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Computational modeling of infectious diseases: insights from network-based simulations on measles

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Abstract

Background Computational modelling of disease spread is crucial for understanding the dynamics of infectious outbreaks and assessing the effectiveness of control measures. In particular, network-based models for disease spreading offer detailed, granular insights into heterogeneous interactions and enable dynamic simulation of intervention strategies. Therefore, they offer valuable insights into the factors influencing disease spread, enabling public health authorities to develop effective containment strategies. Vaccination is among the most impactful interventions in controlling disease spread and has proven essential in preventing the spread of infectious diseases such as measles. However, recent trends indicate a concerning decline in the fraction of vaccinated individuals in various populations, increasing the risk of outbreaks.

Methods In this study, we utilize computational simulations on graph-based models to analyze how vaccination affects the spread of infectious diseases. By representing populations as networks in which individuals (nodes) are connected by potential spread pathways (edges), we simulate different vaccination coverage scenarios and assess their impact on disease spread. Our simulations incorporate high and low vaccination coverage to reflect real-world trends and explore various conditions under which disease spread can be effectively blocked.

Results The results demonstrate that adequate vaccination coverage is critical for halting outbreaks, with a marked reduction in disease spread observed as the fraction of vaccinated individuals increases. Conversely, insufficient vaccination rates lead to widespread outbreaks, underscoring the importance of maintaining high vaccination levels to achieve herd immunity and prevent resurgence. These findings highlight the vital role of vaccination as a preventative tool and emphasize the potential risks posed by declining vaccination rates.

Conclusion This study provides a deeper understanding of how vaccination strategies can mitigate the spread of infectious diseases and serves as a reminder of the importance of maintaining robust immunization programs to protect public health.

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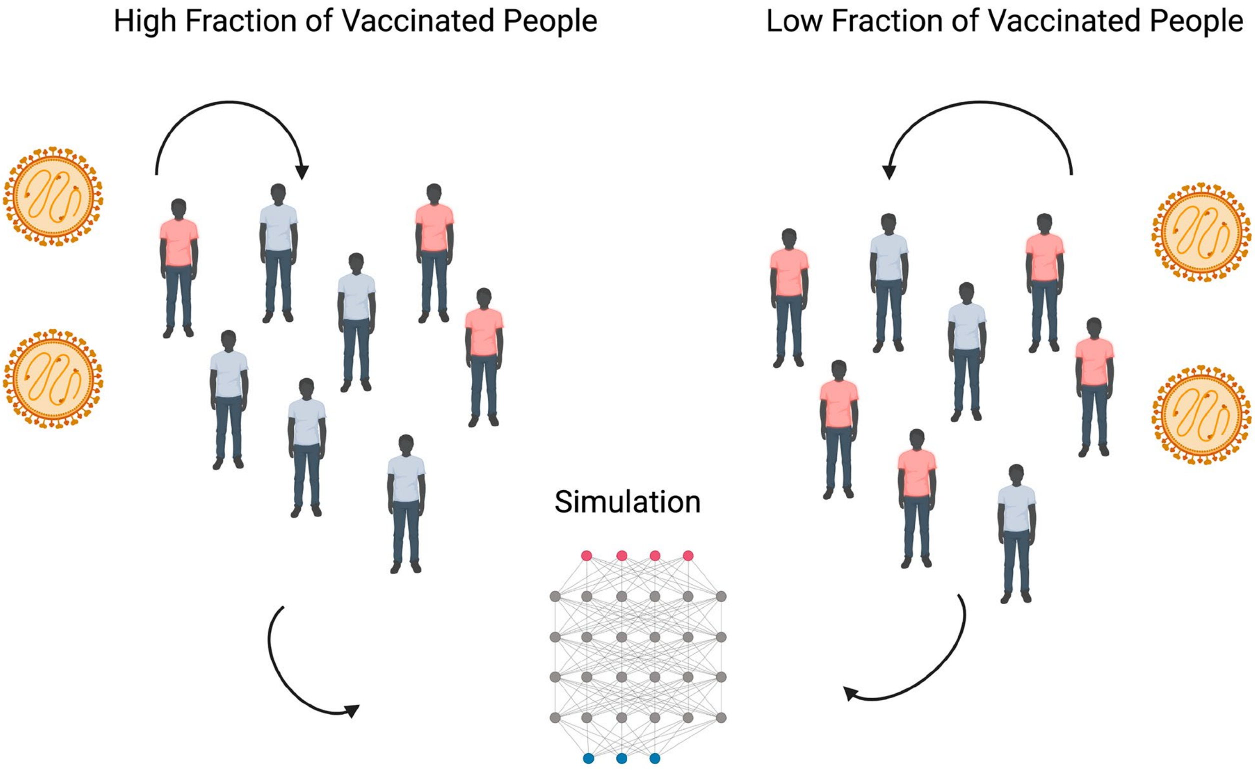
Graphical Abstract



Keywords Infectious disease modeling, Vaccination strategies, Measles outbreaks, Graph-based simulations, Network epidemiology, Disease spread dynamics

Introduction

The COVID-19 pandemic has shown that control of spread of infectious diseases requires the design and implementation of complex strategies of public health intervention [1]. These lessons may be relevant to control the spread of other diseases like measles [1, 2].

In this complex landscape, computational simulations grounded in mathematics and computer science [3] allow to dynamically observe the spread of the diseaseand pinpoint variables crucial for altering disease progression [4] such as guiding vaccination strategies and predicting disease onset and spread within populations [5].

The importance of studying infectious disease vaccination strategies and the impact of vaccination coverage is crucial; effective vaccination can significantly mitigate the spread of highly infectious diseases and prevent large-scale outbreaks [4, 6].

Computational modeling is crucial in this endeavor because it allows for the simulation of various scenarios and interventions, providing insights into potential future outcomes without the need for real-world testing. Specifically, network-based approaches are advantageous as they realistically model how diseases spread through social connections and geographical proximity. By incorporating the structure of human interactions into simulations, network models can predict localized outbreaks and the effectiveness of targeted vaccination campaigns, thus enhancing the precision of public health responses [7–10]. These models not only forecast outbreaks but also evaluate the impact of vaccination strategies on heterogeneous population [11, 12] as represented in Fig. 1.

In this work, we particularly examine how vaccination coverage influences the prediction and management of potential outbreaks of Measles [13–15]. Measles, a highly infective virus with a basic reproduction number (R0) between 12 and 18, serves as a key case study [16]. Despite an effective vaccine, recent declines in vaccination rates have led to a resurgence of measles globally [17, 18] highlighting the vital need to maintain high vaccination coverage and continuous genetic surveillance to prevent outbreaks [19–21]. The virus, belonging to the genus *Morbillivirus*, is characterized by its high basic reproduction number (R0) of 12–18, making it one of the most infectious human pathogens [16]. Recent years have seen a resurgence of measles outbreaks in various parts of the world, largely attributed to declining vaccination rates [17]. This emphasizes the critical need for maintaining high vaccination

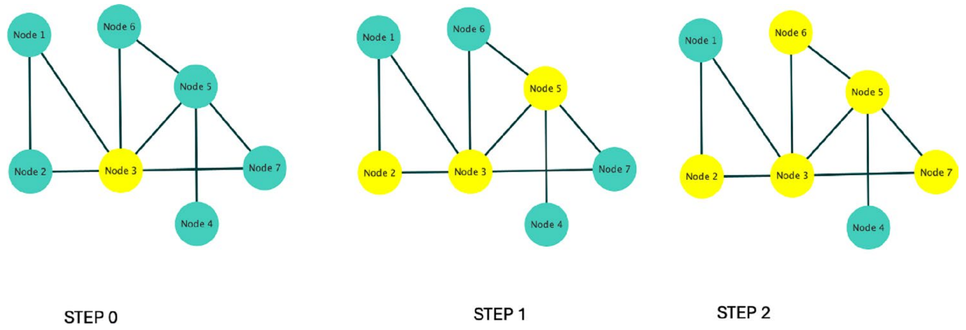


Fig. 1 Contact-based model representation of disease spread in a population. Blue nodes represent susceptible or recovered individuals, while yellow nodes indicate infected individuals. The model demonstrates how disease spread is influenced by both the characteristics of the pathogen and the structure of the contact network

coverage and uninterrupted genetic surveillance to monitor and mitigate the risk of outbreaks [18].

For example, studies have shown that supplemental immunization can drastically reduce measles risk in highly vaccinated communities [22]. Furthermore, targeted vaccination efforts in susceptible regions can curb the spread of outbreaks, emphasizing the critical role of computational approaches [4, 13, 15, 23, 24].

By integrating computational models with a network-based approach, this work aims to refine our understanding of disease dynamics and enhance the strategic deployment of vaccinations. We use a network-based model to analyze the impact of vaccination coverage on the spread of measles. This approach allows us to simulate how the disease transmits through various types of interpersonal connections and assess the effectiveness of vaccination programs in curbing its spread. By modeling different scenarios, we can observe how changes in vaccination coverage affect the dynamics of the disease across diverse population structures. This method provides a robust framework for understanding the potential benefits of increasing vaccine uptake and its crucial role in public health strategies.

To underscore the importance of vaccination, we utilize various network models to reflect different community interactions and social behaviors. These models help demonstrate the significant role that vaccination plays in controlling measles outbreaks under varying conditions. Our findings consistently indicate that vaccination is a key factor in mitigating the spread of measles. By presenting these different scenarios, the research highlights how essential widespread immunization is, regardless of the community structure or the network model used. This reinforces the universal value of vaccination campaigns in preventing the spread of infectious diseases like measles.

Main contribution of this paper are:

1. Developing a computational model that simulates the impact of vaccination on infectious disease spread across different network structures.
2. Demonstrating that increasing vaccination coverage consistently reduces disease spread potential across various network topologies.
3. Showing that vaccination effectiveness is independent of specific network structures or disease characteristics, serving as a universal mechanism for mitigating disease spread across different population contact patterns.
4. Providing quantitative evidence through simulations that supports the critical role of maintaining high vaccination coverage for controlling outbreaks, with significant implications for public health policy and intervention strategies.

The paper is organized as follows: the Methods section describes the computational modeling approach used, including the network models used and the simulation framework implementation. The Results section presents the findings on the impact of vaccination rates on virus diffusion and the implementation of vaccination campaigns across different network structures. The Discussion interprets these results in the context of public health strategies and disease control, while the Conclusion summarizes the key findings and their implications for vaccination policies.

Materials and methods

The Italian National Institute of Health (known as Istituto Superiore di Sanità (ISS)) publishes periodic surveillance reports on measles cases (https://www.epicentro.iss.it/morbillo/bollettino), collected through the Integrated Measles-Rubella Surveillance System, established in 2007 to monitor epidemiological situation of measles in accordance with the “National Plan for the Elimination of Measles and Congenital Rubella 2010–2015” (https://www.epicentro.iss.it/morbillo/PianoEliminazioneMorbilloRosoliaCongenita2010-2015), and coordinated by the Department of Infectious Diseases at the ISS, which also manages the MoRoNET network of accredited laboratories to ensure laboratory confirmation and genotyping of cases.

However, significant pre-processing was required to make these data usable for research purposes. The original reports are published in PDF format, which poses several challenges as some key details are embedded in narrative sections, while others are presented in tabular format with different layouts depending on the topics. In addition, inconsistencies in terminology and formatting required careful handling to ensure data uniformity. To address these issues, we implemented a multi-step data extraction and structuring process. First, we converted the PDF files into machine-readable text using optical character recognition (OCR) when necessary. We then applied automated parsing techniques to extract tabular data, leveraging regular expressions and pattern recognition to correctly identify relevant fields. For unstructured text, we employed natural language processing (NLP) methods to extract key epidemiological details, such as case demographics, vaccination status, and clinical outcomes. Given the variability in data presentation across reports, we performed manual validation to correct misclassifications, resolve ambiguities, and standardize terminology. Finally, we structured the extracted data into a coherent format, ensuring consistency across all records. The resulting dataset includes information on key epidemiological parameters such as demographic details, including the age and sex of reported cases, as well as geographic information down to the regional level. Clinical details, such as the presence of comorbidities, and vaccination status are also recorded, specifying whether individuals received the first dose, second dose, or no dose of measles vaccine. In addition, the dataset contains information on case severity, including the number of individuals who required hospitalization or emergency medical care.

To enhance accessibility, we have structured the dataset into separate folders, each corresponding to a specific surveillance year, named sequentially from the first to the last available year. Each folder contains: (i) a subfolder named “bulletins”, which includes all the PDF bulletins published in that year; (ii) a subfolder named “surveillance”, which is organized into multiple CSV files, each corresponding to a specific epidemiological characteristic extracted from the text. These files provide data on the national and regional trends of measles cases, as well as information categorized by age group and the presence of comorbidities. Data used in this study covers the period from 2014 to September 2024, with the latest update available at the time of submission of the work. However, the dataset continues to be updated on a monthly basis, ensuring that the latest surveillance data remain available at https://tinyurl.com/measles-data-ita. Furthermore, to facilitate real-time data exploration and visualization, we have developed “MeaslesTracker”, an interactive web application that enables users to analyze trends, apply dynamic filters, and generate visual representations of measles incidence. The application is accessible at https://tinyurl.com/measles-tracker-ita.

To model the spread of measles, we considered different types of random network networks: (i) Erdős-Rényi; (ii) Random Geometric Graph (RGG); and (iii) stochastic block model (SBM). An Erdős-Rényi network is a type of random graph where each pair of nodes is connected with a fixed probability, resulting in a structure that follows a Poisson degree distribution. This model is widely used in social network analysis because it simulates the random formation of links between individuals, mirroring real-world scenarios where connections are established independently without any influence from existing relationships [25]. In contrast, the SBM organizes nodes into distinct communities or blocks and assigns different probabilities for forming edges based on whether nodes belong to the same group or different groups. This makes SBM particularly useful for modeling social networks that exhibit community structures, where individuals form tightly-knit groups with frequent internal connections, resembling cliques or social clusters [26, 27]. A RGG, on the other hand, is created by placing nodes in a continuous metric space, with connections established between nodes that fall within a specified distance from each other. This model captures the influence of spatial proximity, representing either physical closeness or social similarity, and is often used to model networks where geographic or social proximity impacts how communities form and interact [28].

For our simulations, we generated an initial network for each structure with 10,000 nodes. To ensure robustness, we maintained the same network structure throughout multiple simulations while varying only the number of vaccinated individuals. Additionally, to introduce variability in the connections without altering the overall topology, we shuffled the edges of the network for each iteration. We also calculated the eigenvalues of the adjacency matrices for each of these networks to further analyze the network dynamics. For the Erdős-Rényi network, we set the edge probability to $p = 0.1$, meaning each pair of nodes had a 10% chance of being connected, representing random connections between individuals with no predefined community structure [29]. For the SBM, we generated a network with 10,000 nodes distributed across three large communities of 5,000, 3,000, and 2,000 nodes, where intra-community connections were more frequent than inter-community ones. Lastly, for the RGG, we placed 10,000 nodes uniformly at random within a unit cube, connecting nodes if the distance between them was less than or equal to a specified radius. Each of these network structures allowed us to explore the impact of vaccination coverage under varying topological conditions, providing insight into how different social network

Table 1 Epidemic threshold values for varying fractions of vaccinated individuals. Increasing the fraction of vaccinated individuals raises the threshold, making it more difficult for an outbreak to occur. Data is based on a network with 10,000 nodes following the Erdős-Rényi model having edge probability $p = 0.1$

Percentage of Vaccinated People	**0.05**	**0.1**	**0.2**	**0.3**	**0.4**
$\frac{1}{\lambda max}$	0.0008	0.0009	0.0011	0.0012	0.0016

Table 2 Epidemic threshold values for different fractions of vaccinated individuals. As the fraction of vaccinated individuals increases, the threshold rises, making outbreaks more difficult. Data is based on a network with 10,000 nodes following a SBM with three major communities of 5,000, 3,000, and 2,000 nodes.

Percentage of Vaccinated People	**0.05**	**0.1**	**0.2**	**0.3**	**0.4**
$\frac{1}{\lambda max}$	0.00025	0.00027	0.00032	0.00033	0.0004

Table 3 Epidemic threshold values for different fractions of vaccinated individuals. As vaccination coverage increases, the threshold rises, making outbreaks less likely. Data is based on a RGG with 10,000 nodes and a radius of 0.3.

Percentage of Vaccinated People	**0.05**	**0.1**	**0.2**	**0.3**	**0.4**
$\frac{1}{\lambda max}$	0.0052	0.052	0.07	0.1	0.52

models respond to interventions aimed at controlling disease spread.

Simulation framework implementation

In this work, we used a susceptible–infected–recovered/removed–vaccinated (SIRV) model [30] to represent the spread of the disease. Each individual can be in a susceptible ($\mathcal{S}$), infectious ($\mathcal{I}$), vaccinated ($\mathcal{V}$), or recovered ($\mathcal{R}$) state. Once a susceptible individual comes into contact with an infected one, it gains a probability of becoming infectious. Each person can infect a susceptible neighbour and recover after a fixed or variable time span. Vaccinated people and recovered people do not play any further role in the simulation since they cannot change its state.

This model represent an extension of the classical Susceptible-Infectious-Recovered (SIR) model that accounts for vaccination of the susceptible population. It is based on the following system of differential equations:

$$\frac{dS}{dt} = -\frac{\beta(t)IS}{N} - v(t)S, \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta(t)IS}{N} - \gamma(t)I, \tag{2}$$

$$\frac{dR}{dt} = \gamma(t)I, \tag{3}$$

$$\frac{dV}{dt} = v(t)S, \tag{4}$$

where β, γ, v are the rates of infection, recovery, and vaccination, respectively. To simulate the spreading of the measles, we implemented this model by adapting the Python library provided by Menczner et al. [31]. We simulated each of the above-described networks, and then we measured averaged the results. At the beginning of the simulation, the large part of the population was in the $\mathcal{S}$ state, and a small fraction was in the $\mathcal{V}$ state, considering an increasing value of this fraction (0.05, 0.1, 0.2, 0.3). The initial fraction of infected nodes is always set to 0.01 and nodes are randomly selected. Then, we set constant infection (β), recovery μ, and vaccination ϱ rates, considering different times. For each simulation step we rewired the contact graph to simulate the dynamic nature of contacts. We also measured the epidemic rate to predict first and demonstrated through the simulation the impact of different vaccination strategies. Finally, we restarted the simulations and evaluated the spreading of the infection by measuring the number of infected individuals over time.

Results

Impact of fraction of vaccinated people on virus diffusion

In the first experiment, we used an Erdős-Rényi network model with 1000 nodes and an edge probability of 0.2 (p = 0.2). We gradually increased the proportion of vaccinated individuals at rates of 0.05, 0.1, 0.2, and 0.3, while keeping the infection and recovery rates constant across all simulations. At the start of each simulation, 0.01 of the nodes are randomly initialized as infected. As the number of people vaccinated increased, we observed a corresponding increase in the diffusion coefficient, indicating that the network structure became more resistant to the outbreak. The increased vaccination rate significantly reduced the potential for widespread infections, demonstrating greater resistance to disease spread. The results for the Erdős-Rényi model are reported in Table 1.

The second experiment utilized SBM with 10,000 nodes distributed across three large communities. The SBM, a network model that generates graphs by partitioning nodes into groups (or blocks) with different probabilities of forming edges within or between groups, is particularly effective in simulating the community structure observed in real-world social networks. This realistic nature of the SBM model, where individuals are more likely to create connections within their own community but maintain some links with other groups, instils confidence in the validity of our research. By capturing this modular structure, the SBM allows us to study how disease spreads in more realistic, community-based settings.

In this setup, we varied the fraction of vaccinated individuals (0.05, 0.1, 0.2, 0.3, and 0.4) while keeping the infection and recovery rates constant. As the vaccination rate increased, the diffusion coefficient also rose, indicating that the SBM network, with its community structure, became progressively more resilient to the outbreak as indicated in Table 2.

In the third experiment, we employed a Geometric Random Graph (GRG) with 10,000 nodes, where each node is placed randomly in a geometric space, and edges are formed between nodes within a certain distance. This model captures spatial constraints often seen in real-world networks, such as physical proximity influencing connections, and is particularly useful for simulating networks like wireless or social networks, where individuals connect based on location or range. We increased the fraction of vaccinated individuals with rates of 0.05, 0.1, 0.2, 0.3, and 0.4 while maintaining constant infection and recovery rates. As the vaccination rate increased, the diffusion coefficient also rose, showing that the network's geometric structure became more resistant to disease spread as summarised in the Table 3.

Implementation of a vaccination campaign

In our second experiment, we examined how an outbreak behaved across three types of random graphs: Erdős-Rényi, SBM, and RGG. The study compared the outbreak's progression under two conditions: without any vaccination and with an increasing number of vaccinated individuals. The goal was to assess the impact of vaccination on the spread of the outbreak within each network structure.

For each graph model, we observed the outbreak's spread when no vaccinations were administered, noting a rapid increase in infected individuals. As we gradually increased the number of vaccinated individuals, we tracked how the outbreak evolved, focusing on the number of susceptible individuals over time. The results consistently demonstrated that increasing the number of vaccinated individuals slowed the outbreak. In all three graph models, the increase in vaccinated populations led to a noticeable reduction in the number of susceptible individuals, preventing the outbreak from spreading unchecked. This effect was observed in all scenarios regardless of the specific graph topology.

In the Erdős-Rényi graph, a random graph model where each edge exists with equal probability, the introduction of vaccinations rapidly curtailed the growth of the outbreak. Figure shows rapid and widespread infection, with the number of infected individuals rapidly increased and it also demonstrates how vaccination significantly slowed the outbreak's progression, with a lower peak of infections and a larger proportion of the population remaining uninfected.

Similarly, vaccinations successfully prevented the outbreak from crossing community boundaries in the SBM, which divides the graph into distinct communities, as depicted in Fig. 2. The introduction of vaccinated

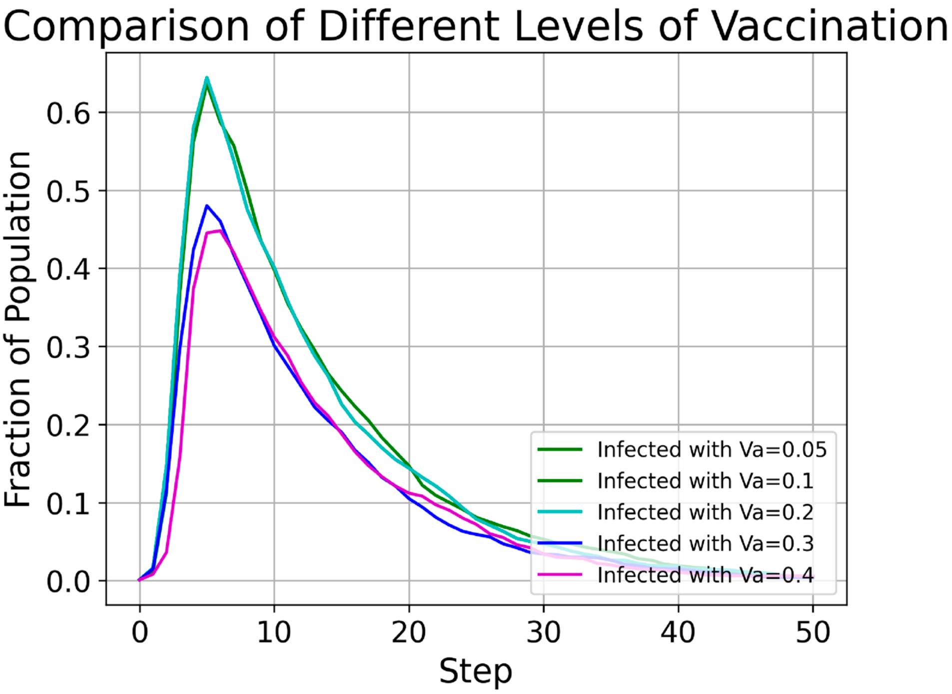


Fig. 2 Comparison of Disease spread simulation in an unvaccinated population using a SBM network

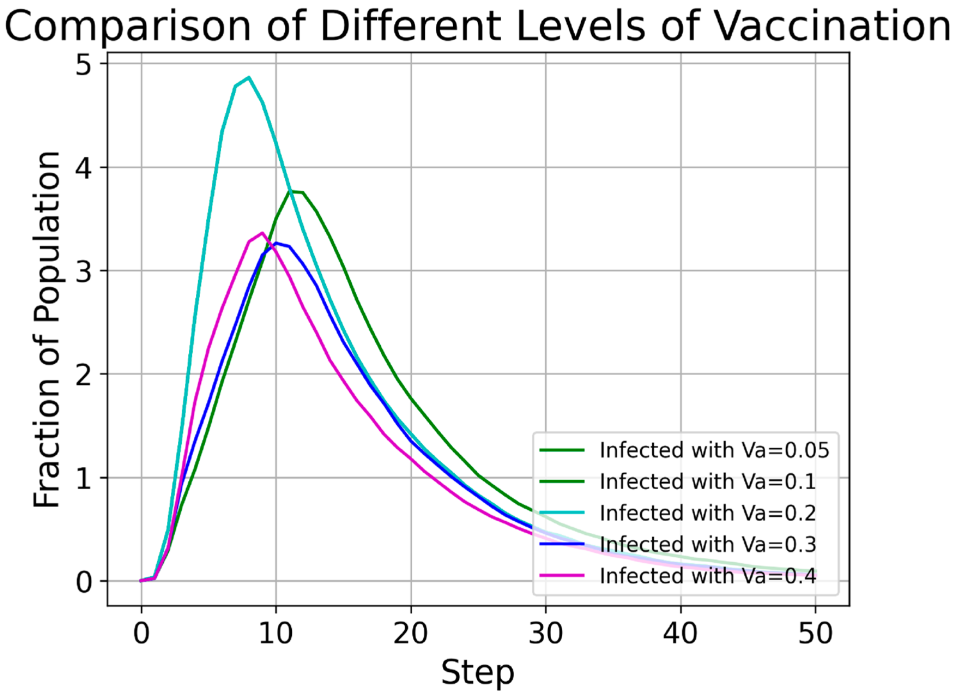


Fig. 3 Comparison of Disease spread simulation in an unvaccinated population using a Geometric Random Graph network

individuals caused the containment of outbreak within specific communities, with vaccinated individuals acting as barriers to inter-community spread.

In the RGG, as represented in Fig. 3, where nodes are placed in a geometric space, we found that vaccinations created localized barriers to the outbreak, effectively controlling its spread. The spatial nature of this model allowed us to visualize how vaccination strategies can create 'firebreaks' in the population, limiting the geographic spread of the infection. This effect was particularly pronounced in densely populated areas, where vaccinated individuals disrupted potential pathways for the spread of the virus.

Across all three models, increasing the number of vaccinated people consistently reduced the infection rate and controlled the overall scale of the outbreak. This was evidenced by lower peaks in the infected population curves, slower rates of decline in the susceptible population, and final network states showing a higher proportion of uninfected individuals. The effectiveness of vaccination was particularly notable in the SBM and RGG models, where the community structure and spatial relationships amplified the protective effects of vaccination.

These results underscore the universal effectiveness of vaccination strategies across different network topologies, highlighting their crucial role in outbreak control regardless of the underlying social or spatial structure of the population.

Discussion

The simulation results demonstrate that vaccination plays a crucial role in controlling outbreaks, independent of the underlying network structure or disease-specific characteristics. Although our contact-based model allowed us to explicitly account for how different network configurations (SBM, RGG, and Erdős-Rényi) influence disease spread, the consistent pattern in all simulations is the apparent reduction in outbreak potential as vaccination coverage increases. This outcome emphasises the generalizability and robustness of vaccination as a critical public health tool.

In each of the three network configurations, we observed that an increase in vaccinated individuals led to a measurable improvement in network resilience, evidenced by a lower outbreak coefficient (the inverse of the largest eigenvalue of the adjacency matrix). Importantly, this reduction occurred consistently, regardless of the structural properties of the network. This suggests that vaccination efficacy is not dependent on the precise details of how individuals are connected but instead serves as a universal mechanism for mitigating disease spread.

In networks characterized by community structure, where connections within tightly-knit groups are more frequent, vaccination effectively disrupts spread pathways. Even in such highly clustered configurations, as modeled by the stochastic block approach, the presence of vaccinated individuals prevents outbreaks from taking hold within or between communities. Similarly, in networks organized by spatial proximity, such as RGGs, vaccination weakens the likelihood of local clusters forming outbreaks. Despite the spatial organization, the introduction of vaccinated individuals leads to substantial reductions in both outbreak size and probability, showing that physical proximity does not diminish the effectiveness of immunization. Even in more random, unstructured networks, where individuals have an equal probability of connecting to any other individual, as in the Erdős-Rényi model, vaccination still significantly reduces the outbreak potential. This highlights that immunization disrupts the potential for widespread spread, regardless of the randomness or lack of structure in the connections. This consistency across different types of networks underscores a crucial point: while the specific structure of a population's contacts can influence the dynamics of disease spread, vaccination remains a potent intervention tool in any configuration. The universal applicability of vaccination as a strategy, transcending the nuances of network topology, reaffirms its effectiveness in diverse scenarios and serves as a reassuring message for public health strategies.

Another key observation from these simulations is that the effectiveness of vaccination in controlling outbreaks is not inherently tied to the particular disease being modelled. The model measured outbreak control in terms of network dynamics (through the largest eigenvalue of the adjacency matrix), which provides a generalised framework for understanding disease spread. By removing susceptible nodes from the network through vaccination, we are fundamentally altering the capacity of the network to sustain an outbreak, regardless of the specific spread dynamics of the disease. This observation implies that vaccination can be effective across a wide range of diseases, even those with varying spread parameters. Whether a disease is highly infectious or less sections are irrelevant of reducing the number of susceptible individuals consistently limits the potential for sustained spread. The mathematical structure of the outbreak coefficient evidences this fact, as it reflects the connectivity and susceptibility within the population rather than disease-specific features.

The importance of these results cannot be overstated. Vaccination remains one of the most effective interventions in public health, and our findings support the idea that its benefits extend across a variety of contact networks and diseases. Whether populations are structured in tightly knit communities, spread across spatially constrained regions, or randomly connected, vaccination serves as a universal defence against the spread of infectious diseases. This has far-reaching implications for public health policy, especially in situations where the exact nature of a disease's spread dynamics or the population's contact structure may not be fully known. For example, in the early stages of novel outbreaks (like the COVID-19 pandemic), where both the disease's characteristics and population contact networks were not immediately understood, vaccination campaigns proved essential in reducing spread, supporting the claim that vaccination is broadly effective irrespective of such unknowns. Moreover, in real-world scenarios, the structure of social interactions is often dynamic and not easily captured by a single static network model. Vaccination proved beneficial across a spectrum of network structures in our simulations, further underscoring its importance in real populations where connections are often a mixture of random, community-based, and spatially constrained interactions.

The universality of vaccination as an outbreak control measure, independent of network topology or disease characteristics, suggests that broad-based vaccination strategies should be prioritised in pandemic preparedness and routine immunisation campaigns. This is particularly critical in scenarios where specific interventions, such as contact tracing or social distancing, may be challenging to implement effectively or may be subject to delays. Furthermore, our findings emphasise the need for robust vaccination coverage despite emerging diseases with unknown epidemiological properties. The simulations suggest that vaccination campaigns do not need to be finely tuned to the particular network structure or disease dynamics to be effective–underscoring the importance of widespread vaccination as a first-line defence in public health responses.

Limitations

While network models and compartmental frameworks offer valuable insights for analyzing the impact of vaccination strategies on the spread of infectious diseases, it's crucial to acknowledge that the simplifications inherent in these models may limit their practicality and precision in real-world settings [32–34]. It's important to recognize that reducing complex human interactions to fixed or dynamically modeled networks doesn't fully encapsulate the subtleties and variations of actual human behavior, which significantly influence disease spread [35]. For instance, the assumption that contacts among individuals remain constant over time overly simplifies the fluid nature of human interactions, as individuals often change their contact patterns. Therefore, introducing dynamic network models that account for these changes is crucial. Moreover, to accurately gauge the effectiveness of vaccination campaigns, network models must also consider variations in susceptibility and infectiousness among individuals. From a data-centric perspective, the data used to construct these networks may not accurately reflect the broader population due to limitations in data collection and inherent biases in observing population dynamics. Furthermore, the definition of a "contact" in these models needs to adequately consider the duration and proximity of interaction necessary for spread, which can vary widely among different diseases and even among strains of the same disease. This observation leads to the argument that models should be disease-specific rather than aiming for a one-size-fits-all approach. The potential to harness artificial intelligence in computational modeling for creating innovative systems that integrate deep learning, computational statistics, and data science is gaining traction [34]. Firstly, employing AI could enhance data collection processes by facilitating the capture of data while minimizing noise impact. Secondly, deep learning techniques could accelerate the simulation and prediction phases, offering faster insights into potential outbreak scenarios and the effectiveness of intervention strategies.

Conclusion

This study emphasized the critical role that vaccination plays in controlling the spread of infectious diseases with application to *morbillivirus*. Through computational simulations across different network configurations the results consistently showed that higher vaccination coverage significantly reduces disease spread. This was evident in all network structures, regardless of their specific properties. The robustness of vaccination as a tool for outbreak control highlights its universal applicability in diverse epidemiological and social contexts, making it an indispensable strategy in public health efforts to prevent widespread disease spread.

Author contribution

PHG and FB contributed equally to this work, including the conceptualization and design of the research. FB conducted data collection, while PHG performed the analysis. FC developed the main software modules, and FS carried out the investigation. PV contributed to the conceptual design of the key ideas. MC provided supervision and validation of the work. All authors reviewed and approved the final version of the manuscript.

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Data Availability

Data are available at http://github.com/fbranda/measles.

Declarations

Ethics approval and consent to participate

Not applicable.

Relevant guidelines and regulartion consent for publication

All the authors read and approved the manuscript.

Competing interests

The authors declare no competing interests.

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