

STUDY OF THE SPREAD OF MEASLES IN NGELWANDE CITY USING MODLING OF ORDINARDY DIFFERENTIAL EQUATIONS.

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Article Received on 24/06/2019

Article Revised on 14/07/2019

Article Accepted on 04/08/2019

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ABSTRACT

Despite the availability of the measles vaccine since 1963, the infectious disease is still endemic in many parts of world including developed countries and continued causing economic and health problems. Due to these impacts, the study addressed mathematical model technique using first order differential equation in order to demonstrate the spread of measles disease among unvaccinated

populations in host communities. The model provides much insight into the dynamic of disease epidemics and spread within a host population. It found that, the first order differential equation will define and represent the spread of measles in host communities. It's worth mentioning, all these information will help the decision makers about public health policies.

KEYWORD: Measles, Contagious Disease, Unvaccinated Populations, Ordinary Differential Equations, Epidemiology, Transmission.

1.0. INTRODUCTION

No doubt, the history of mankind has been shaped by the pitiless outbreaks of infectious diseases pandemics, whole nations and civilization have been copied off the map through the

ages. The epidemics which occurred during the 16th Century resulted in 13 million death decimating Mesoamerican native population, the black bubonic plague burst in Europe in 1348 and is estimated to have killed over 25 million people just in five(5) years . The 1957 and 1963 influenza pandemic resulted in two and one million death respectively [1]. Communicable diseases such as measles, influenza, or tuberculosis, are a fact of modern life. The mechanism of transmission of infections is now known for most diseases. Generally, diseases transmitted by viral agents, such as influenza, measles, rubella (German measles), and chicken pox (small pox), confer immunity against reinfection, while diseases transmitted by bacteria, such as tuberculosis, meningitis, and gonorrhoea, confer no immunity against reinfection. Other diseases, such as malaria, are transmitted not directly from human to human but by vectors, which are agents (usually insects) who are infected by humans and who then transmit the disease to humans. The West Nile virus involves two vectors, mosquitoes and birds. For sexually transmitted diseases with heterosexual transmission each sex acts as a vector and disease is transmitted back and forth between the sexes.^[8]

Epidemiology is one of the areas in biology to which mathematical modeling has been applied most successfully. Recent Epidemiology studies distribute the infectious diseases within a host population in to different classes that correspond to the different stages of the infectious process (e.g., Susceptible, Infectious, and Recovered) and transition between these classes. However these models work particularly well for diseases caused by micro parasites, Mathematical epidemiology has concentrated on cases for which the disease is endemic or in which large epidemics occurs.^[5]

1.1. The Epidemiology of Measles

Measles is caused by the measles virus. It is transmitted on close contact via airborne propagules. Infection leads to the development of a typical rash. The infectious period is a week, after which the hosts recover and develop lifelong immunity. Hosts, therefore, are normally infected only once in their lifetime and, if the force of infection is sufficiently large, this happen at a young age, and hence measles is a childhood disease. Although unvaccinated populations measles is a common disease, infection is not without danger. In large, unvaccinated populations measles is endemic. Before mass vaccination was introduced, measles used to follow a cyclic pattern, with a period of about 2 years in Europe and North American. In small isolated populations, an outbreak of measles can immunize a large part of

the population, so the disease disappears even if the reproductive number was larger than one initially, therefore, measles cannot persist in small populations.^[5]

Measles virus is a paramyxovirus, genus Morbillivirus and it's an infectious disease highly contagious respiratory disease through person-to person transmission mode, with > 95% secondary attack rates among susceptible persons. It is the first and worst eruptive fever occurring during childhood. It produces also a characteristic red rash and can lead to serious and fatal complications including pneumonia, diarrheal and encephalitis. Many infected children subsequently suffer blindness, deafness or impaired vision. Measles confer lifelong immunity from further attacks.^[6] Protection of children from vaccine-preventable diseases, such as measles, is among primary goal for health workers. Since vaccination has turned out to be the most effective method against childhood diseases, developing a framework that would predict an optimal vaccine coverage level needed to control the spread of these diseases is important and essential. Epidemiologists use mathematical models to understand previous outbreak of diseases and to better understand the dynamics of how infections spread through populations. Many existing models closely approximate historical disease patterns.^[6]

In this study the use of a population with variable size to provide this framework was adopted. It majorly relied on a compartmental model expressed by a set of ordinary (O.D.E) based on the dynamics of measles infections. The mathematical model equations, the mathematical analysis and the numerical simulations that followed served to reveal quantitatively as well as qualitatively the consequences of the mathematical modeling on measles vaccination. The numerical and qualitative analyses of the model were performed and different state variables were determined. Simulation of different epidemiological classes revealed that most of the individuals undergoing treatment join the recovered class.^[4]

In countries that have made considerable progress with measles elimination, a significant means of transmission of measles can be acquired at hospitals and other health facilities. In such situations, measles may be relatively rare, and health staff may not immediately recognize measles. In addition to direct contact between children attending hospitals, measles can be transmitted from patients to health care workers and then to other patients. Since measles can be highly infectious in the three days before the onset of rash, there can be considerable difficulties in separating suspected measles cases from other patients who, for example, may be attending a crowded hospital outpatients unit, so that the control measures should be consider.^[4]

1.2. Measles Infection and Symptoms

The first symptoms of infection with measles are fever, tiredness, runny nose, cough and sore red eyes. These symptoms usually last for several days before a red blotchy rash appears. The rash starts on the face over 1 to 2 days and spreads down the body and sometimes the rash peels. The rash will last for 4 to 7 days. Up to a third of people infected with measles will experience a complication. Complications are more common in young children and in adults, complications include ear infectious, diarrhea, pneumonia, and may require hospitalization. Whoever the measles develops encephalitis (swelling of the brain). Measles can be difficult to diagnose because there are many other viruses that cause similar illness with a fever and a rash.^[9]

1.3. A General Model for Measles

In the last decade emergence and re-emerging pandemic such as Aids, Measles, Malaria and Tuberculosis cause death to millions of people each year. According to the UNAIDS report on the global Aids epidemic an estimated 34 million people including 3.4 million children were living with the HIV worldwide at the end of 2010 while the related death and near infection were 1.8 and 2.7 million respectively, Problems stems mainly from two reasons, firstly, the continuous everlasting mutation of viruses and secondly the complexity in the disease transmission. The complex multi-scale interplay between the host factor ranging from the micro-host pathogen and individual scale host, host interaction of macro-scale ecological, social, economic and demographic condition across the globe complicated, by technical issues such as time long between vaccine prototype development and commercial distribution and production imposes a real impediment to central strategy. Partially, mathematical and statistical modeling are playing a most valuable role shading light on the problem and for helping make decision.^[2,3]

The emergence and re-emergence of pandemic such as measles that causes death to millions of people especially children each year is the point of concern. A special attention has to be given by the government to temperate states of this country to be able to put measles issues to rest.

In 1997-2000 Helbing *et al* and Wilson 2008 have put effort to study human behavior in the context of epidemics usually concentrated on judging the effectiveness of various instructionally enforced public health measures such as school closure. Bootsma and Ferguson 2007 and Hatcher *et al* 2007. Recently, however, the impact of self initiated actions

on the progression of an infection disease has received increase attention. After all individual self initiated action (behavior) can change the self initiated action (Behavior) can change the effect of an outbreak and its interaction with diseases dynamic requires proper understanding if we are to fully comprehend what happens when a disease spreads through human population (Ferguson 2007).

Here we aim to systematically review the theoretical studies undertaken so far to study the impact of individual on the epidemiology of infection diseases. Firstly, we propose a classification system that we believe is useful to help bring order to the complex diversity of models. Secondly we aim to assess the contribution that the model makes towards understanding dynamic control of disease, as well as suggestions that follow as to how response to outbreak could be measured and quantified in a reasonable way.

All the effort made by the previous scientists such as Helbing *et al.* 2008, Wilson 2008, Bootsma and Ferguson 2007, Hatchett *et al.* 2007 were able to control the spread of contagious diseases such as measles based on public health measures. This study is centrally on determining and predicting the rate at which a contagious disease spreads with time in a given community of hosts which was not made clear by their work. We assume that a linear differential equation is a model that predicts the exponential growth rate of measles in a community of hosts if no isolation was made especially in a closed population.

2.1. Important Terminologies

2.1.1. Susceptible

This refers to the potential people in the community of hosts that are likely to be infected in an outbreak.

2.1.2. Infected

The group of people being infected by a disease in an outbreak. Are referred to as infected persons.

2.1.3. Epidemics

A large outbreak of a disease over a short period of time is called epidemics.

2.2. Mathematical Modeling

The mathematical description of a system of phenomena is called a mathematical modeling and is usually constructed with certain goals in mind for example the spread of Measles disease in a

certain community of host at a certain in rate in time can reliably assure that the rate at which the measles spread is directly proportional to both the infected and non-infected person.

Written as

$$\frac{dN}{dt} \propto y(N - N) \Rightarrow \frac{dN}{dt} = ky(N - y) \quad (2.1)$$

Where, N = number of population, k = proportional factor, y = infected person and $N - y$ = non-infected persons and k is always greater than 0 i.e. $k > 0$.^[7]

2.2.1 Differential Equations

A differential equation is a mathematical equation that relates some function with its derivative. In application, the function usually represents physical quantities, the derivatives represent their rate of change, and the differential equation defines the relationship between them. Differential equations first came into existence with the invention of calculus by Newton and Leibniz.^[7]

2.2.2. Initial Conditions

Initial conditions are a condition or set of conditions on the solution that will allow us to determine which solution we are after. Initial conditions are of the form $y(t_0) = y_0$ and $y^{(k)}(t_0) = y_k$. In other words, initial conditions are values of the solution and its derivatives at specific points. Differential equations are unique, hence only one solution will meet the given conditions. The number of initial conditions required for a given differential equation will depend upon the order of the differential equations.

2.2.3. Variable Separable Method

The differential equation $\frac{dN}{dt} = ky(N - y)$ is called a first-order differential equation and can

be solved by the separable method, as follows $\frac{dN}{dt} = ky(N - y)$

$$\frac{dN}{y(N-y)} = k dt \Rightarrow \int \frac{dN}{y(N-y)} = \int k dt \quad (2.2)$$

$$\text{Thus } \int \frac{dN}{y(N-y)} = kt + c$$

$$\text{By using partial fraction for } \frac{1}{y(N-y)} = \frac{A}{y} + \frac{B}{N-y} \Rightarrow \frac{A(N-y) + By}{y(N-y)} = \frac{1}{y(N-y)}$$

$$\text{Thus } A(N - y) + By = 1$$

$$\text{Let } y = N, \text{ then } A(N - N) + BN = 1 \Rightarrow A(0) + BN = 1 \Rightarrow B = \frac{1}{N}$$

Also let $y = 0$, then $A(N - 0) + B(0) = 1 \Rightarrow AN + 0 = 1 \Rightarrow A = \frac{1}{N}$

$$\text{Hence } \frac{A}{y} + \frac{B}{N-y} = \frac{\frac{1}{N}}{y} + \frac{\frac{1}{N}}{N-y}$$

$$\begin{aligned} \text{Therefore } \int \frac{1}{y(N-y)} dN &= \int \left(\frac{A}{y} + \frac{B}{N-y} \right) dN \\ &= \int \left(\frac{\frac{1}{N}}{y} + \frac{\frac{1}{N}}{N-y} \right) dN = \frac{1}{N} \int \left(\frac{1}{y} + \frac{1}{N-y} \right) dN = kt + c \end{aligned}$$

$$\frac{1}{N} (\ln|y| - \ln|N-y|) = kt + c \Rightarrow (\ln|y| - \ln|N-y|) = Nkt + Nc$$

$$\ln \left| \frac{N}{N-y} \right| = Nkt + c_0 \Rightarrow \frac{N}{N-y} = ae^{Nkt} \quad (2.3)$$

Where $a = e^c$

2.3. Deterministic Modelling Technics

The first step of deterministic modeling consists of having a complete and realistic picture of the biology of the diseases, example duration of the period of infection, incubation periods, and immune status after infection. The second step is to collect the data on the demographic epidemiology and the biologic characteristic of the infection (transmission rate) and the population (birth rate and death rate).

The third step a parsimonious model is selected.^[10]

2.4. A Threshold Theorem of Kermack And Mc Kendrick Of Spread Of Contagious Disease

Before going on with deterministic modeling it is important to understand how epidemics set up in a population for disease conferring long lasting immunity infection. i.e. measles. The number of susceptible (s) decrease with time. Before the outbreak of a first measles case the population of susceptible (s) is 100% in the population because everyone is susceptible, the proportion of expose(E), infection (I) and recovered (R) is zero (0), when epidemic starts to spread susceptible decrease while immune and infection increase until everyone get immunized. The potential of infected person in a population depend on the basic in a population depends on the basic reproduction number (R) is define as the average number of person directly infected by an infection disease during his/her entire infection period when he/she enters a totally susceptible persons.^[8,7]

3.1 METHODOLOGY

Here the method and the process of computing the values in data obtained and implemented here in this work. Therefore, below is the data obtained from the primary health care management Board Yobe State. An epidermis of measles in Ngelwande primary village unit to Fune local government Yobe State in the months of April, 2010. The graphs are displayed using MTLAB.

4. RESELTS AND DISCUSSION

The following data obtained from the primary health care management Board Yobe State. An epidermis of measles in Ngelwande primary village unit to Fune local government Yobe State in the months of April, 2010.

Table 1: Show the Susceptible, infected people and the time period.

t	0	1	2	3	4	5
S	12,000	11,991	11,920	11,318	7,790	2,051
I	1	9	80	682	4,210	9,949

s = Susceptible people, t = Time period and I = Infected persons

Since the rate of speed of measles contagious disease is directly proportional to the infected and non infected person, the village (Ngelwade) has a total population of twelve thousand (12,000) people. If the infected people is represented as N then the non-infected people is $12000 - N$ ” hence $\frac{dN}{dt} \propto N(12000 - N)$

$$\frac{dN}{dt} = kN(12000 - N) \quad (3.1)$$

To solve equation (3.1), the method of variable separable can be used

$$\frac{dN}{N(12000-N)} = k dt$$

Then by using partial fraction technique and integration of both sides we get

$$\int \frac{dN}{N(12000-N)} = k \int dt \Rightarrow \int \frac{1}{12000} \frac{dN}{N} + \int \frac{1}{12000-N} dN = k \int dt$$

$$\frac{1}{12000} \left[\int \frac{1}{N} dN + \int \frac{1}{12000 - N} dN \right] = kt + c$$

$$\text{Therefore } \frac{1}{12000} (\ln|N| - \ln|12000 - N|) = kt + c$$

$$(\ln|N| - \ln|12000 - N|) = (kt + c)12000$$

$$\ln \left| \frac{N}{12000 - N} \right| = k_1 t + c_1$$

Where $k_1 = k \cdot 12000$ and $c_1 = c \cdot 1200$ are constant and N is always between 1 and 12000,

$$\text{we can drop the absolute value. } \ln \left| \frac{N}{12000 - N} \right| = k_1 t + c_1$$

at the initial condition $N(t) = N, N(0) = 1$

$$\ln \left| \frac{N}{12000 - N} \right| = k_1(0) + c_1 \Rightarrow c_1 = \ln \left| \frac{1}{11999} \right|$$

Again let $N(2) = 80$

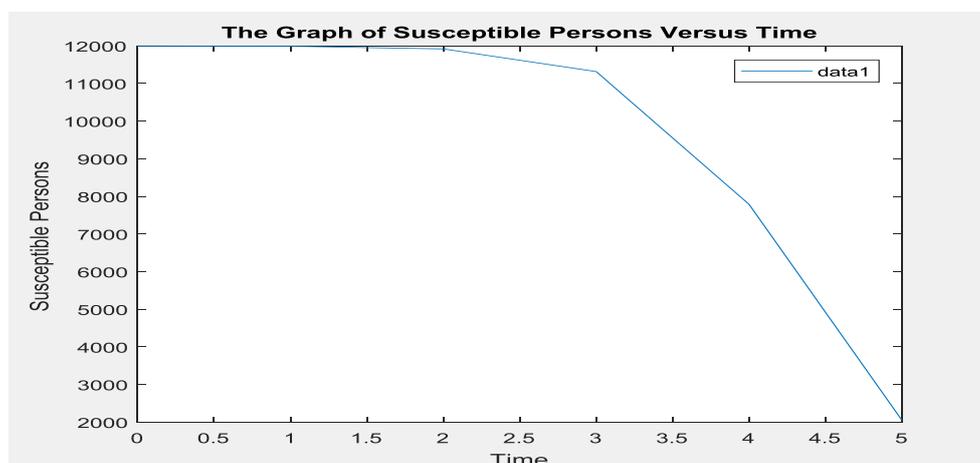
Implies that,

$$\ln \left| \frac{80}{12000 - 80} \right| = 2k_1 + \ln \left| \frac{1}{11999} \right| \Rightarrow 2k_1 = \ln \left| \frac{80}{12000 - 80} \right| - \ln \left| \frac{1}{11999} \right|$$

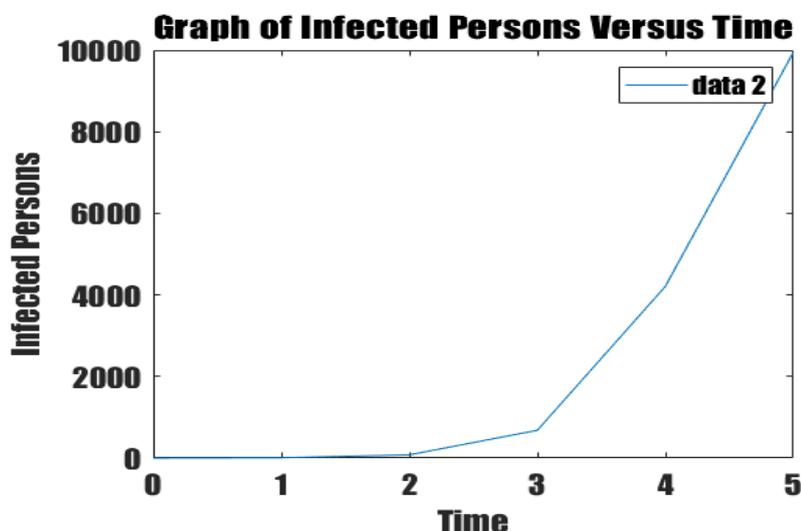
Then $k_1 = 2.194316143$

From here we can plug in the values of t and solve for the values of N . The formula take exponential form and the number of infected people increase meanwhile the susceptible people decrease in unvaccinated populations, we could predict for seven days the population will infect if there are no isolation between infected and susceptible people and good vaccination plans.

The following graphs are display the decreasing of susceptible numbers and increasing of infected persons versus time respectively.



However, above graph depicts that an epidemics has set up and the level of the epidemic is totally at the final stage affecting on average of 996. People in just five days, that is it infected positive is steady from the onset and later it exponentially increase causing a very large damage to the community.



The graph above depicted the infected people against the time in the same community of host at that period in time.

5. CONCLUSION

According to our assumption that there is no separation between infected and non- infected in host communities. In the graphs, there is a decline in the number of non-infected person in that community of host, although, the number of non-infected person ($12000-N$) decline steady and latter reduces sharply showing a threat to the community.

REFERENCE

1. World health Organization, Report 3 April, 2013.
2. World Health Organization “AVIAN Influenza Assessing the pandemic threat” January 2005; WHO/CDS/2005. 29.
3. Blower S, Benoud, Devek, An attempt at a new analysis of the mortality caused by small pox and advantages of innaculation to prevent it, England in, 1966.
4. Mose Ongau Fred, Johana K. Sigey, Jeconiah A. Okello, James M. Okwoyo and Giterere J. Mathematical Modeling on the Control of Measles by Vaccination: Case Study of

- KISII Country, Kenya. The STJ Transaction on Computer Science Engineering and its Application, 2014; 2(3).
5. V.A.A. Jansen and N. Stollenwerk. Model in Measles Outbreaks. Branching Processes: Variation, Growth, and Extinction of Populations. Cambridge University Press @ International Institute for Applied Systems Analysis, 2005.
 6. Differential Transformation Method for SEIR Measles Model. Farah Ashraf. Romana Ashraf, Muhammed Farman, M. O. Ahmed and Maryam Shahid. Department of Mathematics and Statistics, University of Lahore, Pakistan, Sci.In.(Lahore), 2016; 28(5): 4291-4295.
 7. P Abbott and H. Neill, Teach yourself calculus, 2003; 266-277.
 8. Fred Brauer. Compartmental Models in Epidemiology. Department of Mathematics, University of British Columbia, Springer Publication, 2008.
 9. Isaac Bentil (M.Sc Theses). A comparative Analysis on the mathematical models of Pertussis and Measles. Kwame Nkrumah University of Science and Technology, July 2013.
 10. Wayne M. Getz and James O. Lloyd-Smith. Basic Methods for Modeling the Invasion and Spread of Contagious Diseases, American Mathematical Society, 2005.