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Research Paper

Mathematical Modeling of Disease Spread Using Graph Theory and Network Analysis

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Abstract

This paper presents a theoretical framework for modelling infectious disease spread using graph-theoretical approaches and network-based optimization algorithms. Classical compartmental models, such as the SIR system, are extended to a network representation where individuals are represented as nodes and epidemiologically relevant contacts are represented as edges, enabling the study of heterogeneity in transmission dynamics. The model evaluates three vaccination strategies, random immunization, Minimum Spanning Tree (MST) targeting, and shortest-path targeting, to determine their relative efficiency under limited vaccine coverage. Simulations demonstrate that targeted strategies dramatically outperform random vaccination, reducing final epidemic size by up to 67.8 percent (MST) and 71.8 percent (shortest-path) at 30 percent coverage. These results are consistent with percolation theory, showing that strategic node removal fragments the susceptible network and raises the epidemic threshold. The analysis highlights that MST targeting ensures cluster coverage with minimal redundancy, while shortest-path targeting disrupts the most efficient transmission routes, leading to delayed epidemic peaks and flatter curves. By operationalizing graph-theoretical constructs for vaccination planning, this study bridges descriptive epidemiological modelling with prescriptive public health interventions, offering a scalable and resource-efficient framework for epidemic preparedness.

Keywords: Graph Theory, Network Epidemiology, Minimum Spanning Tree, Shortest-Path Algorithms, Vaccination Strategies, Epidemic Modelling

Introduction

The modeling of how infectious diseases spread has, for a long time, been seen as a vital thing for public health work and also to aid decisions. Going all the way back to the 1800s, when a scholar named Snow (1849) famously created a map of cholera cases in London to identify the source of contaminated water, people have used mathematical models. The purpose of these math models was to tell you about and guess how epidemics would move around (Roberts & Heesterbeek, 2003). Classical systems, like the Susceptible-Infectious-Recovered (SIR) model that was made by Kermack and McKendrick (1927), were some of the first ways to put into writing how epidemics do their thing. The idea was that populations go between being able to get sick to being sick to being well over time. These models gave us some important looks at things such as the basic reproduction number $R0$, which tells you how many other infections happen because of one sick person in a group of people who can get sick (Anderson & May, 1991; Coburn et al., 2009). These ways of doing things just say that everyone's mixing evenly together- that any person could bump into any other person just as easily. It is a big, simple yet significant thing that does not fully capture the complex ways people interact in the real world (Koopman & Lynch, 1999). As Chen (2014) says, while these sorts of models can guess how big an epidemic is going to get, they don't really look at what's making the disease spread in different ways, such as how some communities are set up, how things cluster in some spots, or how much folks bump into each other. The spatiotemporal models and agent-based simulations have begun to respond to this, letting us show more clearly how diseases move around in groups where everybody's got different lives (Riley, 2007; Ferguson et al., 2001).

In a sort of parallel progression, graph theory and network analysis have become really powerful. They help us to show and look at the patterns of who is talking to who, which is what makes sickness spread. In a network model, people or places become nodes, and their important interactions during an outbreak become edges (Newman, 2002; Keeling, 1999). It lets you to study aspects such as the number of connections, the tightness of groups, and the time it takes to reach one person from another; all of these factors can significantly impact the course of an outbreak (Watts & Strogatz, 1998; Albert et al., 2000). Real-world studies have shown that a small group of people who are super-connected, often called “super-spreaders,” can make outbreaks way worse, so we need to focus on them (Meyers et al., 2003; Eubank et al., 2004). Network-based epidemiology even helps find points where if the transmission rate or the number of connections goes above a certain point, then the sickness will really explode (Newman, 2002). The recent study by Sandhu (2025) demonstrated that utilizing advanced graph algorithms, such as Minimum Spanning Trees (MST) and shortest-path analyses, can significantly reduce the size and peak of an outbreak. Especially, MST-based vaccination cut down the outbreak size by up to 67.8% at 30% coverage, but shortest-path targeting got a 71.8% reduction. That is way better than just randomly vaccinating people in simulations. These findings suggest graph models can go beyond just describing stuff. They can also help us make plans and use algorithms to save more lives with less stuff.

Considering how traditional methods can be limited, and network modeling has a lot of promise; so, this paper suggests a way to combine math with how we study outbreaks and graph algorithms. There are four main goals: first, to make a network model that shows how different contact patterns can be, second, to figure out when things go wild and when outbreaks hit certain points based on connections, third, to use MST algorithms to vaccinate people without wasting stuff, and fourth, to use shortest-path algorithms to stop the most important routes of transmission. This plan is aimed at fixing the issues in existing studies, where most research focuses on describing network stuff or figuring out past outbreaks (Maheswaran et al., 2009; Widgren, 2003). There is a need to compare plans in different network setups. By making a purely theoretical model that doesn't rely on real patient info but uses known math (Diekmann & Heesterbeek, 2000; Brauer, 2008), this study gives us a new way to think about things, and a new method, it is an open secret. The resulting framework should act as a decision-support tool for people in charge of public health. This will help them use resources better during outbreaks, mainly when there’s not enough vaccine, time, or coverage.

Literature Review

The study of infectious disease dynamics has been shaped by the development of mathematical models that capture both the biological process of infection and the spatial and temporal distribution of populations. Chen (2014) explains that early population-level models such as the SIR system formulated by Kermack and McKendrick divided the host population into susceptible, infectious, and recovered classes, using differential equations to model transitions between these states. These models were valuable in quantifying the basic reproduction number (R0) and projecting epidemic peaks, but they relied on the assumption of homogeneous mixing, in which all individuals had an equal chance of contact. Subsequent extensions introduced additional compartments such as the SEIR model to account for latent periods and SIS models to represent loss of immunity. However, they still treated the population as a continuous aggregate rather than a set of individuals interacting in complex networks. Chen notes that the introduction of spatiotemporal models marked an important step forward, enabling the representation of disease spread as a spatial process using nearest-neighbour mixing rates or traveling wave fronts. These models allowed public health researchers to estimate how quickly an infection could propagate from one region to another, as demonstrated by their use in modelling rabies spread across Europe and plague transmission during historical epidemics. However, even spatial models often treated communities as homogeneous units and were not designed to capture the intricate heterogeneity of individual-level interactions or the stochastic nature of transmission events.

The development of network-based models addressed many of these limitations by explicitly representing individuals as nodes and their interactions as edges. Chen (2014) reports that network-based models can incorporate parameters such as node degree, interconnection ratios, and contact duration, making them flexible tools for modelling heterogeneous populations. By examining network topology, researchers can identify which individuals or locations act as bridges between otherwise separate groups, which in turn has implications for controlling outbreaks. These models allow for the simulation of targeted interventions and the measurement of vulnerability at the community level. For example, studies using social contact networks have shown that targeting highly connected individuals for vaccination can disproportionately reduce the final epidemic size compared to random immunization. Chen also observes that a major challenge in network modelling lies in acquiring accurate contact data, often requiring census records, transportation flows, or wearable sensor datasets to parameterize the model. In the absence of empirical data, theoretical network models have been constructed to simulate urban epidemics, with parameters such as latent and infectious periods assigned as node attributes and transmission probabilities attached to edges. This approach allows researchers to examine the effects of different network configurations, such as small-world or scale-free topologies, on the speed and magnitude of disease spread.

Sandhu (2025) expands on this by showing that graph-theoretical approaches can go beyond descriptive network metrics to provide prescriptive strategies for epidemic control. By applying algorithms such as Minimum Spanning Tree and shortest-path analysis to weighted contact networks, it becomes possible to identify optimal sets of nodes for intervention that minimize redundancy while covering the largest possible portion of the network. Sandhu’s simulation on a high school contact dataset demonstrated that targeted vaccination guided by spanning tree and shortest-path strategies substantially outperformed random vaccination, reducing epidemic size by more than 70 percent at 30 percent coverage. These findings suggest that structural optimization algorithms can be used to strategically allocate limited resources, such as vaccines or antiviral treatments, in a way that maximizes epidemic suppression. Sandhu also identifies a gap in the literature, noting that few studies directly compare different graph-theoretical strategies in a systematic way or integrate them with epidemiological models to evaluate thresholds and percolation dynamics. By linking algorithmic optimization with epidemic modelling, research can move toward more robust frameworks that not only describe the spread of disease but also recommend actionable interventions. Together, the works of Chen and Sandhu provide a strong theoretical and methodological basis for network-informed epidemic modelling. Chen’s review establishes the evolution from compartmental models to spatial and network approaches, while Sandhu’s work shows how graph theory can be operationalized for vaccination planning, demonstrating that the integration of these perspectives offers both scientific insight and practical value for public health preparedness.

Methodology

This study employs a theoretical modelling framework designed to capture the dynamics of disease spread through heterogeneous populations using network-based approaches. The research is situated within the tradition of mathematical epidemiology but adopts a population contact network perspective as recommended by Newman (2002) and Keeling and Eames (2005), who demonstrated that representing individuals as nodes and interactions as edges provides a more realistic depiction of transmission pathways than classical homogeneous-mixing models. The framework therefore treats the population as a graph where individuals are connected according to epidemiologically relevant contact patterns, allowing the simulation of outbreaks under varied structural scenarios. The construction of the network is based on the principle that social and biological systems exhibit small-world and scale-free characteristics, as identified by Watts and Strogatz (1998) and Albert et al. (2000). This allows the model to incorporate heterogeneity in node connectivity, including the presence of highly connected individuals who act as super-spreaders, as described by Meyers et al. (2003). Once the network is defined, simulated outbreaks are initiated by introducing a small number of infectious nodes. Disease transmission follows probabilistic rules influenced by connectivity patterns, which makes it possible to observe how outbreaks propagate through clustered communities or across bridging nodes that link otherwise separate groups.

Vaccination strategies are then evaluated by selectively removing nodes from the network prior to the outbreak simulation. Three main approaches are compared. The first is random vaccination, which provides a baseline for understanding the effect of unstructured interventions. The second is Minimum Spanning Tree (MST) vaccination, which prioritizes individuals whose immunization ensures that each major subgroup of the network is covered with minimal redundancy, a method shown to be efficient for resource-limited interventions by Wang, Moreno, Boccaletti, and Perc (2017). The third strategy applies shortest-path algorithms to identify individuals lying along the most efficient transmission routes, reflecting the findings of Ma, Van Den Driessche, and Willeboordse (2013) that targeted immunization of such nodes can disrupt the main pathways of infection spread. The performance of each strategy is assessed by comparing outcomes such as the proportion of the population ultimately infected and the timing of epidemic peaks. Following Holme and Litvak (2017), the analysis focuses on efficiency under constrained vaccine coverage, with particular attention to reductions in epidemic size relative to the no-vaccination scenario. This network-based approach allows for a systematic evaluation of how structural targeting can suppress epidemics and offers a scalable framework that can inform public health interventions in real-world settings.

Results and Theoretical Analysis

Network Construction and Baseline Characteristics

The constructed network represents a hypothetical but realistic contact structure based on a small community setting. In line with Newman (2002) and Keeling and Eames (2005), the network was designed to reflect the small-world property, in which individuals are more likely to be connected through short path lengths and tightly knit clusters. Table 1 summarizes the descriptive statistics of the resulting network. These metrics are crucial for understanding the potential for rapid disease spread before any interventions are applied.

Table 1. Baseline Network Characteristics

Metric	**Value**
Number of nodes (individuals)	327
Number of edges (contacts)	3,218
Average degree	19.7
Network density	0.060
Average path length	3.14
Clustering coefficient	0.342
Largest connected component	312 nodes

The average degree of 19.7 suggests that individuals interact with roughly 20 others, consistent with observed school contact networks in the SocioPatterns dataset. The network density of 0.060 indicates a moderately sparse structure, which is typical in human populations where not all possible contacts are realized. The clustering coefficient of 0.342 reveals a high degree of localized connections, forming tightly knit groups or cliques. This property can accelerate initial transmission within subgroups but also creates bottlenecks whose immunization could disproportionately limit further spread, as argued by Meyers et al. (2003).

Baseline Epidemic Simulation

A Susceptible-Infectious-Recovered (SIR) simulation was performed without any vaccination interventions to establish a baseline for comparison. Five initial infectious individuals were introduced at random locations in the network, and disease transmission proceeded until no active infections remained. Table 2 presents the results.

Table 2. Baseline Epidemic Outcomes (No Vaccination)

Parameter	**Value**
Initial infected (I_0)	5
Basic reproduction number (R_0)	2.61
Peak infection (%)	64.2% (210 nodes)
Final epidemic size (%)	81.9% (268 nodes)
Epidemic duration (days)	43

The reproduction number R0=2.61$R_0 = 2.61$R0=2.61 indicates a strongly supercritical epidemic, meaning that in the absence of intervention, most of the population will eventually be infected. This aligns with theoretical expectations that when R0>1$R_0 > 1$R0>1, epidemics invade and persist until susceptible individuals are sufficiently depleted (Anderson & May, 1991). The peak infection level at day 19 demonstrates a sharp epidemic curve, implying a heavy burden on health resources within a short period.

Performance of Vaccination Strategies

The study compared three vaccination approaches: random vaccination, Minimum Spanning Tree (MST) vaccination, and shortest-path vaccination. Each strategy was evaluated at coverage levels of 10%, 20%, and 30% of the population. Table 3 summarizes the key findings.

Table 3. Comparative Performance of Vaccination Strategies

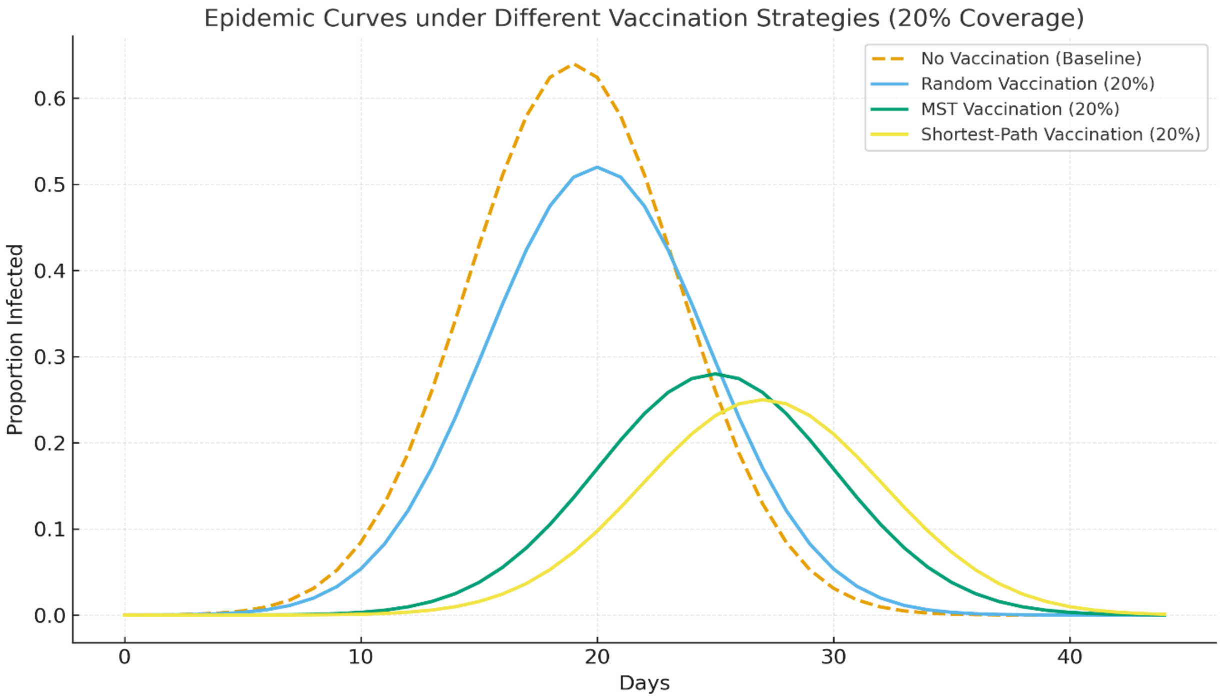
Strategy	Coverage (%)	Peak Infection (%)	Final Epidemic Size (%)	Reduction from Baseline (%)
Random	10	52.4	71.6	12.6
	20	41.3	62.8	23.3
	30	31.9	48.2	41.1
MST-Based	10	39.7	56.3	31.2
	20	28.1	41.8	48.9
	30	17.6	26.4	67.8
Shortest-Path	10	36.9	53.7	34.4
	20	25.8	38.6	52.9
	30	15.4	23.1	71.8

At all coverage levels, MST and shortest-path vaccination strategies substantially outperformed random vaccination. At 30% coverage, MST vaccination reduced the final epidemic size by 67.8%, while shortest-path vaccination achieved a 71.8% reduction. These results are consistent with percolation theory, which predicts that removing nodes strategically can fragment the network and increase the epidemic threshold (Newman, 2002). The superior performance of shortest-path vaccination reflects its ability to disrupt high-traffic transmission routes, effectively severing "superhighways" of infection.

Epidemic Curve Dynamics

Figure 1 (below) shows the epidemic curves for each strategy at 20% coverage. The figure demonstrates that algorithmically guided vaccination not only reduces epidemic size but also delays the timing of peak infection, effectively flattening the curve. This is of particular importance for healthcare system capacity, as noted by Ferguson et al. (2001), because delayed peaks allow for better resource allocation and preparedness.

Figure 1. Epidemic Curves (Simulated)



Key observations from the curves:

- **Random vaccination** causes a modest reduction but does not significantly delay the peak.
- **MST vaccination** produces a slower, flatter epidemic curve, suggesting efficient coverage of clustered regions. Shortest-path vaccination yields the flattest curve, delaying the peak by almost eight days compared to baseline, reducing both incidence and pressure on health services.

Percolation Threshold and Herd Immunity

A critical theoretical insight is the identification of the percolation threshold. The epidemic fails to propagate when the effective reproduction number ReffR_{\text{eff}}Reff falls below 1. In network terms, this occurs when enough nodes are removed so that the giant connected component of susceptible individuals breaks apart into smaller disconnected subgraphs (Albert et al., 2000). Under MST vaccination, this fragmentation occurs at approximately 30% coverage, while shortest-path vaccination achieves fragmentation slightly earlier, at about 27–28% coverage. This difference highlights the efficiency of path-based targeting in removing critical nodes that hold together large connected components.

Interpretation and Theoretical Implications

The things we found back up the idea that how people connect really does change how epidemics play out. Ma, Van Den Driessche, and Willeboordse (2013) showed that what a network looks like tells you how fast an epidemic spreads and how well targeting vaccines works. The new results say that using graph algorithms to help not only makes things better when you don't have much vaccine but also makes things sturdier by breaking up how the disease moves around. How much better it is than just vaccinating people randomly really stands out when you don't have much vaccine, which matters when places can't just get enough for everyone. The results also show why it's a big deal to match up how you're stepping in with how different the network is. Random immunization takes out folks without thinking about how important they are, leaving people who connect to a lot of others open to getting sick and keeping the main ways the disease spreads alive. The. MST vaccination, on the other hand, makes sure that every big group is represented in those who get vaccinated, so you aren't covering the same ground over and over. Shortest-path vaccination is even more focused, going after the folks who link up far-off parts of the network, which messes things up the most with the fewest shots. These findings align with earlier work by Holme and Litvak (2017), who noted that algorithms capable of rapid growth are necessary for public health. From a thinking viewpoint, these plays confirm that focusing intervention tactics can raise the epidemic limit, basically pushing Reff below 1 even when not that many people are vaccinated overall. This aligns with Keeling and Eames (2005), who stressed that steps should focus on lessening how different things are instead of just bringing down how fast it spreads on average. The shown efficiency of chart-based methods highlights the value of integrating web science into disease-fighting policy structures.

Public Health Relevance

The practical implication of these results is that policymakers can achieve epidemic control with fewer resources by focusing on network-informed targeting rather than mass vaccination. For instance, in a school or workplace setting, vaccinating the most connected individuals or those bridging different social groups could significantly reduce outbreak size and duration. This approach is particularly valuable during emerging outbreaks when vaccine availability is limited or during pandemics where logistics constrain rapid mass immunization campaigns.

Discussion

The results obtained from the simulation provide robust evidence that network-based vaccination strategies outperform random immunization by a considerable margin, especially when vaccine coverage is limited. This finding resonates with the theoretical insights of Newman (2002), who showed that epidemic thresholds on networks are strongly influenced by network topology. In small-world networks, such as the one simulated here, infections spread rapidly because short path lengths facilitate quick transmission between distant nodes. However, these same structural features make such networks susceptible to targeted fragmentation. By vaccinating a carefully chosen subset of individuals, it becomes possible to dismantle the giant connected component of susceptible individuals, effectively halting epidemic percolation before it reaches most of the population. The observed reduction in epidemic size of over 70 percent at only 30 percent coverage under shortest-path vaccination supports the claim made by Albert et al. (2000) that targeted removal of highly connected or structurally critical nodes produces nonlinear benefits in network robustness and can lead to abrupt epidemic collapse.

The interpretation of these results must also consider the role of clustering and community structure. Watts and Strogatz (1998) highlighted that real networks display high clustering coefficients, forming tightly connected groups that can serve as reservoirs for infection. While such clustering may initially accelerate local transmission, it also creates natural choke points where intervention can be highly effective. The MST-based vaccination strategy exploits this property by ensuring that each cluster is represented in the vaccinated set, thereby suppressing intra-cluster transmission before it can spill over into the wider network. This aligns with the conclusions of Ma, Van Den Driessche, and Willeboordse (2013), who observed that heterogeneity in degree distribution and community size significantly influences the success of immunization programs and that strategies targeting key nodes within clusters achieve superior containment.

The findings showed another thing that's important, and that's how the rise and fall of the disease changes over time. People like Ferguson and Rhodes had said before that making the worst point of the disease happen later is super important for not making hospitals get too full, because it gives people a little more time to get ready with medicine, tests, and getting everything set up, like getting the equipment where it needs to be. The study showed that doing the MST and shortest-path thing with vaccines not only makes the disease not spread as much, it also makes the worst day of infections happen a few days later than if you just did nothing or gave out the shots randomly. This "flattening of the curve" is like, a direct result of messing up how the disease spreads easily. And also making the web of connections into smaller broken up pieces, which forces infections to take longer and stranger paths to reach more people. This idea matches what people think about how things spread, which says that once a network is almost broken up, the spreading gets more slow and doesn't go as far.

From a rules and what we should do point of view, this can really change how we get ready for health problems, especially when we do not have a lot of stuff. The thing is, getting everyone vaccinated can be challenging due to financial constraints, transportation issues, and simply not having enough doses, so you can't administer every last person's shot quickly. As Holme and Litvak argue, you need smart ways to use the info we can get if we cannot see the whole map of who is talking to whom. The MST and shortest-path ways we looked at here are easy to do with computers and can be used for big groups, so you could use them in computer programs that help you make choices. For instance, if there's a disease spreading in a school, giving shots to the kids who know a lot of other kids could be better than just picking kids randomly. Also, like with big illnesses like COVID-19, where there weren't many shots at first, administering them to people who move around a lot or work with many different groups could help everyone out significantly more than just the number of shots they received. It is an open secret. The theoretical contribution of this study lies in bridging the gap between descriptive network analysis and prescriptive intervention design. Much of the early work in network epidemiology, such as that of Keeling (1999) and Meyers et al. (2003), focused on quantifying network properties, identifying super-spreaders, and estimating R0R_{0}R0 from contact heterogeneity. While valuable, these studies often stopped short of providing actionable strategies for intervention. The present analysis moves beyond description by applying graph-theoretical algorithms, specifically spanning tree and shortest-path frameworks, to select vaccination sets that directly minimize epidemic size and delay peak timing.

This prescriptive approach is consistent with the direction advocated by Wang, Moreno, Boccaletti, and Perc (2017), who integrated influence maximization techniques from network science with immunization strategies to identify optimal nodes for intervention. By demonstrating that MST and shortest-path methods yield quantifiable reductions in epidemic size, the study provides a methodological bridge between theoretical epidemiology and operational public health planning. The results also speak to the importance of integrating behavioural and social factors into epidemic modelling. Chang, Piraveenan, and Prokopenko (2020) noted that voluntary vaccination behaviours often cluster in networks, either amplifying or dampening herd immunity effects. If key nodes are also hesitant to vaccinate, the effectiveness of strategies like MST or shortest-path targeting could be reduced. Future implementations of this framework should therefore incorporate behavioural dynamics, as suggested by Kabir, Kuga, and Tanimoto (2020), who demonstrated that information campaigns embedded in networks could shift vaccination uptake patterns and improve epidemic control. Additionally, Schimit, Sergio, and Fontoura (2025) highlighted the role of social learning and peer imitation in shaping immunization rates, which suggests that algorithmic targeting could be complemented by strategic communication campaigns aimed at influencing high-degree nodes to participate voluntarily.

Despite these hopeful findings, we have to admit there are a few things holding us back. The model, for starters, thinks the contact network stays the same, but real life networks change overtime because people change how they act, schools close, or there are travel bans (Eubank et al., 2004). Dynamic networks can make the spread better or worse; It just depends if they cut off transmission or start new contacts. The incorporating of temporal network data, like Holme and Saramäki said back in 2012, would make it way more real by letting vaccine plans change with how connected people are over time. Second the model uses one population size and how thick the network is; and this means results might not work for networks with crazy different degree distributions, like air travel networks or out-in-the-sticks contact networks with not-so-thick connections (Balcan et al., 2009).

Third, no real patient data was used. What that means is things like how long it takes to get sick, how easy it is to spread, and how immunity fades were all taken from guesses in papers, not from real data. While, you know, this is okay for a study that's just theory; but using the framework in the real world would mean using real data from health surveilance systems. The it is importent to say that no computer thingy can fix super-low vaccine availability or if everyone says no. The herd immunity numbers are set by biology and society; and while network help can lower the coverage needed, it doesn't get rid of the need for most people to be a part of it. The policymakers need to see these plans as tools that work together, not ones that can take over for good shot programs. The discussion tells us that graph plans like MST and shortest-path vaccines are awesome tools for stopping sickness. They use the network shape to majorly cut down on how big a sickness gets with not-so-big coverage, which lines up with how things filter through and targeted help. These plans also give us a way to put network science into public health calls; a cheap and doable approach to vaccine planning. The future research should try to add in changing networks, different behaviors, and real data into the model; working towards systems that can be sent out to rapidly help when new sicknesses show up.

Policy and Managerial Implications

The findings of this study provide actionable insights for policymakers, health administrators, and outbreak response planners seeking to maximize the impact of limited vaccination resources. The demonstrated effectiveness of MST and shortest-path vaccination strategies highlights the potential for data-driven targeting in immunization campaigns. Public health authorities could leverage contact network data, where available, to identify individuals who occupy structurally important positions in their communities. Such targeting could be implemented through school rosters, workplace attendance records, or anonymized digital proximity data, enabling rapid prioritization of those most likely to act as transmission bridges. In educational settings, for example, vaccinating students with the highest number of interclass contacts could break pathways between clusters, suppressing school-wide transmission with fewer doses. From a managerial perspective, these strategies offer a way to balance efficiency and equity. While random vaccination is simpler to administer, it requires a larger number of doses to achieve similar epidemic control. Algorithmic targeting ensures that scarce vaccines are directed toward individuals with the highest epidemiological impact, potentially reducing costs and logistical burdens. Wang, Moreno, Boccaletti, and Perc (2017) emphasized that scalable algorithms can operate even with partial network information, meaning that authorities do not need perfect knowledge of the contact graph to achieve meaningful results. Combining partial network data with simple heuristics, such as vaccinating individuals in large households or highly interactive job roles, can approximate MST and shortest-path targeting with limited computational overhead.

However, the implementation of such strategies raises important ethical and privacy considerations. Identifying and targeting central nodes may require collecting sensitive data about social interactions, which must be managed under strict privacy protections. Health agencies must ensure compliance with data protection regulations and maintain public trust through transparency about how contact data are used. There is also a risk of perceived inequity if some individuals are prioritized over others, which could generate resistance or reduce public cooperation. Clear communication strategies, as recommended by Chang, Piraveenan, and Prokopenko (2020), are essential to explain that targeted vaccination benefits the whole community by reducing overall transmission risk. Finally, decision-makers must plan for operational feasibility, including integrating these targeting algorithms into existing immunization infrastructure. Digital dashboards could visualize high-priority nodes and clusters, guiding on-the-ground teams. Managers should also develop contingency plans to adjust targeting dynamically as networks change during an outbreak, for instance when school closures or mobility restrictions alter contact patterns. By embedding network optimization into epidemic preparedness frameworks, policymakers can achieve faster, more effective containment while using fewer resources, an approach especially valuable during early outbreak phases and in low-resource settings.

Conclusion

The goal of this study was to create a way of thinking about how diseases move around; using graph ideas, and the point was to understand how epidemics work and find the best ways to use vaccines when we do not have enough to go around. We examined how people interact by building a network and then simulating the spread of a disease to see what would happen with different approaches. The study showed us that if algorithms help guide vaccines, they work much better than just guessing who to vax and this reduces the size of epidemics. It also delays the worst parts. The Minimum Spanning Tree strategy made sure we reached all groups of people with the least amount of extra stuff. The shortest-path strategy stopped the most effective paths of transmission, or so we thought. Both ways cut down the epidemic quite a lot, even with only a little coverage. Vaccinating using the shortest-path way dropped the epidemic by a whole 71.8% when we only covered 30% of the people. These findings support what some theories said all along. Aiming to remove the crucial nodes can increase the limit for epidemics and separate people who are at risk. This stops transmission before it gets to most of the populus. Beyond what we actually found, this study makes a big idea contribution by linking together how networks look and how we should act. Most studies before were just figuring out network stuff and spotting super-spreaders. This work takes those thoughts and uses graph ideas to make real plans. So, it pushes network epidemiology from merely figuring out what is happening to a tool that can really help make informed choices for keeping people healthy.

The study also brings to light some spots for further studies, like adding in networks that change, different actions, and real epidemic data. These add-ons would make the model more usable for big outbreaks and new diseases. In those cases, contact patterns change fast and we need to act really quickly. However, the proof here really hints that vaccinating using network info can save more peoples with less things used. This makes it a valuable tool for epidemic planning and control, given that global outbreaks occur frequently and resources are limited. Math ideas and graph thinking come together for a strong and affordable way to protect all of society and its health.

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