Mathematical modelling in epidemiology: A numerical study

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Certificate

It is certified that the work contained in this thesis entitled "**Mathematical modelling in epidemiology: A numerical study**" in partial fulfillment of the requirements for the award of degree of Master of Science in Mathematics and Computing to the School of Mathematics, Thapar Institute of Engineering and Technology, Patiala is an authentic record of my own work studied under the supervision of Dr. Isha Dhiman.
The matter embodied in this thesis has not been submitted by me for the award of any other degree of this or any other University/Institute.

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This is to certify that the above statement made by the candidate is correct and true to the best of my knowledge.

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Abstract

In order to understand the complexity of real world processes, one need to model these processes mathematically. In this thesis, we review a epidemic compartmental models and their classifications. The aim of our approach is to develop an intuitive understanding of epidemic models and adapt a new technique Monte Carlo simulations for the validation of various epidemic model. A new model SEIQR has been introduced and results are validated using Runge Kutta method and Monte Carlo simulations

Keywords: Mathematical modelling; Epidemic models; Compartmental models; Monte Carlo simulations; Quarantine; SEIQ model; SEIQR model

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Chapter 1

Introduction

1.1 Mathematical models

A mathematical model is a system which uses mathematical ideas and language. The process of developing a mathematical model is called mathematical modeling. Mathematical models [1] are extensively used in sciences and engineering fields, also in social sciences. A model can guide to explain a system and to study the consequences of different components, and to make predictions about behaviour.

There are many interacting systems in the real world that are much difficult to model in their entirety. The models require many settlements to be represented in the computerised system. The very first settlement is to recognise the essential parts of the system. Those essential parts will be included in the model and the rest will be excluded. The second kind of settlement is concerned with the amount of mathematical calculations and observations, which is worthwhile. Although, mathematics has the capability to prove the general results, these results depend purely on the types of the equations used in the model. Even a very small changes in the structure of equations may result into huge changes in the mathematical results.

Mathematical models can be seen as an imaginary microworlds [2] which consist of the systems behaving according to the precisely framed assumptions. Mathematics provides a language for formulating the rules of conduct of model in a concise and absolute way. This helps to clearly define the assumptions for the system. Once a mathematical model is prepared, mathematical analysis when collaborated with computer simulations helps to investigate the universal behaviour of the system. This helps in finding the consequences of the predictions that were made for the system. Thus, within the context of the model, one can make different assumptions of imaginative world and also study how these assumptions would change the system described by the model.

Clearly, the suppositions made in the model's virtual world to be relvant to reality, the model itself must correspond to or represent every event and activity happening in the real world. One can never awaits to obtain good predictions from false assumptions. The creators of models, however, are aware of the fact that all models are at their best performance only if partial descriptions or imitations of the mechanisms operating in

reality, containing varieties of simplification, idealization, approximation, and abstraction, are present. Indeed, many researchers have much of the discussions and debates among them which involves the nature of the simplifications and appropriateness of the models. If one accepts this general idea of creating models, then even simplified models which clearly dominate and even contradict some attributes of reality, can provide few valuable predictions. This is only possible as long as the assumptions of model mirror some realistic aspects.

1.1.1 Elements of a mathematical model

Mathematical models can be of many forms. They may be dynamical systems, static models, differential equations system or models based on game theory. Mathematical models may also involve logic models. In many cases, the distinction of a scientific field wholly depends on how better the mathematical models are presented on the conceptual side approved with the results of rigorously performed experiments. Moreover, absence of consistency between conceptual based mathematical models and experimental observations lead to the important advances. As in accordance with those advances better theories are invented.

A traditional mathematical model basically contains the following elements:

1. Governing equations

The governing equation [3] explains how the values of dependent variables change when one or more independent variables are changed. For example, continuity equations like Navier-Stokes equations and energy equations are the governing equations that master the physics of fluid dynamics and thermal sciences.

2. Assumptions and Constraints

(a). Initial and boundary equations [4]

Boundary equation has conditions specified at boundaries(extreme points) of independent variable in a equation. An initial value problem has all the conditions mentioned at same value of independent variable. One can understand the initial equations from population growth models [5] and boundary equations with the concept of logistic equations [6]

(b). Classical constraints and Kinematic equations

Constraint is a parameter that the system must obey. The kinematic equations are the equations of motion that are described as continuous velocity motion or continuous acceleration motion that means velocity or acceleration are constant with time. They are never used for any time interval during which acceleration is changing. Motion of two inflexible bodies with rolling constraint can be considered as an example [7] for this.

1.2 Classification of mathematical models

While studying epidemic models, it is beneficial to understand the various classifications of models. Classifications [8] of various epidemic models can be done into different categories.These categories tell about some essential facts of their structures. Mathematical models mainly consist of relationships(connections) and variables. Connections can be

represented as operators, for example, algebraic operators, functions, differential functions, and many more. Variables are generalization of system parameters, that can be quantified. In accordance with structure of mathematical model, various classification norms can be used.

A model which comprises large amount of theoretical knowledge, generally explains what happens at particular level in ladder by considering the processes which are performed at lower levels. These are called mechanistic models. They consider mechanisms which are responsible for the variations in the system. In empirical models, mechanisms are not much of interest which are responsible for the changes in the system. Instead, it is purely noted that changes do occur and the model trys to account quantitatively for changes affiliated with different conditions.

The system model is also worth of mentioning. This is the build up of various successions of sub-models which describe the nature of some interacting components.

Other classifications are seen as below:

- **Linear vs Non-Linear**: Mathematical models which have all the variables behaving linearly, are known as linear models. Else, the models are considered as non-linear models. A definition of linearity and non linearity completely depends on the context. Linear models may or may not show non linear character in them. For example, in a statistical linear model [9], it is presupposed that a correlation between the parameters is linear, and it may be non linear in the predicted alterations. Similarly, a linear differential equation can be represented with linear differential operators, but, it can show non linear behaviour after some calculations. If the objective functions and constraints are represented entirely by linear equations, then a model is treated as linear model in mathematical programming model. If more than one of the objective functions and constraints are represented with a non linear equation, then the model is considered as non linear model.

  In simple systems, non linearity is often associated with phenomena such as chaos and irreversibility [10]. Non linear systems and models are far more difficult in studying than linear ones. Though, there are many exceptions. An usual approach to non linear problems is linearization and this can be controversial if one is trying to study features such as irreversibility, which are strongly to non linear.

- **Static vs Dynamic**: A dynamic model [11] is the model in which variables are time-dependent changes with the time in the system. On the other hand, a static or steady-state is a time variant model in which variables are time independent. The calculations are performed on the system in equilibrium state. Typically, differential or difference equations are used to present the dynamic models.

  For example, the calculation of mechanical stress in a bridge is a simple picture of linear model. In actual, cars and trucks are driven over it. One of the basic models that normally be created is the one which assumes that few weight distribution has been placed on the bridge in the past at some point, and everything has resolved into a steady/constant state condition. While these types of models cannot be

considered for studying the effects of moving traffic, heavy winds, earthquakes, or other happenings that change in course of time. It does provide a useful first order analysis of whether the bridge can support the weight or not. If the stress in any of the statistics simulates, bridge's structural components may exceeds or even approach to failure limits. The static simulation model of a bridge does not measure for the effects of the weights created by time varying phenomena such as moving traffic, wind and earthquakes. Dynamic models provide a way of simulating the time dependent variations of systems.

In a formulation of static model, the input and output variables are defined as functions of time but it is more necessary to specify in a dynamic model. Same set of variables given as input in static model results in the similar set of output variables. While in case of dynamic model, the resulted values at any instant of time are dependent on input values at that time. Also, they may depend on all input variables presented in the model at previous time instants as well.

- **Explicit vs Implicit**: In explicit models, the input variables are known and the output variables can be calculated by performing finite number of computations. Similarly, it can be vice-versa. Output parameters are known and the corresponding input parameters are calculated, these types of models are known as implicit models. These models can be solved by an repetitive computational methods, such as Newton's method(for linear models) or Broyden's method(for non linear model). For example, an explicit modelling can be seen in physical properties of jet engine, turbine and nozzle throat areas represented by a designed thermodynamic cycle at a particular flight conditions. Power setting, the engine's operating cycles at different flight conditions and cannot be calculated from the constant physical properties explicitly.

- **Discrete vs Continuous**: A mathematical model that treats particle or object as discrete, the model is discrete. The particle in a molecular model or the state in a statistic model are the simple examples of discrete modelling. In other context, a model presenting the objects in a continuous manner is a continuous model. For example, velocity field of fluids in pipe flows, temperature and stress in a solid matter and electric field that moves continuously over the entire model due to point charge.

- **Deterministic vs Probabilistic(Stochastic)**: A deterministic model is a model comprising of set of variables that are uniquely determined by the parameters and by set of previous states of these variables. Therefore, similar calculations are performed for a given set of initial conditions. However, in a stochastic model, generally called as "stochastical model", randomness is present. Variable states are not given by unique values, rather they are given by probability distributions.

  Stochastic model can be simply understood by an example of process over time considering as the number of the individuals (X) in a checkout line. As time 't' varies, so does X- individuals, they come and leave, one or more at a time. X will fluctuate

a bit if time is sampled in closed(small) intervals, say 1 second. Fluctuations in X will be visibly larger for greater time intervals. For example, if 't' is calculated every hour, then the number of customers could change by tens, hundreds or even thousands at time.

1.3 Mathematical models of epidemiology(epidemic model)

There is no doubt in claiming that the infectious diseases are born from infectious micro-organisms, such as bacteria,virus,protozoa,fungi,parasites and worms. These infectious diseases may spread either directly or indirectly, from human to human. Also it may transfer from animals and birds to humans. The infectious diseases are the major cause of mortality worldwide. The reason behind maximum deaths due to infections are medical facilities available are not up to the required level. Medical administer is not genuine and costs payable are not affordable for an average person. It has been believed and proved that the mathematical modelling is a beneficial tool to study the spread of infectious diseases. Mathematical models and tools assist in developing the control measures for the spread of an infectious diseases.

Mathematical epidemiology is perturbed with modelling the spread of disease in people. An essential goal is to understand the period of spread of the disease, with the aim of controlling the spread. Such models are used to guide the strategy in vaccination policies for various childhood diseases. Models work on some basic suppositions and mathematics. They find parameters for different infectious diseases and use those parameters for calculating the consequences of different mediations. Example of such an mediation is mass vacination programme.

Mathematical modelling in epidemiology was introduced by Bernouli [12] in 1970 in his work explaining the effect of the method of vaccination against the very popular disease, smallpox. An epidemic model is the simplest means of explaining the transmission of infectious diseases through population. Nevertheless, the work of Kenmark and McKendrick in 1927 can be considered as the initial point for the design of modern mathematical models. Their study consisted of SIR model. Specifically, one can categorise mathematical models depending on the division of the population into classes. So, in SIR models, susceptible(S), infected(I), and recovered(R) are considered as departments or compartments or subdivisions in which population is divided. The susceptible people are capable of being in contact with the disease; the infected class is able of spreading the infection or disease; and the recovered people are immune from the diseases. They either die from the disease or naturally, or have recovered and are completely immune to the disease. For various infections, there is a span of time during which the humans has been infected but is not yet infectious; during this latent period of time the individual is said to be exposed. In this case, SEIR models come into the role, where the new class of exposed population (E) is considered. Some infections like common cold, do not have any ever lasting immunity. Such infections do not recover completely and their models

have no recovered component. The population become susceptible again after infection. Then there are SIS models. Other variations of these models are such as SIRS model or the SEIRS model.

Epidemic models are used for understanding the mechanism of infectious disease spread. This is an important for disease control or eradiction. Epidemic models are natural tool for preparing for a forthcoming epidemic/pandemic, dealing with an existing disease for bioterrorism. Also, they provide the skeleton for control methods such as measuring the critical vaccination coverage and the desirable vaccination policy. It also helps in evaluating the cost effectiveness of different interventions.

1.3.1 Types of Epidemic models

Stochastic model

Stochastic [13], literary means randomness. A stochastic model works with a technique of approximating probability distributions of likely outcomes by allowing random variables in more than one inputs over a period of time. Stochastic model completely depends on the chance differences in the prospect of exposure, disease and other disease dynamics.

There are many reasons which states that stochastic models are considered when their analysis is possible. Firstly, stochastic is the best and simple possible way to study the spread of disease. One defines the probabilities of disease transmission between various categories or classes of population, rather than considering whether or not transmission will occur. In fact, a necessary part in stochastic modelling is to exhibit where the model converges when the population size is too large. In a large community, good amount of models will direct either to a minor spread infecting only few individuals, or, to a major outbreak infecting more or less measurable percentage of the community. Also, calculating probabilities of two events is only possible by stochastic model. Estimation is the another major advantage of stochastic models. Knowledge about uncertainity in estimates needs a stochastic model. An estimate is not of a purpose without knowledge of its uncertainity.

Deterministic model

One needs deterministic or compartmental mathematical models to deal with the large proportion of population. Deterministic models are very common where division of population is required. In deterministic models [13], various groups of population are assigned to different subgroups or compartments, each representing a particular stage of the epidemic with similar symptoms.

Basically, the parameters involved in such models are the transition rates of individuals to travel from one compartment to another. While creating deterministic models, it must be supposed that the population sizes in a various compartments, differentiable with respect to time and the epidemic process, is measurable. In simple language, the variety in population of various compartments can be measured by using the history that was used to develop the model.

The key advantage of deterministic models is their simpler analysis. Even the complex deterministic models are easy to analyse, atleast when numerical solutions are sufficient.Moreover, deterministic model explains the spread under the assumption of mass action, depending on the law of large numbers. Deterministic model are also seen as introductory model for new phenomena.

1.4 SIR model

One of the simplest and basic compartmental model is the SIR model. This model is considered as the foundation of other epidemic models. The model consists of three compartments or sub divisions as S, I, and R. The SIR model is fairly predictive for communicable diseases which are transmitted from individual to individual. This model has been formulated for diseases like measles, mumps and rubella. Introduction to mathematical modelling in epidemiology is basically made through the first epidemic model given by Kermack and McKendrick [14] in 1927. This model is popularly known as SIR epidemic model. The compartments or subdivisions used in this model consist of three classes:

- S(t) represents the number of people in susceptible class, people who are not yet infected but are suspected to disease.
- I(t) represents the proportion of infected people and these individuals are capable of spreading the disease to those who are in susceptible category.
- R(t) is the compartment for recovered people. They have been infected and then immuned from the infection, either because of recovery or death. Individuals in this category are not prone to infection again.

The passage of SIR model can be considered as:

$$S \to I \to R$$

Considering fixed population,

$$N = S(t) + I(t) + R(t)$$

, Kermack and McKendrick have obtained the following equations:

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Various assumptions were considered while formulating the equations for model: First, every human must have equal probability as every other individual of contracting the disease with the rate of β, which is referred as contact or infection rate of the disease. Therefore, an infected human makes contact and is able to transmit the disease with βN others per unit time and the fractions of contacts by an infected individual with the susceptible class is $\frac{S}{N}$. The number of new infections in unit time per infective population then becomes, βN $\frac{S}{N}$, giving the rate of new infections as

$$\beta N \frac{S}{N} I = \beta S I$$

For the second and third equations, the population leaving the susceptible class is considered equal to the population entering the infected class. However, a number equal to the fraction (γ, which represents the mean recovery rate, or $\frac{1}{\gamma}$, the mean infective period) of infectives are leaving this class per unit time to enter the removed class. These processes occuring simultaneously are referred to as the law of Mass Action. The idea of accepting that the rate of contact between two sub divisions in a pouplation is proportional to the size of each of the sub division concerned.

It is considered that the infection rate and recovery rate are much faster than the time scale of births and deaths. Therefore, birth and death factors are ignored in this model.

1.5 SIRS model

The SIR assumes people carry lifelong immunity or recovery to a disease upon recovery; this is the case for various diseases. For another class of air borne diseases, like seasonal influenza, an immunity may vanish over time and individual may come in susceptible class again. In this case SIRS [15] model is used. It allows recovered humans to return to a susceptible class. Individuals stay immune for a particular period of time and then the immunity wanes and individuals are suspected to come again into susceptible class.

1.6 SEIR model

In this section, we concentrate on SEIR models. These models are based on the categorisation of the population into four compartments; susceptible(S), exposed but not yet infected(E), infectious(I) or recovered (immune)(R). SEIR [16] models can be used to represent various infectious diseases such as measles, pox, flu, dengue etc. Since, the immunity is not hereditary. SEIR models suppose that all individuals are suspected to disease by birth. The disease is also supposed to be transmitted between individuals by horizontal incidence, i.e susceptible people become infected when they come in contact with infectious people. This contact may be direct (like touching or biting) or indirect (through coughing and sneeze). The infected population may die or recover completely

and this recovered population (vaccinated or recovered from infection) is considered immune.

In this four compartmental model, S(t), E(t), I(t) and R(t) denote the count of people in every class or compartment at time 't' respectively. The total population at time 't' is:

$$N(t) = S(t) + E(t) + I(t) + R(t)$$

. The flow of the model can be understood as:

$$S \to E \to I \to R$$

The evolution and dynamics of SEIR model is explained by governing equations which can be described by a set of ordinary differential equations as:

$$\frac{dS}{dt} = \frac{-\beta(t)SI}{N}$$

$$\frac{dE}{dt} = \frac{\beta(t)SI}{N} - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

N(t) is constant and denotes the total population in the system. That is, the population is constant in the sense that the immigrations, new births and deaths of people are not considered. The parameter β is rate of transmission of disease from susceptible to exposed. Similarly, $\frac{1}{\sigma}$ $\frac{1}{\gamma}$ are the average time periods of incubation (exposed) and infectiousness (infected) respectively. For better mathematical analysis, we use dimensionless or scaled system of equations with improved variables as S=uN , E=vN , I = wN , R = zN and $\tau = \gamma t$ as follows:

$$\frac{du}{dt} = -R_0 uw$$

$$\frac{dv}{dt} = R_0 uw - Kv$$

$$\frac{dw}{dt} = Kv - w$$

$$z = 1 - u - v - w$$

where

$$R_0 = \frac{\beta}{\gamma}$$

and

$$K = \frac{\sigma}{\gamma}$$

. The first and last equations above represent the dimensionless equations of the SEIR model.

1.6.1 Reproduction number R_0

The basic reproductive number [17] or reproduction number, R_0 is the count of secondary infections(infection occuring while or after the medication of another disease) that infected individual would produce in a susceptible population through the entire expanse of the infectious period. For most of the models, R_0 provided is an entrance or doorway condition for the stability of the disease free equilibrium point.

- The disease free equilibrium point is locally asymptotically stable when $R_0 < 1$: the disease dies out.
- The disease free equilibrium point is unstable when $R_0 > 1$: the disease builts itself in a population or one can say an epidemic occurs.

The given description for reproduction number is only valid for simple homogeneous autonomus models. Similarly, one can create more complicated model by giving similar assumptions that include heterogeneity but the basic definition no longer holds.
Generally, R_0 is expressed as:
$R_0 =$ (Number of contacts per unit time)(Probability of transmission per contact)(Duration of infection)

1.7 Limitations

Traditionally, the maximum number of existing mathematical models are formed as systems of ordinary differential equations. These pre-existing models have some markable drawbacks. The local characteristics of the spreading process/disease are ignored. Also, these models do not involve any variable susceptibility of individuals. Specifically, they fail to simulate in an adequate way,

- the individual contact processes,

- the effects of individual behaviour,
- the spatial aspects of the epidemic spreading, and
- the effects of mixing patterns of the individuals.

Chapter 2

A new epidemic model: SEIQR

2.1 Need of Quarantined and/or isolation

The study of mathematical modelling in epidemiology [18] introduced by Ross, McDonald, Kermack, McKendrick and others play an essential part in the field of control and prevention of infectious diseases.

Many of the researchers [19] took the perspective of simple ordinary differential equations models to draw the opinion in terms of the effectiveness of many disease control schemes. The models without the concept of quarantine and/or isolation or isolation is predicted to be perfect, then EDA(exponential distribution assumption) and models that use this prediction gives valuable knowledge and important intuitions into the disease ambulation. However, the EDA may not be worthy in models for diseases with relatively long incubation and/or infectious periods when isolation.

Particularly, in recent few years, mathematical models have been extensively used to explore more effective methods to control the disease SARS(Severe Acute Respiratory Syndrome) disease with symptoms fever and cough and in few cases, it leads to pneumonia and respiratory failure. The various disease control methods include vaccination, quarantine and isolation. Dye and Gay [20] and Lipsitch [21] contributed a typical SEIR model, consisting of four sub populations, namely susceptible, exposed, infectious, and recovered. Wnag and Ruan [22] gave a mathematical model that comprising of six sub populations, suceptible, exposed, quarantined, suspect, probable and removed to imitate the spread of SARS in Beijing. Shi [23] and Lloyd-Smith [24] introduced the stochastic dynamic model, and the discrete model has been considered by Zhou and Ma [25]. In addition, small world network has been introduced to study the transmission of the SARS by Nauki Masuda [26] and Small [27]. It has been observed, if all the infectious humans are isolated as soon as they are diagnosed with the disease, the extremity of the outbreak would be least. Futhermore, Chowell [28] attempted to obtain a gateway for the basic reproductive number R_0 for evaluating the techniques of quarantine and isolation. He also discussed the control of spread of SARS by including the role of disease transferring parameters in the depletion of R_0 and the universality of disease. Moreover, Gumel and Ruan investigated mathematically the consequences of concept of isolation and quaran-

tine on the spread of SARS during the outbreaks in Toronto, Hong Kong, Singapore and Beijing. Their study contributed well to prevent the outbreak of SARS

These recent experiments with SARS [29] has given birth to two main questions that must be questioned in the era of an emerging and re-emerging infectious diseases. The very beginning question is, basic public health methods, such as isolation and quarantine, are likely to be enough or not to watch the spread of disease. According to the researcher, Fraser [29] has given a very general and relevant answer, and revealed that the important factors are the measurements to which the disease is asymptotic and its basic reproductive number.

Where the public health measures are adequate, the second question arises, should isolation and quarantine be practiced in the population or not. It is not clear whether isolation or quarantine have the better impact in preventing the spread of disease, or whether both controlling techniques were essential to use for prevention. This is a necessary agenda because the usage of quarantine in mass proportion is disputable. Specifically, in case of SARS, a small percentage of the quarantined people were actually infected. It is also true that with the removal of even a small percentage of infected individuals from the population, better results were seen in regard of public health. It definitely touches the rights and freedoms of a human. Moreover, particularly in case of SARS, it urges appreciable economic and social costs.

In [29], Fraser have derived common mathematical results. The prediction was made as proportion of infectious individuals stopped when quarantine is used in collaboration with isolation for unpredictable diseases. Their essential goal was to explain the factors to make a quarantine an effective controlling method for the spread of infections. The quantity of quarantine is the proportion of infectious individuals that can be prevented if quarantine and isolation are used collectively in treatment. They relate the expected use of quarantine to noticable parameters of a disease spread, so that it might be used to notify strategy decisions.

Various models have incorporated the idea of quarantine and isolation. Few of them already existing and their literature has been discussed below:

2.2 SEIQ model

Chen, Xiangyong and Cao, Jinde and Park, Ju H and Qiu, Jianlong [30] proposed the SEIQ model. They considered that once the population is diagnosed infected, few of the exposed and infected people are quarantined and some of them are recovered. They assumed S(t), E(t), I(t) and Q(t) are number of susceptible, exposed, infectious and quarantined population in the total population N(t) at time 't'. β SI is the standard bilinear incidence rate, where β represents how quickly the suspected people come into the exposed class. 'A' is considered as the constant recruitment/enrolled rate of the population, μ is taken as the natural mortality rate of all populations, α is the mortality rate of infected and quarantined people died because of infection/disease, ϵ is the rate of exposed people becoming infective, 'c' is the rate of infected becoming recovered and coming back into the susceptible class, σ_1 and σ_2 are the rates of becoming exposed and

infected individuals to quarantined class respectively. γ_1, γ_2 and γ_3 represent the rate of recovery of the exposed, infected and quarantined individuals respectively. The SEIQ model is represented as:

$$\frac{dS}{dt} = A - \beta SI - \mu S + cI$$

$$\frac{dE}{dt} = \beta SI - (\mu + \epsilon + \sigma_1 + \gamma_1)E$$

$$\frac{dI}{dt} = \epsilon E - (\mu + \alpha + c + \sigma_2 + \gamma_2)I$$

$$\frac{dQ}{dt} = \sigma_1 E + \sigma_2 I - (\mu + \alpha + \gamma_3)Q$$

2.3 SEII_hR model

This model is described very crisply. The SEIR model does not consider the concept of isolation or quarantine of an infected individuals from the various sub divisions so as to restrict the spread of virus. The concept of isolation has been included in model, named as SEII_hR. The SEII_hR [16] is pictured as system of differential equations as:

$$\frac{dS}{dt} = \mu N - \frac{\beta(t)SI}{N} - \mu S$$

$$\frac{dE}{dt} = \frac{\beta(t)SI}{N} - \sigma E - \gamma E - \mu E$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \alpha I - \mu I$$

$$\frac{dI_h}{dt} = \lambda E + \alpha I - \omega I_h - \mu I_h$$

$$\frac{dR}{dt} = \gamma I + \omega I_h - \mu R$$

In this model the parameter 'N' is represents the total population of the system. It is considered as constant and birth and death rates are equal.

The assumption is made that model assumes that the total population is divided in five compartments or sub populations. The parameter μ depicts the death rate and birth rate of the population during the short period of the epidemic spread and β is the transient rate of the disease from the division S(t) to E(t). Similarly, $1/\sigma$ and $1/\gamma$ are the average rates of stay in the compartments E(t) and I(t). Also, the parameter $1/\omega$ shows the average time that taken by an individual to travel from isolation compartment, I_h(t) to R(t). The parameters λ and α are the probable rates of isolated human from exposed and infected compartments respectively.

2.4 Aims and Objectives

The key objectives of this thesis are:

- to review the concept of epidemic compartmental models
- to propose a new epidemic model, SEIQR
- to validate the results of existing models using Runge Kutta method of fourth order
- to present a new technique, Monte Carlo simulations for studying epidemic models

2.5 SEIQR model

Various studies about the outbreak and spread of infectious disease have been done by means of establishing mathematical epidemic models. Reasearchers provide some useful and authentic references for the characteristics of disease transmission. Based on the results of conceptual analysis and work of Zhigang Wang, Xiaoming Fan and Qixing Han [31], we propose, SEIQR epidemic compartmental model where S is for Susceptible, E is for exposed, I is for infected, Q is for quarantined and R is for recovered individuals. As dicussed in previous models, we take N=S+E+I+Q+R as constant population. For a particular instant of time 't', S(t), E(t), I(t), Q(t) and R(t) are the populations in the susceptible, exposed, infected, quarantined and recovered sub divisions of model respectively. The model is governed by the following equations:

$$\frac{dS}{dt} = A - \beta SI - \mu S + cI$$

$$\frac{dE}{dt} = \beta SI - (\mu + \epsilon + \sigma_1 + \gamma_1)E$$

$$\frac{dI}{dt} = \epsilon E - (\mu + \alpha + c\sigma_2 + \gamma_2)I$$

$$\frac{dQ}{dt} = \sigma_1 E + \sigma_2 I - (\mu + \alpha + \gamma_3)Q$$

$$\frac{dR}{dt} = \gamma_2 I + \gamma_3 Q - \mu R + \gamma_1 E$$

In the above equations, different rates of transmission are as follows:
A signifies the constant recruitment rate of the population
β is the infectious rate of the susceptible population
μ represents the natural mortality rate of all sub populations
c is the rate of travelling from infected to susceptible
ϵ is the rate of travelling from exposed class to infected
α depicts the mortality rate of infected and quarantined population because of disease
σ_1 shows the quarantined rate of exposed population
σ_2 is the rate of travelling from infected population to quarantined
γ_1 is the rate of recovery of exposed population
γ_2 gives the recovery rate of infected population
γ_3 depicts the rate of recovery of quarantined population.
Many people argue that death rate for each class should be different. It is very obvious that a person can die anytime and due to any reason but we take same mortality rate in every compartment to prevent the complexity of our model. So, for simplicity, we take constant transition rates for various ways to reach to demise.

2.6 Methodology

In this section, we describe briefly numerical techniques used to analyse the models. We have worked on various existing epidemic models using 2 methods, Runge Kutta method and Monte Carlo simulations.

- **Runge Kutta method**: Runge Kuta method [32] is a powerful method used to solve the differential equations. Primarily, RK method provides an approximate solutions for the systems of ordinary differential equations with intial conditions known. It is a numerically integrating ODEs method using trial step at the mid points of an intervals to cancel the lower order error terms. The Runge Kuta method of fourth order is reasonbly simple and robust. It converges rapidly to the solution of ODE. RK method uses four approximations to the slope and these approximations are then estimated at some time interval.

The ODE solvers are not as good as analytic solutions. They donot provide any insight into generalizations. Moreover, an exact value may not be clear. Considering these limitations, we proposed an another technique to study epidemic compartmental models

- **Monte Carlo Simulations**: Monte Carlo simulation [33] is a widely used method in a probabilistic analysis of engineering systems. It is a numerical experimentation technique which gives the statistics of the output variables of a system computational model when the statistics of input variables are given. A simulation is an imitation of the performance of the real world process or system. It is a process of scheming the model of a real system and conducting numerous experiments with this model for the purpose of understanding the performance of the system and/or evaluating different strategies for the operation of the system. Simulation is used before an existing system is altered or a new system is built. This is the efficient method to reduce the probability of failure to meet specifications, to eliminate unforseen bottlenecks, to check under or over-utilization of resources and to optimize system performance.

  Brief algorithm: In Monte carlo simulation, a random value is choosed for each task, based on the range of estimates. A class is chosen at random for i^{th} iteration. Depending upon the selected class, transitions are performed based on various transition rates. For example, if S(Susceptible) class is selected at random, then an individual can enter into S by birth or can travel from S to either I(Infected) class or D(Death) class. After rigorous computations, taking usually 10^6 time steps, averages are computed by ignoring the transient and then the results are are plotted. They signify the steady state of the system.These results are used to explain the concepts like likelihood, or probability or reaching different results of model.

2.7 Results and discussions

2.7.1 Comparison of results of existing epidemic models using Runge Kutta Method and Monte Carlo Simulations

- **SIR model**
  Fig. 2.1 shows the graphs drawn using RK method and fig. 2.2 shows the graphs drawn using Monte Carlo simulations for SIR model. The values taken for transition rates involved in this model are as follows:
  N (total population)=1000, r $\beta = 0.3$ days, $\gamma = 0.1$ days, S(0)=999, I(0)=1, R(0)=0, $\mu = 0.000045$ days, G=0.04. In fig. 2.1(a) the time period taken is 100 days.One can observe from the graph that the number of infected people decreases with time and number of recovers increases with time. That means the disease slowly gets vanish by the period of time. Similarly, in fig. 2.1(b), time period is taken 10^5 days, infected are decreased and recovered people are increased in number and curves become stable after a time period.

In fig. 2.2(a) simulations are done for 10000 days and in fig. 2.2(b) for 10^5 days. One can observe from the obtained graphs that our results match well qualitatively with those obtained with RK method.

- **SEIR model**
  Fig. 2.3 shows the graphs drawn using RK method and fig. 2.4 shows the graphs drawn using Monte Carlo simulations for SEIR model. The values taken for various transition rates involved are as follows: N=1000, $\mu = 0.000045$ days, G=0.04; $\beta = 0.3$ days, $\gamma = 0.1$ days, $\epsilon = 0.2$ days, S(0)=6, E(0)=20.1818, I(0)=6.7273, R(0)=3.3636. In fig. 2.3(a) the time period taken for the system is 50 days. As in SIR model, infected population decreases and recovered population increases.The new compartment introduced here also decreases becomes stable with time. Similarly, in fig. 2.3(b) time period is taken 100 days.

  In fig. 2.4(a) simulations are performed for 10000 days time period and in fig. 2.4(b) for 10^6 days. The behaviour of curves matches as obtained with RK method.

- **SEIQ model**
  Fig. 2.5 depicts the graphs drawn using RK method and fig. 2.6 depicts the graphs drawn using Monte Carlo simulations for SEIQ model. The values taken for various transition rates involved are as follows: N=1000, A=20, $\beta = \alpha = \gamma_3 = 0.5$, $\mu = \epsilon = c = \sigma_2 = \gamma_2 = 0.25$, $\sigma_1 = \gamma_1 = 0.125$, S(0)=6, E(0)=20.1818, I(0)=6.7273, Q(0)=3.3636.
  In fig. 2.5(a) the system has been evaluated for 50 days and in fig. 2.5(b) for 100 days. As in previous verified models, infected individuals decreases with time. New introduced class quarantine increases with time and then becomes stable.

  In Monte Carlo simulations we have used A=0.3 so as to stable the system in less time. In fig. 2.6(a) the time period is considered of 10000 days and in fig. 2.6(b) for 10^6 days. The graphs obtained with Monte Carlo simulations are similar in behaviour with that obtained with RK method. Fluctuations are seen because of less time run. These can be removed while running the system for large period of time. We were not able to obtained due to less computational methods.

2.7.2 Verification of results of proposed SEIQR model

Fig. 2.7 depicts the graphs drawn using RK method and fig. 2.8 depicts the graphs drawn using Monte Carlo simulations for SEIQR model. The values of transition rates considered are as follows: N=1000, A=20, $\beta = \alpha = \gamma_3 = 0.5$, $\mu = \epsilon = c = \sigma_2 = \gamma_2 = 0.25$, $\sigma_1 = \gamma_1 = 0.125$, S(0)=6, E(0)=20.1818, I(0)=6.7273, Q(0)=3.3636. R(0)=0. In fig. 2.7(a) the time period is taken 50 days and in fig. 2.7(b) the time period is 100 days. The infected population decreases with time and recovered population increases. In this system, the rate of settling the infection is more.

For performing simulations, we take A=0.3. In fig. 2.8(a) the time period is considered of 10000 days and in fig. 2.8(b) for 10^6 days. The graphs obtained with Monte Carlo

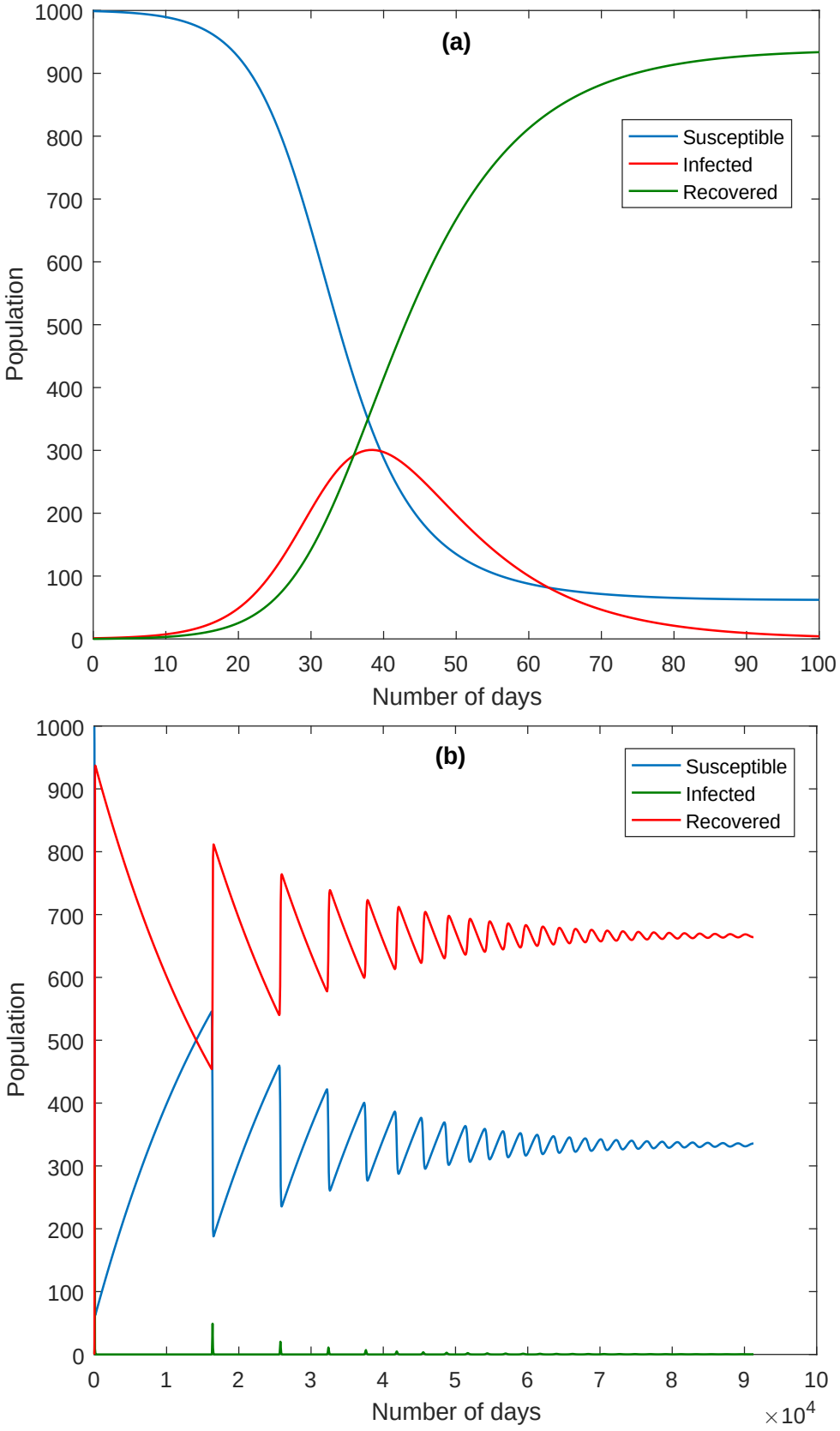

Figure 2.1: SIR model recorded for 100 days in fig 2.1(a) and for 10^5 days in fig 2.1(b)

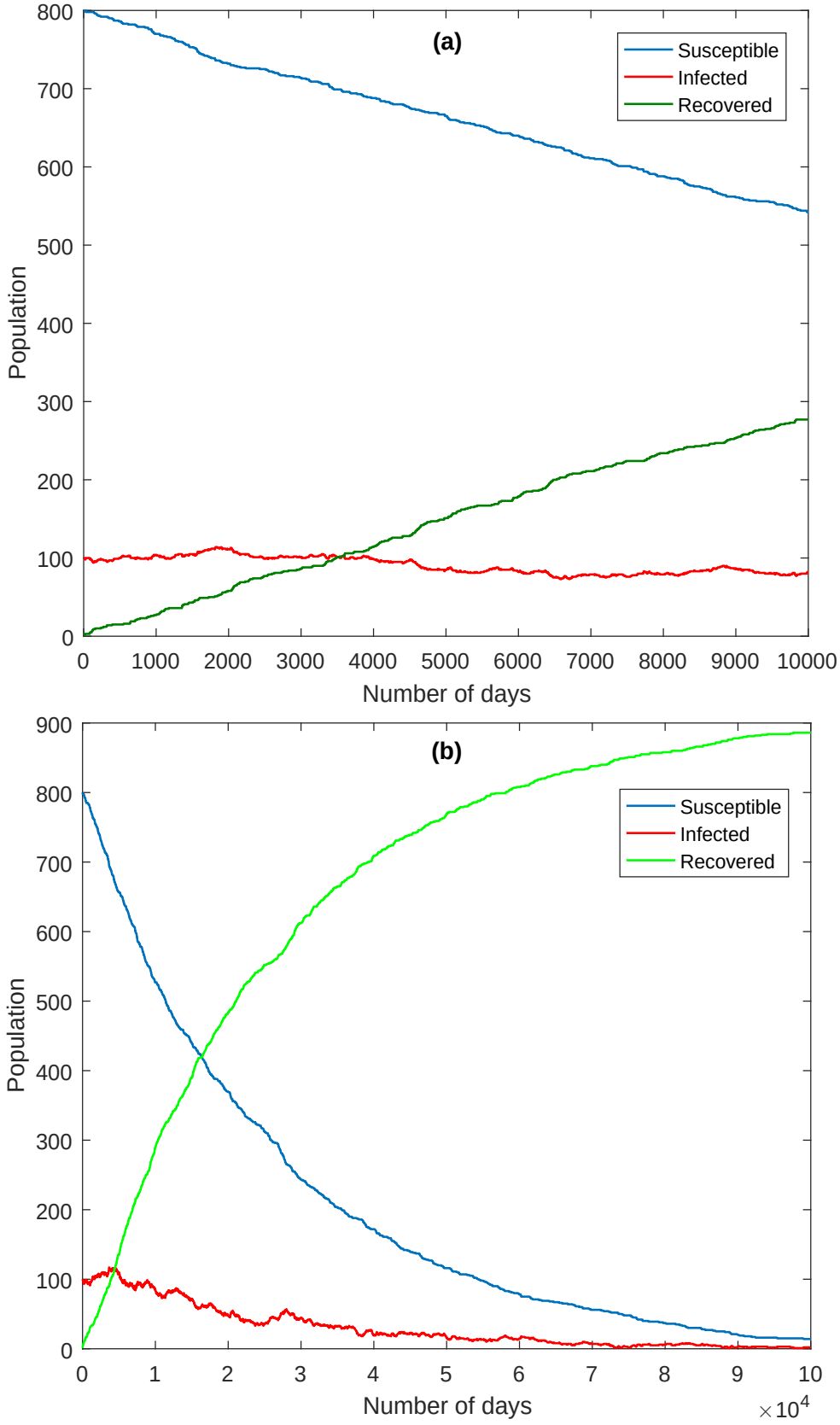

Figure 2.2: SIR model recorded for 10000 days in fig 2.2(a) and for 10^5 days in fig 2.2(b)

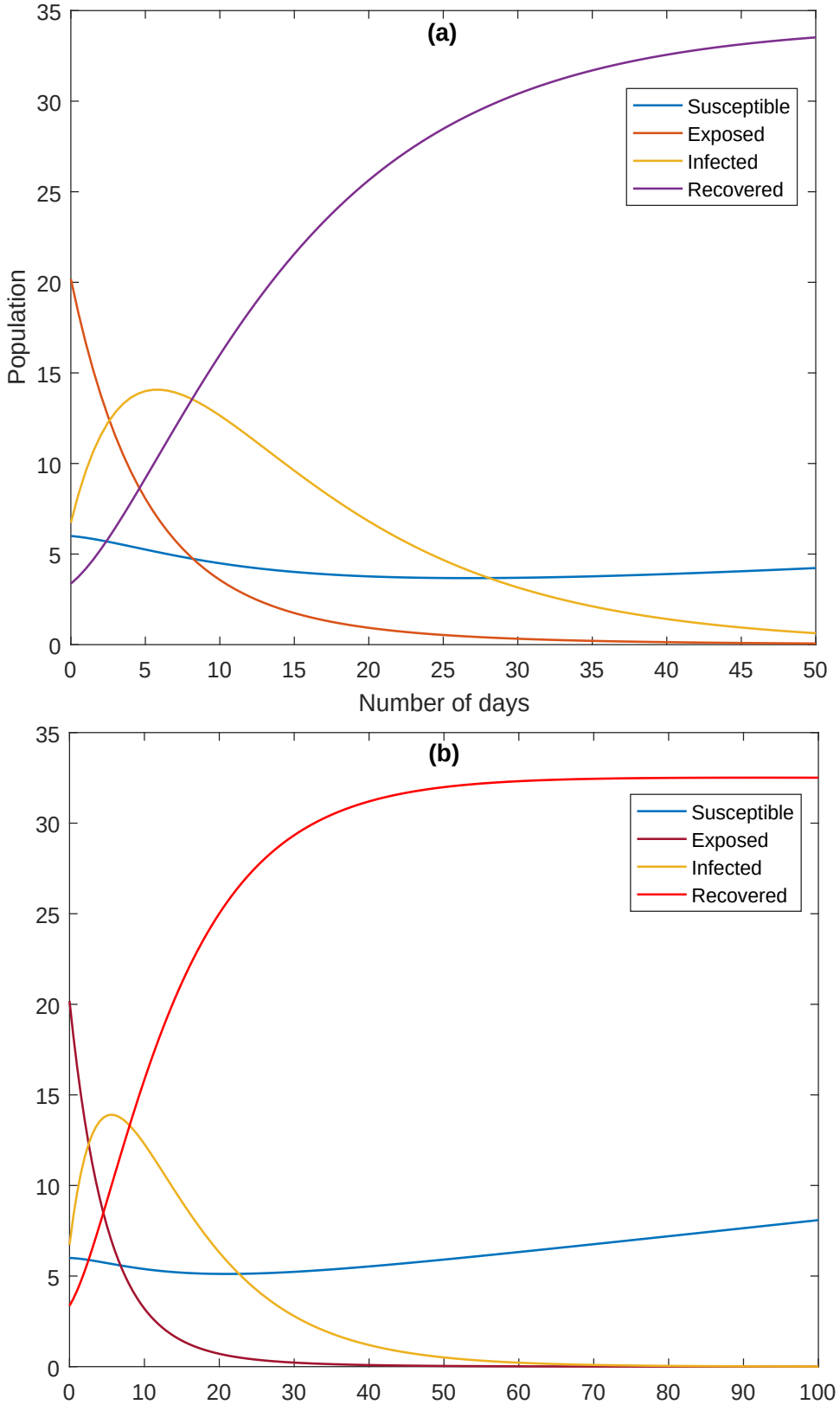

Figure 2.3: SEIR model recorded for 50 days in fig 2.3(a) and for 100 days in fig 2.3(b)

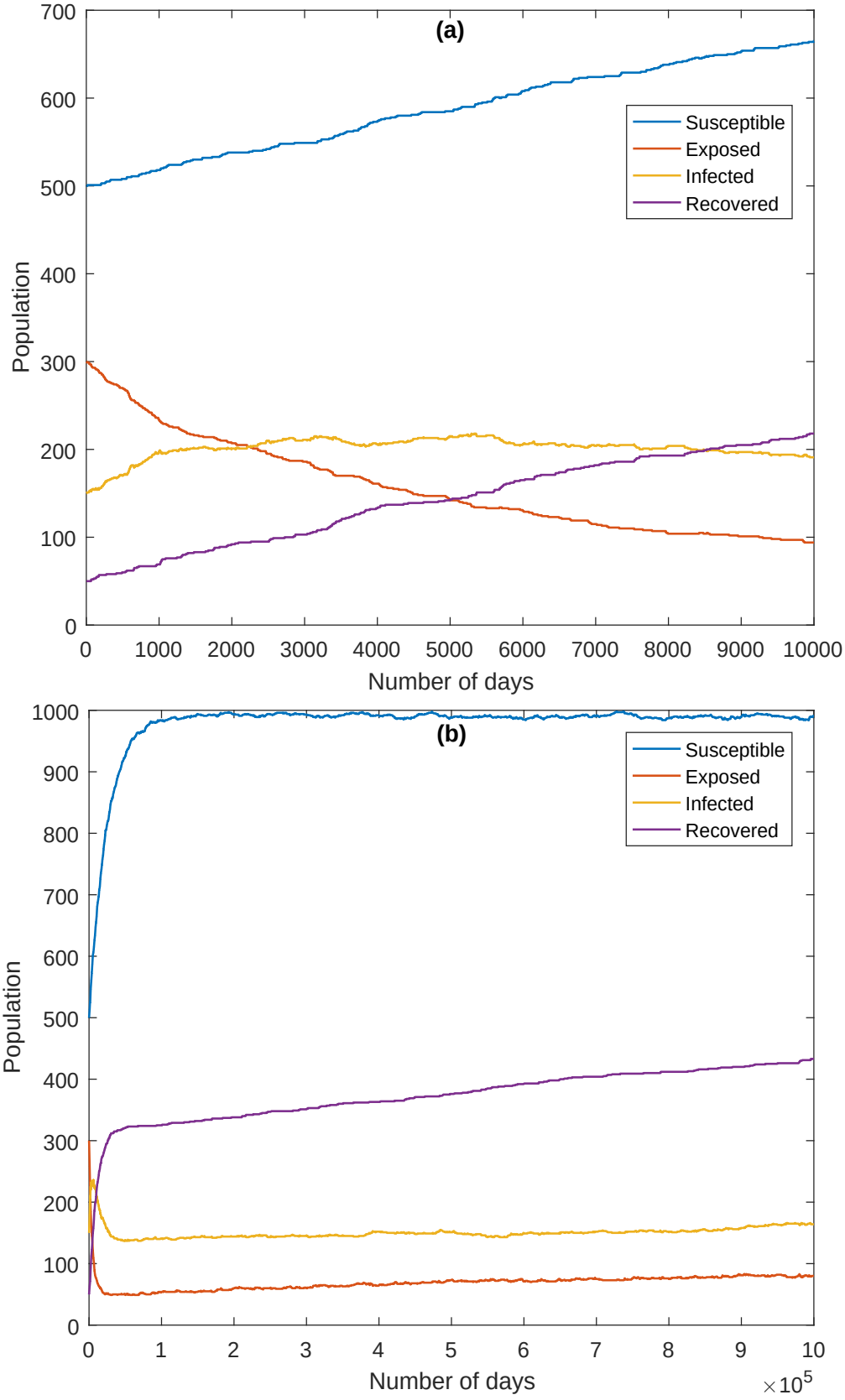

Figure 2.4: SEIR model recorded for 10000 days in fig 2.4(a) and for 10^6 days in fig 2.4(b)

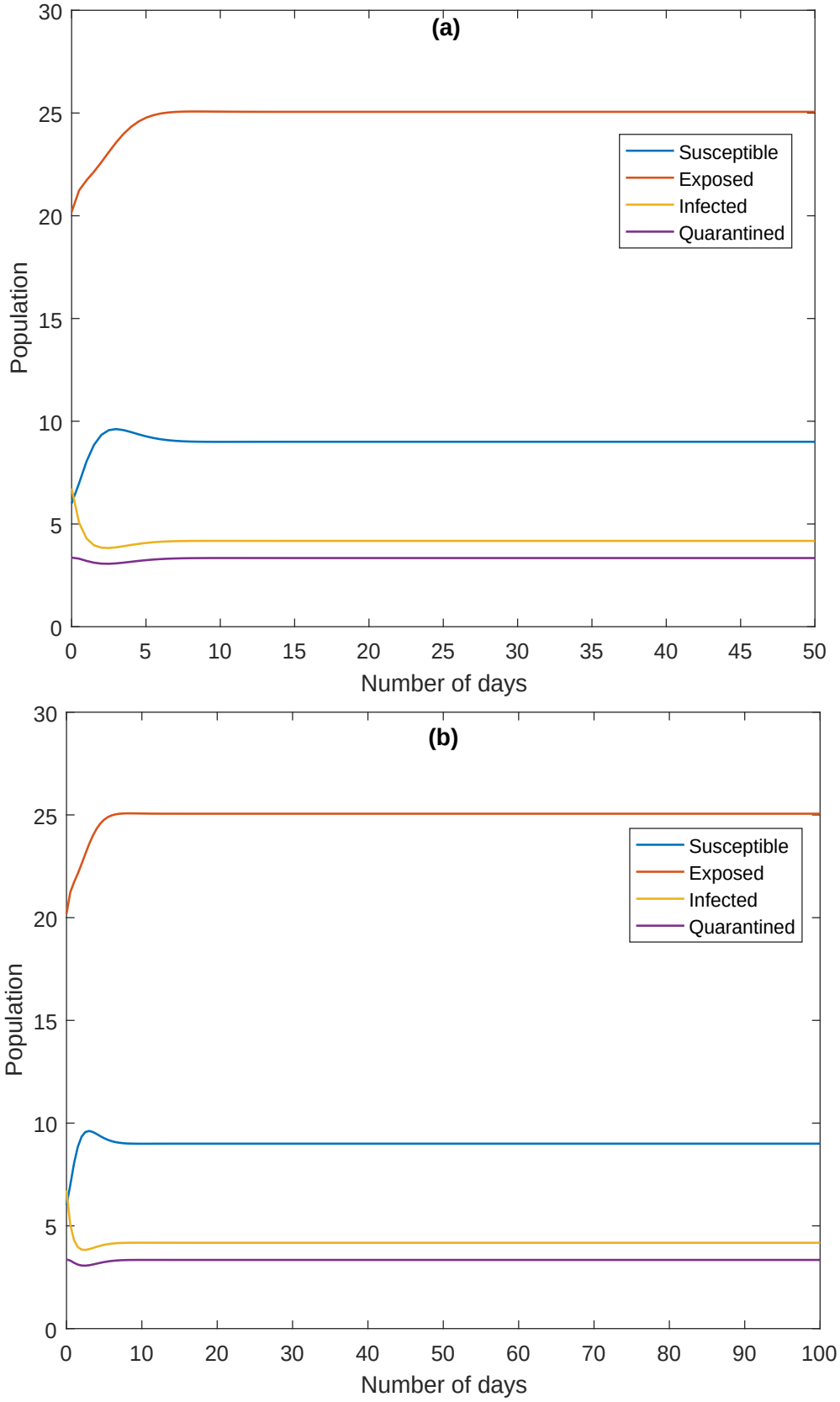

Figure 2.5: SEIQ model evaluated for 50 days in fig 2.5(a) and 100 days in fig 2.5(b)

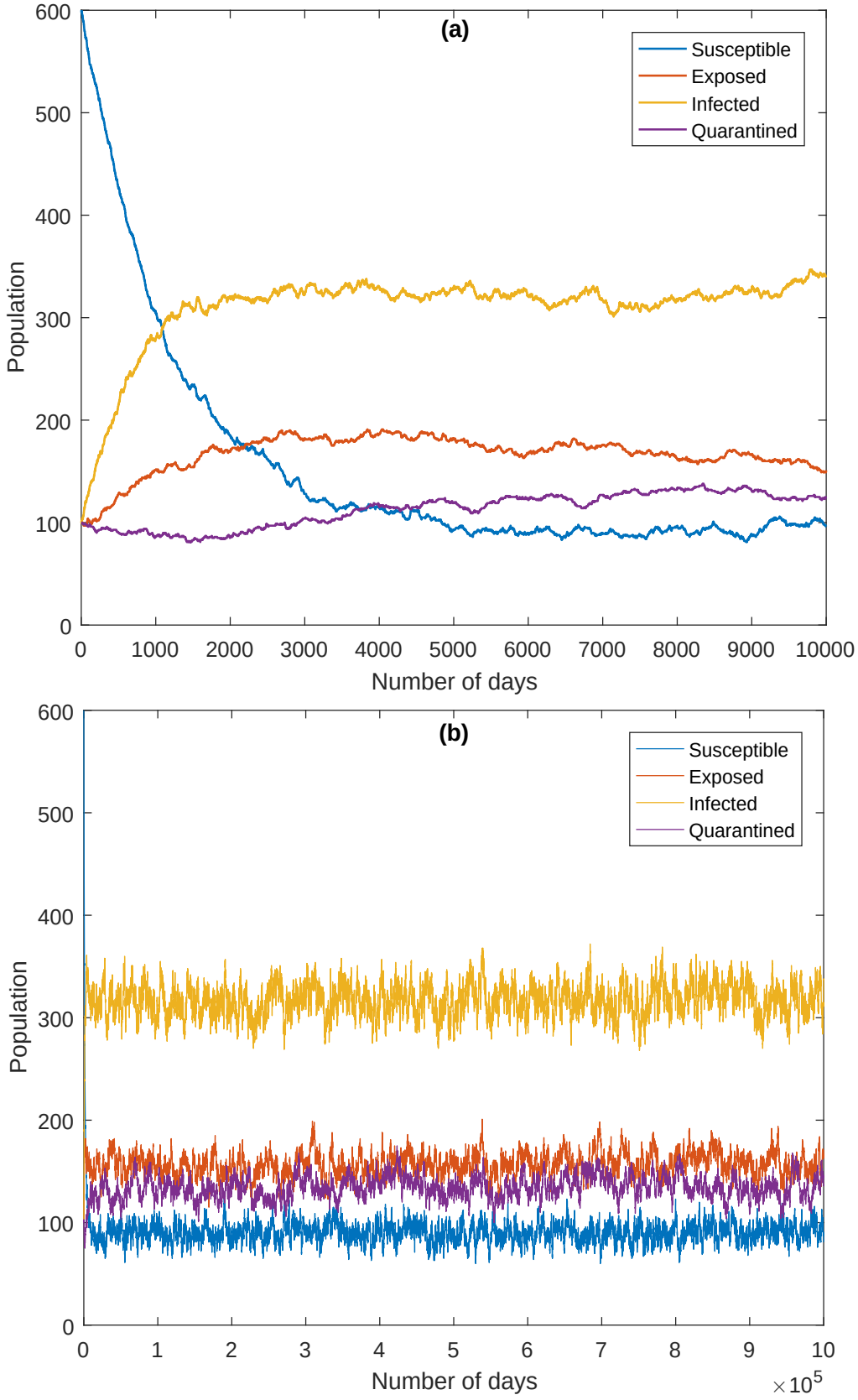

Figure 2.6: SEIQ model evaluated for 10000 in fig 2.6(a) and 10^6 days in fig 2.6(b)

simulations are similar in behaviour with that obtained with RK method. Fluctuations are seen and can be rid off by running the system for more time period.

2.7.3 Effects of changes in various parameters in SEIQR model

In order to thoroughly examine the proposed model, we have investigated the effects of changes in various transition rates which has been described below:

- μ **Natural mortality rate of population**
  Fig. 2.9 shows the results with different values of μ. Initially, μ is taken as 0.5 and then increased its value to 0.9. Due to the increase in natural mortality rate, people die fast, population is reduced rapidly and the disease dies out in a lesser period of time. The stable values are attained faster for the curves. Also, one can see the larger disturbance in the initial time steps. This is because of increase in mortality rate.

- σ_1 **Quarantined rate of exposed population**
  Fig. 2.10 shows the system with different values of σ_1. Initially, the value of σ_1 is 0.125 and then it's increased to 0.9. If the maximum population is quarantined and at a greater rate, the recovery rate increases automatically. The recovered population can be seen has increased with tremendous difference and infected population has been reduced and is almost minimum.

- γ_2 **Recovery rate of infected population**
  Fig. 2.11 shows the results with different values of γ_2. Initially the substituted value is 0.25 and then it's value has been increased to 0.9. it is clear from the obtained results, if recovery rate is more, people are healed in short period of time and disease vanishes quickly. With greater recovery rate, recovered curve is maximum. Also, the infected populations is reduced and is almost equal to quarantined population.

- **A, The recruitment rate of the population**
  Fig. 2.12 shows the system with different values of A. Initially, A=20 and then it's value has been decreased to 0.5. As it is the number of people initialising our model, so slight change in it, changes the whole behaviour of the graph. Stability has been attained here, but the values of stable graph has been reduced. This is because the birth rate or recruitment rate is decreased. One can see that here susceptible population is more than the recovered population.

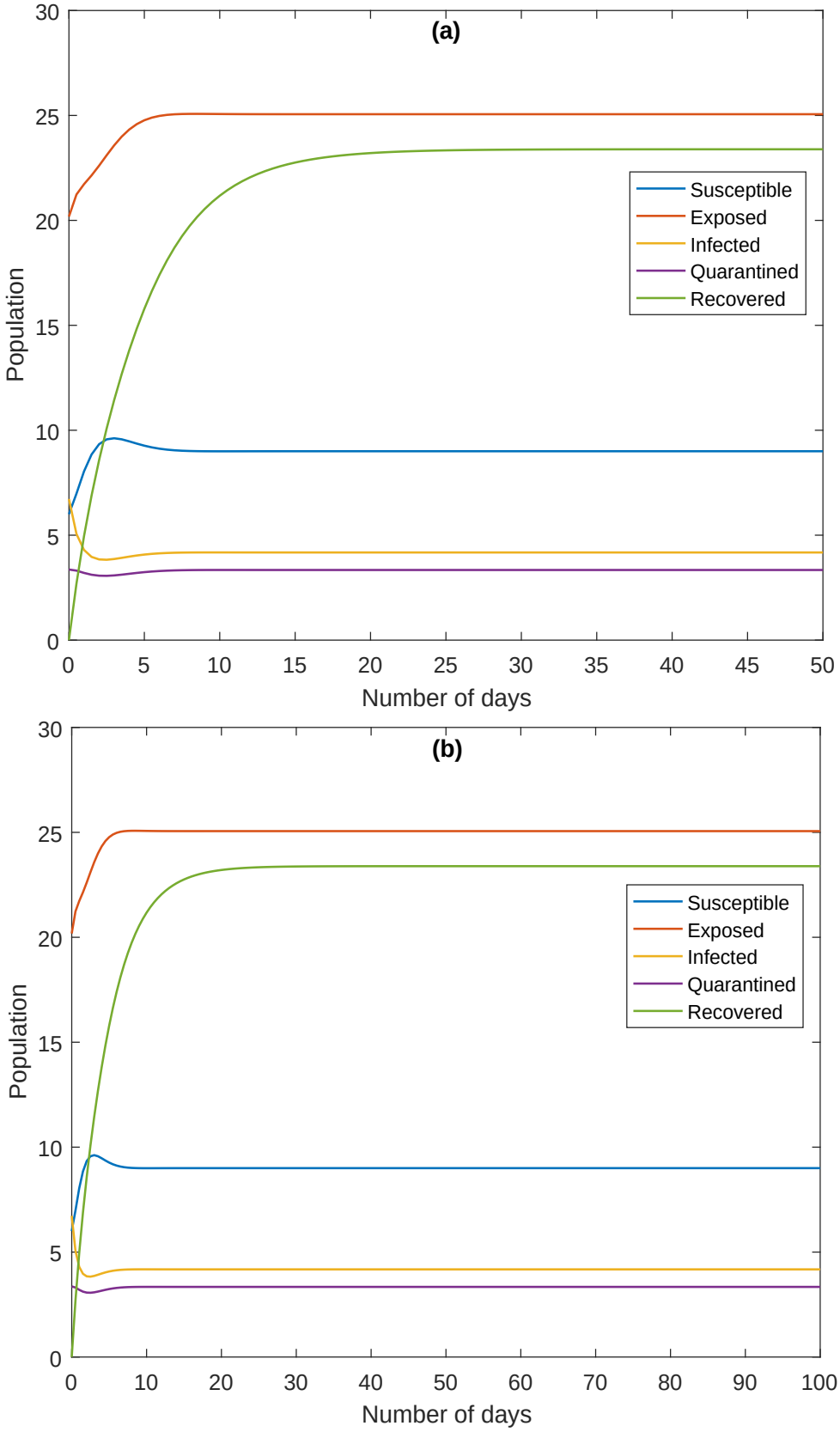

Figure 2.7: SEIQR model verified for 50 days in fig 2.7(a) and 100 days in fig 2.7(b)

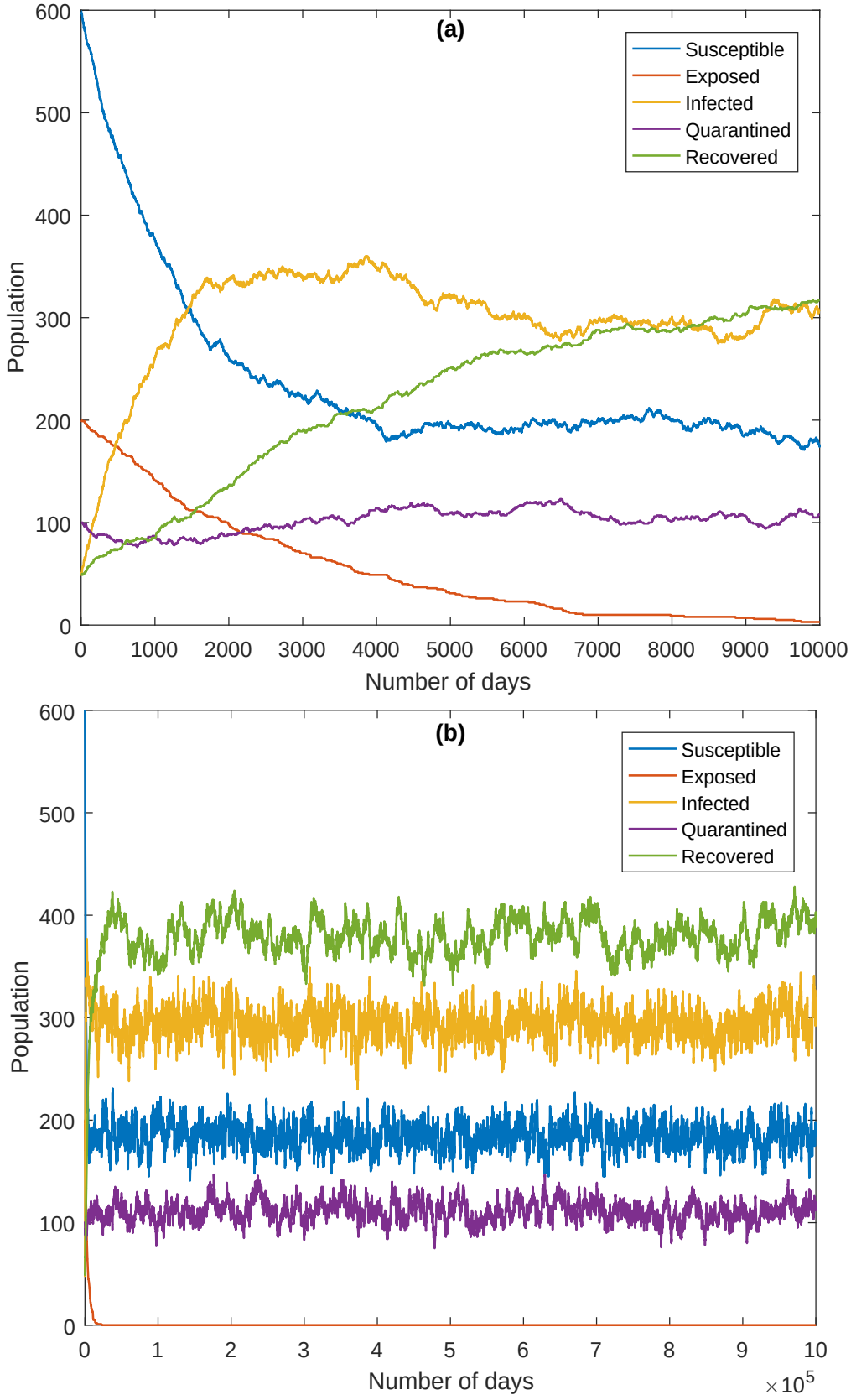

Figure 2.8: SEIQR model verified for 10000 in fig 2.8(a) and 10^6 days in fig 2.8(b)

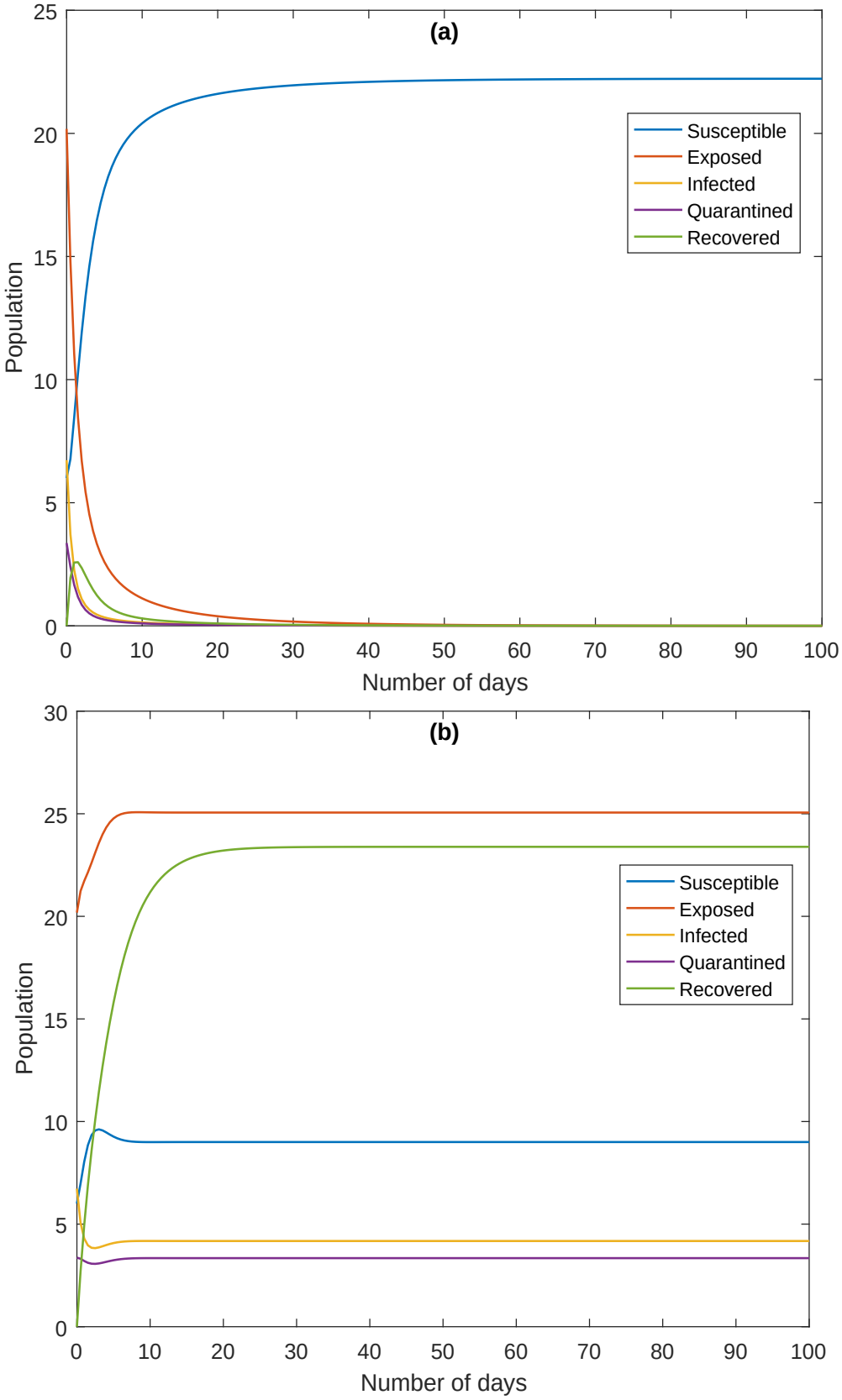

Figure 2.9: Fig. 2.9(a) presents results with $\mu = 0.9$ and fig. 2.9(b)with $\mu = 0.5$

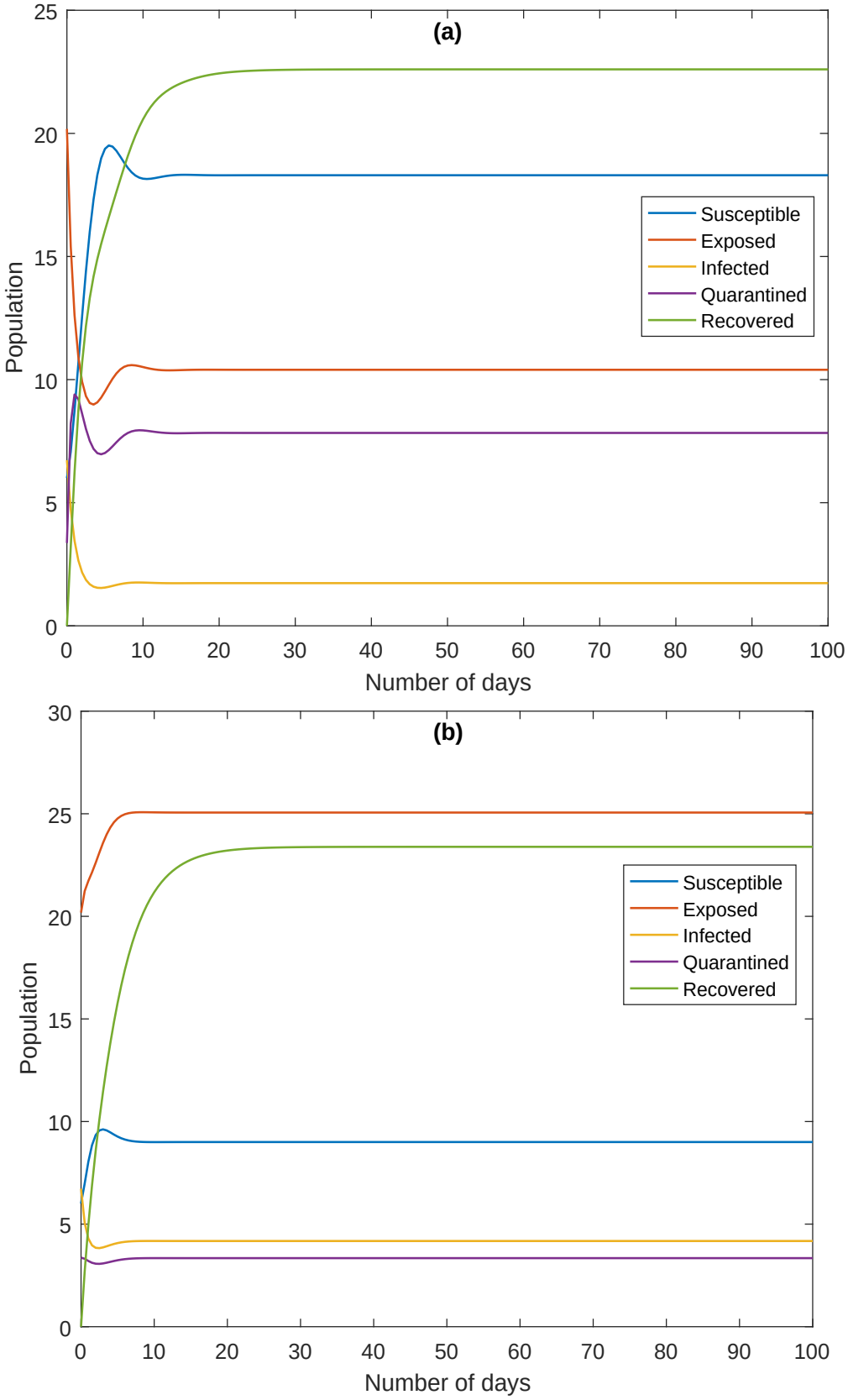

Figure 2.10: Fig. 2.10(a) shows results with $\sigma_1 = 0.9$ and fig. 2.10(b) with $\sigma_1 = 0.125$

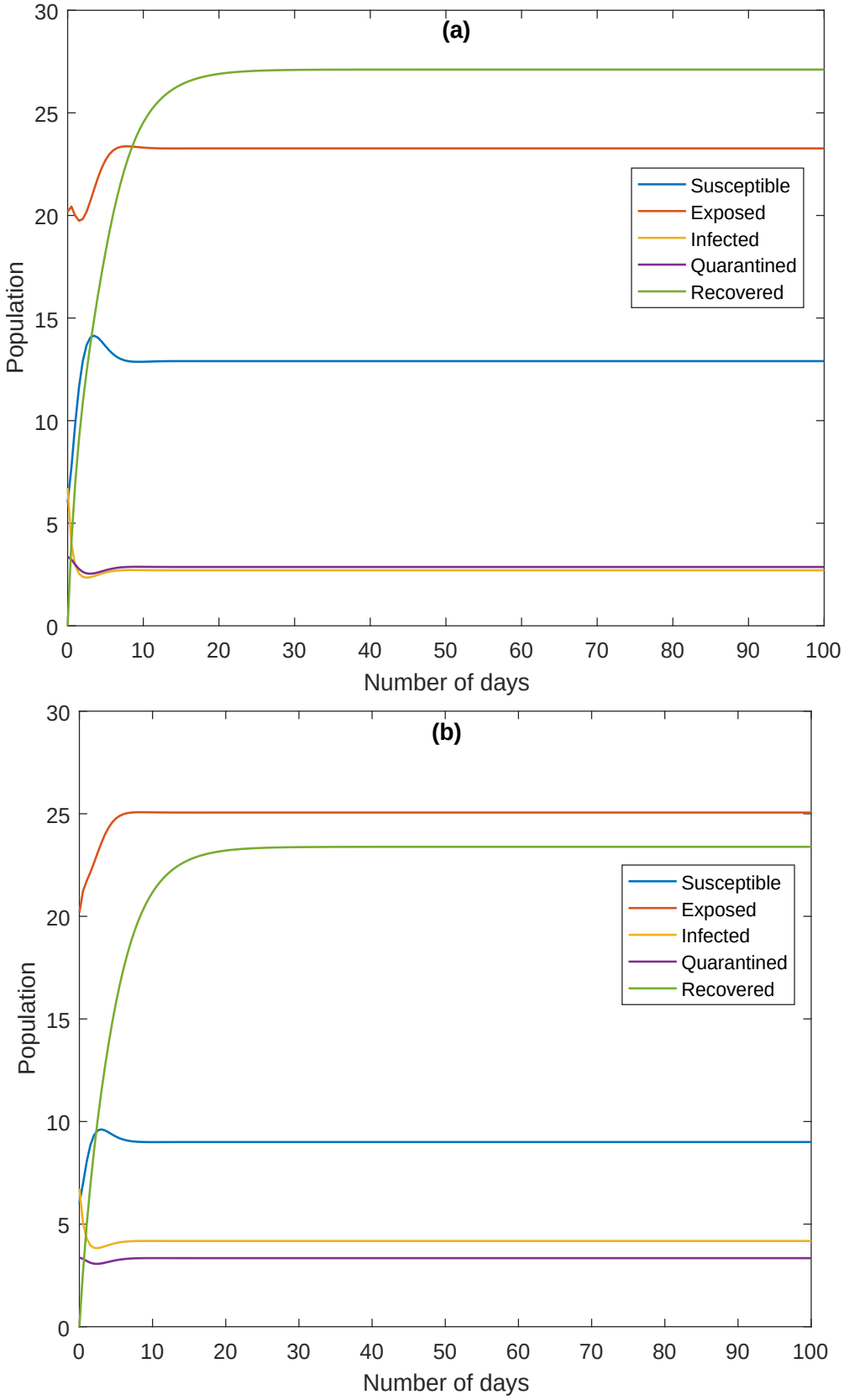

Figure 2.11: Fig. 2.11(a) shows results with γ_2 =0.9 and fig. 2.11(b) with $\gamma_2 = 0.25$

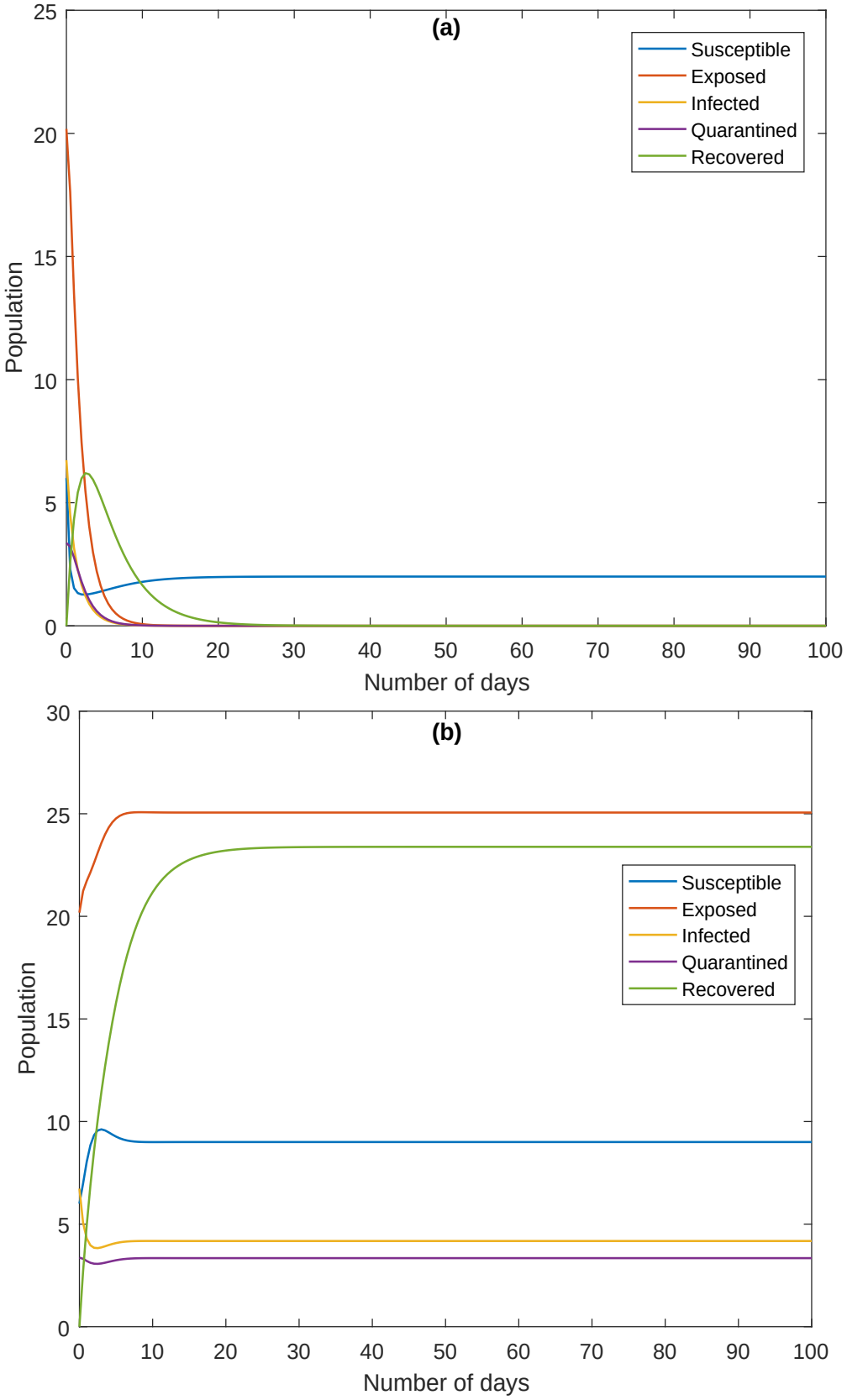

Figure 2.12: Fig. 2.12(a) gives results with A=0.5 and fig. 2.12(b) is for A=20

Chapter 3

Conclusion

3.1 Summary

In this thesis, epidemic compartmental models are studied. Compartmental model is a technique used to simplify the mathematical modeling of infectious disease. The population is divided into various compartments with the assumption that people in one compartment have similar characteristics. Depending on the number of classes in which population is divided, we have large variety of models like SIR, SIRS, SEIR, SEIRS and SEIQ where S is for Susceptible, E is for Exposed, I is for Infected, R is for Recovered and Q for Quarantined

Quarantine means to separate and restrict the movement of infected people. Based on the concept of quarantine, we proposed another compartmental model, SEIQR.

Also, our work comprises of two techniques to study the stability of disease, using which we have validated the results of various existing epidemic models qualitatively. One is Runge-Kutta method of fourth order. Second technique is Monte Carlo simulations. This is an efficient technique that works on realistic assumptions and requires less manual power.

One can easily see that in every possible subdivisions taken of population, infected individuals are decreasing with time and recovered are increasing. Moreover, effects of change in various parameters in SEIQR model have been observed. Transition rates like μ, mortality rate, σ_1, quarantined rate of population, γ_2, recovery rate of infected population, have given the markable difference in values of curves. With increased values of these transition rates, infected population decreases rapidly and recovered increases in short span of time.

3.2 Future outlook

Research is a continuous investigation. So one can study the models described in this thesis more deeply. One can create more compartments, the difference between vaccinaton and isolation, effects of changes in rates of travelling from one compartment to another

can be studied. The proposed models can be used in real world to study the spread of an infectious disease. These models might be used in another fields like, computer virus, effect of medicine in human body, extinction of any specie. Monte Carlo simulations can be used for studying mathematical modelling. It is a realistic and efficient method and works on real life assumptions.

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