

Digital Epidemiology

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Introduction

Digital epidemiology is a branch of epidemiology that utilizes digital data sources and computational methods to study the distribution and determinants of health and disease in populations. It involves analyzing various types of data generated through digital platforms such as mobile apps, electronic health records, and other sources to track and understand patterns of disease spread, monitor public health trends, detect outbreaks early, and inform public health interventions.

Digital contact tracing is a crucial tool of Digital epidemiology for managing and controlling the spread of infectious diseases, particularly in the context of rapidly spreading viruses such as Corona. It involves the use of technology, such as mobile applications, to quickly and efficiently notify individuals who may have been exposed to the virus, allowing them to take necessary precautions such as getting tested or going into quarantine. The technology was developed in response to the realization that traditional contact tracing methods, which involve public-health workers interviewing infected individuals and reaching out to their contacts, were being outpaced by the speed of transmission during the COVID-19 pandemic.

History:

Epidemics have far-reaching consequences on public health, economies, and healthcare infrastructure. They lead to increased morbidity and mortality rates, economic downturns, and strain on healthcare systems, highlighting the urgent need for effective prevention and control measures.

The COVID-19 pandemic, caused by the novel coronavirus SARS-CoV-2, has had unprecedented global impacts since its emergence in late 2019. It has resulted in millions of deaths, widespread illness, economic disruptions, and strains on healthcare systems worldwide, highlighting the interconnectedness of public health and global economies.

Impact of pandemic:

The COVID-19 pandemic has had far-reaching effects across various aspects of society, profoundly impacting public health, the economy, and healthcare infrastructure.

Public Health: The pandemic has resulted in millions of confirmed cases and fatalities worldwide, overwhelming healthcare systems and exacerbating existing health disparities. Shortages of medical resources and personal protective equipment have strained healthcare facilities, while concerns about virus transmission have led to disruptions in routine healthcare services. Additionally, the mental health toll of the pandemic, including increased stress, anxiety, and depression, has been significant.

Economy: The global spread of COVID-19 triggered an economic downturn of unprecedented scale, characterized by widespread job losses, business closures, and decreased consumer spending. Industries heavily reliant on in-person interactions, such as travel, tourism, and hospitality, experienced severe setbacks, with many facing long-term challenges for recovery. Governments around the world have implemented various fiscal and monetary measures to mitigate the economic impact and stimulate recovery efforts.

Healthcare Infrastructure: Healthcare systems faced unprecedented challenges during the pandemic, including shortages of medical supplies and personal protective equipment. Adaptation and innovation became crucial strategies for maintaining healthcare services, with the widespread adoption of telemedicine and remote consultations. Vaccination efforts emerged as a pivotal tool in controlling the spread of the virus and alleviating strain on healthcare infrastructure, with governments and health organizations mobilizing resources to ensure widespread vaccination coverage.

Prevention Methods:

Vaccination: Vaccination programs are integral in preventing and controlling epidemics by inducing immunity within populations. They contribute to herd immunity, protecting not only vaccinated individuals but also those who cannot be vaccinated due to medical reasons or age. Various types of vaccines, including live attenuated, inactivated, subunit, recombinant, or mRNA-based vaccines, offer different mechanisms of action and efficacy profiles. However, vaccination programs face challenges such as vaccine hesitancy, limited access in some regions, distribution logistics, and ensuring equitable vaccine distribution.

Healthcare System Strengthening: Strengthening healthcare systems involves improving infrastructure, facilities, and equipment to handle increased patient loads during epidemics. This includes training healthcare personnel, recruiting additional staff, and enhancing surveillance systems to detect, monitor, and respond to outbreaks promptly. Challenges in healthcare system strengthening include engaging communities, disseminating accurate information, and promoting preventive behaviors, which can be resource-intensive and time-consuming, with obstacles such as funding and workforce shortages.

Isolation and Quarantine: Isolation and quarantine are public health measures aimed at preventing the spread of infectious diseases by separating infected or exposed individuals from others. Isolation entails separating confirmed cases from the general population to prevent further transmission. The duration of isolation and quarantine varies based on factors such as the disease's incubation period and the individual's risk of transmission. Challenges include providing support services and enforcing compliance, especially in resource-limited settings.

Contact Tracing: Contact tracing involves identifying and monitoring individuals who have been in close contact with an infected person to prevent further transmission. Methods include manual tracing and digital technologies like mobile apps and GPS data. Contact tracing helps interrupt transmission chains by isolating potentially infectious individuals before they spread the disease. However, challenges such as incomplete information, difficulty reaching contacts, and privacy concerns may hinder its effectiveness.

Manual Contact Tracing:

Manual contact tracing is a traditional method used to identify and monitor individuals who may have been exposed to infectious diseases, such as COVID-19. It involves several steps to trace and notify potential contacts of their exposure.

Health authorities initiate the process by identifying individuals who have tested positive for the disease, such as COVID-19, through testing and laboratory confirmation. Trained public health workers then conduct interviews with confirmed cases to gather information about their activities, movements, and close contacts during the period when they may have been infectious. Based on the information provided by confirmed cases, public health workers identify individuals who may have been in close contact with them. Once contacts are identified, they are notified of their exposure to the disease and provided with guidance on quarantine, testing, and monitoring for symptoms.

Drawbacks: Despite its effectiveness in identifying potential transmission chains, manual contact tracing has several drawbacks. Firstly, it is resource-intensive, requiring significant resources such as trained personnel to conduct interviews, gather information, and follow up with contacts. Secondly, manual contact tracing is time-consuming, relying on interviews and investigations to gather information about cases and contacts. Additionally, it may suffer from incomplete information, as it relies on individuals' ability to recall and provide accurate information about their activities and contacts. Lastly, manual contact tracing may have limited reach, particularly in communities with low health literacy, language barriers, or distrust of authorities.

Digital Contact Tracing:

Digital contact tracing uses technology, such as mobile apps and Bluetooth, to automate and expedite the contact tracing process. Here's how it works and its significance over manual contact tracing:

- **Automated Contact Tracing:** Digital contact tracing uses smartphones and mobile apps to track individuals' movements and interactions.
- **Notification of Exposure:** If a user tests positive for the disease, they can report their diagnosis through the app.
- **Efficiency and Scalability:** Digital contact tracing is more efficient and scalable than manual methods, as it automates the process of identifying and notifying contacts.
- **Real-time Monitoring:** Digital contact tracing allows for real-time monitoring of potential exposures and disease transmission.

NHS COVID-19 : The NHS COVID-19 app, developed in the UK, has significant significance as it was found to have prevented around one million infections and saved more than 9,600 lives in England and Wales between September 2020 and September 2021. This demonstrates the app's effectiveness in curbing the spread of COVID-19 and reducing the impact of the pandemic. Additionally, the app was able to trace more than twice as many contacts as conventional contact tracing, demonstrating its potential to enhance contact tracing efforts.

However, there are also drawbacks associated with the app. For instance, the app's usage was only around 25% of the population on average over the year, indicating a relatively low adoption rate. This could limit its overall effectiveness in controlling the spread of the virus. Moreover, there may be concerns about public trust in the app, as people may be skeptical about the effectiveness and trustworthiness of digital contact tracing, particularly when it was rolled out at scale during challenging times.

Health Code Apps : This app is a mobile phone application designed for instantaneous contact tracing and notification of close contacts upon confirmation of a COVID-19 case. It operates by recording proximity events between individuals using mobile phones and promptly alerting recent close contacts of diagnosed cases, prompting them to self-isolate. The app also serves as a central hub for accessing COVID-19 health services, information, and instructions, as well as a mechanism for requesting food or medicine deliveries during self-isolation.

The app's significance lies in its potential to reduce infection growth by enabling instantaneous contact tracing and notification of close contacts. This rapid response can effectively prompt individuals to self-isolate, thereby reducing the spread of the virus. The app's ability to provide immediate alerts to recent close contacts of diagnosed cases can significantly minimize the delay in quarantine and isolation measures, contributing to the overall reduction of transmission rates.

However, the app also has drawbacks and ethical considerations. It raises concerns regarding data protection and privacy, as it involves the collection of user movement and coronavirus diagnosis data. Additionally,

there are potential issues related to equity of access and treatment, as well as the need for transparent and auditable algorithms to ensure ethical implementation. The app’s effectiveness also relies on a high level of public understanding and compliance, and its success is contingent on a significant proportion of the population using the app.

1 Objectives

Our study aims to achieve several key objectives in the analysis and modeling of contact networks. Firstly, we seek to develop a robust methodology for generating accurate infected lists based on real-world data. By accurately estimating the percentage of infected individuals per day and incorporating this information into our model, our objective is to generate targeted infected lists for efficient contact tracing efforts.

Secondly, we aim to optimize the utilization of storage resources through the implementation of efficient data structures such as linked lists. By strategically storing contacts beyond the average degree in linked lists while utilizing arrays for more frequently occurring contacts, our objective is to minimize storage overhead while maintaining accessibility and scalability.

Thirdly, our objective is to enhance the efficiency of contact tracing through effective level traversal techniques. By systematically tracing contacts through multiple levels of interaction, our aim is to comprehensively map potential transmission pathways, identifying both direct and indirect contacts for targeted intervention strategies.

Lastly, our overarching objective is to maximize the efficiency and effectiveness of our model in capturing the dynamics of contact networks. By considering factors such as random distribution, degree centrality, population size, and dependency on previous contacts, our objective is to develop a holistic understanding of interpersonal interactions and inform strategies for managing and controlling the spread of infectious diseases, optimizing communication networks, and enhancing social connectivity.

By addressing these objectives, digital contact tracing can play a crucial role in controlling the spread of infectious diseases and supporting public health efforts.

2 Contacts between People Using Random Distribution

Random distribution is fundamental in probability theory and statistics, commonly applied in data science, mathematics, and physics. When generating data, understanding random distributions is vital for simulating realistic scenarios and analyzing system behavior.

In a population of size N , the maximum potential contacts between individuals are $\frac{N(N-1)}{2}$. However, in reality, not every person interacts with every other person. To account for this, we introduce a reducing factor f (where $f \in [0, 1]$), scaling down the maximum potential contacts to $\frac{N(N-1)}{2} \times f$.

Contacts between people are represented as edges. Thus, the range of possible edges (contacts) lies between 1 and $\frac{N(N-1)}{2} \times f$. If there are E edges in a given period, each involving two nodes (representing individuals), we need to generate $2 \times E$ numbers from a random distribution.

3 Reducing Factor (f)

Given a population of size N , let’s determine f , the reducing factor. Each person can make a maximum of $N - 1$ contacts. Suppose the average degree for this population is $\langle q \rangle$, indicating that on average, a person has q contacts. The ratio of contacts made by a person to the maximum possible contacts is $R_{\text{contact}} = \frac{\langle q \rangle}{N-1}$.

Since the ratio of possible contacts to maximum contacts equals R_{contact} , we have:

$$\text{possible contacts} = \text{maximum contacts} \times R_{\text{contact}}$$

Substituting the expressions for possible and maximum contacts, we get:

$$\text{possible contacts} = \frac{N(N-1)}{2} \times \frac{\langle q \rangle}{N-1}$$

Comparing this with the reduced contacts $\frac{N(N-1)}{2} \times f$, we obtain:

$$f = \frac{\langle q \rangle}{N-1}$$

For $N \gg \langle q \rangle$, we approximate f as:

$$f \approx \frac{\langle q \rangle}{N}$$

Now that we have f , the possible contacts in a day are given by:

$$\text{possible contacts} = \frac{N\langle q \rangle}{2}$$

This illustrates that the possible contacts depend on both N and $\langle q \rangle$.

To observe the degree distribution, we generate contact data for $N = 100,000$ and $\langle q \rangle = 10$, as shown in Figure 1. The figure illustrates that individuals with a degree close to $\langle q \rangle$ are most frequent, with the frequency decreasing as the degree deviates from $\langle q \rangle$.

Next, we generate data for varying $\langle q \rangle$ with the same population size, as depicted in Figure 2. Here, we observe a similar trend, but as $\langle q \rangle$ increases, the number of individuals with a degree close to $\langle q \rangle$ decreases.

4 Estimate of Infected List

The term "Infected List" refers to a compiled or predicted list of individuals found to be infected with a particular disease or condition on a specific day. This list is typically generated based on various data sources, such as reported cases, testing results, and visible symptoms. The next step after obtaining the infected list is to trace all the persons who made close contacts with the listed infected individuals.

To understand how infected cases are detected in different countries, let's analyze real-world COVID-19 data for India, USA, France, and Germany, and calculate the average cases detected per day.

India

Total cases (infected persons) detected over 3 years: 45,023,148 as shown in Fig.3a.

$$\text{Average cases per day} = \frac{45,023,148}{3 \times 365} = 41,117.$$

Population of India: 1,407,600,000. Percentage infected per day:

$$\text{Percentage infected per day} = 0.003\%.$$

USA

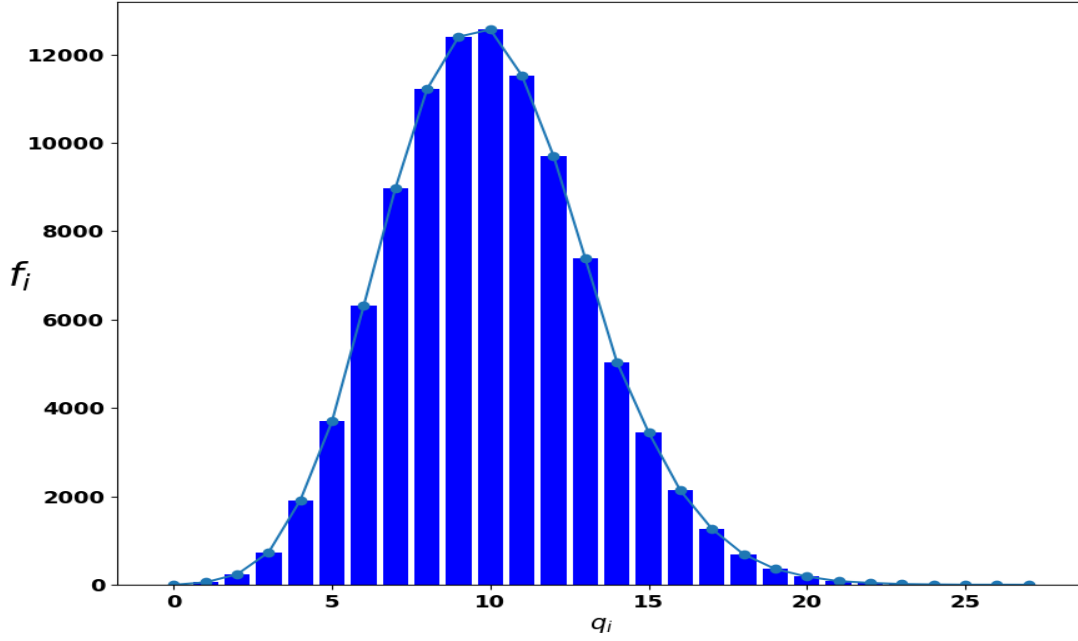


Figure 1: Degree distribution for $N = 100,000$ and $\langle q \rangle = 10$ using random distribution.

Total cases detected over 3 years: 110,766,307 as shown in Fig.3b.

Average cases per day = 101,156.

Population of the USA: 331,900,000. Percentage infected per day:

Percentage infected per day = 0.03%.

France

Total cases detected over 3 years: 40,138,560 as shown in Fig.3c.

Average cases per day = 36,656.

Population of France: 67,700,000. Percentage infected per day:

Percentage infected per day = 0.05%.

Germany

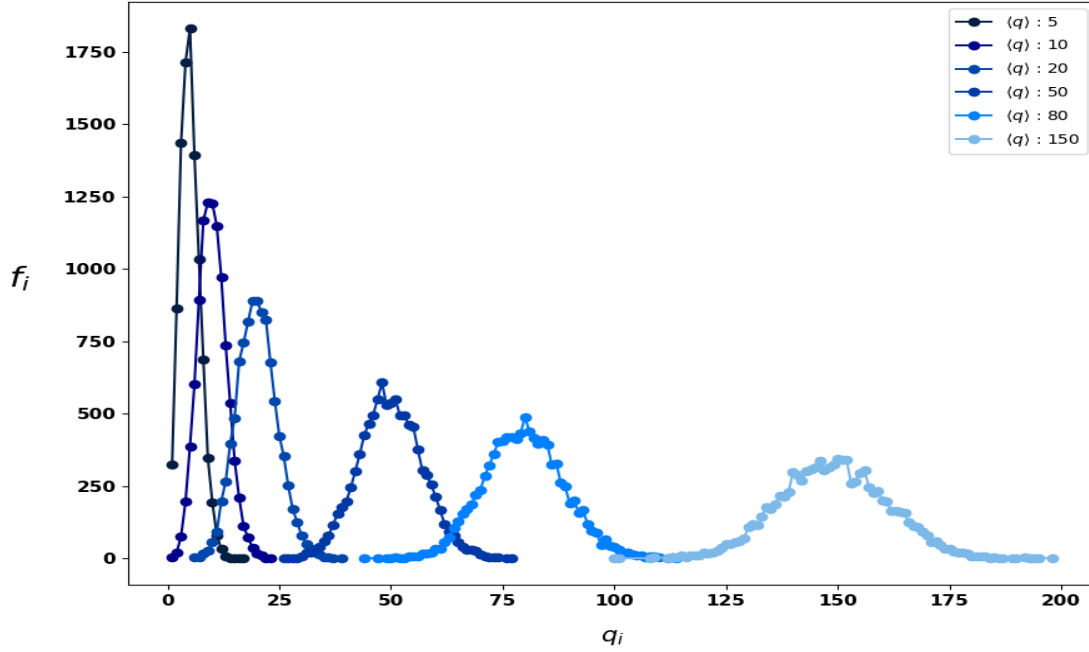


Figure 2: Degree distribution for $N = 100,000$ and varying $\langle q \rangle$ using random distribution.

Total cases detected over 3 years: 38,805,188 as shown in Fig.3d.

Average cases per day = 35,438.

Population of Germany: 67,700,000. Percentage infected per day:

Percentage infected per day = 0.05%.

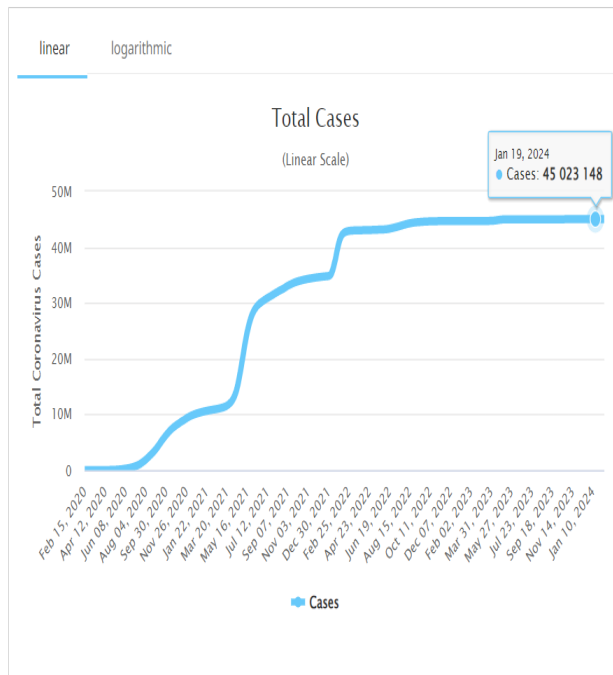
The percentage of people found infected per day ranges from 0.001% to 0.05% of the total population, depending on the country.

Let's assume for a population $N = 100,000$ and average degree $\langle q \rangle = 10$, the infected list size is 0.002% of N . Hence, on any random day, the number of persons found infected is 2.

Now, let's generate data for 300 days with $N = 100,000$ and $\langle q \rangle = 10$, with infected persons found on random days. Our task is to trace all the persons who made contacts (direct and indirect) with infected persons, as depicted in Figure 4.

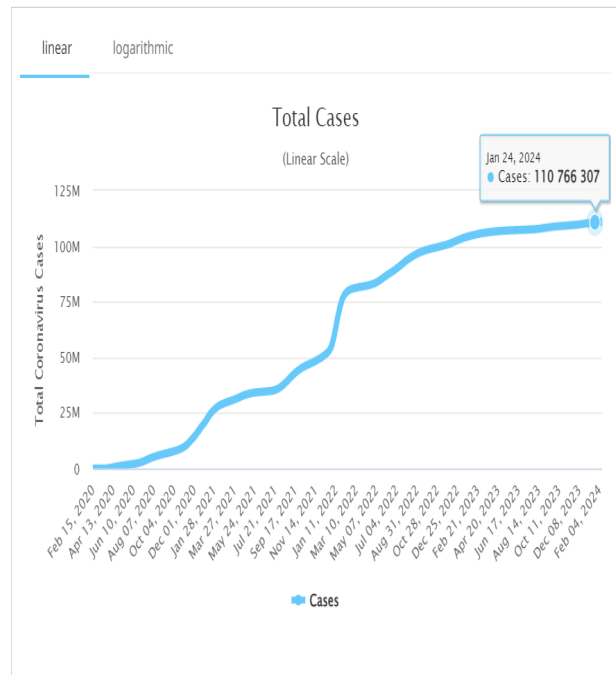
In Figure 4, as the level increases, the number of traced persons also increases. Initially, at the first level, we trace all direct contacts (persons making direct contacts) equal to the degree of the infected person. At the second level, we trace all persons traced at the first level, resulting in a greater number of traced persons. Similarly, at the third level, the number of traced persons increases further as we trace all persons from the second level.

Total Coronavirus Cases in India



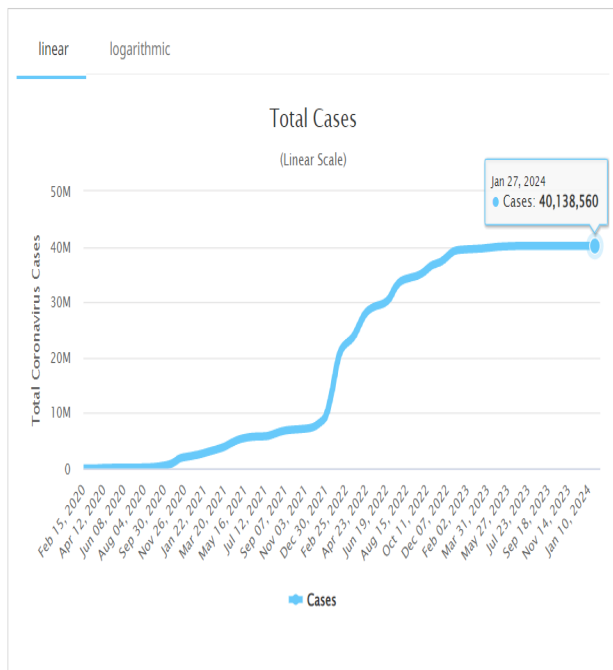
(a) Daily cases of COVID-19 in India over 3 years.

Total Coronavirus Cases in the United States



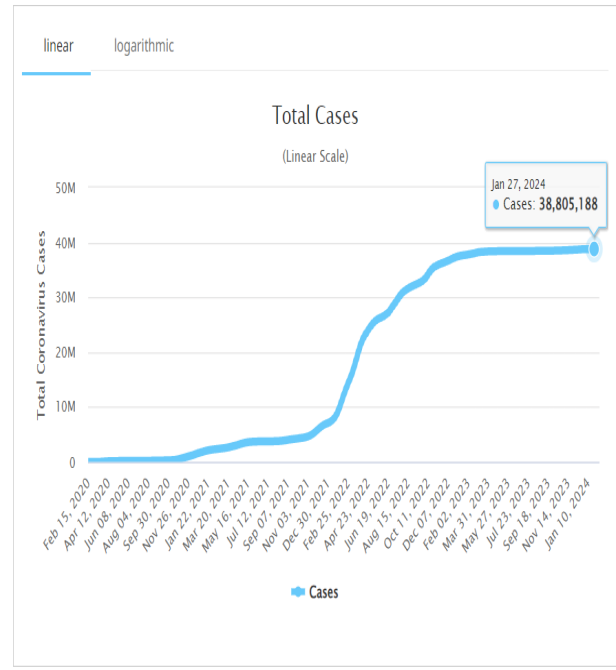
(b) Daily cases of COVID-19 in the USA over 3 years.

Total Coronavirus Cases in France



(c) Daily cases of COVID-19 in France over 3 years.

Total Coronavirus Cases in Germany



(d) Daily cases of COVID-19 in Germany over 3 years.

Figure 3: Daily cases of COVID-19.

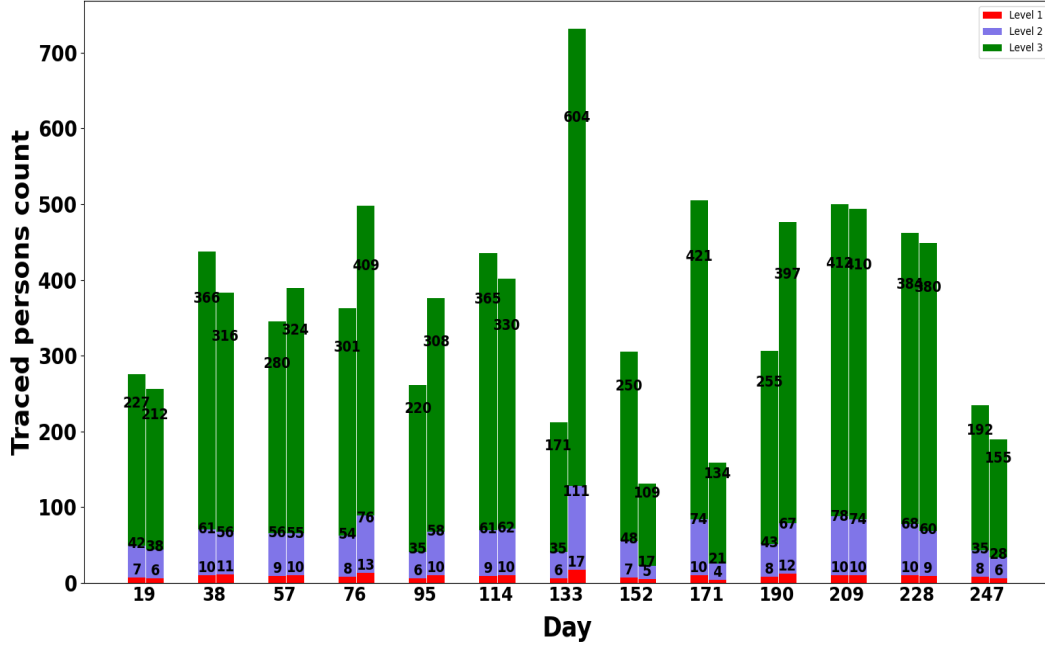


Figure 4: Counts of traced persons on each level for any random day. Red indicates the count of traced persons on the first level (direct contact), blue indicates the count on the second level (indirect contacts), and green indicates the count on the third level (further indirect contacts).

5 Estimate of Linked List Size

When generating data, such as edges or contacts using a random distribution with an average degree $\langle q \rangle$, it's common to observe that some individuals will have a degree greater than this average. To manage and store these contacts efficiently, a strategy is often employed where the contacts of a person whose degree is within the average are stored in a fixed-size array, typically of size $N \times \langle q \rangle$, where N is the total number of individuals in the dataset. However, for individuals with degrees exceeding the average, the contacts beyond the average degree are stored in a linked list structure. This approach results in a scenario where the number of contacts stored in the linked list is significantly lower compared to those stored in the array.

The reason for this lies in the nature of random distributions and the concept of degree centrality. In networks generated with a random distribution, the degrees of individual nodes or individuals follow a probabilistic pattern. While the average degree $\langle q \rangle$ provides a central tendency measure, there will inevitably be nodes with degrees higher than this average due to the stochastic nature of the process. These highly connected nodes, often referred to as hubs, contribute disproportionately to the overall degree distribution. Consequently, a relatively small number of individuals will have degrees significantly higher than the average, while the majority will have degrees closer to the average.

By storing the contacts of individuals with degrees below the average in a fixed-size array, computational resources are efficiently utilized since the array size is predetermined based on the expected average degree. However, for individuals with higher degrees, using a linked list allows for flexibility in accommodating the varying number of contacts beyond the average. This adaptive structure ensures that memory usage remains

efficient while accommodating the inherently uneven distribution of contacts in the network.

Reasons for Using Linked Lists

Linked lists offer several advantages over other data structures for storing contacts:

- **Efficient Addition:** Adding a new contact to a linked list can be done in constant time ($O(1)$). This is because new contacts can be inserted at the front of the linked list without the need for shifting existing elements.
- **Efficient Removal:** If we need to move a contact from the linked list to the array (e.g., when an index in the array becomes available), we can do so in constant time ($O(1)$). This is again because we can remove the contact from the front of the linked list without the need for shifting elements.
- **Contact Checking:** When determining whether any contact is with an infected person, we need to traverse the linked list. While this operation takes linear time ($O(n)$), it is still efficient. Additionally, alternative data structures would also require linear time or worse for this operation.

Thus, utilizing linked lists for storing contacts in digital contact tracing systems proves beneficial due to their efficient addition, removal, and contact checking operations, especially for individuals with high connectivity.

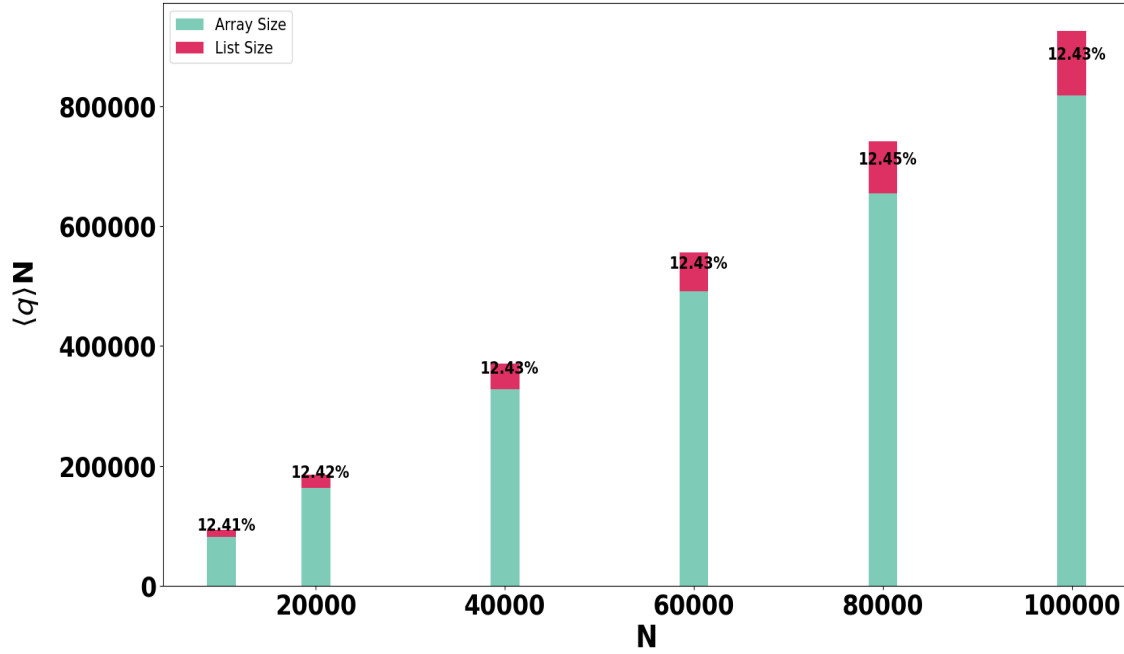


Figure 5: For total contacts $\langle q \rangle N$ red portion shows number of contacts in linked list and green portion shows number of contacts in main structure(array). Here number of contacts lying in linked list is always 11-12% of total contact.

Let's generate data(contacts) for different populations using random distribution. This contact distribution is shown in fig.5

It’s intriguing to observe that only around 11-12% of the total contacts end up in the linked list, with the vast majority stored in the array. This observation aligns with our earlier understanding of random distributions and degree centrality in networks. In such distributions, while there are individuals with degrees significantly higher than the average, they form only a small proportion of the total population. As a result, the number of contacts exceeding the average degree is relatively low compared to the total number of contacts.

The reason behind this phenomenon lies in the inherent characteristics of random distributions. In any given population, the distribution of connections follows a probabilistic pattern, with some individuals having many more connections than others. These highly connected individuals, or hubs, contribute disproportionately to the overall number of connections but represent only a small fraction of the total population. Conversely, the majority of individuals have degrees closer to the average, resulting in a lower number of contacts that exceed this average.

By storing the majority of contacts in a fixed-size array, we efficiently utilize memory resources since the array size is determined based on the expected average degree. This method accommodates the typical scenario where most individuals have degrees around the average. For the relatively few individuals with degrees significantly higher than the average, using a linked list for their extra contacts provides a flexible and adaptive approach without wasting memory on unnecessarily large arrays.

In essence, the observation that only a small percentage of total contacts end up in the linked list reinforces our understanding of random distributions and degree centrality. It underscores the fact that while some individuals may have many connections, they constitute only a minority within the population, and most contacts are distributed more evenly around the average degree. This distribution pattern validates our approach of efficiently managing contacts based on the expected degree distribution within different populations.

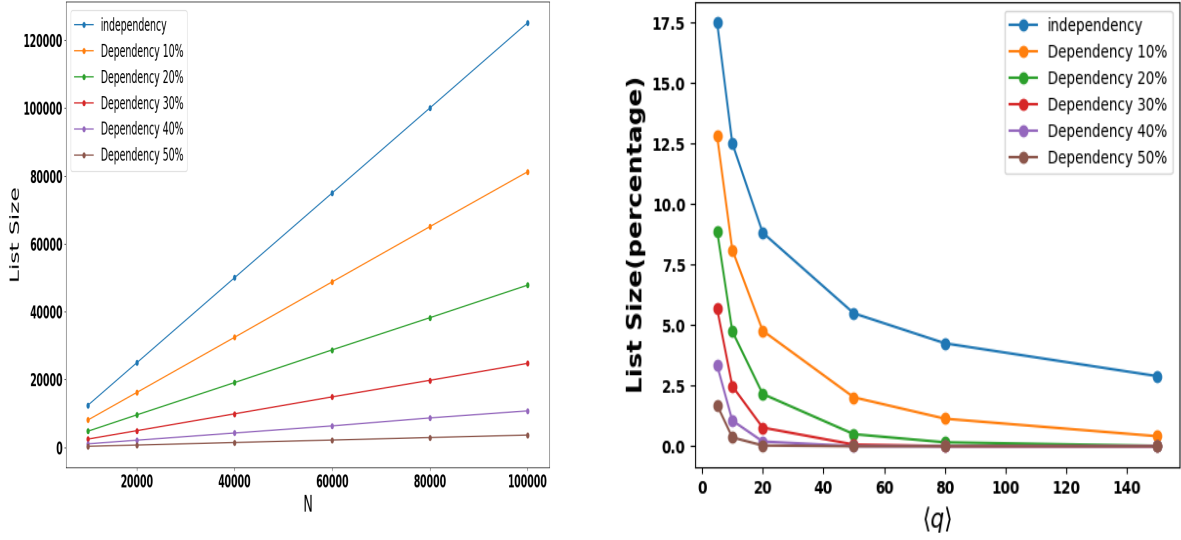
6 Contacts with Dependency on Previous Contacts

In real-world scenarios, people often maintain regular contacts with each other, with many interactions being repetitions of previous contacts. However, there are also occasions where individuals make new contacts, either meeting someone for the first time or reconnecting after a significant period. To model this behavior, our approach is to generate a mixture of repeated contacts based on dependency and new contacts.

The model we develop aims to balance between repeating previous contacts and generating new ones. This balance is achieved by incorporating a parameter representing the level of dependency. A higher dependency value implies a greater tendency to repeat contacts from previous days, while a lower dependency value favors the generation of new contacts.

We visualize the impact of different dependency levels on the size of the generated contact lists for various population sizes in Figure 6a. As the population size increases, the size of the contact list also increases, reflecting the greater number of potential interactions. Additionally, for any given population size, we observe that increasing the dependency level leads to a decrease in the size of the contact list. This trend arises because higher dependency results in a higher proportion of repeated contacts, reducing the number of new contacts generated, thus the list size.

Further exploration in Figure 6b focuses on a fixed population size of $N = 100,000$ with varying average degrees ($\langle q \rangle$). Here, we maintain the same trend: increasing dependency leads to a decrease in the size of



(a) Here as N increases list size is also increases and for (b) Here for $N=100,000$ and varying $\langle q \rangle$ as dependency any N as we increase dependency then list size decreases. increases list size decreases.

Figure 6: List Size with varying N , $\langle q \rangle$ and dependency

the contact list. This outcome underscores the impact of dependency on the generation of new contacts, as higher dependency values prioritize repeating previous interactions, reducing the number of new contacts generated, thus the list size.

In summary, our model captures the balance between repeating previous contacts and generating new ones by adjusting the level of dependency. By visualizing the relationship between dependency and contact list size, we gain insights into how different factors influence the dynamics of contact generation.

7 Conclusion

The analysis and modeling of contacts between individuals provide valuable insights into the dynamics of interpersonal interactions. By leveraging random distribution and considering factors such as average degree, population size, and dependency on previous contacts, we gain a deeper understanding of how contact networks evolve over time.

Through our exploration, we observe that random distribution plays a fundamental role in shaping the pattern of contacts within a population. The concept of degree centrality highlights the presence of highly connected individuals, or hubs, which influence the overall structure of the network. Efficient storage strategies, such as using arrays and linked lists, are essential for managing contact data, particularly in scenarios where some individuals have significantly higher degrees than others.

Furthermore, the analysis of contacts with dependency on previous interactions reveals the balance between repeating previous contacts and generating new ones. By adjusting the level of dependency, we can control the proportion of repeated contacts within the network, influencing the overall size of the contact lists.

In addition to network structure, our model demonstrates efficiency in handling infected lists. By accurately estimating the percentage of infected individuals per day based on real-world data, we can generate targeted infected lists for contact tracing efforts. This enables swift identification of potential infection clusters and effective containment measures.

Moreover, our model facilitates efficient level traversing for contact tracing purposes. By tracing contacts through multiple levels of interaction, we can identify not only direct contacts but also indirect contacts, thereby comprehensively mapping potential transmission pathways.

The incorporation of dependency on previous contacts further enhances the efficiency of the model. By balancing repeated contacts with new ones, we optimize the utilization of resources and minimize redundancy in contact lists. This adaptive approach ensures that contact lists remain manageable while capturing the complexities of real-world interpersonal interactions.

In conclusion, our study underscores the importance of considering various factors, including random distribution, degree centrality, population size, and dependency, when modeling and analyzing contact networks. These insights, coupled with the efficiency of our model in handling infected lists, level traversing, and list size with dependency, contribute to a better understanding of interpersonal interactions and inform strategies for managing and controlling the spread of infectious diseases, optimizing communication networks, and enhancing social connectivity.

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