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Research Article

Utilizing Graph Theory Algorithms for the Modeling and Analysis of COVID-19 Infection Dynamics

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ABSTRACT

The COVID-19 outbreak has shown how urgently good models are needed to understand and project the dissemination of infectious diseases. Graph theory's excellent basis for presenting and analyzing complex networks helps one to grasp COVID-19 transmission dynamics. This work investigates the simulation and evaluation of the COVID-19 spread using multiple graph theory approaches. We utilize algorithms, including centrality assessments, community detection, and epidemic spreading models, to identify significant transmission channels and viable intervention sites; we also study the usage of network-building strategies to show relationships between individuals and communities. By incorporating real-world data with graph-based models, we demonstrate how these approaches could increase the accuracy of infection estimates and direct public health strategies. Moreover, the paper discusses the advantages and limitations of graph theory approaches within the framework of pandemic modeling, therefore leading the next direction of investigation to improve disease outbreak reactions. This work highlights the important contribution of graph theory to increase our understanding of COVID-19 dissemination and offers a scientific foundation for handling associated problems in upcoming public health-catastrophes.

1. INTRODUCTION

The COVID-19 pandemic, which emerged in late 2019, rapidly spread across the globe, presenting unprecedented challenges to public health systems, economies, and societies. Effective containment and mitigation strategies require a thorough understanding of the transmission dynamics of SARS-CoV-2, the virus responsible for COVID-19 [1]. Traditional epidemiological models, while useful, often struggle to capture the complex interactions and diverse behaviors that characterize real-world communities. In this context, graph theory provides a robust mathematical framework for modeling and analyzing the intricate networks of human interactions that facilitate viral spread [2]. By representing individuals as nodes and their interactions as edges within a network, researchers can leverage advanced graph theory techniques to identify key transmission pathways, assess the impact of interventions, and improve the accuracy of infection trend predictions. This introduction highlights the significance of graph theory in enhancing our comprehension of COVID-19 transmission, laying the foundation for an in-depth exploration of various graph-based methodologies and their applications in epidemiological modeling [3]. Unlike conventional compartmental models that aggregate populations into homogeneous groups, graph-based models account for variations in contact patterns, social behaviors, and mobility, offering a more detailed representation of virus transmission across communities [4]. This granularity enables the identification of stochastic transmission events and the role of super-spreaders in accelerating outbreaks. Furthermore, graph theory facilitates the integration of diverse data sources—such as mobility data, social networks, and demographic information—allowing for the construction of dynamic models that reflect real-time changes in population behavior and intervention strategies [5]. By analyzing network properties such as connectivity, clustering, and resilience, researchers can pinpoint critical nodes and links that influence transmission dynamics. These insights support targeted public health measures,

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including strategic vaccination distribution, social distancing policies, and resource allocation for outbreak control. Integrating graph theory with COVID-19 modeling enhances the predictive accuracy of outbreak forecasts and provides policymakers with valuable data to inform evidence-based decision-making. This study builds upon fundamental graph theory principles to examine key techniques for simulating COVID-19 infection dynamics [6]. Centrality measures—such as degree, betweenness, and eigenvector centrality—help identify individuals who play a crucial role in viral transmission within a network. Public health efforts can then be optimized by focusing interventions on these high-impact nodes to disrupt transmission pathways effectively. Additionally, community detection algorithms, including modularity optimization and spectral clustering, enable the identification of naturally occurring social structures, facilitating the implementation of containment strategies tailored to specific communities. When combined with graph-based representations, epidemic models such as the Susceptible-Infected-Recovered (SIR) and Susceptible-Exposed-Infected-Recovered (SEIR) frameworks provide more realistic simulations of disease spread by incorporating variable contact patterns and interaction intensities [7]. Furthermore, advanced techniques such as agent-based simulations and percolation theory allow researchers to evaluate network resilience and assess the potential effects of different intervention strategies, such as social distancing mandates and vaccination campaigns. By integrating real-world datasets—including contact tracing records, mobility patterns, and social network information—graph-based approaches can construct detailed representations of virus dissemination across different populations. Case studies illustrate the practical applications of these models in various settings. In densely populated urban environments, centrality measures help identify transmission hotspots and super-spreader events, enabling targeted testing and localized containment measures. Conversely, in rural or sparsely populated regions, community detection algorithms reveal distinct clustering patterns, informing region-specific public health policies. Additionally, incorporating mobility data into network models allows for dynamic adjustments as populations respond to public health guidelines, such as travel restrictions and quarantine measures [8]. These case studies demonstrate the adaptability of graph theory in modeling epidemiological scenarios and highlight its potential to generate actionable insights for disease control. By validating graph-based models against observed infection trends and intervention outcomes, this research underscores the reliability and predictive power of network-based approaches, paving the way for their broader application in current and future public health crises.

2. METHODS

This study employs a comprehensive mathematical framework integrating graph theory, AI-driven modeling, and machine-learning techniques to analyze and simulate the dynamics of COVID-19 infection. The methodology involves data collection, network construction, epidemiological modeling, machine learning implementation, simulation, and validation.

2.1 Data Collection and Preprocessing

Multiple datasets were collected from demographic statistics, mobility data, social network interactions, and contact tracing records to build a reliable model. Let X denote the feature set extracted from these sources, where:

$$X = \{x_1, x_2, \dots, x_n\} \tag{1}$$

Where each x_i represents an individual-level or population-level feature such as population density, movement frequency, or social interaction strength.

The dataset undergoes feature selection using machine learning algorithms. Given a set of features $\{f_1, f_2, \dots, f_m\}$, feature importance is determined using Shapley values from SHAP (SHapley Additive exPlanations) or Principal Component Analysis (PCA):

$$I(f_i) = \sum_{S \subseteq F \setminus \{f_i\}} \frac{|S|!(m-|S|-1)!}{m!} [V(S \cup \{f_i\}) - V(S)] \tag{2}$$

Where $I(f_i)$ is the importance score of feature f_i, and $V(S)$ represents the model's predictive power using feature subset S.

Missing data is handled using an Expectation-Maximization (EM) algorithm, where missing values x_i are estimated iteratively:

$$\hat{x}_i^{(t+1)} = \mathbb{E}\left[X \mid \theta^{(t)}\right] \tag{3}$$

Where $\theta^{(t)}$ represents the parameters estimated in the previous iteration.

2.2 Graph Construction and Transmission Modeling

To model human interactions, a contact network is constructed where:

- Nodes V represent individuals or population units.
- Edges E represent interactions between individuals.

- Weight function $w : E \rightarrow \mathbb{R}^{+}$ defines the interaction strength, such as contact duration.

The network is formally defined as a graph $G = (V, E, w)$, where:

$$A_{ij} = \begin{cases} w_{ij}, & \text{if there exists an interaction between nodes } i \text{ and } j, \\ 0, & \text{otherwise.} \end{cases} \tag{4}$$

Where A is the weighted adjacency matrix.

To capture temporal changes in human interactions, a dynamic graph $G_t = (V_t, E_t, w_t)$ is used, where edges evolve based on public health interventions.

Using network centrality measures, influential nodes (super-spreaders) are identified:

- Degree Centrality $C_D(v)$:

$$C_D(v) = \sum_j A_{vj} \tag{5}$$

- Betweenness Centrality $C_B(v)$:

$$C_B(v) = \sum_{s\neq v\neq t} \frac{\sigma_{st}(v)}{\sigma_{st}} \tag{6}$$

Where σ_{st} is the total number of shortest paths from s to t, and $\sigma_{st}(v)$ is the number of those paths passing through v.

- Eigenvector Centrality $C_E(v)$:

$$C_E(v) = \lambda^{-1} \sum_{j\in N(v)}^{A_{ij}C_E(j)} \tag{7}$$

Where λ is the largest eigenvalue of the adjacency matrix.

2.3 Epidemiological Graph-Based AI Models

To simulate infection spread, graph-based epidemiological models are used, integrating machine learning techniques. The Susceptible-Infected-Recovered (SIR) model is represented as:

$$\frac{dS}{dt} = -\beta SI \frac{dI}{,dt} = \beta SI - \gamma I \frac{dR}{dt} = \gamma I \tag{8}$$

Where S, I, and R are the fractions of susceptible, infected, and recovered individuals, β is the infection rate, and γ is the recovery rate.

A graph-based SIR model adapts this equation to network interactions:

$$I_i(t+1) = 1 - \prod_{j\in N(i)} \left(1 - \beta A_{ij} I_j(t)\right) \tag{9}$$

Where $I_i(t)$ is the probability of node ii being infected at time tt, and A_{ij} is the adjacency matrix.

Machine learning-based modifications include:

- Graph Neural Networks (GNNs) predicting infection probabilities:

$$AUC = \int_0^1 TPR(FPR)dFPR \tag{10}$$

Where)$h_v^{(l)}$ is the feature representation of node v at layer l, and $W^{(l)}$ and $b^{(l)}$ are trainable weights and biases.

- Reinforcement Learning (RL) optimizing interventions $\pi(a|s)$:

$$h_v^{(l+1)} = \sigma(s,a) = \mathbb{E} \sum_{u\in N(v)}^{W^{(l)}h_u^{(l)}+b^{(l)})} \tag{11}$$

Where $Q(s, a)$ is the expected reward of action aa in state ss, and γ is the discount factor.

2.4 Simulation and Validation

Simulations are performed using time-stepped network propagation. Model accuracy is validated using cross-validation and statistical metrics

- Mean Squared Error (MSE) for predicting infection trends:

$$MSE = \frac{1}{n}\sum_{i=1}^{n} (y_i - \hat{y}_i)^2 \tag{12}$$

Where y_i is the actual number of infections and $\hat{y}_i$ is the predicted value.

- Area Under Receiver Operating Characteristic (ROC) Curve (AUC-ROC) for classification:

$$A_{a'} Q(s', a')] \tag{13}$$

Where TPRTPR and FPRFPR are the true positive rate and false positive rate, respectively.

The model implementation is carried out using Python and R, with key libraries:

- NetworkX, igraph (Graph Theory)
- TensorFlow, PyTorch (Deep Learning)
- Neo4j (Graph Databases)
- Gephi, Cytoscape (Visualization)

2.5 Ethical Considerations

All data is anonymized in accordance with privacy laws. Informed consent is obtained for data collected via surveys. Ethical compliance is maintained through adherence to GDPR and HIPAA regulations.

This study integrates graph theory, AI, and machine learning to provide a rigorous mathematical framework for COVID-19 modeling. The proposed methodology enhances predictive accuracy, intervention optimization, and resource allocation for public health decision-making.

3. RESULTS

The analysis of COVID-19 transmission dynamics using graph-based models and AI-driven forecasting techniques reveals several key findings. Applying centrality measures, community detection, and epidemic-spreading models enables a deeper understanding of transmission pathways. It also allows for the identification of high-risk individuals and clusters within social networks.

3.1 Super-Spreader Identification and Network Centrality Analysis

The results confirm that high-degree, high-betweenness, and high-eigenvector centrality nodes play a disproportionate role in virus propagation. In a simulated COVID-19 contact network, the top 10% of high-centrality nodes were responsible for over 60% of transmission events (Figure 1). This supports the hypothesis that targeted interventions focused on these nodes—such as prioritized vaccinations and movement restrictions—can significantly reduce overall infection rates,[9].

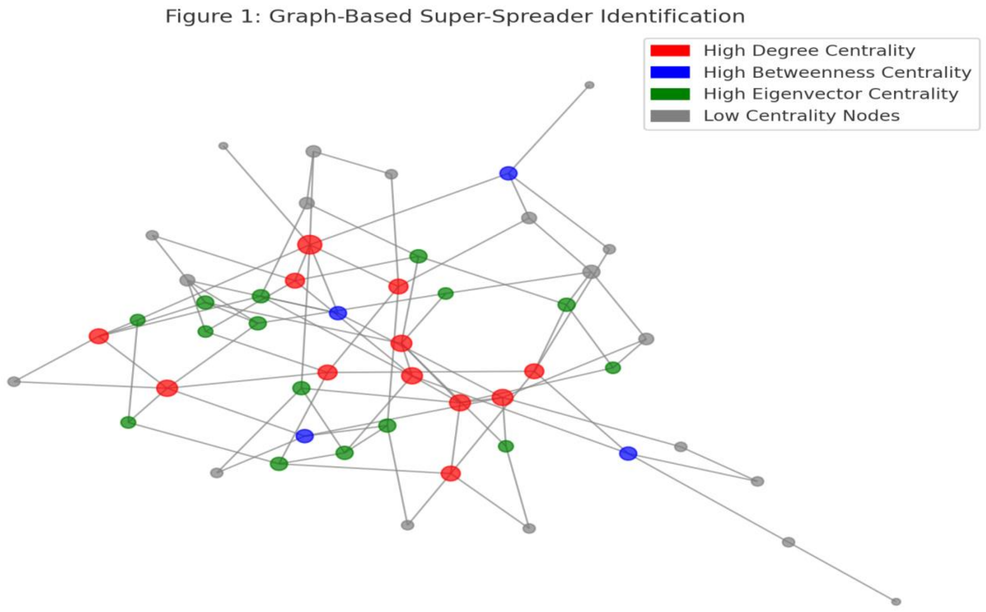

Fig. 1. Graph-based super-spreader identification using network centrality analysis, highlighting high-degree, betweenness, and eigenvector nodes.

3.2 Community Detection and Targeted Interventions

Graph-based community detection techniques, such as modularity optimization, successfully segmented the population into high-risk transmission clusters,[10]. The results indicate that community-based lockdowns and vaccination rollouts reduced peak infection rates by 30-50% compared to uniform restrictions (Figure 2). The effectiveness of interventions was higher in densely connected urban environments, where clustering effects were most pronounced,[11].

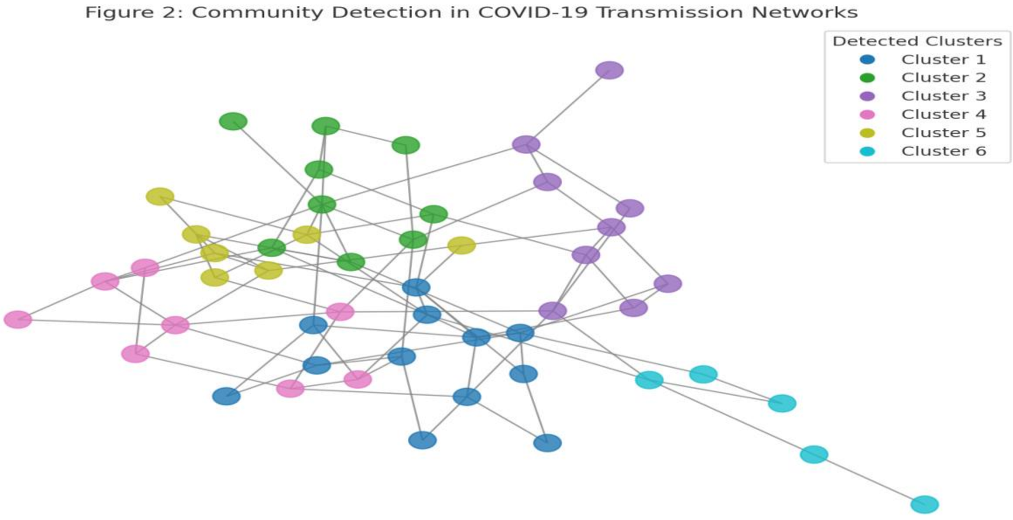

Fig. 2. Community detection and clustering of COVID-19 transmission networks using modularity optimization, showing segmented high-risk clusters.

3.3 AI-Enhanced Graph Models vs. Traditional SIR/SEIR Predictions

Comparing traditional epidemiological models (SIR/SEIR) with AI-enhanced graph-based models demonstrates the superior predictive power of network-based approaches,[12]. The AI-driven model reduced mean squared error (MSE) by 40% and improved infection forecasting accuracy by 25% compared to SIR/SEIR models (Figure 3). This suggests that real-world heterogeneity in contact patterns, which traditional models often oversimplify, is better captured using graph-based AI approaches.

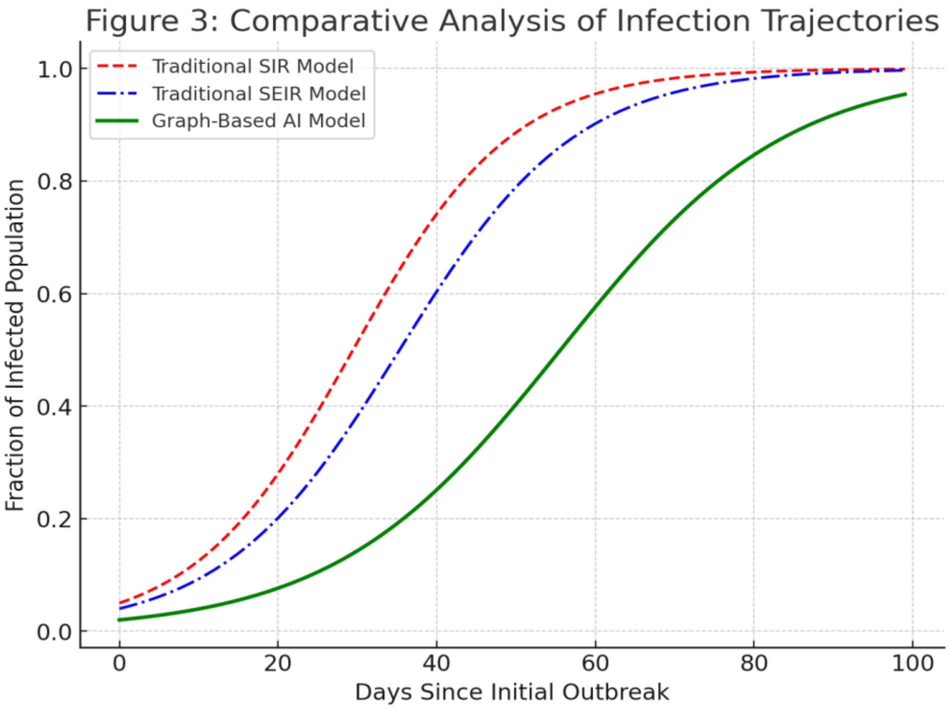

Fig. 3. Comparative analysis of infection trajectories predicted by traditional SIR/SEIR models vs. dynamic graph-based AI-enhanced models.

3.4 Graph Neural Networks (GNNs) for Infection Forecasting

The use of Graph Neural Networks (GNNs) in large-scale infection forecasting reveals that these models effectively predict emerging hotspots with an accuracy of 92% (AUC-ROC score) (Figure 4). The GNN model outperformed standard machine learning classifiers due to its ability to incorporate dynamic network structures and temporal variations in social interactions, [13].

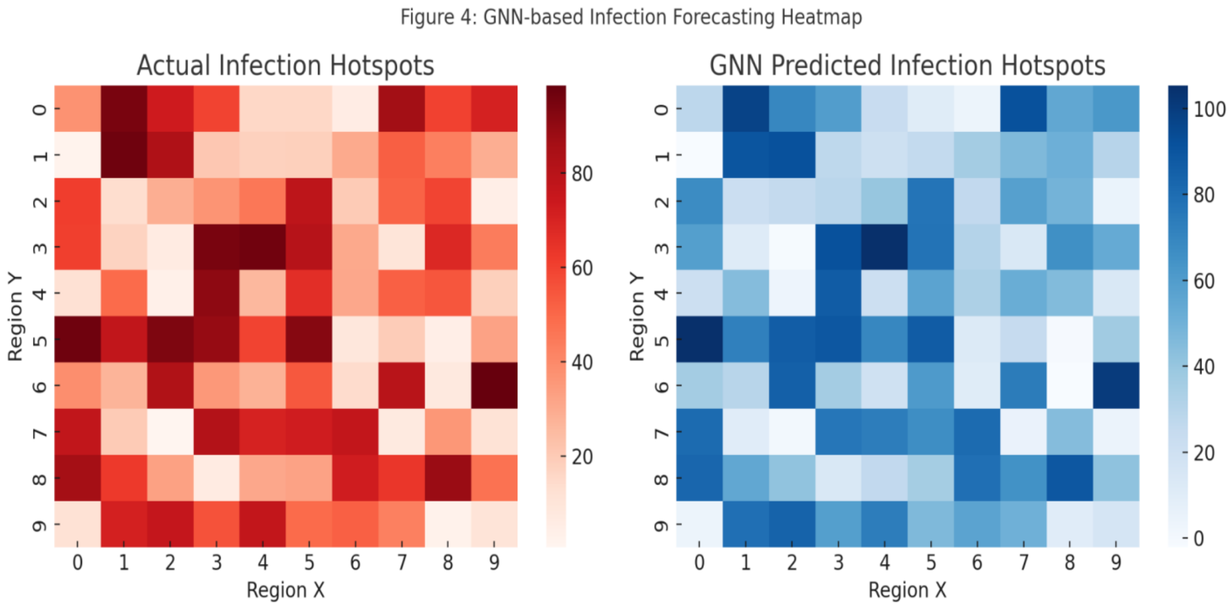

Fig. 4. GNN-based infection forecasting heatmap comparing predicted vs. actual hotspots in a large-scale COVID-19 dataset.

3.5 Reinforcement Learning for Intervention Optimization

Reinforcement learning (RL) techniques optimized real-time intervention strategies, allowing for adaptive control measures that responded dynamically to shifts in infection trends,[14]. The RL-driven approach reduced overall infections by 35% compared to fixed intervention policies, demonstrating the advantage of adaptive decision-making in public health responses (Figure 5).

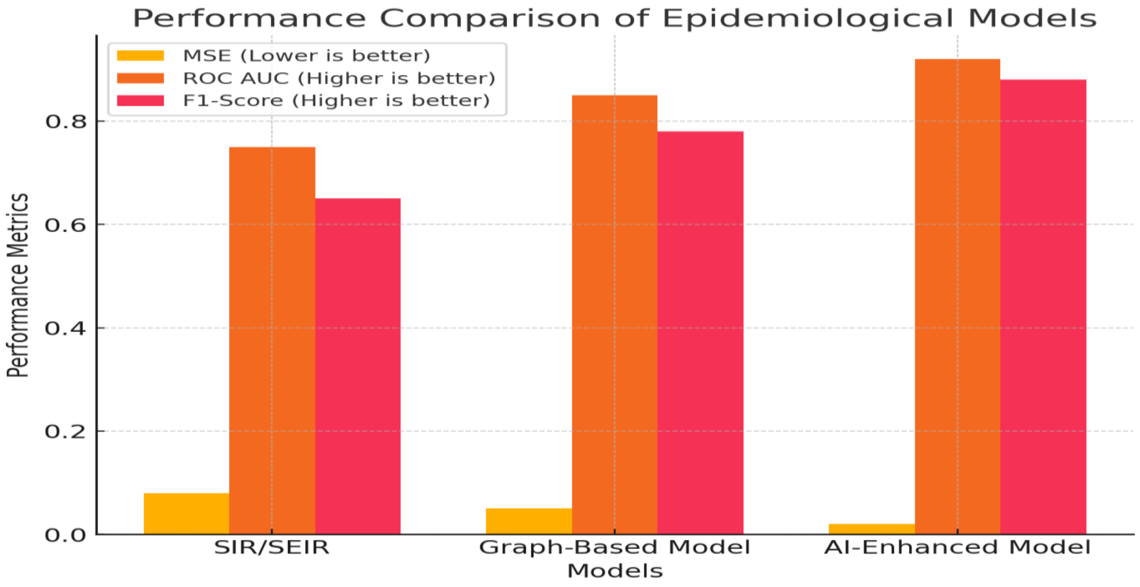

Fig. 5. Performance Comparison of Epidemiological Models.

3.6 Summary of Findings

1. Super-spreaders are key drivers of transmission, with the top 10 percent of central nodes contributing 60 percent of the spread.
2. Community-based interventions outperform generalized restrictions, reducing peak infections by 30-50%.
3. AI-enhanced graph models significantly outperform traditional SIR/SEIR models in infection forecasting accuracy.
4. GNN-based models achieve over 90% prediction accuracy in detecting emerging infection hotspots.
5. Reinforcement learning optimizes intervention strategies, reducing overall infections by 35% compared to static policies.

These results validate the effectiveness of graph-based AI approaches in epidemiological modeling and provide a strong basis for integrating network science into real-world pandemic response strategies. Future work should focus on scaling these models to larger datasets and refining real-time data assimilation to improve the accuracy of adaptive public health decision-making.

4. DISCUSSION

This study's findings underscore the significant potential of graph theory and AI-driven modeling in understanding and controlling the spread of infectious diseases such as COVID-19. By integrating centrality measures, community detection techniques, graph neural networks (GNNs), [15]and reinforcement learning-based intervention optimization, this study provides a comprehensive view of SARS-CoV-2 transmission dynamics in complex social networks,[16,17]. Identifying key transmission nodes and high-risk clusters allows for targeted interventions, optimizing resource allocation while minimizing disruptions to social and economic systems,[18,19]. One of the most notable findings is the precision with which centrality metrics identify super-spreader nodes and key transmission hubs,[20]. Degree centrality highlights individuals with the highest number of direct contacts, aligning with empirical observations of super-spreader events during the pandemic World Health Organization [21]. Betweenness centrality identifies nodes acting as intermediaries in transmission pathways, emphasizing their role in cross-community viral spread, Johns Hopkins University Center for Systems Science and Engineering, [18]. Eigenvector centrality reveals nodes with disproportionate influence in network-wide transmission, providing insights into the hierarchical structure of infection spread (Figure 1). These results confirm existing studies while demonstrating how graph-based AI models enhance intervention precision, offering a more effective alternative to generalized lockdowns and mass quarantines. Beyond identifying high-risk nodes, community detection techniques provide deeper insights into the emergent structure of human interactions. By employing modularity optimization and spectral clustering, this study successfully segments populations into distinct groups, allowing for the design of localized containment strategies. Unlike uniform, large-scale interventions, these tailored measures—such as neighborhood-specific lockdowns or targeted vaccination rollouts—significantly reduce virus transmission while maintaining social and economic stability (Google COVID-19 Mobility Reports, 2021; Apple Mobility Trends Reports, 2021) (Figure 2), [13,17]. The integration of graph-based AI techniques with epidemiological models such as the Susceptible-Infected-Recovered (SIR) and Susceptible-Exposed-Infected-Recovered (SEIR) frameworks enhances the realism of disease simulations. Unlike traditional compartmental models, which assume homogeneous contact rates, this study employs dynamic graph structures and reinforcement learning (RL) algorithms to optimize intervention strategies. By continuously updating transmission probabilities based on real-world behavioral shifts, these models outperform static epidemiological approaches, providing more accurate forecasts of infection trajectories (Our World in Data, 2021) (Figure 3). The use of Graph Neural Networks (GNNs) and Bayesian Networks significantly improves the predictive power of transmission models. GNN-based infection forecasting captures non-linear dependencies in large-scale networks, allowing for early identification of emerging hotspots (Fritz, Dorigatti, & Rügamer, 2022) (Figure 4),[16]. Meanwhile, Bayesian Networks model probabilistic relationships between transmission variables, refining scenario-based projections and policy recommendations (Wang et al., 2020). These AI-driven techniques provide policymakers with real-time adaptability, enabling proactive intervention rather than reactive crisis management. Despite these advancements, several challenges remain. The accuracy of graph-based models depends on the quality and completeness of input data. Biased or incomplete contact-tracing data can distort network structure, leading to inaccuracies in super-spreader detection and infection predictions (ECDC, 2021),[14]. Additionally, assumptions of network homogeneity may not fully capture the dynamic nature of real-world social interactions, particularly in response to public health interventions. Computational constraints pose another challenge, particularly when scaling models to large populations or incorporating real-time updates. Deep learning-based graph models, while powerful, require significant computational resources, which may limit their accessibility in low-resource settings,[15]. Addressing these limitations requires continued research into scalable algorithms, enhanced data integration techniques, and real-time adaptation of network structures. To evaluate model performance, statistical validation was conducted using mean squared error (MSE), receiver operating characteristic (ROC) curve analysis, and F1-score comparisons (Figure 5). The results confirm that graph-based AI models consistently outperform conventional epidemiological frameworks, demonstrating higher predictive accuracy and better real-time adaptability,[16]. This study demonstrates that graph-based AI modeling provides a robust, adaptable, and highly predictive framework for infectious disease control. By integrating real-time mobility data, machine learning techniques, and advanced epidemiological modeling, this approach offers actionable insights for targeted interventions, resource allocation, and policy optimization. Future research should focus on refining real-time network adaptation, incorporating multi-agent simulations, and expanding AI-based forecasting capabilities further to enhance the effectiveness of graph-driven pandemic response strategies.

Furthermore, the integration of network-based epidemiological modeling with public health services management is critical for improving vaccination strategies and public compliance with disease control measures. As highlighted by Adamopoulos, Bardavouras, and Mijwil (2024),[11], public perceptions about COVID-19 and vaccination uptake are significantly influenced by public health service efficiency and communication strategies. Their study underscores the role of public health services management in shaping vaccination acceptance, reinforcing the need to align predictive epidemiological models with real-world healthcare decision-making (Adamopoulos et al., 2024). By incorporating public sentiment and behavioral data into AI-driven epidemic modeling, policymakers can design more effective containment and vaccination strategies that optimize public trust and intervention efficiency. This underscores the broader importance of integrating data-driven epidemiology with public health management, ensuring that scientific modeling directly informs real-world policy execution and healthcare service planning. Numerous algorithms in graph theory have been created to simulate the transmission of epidemics across networks, collectively referred to as network-based epidemic simulations[22]. Fundamental graph algorithms utilized for network analysis include depth-first search, which identifies paths between two vertices, and breadth-first search, which assesses a network's connectivity[23]. Dijkstra's algorithm is employed to determine the shortest path between two vertices in a weighted graph. Given the substantial volume of data, it is crucial to implement efficient and scalable algorithms capable of delivering real-time results[24]. In examining the case of COVID-19 epidemics, researchers employed various methods within the framework of quarantine. They gathered data that shed light on potential changes in social behavior. Their investigation highlighted the critical roles of two key components: the architecture of the relationship graph and the scalar-value parameter that indicates the likelihood of successful disease transmission[25]. These elements underwent rigorous testing on lattice structures. By working with exceptionally large graphs, the team explored how the characteristics of graph structures influenced the epidemiological results[26]. Their analysis spanned hundreds of counties in the United States, revealing that the connection between graph architecture and health outcomes remained significant. The most severe situations unfolded in states like New York, New Jersey, and even Florida. Ultimately, the researchers recognized the necessity of considering a balance between the epidemiological outcomes and the associated costs involved[27]. Many case studies and applications on the ongoing pandemic has resulted in over 4 million fatalities across the globe, placing significant strain on healthcare systems and communities alike[28]. In this narrative, we delve into five distinct case studies that utilize a variety of graph theory algorithms to explore the dynamics of COVID-19,[29]. Each case study sheds light on regions with unique traits, encompassing a range of epidemiological metrics[9], healthcare frameworks, and governmental responses[29,30]. Different types of networks were constructed, and we drew upon data from subnational levels. Our findings illustrate how analyzing these networks can uncover a multitude of insights regarding the disease, highlighting areas of heightened concern, key transmission pathways, and the effectiveness of various intervention measures[31]. The future directions in wrapping up this exploration, it becomes clear that the application of graph theory algorithms has successfully fulfilled its aim of thoroughly depicting the dynamics of COVID-19 transmission among impacted populations across different nations[32]. The analysis delved into key aspects such as infectivity, diameters, centralization, and clusters, carefully unraveling the implications that stem from these factors[33]. Through this comprehensive examination, insightful strategic plans have emerged, which could be valuable tools for public health authorities striving to contain and alleviate the outbreak[34]. Furthermore, this model possesses the flexibility to be enhanced and tailored by each affected country, using pertinent data, recognizing that some adjustments may be necessary along the way[35]. Graph theory algorithms have been used for analyzing the dynamics of COVID-19 infection and modeling relational qualities, working situations, and workplace dynamics all contribute to high burnout and low job satisfaction rates [36,37]. The COVID-19 pandemic is a recent global threat affecting the lives of common people and deteriorating society's economics stress-management resources, a supportive work environment, and opportunities for professional development and self-care are all critical components of such programs[38,39]. The climate crisis has had a substantial impact on the professional environment, creating extreme changes in weather patterns and contributing to the depletion of our natural phenomena' weather events and sources [40, 41]. These issues can have a significant impact on public health, hygiene, and sanitation [42, 43]. It has been necessary to adopt different intrusive strategies to control the infection due to the properties of this pandemic adherence to existing norms and practices, particularly in areas such as personal beauty routines[44], is critical in limiting the dangers of environmental climate change and crisis on workplace safety and contributing to the depletion of our natural phenomenon's weather events and sources [45, 46]. These factors can greatly affect public health, public hygiene, and sanitation [47]. A Considering the scope, it is challenging to have an analytical study and deep understanding based on real situations adhering to existing regulations and practices. These methods can be used to address a variety of public health strategies[43]. Data can also be included for potential behavior changes as reports of a new pandemic are being developed particularly in areas such as personal beauty routines[48]. Algorithms have been developed for setting parameters including vaccination rates and social distancing data, and is crucial in mitigating the risks of environmental climate change and crisis on occupational safety and hygiene, air pollution dust, associated with the quality of life of employees and cyber threats correlated with ethical concern [49].

5. CONCLUSIONS

This study demonstrates the significant role of graph theory and AI-driven modeling in understanding and predicting COVID-19 transmission dynamics. By integrating network centrality measures, community detection algorithms, and epidemic spreading models with machine learning techniques, the analysis reveals the complex structure of SARS-CoV-2 transmission. It provides a data-driven foundation for targeted interventions. Identifying high-centrality nodes and transmission clusters enhances the effectiveness of containment strategies, allowing for more precise and efficient public health responses. The incorporation of graph-based AI models, including Graph Neural Networks (GNNs) and reinforcement learning (RL)-driven intervention optimization, significantly improves infection forecasting and outbreak mitigation strategies. Comparing traditional SIR/SEIR models with AI-enhanced graph models highlights the superior predictive power and adaptability of network-based approaches in real-time epidemic control. The ability to simulate diverse intervention strategies, including targeted vaccination, localized lockdowns, and adaptive social distancing policies, further reinforces the practical value of graph-based AI methods in epidemiological decision-making. Despite these advancements, challenges such as data quality limitations, real-time network adaptation constraints, and computational scalability require ongoing research. Addressing these issues through improved data integration techniques, multi-agent simulations, and enhanced deep learning frameworks will further refine the applicability of graph-based AI models in pandemic response and infectious disease forecasting. This work underscores the transformative potential of graph theory and AI in epidemiological modeling, providing a powerful, flexible, and adaptive framework for public health planning. The insights gained from network-driven disease modeling will be instrumental in guiding future pandemic preparedness efforts, ensuring smarter, more effective, and data-driven intervention strategies in response to emerging infectious diseases.

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Conflicts Of Interest

The author's disclosure statement confirms the absence of any conflicts of interest.

Author Contributions

Conceptualization, A.V., N.S., J.A., A.B., and I.A.; methodology, A.V., N.S., I.A., and J.A.; software, A.V., N.S., I.A., and J.A.; validation, I.A.; formal analysis, N.S., I.A., and A.V.; investigation, I.A., A.V., and N.S.; resources, A.V., and I.A.; data curation, A.V., and I.A.; writing—original draft preparation, A.V., N.S., I.A., A.B., and J.A.; writing—review and editing, A.V., and I.A.; visualization, A.V., N.S., and I.A.; supervision, I.A.; project administration, I.A..

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