a large  $k$  value—increases the randomness of COVID-19 transmission, making it challenging to monitor and prevent[10]. Therefore, it can be assumed that approximately 10 percent to 20 percent of COVID-19 infected individuals are in charge of 80 percent of the virus' dissemination.

According to the studies, being knowledgeable about the illness and the virus's transmission is the greatest method to avoid and delay transmission. By keeping at least one meter of space between people, putting on a mask, by making sure your clothing fits right and washing your hands often or using an alcohol-based rub, you can keep yourself and other people from getting sick. Get your shots on time, and heed any local advice[3].

The primary catalysts of the coronavirus disease 2019 (COVID-19) pandemic are superspreading and variants of concern (VOC) of the human pathogen severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It can be difficult to assess each one's specific influence, though. We show evidence that superspreading has played a significant role in the epidemiological predominance of VOC by analyzing the biggest database of SARS-CoV-2 genomes, the Global Initiative on Sharing Avian Influenza Data [GISAID;  $n > 1.2$  million high-quality (HQ) sequences]. The database contains distinct signatures that are consistent with significant superspreading events (SSEs) that occurred temporally at the same time as the worst epidemiological scenarios brought on by VOC. The statistics indicate that the chances of the new SARS-CoV-2 VOC surviving would have been lower without the genetic drift's unpredictability effect, which was made possible by superspreading[7].

It can be challenging to analyze the transmission of SARS-CoV-2 due to a variety of circumstances. For instance, among those who have the infection, it can be very challenging to pinpoint where and how they contracted it because some people are asymptomatic. Since infectious diseases do not spread evenly throughout the population, there are certain situations that make infections more likely than others. Additionally, there are common chains of infection that may be studied in both the actual world and in accurate simulations. Superspreaders are a vital starting point for quick intervention in the acute phase of a viral threat like SARS-CoV-2 because they represent a particular type of uncertainty with an enormous leverage impact. Therefore, a key element of a successful intervention portfolio is building organizational frameworks that allow regulating the influence of superspreaders and comprehending their prop-

agation mechanisms. In light of this, the paper is divided into two main sections: (1) what we currently know about COVID-19 superspreading, and (2) how to handle uncertain situations brought on by superspreading events in the sense of "trying to manage the unexpected," where getting ready to improvise becomes essential[15].

Our main goal is to provide a mechanism for learning more about the superspreading infection pattern and to give data analysis on the kinds of activities or gatherings that are most likely to cause a COVID-19 outbreak. We need to determine the societal patterns, the precise factors that contributed to the outbreak's spread, the kind of areas that are most affected, and any further precautions or actions that should be taken in light of the current circumstances.

## 2 Related Work

As there was no proof of host sex/age biases or modifications to the viral genome, we looked at additional variables that might affect coronavirus superspreading. The virus must continue to be infectious in order to infect a recipient host for the transmission event to be effective. However, it is evident from the infection data that there are additional elements that affect a person's capacity to contract an infection. For instance, a virus that has been expelled from a superspreader may be more resistant to environmental changes or have changes that enhance attachment or penetration. Superspreading capacity may be influenced by certain environmental or physical conditions, which may be controlled by permanent or cyclical host factors. These possibilities, both separately and collectively, are important promoters of superspreading in coronavirus infection[9].

Basically, a superspreading event is when a small number of people disseminate an infection to a huge number of others they come into contact with. As various researchers have varied thresholds for deciding how many people must be involved, this gives us a lot of leeway for interpretation. Three distinct schooling operations strategies based on the provided dataset have also been examined in light of various scenarios[14]. The following three options were then simulated and assessed. 1. Regular education with few connections 2. School Closures 3. Rotation of classes that have been cut in half (school rotation). Frequent tests were run to identify affected students as early as feasible in order to protect the safety of the students. The schooling tactics here are the sole difference between the three scenarios. To reflect the fact that fewer pupils attend school in the school rotation scenario, the number of school interactions is further decreased to 2. This causes fewer people to use public transportation, more social group fragmentation, and easier social distancing in classrooms. Following a review of the paper[14], it was determined that the total population on which the analysis was conducted is 102,798 individuals, including those who are recovered, susceptible, and deceased. Simulations were conducted for various individuals from various departments, such as employees of a workplace, which could be a private corporation or a public service agency, as well as universities or other facilities. All agents and individuals below the age of 18 attend education. In-

dividuals of any age adhere to a household in which they reside alone or with others, depending on the population data provided. Moreover, all of the people's frequent recreational facilities, such as cinemas, gyms, stadiums, concerts, and other public venues where a variety of recreational activities were conducted, represent stores as providers of both essential and non-essential products. In addition to the data provided about specific locations, infrastructures such as school buses and public swimming facilities have been implemented and analyzed at the city's request in order to investigate the impact of policy decisions on the spread of infections throughout the city.

In one of the research papers[5], the occurrences were described using descriptive statistics, which also revealed how frequently they occurred, where they occurred, and how many instances were documented at each event. Then, using univariate logistic binomial regression, odds ratios (ORs) and 95percent confidence intervals (CI) were calculated. The research identifies a number of scenarios where there are few SSEs and a considerable burden on the community as a result of these SSEs. As suggested by several recent articles, these settings were preschools and primary schools[11]. The workplace environments in the private and public sectors were remarkably similar, with few incidents happening but nevertheless carrying a heavy load in terms of the overall number of cases.

A so-called SIR model[12] was also referred which is a simple mathematical explanation of the transmission of a disease in a community. It splits the (fixed) population of  $N$  persons into three "compartments" that may vary as a function of time,  $t$ [1]:

- $S(t)$  are the ones which are susceptible but are not infected with the disease yet;
- $I(t)$  is the number of individuals who could be infectious;
- $R(t)$  are the individuals who have now recovered from the disease and have immunity to it.

When referred to another research[13], details on data slicing were acquired to determine which events or aspects of meetings pose the most danger for the propagation of COVID-19. The study focused on the vast majority of cases that took place in communal living quarters, healthcare settings with extended stays, workplaces or large gatherings (conferences, concerts, sporting events, religious events). Offices have the lowest incidence rate, factories and facilities that manufacture food are far more at risk, and outbreaks in non-office work situations are more severe than those in offices. Large gatherings have resulted in accelerated growth, despite the fact that there were considerably more occurrences of small gatherings (parties, meals, community center events) due to the smaller number of attendees. Sports participation is not as high risk compared to indoor, fully live events, which plainly carry enormous risks. Additionally, it was shown that healthcare facilities, nursing homes, and jails are sadly significant common hotspots for superspreading incidents. It was discovered that, despite

receiving prominent news coverage, funerals, weddings, and protests don't occur as frequently as you may assume while a greater proportion of events are smaller, less obligatory social meetings including going to bars and clubs, restaurants, worship services, and small private parties where the cases spiked.

## 3 Research Design

### 3.1 Overview

Seven datasets that were generated have been recovered from the DFKI(German Artificial Intelligence Research Centre). In this research paper, three datasets have been analysed - 'Infection Chain', 'Infection States' and 'Location infection' and the simulation is conducted for the same with 101 runs and 60 ticks, merely changing the parameters for various techniques. Within the simulation, a day is represented by the ticks.

### 3.2 Infection States

In case of infection states we are referring to the SIR model and applied the same with beta and gamma values where in we have a count of people who are infected and for each tick we have 101 runs and then we further plan to aggregate the results for the same.

The SIR model represents population change in each of these compartments using two parameters,  $\beta$ , which corresponds to the value 0.21 in Figure 2, and  $\gamma$ , which corresponds to the value 1/4.  $\beta$  summarizes the disease's effective contact rate: Per unit of time, an infected individual comes into touch with  $\beta N$  additional individuals, of whom  $S/N$  are vulnerable to developing the disease. It basically represents the rate of transmission.  $\gamma$  is the typical recovery rate; hence,  $\frac{1}{\gamma}$  is the mean duration of time an infected individual may transmit the disease.[12][1]

All population members who are susceptible to contracting an infection are considered susceptible. Considering that there is an infection that is likely to infect everyone, everyone will be vulnerable in the beginning. As a population member becomes infected, it ceases to be susceptible and is transferred to the afflicted state compartment. Either the diseased category can infect the others or it will recover from the infection. If the sick members of a population recover, they are considered to be in the recovered compartment condition. With the help of the below flow chart we'll now try to understand the presumptions of the model and differential equations which govern the movement rates between the compartments[8].

The above can be turned into an equation by saying that the number of people who are susceptible, infected, and recovered adds up to the total population, which is considered to be (N).

$$S(t) + I(t) + R(t) = N$$

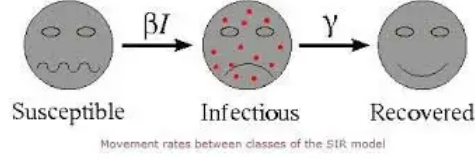


Figure 1: SIR Model flow[8]

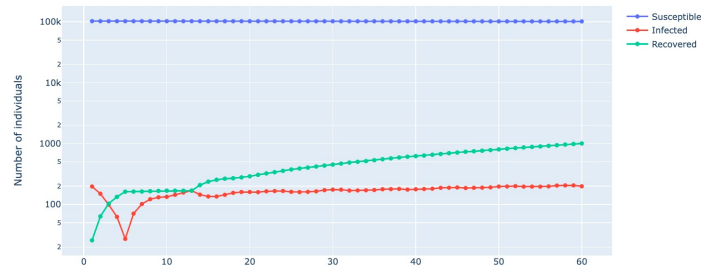


Figure 2: SIR Model  $\beta : 0.21$ ,  $\gamma : 1/4$

As per this model's assumptions, we will now examine the model's system of ordinary differential equations[8].

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Here:

$\frac{dS}{dt}$ : The change rate of susceptible individuals with respect to time.

$\frac{dI}{dt}$ : The change rate of Infected individuals with respect to time.

$\frac{dR}{dt}$ : The change rate of Recovered individuals with respect to time.

The technique for the SIR Model that was described earlier provided us with the graph that is shown in figure 2, and the dataset that is currently being worked on provided us with the data for the other three graphs. Considering the above graph in figure 3, we can conclude that there was a gradual drop in susceptibility over a period of time, but for a brief while it remained constant, culminating to a rapid decline after the 12th day; this occurred over a period of 60 days. Figure 4 depicts an initial infection peak, followed by a steady



Figure 3: Susceptible



Figure 4: Infected

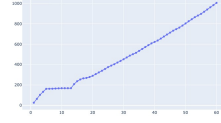


Figure 5: Recovered

reduction in the number of infections on the sixth day, followed by a dramatic increase in infections that continues to rise throughout the duration of 60 days. On day 59, we may once again see a decline in the number of illnesses. According to the graph in figure 5, we can see that initially there were a good number of recoveries, and for the time being we can see no change in the same. However, after day 12, we can see that there was an abrupt increase in the total number of recoveries that occurred over the course of 60 days.

### 3.3 Infection Chains

The "infection chains" data set consists of run, tick, location id, and location class with the following infected locations: leisure (including outdoor pools), domestic, workplace, and school. The column infected person contains the id of the person who will cause infection, while new person infected contains the id of the person who contracted the infection.

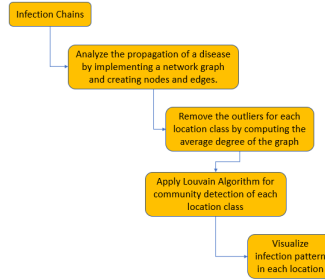


Figure 6: Workflow: Infection Chains

#### 3.3.1 Social Network Analysis

As we have two columns, infected person and newly infected, representing the sequence of infections, we employ social network analysis in order to analyze this data more effectively. Social network analysis is the investigation of social systems utilizing networks and graph theory. We will begin with a quick introduction to the nodes and edges of a network[6].

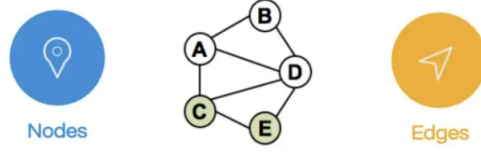


Figure 7: Example Network[6]

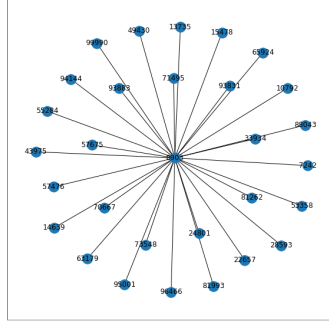


Figure 8: One Person ID

**Nodes** (A,B,C,D,E in the example) often represent things in the network and can store both self-properties (such as weight, size, location, and other attributes) and network-based characteristics (such as Degree, which is the number of neighbors, or Cluster, which is a connected part of which the node is a part and so on). You can see the graph worked on in the below figure 8. The already infected individual with the identifier "8903" who is in the center is deemed to be the node and is thus the source of the spread. **Edges** represents the connections between the nodes and may also have characteristics (such as weight representing the strength of the connection, direction in case of asymmetric relation or time if applicable). These two basic parts can be used to describe many types of relationships, which would include social connections, virtual routing networks, physical electricity networks, road networks, biological relationships networks, and many more. To further illustrate the graph, figure 8 shows that the main node has a connection forming with other sub nodes such as "93883, 57675, 70667," etc. These interconnections are what are commonly referred to as the edges.

### 3.3.2 Removal of Outliers

We will remove the outliers based on the number of the edges that are connected to the nodes. The degree of a node in a graph is the number of edges that are connected to it. If the degree of the current node is more than 1.5 times the average degree or less than half of the average degree, the code removes the node



from the graph . This operation is used to remove nodes that are significantly less or more connected than the average node in the graph. The final result is a graph with nodes that have degree values that are close to the average degree of the graph. It's important to note that this operation can affect the overall structure of the graph and the insights you can extract from it.

### 3.3.3 Louvain Method

The Louvain algorithm has the potential to be an effective tool for recognizing communities within the COVID-19 infectious pattern[2][4]. It also has the potential to provide insights into the fundamental social structures and transmission patterns of the pandemic. Louvain algorithm is used to identify communities of nodes that are more closely interconnected than other communities' nodes. In order to obtain insight into the factors that contribute to the dissemination of COVID-19, we calculated the degree of each network node. The degree of a node is the number of edges connected to it, which can be interpreted as a measure of the node's importance or influence within the network. We were able to identify concentrations of individuals or locations that are more likely to transmit the virus to one another by applying the Louvain algorithm to the network and visualizing the community structure.

## 3.4 Location Infections

In this section, analysis is performed on the Location Infections dataset using School infected as the foundation. This data collection includes the following categories: infected schools, uninfected schools, infected leisure(including outdoorpools), infected households, infected school buses and infected workplaces. For the purpose of analyzing this information, the average performance of the trials is being taken into consideration. The total number of infected and uninfected number of people in School is 15,699, for leisure it's 102,741, for household it's 102,640 and for workplace is 46,130.

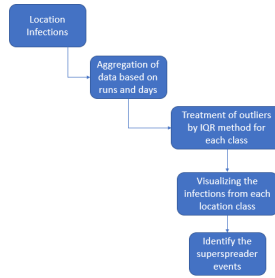


Figure 9: Workflow: Location Infections

### 3.4.1 Data Transformation

Few patterns were observed in the simulated runs, and since the per-day runs were relatively similar, the data was aggregated per day. Using the Interquartile method, outliers were found. If the values are greater than the upper fence and less than the lower fence, they are outliers. In order to impute the outliers they are simply replaced by the mean values.

## 3.5 Results

### 3.5.1 Infection Chains

The results of this analysis will lead to a better understanding of the transmission of COVID-19 and will influence measures aimed at improving public health. In addition, the findings of this study shed light on the significance of SNA in the field of infectious disease research as well as the promise of network-based techniques in the field of public health.

The graph in Figure 9 is a graphical depiction of the network of people who are affected with the disease. Each node in the graph represents an infected individual, and each edge illustrates how an illness might travel from one person to another. The community that each node belongs to is denoted by the color of the node that corresponds to it, the larger the community number, the darker the color of the node that represents it.

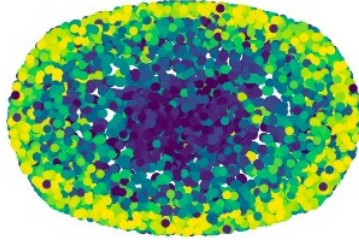


Figure 10: Overall infection spread(Black nodes represent superspreaders)

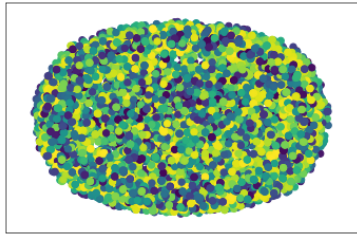


Figure 11: Household Infected

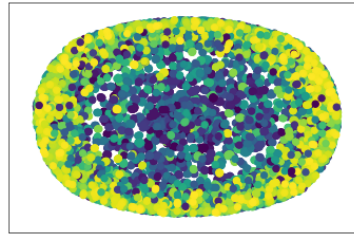


Figure 12: Leisure Infected

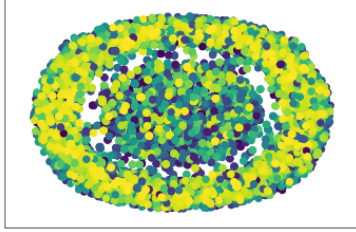


Figure 13: Workplace Infected

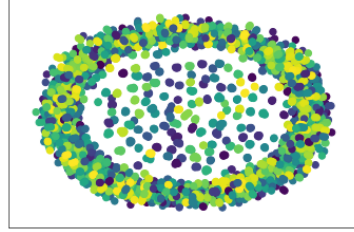


Figure 14: School Infected

With respect to our dataset there are 67,412 nodes and 103,404 edges in total. After the outliers have been eliminated, the number of nodes and edges for Leisure is 10634 and 5940, for Households it's 33556 and 20517, for Workplace it's 12611 and 7160, and for Schools is 3165 and 1822. In figures 10, it is observed that certain household location classes have a greater connection density, which would suggest that the infection is moving through this community at a quicker rate. Alternately, we could also notice in figures 11, 12 and 13 that people in location classes such as leisure, workplace, and school are more isolated, which would imply that the virus is spreading more slowly within those communities. The research concluded that various location classifications had differing degrees of connection density as well as levels of isolation, both of which could correspond with differences in infection rates. To be more specific, certain household location classes had a greater connection density, which lends credence to the hypothesis that the virus was moving through these neighborhoods at a faster rate. People who were located in location classes such as leisure, workplace, and school were more isolated, which suggests that the virus propagated more slowly within those communities. In comparison, people who were located in location classes such as leisure were not. For this reason, variables that may correspond with infection rates and create typical patterns could include the size and intensity of social networks, in addition to the degree of interaction both within and between different geographic classes. For instance, individuals who reside in households with a large number of occupants or work in workspaces with a high volume of foot traffic may be at a greater risk of infection as a result of the increased opportunities for exposure. In a similar vein, those who partake in dangerous hobbies for fun or go to gatherings with a large number of people present may have a higher risk of catching the virus.

### 3.5.2 Location Infections

The below figure 15 represents the percentage of infection per location. Household\_infected holds the maximum transmission of infections with the percentage of 62.25 percent. Following we have Leisure\_infected with 25.17 percent and then further we have the least infection transmission in case of Workplace\_infected and School\_infected with the percentage of 8.63 percent and

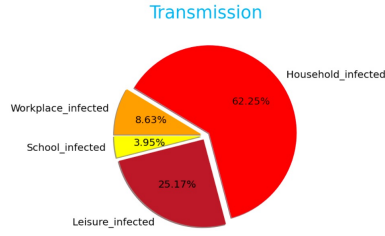


Figure 15: Percentage of infections per location

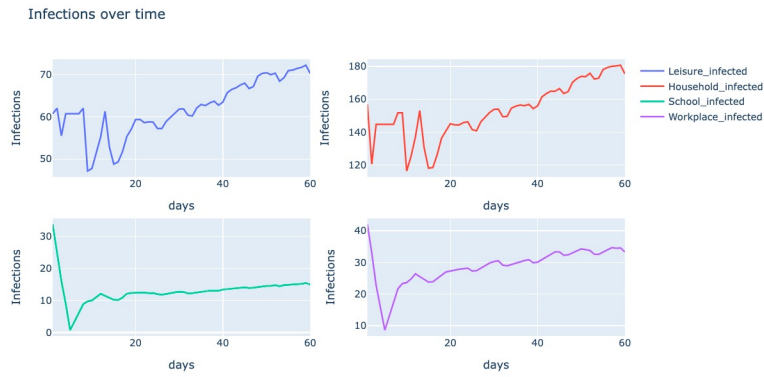


Figure 16: Infections per day in each location

3.95 percent respectively.

Figure 16 individually represents the infections per day in each location. Red represents Household\_infected, where we can see a lot of variation in the infections in the first 18 days but after the 20th day, there is a gradual increase in the infections with a few days having a less count than the others. Blue represents Leisure\_infected and almost the same pattern can be observed for this as above, only difference is the number of infections. Green represents the School\_infected, on the 5th day, we see a sudden decrease in the infection count and after the 6th day, we can see a gradual increase in the infections. Almost the same results are observed for Workplace\_infected, represented by violet color with only difference in the number of infections. Therefore, it can be said that Household has recorded the maximum number of infections, thus can be considered as superspreader.

## 4 Conclusion

The analysis of the output data from DFKI's social simulation of Covid-19 infection dynamics has provided valuable insights into the social patterns. This was accomplished with the assistance of a social network analysis approach, which

was found to be useful in capturing transmission in different location classes and identifying the super spreader events from a network perspective. Another strategy, in which we have utilized statistical analysis to identify the locations with the highest number of infections. These findings might prove helpful in the process of coming up with effective strategies to stop the further proliferation of the Covid-19 virus. In general, the results of this research demonstrate the significance of utilizing methods that are guided by data in order to comprehend the dynamics of infectious illnesses and to design appropriate interventions.

The analysis of the output data from DFKI's social simulation of Covid-19 infection dynamics has yielded valuable insights into the social patterns, significant variables, and correlations that influence the disease's spread. First, we learned the epidemic curve, which consists of susceptible, infected, and recovered states, using the SIR model. We were able to obtain transmission rate and recovery rate as a result. Second, in the location class, social patterns were analyzed using a social network analysis approach, which was found to be beneficial for capturing COVID-19 transmission in various location classes and identifying super spreader events from a network perspective. We have utilized statistical analysis to identify the locations with the highest infection rate as part of a second strategy. Taking into account the location classes, these findings may prove useful in the development of effective strategies to identify patterns of infection and proliferation of the Covid-19 virus. In general, the findings of this study demonstrate the importance of employing data-driven methodologies to fathom the dynamics of infectious diseases and to design effective interventions. There is space for improvement in terms of identifying places(location id) where infections occur; additional analysis could be conducted to determine the correlation between specific location categories and infection rates. We could investigate the use of machine learning algorithms to identify patterns and correlations in the data in order to identify super spreading events. By training models on the dataset, we can identify factors that are predictive of infection rates and create models that can be used to predict future outbreaks.

## References

- [1] The sir epidemic model. <https://scipython.com/book/chapter-8-scipy/additional-examples/the-sir-epidemic-model/>.
- [2] Ayan Kumar Bhowmick, Koushik Meneni, Maximilien Danisch, Jean-Loup Guillaume, and Bivas Mitra. Louvainne: Hierarchical louvain method for high quality and scalable network embedding. In *Proceedings of the 13th international conference on web search and data mining*, pages 43–51, 2020.
- [3] Naif K Binsaleh, Abdulrahman S Bazaid, Abdu Aldarhami, Subuhi Sherwani, and Omar W Althomali. Awareness and practice of covid-19 precautionary measures among healthcare professionals in saudi arabia. *Journal of multidisciplinary healthcare*, 14:1553, 2021.
- [4] Pasquale De Meo, Emilio Ferrara, Giacomo Fiumara, and Alessandro Proveti. Generalized louvain method for community detection in large networks. In *2011 11th international conference on intelligent systems design and applications*, pages 88–93. IEEE, 2011.
- [5] Antoine Deslandes, Clementine Calba, Sarah Mahdjoub, Aurelien Zhu-Soubise, Damian Mathey, and Alexis Ardoin. Superspreading events of sars-cov-2 in paris: A retrospective analysis of data from the first wave of covid-19 in 2020. *Journal of infection and public health*, 14(11):1733–1738, 2021.
- [6] Dima Goldenberg. Social network analysis: From graph theory to applications with python. <https://towardsdatascience.com>. Accessed: 2021-16-01.
- [7] Alberto Gómez-Carballa, Jacobo Pardo-Seco, Xabier Bello, Federico Martín-Torres, and Antonio Salas. Superspreading in the emergence of covid-19 variants. *Trends in Genetics*, 37(12):1069–1080, 2021.
- [8] Shalini Harkar. Sir model for spread of disease- the differential equation model. <https://medium.com/@shaliniharkar>. Accessed: 2020-05-07.
- [9] Seema S Lakdawala and Vineet D Menachery. Catch me if you can: superspreading of covid-19. *Trends in Microbiology*, 29(10):919–929, 2021.
- [10] Betsy Ledyzhets. Your thanksgiving could be a superspreading event). <https://covidatadispatch.substack.com/p/your-thanksgiving-could-be-a-superspreading.com>. Accessed: 2020-11-08.
- [11] Anna A Mensah, Mary Sinnathamby, Azad Zaidi, Laura Coughlan, Sharif Ismail, Mary E Ramsay, Vanessa Saliba, and Shamez N Ladhani. Sars-cov-2 infections in children following the re-opening of schools and the impact of national lockdown during autumn 2020: prospective, national observational cohort surveillance, england. *Mensah AA, Sinnathamby M, Zaidi A,*

*Coughlan L, Simmons R, Ismail SA, Ramsay ME, Saliba V, Ladhani SN. SARS-CoV-2 infections in children following the full re-opening of schools and the impact of national lockdown: Prospective, national observational cohort surveillance, 2020.*

- [12] Gaurav Pandey, Poonam Chaudhary, Rajan Gupta, and Saibal Pal. Seir and regression model based covid-19 outbreak predictions in india. *arXiv preprint arXiv:2004.00958*, 2020.
- [13] Micheal Stock. Characteristics of high risk covid-19 settings (superspreader events). <https://probabilis.blogspot.com/2020/10/characteristics-of-high-risk-covid-19.html>. Accessed: 2020-10-26.
- [14] Lukas Tapp, Veronika Kurchyna, Falco Nogatz, Jan Ole Berndt, and Ingo J Timm. School’s out? simulating schooling strategies during covid-19. In *International Conference on Autonomous Agents and Multiagent Systems*, pages 48–59. Springer, 2022.
- [15] Lukas Zenk, Gerald Steiner, Miguel Pina e Cunha, Manfred D Laubichler, Martin Bertau, Martin J Kainz, Carlo Jäger, and Eva S Schernhammer. Fast response to superspreading: uncertainty and complexity in the context of covid-19. *International journal of environmental research and public health*, 17(21):7884, 2020.