

## **Simulating Measles Vaccination on Complex Graphs**

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**Abstract:** *Measles is a highly contagious illness caused by the measles virus. Measles remains one of the leading causes of death among young children around the world. The objective of this study is to examine the effect of vaccination and human contact interactions on the transmission of measles virus. Data on contact interactions among 3000 young children in Ajaka community, Kogi State, Nigeria were collected. A graph representing this population and their interconnectedness was generated. The effects of different converges of vaccination on the epidemiology of measles virus were investigated. The results show that effective measles vaccination is crucial for the elimination of measles among the children in the community. Therefore, mass vaccination for measles is recommended in order to eliminate or at least significantly reduce the menace of measles outbreaks.*

**Keywords:** *measles, graph, network, vaccination, simulation, model*

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### **I. Introduction**

Measles is a highly infectious illness caused by a paramyxovirus, of genus morbillivirus. The virus lives in the mucus of the nose and the throat of people with this infection. It is one of the first and worst childhood diseases. Sign and symptoms of measles include cough, runny nose, inflamed eyes, sore throat, fever and a red blotchy skin rash. It can lead to serious and fatal complications including pneumonia, diarrhea, encephalitis, blindness, deafness or impaired vision. Physical contact, coughing and sneezing can spread the infection. Once quiet common, measles can now almost always be prevented with a vaccines [1].

Measles is still a leading cause of death among young children, despite the availability of an effective vaccine for the past 40years. Although it is rare in many developed countries, it remains a common illness in many developing countries and more than half a million people, mostly children, died from measles in 2003 [2]. As reported in [3], measles caused an estimated 2.6 million deaths in 1980, 75% decrease in deaths from 2000 through 2013, 145,700 deaths in 2013, and estimated 20 million cases every year.

### **II. Graphs and Modeling**

Models are available to capture the important processes in measles disease transmission. As reported in [5], Allen and his collaborators, in 1991, studied a discrete-time model with vaccination for measles epidemic. They used a discrete-time, age-independent *SIR*-type epidemic model. They applied their model to measles epidemic on a university campus. [6] developed a simple stochastic mathematical model to investigate the dynamics of measles epidemic. Their model is a multi-dimensional diffusion process with SEIR compartments. An analysis on extensive simulations of a stochastic metapopulation model (SEIR type) focusing on Seasonality and extinction in chaotic metapopulations can be seen in [7]. [8] presented a detailed analysis of the pattern of measles outbreaks in the small isolated community of the Faroe Islands. Measles outbreaks in that population showed frequent fade-out of infection resulting in long intervals when the disease was absent from the islands. They used a Lattice-based epidemic model to provide a theoretical estimate of the scaling exponents. A mathematical model for the simulation of a localized measles epidemic was presented in [9]. Susceptible-Exposed-Infected-Recovered (SEIR) model was used in [10] to study the transmission dynamics of measles. A univariate time series analysis on pertusis, mumps, measles and rubella based on Box-Jenkins or Auto-Regressive Integrated Moving Average (ARIMA) model was carried in [11].

As reported in [11], most mathematical models are used to study the epidemiology of childhood viral diseases, such as measles. He described the period of infectiousness by an exponential distribution. He used Susceptible Infectious Recovered (*SIR*) model in his study. [13] used SEIR deterministic model to provide useful insights into the mechanic of many common childhood diseases such as measles. A survey of stochastic epidemic models can be seen in [14].

The aforementioned models have an obvious limitation. Most of these models assume random interactions, but in reality interactions are usually not random. Human contact interactions are a network and this network can be described by a graph. In this article, attention is focused on a graph-based model.

Graphs used in the literature can be classified on the properties of interest. From the dynamism point of view, graphs or networks can be classified as static or dynamic depending on whether their structures change with time. From the field of application perspective, we have social networks, information networks, technological networks, epidemic networks, to mention a few. Each of these types of networks can be narrowed to specific networks. Graph classifications based on degree distribution exist. For instance, scale-free graphs, Poisson graphs. Graphs such as unipartite, bipartite or multipartite are based on the node types. For a general knowledge of graphs and their theory, the reader is referred to [16, 17, 19, 20, 21, 22].

Real world network are large, and in most cases it is virtually impossible to describe them in detail or to give an accurate model for how they came to be. To circumvent this problem, random graphs have been considered as network models. The field of random graphs was established in late 1950s and early 1960s. For detail, see [16].

In this article, our interest is in social networks and how they affect the epidemiology of diseases. A social network is a social structure made up of individuals (or organizations) called nodes which are connected by some specific types of interdependency, such as friendship, enmity, common interest, financial exchange, dislike, sexual relationship or relationship of beliefs, knowledge or prestige. For detail of social network analysis, the reader is referred to [23].

The plan of this paper is as follows. In section 2, we present graphs and modeling; and model description is presented in section 3. Simulation is presented in section 4. Section 5 is devoted to results. Finally, discussion of results and conclusive remarks are passed in section 6 and 7 respectively

### III. Model Description

We construct a graph or network model, wherein each individual is represented by a node and the edges are the links between the individuals. A Poisson distribution is used to generate degree sequence; and the graph is constructed using the mechanism of configuration model.

We simulate epidemics on our graph based on the following procedure.

1. Specify the proportion already vaccinated at initial time  $t_0$ .
2. Specify the total population  $T = N$ .
3. Specify the degree distribution as a Poisson distribution with the parameter value  $\lambda$ .
4. Generate the graph by the mechanism of configuration model.
5. At each time step, apply the infection operator  $\xi_1$ . A susceptible node may be exposed by neighbouring infected nodes with probability  $p_1$ , which is determined by the number of infected nodes  $i, i = 1, \dots, k$ .
6. At each time step, apply local progression operator  $\xi_2$ . An exposed individual progresses to an infectious state  $p_2$ .
7. At each time step, an infectious individual recovers with probability  $p_3$ .

Repeat these steps until statistical significance is obtained.

### IV. Simulation

We use the following parameter values in Table 1.

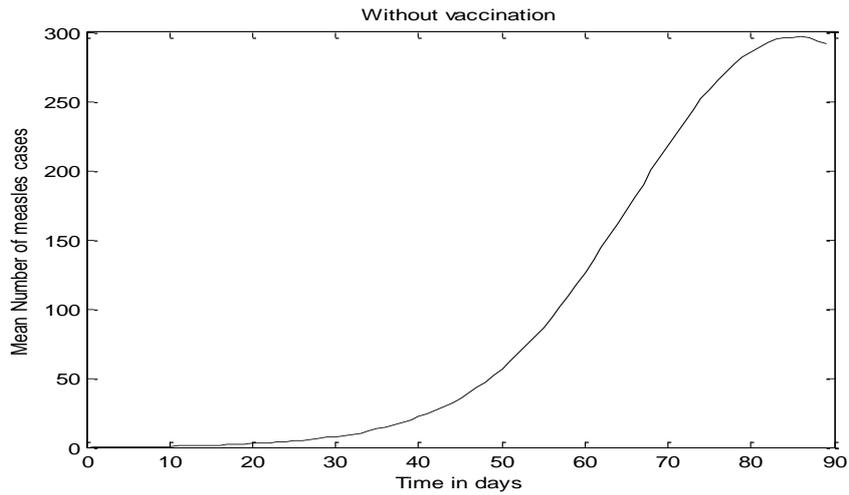
*Table 1: parameters for numerical simulations*

parameters	Definition	Parameter value	source
$p_1$	Transmission probability per day	0.09091	[24]
$\sigma$	Rate of progression from exposed to infectious state	0.125	[24]
$p_3$	Fixed probability for recovery	0.1429	[2, 15]
c	Proportion vaccinated before start of outbreak	0 – 0.95	variable

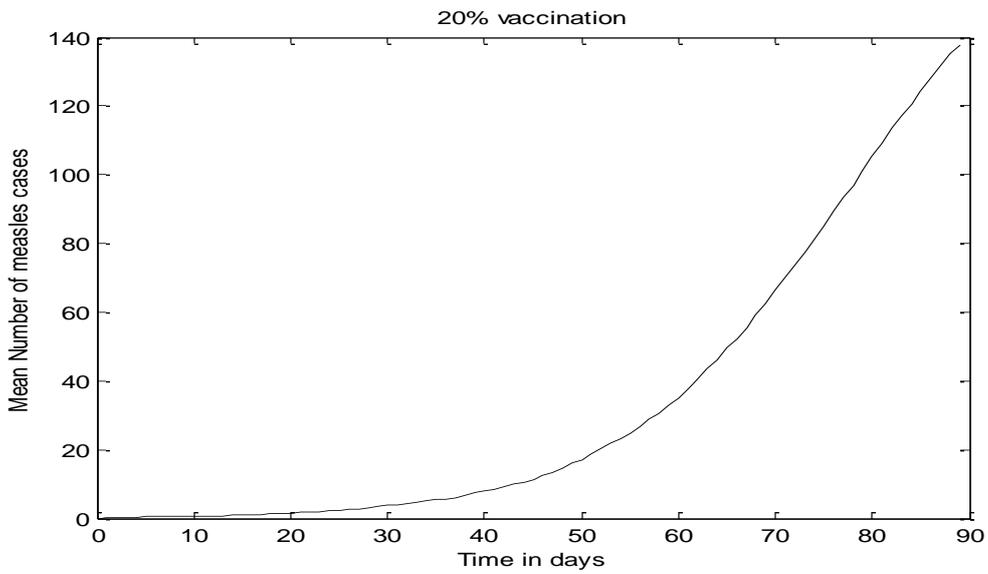
The values of our model parameters are based on published epidemiological data shown in Table 1.

### V. Results

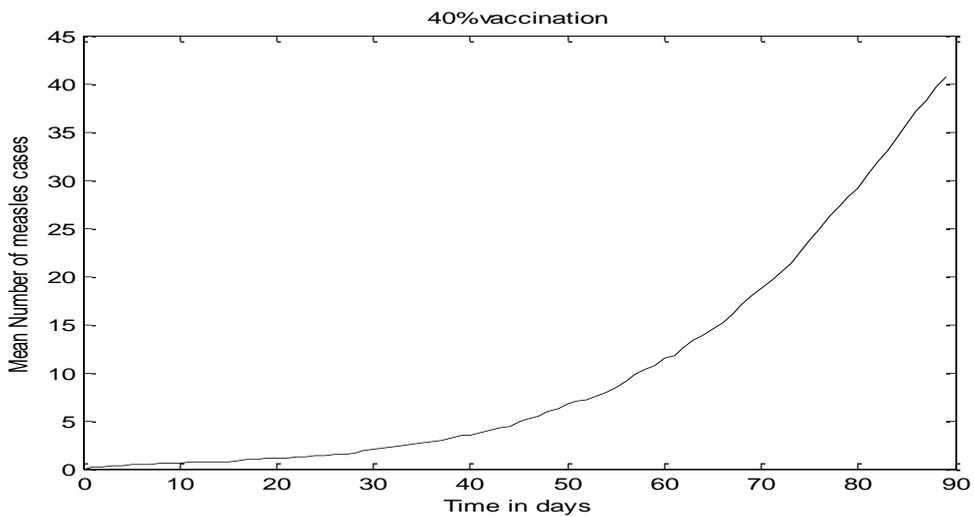
The results of our simulation experiments are displayed in the sequel.



**Figure 1: Graph showing the mean number of measles cases without control**



**Figure 2: Graph showing the mean number of measles cases with 20% vaccination**



**Figure 3: Graph showing the mean number of measles cases with 40% vaccination**

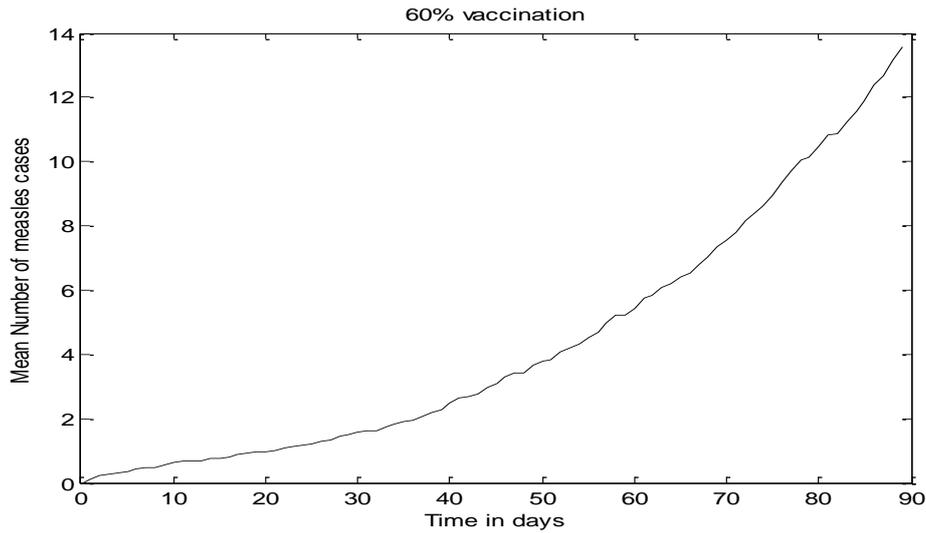


Figure 4: Graph showing the mean number of measles cases with 60% vaccination

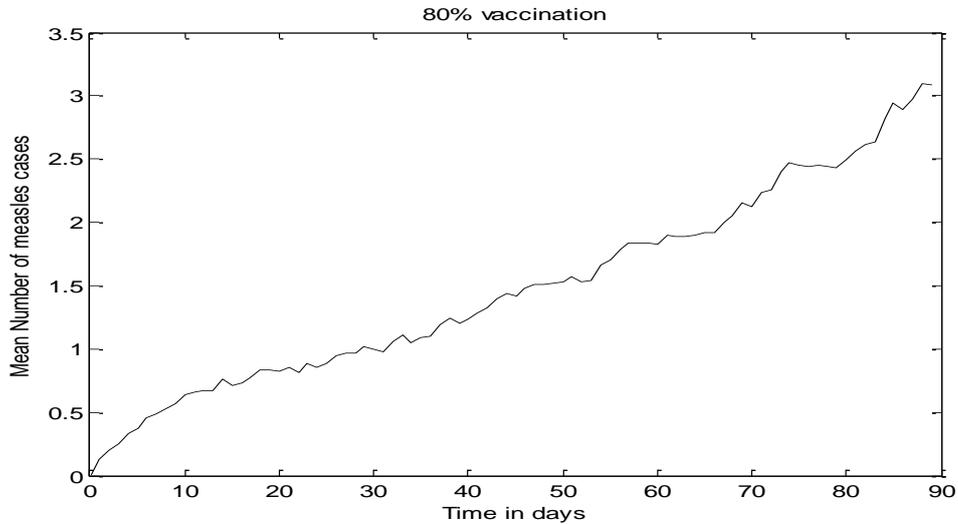


Figure 5: Graph showing the mean number of measles cases with 80% vaccination

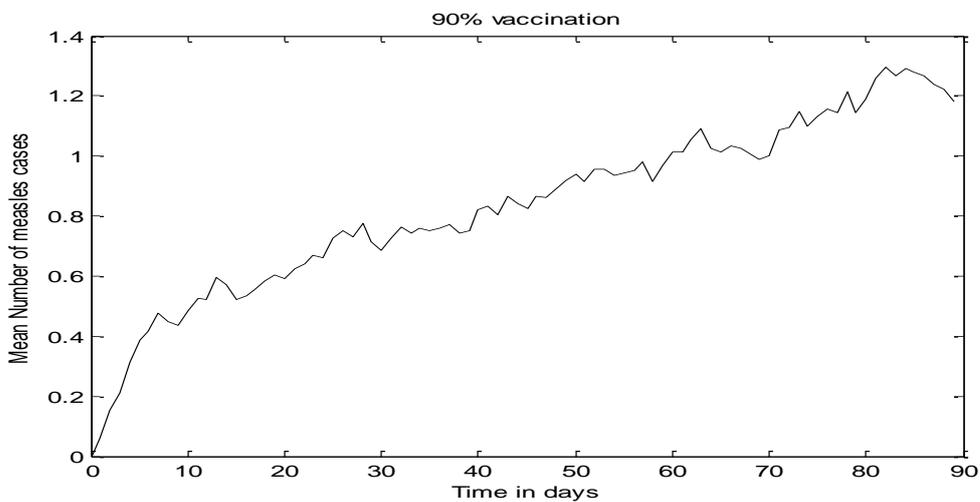
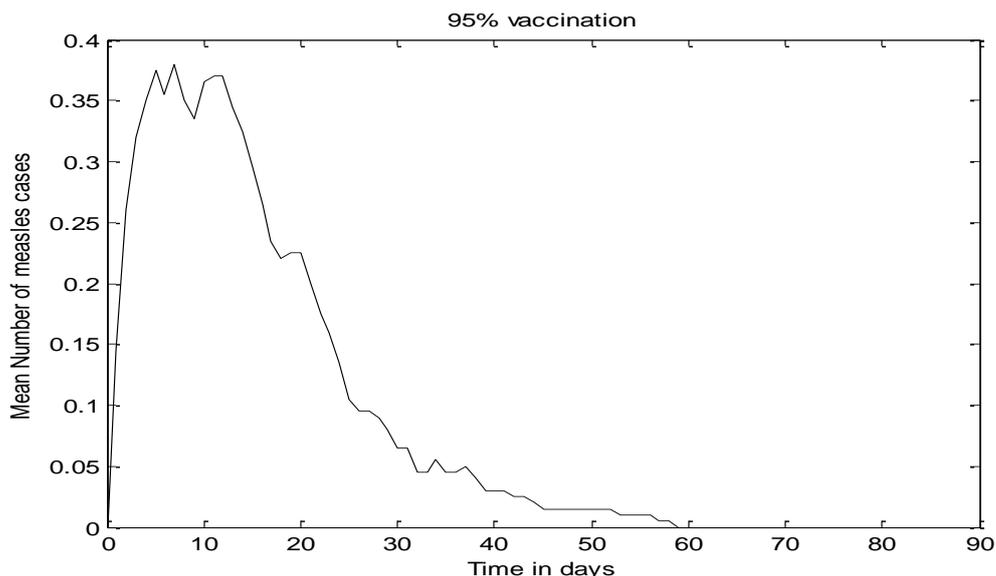
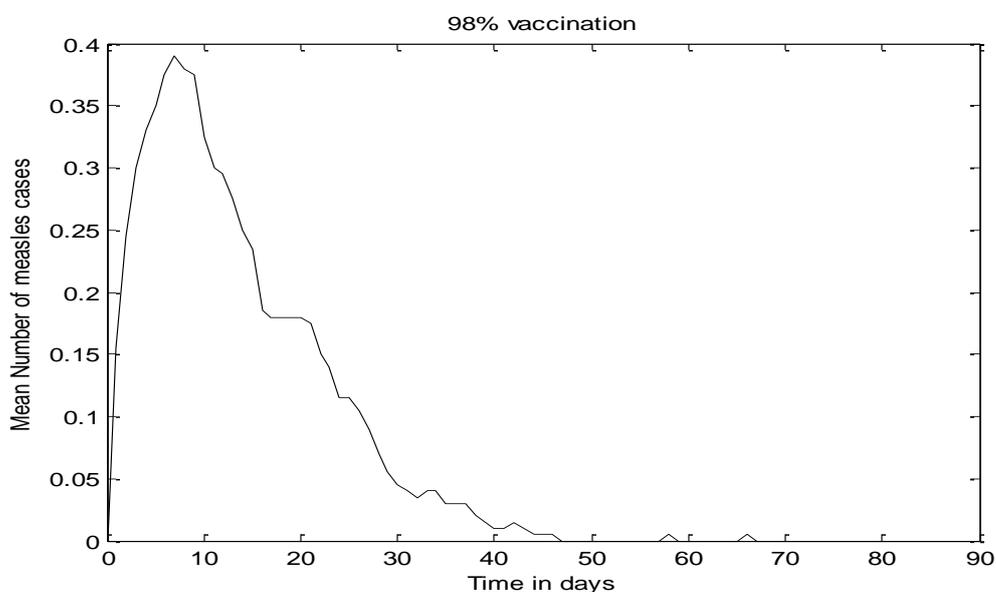


Figure 6: Graph showing the mean number of measles cases with 90% vaccination



**Figure 7: Graph showing the mean number of measles cases with 95% vaccination**



**Figure 8: Graph showing the mean number of measles cases with 98% vaccination**

### VI. Discussion

Measles is a highly infectious disease caused by measles virus. Vaccination is one of the preventive interventions for measles spread. Vaccination confers some level of immunity on individuals so that when they are exposed to an infected person they remain protected. Our graph-based model is used to simulate the effects of vaccination on the transmission dynamics of measles disease. Our results show that in absence of vaccination or any other measure, the presence of an index case in a population can lead to an exponential increase in the number of cases because of high infectivity of the virus. This can be seen in Figure 1. Small vaccination coverage cannot stop measles epidemics; it can only relatively reduce the number of cases. We observe from our results that the size of epidemic decreases with the vaccination coverage and that there is an outbreak for any vaccination coverage less than 95%. Herd immunity can be achieved for vaccination coverage of 95% and above. Our findings show that high vaccination coverage guarantees herd immunity and prevent measles outbreak. Therefore high vaccination coverage can only be sufficient for the elimination of measles in a population.

## VII. Conclusion

In this article, we have developed a graph-based model and used it to simulate the transmission dynamics of measles disease. The main results are shown in Figures 1 through 8. Our results show that measles is highly infectious; that small coverage can still precipitates measles outbreak. Therefore, to eliminate measles from the society mass vaccination is recommended.

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