KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY

MATHEMATICAL MODELING OF THE EPIDEMIOLOGY OF VARICELLA

By

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of

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Declaration

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

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Dedication

To my family and friends

Acknowledgement

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Abstract

In this thesis a modified SIR mathematical model on the spread of Varicella (Chickenpox) in Ghana was developed.

Here the population is divided into three compartments: the susceptibles, the infectives, and the recovered. The resulting system of non-linear differential equations was analysed, thus in respect of the stability of the equilibrium points. The model focuses on the spread of the disease at the initial stages of the infection when the infected persons are absent and when they are present taking into consideration birth rate and natural death rate. The study is based on the assumption that the population of Ghana is constant, and the natural death rate was assumed to be equal to the birth rate. We then determine how the various compartments react to increasing proportion of persons at the initial stages of their infection.

We perform sensitivity analysis on the already estimated model parameters to determine their effect on the reproductive number and at what values of the reproductive number are the disease free and endemic equilibra stable.

Table of Content

Declaration ii

Dedication iii

Acknowledgments iv

Abstract v

List of Tables ix

List of Figures ix

Chapter 1 Introduction 1

1.1 Background ……1

1.2 Varicella (Chicken Pox). ……2

1.2.1 Description of Varicella . . . . . ……..... 2

1.2.2 Epidemiology of Varicella…….. 3

1.2.3 Diagnosis of Varicella……. 4

1.2.4 Varicella Infection in Pregnancy and Newborn Babies…... 4

1.2.5 Treatment of Varicella Infection in Adults……. 6

1.2.6 Treatment of Varicella Infection in Children…….6

1.2.7 Prevention…….. 6

1.2.7.1 Vaccination…….……. 7

1.2.7.2 Hygienic Measures…….. 8

1.3 Problem Statement ……. 8

1.4 Objectives of the Study …….. 9

1.5 Methodology …….. 9

1.6 Justification of Study…….. 10

1.7 Structure of the Thesis …… 11

Chapter 2 Review of Related Work 12

Chapter 3 Mathematical Model 21

3.0 Introduction……..21

3.1 Model Formulation ……. 21

3.2 Model Equations…….. 22
3.2.1 Equilibrium Points. ……... 26
3.2.2 Stability of the model……28
3.2.2.1 Disease Free Equilibrium ……. 29
3.2.2.2 The Endemic Equilibrium ……31
3.3 Reproductive Number . …….. 33
3.4 Herd Immunity Threshold . …… 34
3.5 Effective Reproductive Number…… 35
3.6 Control Vaccination Number…… 35

Chapter 4 Analysis of Model 37
4.1 Introduction 39
4.1.1 Simulations and Results ……39
4.1.2 Effects of initial proportions of infectives on the various compartments ……41
4.2 Stability Analysis ……45
4.2.1 Stability of infectious free equilibrium ……45
4.2.2 Stability of the endemic equilibrium …… 45
4.2.3 Sentivity Analysis .....…….. 47
4.2.4 Herd immunity threshold . .....…… 48
4.2.5 Control Vaccination Number……..... 49

Chapter 5 Discussion, Conclusion and Recommendations 50
5.1 Introduction……50
5.2 Discussions ……. 50
5.3 Conclusion ……..... 52
5.4 Recommendations ……. 53
References 54

List of Figures

4.1 The dynamics of the various compartments during the outbreak ……. 40

4.2 Effect of an increase in initial proportion of infectives on susceptible population with time. . . . . ……. 42

4.3 Effect of an increase in initial proportion of infectives on the infective population with time. …… 43

4.4 Effect of an increase in initial proportion of infectives on the recovered population with time . ……... 44

List of Tables

4.1 Parameters values for the model ……..37

4.2 Initial proportions of various compartments . ……..41

4.3 Parameter values, eigenvalues and classification of disease free equilibrium point…… 47

4.4 Parameter values, eigenvalues and classification of endemic equilibrium point. . ……... 48

CHAPTER 1

INTRODUCTION

1.1 Background

Mathematical modeling has significantly enhanced the understanding of the epidemiology and control of infectious diseases. Knowledge from this important and exciting field have helped in various levels of decision making.

The communicable nature of infectious diseases makes them basically different from non-infectious diseases, so techniques from 'classical' epidemiology are often invalid and hence lead to incorrect conclusions - not least in health-economic analysis.

"Mathematical modelling now plays a key role in policy making, including health-economic aspects; emergency planning and risk assessment; control-programme evaluation; and monitoring of surveillance data. In research, it is essential in study design, analysis (including parameter estimation) and interpretation.

With infectious diseases frequently dominating news headlines, public-health and pharmaceutical-industry professionals, policy makers, and infectious disease researchers, increasingly need to understand transmission patterns and to interpret and critically-evaluate both epidemiological data, and the findings of mathematical modeling studies. Recently there has been rapid progress in developing new models and analysis techniques for outbreaks and emerging epidemics, such as influenza A ($H1N1$) and $SARS$." C Fraser, 2008

Also with the betterment of human society cleanliness, the improvement of medical level and science technology, many diseases, such as cholera, smallpox, have been greatly controlled by humans. However, more and more new viruses are emerging. How to regulate the widespread of diseases and form the system of forecasting for the epidemic diseases is a tough task and problem given much consideration by countries and research departments. More researchers nowadays use mathematical methods to study the spread of infectious diseases. It therefore deemed very important to form a mathematical method that reflects the epidemic features for the revelation of the spreading law and forecasting of the epidemic. Many research work have been undertaken in this field.

In this thesis, we study the epidemiology of Varicella (chicken pox) using a mathematical model. We consider some of the recent mathematical developments that have improved our understanding and predictive ability.

1.2 Varicella (Chicken Pox)

1.2.1 Description of Varicella

Chickenpox or varicella is a highly transmissible infection primarily caused by an α-herpes virus called Varicella Zoster, and is one of the commonly reported childhood disease.

This disease is an airborne disease and highly communicable which spreads from person to person by either by direct contact with the fluid from the blisters or through secretions from the respiratory tract (i.e. infected person's coughing or sneezing) or by coming in contact with infected person's clothing.

The chicken pox patient is normally infectious from five days before the appearance of the blisters and remains infectious until all the blisters have formed scabs, and this usually takes five to six days. It usually takes from ten(10) to twenty-one (21) days after coming in contact with an infectious patient for one to develop the disease. Early rash of chickenpox is mostly on the upper body.

1.2.2 Epidemiology of Varicella

Primary varicella is an endemic disease. Cases of Varicella are experienced throughout the year.

Varicella is one of the classic diseases of childhood, with maximum occurrence in children with ages between four (4) and ten(10) years. It is highly contagious with and infection rate of 90% in close contacts. In general most people get infected before reaching adulthood but about 10% of adults still remain susceptible.

From history, varicella has been a disease mostly affecting infants and school-aged children. As compared to children the pock marks in adults are darker and the scares more noticeable.

1.2.3 Diagnoses of Varicella

The diagnosis of chickenpox is mostly clinical. The diagnosis of varicella is mostly clinical, with typical early symptoms, and then the onset of a characteristic itchy rash.

Confirmation of the diagnosis can be sought through either the examination of fluids of the rash or by blood test for eh presence of and acute immunologic response.

Vesicular fluids can also be examined for the presence of fluorescent antibody. Where attempts are made to grow the virus for a fluid sample the fluid is cultured (McPherson & Pincus, 2007).

In pregnant mothers, the diagnosis of fetal infection of varicella can be done by using ultrasound. A delay of 5 weeks after maternal infection is usually advised. Though there is the risk of abortion due to amniocentesis, a DNA test of the mothers' amniotic fluid can also be carried out.

1.2.4 Varicella Infection In Pregnancy And Newborn Babies

For pregnant women, immunity gotten through immunization or previous infection is transferred to the foetus through the placenta, (Branon,2007). On the other hand varicella infection during pregnancy can lead to viral transmission through the placenta and foetal infection.

If there is an infection within the first 28 weeks of gestation, it can lead to foetal varicella syndrome. This is also referred to as congenital varicella syndrome. Foetal varicella can cause lesser effects such as finger and toes underdevelopment to severe ones such as bladder malformation.

Some other possible effects include:

- Brain damage: microcephaly, encephalitis, hydrocephaly, etc.
- Eye damage: optic cap, optic stalk and lens vesicles, e.t.c.,
- Neurological disorder:
- Skin disorder;
- Body damage: hypoplasia of lower/upper extremities, bladder and anal sphincter dysfunction.

Infection during the latter part of gestation or immediately after birth is referred to as neonatal varicella. Maternal infection is associated with premature delivery. Exposure of the baby to the infection 7 days prior to delivery or 7 days after delivery has the greatest risk of the baby developing the disease.

Neonates that develop the symptoms are at a high risk of pneumonia and other severe problems.

After an infection of chickenpox, the virus remains latent in the body's nerve tissues and later in life, reactivates and causes a different form of the virus called shingles.

1.2.5 Treatment of Varicella Infection in Adults

Infection in adults is more severe and active. Treatment with antiviral drugs is mostly advised. Remedies to ease the symptoms of chicken pox in adults are basically the same as those used on children. However, adults are prescribed antiviral medications with the aim to reducing the severity of their illness and the likelihood of complications. This however does not kill the virus, but only prevents its growth.

Painkillers such as ibuprofen and paracetamol are also prescribed to relieve itching and other symptoms such as fever and pains. Increased intake of water is also recommended to reduce dehydration and relieve headache. Antihistamines mays also used as they are effective in easing itching and they also act as a sedative.

Sorivudine, has been found in some cases to be effective in the treatment of primary varicella in healthy adults.

1.2.6 Treatment of Varicella Infection in Children

Treatment of chicken pox in children is aimed symptoms whilst the immune system is allowed to deal with the virus. Nails of children younger than 12 years are cut and kept clean to prevent them from crashing themselves and further infection of the blisters. Children between the ages on one month and 12 years are not meant to receive antiviral treatment if they are not suffering from other condition that might expose them to other complication.

Increased water intake is also advised for children to avoid dehydration, especially if the child develops fever.

Painkillers such as paracetamol or ibuprofen can be used to relieve pain, headaches and fever. In some cases children who are more than a year old may be administered antihistamine tablets or liquid medicine are helpful in cases when the child is not able to sleep because of the itching.

Immunoglobulin or Acyclovir is mostly recommended in children who are at a high risk of developing complications from the disease. Their treatment is similar to the one mentioned above plus additional antiviral medication. Children with suppressed immune system, infants less than a month, those on steroids or immune suppressing medication or other immune-compromised diseases are those who are considered at risk of complications from the disease. Administration of Aspirin to children younger than 16 years may lead to a fatal condition called Reyes syndrome.

1.2.7 Prevention

1.2.7.1 Vaccination

The first varicella vaccine was developed by Michiaki Takahashi in 1974 derived from the Oka strain. Some countries require the varicella vaccination before entering elementary school. Immunity derived from the vaccine is not lifelong and subsequent vaccination is necessary usually after five years after the initial vaccination. Chickenpox vaccination is not part of the routine childhood vaccination schedule in Ghana but in the

UK, for example, the vaccine is currently offered to people who are particularly vulnerable to the disease.

1.2.7.2 Hygienic Measures

The spread of varicella can be controlled by the isolation of infected persons. Contraction is by direct contact with lesions or exposure to respiratory droplets of patients within their infectious period. That is from 3 to 5 days before the appearance of the rash to 4 to 5 days after the onset of the rash.

Therefore the avoidance of physical contact or close proximity with affected persons during this period will aid prevent contagion. The varicella virus is susceptible to disinfectants and also sensitive to desiccation, heat and detergents.

1.3 Problem Statement

Chickenpox has long been considered not dangerous, unavoidable disease of childhood. Complications are generally mild and rarely severe, and virtually every individual is infected by adulthood. Infection is related, however, with a high risk of serious complications in certain high-risk groups, such as leukemic children or immuno-compromised patients.

It was reported by Joy news reporter Isaac Essel on the 26th of August 2008 that an outbreak of chicken pox at the Accident and Emergency Unit of the Korle-Bu Teaching

Hospital had forced hospital authorities to close the unit temporarily. This has also been experienced in other hospitals and polyclinics in Ghana.

The epidemiology of varicella in Ghana has not been carefully studied and most recent outbreaks indicate a large proportion of people been infected. Fears about the severity of the disease (that is Chickenpox) in Ghana have led to this thesis.

1.4 Objective of the Study

The objective of this research involves the following

1. Developing a mathematical model for varicella or chicken pox in Ghana
2. Determine the nature of the outbreak
3. Estimate the proportion of the population that should be vaccinated
4. Show how the proportion of susceptible, infectious, and recovered people change with time
5. Determine the effect of the initial number of people infected with varicella on the population

1.5 Methodology

We employ the simple Susceptible-Infective-Recovered (SIR) compartmental model which is used to describe the epidemiology of infectious diseases.

The SIR model is used in epidemiology to compute the amount of susceptible, infected and recovered people in a population. This model does not work for all diseases. For the SIR model to be applicable, once a person has recovered from the disease, they receive

lifelong immunity. The SIR model is also not appropriate if a person was infected but is not infectious.

The model equations are solved numerically with MatLab which employs Runge-Kutta method. Simulation and sensitivity analysis are then performed on the model equations to determine the effect of the parameter values on the spread of the disease.

1.6 Justification of Study

Epidemiology has provided valuable insights for analysis of different types of diseases in the world. This study seeks to be justified based on the following;

- The disease (that is varicella) has been extensively studied in other countries but not in Ghana. As at now we are unaware of any mathematical publication specifically looking at chicken pox epidemics in Ghana.
- Although there are records on chicken pox, they normally underestimate the number of those who have been infected by the disease. Some people have the disease but have not been diagnosed.
- People get infected daily but we are generally unaware of the trend of the spread of the disease.
- The occurrence of death from the disease generally affects the productivity of the country but we are not taking into consideration other measures apart of isolation of infected persons of controlling the disease.

1.7 Structure of the Thesis

This thesis is organized into five (5) main chapters. Chapter one gives the introduction of the thesis. This consists of a biological background of Varicella, statement of problem, objectives, methodology, limitation and organization of the thesis. In the second chapter we review related research works. This includes diseases modeled as SIR model and works on varicella. The formulation of the mathematical model is presented in chapter three. Chapter four presents the analysis and results of model. Chapter five concludes the study with discussion of results, conclusions and suggestions for further studies.

CHAPTER 2

REVIEW OF RELATED WORK

In this chapter some of the previous related studies on the spread of communicable diseases especially varicella have been reviewed.

The spread of several communicable diseases have been gainfully studied with mathematical models. Information contained in such models either fails to include reality in the field or does not admit full quantitative and qualitative description of the disease. 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.

Nokes et al (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-McKendrick (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 removal class equation was approximately by Taylor series to second degree for small number of removals over relateive removal rate. 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 Kemack-McKendrik (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-McKendrick (1927) SIR model.

Herpes-zoster is caused by the reactivation of varicella-zoster virus (VZV). In a paper Garnett and Grenfell,(1992), reviewed and discussed different hypotheses of how this re-emergence of virus comes about. From these hypotheses, and epidemiological data describing the initial transmission of the virus, a mathematical model of primary disease (varicella) and reactivated disease (zoster) in developed countries was derived. The steady-state age distributions of zoster cases was predicted by this model and were compared with the observed distribution, derived from a review and analysis of published epidemiological data. Their model allows differentiation between published hypotheses in which age of host may or may not influence the probability of viral reactivation. Their results indicated that the probability of reactivation must increase with age to allow the observed pattern of zoster cases.

The basic mathematical model they presented provides a conceptual framework, which may be extended to assess possible control programmes.

Tuckwell and Williams (2006), investigated the properties of a simple discrete time stochastic epidemic model. The model was Markovian of the *SIR* type in which the total population was constant and individuals met a random number of other individuals at each time step. Individuals remained infectious for R time units, after which they become removed or immune. Individual transition probabilities from susceptible to diseased states were given in terms of the binomial distribution. An expression was given for the probability that any individuals beyond those initially infected become diseased. In the model with a finite recovery time R, simulations revealed large variability in both the total number of infected individuals and in the total duration of the epidemic, even when the variability in number of contacts per day was small. In the case of no recovery,

$R = 1$, a formal diffusion approximation was obtained for the number infected. The mean for the diffusion process could be approximated by a logistic which was more accurate for larger contact rates or faster developing epidemics.

For finite R they then proceeded mainly by simulation and investigated in the mean the effects of varying the parameters p (the probability of transmission), R, and the number of contacts per day per individual. A scale invariant property was noted for the size of an outbreak in relation to the total population size. Most notable were the existence of maxima in the duration of an epidemic as a function of R and the extremely large differences in the sizes of outbreaks which could occur for small changes in R. These findings had practical applications in controlling the size and duration of epidemics and hence reducing their human and economic costs.

Seddighi 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 infectous free equilibrium point was

asymptotically stable. The simple SIR model is same as modified SIR model if the removal rate of infective individuals from to high-infectives equals to zero. 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, economic status of infectives and cultural were not captured in their work.

With the increasing threat of biological warfare and the fear of an epidemic outbreak of influenza, smallpox, and other deadly diseases, the field of epidemic modeling is becoming increasingly important in the scientific fields. Hye Yon Yi, (2009), focused to create a model to study the effects of the rates of reaction and the rates of diffusion within a network based on the different parameters used in the modeling of any disease. Their model combines aspects of the predator-prey and the SIR (Susceptible, Infected, and Recovered) systems to create a first order system of difference equations. For their model, the exact parameters of a specific disease were not as crucial as the qualitative behaviors that occur from the changing parameters. The model was linearly stable when diffusion does not exist. As diffusion is incorporated, turing instabilities occur.

An SIR epidemic model with vital dynamics, incubation time and also with bilinear incidence rate was formulated by Setiawan et al (2002), where incubation time lengths as time delay. The total host population was assumed constant. The threshold value R_0 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_0 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 value R_0 and time delay. If R_0 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_0 exceeds one and for all positive time delay, or it can be called absolutely locally asymptotically stable (ALAS) when R_0 exceeds one.

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. Liu (2009) 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.

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,(2009), 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.

Yang and Wang (2010) studied a nonautonomous *SIR* epidemic model with age structure. Using integro-differential equation and a fixed point theorem, they prove the existence and uniqueness of a positive solution to the model. They obtained existence and uniqueness of this model using integral differential equation and a fixed theorem. Their model was different from the classical age structure epidemic model and non-autonomous epidemic model. The initial condition was nonlocal and dependent on total population. In addition, incidence law was not Lipschitzianity. They established that the classical methods were not valid and constructed a new norm and proved the existence of the model under definition of the new norm. This was illustrated through two simulated examples.

Mathematical models have been used to study the dynamic interaction of many infectious diseases with the host's immune system. Forde and Meeker (2010) studied Varicella Zoster Virus, which is responsible for chicken pox (varicella), and after a long period of latency, herpes zoster (shingles). After developing the model and demonstrating that it exhibited the type of periodic behavior necessary for long term latency and reactivation, they examined the implications of the model for vaccine booster programs aimed at preventing herpes zoster. They then proceed to prove the positivity and boundedness of solutions to the system and explore the existence, location and stability of steady state solutions. They had developed a simple mathematical model based on the known biology of varicella-zoster virus infection, including the latent infection of neurons and the VZV-specific immune response. They had shown that the model explained the long latency period of the infection, and its spontaneous reactivation as a result of declining specific immunity with age. Mathematically, the course of reactivation was represented by a limit cycle. Cycling behavior can only occur when the levels of viral production from the site of latency (the parameter s) and reactivity of the specific immune cells (d/p) lie within a defined set of values. Based on the model, they could make predictions about means of preventing the reemergence of infection, which causes herpes zoster. In particular, the model could be used to make predictions about the ideal timing of the administration of vaccine boosters intended to prevent herpes zoster. As more information about the effects of this booster on patients becomes available, the model could serve as a platform for converting this patient data into recommendations about booster timing. Finally, they had also observed that the mathematical model of infection and immunity demonstrates a wide variety of possible dynamic behaviors. By

choosing two parameters appropriately, the model could be used to simulate many different possible biologically relevant courses of infection, including acute infection followed by clearance and chronic infection. This indicated that the model may be useful not only for the study of varicella-zoster virus, but also of other infectious diseases which have quite different natural histories.

CHAPTER 3

MATHEMATICAL MODEL

3.0 Introduction

Epidemiology is essentially a population biology discipline concerned with public health. As such, epidemiology is thus heavily influenced by mathematical theory. The reason is that most phenomena observed at a population level are often complex and difficult to deduce from the characteristics of an isolated individual. For example, the prevalence of a disease in a population is only indirectly connected to the course of disease in an individual. In this context, the use of mathematical models aims to unearth processes from a large-scale perspective.

This chapter is mainly concerned with developing a modified SIR model for the occurance of chicken pox in Ghana, finding threshold conditions for the disease to become endemic and describing the stability of steady-state solutions, often under the assumption that the population has reached its steady state and the diseases does not affect the death rate of the population.

3.1 Model Formulation

The SIR Model is used in epidemiology to compute the dynamics of the susceptible, infectious and recovered people in a population.

This model is an appropriate one to use under the following assumptions;

1) The population is fixed.
2) The only way a person can leave the susceptible group is to become infected. The only way a person can leave the infected group is to recover from the disease. Once a person has recovered, the person received immunity.
3) Age, sex, social status, and race do not affect the probability of being infected.
4) There is no inherited immunity.
5) The member of the population mix homogeneously (have the same interactions with one another to the same degree).

3.2 Model Equations

The following assumptions were made in addition to the five general assumptions iterated above.

1. This is a closed population (no immigration or emigration) i.e. we assume that the population of Ghana is fixed. Individuals in the population are divided into three classes (compartments): Susceptibles $(S(t))$, Infectives $(I(t))$, and Recovereds $(R(t))$.
2. Susceptible individuals (those who have never had the disease) become infected at a rate that is jointly proportional to the number of susceptible and the number of infectious.
3. An individual who contracts the disease is assumed to be infective immediately after infection. Hence there is no relapse period for the disease.

4. Everybody who gets infected recovers at a rate proportional to the number of people infected.
5. Once recovered from the disease, a person can no longer become susceptible to the disease.
6. The parameters are assumed to be positive constants.
7. The natural death rate is equal to the birth rate (that is, $\alpha = \delta$).

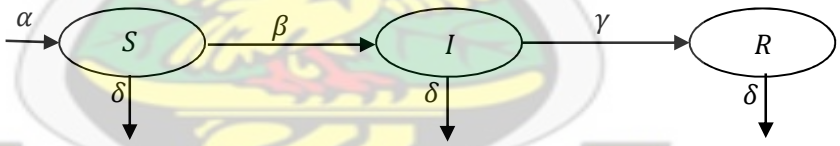
$S(t)$ is the number of susceptible individuals at time t

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

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

N is the total population size

The compartmental diagram shown below summarizes these assumptions.



where

α is the general population birth rate

β is the infection rate

γ is the recovery rate, and

δ is the natural death rate

The dynamics of the chicken pox(varicella) outbreak in Ghana is modeled using the following systems of ordinary differential equations;

$$\frac{dS}{dt} = \alpha N - \beta SI - \delta S \tag{3.1}$$

$$\frac{dI}{dt} = \beta SI - (\gamma + \delta)I \tag{3.2}$$

$$\frac{dR}{dt} = \gamma I - \delta R \tag{3.3}$$

The nonlinear system of differential equations formulated above has initial conditions

$$S(0) = S_0 \ , \ I(0) = I_0, \quad R(0) = 0 \tag{3.4}$$

This is a modification of the classic Kermack–McKendrick (1927) model. We are only interested in nonnegative solutions for *S*, *I* and *R*. This is a basic model but, even so, we can make some highly relevant general comments about epidemics and, in fact, adequately describe some specific epidemics with such a model.

The constant population size is built into the system above since, on adding the equations,

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{3.5}$$

$$N = S(t) + I(t) + R(t) \tag{3.6}$$

A key question in any epidemic situation is, given $\alpha, \beta, \gamma, \delta \geq 0$ and S_0, and the initial number of infectives I_0, whether the infection will spread or not, and if it does how it develops with time, and crucially when it will start to decline.

From the above system of equations and initial conditions the following deductions can be made

Expressing equations $(3.1) - (3.3)$ as a proportionof the population we divide through equation (3.6) by the total population to obtain

$$s(t) = \frac{S(t)}{N}, \qquad i(t) = \frac{I(t)}{N}, \qquad r(t) = \frac{R(t)}{N} \tag{3.7}$$

Thus,

$$s(t) + i(t) + r(t) = 1 \tag{3.8}$$

Where

- $s(t)$ is the proportion of susceptible population at time t
- $i(t)$ is the proportion of the infective population at time t
- $r(t)$ is the proportion of the recovered population at time t

Substituting equation (3.6) into equations $(3.1) - (3.3)$ we obtain the following

$$\frac{dsN}{dt} = \alpha N - \beta sNiN - \delta sN \tag{3.9}$$

$$\frac{diN}{dt} = \beta sNiN - (\gamma + \delta)iN \tag{3.10}$$

$$\frac{drN}{dt} = \gamma iN - \delta rN \tag{3.11}$$

Letting $N = 1$, from equation (3.8) into equations $(3.9) - (3.11)$ we obtain the following

$$\frac{ds}{dt} = \alpha - \beta si - \delta s \tag{3.12}$$

$$\frac{di}{dt} = \beta si - (\gamma + \delta)i \tag{3.13}$$

$$\frac{dr}{dt} = \gamma i - \delta r \tag{3.14}$$

Before analyzing the system of nonlinear equations, there is the need to linearize these systems of equations.

3.2.1 Equilibrium Points

Linearization approximation is a standard phase plane technique used to analyze system dynamics. For an *SIR* system with a constant host population size we have the following system of two independent nonlinear differential equations:

$$\frac{ds}{dt} = \alpha - \beta si - \delta s \tag{3.15}$$

$$\frac{di}{dt} = \beta si - (\gamma + \delta)i \tag{3.16}$$

We then solve the reduced system of nonlinear equations for the equilibrium points. Thus the differential equations above should be equated to zero(0), that is $\frac{ds}{dt} = \frac{di}{dt} = 0$.

$$\alpha - \beta si - \delta s = 0 \tag{3.17}$$

$$\beta si - (\gamma + \delta)i = 0 \tag{3.18}$$

Solving the above equations simultaneously, from equations $(3.17) - (3.18)$ let $i = 0$, substituting the value of i into equation (3.17)we have

$$\alpha - \beta s(o) - \delta s = 0 \tag{3.19}$$

$$\alpha - \delta s = 0 \tag{3.20}$$

Solving the above equation form the value of s, we have $s = \frac{\alpha}{\delta}$, bust since $\alpha = \delta$, implies $s = 1$. Hence the first equilibrium point is

$$(s^*, i^*) = (1, 0) \tag{3.21}$$

This is called the disease free equilibrium.

From equation (3.18), $s = \frac{\gamma+\delta}{\beta}$, substituting the value of s into the equation (3.17) we have,

$$\alpha - \beta\left(\frac{\gamma + \delta}{\beta}\right) i - \delta\left(\frac{\gamma + \delta}{\beta}\right) = 0 \tag{3.22}$$

From which we get

$$i = \frac{\alpha\beta - \delta(\gamma + \delta)}{\beta(\gamma + \delta)} \tag{3.23}$$

Thus the equilibrium points is

$$(s^*, i^*,) = \left(\frac{\gamma + \delta}{\beta}, \frac{\alpha\beta - \delta(\gamma + \delta)}{\beta(\gamma + \delta)}\right) \tag{3.24}$$

This equilibrium point is called the endemic equilibrium point.

3.2.2 Stability of the model

In this section, we consider some important methods of establishing stability of equilibrium points of non-linear differential equations.

Stability by linearization

Let $f: R^n \to R^n$ be a C^1 map and suppose that p is a point such tat $f(p) = 0$, i.e., p is a fixed point for the differential equation $x'(t) = f\big(x(t)\big)$.

The linear part of f at p, denoted $Df(p)$, is the matrix of partial derivatives at p. For $x \in R^n$, we write

$$f(x) = \begin{bmatrix} f_1(x) \\ f_2(x) \\ \vdots \\ \vdots \\ f_n(x) \end{bmatrix} \tag{3.25}$$

The functions f_i are called the component functions of f. We define

$$Df(p) = \begin{bmatrix} \frac{\partial f_1}{\partial x_1}(p) & \frac{\partial f_1}{\partial x_2}(p) & \cdots & \frac{\partial f_1}{\partial x_n}(p) \\ \frac{\partial f_2}{\partial x_1}(p) & \frac{\partial f_1}{\partial x_2}(p) & \cdots & \frac{\partial f_2}{\partial x_n}(p) \\ \vdots & \vdots & \vdots & \vdots \\ \frac{\partial f_n}{\partial x_1}(p) & \frac{\partial f_1}{\partial x_2}(p) & \cdots & \frac{\partial f_n}{\partial x_n}(p) \end{bmatrix} \tag{3.26}$$

Since $f \in C^1$, Taylors theorem for functions of several variables says that

$$f(x) = Df(p)(x - p) + g(x) \tag{3.27}$$

(we have used $f(p) = 0$), where g is a function

The stability of flow of nonlinear systems can be studied in different perspectives. In this work, we will limit ourselves to two different ways: Hartman-Grobman method (linearization) and Liapunov's method.

Hartman-Grobman Theorem

In a continuous model, a steady state will be stable provided the eigenvalues of the characteristic equation (associated with the linearized problem) are both negative (if real) or have a negative real part (if complex).

In determining the stability, we implore the linearization technique to equations (3.26) to find the Jacobian or community matrix. This gives

$$J = \begin{pmatrix} -\beta i - \delta & -\beta s \\ \beta i & \beta s - (\gamma + \delta) \end{pmatrix} \tag{3.28}$$

3.2.2.1 Disease Free Equilibrium

At the initial state of the disease we have only the susceptible present. From earlier calculations, the disease free equilibrium is $(s^*, i^*) = (1, 0)$. In order to determine the stability of the model at this point, we evaluate the Jacobian matrix at this equilibrium point and find the eigenvalues corresponding to this point.

Evaluating the Jacobian in equation at the disease free equilibrium point, we have

$$J(1,0) = \begin{pmatrix} -\beta(0) - \delta & -\beta(1) \\ \beta(0) & \beta(1) - \gamma - \delta \end{pmatrix} = \begin{pmatrix} -\delta & -\beta \\ 0 & \beta - \gamma - \delta \end{pmatrix} \tag{3.29}$$

We then find the characteristic equation which is given by $\det(A - I\lambda) = 0$ where λ is the eigenvalues and A is an $n \times n$ matrix. Here we replace the $n \times n$ matrix(A) by the Jacobian matrix(J). Thus

$$det(A - I\lambda) = det\left\{\begin{pmatrix} -\delta & -\beta \\ 0 & \beta - \gamma - \delta \end{pmatrix} - \lambda \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}\right\} \tag{3.30}$$

$$= det\left\{\begin{pmatrix} -\delta - \lambda & -\beta \\ 0 & \beta - \gamma - \delta - \lambda \end{pmatrix}\right\} \tag{3.31}$$

$$= (-\delta - \lambda)(\beta - \gamma - \delta - \lambda) - (-\beta)(0) \tag{3.32}$$

Because $\det(A - I\lambda) = 0$, implies

$$(-\delta - \lambda)(\beta - \gamma - \delta - \lambda) - (-\beta)(0) = 0 \tag{3.33}$$

Therefore $\lambda_1 = -\delta \ or \ \lambda_2 = \beta - \gamma - \delta$. The eigenvalues corresponding to the disease free equilibrium $(s^*, i^*,) = (1, 0)$ are $-\delta$ and $\beta - \gamma - \delta$.

Further analysis of the disease free equilibrium point will be done in chapter four.

3.2.2.2 The Endemic Equilibrium

At the point in time where all the compartments of the population coexist is called the endemic period. The presence of an infectious person is a problem in the epidemiology of infectious diseases. In this section we consider the situation whereby there is coexistence between the two main categories (i.e. the susceptible and the infectious). This is seen in the endemic equilibrium point in equation below

$$(s^*, i^*) = \left(\frac{\gamma+\delta}{\beta}, \frac{\alpha\beta-\delta(\gamma+\delta)}{\beta(\gamma+\delta)}\right) \tag{3.34}$$

In order to determine the stability of this point, we resort to the same approach used in determining the stability of the disease free equilibrium.

We evaluate the community (or Jacobian) matrix at the endemic point.

$$J(s^*, i^*) = \begin{pmatrix} -\beta\left(\frac{\alpha\beta-\delta(\gamma+\delta)}{\beta(\gamma+\delta)}\right)-\delta & -\beta\left(\frac{\gamma+\delta}{\beta}\right) \\ \beta\left(\frac{\alpha\beta-\delta(\gamma+\delta)}{\beta(\gamma+\delta)}\right) & \beta\left(\frac{\gamma+\delta}{\beta}\right)-(\gamma+\delta) \end{pmatrix} \tag{3.35}$$

$$J(s^*, i^*) = \begin{pmatrix} \frac{-\alpha\beta}{(\gamma+\delta)} & -(\gamma+\delta) \\ \frac{\alpha\beta-\delta(\gamma+\delta)}{(\gamma+\delta)} & 0 \end{pmatrix} \tag{3.36}$$

We then find the characteristic equation which is given by $\det(A - I\lambda) = 0$ where λ is the eigenvalues and A is an $n \times n$ matrix. Here we replace the $n \times n$ matrx(A) by the Jacobian matrix(J).

Thus

$$det(A - I\lambda) = det\left\{\begin{pmatrix} \frac{-\alpha\beta}{(\gamma+\delta)} & -(\gamma+\delta) \\ \frac{\alpha\beta-\delta(\gamma+\delta)}{(\gamma+\delta)} & 0 \end{pmatrix} - \lambda\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}\right\} \tag{3.37}$$

$$= det\left\{\begin{pmatrix} \frac{-\alpha\beta}{(\gamma+\delta)} - \lambda & -(\gamma+\delta) \\ \frac{\alpha\beta-\delta(\gamma+\delta)}{(\gamma+\delta)} & -\lambda \end{pmatrix}\right\} \tag{3.38}$$

$$= \left(\frac{-\alpha\beta}{(\gamma+\delta)} - \lambda\right)(-\lambda) + (\gamma+\delta)\left(\frac{\alpha\beta-\delta(\gamma+\delta)}{(\gamma+\delta)}\right) \tag{3.39}$$

Because $\det(A - I\lambda) = 0$, implies

$$\left(\frac{-\alpha\beta}{(\gamma+\delta)} - \lambda\right)(-\lambda) + (\gamma+\delta)\left(\frac{\alpha\beta-\delta(\gamma+\delta)}{(\gamma+\delta)}\right) = 0 \tag{3.40}$$

$$(\gamma+\delta)\lambda^2 + \alpha\beta\lambda + (\gamma+\delta)\big(\alpha\beta - \delta(\gamma+\delta)\big) = 0 \tag{3.41}$$

$$\lambda_{1,2} = \frac{-\alpha\beta \pm \sqrt{(\alpha\beta)^2 - 4(\gamma+\delta)(\gamma+\delta)\big(\alpha\beta - \delta(\gamma+\delta)\big)}}{2(\gamma+\delta)} \tag{3.42}$$

This gives the eigenvalues of the endemic equilibrium to be

$$\lambda_{1,2} = \frac{\frac{-\alpha\beta}{(\gamma+\delta)} \pm \sqrt{\left(\frac{\alpha\beta}{(\gamma+\delta)}\right)^2 - 4\big(\alpha\beta - \delta(\gamma+\delta)\big)}}{2} \tag{3.43}$$

The stability of the endemic equilibrium depends on the values of $\alpha, \beta, \gamma,$ and δ. A detailed description of the stability of the endemic equilibrium point will be done in chapter four.

3.3 Basic Reproductive Number (R_0)

The basic reproduction ratio of an infectious disease is a pivotal concept in epidemiology. It is defined as the expected number of secondary cases that would arise from the introduction of a single primary case into a fully susceptible population. Clearly, when $R_0 < 1$ each successive 'infection generation' is smaller than its predecessor, and the infection cannot persist. Conversely, when $R_0 > 1$ successive 'infection generations' are larger than their predecessors, and the number of cases in the population will initially increase. This increase does not continue indefinitely. The infection process reduces the 'pool of susceptibles', and hence reduces the probability that an infectious individual contacts a susceptible within its period of infectiousness. This non-linear effect can only be neglected at the beginning of an epidemic.

It represents the average number of secondary infections infected by an individual infective. The basic reproduction number can be used to assess whether a newly infectious disease can invade a population and to estimate the final size of an SIR-type epidemic.

For example, when $R_0 < 1$, the disease-free equilibrium (DFE) is locally asymptotically stable and when $R_0 > 1$, it is unstable.

This basic reproductive number can be computed by the formula

$$R_0 = \lambda^*(infectious\ period) + 1 \tag{3.44}$$

Where λ^* is the dominant eigenvalue whether negative or positive.

The basic reproductive ratio for our model is given by

$$R_0 = \frac{\beta}{\gamma + \delta} \tag{3.45}$$

From the mathematical point of view, usually when $R_0 < 1$, the model has only disease free equilibrium with equilibrium points $(s^*, i^*,) = (1, 0)$ in the SI plane, and also the endemic equilibrium is globally asymptotically stable. When $R_0 > 1$ the equilibrium becomes unstable and usually a positive equilibrium $E^*(s^*, i^*,)$ appears. E^* is called an endemic.

3.4 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. The Herd Immunity Threshold (H_I) is percentage of the population that needs to be immune to control transmission of a disease, i.e. equal to one. The equation (given by Diekmann and Heesterbeek, 2000) for estimating the Herd Immunity Threshold is

$$H_I = 1 - \frac{1}{R_0} \tag{3.46}$$

From equation substituting $R_0 = \frac{\beta}{\gamma+\delta}$, into equation above we have

$$H_I = 1 - \frac{1}{\left(\frac{\beta}{\gamma + \delta}\right)} \tag{3.47}$$

$$H_I = \frac{\beta - \delta - \gamma}{\beta} \tag{3.48}$$

As the amount of vaccinations increase, the herd immunity threshold also increases.

3.5 Effective Reproductive Number

The Effective Reproductive number, denoted E_R, is the average number of secondary cases generated by an infectious case during an epidemic (Johnson, 2009). To estimate this number we used the formula stipulated in Johnsons 2009 article

$$E_R = R_0 \frac{S_t}{N} \tag{3.49}$$

The Effective Reproductive number is important since it helps to determine how effective policies on controlling diseases have been. When $E_R < 1$, the policies concerning the containing of the disease are effective.

3.6 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 measure, in this case vaccination.

The formula form estimating the control vaccination number is given by

$$C_V = R_0(1 - hf) \tag{3.50}$$

Where h is the vaccine efficacy (the effectiveness of the vaccine) and f is the vaccination coverage (the fraction of the population that has been vaccinated).

The goal of researchers is to have $C_V < 1$. To have $C_V < 1$, knowing the efficacy of the vaccine we can estimate the proportion of the population that need to be vaccinated.

This is given by

$$f > \frac{1 - \left(\frac{1}{R_0}\right)}{h} \tag{3.51}$$

CHAPTER 4

ANALYSIS OF MODEL

4.1 Introductions

This chapter deals with the analysis of the models and the discussion of the results obtained. We use MatLab to run our simulations. For our systems of nonlinear differential equations, we use the ode 15s which is a fourth order variable Runge-Kutta method.

Sensitivity analysis is performed on the parameter values to determine the effect of these values on the rate of spread of Varicella.

The estimated parameters of the model which have been used for the analysis are shown in the table below.

Table 4.1: Parameter values for the model

Parameter	Description	Value
α	birth rate	0.03
β	infectious rate	0.124
γ	recovered rate	0.085
δ	natural death rate	0.03

The number of contacts between susceptibles and varicella patients during his/her infectious period is

$$\sigma = \frac{\beta}{\gamma} = \frac{0.124}{0.085}$$

$$\sigma = 1.45882$$

This means that on the average one varicella patient contacts 1.45882 susceptible people in the country during his/her infectious period.

To analyze the data, we calculate the reproductive number R_0. Substituting the parameter values in table into equation (3.45), we have

$$R_0 = \frac{0.124}{0.085 + 0.03} = 1.07826$$

Since the reproductive number, $R_0 = 1.07826 > 1$, an outbreak of varicella will result in an epidemic in Ghana.

4.1.1 Simulations and Results

In these simulations we use the parameter values given in Table 4.1, for the model equations in $(3.12) - (3.14)$

With the introduction of an infective into a susceptible population of Ghana, after sometime, the population changes from being infectious free to the state of endemicity. We study the dynamics of the disease by the use of simulations at the following instances:

(i) The presence of infectives and

(ii) Increase in initial proportion of infectives in the population.

To depict the dynamics of the compartments during the outbreak, we assume the initial proportions of susceptibles, infectives and the recovered to be $s(t) = 0.95$, $i(t) = 0.05$ and $r(t) = 0.0$ respectively.

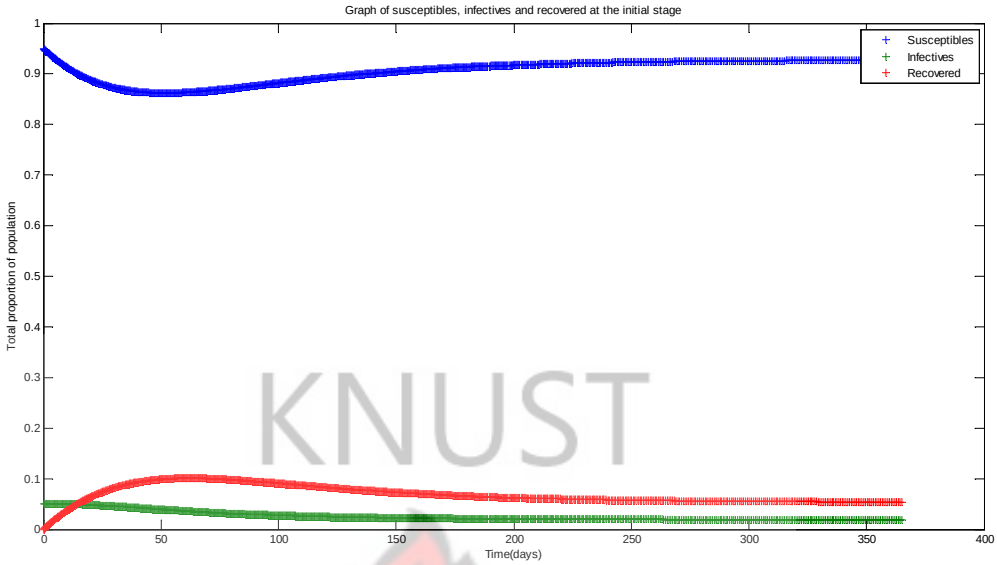


Figure 4.1: The dynamics of the various compartments during the outbreak

From Figure 4:1, when the initial proportion of infectives is 0.05, the proportion of the susceptibles declines from an initial value of 0.95 to an approximate minimum value of 0.84 from day 0 to day 50 and begins to increase gradually afterwards. On the other hand, the proportion of the infectives declines asymptotically from the first day reaching a minimum value of 0.01 on the $270th$ day and maintaining that value onwards. Also, the proportion of the recovered population increases after the initial day (day 0) and reaches maximum of 0.11 on the sixtieth $(60th)$ day and then declining steadily with time. Hence, the susceptibles decrease due to the introduction of the infectives. While even though the infectives infect more susceptibles, due to their high recovery rate the number keeps on reducing. This is exhibited due to the asymptotic decline of the infectives. The rise of the recovered population is due to frequent migration of people from infectives population to the recovered population.

4.1.2 Effects of initial proportions of infectives on the various compartments

In this section we vary the initial proportion of infectives to investigate the effect it will have on the susceptible, infectives and recovered populations.

Table 4.2: Initial proportions of various compartments

Infectives	Susceptibles	Recovered
0.05	0.95	0.00
0.10	0.90	0.00
0.20	0.80	0.00
0.30	0.70	0.00

The following Figures depict the effect of changes in initial proportion of infectives in Table 4.2 on the various compartments in the population.

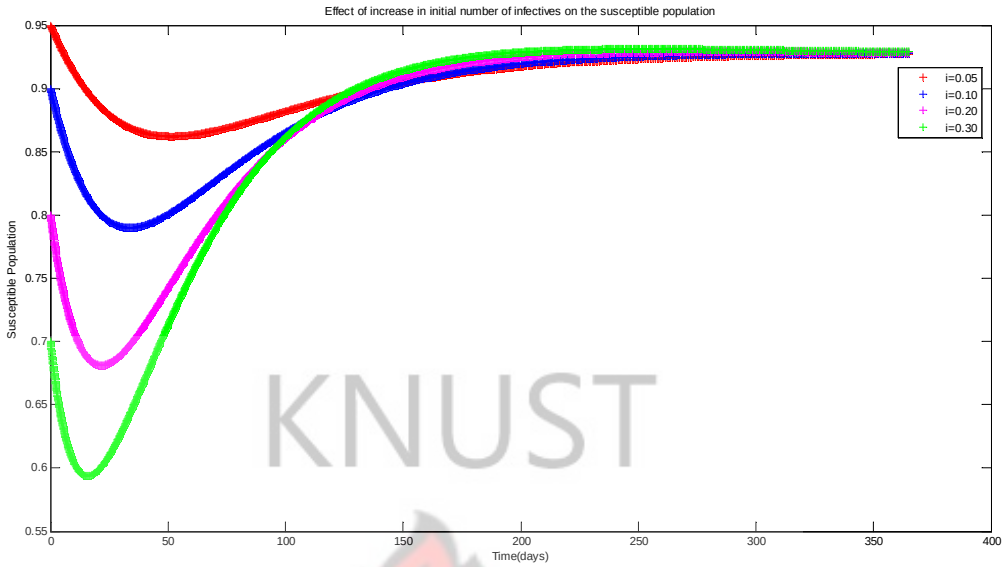


Figure 4.2: Effect of an increase in initial proportion of infectives on susceptible population with time.

From Figure 4.2 above, when the initial proportion of infectives is 0.05, the proportion of the susceptibles declines from an initial value of 0.95 to an approximate minimum value of 0.87 from day 0 to day 50 and begins to increase gradually after day 50 onwards attaining a constant value of 0.925. When the initial proportion of infectives is increased to 0.10, the proportion of the susceptibles, declines from an initial value of 0.90 and reaching its minimum value of 0.79 in thirty (30) days before rising steadily. As we increase the initial proportion of infectives from 0.10 to 0.20 the proportion of the susceptible also decline to a minimum of 0.675 within twenty-five (25) days before increasing thereafter. Lastly at an initial proportion of infectives being 0.30 the proportions of the susceptibles decline to a minimum of 0.58 within twelve (12) days and then rising afterwards.

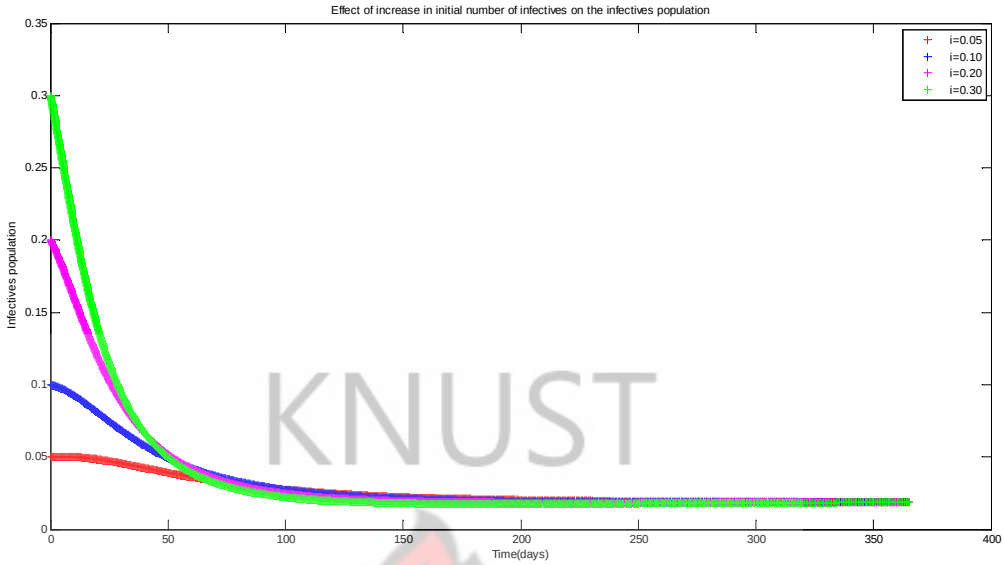


Figure 4.3: Effect of an increase in initial proportion of infectives on the infective population with time.

In Figure 4:3 above, as the initial proportion of infectives is 0.05, the proportion of the infectives declines from its initial of 0.05 to its minimum value of 0.025 within 170 days. With the initial proportion being 0.10, 0.20 and 0.30, the infectives population exhibited similar behavior by declining exponentially to 0.025 by day 170th day.

The higher the initial proportion of the infectives the faster the declination.

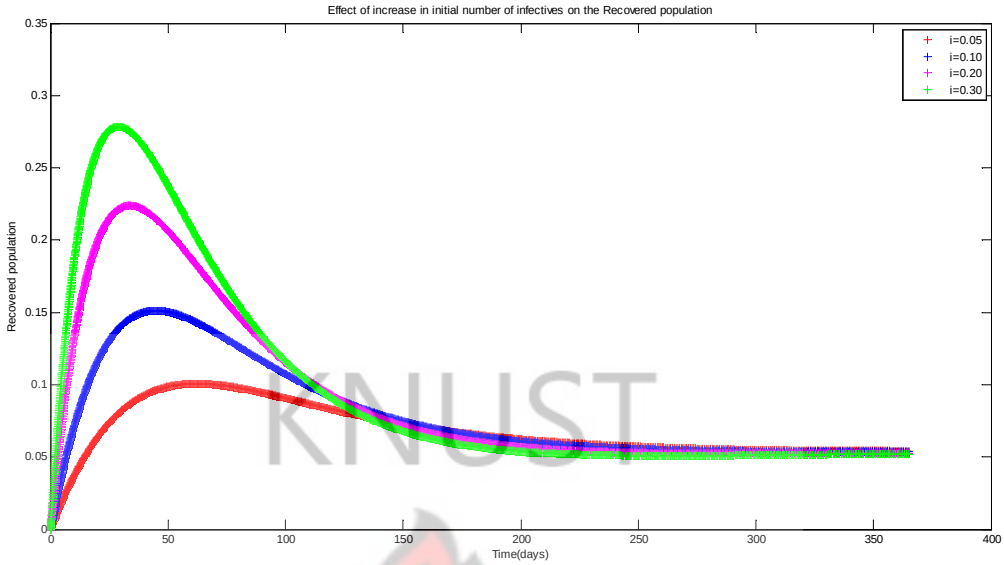


Figure 4.4: Effect of an increase in initial proportion of infectives on the recovered population with time

From Figure 4.4, as the initial proportion of infectives is 0.05, the proportion of recovered population rises exponentially from day 0 to a peak value of 0.1 on day 55 before reducing gradually. As the initial proportion of the infectives is increased to 0.10 the maximum value of 0.15 is observed on the forty-fifth $(45th)$ day.

Similar observations are made for increasing number of initial proportion of infectives. However, each proportion of the recovered population attains different peak values but at different time with all declining to a minimum of 0.05.

4.2 Stability Analysis

4.2.1 Stability of infectious free equilibrium

We now investigate the linear stability of the infectious free equilibrium point $(s^*, i^*) = (1, 0)$. By substituting the parameter values in Table 4.1 above into equation (3.33) the eigenvalues corresponding to the infectious free equilibrium are $\lambda_1 = -0.03$ and $\lambda_2 = 0.009$. Because the two eigenvalues, that is $\lambda_{1,2}$, are both real and λ_1 negative whilst λ_2 is positive, the disease free equilibrium is a saddle point, therefore unstable.

This implies that the presence of a person infected with chicken pox in Ghana will eventually result in an outbreak of the disease.

We will later consider the effect of the changes in the parameter values on the stability of the equilibrium.

4.2.2 Stability of the endemic equilibrium

At the point in time where all the compartments of the population coexist is called the endemic period. The presence of an infectious person is a problem in the epidemiology of infectious diseases. We study the behavior of this equilibrium point.

The endemic equilibrium point is given by

$$(s^*, i^*) = \left(\frac{\gamma + \delta}{\beta}, \frac{\alpha\beta - \delta(\gamma + \delta)}{\beta(\gamma + \delta)}\right) \tag{4.1}$$

Substituting the parameter values in Table 4.1 into the above equation, we obtain our endemic equilibrium as

$$(s^*, i^*) = \left(\frac{115}{124}, \frac{27}{1426}\right) \tag{4.2}$$

$$(s^*, i^*) = (0.927419, 0.018934) \tag{4.3}$$

The eigenvalues corresponding to the endemic equilibrium is given by the equation

$$\lambda_{1,2} = \frac{\frac{-\alpha\beta}{(\gamma+\delta)} \pm \sqrt{\left(\frac{\alpha\beta}{(\gamma+\delta)}\right)^2 - 4\left(\alpha\beta - \delta(\gamma+\delta)\right)}}{2} \tag{4.4}$$

Also by substituting the parameter values into the above equation will have

$$\lambda_{1,2} = \frac{\frac{-0.03(0.124)}{(0.085+0.03)} \pm \sqrt{\left(\frac{0.03(0.124)}{(0.085+0.03)}\right)^2 - 4\left(0.03(0.124) - 0.03(0.085+0.03)\right)}}{2} \tag{4.5}$$

which yields

$$\lambda_1 = -0.016174 + 0.002899i \text{ and } \lambda_2 = -0.016174 - 0.002899i$$

Since the eigenvalues are complex conjugate with negative real parts the endemic equilibrium is asymptotically stable.

From further analysis the endemic equilibrium $(s^*, i^*) = \left(\frac{\gamma+\delta}{\beta}, \frac{\alpha\beta-\delta(\gamma+\delta)}{\beta(\gamma+\delta)}\right)$, can be expressed in terms of the reproductive number R_0. Since $R_0 = \frac{\beta}{\gamma+\delta}$ and $\alpha = \delta$ further substitution yields

$$(s^*, i^*) = \left(\frac{1}{R_0}, \frac{\alpha(R_0-1)}{\beta}\right) \tag{4.6}$$

This produces another expression for the endemic equilibrium solely in terms of the parameters and the reproductive number

4.2.3 Sensitivity analysis

Table 4.3: Parameter values, eigenvalues and classification of the disease free equilibrium.

α	β	γ	δ	λ_1	λ_2	R_0	$Nature\ of\ the\ equilibrium$
0.03	0.124	0.1240	0.03	-0.03	-0.03	0.80519	$Stable\ centre$
0.03	0.124	0.085	0.03	-0.03	0.009	1.0783	$Saddle\ point, unstable$
0.03	0.124	0.095	0.03	-0.03	-0.001	0.992	$Asymptotically\ stable$

From the equations for the eigenvalues, $\lambda_1 = -\delta$ and $\lambda_2 = \beta - \gamma - \delta$

Since $\delta > 0$, it implies that $\lambda_1 < 0$

For stability to be obtained $\lambda_2 < 0$ implying $\beta - \gamma - \delta < 0$

$$\beta < \gamma + \delta$$

$$\frac{\beta}{\gamma + \delta} < 1 \quad \Rightarrow \quad R_0 < 1$$

This implies that when the reproductive number is less than unity, i.e. $R_0 < 1$, that disease free equilibrium is stable. Whilst when the reproductive number is greater than unity the diseases free equilibrium is unstable.

Table 4.4: Parameter values, eigenvalues and classification of equilibrium point of the disease endemic equilibrium.

α	β	γ	δ	λ_1	λ_2	R_0	*Nature of the equilibrium*
0.03	0.124	0.124	0.03	0.02026	-0.04441	0.80519	*Unstable saddle point*
0.03	0.124	0.085	0.03	$-0.016174 + 0.002899i$	$-0.016174 - 0.002899i$	1.07826	*Asymptotically stable*
0.03	0.120	0.095	0.03	0.004504	-0.03330	0.96	*Unstable saddle point*

From the above table perturbation of parameter the endemic equilibrium is stable when the reproductive number is greater than unity, i.e. $R_0 > 1$, and unstable when the reproductive number is less than unity, i.e. $R_0 < 1$.

4.2.4 Herd Immunity Threshold

From equation (3.46), the herd immunity ratio is given as

$$H_I = 1 - \frac{1}{1.07826}$$

$$H_I = 0.0725799$$

Thus about 7.257996% of the susceptible population should be immune in order to bring the spread of varicella under total control.

4.2.5 Control Vaccination Number

Research has shown that that the vaccine for varicella has 99% effectiveness in the first year, and after eight years the effectiveness drops to 87% [Karen, 2004]. Knowing the efficacy of the vaccine we estimate the proportion of the population that need to be vaccinated.

This is given by

$$f_1 > \frac{1-\left(\frac{1}{1.07826}\right)}{0.99} \text{ and } f_2 > \frac{1-\left(\frac{1}{1.07826}\right)}{0.87}$$

$$f_1 > 0.073313 \text{ and } f_2 > 0.083425$$

We can observe from calculations above that when the effectiveness is 99%, then about 7.3313% of the population need to be vaccinated in order for $C_V < 1$. When the effectiveness is 87%, then about 8.3425% of the population need to be vaccinated in order for $C_V < 1$.

CHAPTER 5

DISCUSSION, CONCLUSION AND RECOMMENDATION

5.1. Introduction

In this chapter we discuss the results obtained from the analysis, conclude and give necessary recommendation for further study

5.2. Discussions

From the preliminary analysis, one Varicella patient contacts on the average 1.45882 susceptible people in the country during his/her infectious period

From the simulations, Figure 4.2 exhibits a decline in the susceptible population as the initial proportion of infectives is increased. This implies that, the larger the initial proportion of infectives in the country the larger the proportion of the susceptibles that are infected, and on the other hand the smaller the proportion of the susceptibles left in the country.

Thus when there are many people infected with varicella in Ghana, the susceptibles are at a higher risk of acquiring the disease.

The study of Figure 4.3 also revealed that, an increase in the initial proportion of infective increases the infective in the population. But as the initial proportion increase,

the reduction in the number of infectives with time is faster as compared to a lower initial proportion of infectives

This is because there is a relatively high recovery rate such that even though the susceptible population are been infected, a high amount of them recover quickly there by providing herd immunity. This means that the higher the number of infectives in Ghana the faster they recover adding up to the number of immune persons thereby reducing the number of people to be contacted by an infected person before recovery.

Furthermore, the simulation in Figure 4:4 indicates that the recovered population increases as the initial proportion of infectives remains high. Since the infectives population increases with high recovery rate, more people become infected with varicella and all this people recover.

The sensitivity analysis indicates as illustrated in Table 4.4, that there exist a direct (linear) relationship between the transmission rate, and the reproductive ratio, R_0. The higher the transmission rate relative to the recovery rate the higher the reproductive number whilst the lower the transmission rate relative to the recovery rate the lower the reproductive number since the natural death rate is relatively small.

The perturbation analysis of the disease free equilibrium revealed that when the reproductive number R_0 is less than unity the disease free equilibrium is stable, whilst when it is greater than unity the disease free equilibrium is unstable (Diekmann and Heesterbeek, 2000).

On the other hand the perturbation analysis of endemic equilibrium revealed stability when the reproductive number is greater than unity and instability when the reproductive number is less than unity.

The herd immunity threshold shows that about 7.26% of the susceptible population of Ghana should be immune in order for the disease not result in an epidemic

From further analysis with a control measure such a vaccination, and having a vaccine efficacy of 99% about 7.33% of the susceptible population should be vaccinated in order to have Varicella under total control whilst with a vaccine efficacy of 87% about 8.34% 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.

5.3. Conclusion

The derivation and analysis of the modified SIR mathematical model (SIRS), enabled a better understanding of the dynamics of the spread of varicella within the Ghanaian population.

Numerical simulations and sensitivity analysis was extensively helpful in the determination of the effect of the various parameters especially the transmission rate and recovery rate on the spread of the disease.

The reproductive ratio estimated indicates that the disease outbreak will be epidemic in the country. About 7.26% of the susceptible population should be immune or recovered in order not to have an epidemic during an outbreak.

The simulation results and the sensitivity analysis of the study confirmed the transmission rate and recovery rate as the dominant parameters in the spread of the disease in Ghana. Essentially, the chances of an epidemic is possible as far as the reproductive ratio is greater than one.

5.4. Recommendations

Further research work is recommended particularly for non-constant and heterogeneous population and also on vaccination.

Vaccination programmes should be introduced by the ministry of health and should target at vaccinating the about 7.33% of the susceptible population in order to fully bring the disease under control where the outbreak is considered epidemic.

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APPENDIX

Matlab Code for Simulations

```
function dy=csm(t,y,alpha,beta,delta,gamma)
dy=zeros(3,1)
dy(1)=alpha-beta*y(1)*y(2)-delta*y(1)
dy(2)=beta*y(1)*y(2)-(delta+gamma)*y(2)
dy(3)=gamma*y(2)-delta*y(3)
```

Call Function for the Graph of the susceptibles, infectives, recovered at the initial stages

```
alpha=0.03;beta=0.124;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.95 0.05
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,1),'+',t,y(:,2),'+',t,y(:,3),'+')
legend('Susceptibles','Infectives','Recovered'), ylabel('Total
proportion of population'),
xlabel('Time(days)'), title('Graph of susceptibles, infectives and
recovered at the initial stage')
print
```

Call function for the change in the initial infectives on the susceptible population

```
alpha=0.03;beta=0.124;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.95 0.05
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,1),'r+')
hold on

alpha=0.03;beta=0.124;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.90 0.10
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,1),'b+')
hold on

alpha=0.03;beta=0.124;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.80 0.20
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,1),'m+')
hold on

alpha=0.03;beta=0.124;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.70 0.30
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,1),'g+')
legend('i=0.05','i=0.10','i=0.20','i=0.30'),xlabel('Time(days)'),
ylabel('Susceptible Population'),title('Effect of increase in initial
number of infectives on the susceptible population')
print
```

Call function for the change in the initial infectives on the infective population

```
alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.95 0.05
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,2),'r+')
hold on

alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.90 0.10
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,2),'b+')
hold on

alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.80 0.20
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,2),'m+')
hold on

alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.70 0.30
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,2),'g+')
legend('i=0.05','i=0.10','i=0.20','i=0.30'),xlabel('Time(days)'),
ylabel('Infectives population'),title('Effect of increase in initial
number of infectives on the infectives population')
print
```

Call function for the change in the initial infectives on the recovered population

```
alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.95 0.05
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,3),'r+')
hold on

alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.90 0.10
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,3),'b+')
hold on

alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.80 0.20
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,3),'m+')
hold on

alpha=0.03;beta=0.1240;delta=0.03;gamma=0.085;
options=odeset('RelTol',2e-29,'AbsTol',1e-19);
[t,y]=ode15s(@csm,[0 365],[0.70 0.30
0.00],options,alpha,beta,delta,gamma);
plot(t,y(:,3),'g+')
legend('i=0.05','i=0.10','i=0.20','i=0.30'),xlabel('Time(days)'),
ylabel('Recovered population'),title('Effect of increase in initial
number of infectives on the Recovered population')
print
```