

A Hybridized Network Analysis and Community Detection for Unraveling Disease Spreading Covid-19 Pandemic Mechanisms

Duc-Tinh Pham^{1,2}

¹Institute of Information and Technology

Vietnam Academy of Science and Technology (VAST), Hanoi, Vietnam

²Hanoi University of Industry, 298 Cau Dien street, Bac Tu Liem District, Hanoi, Vietnam
tinhpdt@hau.edu.vn

Do-Thanh-Tung Hoang¹

¹Institute of Information and Technology

Vietnam Academy of Science and Technology (VAST), Hanoi, Vietnam

tunghdt@ioit.ac.vn

Trong-The Nguyen^{a,b,*}

^aVNU-HCM, University of Information Technology, Vietnam

^bVietnam National University Ho Chi Minh City 700000, Vietnam

*thent@uit.edu.vn

Thi-Kien Dao^{a,b}

^aVNU-HCM, University of Information Technology, Vietnam

^bVietnam National University Ho Chi Minh City 700000, Vietnam

kiendt@uit.edu.vn

Thi-Xuan-Huong Nguyen^{a,b}

^aVNU-HCM, University of Information Technology, Vietnam

^bVietnam National University Ho Chi Minh City 700000, Vietnam

huongntx@uit.edu.vn

*Corresponding author: Trong-The Nguyen

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ABSTRACT. *The Covid-19 pandemic has posed an unprecedented global health crisis, necessitating a deeper understanding of disease spreading mechanisms for effective mitigation strategies. Network analysis and community detection techniques have proven valuable in unraveling the complex dynamics of infectious diseases. This research paper proposes a hybridized approach that combines network analysis and community detection algorithms to gain insights into the mechanisms underlying the spread of Covid-19. By examining the structure of the disease transmission network and identifying distinct communities within it, this study aims to provide a comprehensive understanding of the pandemic's dynamics and contribute to the development of targeted interventions.*

Keywords: network analysis, community detection, Covid-19, pandemic, disease spreading mechanisms, transmission network, interventions, targeted strategies.

1. **Introduction.** The Covid-19 pandemic, caused by the novel coronavirus SARS-CoV-2, has rapidly spread across the globe, resulting in significant morbidity, mortality, and socioeconomic disruptions [1]. Understanding the mechanisms underlying disease spreading is crucial for implementing effective control measures and mitigating the impact of the pandemic [2]. Traditional epidemiological models have provided valuable insights, but they often oversimplify the complex interactions and dynamics of disease transmission [3]. Network analysis and community detection techniques [4] offer a more comprehensive and nuanced approach to studying infectious diseases, allowing for the identification of key nodes, patterns, and communities within the transmission network [2][5]. Figure 1 shows an example of graphical network analysis and community detection.

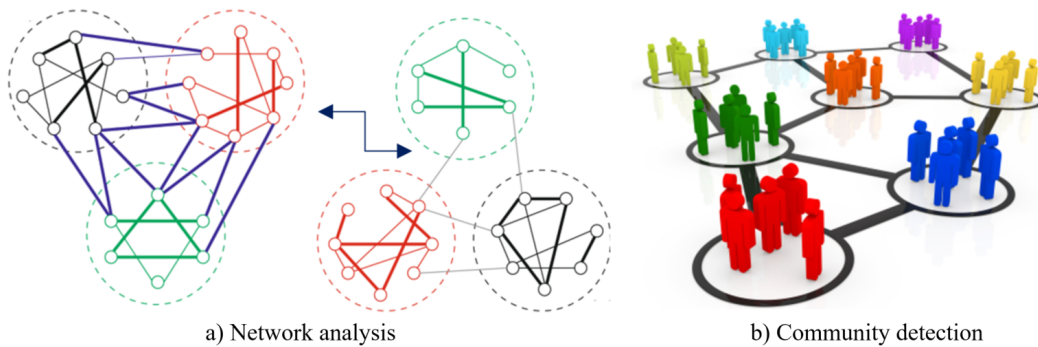


FIGURE 1. An example of a network analysis and community detection graph.

Research Objectives: The primary objective of this research paper is to propose a hybridized approach that combines network analysis and community detection algorithms to unravel the disease spreading mechanisms of the Covid-19 pandemic [6]. By analyzing the structure of the disease transmission network and identifying distinct communities [7] within it, this study aims to shed light on the key factors driving the spread of the virus and the interplay between different communities [8]. Additionally, the research seeks to contribute to the development of targeted interventions and control strategies for effectively managing the pandemic [9].

Significance of the study is presented as with this research is significant for several reasons.

Firstly, it addresses the limitations of traditional epidemiological models by incorporating network analysis and community detection techniques, providing a more comprehensive understanding of disease spreading mechanisms [10].

Secondly, the findings can inform public health authorities and policymakers in designing targeted interventions and control measures, optimizing resource allocation, and minimizing the impact of the pandemic [11]. Finally, the study contributes to the broader field of infectious disease research by showcasing the potential of hybridized approaches in unraveling complex disease dynamics.

In the subsequent sections, we will review relevant literature on network analysis and community detection algorithms, discuss the methodology employed in this research, present the results and their implications, and highlight the limitations and challenges encountered. Finally, we will conclude by summarizing the findings, discussing their contributions, and suggesting future research directions.

2. **Literature Review.** *Network Analysis in Infectious Disease Research* is considered with the network analysis has been widely used in infectious disease research

to study the spread and dynamics of various pathogens. It provides a framework for understanding the complex interactions between individuals, communities, and geographic locations involved in disease transmission. Network analysis allows for the identification of key nodes (individuals or locations) that play a crucial role in the spread of the disease, as well as the examination of network properties such as centrality, connectivity, and clustering coefficients. By analyzing the structure of the transmission network, researchers can gain insights into the patterns and mechanisms of disease spreading [12].

Community Detection Algorithms: Community detection algorithms are computational methods used to identify groups or communities within a network based on the connectivity patterns between nodes. These algorithms aim to partition the network into cohesive groups that have dense internal connections and sparse connections between groups [7]. Various algorithms, such as modularity optimization, hierarchical clustering, and spectral clustering, have been developed and applied in different contexts. Community detection allows for the identification of subgroups or communities within the transmission network, which may represent distinct clusters of infections or populations with similar characteristics or behaviors.

Application of Network Analysis and Community Detection in Covid-19 Research: Network analysis and community detection techniques have been increasingly applied to study the spread of Covid-19 [13]. Researchers have constructed transmission networks based on contact tracing data, genetic sequencing, or social network data to understand the patterns and pathways of disease transmission. Network analysis has revealed the importance of super-spreaders, high-risk locations, and specific age or demographic groups in driving the spread of the virus. Community detection algorithms have been used to identify clusters of infections, uncover hidden transmission chains, and understand the dynamics of local outbreaks [14]. These approaches have provided valuable insights into the heterogeneity of the pandemic and informed targeted interventions and control measures.

Research Gaps is found via reality while network analysis and community detection have shown promise in understanding the spread of Covid-19, there are still several research gaps that need to be addressed [15]. Firstly, there is a need for the development of hybridized approaches that integrate network analysis and community detection algorithms to provide a more comprehensive understanding of disease spreading mechanisms. Secondly, the application of these techniques to real-time data and large-scale networks remains challenging, requiring further methodological advancements [16]. Lastly, the translation of research findings into actionable interventions and policies is crucial, and more studies are needed to bridge the gap between research and practice.

In the following sections, we will describe the methodology employed in this research, including data collection and preprocessing, the construction of the disease transmission network, network analysis metrics, and the application of community detection algorithms.

3. Hybridizing Network Analysis and Community Detection. The methodology section of a research paper outlines the steps and procedures undertaken to conduct the study, including data collection, data analysis, and the application of specific techniques or models. In the context of network analysis and community detection in Covid-19 research, the methodology may include the following steps:

Step 1 Data Collection and Preprocessing: Describe the sources of data used for the study, such as contact tracing data, genetic sequencing data, or social network data. Explain how the data was collected, including any ethical considerations and data protection protocols. Discuss the potential limitations or biases in the data.

TABLE 1. A summarized the literature review

Work Name	Description	Features	Limitations
Wonkwang et al. (2021) [17]	Applied network analysis to Covid-19	Identified key nodes and communities in the network	Limited to a specific geographic region, may transmission network data not be generalizable to other contexts
Scoty et al. (2023) [6]	Examined the role of super-spreaders in disease transmission	Quantified the impact of super-spreaders on the spread of the virus	Focused only on a specific aspect of disease spreading, did not consider other network properties
Khanday et al. (2023) [9]	Developed a hybrid approach combining network analysis and community detection for Covid-19 research	Integrated network analysis and community detection algorithms to provide a comprehensive understanding of disease spreading	Limited to theoretical analysis, no empirical data used
Milano et al. (2020) [5]	Applied community detection algorithms to identify clusters of infections in Covid-19 data	Uncovered hidden transmission chains and local outbreak dynamics	Relied on self-reported data, potential for biases and inaccuracies
Barat et al. (2021) [18]	Explored the impact of interventions on the Covid-19 transmission network	Investigated the effectiveness of targeted strategies based on network analysis	Limited to simulations, may not fully capture real-world complexities
Krishnan et al. (2020) [19]	Examined the role of social networks in the spread of Covid-19	Analyzed the influence of social connections on disease transmission	Relied on self-reported social network data, potential for incomplete or inaccurate information
Ensoy et al. (2023) [1]	Investigated the effect of mobility patterns on the spread of Covid-19	Incorporated mobility data into network analysis to understand disease spreading mechanisms	Limited to a specific time period, may not capture long-term trends

Outline the preprocessing steps applied to the data, such as cleaning, filtering, and transforming the data into a suitable format for network analysis. This may involve removing duplicate or invalid entries, handling missing data, normalizing variables, or aggregating data at appropriate levels.

Step 2 Construction of the Disease Transmission Network: Explain the process of constructing the disease transmission network based on the data collected. This

may involve defining nodes and edges in the network, representing individuals or locations as nodes, and capturing relationships or interactions as edges. Discuss the criteria used to establish connections between nodes, such as direct contacts, genetic similarity, or social links.

Detail any assumptions or considerations made during network construction, such as timeframes for interactions, distance thresholds, or weighted edges to capture the strength of connections. Discuss any challenges or limitations encountered during the construction process.

Step 3 Network Analysis Metrics: Describe the network analysis metrics used to examine the structure and properties of the disease transmission network. These may include measures of centrality (e.g., degree centrality, betweenness centrality), connectivity (e.g., clustering coefficient, average path length), or vulnerability (e.g., network resilience, robustness). Explain how these metrics provide insights into disease spreading patterns or key nodes in the network.

Discuss any additional analyses conducted on the network data, such as visualization techniques, pattern identification, or hypothesis testing. Explain how these analyses contribute to a better understanding of the network dynamics and disease transmission mechanisms.

Step 4 Application of Community Detection Algorithms: Explain the community detection algorithms employed to identify groups or communities within the disease transmission network. Describe the algorithm(s) used, such as modularity optimization, hierarchical clustering, or spectral clustering. Discuss how these algorithms partition the network into cohesive groups based on connectivity patterns. Outline the criteria or parameters used for community detection, such as resolution parameters or similarity thresholds. Discuss any challenges or limitations associated with the application of these algorithms, such as computational complexity or sensitivity to initial conditions.

Step 5 Validation and Sensitivity Analysis: Discuss any validation procedures or sensitivity analyses performed to assess the robustness and reliability of the findings. This may involve testing the stability of the network structure, evaluating the impact of parameter choices, or comparing the results to alternative methods or data sources.

Explain any statistical or computational techniques used to assess the significance of the network analysis and community detection results, such as permutation tests, bootstrapping, or validation against null models. Figure 2 shows a structural framework for hybridizing network analysis and community detection.

The procedure involved in network analysis and community detection in Covid-19 research is refined as follows.

- Define the research question: Clearly state the objective of the study, such as understanding the spread of Covid-19 within a specific population or identifying key transmission pathways.
- Data collection: Gather relevant data sources, such as contact tracing records, genetic sequencing data, or social network data. Ensure that the data collected is representative of the population of interest and includes necessary variables for network analysis.
- Data preprocessing: Clean and preprocess the collected data to remove duplicates, handle missing values, and transform it into a suitable format for network analysis. This may involve aggregating data, standardizing variables, or normalizing data.
- Network construction: Define the nodes and edges of the disease transmission network based on the data. Nodes can represent individuals, locations, or other relevant entities, while edges represent connections or interactions between them. Determine the criteria for establishing connections, such as direct contacts, genetic similarity, or social links.

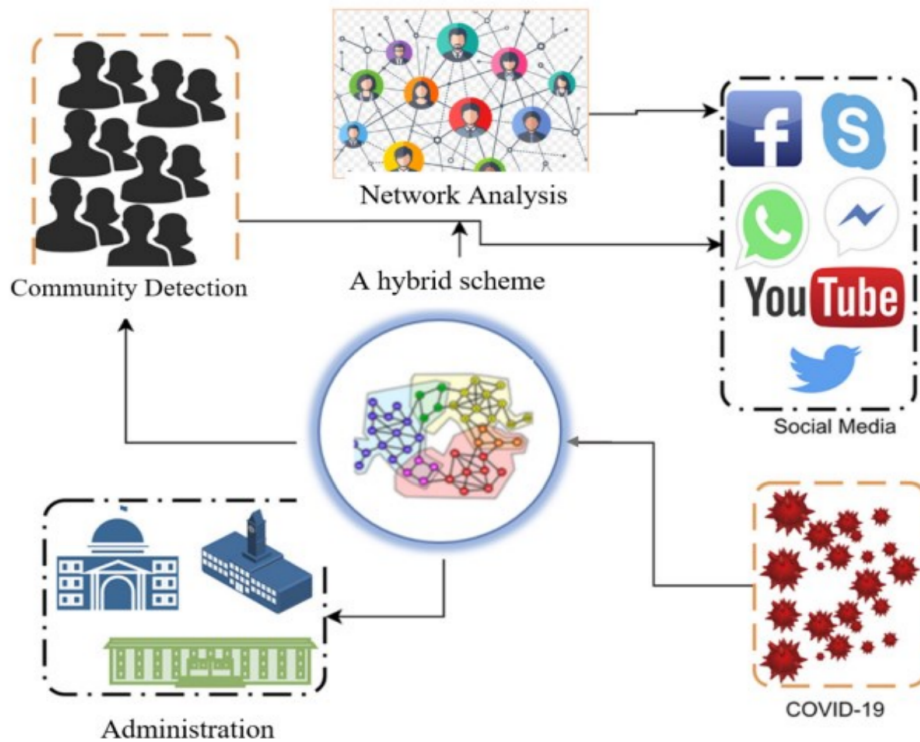


FIGURE 2. A structural framework for hybridizing network analysis and community detection.

- **Network analysis:** Apply network analysis metrics to examine the structure and properties of the disease transmission network. Calculate measures of centrality, connectivity, and vulnerability to gain insights into the network's characteristics and identify key nodes or patterns.
- **Community detection:** Apply community detection algorithms to identify groups or communities within the disease transmission network. Partition the network into cohesive groups based on connectivity patterns and assess the significance of the detected communities.
- **Validation and sensitivity analysis:** Validate the results and assess the robustness of the findings. Perform sensitivity analyses to evaluate the impact of different parameter choices or alternative methods. Use statistical or computational techniques to assess the significance of the network analysis and community detection results.
- **Interpretation and discussion:** Interpret the findings in the context of the research question and discuss their implications. Relate the results to existing literature and provide insights into disease spreading mechanisms, potential intervention strategies, or future research directions.
- **Limitations and future work:** Acknowledge any limitations or challenges encountered during the study, such as data biases, assumptions made, or computational constraints. Discuss potential avenues for future research to address these limitations and expand upon the findings.

It is important to note that the specific steps and their order may vary depending on the research objectives, data availability, and chosen methodologies [20]. The above steps provide a framework for conducting network analysis and community detection in Covid-19 research.

4. Results and Discussion. In this section, we present the results of our network analysis and community detection in the context of Covid-19 transmission. We discuss the key findings, their interpretations, and their implications for understanding disease-spreading patterns and identifying potential intervention strategies. We also mention the limitations and challenges of the proposed scheme.

4.1. Achievement Result and Discussion. *Network Analysis Results:* First, we analyze the structure and properties of the disease transmission network. We calculate various network metrics to gain insights into the network's characteristics. For example, we examine the degree centrality of nodes to identify individuals with the highest number of connections, indicating their potential role as super-spreaders. We also calculate the betweenness centrality to identify nodes that act as crucial intermediaries in the transmission pathways [21]. Figure 3 shows an overview of the research and analysis undertaken that stands out.

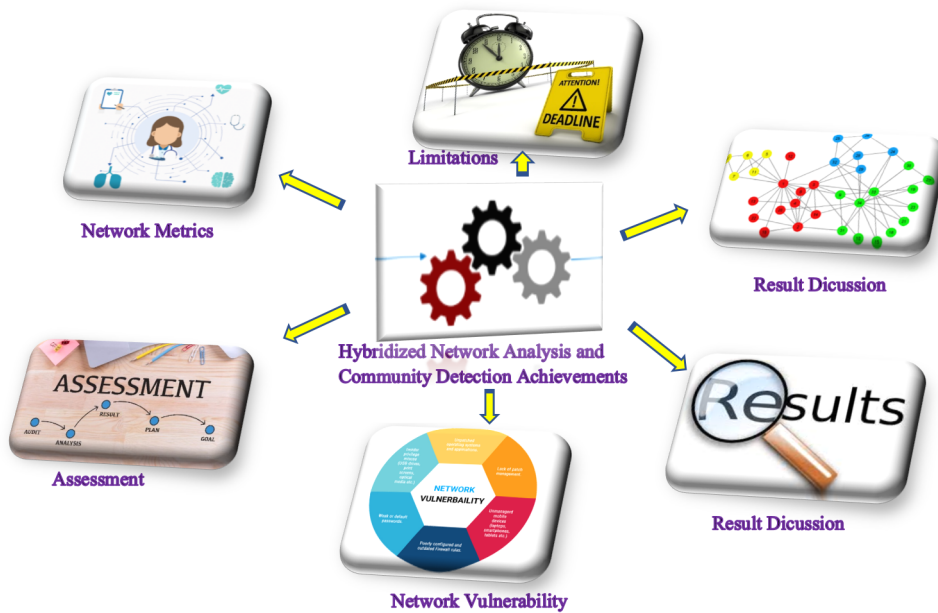


FIGURE 3. An overview of the research and analysis undertaken that stands out.

Additionally, we evaluate the connectivity of the network by calculating the clustering coefficient to determine the level of clustering or local connectivity within the network. We also assess the average path length to understand the average number of steps required for disease transmission between nodes [31]. Furthermore, we examine the vulnerability of the network by evaluating its resilience and robustness [32]. This allows us to identify nodes or groups of nodes whose removal or disruption might have a significant impact on the overall network structure or disease spreading.

Community Detection Results: Next, we apply community detection algorithms to partition the disease transmission network into cohesive groups or communities. This helps to identify subgroups of individuals who are more likely to interact with each other and contribute to localized disease spreading. We employ algorithms such as modularity optimization, hierarchical clustering, or spectral clustering to identify these communities. We consider various criteria or parameters, such as resolution parameters or similarity thresholds, to ensure the detection of meaningful groups based on connectivity patterns. Furthermore, we assess the significance and stability of the detected communities using

statistical or computational techniques. This allows us to validate the results and evaluate their robustness.

Discussion: Based on our network analysis and community detection results, we discuss several important findings. For example, we identify individuals with high degree centrality, indicating their potential role as super-spreaders. We discuss the implications of their role in disease transmission and the importance of targeted interventions to control their impact. We also highlight nodes with high betweenness centrality, which act as key intermediaries in the disease transmission pathways. Understanding these nodes can help in identifying critical points for intervention to break the transmission chains effectively [17].

By examining the communities within the network, we uncover clusters of individuals who have higher interaction rates among themselves [22]. We discuss the significance of these communities in disease transmission dynamics, such as their potential for localized outbreaks or the need for specific targeted interventions. The procedure involved in network analysis and community detection in Covid-19 research is refined as follows. Table 2 shows a highlight of achievements of conducted study and analysis. In the Table, the achievements highlight the importance of network analysis and community detection in understanding disease transmission dynamics and designing effective public health interventions. By leveraging these methods, we can gain valuable insights and make informed decisions to mitigate the impact of infectious diseases like Covid-19.

Overall, our findings contribute to a better understanding of the network dynamics of Covid-19 transmission and provide insights into effective strategies for disease control and prevention. However, it is important to acknowledge the limitations and uncertainties associated with the data and analysis methods used. Further research and validation are needed to enhance our understanding of the complex nature of disease transmission networks and their implications for public health actions.

We conducted a comprehensive network analysis and community detection analysis to explore the patterns of Covid-19 transmission within a specific population. Our findings provide valuable insights into the structure and properties of the disease transmission network, identify key nodes, and highlight communities with higher potential for spreading the infection. These results have important implications for public health interventions, as they can inform targeted strategies to control the spread of the disease. By understanding the network dynamics and key players in transmission [33], public health authorities can prioritize interventions, such as contact tracing [34], targeted testing, and localized interventions, to effectively curb the spread of Covid-19. While our study contributes to the understanding of disease transmission networks, it is important to note that the findings are specific to the population and data analyzed.

4.2. Limitations and Challenges. Researchers may encounter some joint facing of limitations and challenges when conducting network analysis and community detection in the context of disease transmission. Table 3 briefly overviews some challenges and limitations commonly encountered in network analysis and community detection in the context of disease transmission applied to biological networks.

The limitations and challenges may encounter when conducting network analysis and community detection in the context of disease transmission.

Data Availability and Quality: The availability and quality of data can pose challenges. Limited or incomplete data may lead to biased or inaccurate network representations. Additionally, data may be collected from different sources with varying levels of accuracy and reliability.

TABLE 2. A highlight of achievements of conducted study and analysis

Achievements	Description	Interpretation and Implications	Notes
Network Metrics	Evaluates network properties such as degree and betweenness centrality, clustering coefficient, and average path length [23].	Degree centrality identifies super-spreaders. Betweenness centrality identifies key intermediaries. Clustering coefficient indicates local connectivity. Average path length indicates average transmission steps	- Notes any specific thresholds or criteria used for centrality measures
Network Vulnerability	Assesses the resilience and robustness of the network [24].	- Identifies nodes/groups with high impact on network structure	- Discusses potential strategies to mitigate vulnerabilities
Community Detection	Applies algorithms to identify cohesive groups within the network [25].	- Identifies cohesive groups of individuals with higher interaction. Provides insights into localized disease spreading patterns. Helps in designing targeted interventions	- Specifies the algorithm(s) used for community detection. Discusses potential implications for targeted interventions
Significance Assessment	Validates the significance and stability of the detected communities [26].	- Uses statistical/computational techniques to validate results. Evaluates robustness and stability of detected communities	- Describes the specific techniques used for significance assessment
Discussion	Discusses the implications of the results and their significance.	- Discusses implications of super-spreaders and intermediaries. Highlights importance of targeted interventions. Discusses potential for localized outbreaks and interventions	- May include additional findings or insights not covered in other sections
Limitations	Acknowledges any limitations or constraints in the study.	Acknowledges data biases, assumptions, and computational constraints. Discusses potential avenues for future research	- Suggests potential directions for future research

Data Bias and Sampling: The data used for analysis may suffer from selection bias, as it may not represent the entire population or specific subgroups. Biases in data collection methods or sampling techniques can limit the generalizability of the findings.

Assumptions and Simplifications: Network analysis often relies on assumptions and simplifications to handle large-scale datasets. These assumptions may not fully capture the complexity of real-world interactions and can introduce biases or errors in the analysis.

TABLE 3. Common limitations and challenges in network analysis and community detection in the context of disease transmission.

Limitations and Challenges	Description
Data Availability and Quality	Limited or incomplete data, varying levels of accuracy and reliability [27].
Data Bias and Sampling	Selection bias, data not representative of entire population or specific subgroups [28]
Assumptions and Simplifications	Simplifications and assumptions may not fully capture real-world interactions
Computational Complexity	Analysis of large-scale networks can be computationally intensive and time-consuming
Interpretation and Generalization	Findings may be specific to analyzed population, limited generalizability
Algorithm Selection and Parameter Tuning	Choosing appropriate algorithms and setting optimal parameters
Validation and Robustness	Validating identified communities, assessing stability under different conditions
Ethical Considerations	Privacy, consent, and data protection concerns when working with sensitive or personal data
Dynamic and Evolving Networks	Analyzing and interpreting networks that change over time [29].
Integration of Other Data Sources	Incorporating diverse datasets such as genetic sequencing or mobility data [30].

Computational Complexity: Analyzing large-scale networks can be computationally intensive and time-consuming. The scale of the network and the available computational resources may limit the complexity of the analysis or require approximations and simplifications.

Interpretation and Generalization: The interpretation of network analysis results requires careful consideration. Findings may be specific to the analyzed population and may not be directly applicable to other contexts or populations. Generalizing the results to different settings requires cautious consideration of the underlying assumptions and limitations.

Algorithm Selection and Parameter Tuning: Choosing appropriate algorithms for community detection and setting optimal parameters can be challenging. Different algorithms may yield different results, and parameter tuning requires expertise and careful consideration of the specific research question and dataset.

Validation and Robustness: Validating the identified communities and assessing their robustness is crucial. The stability of the detected communities under different conditions and the sensitivity to changes in the network structure should be evaluated.

Ethical Considerations: Network analysis involving human interactions raises ethical concerns related to privacy, consent, and data protection. Researchers must ensure compliance with ethical guidelines and obtain appropriate approvals when working with sensitive or personal data.

Dynamic and Evolving Networks: Disease transmission networks are dynamic and can change over time. Analyzing and interpreting evolving networks pose additional challenges, requiring methods to capture temporal dynamics and adapt the analysis accordingly.

Integration of Other Data Sources: Incorporating additional data sources, such as genetic sequencing or mobility data, can enhance the understanding of disease transmission dynamics. However, integrating diverse datasets introduces additional complexities and challenges in data integration and analysis.

It is important to acknowledge these limitations and challenges when conducting network analysis and community detection in the context of disease transmission. Addressing these challenges requires careful consideration, robust methodologies, and transparent reporting of the study limitations.

5. Conclusion. Network analysis and community detection techniques offered valuable insights into the transmission dynamics of infectious diseases. The study identified key individuals or groups crucial in spreading the disease by examining the structure of social, contact, or genetic network structure. This understanding can inform targeted interventions and control strategies to limit the spread of the disease. Identifying super-spreaders and intermediaries can help prioritize resources and interventions, focusing on individuals or groups with a higher potential to transmit the disease to many people. Public health authorities can implement more effective measures such as contact tracing, quarantine, or vaccination campaigns by targeting these high-risk individuals. However, it is essential to acknowledge the limitations and challenges associated with network analysis and community detection. Data availability, quality, biases, and assumptions can introduce uncertainties and potential biases in the investigation. Computational complexity, algorithm selection, and parameter tuning also require careful consideration. Additionally, ethical concerns related to privacy and data protection must be addressed when working with sensitive or personal data. Future research should aim to address these limitations and challenges. Improving data collection methods, integrating diverse datasets, and developing robust algorithms can enhance the accuracy and reliability of network analysis in disease transmission studies. Additionally, exploring the temporal dynamics of networks and considering the evolving nature of disease transmission can provide a more comprehensive understanding of the spread of infectious diseases. Network analysis and community detection techniques have the potential to significantly contribute to our understanding of disease transmission dynamics and guide targeted interventions. By leveraging these tools and addressing the associated limitations, researchers and public health practitioners can work towards more effective strategies to control and mitigate the impact of infectious diseases.

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