KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, KUMASI

A SEIR Model to Control Varicella Transmission in Ghana

By

Precious Dakeh Torgbenu

(Bsc. Physics, Postgraduate Diploma in Optometry)

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Declaration

I hereby declare that this submission is my own work towards the award of the M. Phil degree and that, to the best of my knowledge, it contains no material previously published by another person nor material which had been accepted for the award of any other degree of the university, except where due acknowledgement had been made in the text.

Precious Dakeh Torgbenu	.....	.....
Student	Signature	Date

Certified by:

Dr. F.T. Oduro	.....	.....
Supervisor	Signature	Date

Certified by:

Prof. S.K. Amponsah	.....	.....
Head of Department	Signature	Date

Dedication

I dedicate this work to the God of all creations, my wife, children, extended family and all those who inspired me.

Abstract

In this thesis, a SEIR epidemiological model is formulated to help control the transmission of varicella, using clinical varicella data from Ghana Health Service. The thesis is based on the assumption that the population is constant with birth rate equals death rate. First it is shown that there exists a domain where the model is epidemiologically and mathematically well-posed as desired in any population dynamics. Qualitative results show that the model has the disease-free equilibrium point which is locally asymptotically stable for $R_0 < 1$ and unstable for $R_0 > 1$. The Routh-Hurwitz criterion is used to show that the model has an endemic equilibrium point which is locally asymptotically stable when $R_0 > 1$. The basic reproduction number for Ghana is found to be $R_0 = 1.2869$, whiles the herd immunity threshold is found to be $H_I = 22.3\%$. Numerical simulation of the model, using MATLAB and a fouth order Runge-Kuta method suggests that one practical measure, to bring the transmission of the disease under control is early detection of the infectious, for isolated supervised treatment. It is concluded that vaccination is the most important factor to control the spread of varicella in case of an outbreak and that 22.3% of the susceptible population needs to be vaccinated in order to bring the disease under control.

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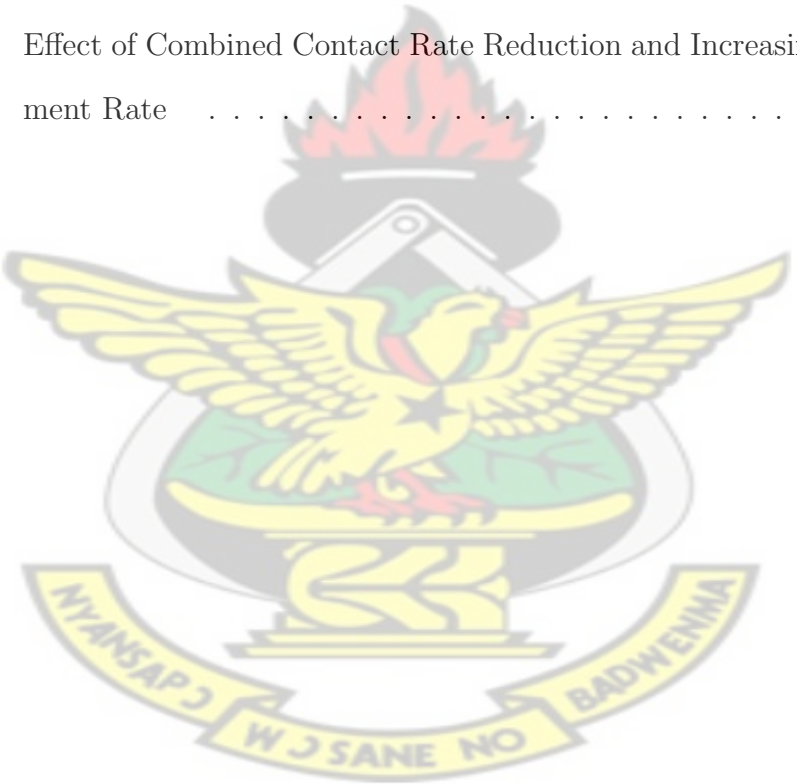

Chapter 1

Introduction

1.1 Background of the Study

Mathematical methods have been proved to be an essential tool in epidemiology. Using mathematical methods to model epidemiology, provides understanding of the epidemic features of the spreading law and control measures of the epidemic.

Global incidence of varicella has been significantly reduced through vaccination, but varicella still remains an important public health problem because vaccination coverage is not globally uniform.

According to the World Health Organization (WHO), chickenpox is one of the endemic diseases in the sub-Saharan country (Providential Aid Organization, 2012).

In 2008, 77,790 cases of chickenpox were recorded in Ghana, 45,512 in 2004, and 19,614 in 2003 and 35,667 in 2002 (Ghana Health Service, Prime Division, Accra).

The first vaccine for varicella was invented in 1974, and a one-dose vaccine was approved for the U.S. national immunization program in 1995. This one dose policy effectively decreased incidences, but failed to prevent outbreaks. The two-dose vaccination program was adopted in 2007 and so far it has been virtually 100% effective in preventing severe cases of varicella and 95% effective in preventing the illness entirely, Gommel et al. (2012).

Varicella is a highly contagious skin rash disease caused by varicella zoster virus

(VZV), Schuette and Hethcote (1999). Primary varicella is an endemic disease. In unvaccinated populations, varicella is primarily a classic childhood illness affecting children from 1 to 14 years, Preblud et al. (1984), with more than 90% of the population in temperate countries developing clinical infection by early adulthood. Varicella confers a lifelong immunity after recovery, Watson et al. (2002), but it remains dormant in the dorsal root ganglia and can reactivate later in life, causing herpes zoster (HZ) Holmes et al. (1996), Garnett and Grenfell (1992).
The average incubation period for varicella is 14 to 16 days, with a range of 10 to 21 days. The infectious period is from 5 days before the rash appears, and up to 6 days afterwards, Baker et al. (2000)

Humans are the only source of infection with the VZV. The virus is transmitted from person to person through the air and by direct contact with the fluid of a rash. When an infected person coughs or sneezes, secretions from the nose and throat become airborne and may infect persons who have not been infected before or who have not been vaccinated. Infection can also occur from contact with contaminated items, such as towels, sheets, and clothing. Additionally, contact with the drainage from zoster lesions can cause chickenpox , Baker et al. (2000).

Protecting children from vaccine-preventable diseases, such as varicella, is among primary goals of health administrators worldwide. Since vaccination turned out to be the most effective strategy against childhood diseases, developing a framework that would predict an optimal vaccine coverage level needed to control the spread of varicella is crucial, Tessa (2006).
Using mathematical methods to model epidemiology, provides understanding of the epidemic features of the spreading law and control measures of the epidemic. This situation motivated us to apply the SEIR epidemic model to effectively model and analyze the disease.

1.2 Problem Statement

Varicella is an unavoidable communicable diseases of childhood, and virtually majority of people infected by adulthood.

Even though this incidence has been globally reduced through vaccination, in Ghana, varicella still remains an important public health problem, since the is no vaccination against the disease and everyone is susceptible .

In August 2008 an outbreak of varicella at the Accident and Emergency Unit of the Korle-Bu Teaching Hospital, as reported by Joy news reporter Isaac Essel on August 26th, resulted in the temporal close down of the unit. This has also been experienced in other hospitals nationwide.

On Tuesday 15th April 2014, there was an outbreak of varicella at the Koforidua Central Prisons, with 20 people infected, as reported by Portia Gabor and Abu Issah Mornnie on TV3 7:00 pm news.

Epidemiology of varicella in Ghana has not been carefully studied and most recent outbreaks indicate a large proportion of people been infected. This situation motivated us to apply the SEIR epidemic model to effectively model and analyze the disease.

1.3 Objectives of the Thesis

The objectives of this thesis are as follows:

1. To formulate a mathematical model to control varicella transmission in Ghana.
2. To determine equilibrium points and perform stability analysis of the model.
3. To investigate the role of the reproductive number and perform simulations.
4. To investigate the effect of vaccination against the spread of varicella.

1.4 Methodology

The data used for this thesis is obtained from Ghana Health Service Directorate. We used SEIR model proposed by Anderson and May (1991) to model the spread of varicella and ordinary differential equations were used to formulate the model equations. Equilibrium points (steady states) and stability analysis were determined, and the basic reproductive number found. Numerical simulation using MATLAB and a fourth order Runge-Kuta method is then performed.

1.5 Justification

Epidemiology of varicella have been extensively studied especially in developed countries. However, few studies have been done in developing countries like Ghana, hence there is not enough mathematical publication specifically looking at varicella epidemics in Ghana. Also, there is no control programme against the spread of the disease in Ghana. Therefore, this thesis will assist decision makers to see the need to implement vaccination programme against the transmission of varicella. The thesis may also assist research scientists to further develop suitable models to help public health professionals to make better strategies for controlling the disease.

1.6 Thesis Organization

The thesis contain five chapters. Chapter one presents the background, problem statement, objectives, methodology, justification and organization of the thesis. Chapter two examines the previous works related to the thesis. Model formulation is presented in chapter three, and equilibrium points, stability analysis, and reproductive number were studied. Chapter four apply our results to vaccination policies, numerical simulation of the model using MATLAB and result discussion. Chapter five is devoted to conclusions and recommendations.

Chapter 2

Literature Review

2.1 Introduction

In this chapter we reviewed the work of other researchers related to the topic.

2.2 Abstracts Relevant to this Thesis

The spread of several communicable diseases have been gainfully studied with mathematical models. Varicella occurs in almost every part of the world. In Ghana the study of the epidemiology of this disease has not been given much attention. Mathematical models can be used to study the spread of this disease. In this chapter some of the previous related studies on the spread of communicable diseases especially varicella have been reviewed.

The application of mathematics to the study of infectious disease was initiated by Daniel Bernoulli in 1760, presented at the Royal Academy of Sciences in Paris. His was to influence public health policy, by using mathematical techniques to evaluate the potential effectiveness of universal vaccination against smallpox. He was utilizing quantitative techniques, and specifically mathematical modeling, to influence public health policy, Lachlan (2008)

The mass-action concept was used by Kermack and McKendrick in 1927 who began to provide a firm theoretical framework for the investigation of observed patterns of the course of an epidemic. The framework of Kermack and McKendrick has evolved to become the classic SIR model for studying population biology, and their framework could be considered the birth of modern mathemat-

ical epidemiology, Lachlan (2008).

According to Kermack and Mckenderick (1927), an epidemic, which acts on a short temporal scale, may be described as a sudden outbreak of a disease that infects a substantial portion of the population in a region before it disappears. Epidemics usually leave many members untouched. Often these attacks recur with intervals of several years between outbreaks, possibly diminishing in severity as populations develop some immunity.

Throughout history, epidemics have had major effects on the course of events. One of the early triumphs of mathematical epidemiology was the formulation of a simple model that predicted behavior very similar to this behavior, observed in countless epidemics. The Kermack and Mckenderick (1927) model is a compartmental based on relatively simple assumptions on the rates of flow between different classes of members of the population.

Another important distinction is between epidemics and endemic situations. An epidemic acts on a short time scale and may be described as a sudden outbreak of a disease that infects a substantial portion of the population in a region before it disappears. Epidemics usually leave many members untouched. In an endemic situation, a disease becomes established in a population and remains for a long time.

In models for epidemics, one usually ignores demographic effects (births and deaths not due to disease) because of the short time scale. The justification for ignoring demographic effects is that the demographic time scale is normally much longer than the disease time scale, and may be neglected. Endemic situations, on the other hand, may endure for years, and it is necessary to include demographic effects in modeling them, Dietz (1982).

According to Arino et al. (2007), in the mathematical modeling of disease trans-

mission, as in most other areas of mathematical modeling, there is always a trade-off between simple models, which omit most details and are designed only to highlight general qualitative behavior, and detailed models, usually designed for specific situations including short-term quantitative predictions. Detailed models are generally difficult or impossible to solve analytically and hence their usefulness for theoretical purposes is limited, although their strategic value may be high.

In their example, very simple models for epidemics predict that an epidemic will die out after some time, leaving a part of the population untouched by disease, and this is also true of models that include control measures. This qualitative principle is not by itself very helpful in suggesting what control measures would be most effective in a given situation, but it implies that a detailed model describing the situation as accurately as possible might be useful for public health professionals.Such a model might have many equations and in practice could only be solved approximately by numerical simulations. This has become feasible in recent years because of the developments in high-speed computing.

Anderson et al. (1986) studied an epidemic such as mumps in the United Kingdom. The work was done on virus transmission, herd immunity and the potential impact of immunization. On their findings children are mostly affected by the disease. However vaccination of susceptible population does not confer permanent immunity, but with regards to SEIR model, permanent immunity would be attained with effective vaccination for a longer period before the vaccination will lose it effectiveness.

Hethcote (2000) introduced SEIR model to describe the spread of epidemics. According to his studies, the dynamics of the disease depends on infection rate, and the removal rate. There is an outbreak of the disease if the reproductive number exceeds unity. The disease dies out in the susceptible population if the

reproductive number is less than one . Moreover, an outbreak of the disease is likely to ensure, if the density of susceptible is high and the removal rate of infection is low. The solution of number of removals depend on infection rate, removal rate, initial number of susceptible and population size. On the other hand the solution of the removal class cannot be used to estimate removals if the outbreak results in large population.

Nokes and Anderson (1986) studied rubella epidemiology in south east England. The disease was characterized by age-dependent changes in the pattern of virus transmission. The rate of infection was low in children than in adults. Immunization against people raised levels of immunity in both children and adults. On average, antibody concentrations recorded a reduction with age and low in vaccinated females than in unvaccinated males.

Kermack and Mckenderick (1927) studied epidemics of measles in United Kingdom. In their study the dynamics of the disease depended on infections rate, the removal rate and relative removal rate. Their work observed that the disease threshold occurs when reproductive number equals to one. There will be an outbreak of the disease if the reproductive number exceeds unity. The disease dies out in the susceptible population if the reproductive number is less than one. Moreover, an outbreak of the disease is likely to ensue if the density of susceptible is high and the removal rate of infectives is low. The expression for the number of the removal or recovered class was ascertained from other equations of the system as a function of time. The solution of number of removals depend on infection rate, removal rate, initial number of susceptibles and population size. Their work observed that the solution of the removal class be used to estimate removals if the outbreak results in large population. More importantly, the qualitative solution of the removal class at equilibrium was not captured in their work.

Li and Zou (2009) applied a generalization of the Kermack and Mckenderick (1927) SIR model to a patchy environment for a disease with latency. Their work assumed that the infectious disease had a fixed latent period in a population. The SIR model for a population living in two cities were formulated. Their model used system of delay differential equations with a fixed delay accounting for the latency and non-local terms caused by the mobility of the individuals during the latent period. The disease later dies out, leaving a certain portion of the susceptible population untouched. Their work revealed that the ratio of the final sizes in two compartments is determined by the ratio of the dispersion rates of the susceptible individuals between the two compartments. Numerical methods were used to explore the dynamics under which the disease dies out and the existence of multiple outbreaks. Their work was found to be inconsistent with that of Kermack and Mckenderick (1927) SIR model.

Alli et al. (2010) reported on the stability of two SIR type models for HIV. An SIR model with birth rate equal to natural death rate was compared with the SIR model with two different infectivies for HIV. The reproductive numbers for the models were determined from spectral radius of the next generation matrix. Two different expressions of reproductive numbers were obtained for the models. In the modified SIR model there were high-infective and higher-infective individuals in the infective class.

Their work observed three different removal rates for infective to high-infectives, from infective to higher-infectives and from infective class to removed class. Modified SIR model involved more dynamics than simple SIR. They observed that if reproductive number is less than unity the infection free equilibrium is locally asymptotically stable for the modified SIR model and unstable for modified SIR model if reproductive number is greater than unity. In simple SIR model, an infectious free equilibrium point was asymptotically stable.

They concluded that the modeled disease observed disease-related factors such

as the infectious agent, mode of transmission and infectious period. Factors such as geographic factors, demographic and economic status of infectious were not captured in their work.

An SIR epidemic model with vital dynamics, incubation time and also with bilinear incidence rate was formulated by Setiawan (2008). The total host population was assumed constant. The threshold value R_O determining whether the disease dies out found. They used Taylor series method to find the root of characteristics of the system. Then, the root of characteristic and the threshold value R_O will be determining the stability of the equilibria of the model which is in the absence of time delay or if it's exist. The result obtained showed that the global dynamics were completely determined by the values of the threshold valueR_O and time delay. If R_O is less than or equal to one, the disease-free equilibrium was globally asymptotically stable (GAS) and the disease always dies out, while if it exceeds one there will be an endemic. Then, by using incubation time length as constant time delay, the local stability for endemic equilibrium was investigated.
The result obtained that the endemic equilibrium was locally asymptotically stable (LAS) for R_O exceeds one and for all positive time delay, or it can be called absolutely locally asymptotically stable (ALAS) when R_O exceeds one.

Age structure of a population affects the dynamics of disease transmission. Traditional transmission dynamics of certain diseases cannot be correctly described by the traditional epidemic models with no age-dependence. A simple model was first proposed by Lotka and Von Foerster where the birth and the death processes were independent of the total population size and so the limitation of the resources were not taken into account. To overcome this deficiency, Gurtin and MacCamy (1974) in their pioneering work considered a nonlinear age-dependent model, where birth and death rates were function of the total population. Various age-structured epidemic models have been investigated by many authors,

and a number of papers have been published on finding the threshold conditions for the disease to become endemic, describing the stability of steady-state solutions, and analyzing the global behavior of these age-structured epidemic models.

With the improvement of human society sanitation, the enhancement of medical level and science technology, many diseases, such as cholera, smallpox, have been controlled by human. However, more and more new viruses are coming. Yulian (2010) investigated the prediction and establishment of SIR model for H1N1 epidemic disease. The H1N1 SIR epidemic model of Hong Kong has been established and the software MatLab was used to write a program for solving the established SIR epidemic model. Through their numerical calculation, their predicted infected curve agrees with their fact infected curve well. The result of the investigation proved that the established SIR epidemic model of H1N1 in Hong Kong is accurate and can be used to analyse the development of H1N1 of Hong Kong in the future. Their result could provide the condition and investigation method for their sanitation department.

Several studies have modeled VZV transmission. Most of these studies are concerned with the effect of vaccination on the long-term epidemiology. Factors such as changes in the age distribution of infection, reduction in case numbers, reductions in morbidity and mortality, and the economic effects of vaccination have all been investigated. The effect of vaccination on herpes zoster (HZ) incidence has also generated substantial interest from the modeling community.

Esson et al. (2014), used the SEIR model to study epidemiology of chickenpox in the Agona West Municipality of Ghana. The study showed that chickenpox is persistent in the municipality with $R_0 = 2$. The stability analysis of disease free and endemic equilibrium point of varicella transmission without vaccination was estimated to be a center. He concluded that varicella in the Municipality

can be prevented by reducing the rate at which people are exposed to the disease.

Martey (2012), used the SIR epidemic model to study varicella transmission in Ghana. He concluded that chickenpox is endemic in Ghana with average patient contact rate of 1.4588 and the reproductive number $R_0 = 1.078$ and that about 7.26% of the susceptible population should be immune in order not to have an epidemic during an outbreak.

Garnett and Grenfell (1992) introduced a quantitative model with the aim of describing VZV transmission dynamics as well as HZ. Their model is a simple compartmental, deterministic model. Infants enter the model into a class with maternal antibodies (M), become susceptible (S), then exposed (E), infectious (I), and finally recover with permanent immunity (R). In the terminology presented above, this is an MSEIR model. The parameters that describe the flow from one compartment to the next are estimated from observed data. Age structure and the rate of zoster occurrence among the recovered add complexity to the model. The effect of age is accounted for by including age-specific forces of infection. Their results concern rates of viral reactivation, which causes HZ in previously infected and recovered individuals. They find that an age-dependent reactivation rate approximates real data better than a constant reactivation rate.

Mathematical modeling is used to investigate VZV transmission in the US population as well as the effectiveness of various control measures by Gommel et al. (2012). In their effort to mathematically model Varicella-Zoster Virus (VZV) and still be able to analyze the models without numerical computer simulation, developed several models to capture the transmission dynamics. In these models, the population is divided into up to seven distinct, disjoint classes, denoted S, I, P, V, J, Z,R and N, respectively standing for susceptible, infected/infectious (with chickenpox), partial immunity (immune to chickenpox), vaccinated against vari-

cella, breakthrough infected/infectious, infected with zoster, recovered/removed and entire population.

Their first and simplest model divides the population into four classes: S, I, R, and Z. Their second model improves upon the first one by removing the ambiguity of the class R; they were not sure whether an individual in the R class is only immune to chickenpox, or immune to both zoster and chickenpox. With this in mind, they created the class P, for individuals who have contracted and recovered from chickenpox but have not yet been infected with shingles. Their third model accounts for the potential for breakthrough cases after vaccination by adding a vaccinated class V (not just by moving vaccinated people to the class P) and a breakthrough infected/infectious class J. Their fourth model is an extension of the third model; it adds the P class back in, and accounts for the zoster vaccine. In addition, they accounted for both doses of the varicella vaccine (not just one), and provided a path for an individual to bypass both chickenpox and zoster and end in the recovered/removed class with the vaccinations and the P class.

For the first two models, the Vaccination Reproduction Number (also known as the basic reproduction number, the basic reproduction ratio, or the basic reproductive rate) was the same and the interpretation for this vaccination reproduction number was identical. The last two model was too complex to find the endemic equilibrium, either by hand or using a computer program, and thus they were unable to list the Endemic Equilibrium (EE). They were, however, able to use the Next Generation Operator Method to find the vaccination reproduction numbers, but could make no claims about the stability of the EE since they were unable to find it.

They developed these four models in an effort to accurately depict the transmission dynamics of the VZV without being so complex that they could not analyze them without computer simulation. As such, more complex models, such as that of Shuette and Hethcote, predict a rise in zoster incidence with a universal vaccination program. Using model number four, their results seem to agree with

the claim that higher zoster rates coincide with higher values for varicella vaccination rate. Their research data also backs the claim that conditions where the Disease-Free Equilibrium (DFE) is unstable do exist when the one-shot varicella vaccination is given at a 90% coverage rate, meaning that breakouts could happen given these conditions, which lead them to believe that the two-dose varicella vaccination program is the most effective way to prevent outbreaks and achieve maximum efficacy.

Socan et al. (2010) studied varicella susceptibility and transmission dynamics in Slovenia. their research revealed that the most appropriate approach to reduce the burden of varicella in Slovenia would be a universal, standard two dose varicella vaccination programme (the first dose administered at 12-18 months and the second at 3-6 years). After the introduction of varicella vaccine in the childhood immunization schedule, a vigilant surveillance of varicella epidemiology should continue in order to promptly identify gaps and unexpected epidemiological changes in both varicella and herpes zoster.

According to Valeika (2008), in 1995, the United States implemented a single-dose strategy of varicella vaccination in infants. Varicella incidence, morbidity, and mortality declined dramatically by roughly 80%, though outbreaks continued, even in highly vaccinated populations, and the incidence of varicella began rising in 2003. These events prompted the recommendation of a two-dose vaccination strategy in 2005. He therefore researched on the epidemiology of varicella under a two-dose vaccination strategy.

A deterministic, age-structured transmission model of the two-dose strategy predicts a large epidemic of varicella in the near future, even with high second-dose coverage rates. In the long-term, incidence rates under a two-dose regime will be 10% or less compared with pre-vaccination rates, compared with up to 50% with a continued one-dose strategy. This study predicts that the resurgence in vari-

cella incidence that has been observed since 2003 will continue and peak in 2015, 20 years after the beginning of the single dose varicella vaccination strategy. The resurgence is a result of a buildup of susceptibles (S) protected by herd-immunity, as well as a buildup of partially susceptible vaccinated individuals (VS) due to waning immunity or sub-optimal response to vaccine, compounded by the decreasing circulation of VZV.

Yusuf and Benyah (2012) presented Optimal control of vaccination and treatment for an SIR epidemiological model. They considered an SIR model with variable size population and formulated an optimal control problem subject to the model with vaccination and treatment as controls. Their main aim was to find the optimal combination of vaccination and treatment strategies that will minimize the cost of the two control measures as well as the number of infectious. The analysis of the model show that the disease free equilibrium is globally asymptotically stable if the basic reproduction ratio is less than one while the endemic equilibrium exists and it is globally asymptotically stable whenever the basic reproduction ratio is greater than one. Their results confirm that the optimal combination of vaccination and treatment approach required to achieve the set objective will depend on the relative cost of the control measures. In conclusion, the results indicate that the case where it is more expensive to vaccine than to treat, resources should be invested in treating the disease until the disease prevalence begins to fall. This option, does not decrease the number of susceptible quickly enough, but rather result in an overall increase in the infected population. On the other hand, if it is more expensive to treat than to vaccine, then more resource should be put into vaccination. This case rather resulted in a rapid decrease in the susceptible as well as an appreciable decrease in the number of infectives. However, the case where both measures are equally expensive showed that the optimal way to derive the epidemic towards eradication within the specified period is to use more of the vaccination control and less of the treatment control initially to de-

rive the epidemic to below certain threshold after which we can then apply less of vaccination control and more of the treatment control.

Flavio and Rowthorny (2009), in their paper used the SI model to fully characterizes the optimal control of a recurrent infectious disease through the use of (non-vaccine) prevention and treatment. The dynamic system may admit multiple steady states and the optimal policy may be path dependent. They found that an optimal path cannot end at a point with maximal prevention; it is necessarily zero or at an intermediate level. In contrast, an optimal path must end at a point at which treatment is either maximal or minimal. They showed that treatment and prevention are imperfect substitutes and may or may not be used in conjunction, depending on the state of the system. This means that optimal paths do not generally approach steady states as rapidly as possible. They showed that for some parameterizations, it is always optimal to go to a specific steady state (either a high or a low prevalence one) while for others, the optimal path and steady state depend on initial conditions and thus there is hysteresis. They found that the comparative statics with respect to the rates of infectivity and recovery may radically differ across steady states, which has important policy implications.

According to Gaff and Schaefer (2009), mathematical models provide a powerful tool for investigating the dynamics and control of infectious diseases, but quantifying the underlying epidemic structure can be challenging especially for new and under-studied diseases. They considered the variations of standard SIR, SIRS, and SEIR epidemiological models to determine the sensitivity of these models to various parameter values that may not be fully known when the models are used to investigate emerging diseases. Optimal control theory was applied to suggest the most effective mitigation strategy to minimize the number of individuals who become infected in the course of an infection while efficiently balancing vaccination and treatment applied to the models with various cost scenarios. The

optimal control simulations suggest that regardless of the particular epidemiological structure and of the comparative cost of mitigation strategies, vaccination, if available, would be an essential tool of any intervention plan. However, if resources allow for the provision of treatment as well, this additional tool is a valuable resource in decreasing the number of individuals who are affected.

Chapter 3

Methodology

3.1 Introduction

This chapter is mainly concerned with developing a SEIR model to control varicella transmission in Ghana, finding threshold conditions for the disease to become endemic and describing the stability of steady-state solutions.

3.2 Why Epidemiological Models

Epidemiology is the study of the distribution and determinants of disease prevalence in humans. One function of epidemiology is to describe the distribution of the disease, i.e. find out who has how much of what, where and when. Another function is to identify the causes or risk factors for diseases in order to find out why everyone does not have the same thing uniformly. A third function of epidemiology is to build and test theories. A fourth function is to plan, implement and evaluate detection, control and prevention programs.

Epidemiology modeling can play an important role in these last two functions. Mathematical models have become important tools in analyzing the spread and control of infectious diseases.Understanding the transmission characteristics of infectious diseases in community, regions and countries can lead to better approaches to decreasing the transmission of diseases.

3.3 Model Formulation

The model we study in this thesis is a SEIR epidemic model. Even though the SIR model provides a general framework to understand the spread of a disease, it may be too simple to accurately model a real epidemic like the outbreak of varicella in Ghana. The limitations in this model, can be overcomed by introducing an Exposed (but not yet infected) class; people have to be exposed to the disease before they can be infected and consequently become infectious, and this is the case for the varicella. A varicella patient becomes infectious only after the infected person develops the symptoms. Hence, the limitations and flaws in the SIR model can be modified and extended to the SEIR model.

The total constant population N(t), is divided into four disease-state compartments: susceptible individuals (S), people who can catch the disease; exposed individuals (E), people whose body is a host for the infectious agent but are not yet able to transmit the disease; infectious (infective) individuals (I), people who have the disease and can transmit the disease; recovered individuals (R), people who have recovered from the disease with permanent immunity.

Let γ be the Recruitment rate , μ be the natural death rate, β be the rate (force) of infection per unit time - the average number of effective contacts with other(susceptible) individuals per infective per unit time , ω is rate at which an infected individual becomes infectious per unit time, α is the rate at which an infectious individual recovered per unit time.

3.3.1 Model Assumptions

The model assumptions for the SEIR model are as follows:

1. People can be infected only through contacts with infectious people except those who are immune, and recovered individuals are permanently immune.

2. The disease does not inflict death on the infected hosts so that the total population density is constant. Thus S(t) + E(t) $+I(t) + R(t) = 1$.

3. There is equal birth and death rates, and all persons, including Newborns are assume to be susceptible.

4. The population is homogeneously mixed (A population that interacts with one another to the same degree) and fixed.

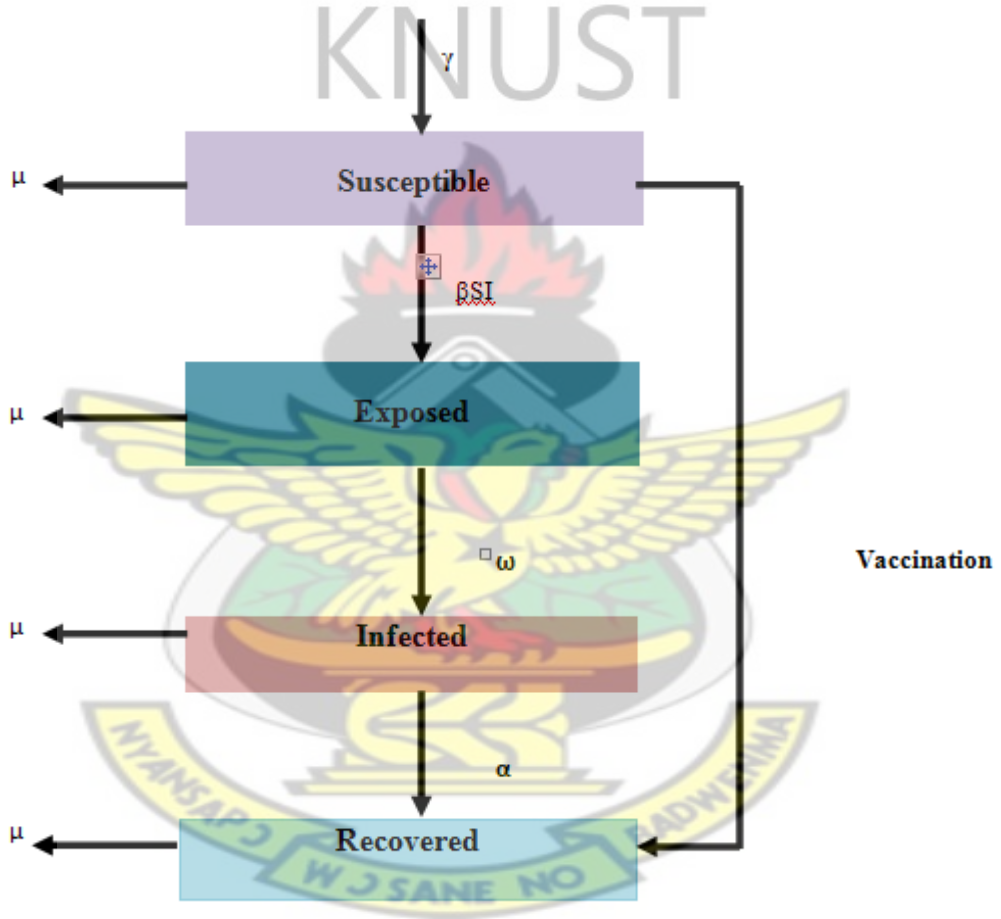

Figure 3.1: The compartmental diagram of SEIR model for Varicella

Where:

S(t) is the number of susceptible individuals at time, t

E(t) is the number of exposed individuals at time, t

I(t) is the number of infected individuals at time, t

R(t) is the number of recovered individuals at time, t

and

γ is the recruitment rate

μ is the natural death rate

β is the contact rate (rate of infection)

ω is the rate at which an infected individual becomes infectious

α is the clinical treatment -recovery rate of humans from the infectious state to the recovered state.

3.3.2 The SEIR Model Equation

From the assumptions, definitions of state variables and parameters and compartmental diagram above, the system of non-linear differential equations which describe the dynamics of varicella outbreak in Ghana are formulated below:

$$\frac{dS}{dt} = \gamma - \mu S - \beta SI$$

$$\frac{dE}{dt} = \beta SI - (\mu + \omega)E$$

$$\frac{dI}{dt} = \omega E - (\mu + \alpha)I$$

$$\frac{dR}{dt} = \alpha I - \mu R$$

with initial conditions

$$S(0) = S_0, \quad E(0) = E_0, \quad I(0) = I_0, \quad R(0) = R_0$$

The total population size $N = S + E + I + R$, is constant and thus $\frac{dN}{dt} = 0$. The disease is assumed not to inflict death on the infected hosts so that the total population density is constant. Thus $S(t) + E(t) + I(t) + R(t) = 1$

The variable R(t) does not appear in the first three equations of the model,

and can always be determined from the relation $R(t) = 1 - S(t) + E(t) + I(t)$. Hence, we will analyze the first three equations, forming our new reduced system of equations as

$$\frac{dS}{dt} = \gamma - \mu S - \beta SI \tag{3.1}$$

$$\frac{dE}{dt} = \beta SI - (\mu + \omega)E \tag{3.2}$$

$$\frac{dI}{dt} = \omega E - (\mu + \alpha)I \tag{3.3}$$

3.3.3 Feasible and Non-Negative Solutions

The feasible solution shows the region in which the solutions of the system (3.1) - (3.3) are biologically meaningful and the positivity of the solutions describes the non-negativity of the solutions of the system (3.1)- (3.3)

Invariant Region

This region can be obtained by the following theorem.

Theorem 3. 1

The solutions of the system (3.1)- (3.3) are feasible for all $t > 0$ if they enter the invariant region Ω.

Proof:

Let $\Omega = (S, E, I) \in R_+^3$ be any solution of the system (3.1)- (3.3) with non-negative initial conditions.

From the model equations, the total population of individuals is given by $N = S + E + I + R$. Therefore adding the first 4 differential equations, results in a first-order linear differential equation of the form

$$\frac{dN}{dt} = \gamma - \mu N \tag{3.4}$$

with an integrating factor $(IF) = e^{\int \mu dt} = e^{\mu t}$

Multiplying both sides of the equation with $e^{\mu t}$ gives

$$\frac{dN}{dt}e^{\mu t} = \gamma e^{\mu t} - \mu N e^{\mu t}$$

and when rearranged it becomes

$$\frac{dN}{dt}e^{\mu t} + \mu N e^{\mu t} = \gamma e^{\mu t} \tag{3.5}$$

and finally

$$\frac{d}{dt}(Ne^{\mu t}) = \gamma e^{\mu t} \tag{3.6}$$

Integrating equation (3.6) on both sides, we have

$$Ne^{\mu t} = \frac{\gamma}{\mu}e^{\mu t} + C \tag{3.7}$$

where C is a constant of integration. Dividing (3.7) through by $e^{\mu t}$ gives

$$N(t) = \frac{\gamma}{\mu} + Ce^{-\mu t} \tag{3.8}$$

applying the initial conditions at $t = 0, N(0) = N_0$ we obtain

$$N_0 = \frac{\gamma}{\mu} + C$$

$\Longrightarrow$

$$C = N_0 - \frac{\gamma}{\mu} \tag{3.9}$$

The solution of the linear differential equation then becomes

$$N(t) = \frac{\gamma}{\mu} + (N_0 - \frac{\gamma}{\mu})e^{-\mu t} \tag{3.10}$$

so that

$$N(t) \leq \frac{\gamma}{\mu} \quad as \;\; t \longrightarrow \infty \tag{3.11}$$

Therefore as $t \longrightarrow \infty$ in (3.11) the population of Ghana N approaches $K = \frac{\gamma}{\mu}$ (that is, $N \longrightarrow K = \frac{\gamma}{\mu}$). The parameter $K = \frac{\gamma}{\mu}$ is usually called the carrying capacity.

Hence all feasible solutions set of the population of the model (3.1) - (3.3) enters the region

$$\Omega = \{(\ S,\ \ E,\ \ I,\ \ ) \in R^3_+ : S + E + I \leq \frac{\gamma}{\mu} \quad S > 0,\ \ (\ \ E,\ \ I) \geq 0,\ \ \}$$

Therefore, the region Ω is positively-invariant (i.e. the solutions exist and remain positive for all times, t) and the model (3.1) - (3.3) is biologically meaningful and mathematically well-posed in the domain Ω.

Positivity of Solutions

For the model to be realistic, we need to make sure that all the variables including R remain positive, since we are dealing with a human population.

Theorem 3. 2

Let the initial data be $\{\ S > 0,\ \ (\ \ E,\ \ I,\ \ ) \geq 0\ \} = \Omega$

Then the solution set { S, E, I, }(t) of the system (3.1) - (3.3) is positive for all $t\ >\ 0$.

Proof

From equation (3.1) we have

$$\frac{dS}{dt} = \gamma - \mu S - \beta SI \geq -\mu S - \beta SI = -(\mu + \beta I)S$$

Rearranging, we have

$$\frac{dS}{S} \geq -(\mu + \beta I)dt$$

Integrating by separation of variables gives

$$\int \frac{dS}{S} \geq -\int (\mu + \beta I)dt \Longrightarrow \ln S \geq -(\mu+\beta)t + C \Longrightarrow S(t) \geq e^{-(\mu+\beta)t+C}$$

$$\Longrightarrow S(t) \geq e^{-(\mu+\beta)t} \times e^{c} = e^{-(\mu+\beta)t} \times A = Ae^{-(\mu+\beta)t}$$

$$At \;\; t = 0, \quad S(0) \geq A = S_0 \Longrightarrow S(t) \geq S_0 e^{-(\mu+\beta)t} \geq 0$$

Therefore

$$S(t) \geq S_0 e^{-(\mu+\beta)t} \geq 0 \;\; since \;\; (\mu+\beta) > 0 \tag{3.12}$$

From equation (3.2)

$$\frac{dE}{dt} = \beta SI - (\mu+\omega)E \geq -(\mu+\omega)E \Longrightarrow \frac{dE}{E} \geq -(\mu+\omega)dt$$

$$\int \frac{dE}{E} \geq \int -(\mu+\omega)dt \Longrightarrow \ln E(t) \geq -(\mu+\omega) + C$$

Therefore

$$E(t) \geq E_0 e^{-(\mu+\omega)t} \geq 0 \;\; at \quad t > 0 \;\; since \;\; (\mu+\omega) > 0 \tag{3.13}$$

From equation (3.3)

$$\frac{dI}{dt} = \omega E - (\mu+\alpha)I \geq -(\mu+\alpha) \Longrightarrow \frac{dI}{I} \geq -(\mu+\alpha)dt$$

$$\int \frac{dI}{I} \geq -\int (\mu+\alpha)dt \Longrightarrow \ln I(t) \geq -(\mu+\alpha) + C$$

Therefore

$$I(t) \geq I_0 e^{-(\mu+\alpha)t} \geq 0 \;\; at \quad t > 0 \quad since \;\; (\mu+\alpha) > 0 \tag{3.14}$$

Hence, all variables are positive for all time $t > 0$. Thus our model has both the invariant and positivity of solutions. Therefore, in the rest of the thesis we will study the system and formulate our results accordingly in the region

$\Omega = \{(\ S,\ \ E,\ \ I,\ \ ) \in R^3_+ \ : S + E + I \leq \ \frac{\gamma}{\mu} \quad S > 0,\ \ (\ \ E,\ \ I) \geq 0,\ \ \}$

3.4 Equilibrium point and Stability

In order to determine the stability of the model, we first evaluate the equilibrium points or steady states of the ordinary differential equations (3.1) - (3.3). Steady state solutions or equilibrium points are the roots or solutions of the system of equations when the right-hand side of a nonlinear system is set to zero.

There two equilibrium points in this model are the Disease-Free (I = 0) and the Endemic ($I \neq 0$). Therefore using the nonlinear system (3.1) - (3.3) , we have

$$\gamma - \mu S - \beta SI = 0 \tag{3.15}$$

$$\beta SI - (\mu + \omega)E = 0 \tag{3.16}$$

$$\omega E - (\mu + \alpha)I = 0 \tag{3.17}$$

3.4.1 The Disease-Free Equilibrium Point (DFE)

Let define the diseased classes as the population that are either exposed or infectious; that is, E and I.

In absence of the disease, this implies that $E = I = 0$, therefore (3.15) - (3.17) reduces to

$$\gamma - \mu S = 0 \tag{3.18}$$

$\Longrightarrow$

$$S^* = \frac{\gamma}{\mu} \tag{3.19}$$

But since birth rate is equal to death rate, i.e $\gamma = \mu \Longrightarrow S^* = 1$. Therefore, the DFE, the state in which there is no infection(in the absence of varicella) in the society, is given by,

$$DFE = (\ S^*, \quad E^*, \quad I^*) = (1, \quad 0, \quad 0\ ). \tag{3.20}$$

3.4.2 An Endemic Equilibrium Point (EEP)

Endemic equilibrium points are steady state solutions where the disease persists in the population.

Adding (3.15) and (3.16), we have

$$\gamma - \mu S - (\mu + \omega)E = 0 \tag{3.21}$$

Let the birth rate be equal to death rate, ie. $\gamma = \mu$

$$S = \frac{-(\mu + \omega)E + \mu}{\mu} \tag{3.22}$$

From (3.17)

$$\omega E = (\mu + \alpha)I$$

$$\Longrightarrow$$

$$I = \frac{\omega E}{(\mu + \alpha)} \tag{3.23}$$

From (3.16)

$$\beta SI - (\mu + \omega)E = 0$$

But from (3.22) and (3.23) above, we have

$$\beta[\frac{-(\mu + \omega)E + \mu}{\mu}][\frac{\omega E}{(\mu + \alpha)}] - (\mu + \omega)E = 0$$

$$\frac{-\beta(\mu + \omega)\omega E^2 + (\beta\mu\omega E)}{\mu(\mu + \alpha)} - (\mu + \omega)E = 0$$

$$E[\frac{-\beta(\mu + \omega)\omega E}{\mu(\mu + \alpha)} + \frac{\beta\mu\omega}{\mu(\mu + \alpha)} - (\mu + \omega)] = 0$$

Therefore either $E = 0$ or

$$\frac{-\beta(\mu+\omega)\omega E}{\mu(\mu+\alpha)} + \frac{\beta\mu\omega}{\mu(\mu+\alpha)} - (\mu+\omega) = 0$$

$$(\mu+\omega)\beta\omega E = \beta\mu\omega - \mu(\mu+\alpha)(\mu+\omega)$$

$$E = \frac{\mu}{(\mu+\omega)} - \frac{\mu(\mu+\alpha)}{\beta\omega} = \frac{\mu}{(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}]$$

Therefore

$$\mathbf{E}^e = \frac{\mu}{(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}] \tag{3.24}$$

From(3.24) and (3.22), we have

$$S = \frac{-(\mu+\omega)E + \mu}{\mu}, \quad E = \frac{\mu}{(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}]$$

$\Longrightarrow$

$$S = \frac{-(\mu+\omega)\{\frac{\mu}{(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}]\} + \mu}{\mu}$$

$$S = -1 + \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega} + 1 = \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}$$

Therefore

$$\mathbf{S}^e = \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega} \tag{3.25}$$

Again from (3.23) and (3.24)

$$I = \frac{\omega E}{(\mu+\alpha)}, \quad E = \frac{\mu}{(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}]$$

Thus

$$I = \frac{\omega\mu}{(\mu+\alpha)(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}]$$

Therefore

$$\mathbf{I}^e = \frac{\omega\mu}{(\mu+\alpha)(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}] \tag{3.26}$$

Therefore, the EEP of the varicella model (3.1) - (3.3) is given by,

$$EEP = \{\frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}, \frac{\mu}{(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}],$$

$$\frac{\omega\mu}{(\mu+\alpha)(\mu+\omega)}[1 - \frac{(\mu+\omega)(\mu+\alpha)}{\beta\omega}] \tag{3.27}$$

3.4.3 Basic Reproductive Number (R_0) of the Model

The basic reproduction number R_o (Kermack and McKendrick, 1927), is defined as the average number of Secondary infections that occur when one infective individual is introduced into a susceptible population with no immunity to the disease, in the absence of interventions.

Therefore, when $R_0 < 1$, the DFE is locally asymptotically stable and the EEP is unstable, that is the disease dies out . When $R_0 > 1$, it follows that an infected individual will cause more than one additional infection on average, and thus the disease will spread and the EEP will be stable, whereas the DFE will be unstable. When $R_o = 1$, then the disease becomes endemic, meaning the disease remains in the population at a constant rate. This means that the threshold quantity for eradicating the disease is to reduce the value of R_o to value less than one. R_o is an important factor in determining targets for vaccination coverage.

R_o is determined by the dominant eigenvalue of the Jacobian matrix at the DFE. We now calculate our R_0 using the Next Generation Matrix Approach comprising

two matrices F and V. The elements in matrix F constitute the new infections that will arise, while that of matrix V constitute the transfer of infections from one compartment to another.

The Next Generation Matrix is defined as

$$K = FV^{-1} \tag{3.28}$$

R_0 is the dominant eigenvalue value or spectral radius of the Next Generation Matrix. Rearranging the system (3.1) to (3.3) and separating new infections F from other transitions V. We have

$$\begin{aligned} \frac{dE}{dt} &= \beta SI - (\mu+\omega)E..... = A(E,I,S) \\ \frac{dI}{dt} &= \omega E - (\mu+\alpha)I..... = B(E,I,S) \\ \frac{dS}{dt} &= \gamma - \mu S - \beta SI..... = C(E,I,S) \end{aligned} \tag{3.29}$$

Linearization of the SEIR model gives the Generation matrix (G) evaluated at the Disease Free Equilibrium.

$$G(E,I,S) = \begin{bmatrix} A_E & A_I & A_S \\ B_E & B_I & B_S \\ C_E & C_I & C_S \end{bmatrix} \tag{3.30}$$

Since A and B form a subsystem describing the generation and transition of infections, the Jacobian matrix associated with the linearized subsystem at Disease Free Equilibrium (DFE) is given by,

$$J(E,I) = \begin{bmatrix} \frac{\partial A_E}{\partial E} & \frac{\partial A_I}{\partial I} \\ \frac{\partial B_E}{\partial E} & \frac{\partial B_I}{\partial I} \end{bmatrix} \tag{3.31}$$

Therefore from equation (3.29) above, the Jacobian matrix becomes

$$J(E,I) = \begin{bmatrix} -\mu-\omega & \beta S \\ \omega & -\mu-\alpha \end{bmatrix} \tag{3.32}$$

Therefore at the DFE,

$$J(1,0) = \begin{bmatrix} -\mu-\omega & \beta \\ \omega & -\mu-\alpha \end{bmatrix} \tag{3.33}$$

$J(1,0)$ is decomposed as $F-V$, where F is the transition matrix describing the changes in individual states. The DFE is locally asymptotically stable provided that $R_o < 1$,where as if $R_o > 1$, then the disease free equilibrium is unstable. For the disease state

$$J(1,0) = F - V = \begin{bmatrix} -\mu-\omega & \beta \\ \omega & -\mu-\alpha \end{bmatrix} \tag{3.34}$$

$$J(1,0) = F - V = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} - \begin{bmatrix} \mu+\omega & 0 \\ -\omega & \mu+\alpha \end{bmatrix}$$

Therefore

$$F = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} \quad and \;\; V = \begin{bmatrix} \mu+\omega & 0 \\ -\omega & \mu+\alpha \end{bmatrix} \tag{3.35}$$

$$V^{-1} = \frac{1}{(\mu+\omega)(\mu+\alpha)} \begin{bmatrix} \mu+\alpha & 0 \\ \omega & \mu+\omega \end{bmatrix} = \begin{bmatrix} \frac{1}{\mu+\omega} & 0 \\ \frac{\omega}{(\mu+\omega)(\mu+\alpha)} & \frac{1}{\mu+\alpha} \end{bmatrix}$$

$$K = FV^{-1} = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\mu+\omega} & 0 \\ \frac{\omega}{(\mu+\omega)(\mu+\alpha)} & \frac{1}{\mu+\alpha} \end{bmatrix}$$

$$K = FV^{-1} = \begin{bmatrix} \frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)} & \frac{\beta}{\mu+\alpha} \\ 0 & 0 \end{bmatrix} \tag{3.36}$$

From (3.36), we can now calculate the eigenvalues to determine the basic reproduction number R_o by taking the spectral radius (dominant eigenvalue) of the matrix K. This is computed as $\left|K - \lambda I\right| = 0,$ and so we have

$$\begin{vmatrix} \frac{\beta\omega}{(\mu+\lambda)(\mu+\alpha)} - \lambda & \frac{\beta}{\mu+\alpha} \\ 0 & -\lambda \end{vmatrix} = 0 \tag{3.37}$$

$$(\frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)} - \lambda)(-\lambda) = 0$$

Therefore

$$(\frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)} - \lambda) = 0 \quad or \quad -\lambda = 0$$

$$\Longrightarrow$$

$$\lambda = \frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)} \quad or \quad \lambda = 0$$

Therefore the dominant eigenvalue of the matrix K is $\lambda = \frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)}$.

Hence the basic reproduction number

$$R_o = \frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)} \tag{3.38}$$

Comparing (3.25) and (3.38) , it is clear that $S^e = \frac{1}{R_o}$.

Therefore, the EEP is given by,

$$EEP = (\ S^e, E^e, I^e) = \frac{1}{R_0}, \quad \frac{\mu}{(\mu+\omega)}[1 - \frac{1}{R_0}], \quad \frac{\mu}{\beta}[R_o - 1] \tag{3.39}$$

3.4.4 Stability Analysis of Disease-Free Equilibrium (DFE)

The DFE of the system is asymptotically stable if $R_0 < 1$. To determine the local stability of the system at the DFE, we consider the linearized form of the varicella model (3.1) - (3.3) below about the equilibrium point.

$$\frac{dS}{dt} = \gamma - \mu S - \beta SI$$
$$\frac{dE}{dt} = \beta SI - (\mu + \omega)E$$
$$\frac{dI}{dt} = \omega E - (\mu + \alpha)I$$

The Jacobian matrix J of the system is

$$J = \begin{bmatrix} -(\mu + \beta I) & 0 & -\beta S \\ \beta I & -(\mu + \omega) & \beta S \\ 0 & \omega & -(\mu + \alpha) \end{bmatrix}$$

Therefore at the disease-free equilibrium

$$J(1,0,0) = \begin{bmatrix} -\mu & 0 & -\beta \\ 0 & -(\mu + \omega) & \beta \\ 0 & \omega & -(\mu + \alpha) \end{bmatrix} \tag{3.40}$$

The eigenvalues of the Jacobian matrix are the solutions of the characteristic equation

$$\left| J - \lambda I \right| = 0$$

That is

$$\begin{vmatrix} -\mu - \lambda & 0 & -\beta \\ 0 & -(\mu + \omega) - \lambda & \beta \\ 0 & \omega & -(\mu + \alpha) - \lambda \end{vmatrix} = 0$$

Thus, $\lambda = -\mu$ is one of the eigenvalues, and the other two are the roots of,

$$\lambda^2 + (\alpha + \omega + 2\mu)\lambda + (\mu + \alpha)(\mu + \omega) - \beta\omega = 0 \tag{3.41}$$

All the eigenvalues being negative means that the disease-free equilibrium is asymptotically stable.

Hence the DFE $(1, 0, 0)$ is locally asymptotically stable provided that $R_o < 1$, that is, $\beta\omega < (\mu + \omega)(\mu + \alpha)$. Where as if $R_o > 1$, then the DFE is unstable, that is the system is said to be uniformly persistent.

3.4.5 Stability Analysis of Endemic Equilibrium Point (EEP)

The endemic equilibrium point is asymptotically stable if $R_0 > 1$. The system has an endemic infection because of the introduction of those with secondary infection. To determine this, we linearized the Jacobian matrix J evaluated at the endemic equilibrium point. The Jacobian matrix of the system is

$$J = \begin{bmatrix} -(\mu + \beta I) & 0 & -\beta S \\ \beta I & -(\mu + \omega) & \beta S \\ 0 & \omega & -(\mu + \alpha) \end{bmatrix}$$

At the endemic equilibrium point $S^e = \frac{1}{R_0}, E^e = \frac{\mu}{(\mu+\omega)}[1 - \frac{1}{R_0}], I^e = \frac{\mu}{\beta}[R_o - 1]$

Inserting (S^e, E^e, I^e) into the Jacobian matrix gives

$$J = \begin{bmatrix} -\mu R_o & 0 & -\beta\frac{1}{R_0} \\ \mu(R_o - 1) & -(\mu + \omega) & \beta\frac{1}{R_0} \\ 0 & \omega & -(\mu + \alpha) \end{bmatrix} \tag{3.42}$$

We determine the eigenvalues by calculating the determinants of the Jacobian matrix. Thus

$$det(J-\lambda I)=\begin{vmatrix} -\mu R_o-\lambda & 0 & -\beta\frac{1}{R_0} \\ \mu(R_o-1) & -(\mu+\omega)-\lambda & \beta\frac{1}{R_0} \\ 0 & \omega & -(\mu+\alpha)-\lambda \end{vmatrix} = 0$$

To compute the determinant of the above matrix, we divide the above matrix into three 2×2 matrices and find their determinants. Let

$$d_1=\begin{vmatrix} -(\mu+\omega)-\lambda & \beta\frac{1}{R_0} \\ \omega & -(\mu+\alpha)-\lambda \end{vmatrix}$$

$$d_2=\begin{vmatrix} \mu(R_o-1) & \beta\frac{1}{R_0} \\ 0 & -(\mu+\alpha)-\lambda \end{vmatrix}$$

and

$$d_3=\begin{vmatrix} \mu(R_o-1) & -(\mu+\omega)-\lambda \\ 0 & \omega \end{vmatrix}$$

$$det(J-\lambda I)=(-\mu R_o-\lambda)\times d_1-0\times d_2+(-\beta\tfrac{1}{R_0}\times d_3)=0$$

$$det(J-\lambda I)=(-\mu R_o-\lambda)\times d_1-\beta\frac{1}{R_0}\times d_3=0 \tag{3.43}$$

Now calculating the values of d_1, d_2 and d_3, we have

$$d_1=(\mu+\omega+\lambda)(\mu+\alpha+\lambda)-\tfrac{\omega\beta}{R_0}=\lambda^2+[(\mu+\omega)+(\mu+\alpha)]\lambda+(\mu+\omega)(\mu+\alpha)-\tfrac{\omega\beta}{R_0}$$

$$d_2=(\mu(R_o-1))(-(\mu+\alpha)-\lambda)$$

$$d_3=\mu\omega(R_o-1)$$

Substituting the values of d_1, d_2 and d_3, we have

$$(-\mu R_o-\lambda)\times[\lambda^2+[(\mu+\omega)+(\mu+\alpha)]\lambda+(\mu+\omega)(\mu+\alpha)-\tfrac{\omega\beta}{R_0}]+\tfrac{\beta\mu\omega}{R_0}(1-R_o)=0$$

$$\lambda^3+[(\mu+\omega)+(\mu+\alpha)+\mu R_o]\lambda^2+\mu R_o[(\mu+\omega)+(\mu+\alpha)]\lambda+\mu(\mu+\omega)(\mu+\alpha)[R_o-1]=0 \tag{3.44}$$

and is of the form

$$\lambda^3+a_1\lambda^2+a_2\lambda+a_3=0 \tag{3.45}$$

where

$$a_1=(\mu+\omega)+(\mu+\alpha)+\mu R_o>0$$

$$a_2=\mu R_o[(\mu+\omega)+(\mu+\alpha)]>0$$

$$a_3=\mu(\mu+\omega)(\mu+\alpha)[R_o-1]$$

which implies that

$$a_3=\begin{cases}>0 & \text{if} R_o>1,\\ <0 & \text{if} R_o<1.\end{cases}$$

Using the Routh-Hurwitz Criteria on (3.44), we can prove that all roots of the polynomial (3.44) have negative real parts. This criteria give the necessary and sufficient conditions for all of the roots of the characteristic polynomial (with real coefficients) to lie in the left half of the complex plane, Flores (2011).

Routh-Hurwitz Criteria

Theorem 3.3

Given the polynomial

$$P(\lambda)=\lambda^n+a_1\lambda^{n-1}+...+a_{n-1}\lambda+a_n$$

where the coefficients a_i are real constants, $i = 1, ...,$ define the n Hurwitz matrices using the coefficients a_i of the characteristic polynomial:

$$H_1 = \begin{bmatrix} a_1 \end{bmatrix}, \quad H_2 = \begin{bmatrix} a_1 & 1 \\ a_3 & a_2 \end{bmatrix}, H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{bmatrix}, H_n = \begin{bmatrix} a_1 & 1 & 0 & 0 & ... & 0 \\ a_3 & a_2 & a_1 & 1 & ... & 0 \\ a_5 & a_4 & a_3 & a_2 & ... & 0 \\ . & . & . & . & ... & . \\ 0 & 0 & 0 & 0 & ... & a_n \end{bmatrix}$$

where $a_j = 0$ if $j > n$. All of the roots of the polynomial $P(\lambda)$ are negatives or have negative real parts if and only if the determinants of all Hurwitz matrices are positive:

$$det(H_j) > 0, j = 1, \ 2, \ ..., n.$$

For the characteristic polynomial in (3.44), when $n = 3$, the Routh-Hurwitz criteria are

$$a_1, a_2, a_3 > 0 \ , \ det(H_1) = a_1 > 0, \quad det(H_2) = \begin{vmatrix} a_1 & 1 \\ 0 & a_2 \end{vmatrix} = a_1 a_2 > 0$$

$$det(H_3) = \begin{vmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ 0 & 0 & a_3 \end{vmatrix} = a_1 a_2 a_3 - a_3^2 = a_1 a_2 - a_3 > 0$$

$$a_1 a_2 - a_3 = ((\mu+\omega)+(\mu+\alpha)+\mu R_o)([(\mu+\omega)+(\mu+\alpha)]\mu R_o) - \mu(\mu+\omega)(\mu+\alpha) > 0$$

$$a_1 a_2 - a_3 = 2\mu^3 R_o^2 + \omega\mu^2 R_o^2 + \alpha\mu^2 R_o^2 + 4\mu^3 R_o + 4\omega\mu^2 R_o + 4\alpha\mu^2 R_o + \omega^2 \mu R_o + 2\alpha\omega\mu R_o + \alpha^2 \mu R_o - \mu^3 - \omega\mu^2 - \alpha\mu^2 - \alpha\omega\mu > 0$$

According to the Routh-Hurwitz criterion, the eigenvalues of the matrix have negative real parts if and only if the following inequalities hold,

$a_1,\ \ a_2,\ \ a_3\ \ > 0 \quad$ and $\quad a_1a_2 - a_3 > 0.$

For $R_o > 1$, we have $a_1, \quad a_2, \quad a_3 \quad > 0 \quad$ and $\quad a_1a_2 - a_3 > 0$, and this shows that the **EEP** is locally asymptotically stable.

3.5 Optimal Vaccination Strategies

3.5.1 Herd Immunity Threshold

Herd Immunity is a type of community protection from disease that occurs when the vaccination of a portion of the population (or herd) provides protection to unvaccinated individuals by making it less likely that any infected individual will contact a susceptible individual and thus pass on the disease.

Vaccination is an effective way to control the transmission of varicella. Interrupting horizontal transmission by appropriate immunization program is expected to have a significant impact on the rate of acquisition of new infected.
One Purpose of vaccination is that it reduces the incidence of the disease in those immunized, the susceptibles. Also, vaccination protects indirectly non-vaccinated susceptibles against infection by producing herd immunity, while having the amount of infected people to be very small, Tessa (2006). The Herd Immunity Threshold H_I is the percentage of the population that needs to be immune to control transmission of a disease.

The Condition for Control

The Herd Immunity Threshold H_I, is the proportion immune after a vaccination campaign. Recall that, for a stable state: $R_o \times S = 1$, so that, S will be $(1 - H_I)$. Hence the control condition to be fulfilled is: $R_o \times (1 - H_I) < 1$. This means $R_o \times (1 - H_I) = 1 \Longleftrightarrow 1 - H_I = \frac{1}{R_o}$

Therefore

$$H_I = 1 - \frac{1}{R_o} \tag{3.46}$$

As the amount of vaccinations increase, the herd immunity threshold also increases. By decreasing the amount of susceptible people, the herd immunity threshold decreases.

3.5.2 Control Vaccination Number

The Control Vaccination Number, denoted C_v , is the average number of secondary cases generated by an infectious case during epidemic with control measures, i.e. vaccinations. The formula for estimating the control vaccination number is given by is the average number of secondary cases generated by an infectious case during epidemic with control measures, i.e. vaccinations Where h is the vaccine efficacy (the effectiveness of the vaccine) and f is vaccination coverage (the fraction of the population that has been vaccinated). The goal of researchers and health officials is to have $C_v < 1$. Having $C_v < 1$, and knowing the efficacy of the vaccine we can estimate the proportion of the population that need to be vaccinated. This is given by

$$f > \frac{1 - (\frac{1}{R_o})}{h} \tag{3.47}$$

Chapter 4

Analysis

4.1 Introduction

In this chapter, we use the varicella model in chapter three to analyze clinical varicella data in Ghana. Numerical simulations using MATLAB and a fourth order Runge-Kuta method will also be performed.

4.2 Parameter Estimation

The parameters in the model were estimated using clinical varicella data and demographics statistics of Ghana. Those that were not available were obtained from literature published by researchers in varicella endemic countries which have similar environmental conditions comparable to Ghana.

The latency rate ω, by which exposed become infectious can be derived from the average latency period $(1/\omega)$, and the recovery rate α, can be obtained from the average duration of the infectious period $(1/\alpha)$. The average latency period $(1/\omega)$ for varicella is about 14 days, Valeika (2008), Schuette and Hethcote (1999), Garnett and Grenfell (1992), and Thrasher (1996), so that the latency rate, $\omega = (1/14)$ per day.

The average infectious period is estimated to be 7 days, Hethcote (2000) and Schuette and Hethcote (1999) so that the recovery rate, $\alpha = 1/7$ per day. The birth rate (γ) and the death rate (μ) are assumed to be equal to keep the total population (N) constant. The death rate (μ) is based on the 65.32 year life expectancy of Ghana, (2013 CIA World Factbook, Index Mundi, 2013 est.).

The contact rate is estimated to be 0.184.

The parameter values are summarized in table 4.1 below.

Parameter	Description	Values	Data Source
γ	recruitment rate	1/(65.32 x 365) per day	Index Mundi, 2013
μ	natural death rate	1/(65.32 x 365) per day	Index Mundi, 2013
β	contact rate	0.184	Estimated
ω	latency rate	1/14 per day	Garnett and Grenfell (1992)
α	recovery rate	1/7 per day	Schuette and Hethcote (1999)

Table 4.1: Estimated Parameter values and their Sources

4.3 Basic Reproductive Number R_o

The basic reproduction number is given by:

$$R_o = \frac{\beta\omega}{(\mu+\omega)(\mu+\alpha)} = \frac{(0.184)(\frac{1}{14})}{(0.00004194+\frac{1}{14})(0.00004194+\frac{1}{7})}$$

$$R_o = 1.2869 \tag{4.1}$$

Since the reproductive number, $R_o = 1.2869 > 1$, the presence of a person infected with varicella virus will eventually result in an outbreak of the disease in Ghana. Also the number of contacts between susceptibles and varicella patients during

the infectious period is

$$\sigma = \frac{\beta}{\alpha} = \frac{0.184}{0.1429} = 1.2876 \tag{4.2}$$

Meaning that on the average 1429 varicella patients contacts 1840 susceptible people in the country during an infectious period.

4.4 Equilibrium point and Stability

4.4.1 Stability Analysis of Disease-Free Equilibrium (DFE)

From (3.20), the DFE is $DFE = (1, \quad 0, \quad 0 \quad)$. From (3.40), the Jacobian matrix (J) of the varicella model at disease-free equilibrium point is given by

$$J(1,0,0) = \begin{bmatrix} -\mu & 0 & -\beta \\ 0 & -(\mu+\omega) & \beta \\ 0 & \omega & -(\mu+\alpha) \end{bmatrix} = \begin{bmatrix} -0.00004194 & 0 & -0.184 \\ 0 & -0.07147 & 0.184 \\ 0 & 0.07143 & -0.1429 \end{bmatrix}$$

Thus, $\lambda_1 = -0.00004194$ is one of the eigenvalues, and the other two are the roots of,

$$\lambda^2 + (\alpha + \omega + 2\mu)\lambda + (\mu + \alpha)(\mu + \omega) - \beta\omega = 0$$

$$\lambda^2 + (\frac{1}{7} + \frac{1}{14} + 2 \times 0.00004194)\lambda + (0.1429)(0.07147) - (0.184 \times \frac{1}{14}) = 0$$

$$\lambda^2 + 0.2144\lambda - 0.002930 = 0$$

Now by using

$$\lambda_{2,3} = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}$$

where $a = 1, \quad b = 0.2144, \quad \text{and} \quad c = -0.002930$, we have

$$\lambda_{2,3} = \frac{-0.2144 \pm \sqrt{(0.2144)^2 - 4(1)(-0.002930)}}{2(1)} = \frac{-0.2144 \pm 0.2402}{2}$$

$$\lambda_2 = -0.2278, \quad \lambda_3 = 0.0129$$

Since all the roots of the equation are not negative, the DFE is locally asymptotically unstable, meaning that the presence of an infectious person in Ghana will eventually result in an outbreak of the disease.

4.4.2 Stability Analysis of Endemic Equilibrium Point (EEP)

From(3.39), the endemic equilibrium point is given by,

$$EEP = (\ S^e, E^e, I^e) = \tfrac{1}{R_0}, \quad \tfrac{\mu}{(\mu+\omega)}[1 - \tfrac{1}{R_0}], \quad \tfrac{\mu}{\beta}[R_o - 1]$$

$$EEP = (\ S^e, E^e, I^e) = (0.7771, \quad 0.0001308, \quad 0.00006539) \tag{4.3}$$

From (3.42), the Jacobian matrix at the endemic equilibrium point is,

$$J = \begin{bmatrix} -\mu R_o & 0 & -\beta\frac{1}{R_0} \\ \mu(R_o - 1) & -(\mu+\omega) & \beta\frac{1}{R_0} \\ 0 & \omega & -(\mu+\alpha) \end{bmatrix}$$

Now we determine the eigenvalues of J by calculating the determinants of the Jacobian matrix above.

Using (3.44), the characteristic equation of the Jacobian matrix is given by

$$\lambda^3 + [(\mu+\omega)+(\mu+\alpha)+\mu R_o]\lambda^2 + \mu R_o[(\mu+\omega)+(\mu+\alpha)]\lambda + \mu(\mu+\omega)(\mu+\alpha)[R_o - 1] = 0$$

and is of the form $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$, where

$$a_1 = (\mu + \omega) + (\mu + \alpha) + \mu R_o > 0$$

$$a_2 = \mu R_o[(\mu + \omega) + (\mu + \alpha)] > 0$$

$$a_3 = \mu(\mu + \omega)(\mu + \alpha)[R_o - 1]$$

Putting in the values of the parameters we have

$a_1 = 2.144 \times 10^{-1}$, $a_2 = 1.157 \times 10^{-5}$, $a_3 = 1.229 \times 10^{-7}$ and

$a_1 a_2 - a_3 = 2.358 \times 10^{-6}$

According to the Routh-Hurwitz criterion, the eigenvalues of the matrix have negative real parts if and only if the following inequalities hold,

$a_1,\ a_2,\ a_3\ > 0$ and $a_1 a_2 - a_3 > 0$.

And from the calculations aboves, for $R_o > 1$, we have $a_1,\ a_2,\ a_3\ > 0$ and $a_1 a_2 - a_3 > 0$, and this shows that the **EEP** is locally asymptotically stable. This means that varicella will spread in Ghana.

4.5 Optimal Vaccination Strategies

4.5.1 Herd Immunity Threshold

Herd Immunity Theory proposes that in contagious diseases that are transmitted from individual to individual, chains of infection are likely to be disrupted when large numbers of a population are immune or less susceptible to the disease. From equation (3.46), we estimate our Herd Immunity Threshold H_I.

$$H_I = 1 - \frac{1}{R_o} = 1 - \frac{1}{1.2869} = 1 - 0.777$$

$$H_I = 0.2229 \tag{4.4}$$

Thus about $H_I = 22.3\%$ of the susceptible Ghanaian population should be immune in order to bring the spread of varicella under total control. This means that if the proportion of immune individuals exceeds this level due to a mass vaccination programme, the disease will die out, because unvaccinated individuals are indirectly protected by vaccinated individuals.

4.5.2 Control Vaccination Number

Research has shown that the vaccine for varicella has 99% effectiveness in the first year, and after eight years the effectiveness drops to 87%, Valeika (2008). Knowing the efficacy of the vaccine we estimate the proportion of the population that need to be vaccinated.

This is given by

$$f > \frac{1-(\frac{1}{1.2869})}{0.99} \quad and \quad f > \frac{1-(\frac{1}{1.2869})}{0.87}$$

$$f > 0.2252 \quad and \quad f > 0.2562$$

We can observe from calculations above that when the effectiveness is 99%, then about 22.5% of the population need to be vaccinated in order for $C_v < 1$. When the effectiveness is 87% then about 25.6% of the population need to be vaccinated in order for $C_v < 1$.

4.6 Numerical Simulations of the Model

In this section, we present the numerical analysis of the model. A numerical simulation of the model is conducted to find out the dynamics of the disease in the human population. The simulations were conducted using MATLAB and a fourth order Runge-Kuta method. The initial conditions in terms of proportion used were $S(0) = 1, \quad E(0) = 0.000926,, \quad I(0) = 0.00176, \quad R(0) = 0.00176$

(Appendix B).

From the simulation we obtain the graph below.

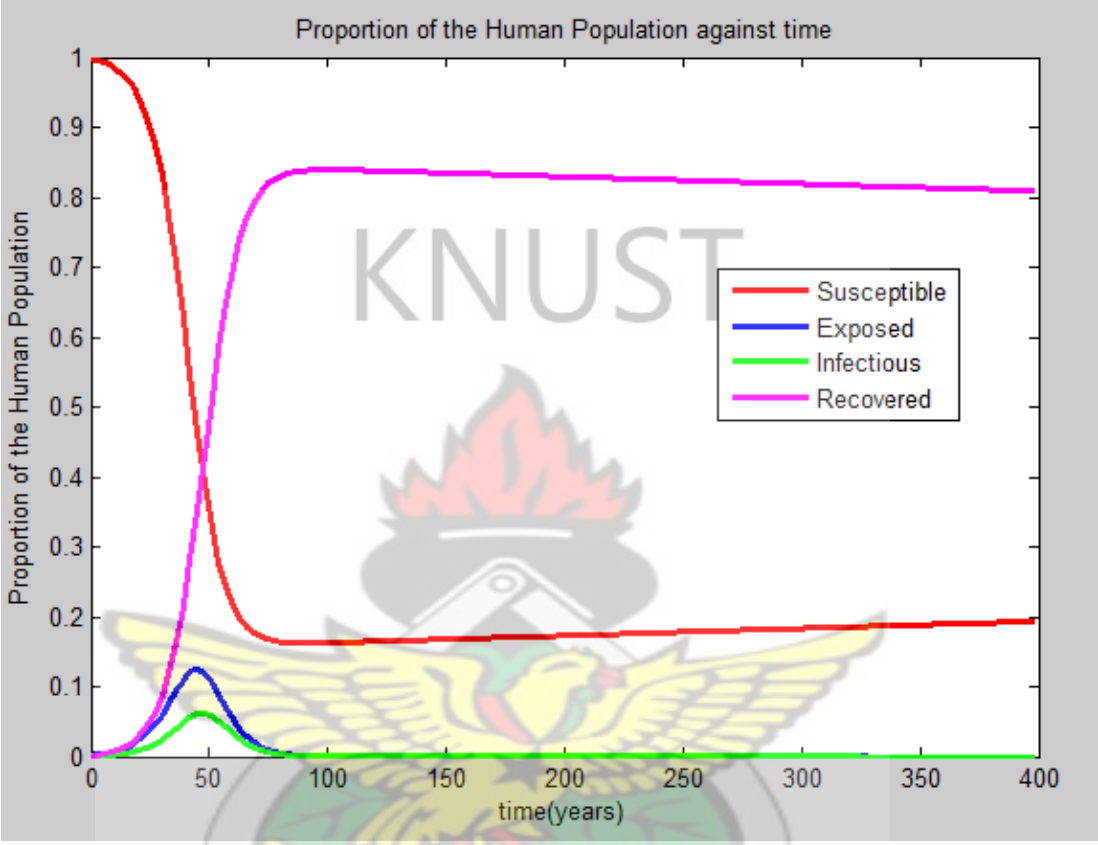

Figure 4.1: Dynamics of SEIR Compartmental Model of Varicella

This simulation shows that the epidemic builds up to where almost 6% of the population is infected, and then declines, whiles the exposed group builds up to about 12% and then declines. In the end almost 80% of the population will have become infected and immune to any subsequent outbreak.

About 20% of the population never gets the disease and remains susceptible to the infectious disease. The simulation also shows that the number of infected individuals and exposed individuals sharply decreases to zero. After about 85 years, the disease seems to disappears from the host population.

We now consider the effects of varying the main parameters responsible for con-

trolling varicella.

We consider the effect of:

- Reducing the contact rate (β) on the model.
- Increasing the treatment rate (α) of infectious humans on model.
- Combining the reduction in the contact rate and the increase in the treatment rate of infectious humans on model.

4.6.1 Simulation of the Effect of Reducing the Contact Rate on the Model

The contact rate of the infection can be reduced by early detection for isolated supervised treatment. The value of the contact rate is reduced to $\frac{2}{3}$, resulting in the portrait below.

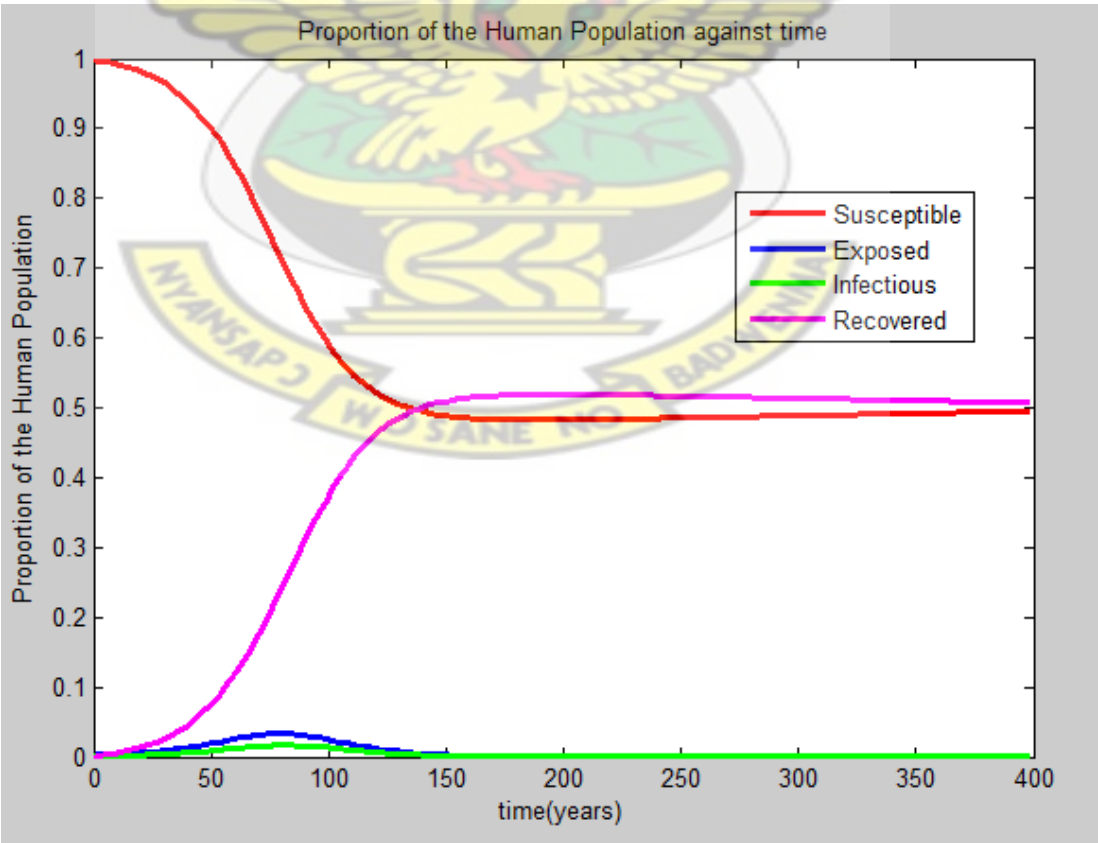

Figure 4.2: Effect of Reducing the Contact Rate

This simulation shows that the epidemics reduced from the initial 6% to about 2%, whiles the exposed also reduced from the initial 12% to about 4%. In the end almost 52% of the population will have become infected and immune to any subsequent outbreak and about 48% of the population never gets the disease and remains susceptible to the infectious disease. The disease seems to disappears from the host population after about 140 years.

4.6.2 Simulation of the Effect of Increasing the Treatment Rate on the Model

Increasing the treatment rate will reduce the transmission rate of infection from an infectious human to the susceptible. Therefore increasing the treatment rate from $\frac{1}{7}$ to $\frac{1}{5}$ give the phase portrait diagram below.

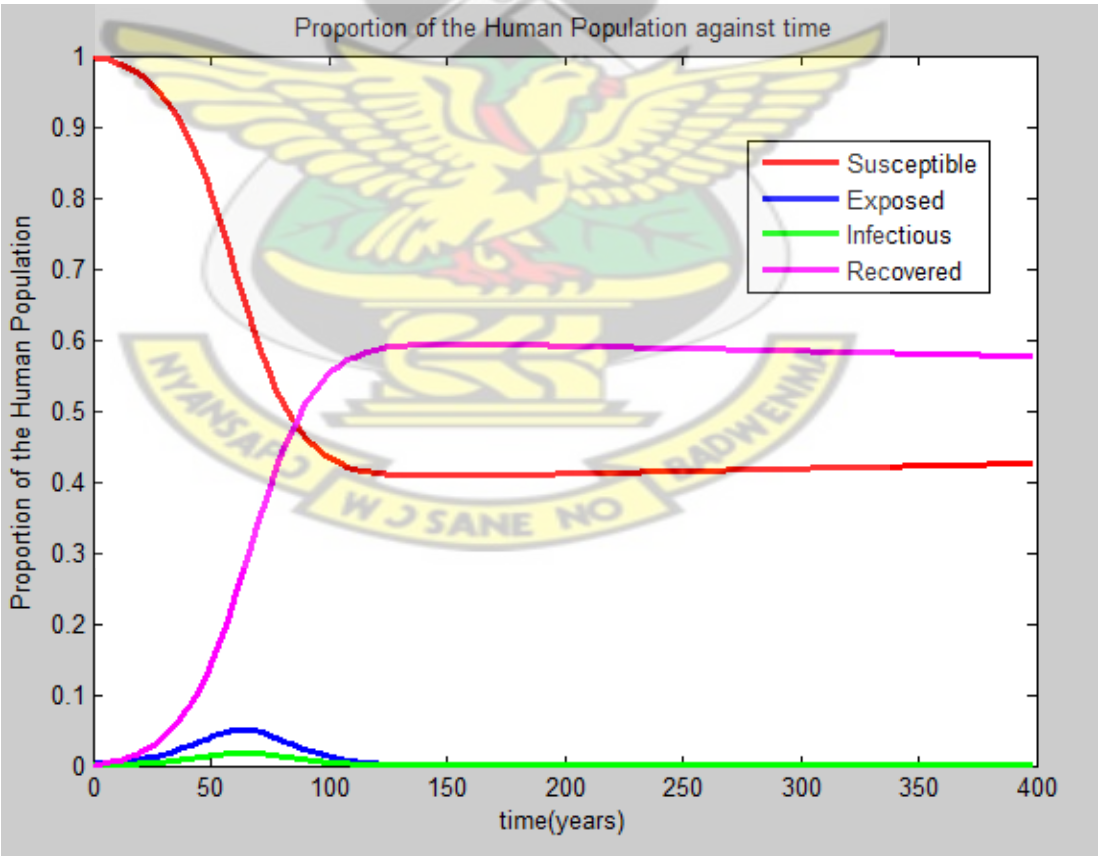

Figure 4.3: Effect of Increasing the Treatment Rate

This simulation also shows that the epidemics reduced from the initial 6% to

about 3%, whiles the exposed also reduced from the initial 12% to about 6%. In the end almost 60% of the population will have become infected and immune to any subsequent outbreak and about 40% of the population never gets the disease and remains susceptible to the infectious disease. The disease seems to disappears from the host population after about 120 years.

Clinical treatment rate could be increased if the pharmaceutical industry produces anti-varicella drug(s) that will reduce the number of days it takes to recover from the infection from 7 to 5 days, reducing R_0 from 1.2869 to 0.9193.

4.6.3 Simulation of the Combine Effect of Contact Rate Reduction and Increasing Treatment Rate

The effects of combining the two interventions in controlling varicella disease are shown below. Less than 1% of the population is exposed to the disease as well as infected. With these two control measures, almost 8% of the population will have become infected and immune to any subsequent outbreak and about 92% of the population never gets the disease and remains susceptible to the infectious disease. The disease seems to disappears from the host population in less than 50 years. This simulation shows that the combination of these interventions can play a positive role in reducing or eradicating the disease in the country.

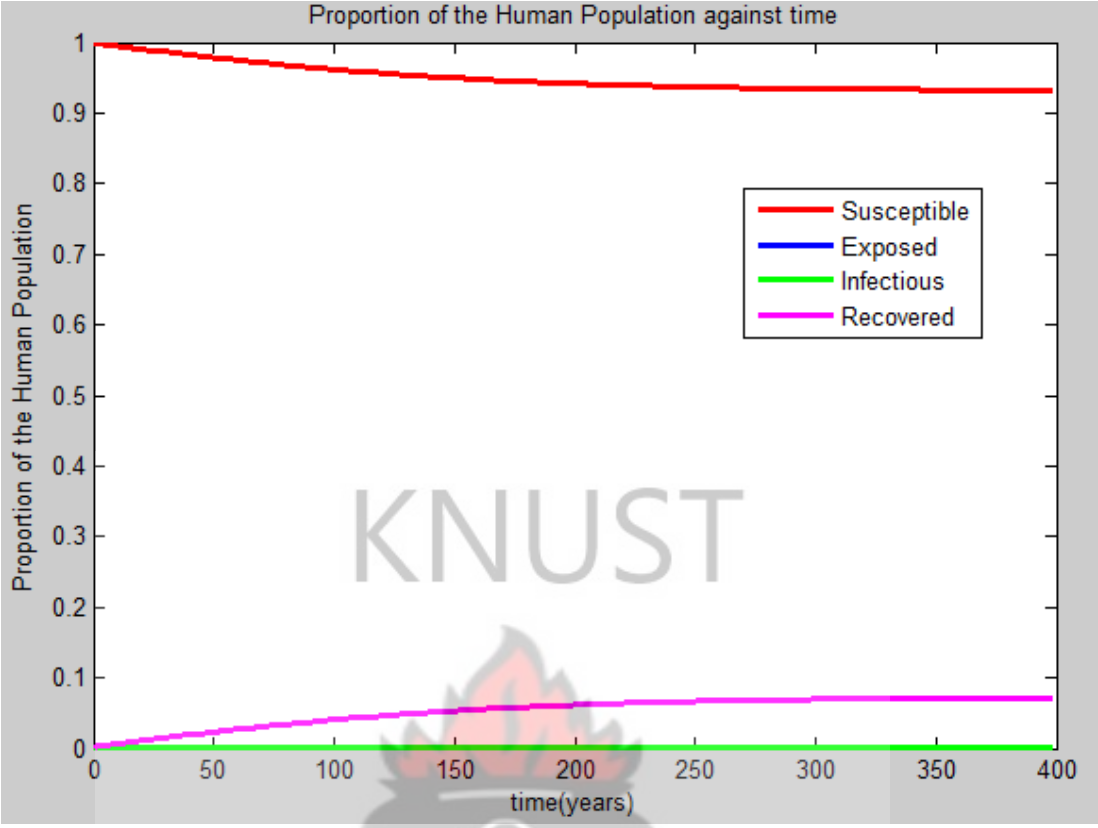

Figure 4.4: Effect of Combined Contact Rate Reduction and Increasing Treatment Rate

4.7 Discussion

A mathematical model was derived and analyzed to control varicella transmission in Ghana. The basic reproduction number R_0 was computed for the model. If $R_0 < 1$, the disease can not persist in the country and when $R_0 > 1$ the disease can persist. It is also shown that the model has both a disease-free and endemic equilibria. The Herd Immunity Threshold and Control Vaccination Number were investigated and finally simulation of the model was performed.

The following results were obtained from the analysis of the model. The basic reproduction number $R_0 = 1.2869$, meaning that the presence of a person infected with varicella virus will eventually result in an outbreak of the disease in Ghana. The number of contacts between susceptibles and varicella patients during the infectious period is $\sigma = 1.2876$, meaning that on the average about

1429 varicella patients contacts 1840 susceptible people in the country during an infectious period.

The disease-free equilibrium point (S^*, E^*, I^*) = (1, 0, 0), and the endemic equilibrium point (S^e, E^e, I^e) = (0.7771, 0.0001308, 0.00006539). The disease-free equilibrium point is locally asymptotically unstable, whiles the endemic equilibrium point is locally asymptotically stable. That means varicella will spread in Ghana.

The herd immunity threshold shows that about 22.3% of the susceptible population of Ghana should be immune in order to bring the spread of varicella under total control. Meaning that if the proportion of immune individuals exceeds this level due to a mass vaccination programme, the disease will die out, because unvaccinated individuals are indirectly protected by vaccinated individuals.

From further analysis with vaccination as the control measure, and having a vaccine efficacy of 99%, about 22.5% of the susceptible population should be vaccinated in order to have Varicella under total control, whilst with a vaccine efficacy of 87% about 25.6 % of the susceptible population of Ghana should be vaccinated in order to bring the disease under control in Ghana. Vaccinating these percentages of the entire population reduces the proportion of the susceptible population who risk infection upon outbreak.

The numerical simulation shows that the epidemic builds up to where almost 6% of the population is infected, and then declines, whiles the exposed group builds up to about 12% and then declines. In the end almost 80% of the population will have become infected and immune to any subsequent outbreak and that bout 20% of the population never gets the disease and remains susceptible to the

infectious disease. The simulation also shows that the number of infected individuals and exposed individuals sharply decreases to zero after about 85 years. Further simulation revealed that if the contact rate can be reduced to $\frac{2}{3}$ its value, by early detection for supervised treatment, and if the number of days it takes to recover from the infection can be reduced from 7 to 5 days, thereby increasing the treatment or recovery rate, then the disease can be effectively controlled in Ghana.

Chapter 5

Conclusion And Recommendation

5.1 Introduction

In this chapter, a conclusion and recommendations are offered to stakeholders, the government, public health agencies and health care providers to enable them determine how best to allocate scarce resources for the prevention and controlling varicella transmission in Ghana.

5.2 Conclusion

A mathematical model is derived and analyzed to better understand the dynamics of varicella transmission in Ghana. First it is showed that there exists a domain where the model is epidemiologically and mathematically well-posed. The basic reproduction number $R_0 = 1.2869$, meaning that the presence of a person infected with varicella virus will eventually result in an outbreak of the disease in Ghana.

From the model the herd immunity level for varicella in Ghana is found to be 22.3%. Meaning that for Ghana to be declared varicella free state, at least 22.3% of the population must attain immunity through mass vaccination programme. The simulation revealed that early detection of the infectious, for isolated supervised treatment, as well as increasing the treatment rate, has a positive impact on the reduction of varicella transmission; that is there is a need to detect new cases as early as possible so as to provide early treatment for the disease and to produce anti-varicella drugs to increase the treatment rate.

Comparing with others, we had situations in 1995, where there were 2934 verified cases reported in Antelope Valley, CA, 3130 cases in Travis County and 1197

cases in West Philadelphia. The number of cases declined in all sites in 1996 and remained stable until 1998. In 1999, the number of cases began to dramatically decrease and in 2000, there were 837, 491 and 250 cases in Antelope Valley, Travis County, and West Philadelphia, respectively. Between 1995 and 2000, the total number of cases in the three surveillance areas declined from 71 to 84%, with the most considerable reduction in preschool children (1 to 4 year olds). By 2005, the number of cases declined by about 90% in both Antelope Valley and West Philadelphia combined, Esson et al. (2014). This supports our thesis that varicella transmission can be controlled in Ghana through vaccination.

5.3 Recommendation

Eradication of contagious diseases such as varicella has remained one of the biggest challenge facing developing countries like Ghana. To eradicate varicella from Ghana, the following recommendations are made:

1. That vaccination against varicella should be added to the National Immunization Programme and should target vaccinating at least 22.3% of the susceptible population in order to fully bring the disease under control where the outbreak is considered epidemic.

2. The simulation results confirmed that the transmission rate is one of the dominant parameters in the spread of the disease in Ghana. Therefore a National Varicella Control Programme should be instituted to educate on the improvement in early detection of varicella cases for isolated supervised treatment so that the disease transmission can be minimized.

3. Stakeholders in the health sector should ensure that up to date data is kept on all diseases reported at the various health facilities to facilitate research work in Ghana.

5.4 Future Work

Researchers can extend the model to non constant population size, unequal birth and death rate, and different age groups.

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Appendix A

Year	Susceptible	Exposed	Infectious	Recovered
2002	20244150	187365	35667	35667
2003	20467750	136776	19614	19614
2004	20757030	278432	45512	45512
2005	---	---	---	---
2006	---	---	---	---
2007	---	---	---	---
2008	23383850	367987	77709	77790

Table 5.1: Source: Ghana Health Service, Prime Division, Accra

Appendix B