FATMA NEŞE EFİL

AGGRAVATİON OF CANCER, HEART DİSEASES AND DİABETES SUBSEQUENT TO COVİD-19 LOCKDOWN VİA MATHEMATİCAL MODELLİNG

NEAR EAST UNIVERSITY
INSTITUTE OF GRADUATE STUDIES
DEPARTMENT OF MATHEMATICS

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Ph.D. THESIS

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Supervisor
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Approval

We certify that we have read the thesis submitted by Fatma Neşe EFİL titled **"Aggravation of Cancer, Heart Diseases and Diabetes Subsequent to Covid-19 Lockdown via Mathematical Modelling"** and that in our combined opinion it is fully adequate, in scope and in quality, as a thesis for the degree of Doctor of Philosophy in Applied Mathematics.

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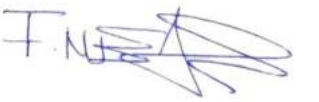
Declaration

I hereby declare that all information, documents, analysis and results in this thesis have been collected and presented according to the academic rules and ethical guidelines of Institute of Graduate Studies, Near East University. I also declare that as required by these rules and conduct, I have fully cited and referenced information and data that are not original to this study.



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Fatma Neşe EFİL.

To my mom...

Abstract

Aggravation of Cancer, Heart Diseases and Diabetes Subsequent to Covid-19 Lockdown
via Mathematical Modelling

EFİL, Fatma Neşe

Supervisor: Prof. Dr. Evren Hınçal

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The main aim of this thesis is to illustrate the future effect of COVID-19 on people who are afflicted by other deadly diseases such as cancers, heart disease, and diabetes. Using ordinary differential equations (ODEs), mathematical models are evolved to explain the affiliation between COVID-19 and cancer and between COVID-19 and heart disease and diabetes. Concordantly, famous mathematical techniques, sensitivity analysis, and equilibrium points are employed in the well-constructed models.

Chapter I specifies the principal factors and opinions of the proffered thesis. General opinions, theorems, and definitions advocating the thesis are presented in Chapter II. The study is separated into two sections, broadly.

In Chapter III, the first model is proposed with the proof of existence of the solution. Afterwards The model is constructed with the help of ODEs to obtain the change in compartments at time t. Then, an analysis of the model with equilibrium points is given. In the analysis of the first model, disease-free equilibrium, $E0,1$, and endemic equilibrium, $E*,1$, points are found with their existence proofs. Moreover, the globally asymptotically stability property of both points is proved under some conditions. This suggest that there can be a population without cancer disease at point $E0,1$ and an endemic situation at point $E*,1$. Model fitting is also provided for interpreting the relationship between real data and the results of this work respectively.

In Chapter IV, the second model of the paper is proposed, and the entity of the solution is demonstrated. the analysis of the second model demonstrated two existing

equilibrium points for this model: the disease-free equilibrium point, $E0,2$, and the

endemic equilibrium point, $E*,2$. Both points are globally asymptotically stable with

necessary conditions, which means that both environments are possible for the diseases to occur. The correlation between diabetes and cardiovascular illness is also illustrated graphically. The effects of smoking and obesity are also found to be significant in disease compartments. Diabetic people, in particular, need to monitor their health conditions closely and practice heart health maintenance. People with heart diseases should undergo regular checks so that they can protect themselves from diabetes and take some precautions including suitable diets.

In Chapter V, Sensitivity analysis is a method that can be applied to the parameters of any mathematical model with the purpose of identifying the effect of the parameters on the compartments. The purpose of this analysis is to demonstrate how a small change in parameters can affect whether a disease exists or dies out. In this section, a sensitivity analysis was applied to the parameters of both models. This analysis aimed to specify the effects of the parameters on compartments Cancer C, Heart disease H, and Diabetes D to demonstrate the result of an increase in smoking and obesity, respectively. The results of the sensitivity analysis should be utilized by healthcare systems and policymakers to develop control strategies to achieve better public health.

As a summary, both of the models indicated that the most dangerous parameter for the diseases is c, (a negative effect of COVID-19), which is a result of the COVID-19 pandemic. The presented study emphasized being aware of COVID-19 and its results may lead to a substantial decrease in deaths due to cancer, heart disease, and diabetes. That, combined with frequent doctor visits, could lead to the earlier diagnosis and treatment of these diseases.

Key Words: cancer, heart diseases, diabetes, mathematical modelling, COVID-19, sensitivity analysis

Özet

Aggravation of Cancer, Heart Diseases and Diabetes Subsequent to Covid-19 Lockdown
via Mathematic Modelling

EFİL, Fatma Neşe
Danışman: Prof. Dr. Evren Hınçal
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Bu tezin ana amacı, COVID-19'un kanser, kalp hastalığı ve diyabet gibi önemli hastalıklar üzerindeki gelecekteki etkisini açıklamaktır. Olağan diferansiyel denklemler (ODE'ler) kullanılarak, COVID-19 ile kanser arasındaki ve COVID-19 ile diyabet ve kalp hastalığı arasındaki ilişkiyi açıklayan matematiksel modeller geliştirilmiştir. Buna uygun olarak oluşturulan modellerde popüler matematiksel tekniklerden ikisi olan duyarlılık analizi ve denge noktalari kullanılmıştır.

Bölüm I sunulan tezin temel noktalarını ve görüşlerini içermektedir. Tezi destekleyen genel görüşler, teoremler ve tanımlar Bölüm II'de sunulmuştur. Çalışma genel olarak iki bölüme ayrılmıştır.

Bölüm III'te, ilk model çözümün kanıtı ile birlikte verilmektedir Daha sonra, kompartmanlardaki değişiklikleri elde etmek için, t zamanda, ODE'lerin yardımıyla model oluşturulur. Ardından, denge noktaları ile modelin analizi verilir. İlk modelin analizinde, teshis olmayan denge noktası $E_{0,1}$, ve endemik denge noktası $E_{*,1}$, kanıtları ile birlikte elde edilir. Ayrıca, her iki noktanın da bazı koşullar altında küresel asimptotik kararlılık özelliği kanıtlanır. Bu, $E_{0,1}$ noktasında kanser hastalığı $E_{*,1}$ noktasında endemik bir durum olabileceğini öne sürer.

Model, ayrica gerçek veriler ile bu çalışmanın sonuçları arasındaki ilişkiyi olmayabileceğini ve E yorumlamak için de elde edilmiştir.

Bölüm IV'te , ikinci model çözümün kanıtı ile birlikte verilmektedir. İkinci modelin analizi, bu modele ait iki mevcut denge noktasını göstermektedir : teshis olmayan denge noktası, E0,2, ve endemik denge noktası, $E*$,2. Her iki nokta da gerekli koşullarla küresel olarak asimptotik olarak kararlıdır, bu da her iki durumun da hastalıkların ortaya çıkabileceği olası ortamlar olduğunu göstermektedir. Diyabet ile kardiyovasküler hastalık arasındaki ilişki grafiksel olarak da açıklanmıştır. Sigara kullanimi ve obezitenin hastalık kompartmanları üzerindeki önemli etkileri de bulunmuştur. Özellikle, diyabet hastalarının sağlık durumlarını yakından izlemesi ve kalp sağlığını korumaları gerektigi belirtilmistir. Kalp hastalığı olan insanlar, diyabetten kendilerini koruyabilmek ve uygun diyetler de dahil olmak üzere bazı önlemler alabilmek için düzenli olarak saglik kontrollerinden geçmeleri gerektigi ortaya konulmustur.

Bölüm V'te, duyarlilik analizinin, herhangi bir matematiksel modelin parametrelerine uygulanabilen bir yöntem oldugu ve amacinin da parametrelerin kompartmanlar üzerindeki etkisini belirlemek oldugu ifade edilmistir. Bu analizin amacının parametrelerdeki küçük bir değişikliğin hastalığın var olup olmadığını veya yok olup olmadığını nasıl etkileyebileceğini göstermek oldugu belirtilmistir. Bu bölümde, her iki modele de parametreler üzerinden duyarlilik analizi uygulanmistir. Bu duyarlilik analizi, sigara içme ve obezitenin artışının Kanser C, Kalp hastalığı H ve Diyabet D kompartmani üzerindeki etkilerini belirlemeyi amaçlamıştır. Duyarlilik analizinin sonuçlarının, sağlık sistemleri ve politikacilar tarafından daha iyi bir halk sağlığına ulaşmak için kontrol stratejileri geliştirmek için kullanılabilecegi belirtilmistir.

Özetle, her iki model de hastalıklar için en tehlikeli parametrenin c (COVID-19'un negatif etkisi) oldugu belirtilmistir, bunun da COVID-19 salgınının bir sonucu oldugu eklenmistir. Sunulan çalışma da, COVID-19 ve sonuçları hakkında ki farkındaligin kanser, kalp hastalığı ve diyabet nedeniyle ölümlerde önemli bir azalmaya yol açabileceği vurgulanmistir. Bu, sık doktor ziyaretleri ile birleştirildiğinde, bu hastalıkların daha erken teşhisi ve tedavisi ile sonuçlanabilecegi de ifade edilmistir.

Anahtar Kelimeler: kanser, kalp hastalıkları, diabet, matematiksel modelleme, COVID-19, duyarlılık analizi.

Table of Contents

CHAPTER V

CHAPTER VI

CHAPTER VII

List of Tables

Page

List of Figures

List of Abbreviations

CCG:	Clinical Commissioning Groups
NHS:	National Health Service
PCT:	Primary Care Trust
PARR:	Predict a Readmittance from Regular Inpatient Data
PDE:	Partial Differential Equation
IVP:	Initial Value Problem
DFE:	Disease Free Equilibrium
EE:	Endemic Equilibrium
SIR:	The Susceptible-Infected-Recovered Model
SEIR:	The Susceptible-Exposed-Infected-Recovered Model
ODE:	Ordinary Differential Equation
SA:	Sensivity Analysis
WHO:	World Health Organization
NGO:	Non-government Organization
SARS:	Severe acute respiratory syndrome
MERS:	Middle East respiratory syndrome

CHAPTER I
Introduction

Mathematical modelling can be defined as the use of mathematical and predictive techniques to explain the behaviour of a given healthcare condition, including explaining its likely occurrence and re-occurrence. The technique leverages on equations that analyse trends of a given phenomenon and then use such trends to underscore why the behaviour of a condition with greater precision and certainty.

Mathematical modelling has an extensive impact in the healthcare sector including aiding in various areas such as health service planning, outcome assessment, financing, budget impact assessment, infectious disease surveillance, and health economic assessments. For infectious diseases, mathematical modelling has been used to study the spread, transmission, and control of various infections. Cassidy et al., (2019) explains that mathematical models help describe the transmission and spread of infectious diseases, providing insights into the factors that drive disease dynamics. Secondly, various models help to explain disease surveillance. By analyzing disease surveillance data, mathematical models can be used to address both the biological process of transmission and the emergent dynamics of infection at the population level (Christen & Conteh, 2021). The other role is in infection control where the models can help determine the effectiveness of interventions, such as vaccination programs, and inform public health policies to control the spread of infectious diseases.

COVID-19 is a contagious disease caused by the virus SARS-CoV-2. The condition which was first reported in Wuhan China, most often causes respiratory symptoms that can feel much like a cold, the flu, or pneumonia. The symptoms of COVID-19 are variable depending on the type of variant contracted, ranging from mild symptoms to a potentially fatal illness. Common symptoms include coughing, fever, loss of smell (anosmia), and taste (ageusia), with less common ones including fatigue, shortness of breath, vomiting, and loss of taste or smell; some cases are asymptomatic. The condition spreads when an infected person breathes out droplets and very small particles that contain the virus.

It is also possible to leverage on some of the models to predict the outcome of an infectious disease, including studying patterns of their occurrence. A good example that demonstrates the value of mathematical modelling is in the study of diseases like COVID-19 pandemic. Mathematical modelling has been extensively used to predict the spread and impact of COVID-19 pandemic. Various mathematical models have been developed to estimate and predict the outbreak of COVID-19, both with and without preventive measures. Other than COVID-19 mathematical modelling can be used to predict the existence of conditions like diabetes, cancer and other cardiovascular conditions. For instance, proposed a mathematical model to depict the risk of cancer in individuals with type-2 diabetes mellitus, highlighting the positive relationship between diabetes and cancer (Deepak et al., 2021). Additionally, mathematical models have been constructed to simulate and comprehend the dynamics of the diabetes population, offering insights into the prevalence of diabetes and its complications, as well as suggesting preventive measures. As explained by Brady & Enderling, (2019), it is also possible to use mathematical modelling techniques to explain the prevalence of specific types of cancer within a given demographic by studying previous prevalence cases.

Purpose of the Study

This thesis is conducted to forecast the future effects of the uncertainty and fear created by COVID-19 on chronic diseases including cancer, heart diseases, and diabetes.

These 3 chronic diseases are chosen to study that cannot be treated by themselves and generally cannot be cured completely. Also, they are the leading most common causes of death and disability all over the world. They are additionally very serious like immediate life-threatening such as heart disease and stroke and need intensive management such as diabetes.

Significance of the Study

The importance of this study stems from the fact that there is no other study in the literature that explains the purpose of the study with the mathematical models used and sensitivity analyses performed in this field.

Research Questions / Hypotheses

The main research question of this thesis is whether individuals may not have sought medical attention adequately (like not going to medical institutions) due to the fear of contracting the contagious disease COVID-19 and whether or not it will be a hazard for these diseases in the future.

The hypothesis is due to the effect of COVID-19, there might be a decline in the number of patients with cancer, heart diseases, and diabetes in the future and it will be a sign of danger for these chronic diseases because of without cure or diagnosis. Therefore, a decrease in the number of patients will not present the right data to help these people who are suffering.

The reason for using two different mathematical models in this study is the observation of a relationship between diabetes and heart disease during the research. Based on this relationship, it was decided that using separate mathematical models for cancer, and for diabetes & heart diseases would be more appropriate.

CHAPTER II

Literature Review

In this chapter, information related to the topic of the presented thesis, including existing literature, conceptual definitions, relevant theorems, and cause-and-effect relationships, is provided.

Theoretical Framework and Definitions

This section consists of the theories, definitions and information about mathematical modelling process, its relation with health sciences and breast cancer are stated.

In this section, definitions, concepts and theorems related to mathematical modelling used in this study are presented. The relationship between mathematical modelling and health sciences is clarified in terms of COVID-19, cancer, diabetes, and cardiovascular diseases, respectively.

Mathematical Modelling

To formally depict some system in mathematical notation is the job of a mathematical model. Developing such a mathematical model is the focus of the field known as mathematical modelling. Mathematical models are used in many disciplines, both in the hard sciences and in the social sciences. The purpose of a mathematical model is to help solve a real-world problem by elucidating and illuminating its hidden dynamics (often in the form of equations). The development of state-of-the-art technologies and our general comprehension of the world's systems are both reliant on modelling to a significant extent. We may use models to view deep into the universe, investigate how atoms function, and foretell the future of our climate. Mathematicians use a method known as "mathematical modelling," which entails creating a mathematical representation of the condition, to foretell or gain insight into an event in the actual world. Developing a mathematical relationship is different from simply using

a formula (Brauer et al, et al., 2019).

General weather predictions, global warming, aviation simulation, hurricane forecasting, nuclear winter, nuclear arms race, and so on are all examples of large mathematical models that could have profound effects on society. Mathematical models describe a wide range of phenomena, including traffic dynamics, stock market potential, predator-prey dynamics, and search techniques (Tuan et al., 2020).

In health service planning, techniques from gravitational physics can be used to estimate catchment areas of new facilities, models utilising network analysis can be used to study patients' travel requirements to services, and so on. Queuing theory-based models can be used to predict the effects of changes on access to services and calculate the required capacity of services given assumptions about patterns of demand and levels of utilisation. Epidemiology, health impact assessment, and clinical auditing are also further applications of modelling. They are useful for pinpointing problem areas, setting priorities, and directing attention (Jewell et al., 2020). If the underlying mathematical problems cannot be solved directly, a simulation is used instead. Modeling is crucial in many different fields:

- To project future health care requirements, such as the prevalence of eye diseases, use the National Eye Health Epidemiological Model.
- Showing the potential outcomes of not acting on pressing public health issues. Projecting the continued rise in childhood obesity, for instance, has helped to establish this problem as a national priority and direct resources toward resolving it.
- Examining how changes to services affect variables like patient wait times and hospital bed utilization.
- In the absence of precise data, an estimate of the prevailing condition can be made.
- Service demand forecasting for specific populations, such as those at high risk for unplanned hospitalization or readmission.

In order to better assist their staff in developing and enforcing health policies, decision- and policy-makers are frequently urged to make greater use of a wide range of resources. To better connect modellers, policymakers, and implementers, it is important to be able to convey modelling knowledge and experience. Authorities in the health care field have profited greatly from mathematical modelling on a variety of difficulties, but researchers may be underusing models of real repercussions. Therefore, it is crucial to keep an eye on how a complete framework for translating model-based findings into policy and code is being put into practise (Atangana & İğret Araz, 2020).

As an example, The Diabetes Prevalence Model is a spreadsheet-based tool for estimating the annual rate of new diabetes diagnoses among the model's population. The local authority and CCG can provide estimates of patients at risk of re-hospitalization (PARR model). Clinical Commissioning Groups (CCGs) have replaced primary care trusts (PCTs) as the local commissioning authority in the NHS. Prior to this change, PCTs employed a risk prediction system called PARR to identify patients who were at a high risk of being readmitted. Predict a Readmittance from Regular Inpatient Data (PARR+) was the first set of algorithms to do this (Heffernan et al., 2019).

Infectious disease epidemiology is a field of study dedicated to learning more about the spread of illness throughout a population. Things include the progress of an epidemic, how to keep it under control, what vaccines to use, etc. Researchers can learn more about an epidemic's spread and, hopefully, cut it down, by modelling the epidemic's development. Public health and plant health measures can be informed by mathematical models that anticipate the spread of infectious illnesses, revealing the likely outcome of an epidemic (even in plants). The study of epidemiology focuses on the effects of disease on communities and the causes of disease outbreaks. Medicine's field of epidemiology attempts to answer questions about the who, what, where, and when of disease outbreaks. Another benefit is that it aids in the study of aetiology, or the study of cause, and so provides insight into the topic of why the incidence of specific diseases varies so considerably. The third function of epidemiology is the formulation and testing of hypotheses. The fourth obligation is to plan, implement, and evaluate surveillance, preventive, and control activities. The preceding two applications illustrate the utility of epidemiological modelling (Liang, 2020).

The Susceptible-Infected-Recovered (SIR) models can be used in many contexts, presuming that infected people can disseminate the disease to others. SEIR models, on the other hand, take into consideration latent infections in the exposed compartment (E) (He et al., 2020). It classifies a population of size N into four states: susceptible (S), exposed (E), infective (I), and removed (R). (R) characteristic of a particular population, habitat, or location. The SEIR model is an epidemiological framework for projecting the development of infectious illnesses. Examples of endemic diseases include the yearly recurrence of

chicken pox among American schoolchildren and the prevalence of malaria in certain regions of Africa (Mwalili et al., 2020).

Based on the number of contacts, the probability of disease transmission, the incubation time, and the infectiousness rate, the SEIR model has been utilised in research to predict the number of infected, recovered, and dead in an epidemic situation. Throughout human history, numerous infectious diseases have appeared and spread. Diseases including dengue fever, malaria, the flu, the plague, and HIV/AIDS are just a handful. Developing a reliable epidemiological model for such epidemics is challenging. Some researchers have begun to see the transmission of disease as a sophisticated network in order to better understand, forecast, and model it. (Zou 2020) created a network-based model based on the connections between cities and the circulation of cars to more accurately depict the COVID-19 epidemic in Hubei province. It is currently possible to model epidemics using the SIS, SIR, and SEIR models. The study's findings have been published in several different journals. Taken as a whole, these findings show that the SIS, SIR, and SEIR models are good surrogates for the dynamics of different epidemics. The COVID-19 has also been modelled in this way. A comprehensive epidemiological model called SEIR has been investigated by scientists. SEIR takes into account quarantine, isolation, and treatment. Alternative representations of the COVID-19 exist. The number of confirmed cases of coronavirus disease in Wuhan in 2019 was calculated using Zhang's phase-adjusted technique (Piccirillo, 2021).

The SEIR model is a popular choice among the numerous mathematical models designed to characterise epidemic dynamics and predict the spread of infectious diseases. In the event of a pandemic, the SEIR model can be utilised to assess the efficiency of potential responses, such as lock-down. A set of dynamic ordinary differential equations (ODE) takes into account the number of susceptible individuals, the rate at which infected individuals recover, and the number of deaths that occur over time (López & Rodo, 2021).

The 2019 coronavirus (COVID-19) has been detected in over 200 nations, posing a threat to economic growth and social stability in addition to people's day-to-day lives. As of August 24, 2021, the World Health Organization had confirmed 211,730,035 cases and 4,430,697 deaths from the outbreak. In a recent study, numerous academics all came to the same conclusion that was investigated

vaccination methods against the COVID-19 disease, tuberculosis, and Rotavirus epidemic. (Baart, & Ahmed, 2020; Nkamba et al., 2019; Kaymakamzade et al., 2022)

Properties of a Mathematical Model

In this section, the essential and significant features for the creation and proof of a mathematical model are presented, along with the necessary theorems.

Existence of a Mathematical Model. A mathematical model is an abstract description of a real-world system using mathematical concepts and language. It involves describing a real-world problem in mathematical terms, usually in the form of equations, and then using mathematics to solve the resulting equations (Kohen & Orenstein, 2021). Mathematical modelling which is the concept of developing mathematical models entails writing relevant equations, simplifying as much as possible, solving the equations, and comparing the results against data. The existence of solutions for mathematical models depends on the specific problem and the assumptions made in the model. In the context of linear simultaneous equations, a unique solution exists if and only if the number of unknowns and the number of equations is equal, all equations are consistent, and there is no linear dependence between any two or more equations, meaning all equations are independent (Erbas et al., 2014). However, there are cases where solutions may not be unique or may not exist at all.

In the context of partial differential equations (PDEs), uniqueness is important because it ensures that the model can make a single prediction about the behavior of the system. Non-uniqueness can indicate that the model is not powerful enough to make a single prediction, or that the system has multiple different equilibria, some of which can occur in reality. Engineers care about uniqueness because it helps them determine the accuracy of their models and avoid potential issues caused by non-uniqueness.

The existence of unique solutions in mathematical problems has significant implications. A solution is unique if and only if a certain condition is met,

such as the invertibility of a matrix in the case of linear equations. This uniqueness ensures that the model can make a single prediction about the behavior of the system, which is important in various applications, such as physical modeling and engineering. On the other hand, non-uniqueness of solutions means that there is more than one solution to the problem. This can arise in various contexts, such as systems of linear equations or PDEs. Non-uniqueness can indicate that the model is not powerful enough to make a single prediction about the system's behavior, or that the system has multiple different equilibria, some of which can occur in reality.

Uniqueness of Solutions of a Mathematical Model. This section contains theorems and definitions related to the unique solutions of any mathematical model.

The uniqueness of solutions in a mathematical model is a fundamental concept with broad applications. It is often formalized through uniqueness theorems, which assert the existence of a single solution under certain conditions. These theorems are essential in various mathematical fields, including differential equations, electromagnetism, and finite group theory. The first mathematical definition of the uniqueness of the solutions of a mathematical model is the unicity theorem, states the uniqueness of a mathematical object, indicating that there is only one object fulfilling given properties, or that all objects of a given class are equivalent (Schlömerkemper & Žabenský, 2018). This concept is important in ensuring that a mathematical model can make a single prediction about the behaviour of the system. Lack of uniqueness can indicate that the model is not powerful enough to make a single prediction, or that the system has multiple different equilibria.

Definition 1. (Existence and Uniqueness Theorem)

In general, on the rectangular region $R: a \le t \le b, c \le y \le d$ including the point $(t0, y0)$ if f / y and f are continuous functions, therefore there consists of an interval : $|t - t0| \le h$ centered at t_0 on which there exists one and only one solution to the initial value problem

$$y' = f(t, y), y(t_0) = y_0.$$

(Abell &Braselton, 2018)

Another mathematical definition is Picard–Lindelöf theorem and the Cauchy–Kowalevski–Kashiwara theorem in differential equations. The theorem guarantees the existence and uniqueness of solutions under specific conditions. In electromagnetism, the uniqueness theorem for the solution of Maxwell's equations is another important application of uniqueness theorem.

The Cauchy–Kowalevski–Kashiwaratheorem: A wide generalization of Cauchy–Kowalevski theorem for analytic PDEs. It guarantees the existence and uniqueness of solutions to certain PDEs under specific conditions (Sugiki & Takeuchi, 2001).

Theorem 1. The Cauchy-Kovalevskaya Theorem): Consider the Cauchy (or Initial value) problem.

$$\partial_n u = A_1(z)\partial_z u + \ldots A_{n-1}(z)\partial_{n-1} u + A_0(z)u + a(z),$$
$$u|_{\{z_n=0\}} = 0$$

When $a: Cn \to Cm, Aj: Cn \to Cmxm, (j=0,\ldots,n-1)$ are analytic at 0.

So, there exist an analytic solution $u: \Omega \to C^m$ and an open set $\Omega \subset C^n$ with $0 \in \Omega$.

This analytic solution is unique between the functions from $C^w(\Omega, C^m)$.

Proof. (Gantumur,2014)

The second theory is the Black hole uniqueness theorem - This theorem states that, given boundary conditions, the electric and magnetic fields in a region are uniquely determined, which has implications for understanding the behavior of electric and magnetic fields in various scenarios. The third theorem is the existence and uniqueness theorem for linear equations which states that the solution to a system of linear equations is unique if and only if the matrix representing the system is invertible. The last theorem is the Cauchy's rigidity theorem and Alexandrov's uniqueness theorem for three-dimensional polyhedra: These theorems assert the uniqueness of a mathematical object, which usually means that there is only one object fulfilling given properties, or that all objects of a given class are equivalent (i.e., they can be represented by the same model).

Basic Reproduction Number, Equilibrium Points and Stability.

The basic reproduction number, denoted as (R0), is a fundamental concept in mathematical modeling, particularly in epidemiology. It is defined as the expected number of secondary cases produced by a typical infective individual in a completely susceptible population. In other words, it represents the average number of individuals who will catch a disease from a single infected person in a population where everyone is susceptible to the disease (Allen & van den Driessche, 2008). The value of (R0) is crucial in forecasting whether a disease will persist or vanish. If (R0) is greater than 1, the disease is likely to persist, while if it is less than 1, the disease is likely to die out. The estimation of (R0) is often done using complex mathematical models that consider various biological, sociobehavioral, and environmental factors governing pathogen transmission. The basic reproduction number is a key parameter in understanding the contagiousness or transmissibility of infectious diseases and plays a significant role in guiding control strategies.

In dynamical systems and ODEs, the basic reproduction number is used to determine the stability of the disease-free equilibrium point. Specifically, if the value of (R0) is less than or equal to 1, the disease-free equilibrium point is stable, meaning that the disease will eventually die out. If the value of (R0) is

greater than 1, the disease-free equilibrium point is unstable, meaning that the disease will persist and spread throughout the population (Hussain & Dutta Borah, 2021). For example, consider the SIR model, which is a system of ODEs used to model the spread of infectious diseases. The basic reproduction number for this model is given by

$R0 = N(\beta/\gamma)$ where (β) is the transmission rate, (γ) is the recovery rate, and (N) is the total population size Van (den Driessche & Watmough, 2008).

If (R0) is greater than 1, the disease will persist and spread throughout the population, while if it is less than 1, the disease will eventually die out.

If the basic reproduction number is greater than 1, the disease is likely to persist and spread throughout the population. This means that each infectious individual, on average, infects more than one other individual, leading to a continuous increase in the number of infected individuals. In this case, the disease is considered contagious and may require intervention measures to control its spread. If the basic reproduction number is less than 1, the disease is likely to die out. This means that each infectious individual, on average, infects fewer than one other individual, leading to a decrease in the number of infected individuals. In this case, the disease may become extinct over time, as the number of infected individuals decreases and if the basic reproduction number is equal to 1, the disease is at the threshold of persistence. In this case, the disease can persist in the population, but the number of infected individuals remains stable. Small changes in the value of (R0) can cause the disease to either die out or persist, making it a critical value for determining the long-term behaviour of the disease.

Solutions with vectors that are either approaching or receding from the equilibrium value are shown in a phase portrait of a dynamical system that has a constant solution. In the form of an attractor, a stable equilibrium value is one that the system's values tend to approach. If the values in the system tend to move away from the equilibrium value, it is unstable and acts as a repelling point. It's been observed that some values tend to drift closer to the equilibrium point, while others prefer to move further away. This area is characterised by a saddle point. It's a precarious scenario (Widyaningsih et al., 2018).

An equilibrium point may occur at the starting point in some cases, but the pathways that approach it will always show some degree of divergence. Although a balance has been attained, it is not globally asymptotically stable. Because the value of x(t) diminishes with time, the ensuing equilibrium point is stable on a global scale, and the resulting phase picture shows all trajectories converging on the equilibrium point. If both eigenvectors are linearly independent and have real, negative, and equal eigenvalues, then the phase picture represents a globally stable equilibrium point.
At the outset, every person in a community is included in the S group; but, over time, some individuals are "removed" from the S group due to sickness and quarantine, or because they are isolated from the population for other reasons. For the S' group, we account for births by assuming a constant rate of addition to the vulnerable population. Multiplying the death rate per person by the total population yields the total number of people "removed" from the R' group (it is a function of how many individuals are removed, not constant like the birth rate).

At a state of equilibrium, all of the determinants of that state's condition remain unchanged. This is the same as asserting that at equilibrium locations in the model, the derivatives are zero because they represent changes in the state variables. The point at which there are no diseases in the population is known as the disease-free equilibrium, and it is represented in the model by the equation I1 = I2 = I3 = 0. The set of equations is made simpler to. $S = \Lambda - \mu S$. An infectious disease-free equilibrium point, where the number of infected people is zero, and maybe other equilibrium points where the number of infected people is less than zero and equal to zero. According to the setting, these are either endemic equilibrium points or outbreak equilibrium points).

It is the attractors of a dynamical system, which are connected to the idea of equilibrium, that define its long-term behaviour. Any given dynamical system may have no equilibrium point, a single equilibrium point, or numerous equilibrium points, any of which may be stable or unstable. A pendulum is a nice illustration of a straightforward mechanical tool. Since the system will remain in the bottom position of the pendulum forever, this is an equilibrium

point. There is no doubt that this equilibrium is stable (if fraction is considered). To a similar extent, standing upright is obviously an unstable equilibrium. An understanding of these equilibria is crucial for extracting the model's defining system behaviours. For a full appreciation of the model, it is essential to grasp these.

An SEIR model with density-dependent mortality and constant infection rate was tested in (Jiao et al., 2020). A total of three equilibria were found in the system: I when the population is wiped out, (ii) when the disease is wiped out, and (iii) while the disease is present in the population. This third equilibrium was found to exist and be unstable close by. Variable-amplitude disease cycles were found numerically for a wide variety of parameters. After showing that the SEIR model is globally stable even when the overall population size changes, (Rezapour et al., 2020) looked at an SEIR model with vertical transmission in a fixed population and an incidence term expressed as a bilinear mass action.

When an infection is not fatal, both the global disease-free equilibrium and the local endemic equilibrium become stable. Taking into account the effect of diffusion on various population subgroups, (Wintachai & Prathom, 2021) created an SEIS model to account for the nonhomogeneous mixing, which leads to differing incidence rates for the exposed and infected populations. Analyzing the diffusive model with matrix stability theory, we obtain the criteria for Turing bifurcation. Finding a globally exact solution for the traditional SIRS model required the application of modal expansion infinite series (Etxeberria-Etxaniz et al., 2020). They demonstrated that the modal expansion series converges for practical initial points.

Sensitivity Analysis

Sensitivity analysis (SA), which can aid in identifying influential model parameters and optimising model structure, has not been frequently implemented in infectious disease modelling despite its usefulness. The aim of doing a sensitivity analysis on a mathematical model or system is to ascertain the degree of influence that individual variables have on the final result.

In recent years, sensitivity analysis has become increasingly popular across many scientific and technological fields. Sensitivity and uncertainty analysis is widely used by scientists who apply mathematical models to simulate biological processes because of its usefulness in establishing key parameters for model performance. This model can be helpful in many contexts, including experiment analysis, parameter estimate, decision making, and policy guidance (De la Sen et al., 2021).

SAs are performed for an analysis of reasons, including but not limited to: characterising the response of model outputs to parameter variation; isolating major sources of parametric uncertainty; identifying parameters that can be shed to yield a simpler model; clarifying the plausible range of system outcomes; forecasting when data is unavailable; and determining the robustness of a modelling stucture. There ought to be a resurgence of interest in SA since newer methods can produce significantly higher levels of comprehension than their predecessors. Once data collection is complete, a posterior distribution over all model parameters should be estimated. Today's SA is analogous to parameter estimation methods for complex models, which are usually based on Bayesian approaches using, for example, Markov Chain Monte

Carlo algorithms (Brauer et al, et al., 2019). It is possible to use this posterior information to marginalise the joint distribution, so revealing the sensitivity of the model fit (often a log likelihood) to each parameter. As a measure of how dependent events are on one another, we use the log probability. But because we don't know enough about the sensitivity of the parameters influencing the other intriguing model outputs, many potential for considerable SA would remain. One's comprehension of a modelled complex system can be enhanced by employing SA before commencing to collect data; in fact, utilising SA can help one decide what data should be collected in order to most informatively narrow parameter and output uncertainty. The idea of elastic demand in economics and ecology, the response surface methodology, and the design of experiments are all approaches that may be used to a variety of contexts and have many similarities in methodology. The Fisher Information Matrix can also be used

to characterise gradients on the log-likelihood surface and to determine which parameters, if investigated, would provide the greatest benefit from experimental investigation. To achieve this goal, it is vital to determine which parameters would most

benefit from further laboratory investigation. This exemplifies the power of SA

techniques like these for studying the parameter-sensitivity of the log-likelihood surface (Widyaningsih et al., 2018).

Covid-19

When discussing viruses, the term "coronavirus" is used to refer to any member of the family Coronaviridae. Coronavirus virions (viral particles) are typically approximately 120 nm (1 nm = 109 meters) in diameter. Glycoprotein spikes in the envelope of these viruses take on a club form, giving the virus a coronal appearance. Nucleocapsids are protein capsids that encase viral nucleic acids in a helical or tubular shape. The coronavirus genome is a single-stranded, positive-sense RNA (ribonucleic acid). It is generally accepted that there are only two genera under the family Coronaviridae, namely Coronavirus and Torovirus, which may be identified from one another by the shape of their nucleocapsids (helical vs. tubular). Humans, hens, and cows are all susceptible to coronavirus infections, which can lead to severe gastrointestinal symptoms. A human respiratory disease known as SARS coronavirus
(or severe acute respiratory syndrome coronavirus) is extremely infectious and manifests with high body temperature, a hacking cough, and aching muscles, followed
by trouble breathing. (Singhal, 2020).

The Natural History of Covid-19. The virus was first found in humans in 2002,
and it is believed that it was transmitted to humans from horseshoe bats, its
initial animal reservoir. In order to infect humans, the SARS (severe acute
respiratory syndrome) coronavirus must have undergone a genetic change.
While the SARS virus in horseshoe bats cannot infect people directly,
researchers assume that the palm civet was the first host of these modifications
(Singhal, 2020). Bats, cats, and camels are all frequent hosts for the coronavirus. It appears that
the viruses are able to live in harmony with the animals without infecting them.
Viruses can change to infect new hosts, such as other species of animals.
Transmission to new species increases the likelihood that the viruses

animals are suspected as the first transmission sites for SARS-CoV-19 (He et al., 2020).

When infected with a coronavirus (CoV), both people and animals are at risk for developing symptoms in their respiratory and digestive systems. Since its discovery in Wuhan, China in response to reports of severe pneumonia, the current coronavirus illness pandemic (COVID-19) has been traced back to SARS-CoV-2 (Yan et al., 2020). It was discovered late in 2019 that Wuhan, China has a coronavirus quite similar to the one that caused SARS. Once known as COVID-19, the disease was later shown to be caused by Coronavirus Type 2. (SARS-CoV-2). Similarly, the virus was highly contagious and had spread from China to the United States and Europe via sick travelers by the beginning of the year 2020. Since the World Health Organization declared the pandemic in March 2020, several countries have severely restricted travel to and from affected areas. Several municipalities instituted "stay-at-home" policies, which strongly advised locals to remain indoors after the closing of local schools and businesses. By 2020, SARS-CoV-2 vaccinations were readily available, allowing a plethora of formerly closed establishments to reopen (Zu et al, 2020).

There are several variants of the COVID-19 virus, including SARS and MERS (Middle East respiratory syndrome) variants. SARS-CoV-2 virus is genetically similar to the SARS-CoV virus, which caused the 2003 SARS outbreak. SARS

MERS caused significant morbidity and mortality in the region, with a high fatality rate and considerable economic, social, and health security effects. MERS-CoV was also classified as a zoonotic virus, meaning it is transmitted between animals and people, and is contractable through direct or indirect contact with infected animals (WHO, n.d). Therefore, its implication spread from people to animals, causing a high mortality.

SARS-CoV-2, the virus that causes COVID-19, belongs to the same Betacoronavirus genus as the viruses responsible for SARS and MERS (Petrosillo et al., 2020). While both COVID-19 and MERS are caused by coronaviruses, they are genetically different and have distinct epidemiological, clinical, and virological characteristics.

Diagnosis and Treatment of Covid-19. The COVID-19 coronavirus, which causes the disease, is covered with spike-like proteins on every one of its particles. Aiding in viral attachment and disease transmission, these spikes are a common feature of many virus capsids. Some vaccines for coronaviruses are designed to "recognize" and eliminate the viruses by targeting their spike proteins (Li et al.., 2020).

If there were an effective vaccination, people wouldn't have to worry about
ending up in the hospital or even dying. Widespread vaccination has the potential to significantly lessen the virus's capacity to propagate inside populations and evolve into new forms (Stokes et al., 2020).

Cancer

The term "cancer" is used to describe a group of diseases in which abnormal cells multiply out of control, invade neighboring tissues, and ultimately destroy them. Cancer is an aggressive disease that can swiftly spread to other parts of the body. Cancer is the second leading killer worldwide. The symptoms of cancer will change depending on where it is located in the body. Cancer patients often encounter the following non-specific symptoms: Weariness a bulging subcutaneous lump or enlarged area Rapid changes in weight gain or decrease Variations in the skin's color, texture, or general appearance, such as the development of a new mole or the transformation of an existing one. Modifications affecting the regularity with which one urinates or defecates Persistent respiratory distress or coughing Trouble swallowing that causes chest pain Hoarseness Recurring discomfort or soreness in the stomach after eating Muscle or joint pain that persists and for no apparent reason Persistent nighttime sweats and/or fever unusually heavy or frequent bleeding (Cox, 2021).

Cancer can develop if there are alterations (mutations) to the DNA within cells. The DNA of a cell is structured into genes, each of which directs a specific aspect of the cell's life cycle. The cell may become dysfunctional or cancerous if the code is flawed (Hanahan, 2022).

Some persons are more likely to acquire cancer because of preexisting conditions. Tabacco use, excessive alcohol use, a diet high in red and processed meat, sugary beverages and salty snacks, starchy meals, and refined carbohydrates such as sugars and processed grains were all highlighted as risk factors for chronic illness in the 2017 evaluation. Air pollution, radiation, and unprotected exposure to UV light, as well as hepatitis A, B, C, and HIV infection, are all risk factors for developing cancer (sunlight). Cancer incidence also rises with age. The chance of having cancer tends to grow until age 70–80, when it seems to level off, as reported by the most reliable sources (Goodall & Wickramasinghe, 2021).

Types, Risk Factors, Diagnosis and Treatment of Cancer. Non-melanoma Skin Cancer: Basal cell carcinoma and squamous cell carcinoma are examples of the non-melanoma skin cancers that occur most frequently. Over a million people in the United States are affected annually. Many of these newly diagnosed cases go unreported to cancer registries because of how easily they may be diagnosed and treated, making it impossible to pin down an exact annual occurrence rate. Basal cell carcinoma can be diagnosed by looking out for the following signs: Repeated episodes of bleeding, whether permanent or transient. Raise, red, and scaly spots caused by scarring. Tiny, smooth, shiny, pink, red, or white pimples. In particular, flat, pale skin discolorations are frequently misunderstood as scars. Any kind of skin growth or lesion characterized by obvious blood vessels, itching, or bleeding. raised or sunken pink lumps. Basal cell carcinoma most frequently manifests itself on the skin of the head and neck, followed by the trunk (Cao et al., 2020).

Breast Cancer: Symptoms like a lump or tumor forming in the breast, armpit, or collarbone area. While most bumps won't cause any discomfort, some people are particularly hypersensitive to them. Male hormones can cause breast growth in females. Redness, scaling, itching, and dimpling (which can make some people's skin look like an orange peel) are all symptoms of breast skin disorders. Discomfort in the breast or genital area Symptoms of a nappy rash other than breast milk The Nipple Pulls Back (sometimes called a "dented" or "bent inward" nipple) These signs, however, are not always indicative of breast cancer.

Lung Cancer: persistent, intensifying, hacking cough Blood can be seen in the patient's cough. suffering from breathlessness or wheezing Constant discomfort in the chest Skeletal pain, or arthralgia Changes in the voice's quality, such as hoarseness Frequent recurrence of an acute respiratory infection (like pneumonia or bronchitis) Constant and unstoppable weight reduction The Ignorance of Hunger Constant ache in the head Clotted blood Symptoms of lung cancer typically do not show up until the disease has spread extensively (also referred to as late-stage cancer). Lung tumors typically generate no symptoms since there are so few nerve endings in the area (Dai et al., 2018).

Prostate Cancer: Problems with the urinary system, such as inability to start or control urination, leakage, pauses in urine flow, or an urgent and unanticipated need to urinate. Discomfort in the urethra (which may also be described as a burning sensation) urinary frequency, especially at night A difficulty in getting or keeping an erection Changes in ejaculatory behavior, such as decreased fluid flow or discomfort during ejaculation Urinary or vaginal bleeding Experiencing pain in one's hips, groin, or lower back Discomfort or pressure in the genitalia Prostate cancer rarely presents with symptoms until it has advanced. If Individual is a man over 55 who hasn't been experiencing any symptoms, he should talk to his doctor about getting checked out (Leone & Powell, 2020)

Colon and Rectal Cancers: Symptoms of colorectal cancer sometimes

do not

appear until the disease has already spread. Colorectal cancer symptoms, while

serious, might be caused by other conditions including hemorrhoids or

irritable

bowel syndrome. effortlessly reducing fat percentage Defeat due to exhaustion

and weakness Changes in bowel habits over time (such as constipation,

diarrhea, or thin stools) Continual yet sporadic abdominal pain (lasting more

than a few days) Pressure felt internally in the abdomen or genitalia.

Another

possible side effect is an increased need to use the restroom. Punctured flesh

Where the toilet paper is stored (which may look dark red or black)

Bleeding

due to rectum damage. This could look like a bright red stain on the toilet paper

(NagY et al., 2021). There are many other common type of cancers

such as

Melanoma, Bladder Cancer, Kidney, etc.

Factors such as obesity, poor diet, tobacco use, and hereditary

predisposition all

contribute to an increased risk of developing cancer. However, having a risk

context of breast cancer patients affected by chemotherapy response, if the basic reproduction number is less than one, the endemic condition will not be achieved, providing an early prediction of the disease's behavior (Harper & Jones, 2005). Mathematical modeling has been used to study the effect of chemotherapy on the growth of solid cancer with angiogenesis. In this study, the reproduction number of the model was obtained, and simulations were conducted to show the effect of chemotherapy on cancer growth.

The negative impact of covid-19 on cancer.

On March 1, 2021, it was reported that over 113 million people had contracted COVID-19, leading to over 2.5 million deaths. The number of verified cases in Norway is incredibly low. Age and co-morbidities like cancer are known to increase the likelihood of a poor result from SARS-CoV-2 infection. No reliable information is available on the outlook for cancer patients with COVID-19 disease. Males and those with hematological malignancies have been found to have a higher chance of developing SARS-CoV-2 than females and those without cancer, according to certain studies. The elderly, particularly those with cancer, as well as those with chronic illnesses or compromised immune systems, are thought to be at a higher risk of hospitalization, treatment in an intensive care unit (ICU), or death as a result of COVID-19. Patients with COVID-19 had
an increased risk of mortality due to the presence of many chronic conditions.
These conditions included hypertension, diabetes, cardiovascular disease,
respiratory disease, and cancer. Mortality from COVID-19 was higher among
individuals with cancer (21% vs. 7.8%). British researchers analyzed data from
16,749 hospitalized patients and found an increased risk of dying from cancer
(hazard ratio 1.13, 95% CI 1.02-1.24) (Miller et al., 2019).

Diabetes

Diabetes is a chronic illness that disrupts the metabolic process, making it difficult for the body to use food as fuel. Humans convert the majority of the food they consume into glucose (sugar) and then inject it into the bloodstream. When there is an excessive amount of glucose in the blood, the pancreas will respond by releasing insulin into the bloodstream. Insulin is a hormone that serves as a gatekeeper for cells, enabling glucose to enter the cell so that it may be utilised as fuel. People who have diabetes either do not produce enough insulin or are unable to use the insulin that they do produce in an efficient manner. Insufficient insulin production or cellular insulin resistance both contribute to the persistence of glucose in the circulation. Some of the long-term consequences include cardiovascular disease, blindness, and even kidney failure. There is currently no treatment for diabetes; but, improvements in food, exercise, and other aspects of daily life can help (Cole & Florez, 2020).

Diabetes is brought on by high blood glucose levels, sometimes known as sugar. Humans rely heavily on glucose in the blood, which originates from the food they consume, for their energy needs. Pancreatic insulin facilitates cellular uptake of sugar from meals. Diabetes develops when either the body's insulin production is inadequate or its use is inefficient (Bloomgarden, 2020). It is impossible for glucose in the blood to reach cells without the hormone insulin. Negative health outcomes have been linked to chronic exposure to elevated blood glucose levels. Although there is currently no treatment for diabetes, those with the disease can take measures to keep themselves healthy through proper management of their condition. Diabetes is sometimes known as "a touch of sugar" or "borderline diabetes" by certain people. Despite what these labels might imply, every case of diabetes is dangerous (Hill-Briggs et al., 2021).

Types, Risk Factors, Diagnosis and Treatment of Diabetes.

Type1: In those with type 1 diabetes, the immune system erroneously attacks healthy cells. The risk factors for developing type 1 diabetes are less well understood than those for developing prediabetes or type 2 diabetes. Having a parent, sibling, or first cousin with type 1 diabetes increases your chance of having the condition, therefore genetic testing can help determine if you are at an elevated risk for developing it. Type 1 diabetes is more frequent in

adolescents, teenagers, and young adults, while it can afflict anybody at any age. The onset of type 1 diabetes has no known preventative measures (Corbin et al., 2018).

Type2: Prediabetic people, those who are overweight, those who are 45 or older, those who exercise fewer than three times per week, and those who have a first-degree relative with diabetes are all at increased risk for developing type 2 diabetes, has ever delivered a baby weighing more than 9 pounds or suffered from gestational diabetes. Some Asian and Pacific Islander Americans are likewise at a higher risk. Individuals at high risk for acquiring type 2 diabetes, such as those with non-alcoholic fatty liver disease, can delay or prevent the onset of the illness by adopting adjustments to their lifestyle. Regular exercise, a healthy diet, and weight loss, if necessary, are all excellent examples (Ngari et al., 2019).

Age, ethnicity, obesity, a personal or family history of diabetes, and cigarette smoking are only few of the risk factors that might contribute to the case for those with type 1. However, their insulin production is inadequate, or their cells are resistant to the hormone, thus their blood sugar levels continue to rise.

Insulin is produced by diabetics with type 2 diabetes, which is not the development of type 2 diabetes. In a variety of ways, smoking is associated with an increased risk of acquiring type 2 diabetes, as detailed in the 2014 Surgeon General's Report. Cigarette smoke contains compounds that are toxic to cells and can disrupt their normal function. Inflammation throughout the body can reduce insulin's efficacy, thus avoiding this is important. Cell damage, known as oxidative stress, can also be caused by the interaction of chemicals from cigarette smoke with oxygen in the body. The risk of developing diabetes may be influenced by both oxidative stress and inflammation. There is a 30–40% increased risk of

Obesity and other lifestyle choices are linked by doctors' research to the development of type 2 diabetes (Bellou et al., 2018).

The high quantities of nicotine in cigarettes reduce the efficacy of insulin, making it more insulin is needed to manage blood sugar in smokers than in nonsmokers. Heart disease, blindness, kidney failure, and damage to the feet and legs' nerves and blood vessels, which can ultimately lead to amputation, are just some of the complications that can arise from uncontrolled diabetes. 8, 9 Diabetic problems are also more likely to occur in smokers (Campagna et al., 2019).”

Experts predict that this increase would lead to over a million new cases of type 2 diabetes, cardiovascular disease, and cancer. “Even though the risk of becoming obese increases with age, the prevalence of obesity in young adults is on the rise, Public Health England reports that 31.2% of children between the ages of 2 and 15 are overweight (Kotsis et al., 2018).

Many of the risk factors for having diabetes mellitus are within a person's control. No one knows for sure what causes diabetes mellitus in humans. Possessing a body mass index (BMI) of 30 or more, which defines one as overweight or obese, is a risk factor for developing type 2 diabetes. People with a body mass index (BMI) of 80 or higher have up to 80 times the chance of having type 2 diabetes compared to those with a BMI of 22 or below, according to recent studies, leading many to conclude that obesity is responsible for 80-85% of the risk of developing type 2 diabetes (Zhou et al., 2021).

One's risk of developing the disease increases if either parent has the disease. A higher prevalence of prediabetes has also been observed, If a person has a prediabetes or diabetes history in their family, they should discuss this with their

been devoted to understanding glucose-insulin dynamics in diabetes with the models providing insights into the physiological processes related to glucose and insulin regulation, which are essential for the diagnosis and treatment of diabetes (Optus et al., 2012). The spread of diabetes transmission through social contact can as well be modelled, which can provide valuable information for understanding the dynamics of the disease and developing strategies for its diagnosis and treatment.

Negative effects of Covid-19 on diabetes

The correlation between COVID-19 and type 2 diabetes is intricate and multifaceted. On the one hand, diabetes mellitus is suspected to have a significant role in determining the severity of COVID-19's progression. Age, a proinflammatory and hypercoagulable state, hyperglycemia, and underlying comorbidities including hypertension, cardiovascular disease, chronic renal disease, and obesity are all factors that are associated with diabetes mellitus and raise this risk. Hyperglycemia is already a problem for those with diabetes, but a severe COVID-19 infection and the medicines used to treat it can make the condition significantly worse by increasing insulin resistance and decreasing -cell function. Additionally, hyperglycemia may allow the development of COVID-19. As the pandemic progresses, more data will become accessible, but understanding the effects of COVID-19 on diabetes will require overcoming some significant challenges (Marfella et al., 2020).

Cardiovascular Disorders(CVD)

Cardiovascular disorders refer to the dysfunction of the heart and constriction of blood vessels leading to failure in the functioning of body organs. The term covers all the disorders that normally occur due to fatty deposits in arteries, which can be a causal factor for life-risking clots (NHS, 2017). Plaque formation can be observed in all major arteries, including the carotid and coronary arteries. Cardiovascular disorders are one of the biggest causes of increasing mortality rates all over the globe.

Types, Risk Factors, Diagnosis and Treatment of Cardiovascular Disorders (CVD)

Coronary heart diseases are disorders that result from the inactivity of heart muscles due to a blocked supply of blood caused by constricted arteries. The fatty deposits (atheroma) in the coronary arteries can restrict the blood supply to heart muscles which is the ultimate cause of death of heart muscles leading to a heart attack. In initial and less severe cases, the constriction of coronary arteries can cause chest pain which is termed angina. However, if the arteries are completely blocked and no blood reaches to heart, then it can lead to cardiac arrest (Valerio et al., 2016).

Stroke is another form of CVD that causes the death of a part of the brain, increasing the risk of fatality. Like all organs, the brain also needs a continuous supply of oxygen which is made possible with the help of carotid arteries. When blood reaches the brain through carotid arteries, oxygen is provided to the brain for its proper functioning. If the supply of oxygen to any part of the brain, due to fatty deposits or clots in coronary arteries, is restricted that it causes the death of brain cells and results in a stroke. A stroke is a serious medical emergency that can lead to the death of an individual with life-long disabilities.

Many risk factors lead to CVD and, consequently, a rise in the global fatality rate (Mozaffarian et al., 2008). One of the most common risk factors is tobacco smoking. Smoking leads to the thickening of blood in arteries, and hence clots are formed easily. Nicotine and other chemicals in cigarette smoke cause the thickening of arteries, termed atherosclerosis. The plaque formation or fatty deposits constrict the arteries supplying blood to the heart, brain, and other parts of the body. This is the major causal factor of CVD.

Obesity is the other major factor leading to the onset of Cardiovascular Disorders through the alterations in body composition. The hemodynamics can deteriorate, and as a result, the structure of the heart may be deformed. Obese people have a high percentage of adipose tissues, which release pro-inflammatory cytokines leading to the dysfunction of the heart (Carbone et al., 2019). This might also cause the thickening and constriction of arteries due to plaques. The atherosclerotic condition is a risk factor for cardiac arrest and, ultimately, death of the individual.

Another noteworthy factor leading to CVD is family history with related cases. A study suggested that positive family history is associated with a greater prevalence of Cardiovascular Diseases (non-stroke in nature) (Valerio et al., 2016). Hypertension, in this regard, is a causal factor for cardiovascular diseases, which leads to myocardial infarction or strokes.

Mathematical models are used to develop risk prediction models that estimate an individual's likelihood of developing cardiovascular events, such as heart attacks or strokes. These models consider various risk factors such as age, gender, blood pressure, cholesterol levels, and smoking status. The other way through which the models are used is in optimizing treatment approaches. The models can help to optimize treatment strategies for cardiovascular diseases (Pajouheshnia, 2017). For example, models may be used to simulate the impact of different drug regimens or interventions on disease progression, allowing identify the most effective and efficient researchers and clinicians to approaches.

Negative effects of Covid-19 on CVD

Furthermore, the infamous Covid-19 pandemic is now a subject of consideration and has profound links with cardiovascular disorders. A noteworthy elevation of cardiac troponins was reported in a study that focused on the onset of CVD in Covid-19 victims (Pina & Castelletti, 2021). This acute cardiac injury was reported in approximately 8 to 12% of all the patients. The postulated mechanisms leading to cardiac injury include the viral involvement

of cardiomyocytes. Apart from that, systemic inflammation is also a leading mechanism.

Sedentary lifestyle habits induced by the Covid-19 pandemic have posed a life-threatening risk to people, particularly due to an increase in the ratio of CVD. A sedentary way of living and lower activity levels might lead to obesity; this is a serious risk to cause the onset of heart-related disorders and stroke.

Related Research

Many studies have been carried out using mathematical models and statistical tools to understand the extent of Covid-19 as an infectious disease. The model has been applied to contain the spread of the infection, undertake risk analysis, and make accurate decisions that can help to reduce the transmission rates. Kucharski et al.; (2020) explored the use of transmission dynamics modelling to understand, predict, prevent, and control the spread of the infectious disease. The model employed in the study helped understand the disease, predict the trend of its spread, and then evaluate control measures that would help to inform further decision-making processes, especially in times of uncertainty.

For the identification of the epidemiological features, the model was used to understand the virus' epidemiological features like the period of incubation and the secondary number of infections that emerge from the first infectious individual in a vulnerable population. The parameters employed at the epidemiological level helped to understand the key features of the infectious condition. As more data was generated, the model was able to be applied to short-term prediction. The model was fit with actual data, and then properly refined to help predict future trends like understanding the number of infections as well as the hospitalization needs (Kucharski et al., 2020). The model was particularly important in explaining short-term trends, proving to be key in disease prevention and control.

One of the ways through which the model was used is by comparing the observed against predicted infections controls. The comparison provided a quantitative assessment that helped to understand the prevention and control measures. For instance, using the mathematical model, it was possible to undertake the Wuhan shutdown and

improve the national emergency response that delayed the spread of the epidemic and also averted the high number of infections.

The mathematical model was also important in exploring the uncertainty that came with the Covid-19 pandemic. It was also possible to underscore the sensitivity of the model by assessing the relationship between diverse parameters used in the study. For instance, the mathematical model warned against completely lifting the non-pharmacological interventions even with the vaccines that were noted to be highly effective. The model showed that such lifting would eventually result in a notable increase in the transmissions. Therefore, the mathematical model improved understanding of the condition and the dynamics within which its spread could be controlled.

Extensive research has demonstrated the use of mathematical models and statistical techniques to explore the progress of cancer, including its treatment. Yin et al., (2019) underscored the use of mathematical model to explain how different changes in the cancer strain results in challenges in cancer treatment. The authors note that the use of mathematical models has helped to understand the heterogeneity of tumors and the general evolution of different types of cancers. Through the mathematical models, a more detailed characteristic understanding of the health condition and the subsequent treatment approach was determined through the model analysis. it is possible to achieve a better characterization of cancer evolution and the subsequent use of personalized treatment mechanisms that would achieve notable resistance to cancer treatment. Both partial and ordinary differential equations as well as algebraic equations helped to characterize cancer tumors.

The purpose of the study was to explore the extent to which mathematical-based models can be used to explore the opportunities and challenges of characterizing changes in the size of tumor cells and the evolution of resistance to treatment. The inhibition dynamic approach employed in the model underscored the understanding of tumor growth and the overall clonal evolution of drug resistance (Yin et al., 2019). The article explains that cancer treatment evolution can be better explained and a personalized treatment approach developed based on the understanding of cancer resistance variants. The research also underscores the diverse stochastic and deterministic models in the evolution of tumor resistance.

The significance of the article is that it provides a clear overview of the progress that has been made in exploring the treatment of cancer. The knowledge gained in the study can be extended to ascertain unique the response to anti-cancer treatment as a function of the highlighted models The findings could support the analysis of anticancer treatment responses using modeling approaches that consider both the inhibition of tumor growth and the evolution of resistance. However, it's crucial to acknowledge that there are significant challenges that still need to be addressed in this context.

The aim of the study by Awad et al., (2022) was to characterize and then forecast the burden of type 2 diabetes mellitus between 2020 and 2050 in Qatar. The overall population is composed of 89% expatriates who come from more than 150 countries. The model applied in the study was an age-structured mathematical model which was noted to be effective in understanding the weight of type 2 diabetes. The influence of other risk factors such as excessive smoking, prevalence of obesity, and lack of physical activity was also assessed with the help of the model. The data used as part of the input parameters were the natural history studies of the disease, a stepwise survey, and an observatory study (Awad et al., 2022). Using the epidemiological and natural history data, it was possible to forecast the prevalence of type 2 diabetes.

The purpose of the mathematical model was to try and improve the characterization of the diabetes burden among the expatriate resident population which constitutes 89% of the total Qatar population. The findings noted using the model were that the prevalence of diabetes was set to double by 2050, with the incidence of the condition projected to increase by 80% (Awad et al., 2022). Another aspect noted in the research was that the diabetes burden and the drivers of the condition substantially varied in diverse nationalities staying in Qatar and that while obesity was perceived to be the main driver of the condition, it was arguably not the main reason for diabetes prevalence among the expatriate population living in Qatar. The research is significant since it provides valuable insights into the epidemiology of T2DM in Qatar and demonstrates the importance of mathematical modeling in understanding and addressing the disease.

A machine learning prediction model was employed in research by Karthick et al., (2022) to explain the risks of cardiovascular conditions. The study employs various machine learning algorithms, such as multi-layer perceptron (MLP), K-nearest

neighbor (K-NN), support vector machine (SVM), Gaussian Naive Bayes, logistic regression, LightGBM, XGBoost, and random forest, to develop a heart disease risk prediction model using the Cleveland heart disease dataset. The approach involves data preprocessing and selection of specific attributes from the Cleveland heart disease dataset using the chi-square statistical test. The second step is training the selected dataset using the chosen machine learning algorithms before the performance of the model is assessed based on their accuracy, area-under-the-curve value, and other relevant metrics.

The purpose of using machine learning mathematical models in explaining the prevalence of heart attacks is to develop effective predictive tools that can aid in the early detection and assessment of heart disease. Machine learning techniques can analyze various health record data and parameters, such as cholesterol levels, genetic factors, blood pressure, physical activity, obesity, and smoking, to identify patterns and risk factors associated with heart disease. By training machine learning models on relevant datasets, it is possible to create accurate prediction models that can assist diagnosticians in reducing misdiagnosis and making more precise health decisions for patients. These models can help in identifying individuals at risk of heart disease, thus enabling timely intervention and medical care.

The different machine learning techniques provide the data visualization feature that provides an easier way of presenting the risks of cardiovascular conditions. The visualization approaches include the use of heat maps and sub-set attribute correlation that gives a better pictorial view of how to present data. The tools also help to provide a better correlation between risk features of cardiovascular disease and other closely linked lifestyle conditions.

Framework of the Thesis

The main purpose of this thesis can be summarized as investigating the future impact of COVID-19 on the patient numbers of the chronic diseases cancer, diabetes, and heart diseases, given in order. The mathematical models used in this study employed 'sensitivity analysis.' The summary of the thesis including purpose and significant of the study, and research questions and hypotheses are stated in Chapter I.

For a better understanding of the future impact of COVID-19 on the patient numbers of the chronic diseases cancer, diabetes, and heart diseases, and the relationship between mathematical model and health sciences, a literature review is done and explained in Chapter II including the mathematical tools (solution techniques, definitions, theorems and corollaries) that are used in the thesis. The data of cancer, diabetes, and heart diseases diagnosed patients is opted for with the aim of designing mathematical models. Chapter III consists of the constructed mathematical model 1 with its necessary properties and theorems with proofs. Chapter IV consists of the constructed mathematical model 2 with its necessary properties and theorems with proofs. Numerical simulations of the results of the model I and model II are also presented in Chapter V respectively. The findings of all thesis and discussions are provided in Chapter VI with the comparison of other works in literature. Chapter VII comprises the conclusions and
recommendations of the thesis. In this chapter, overall conclusions and what can be
done in future in this field are discussed.

CHAPTER III

Methodology

In this section, the evaluation of the number of diagnosed cancer patients is proposed through mathematical modelling. The aim of this section is to create a mathematical model between susceptible individuals to cancer and the number of cancer patients. In doing so, the aim is to assess the relationship between subcategories and find the most effective parameters on state variables or compartments using sensitivity analysis. For this purpose, first, the design and limitations of the research are provided. Following that, the obtained data is explained. Lastly, necessary theorems and proofs are presented in the analysis of the model, accompanied by numerical simulations.

Research Design and Limitations

A mathematical model has been constructed through ODEs to assess the relationship between susceptible individuals to cancer and the number of cancer patients. Subsequently, the proof of the existence of solutions and equilibrium points has been demonstrated and calculated using various computational techniques and theorems.

Data Collection

In this chapter, the data is obtained from the references.

Data Analysis

In this section of the thesis, analysis of the obtained data is given.

Mathematical Model and Its Analysis

While constructing the model, the whole population, denoted by $N(t)$ at time t, is divided into 2 compartments, that is, the model consists of 2 state variables. These are: susceptible individuals ($S(t)$), and cancer diagnosed individuals ($C(t)$). For determining the necessary parameters, the obtained data is analyzed. Hence, the model is constructed as follows:

$$\frac{dS}{dt} = \pi - f1CS - (o+b)S - \mu S + \gamma C + cC$$

$$\frac{dC}{dt} = f1CS + (o+b)S - \mu C - \eta C - \gamma C - cC.$$

In Table 1 and Table 2, descriptions of variables and parameters of the model are explained, respectively.

Table 1.

Description of Variables used in the Mathematical Model

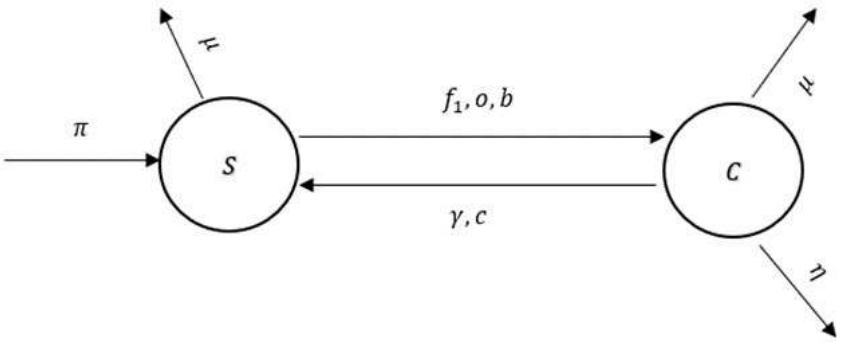
Variables	Descriptions
S	Susceptible individuals
C	Cancer patients

Table 2.

Description of Parameters used in the Mathematical Model

Parameters	Descriptions
π	Recruitment rate
$f1$	Transmission rate of hereditary
o	Rate of obese individuals with cancer
b	Rate of smokers with cancer
γ	Recovery rate
c	Negative effect of COVID-19
η	Disease-caused death rate
μ	Natural death rate

Figure 1: The Flow Diagram of The Model (1)



For the proof of existence of solutions of the proposed model, the following theorem is stated and demonstrated.

Theorem 2. Let (S,C) be a solution of the proposed system with the following initial conditions:

$$S\geq 0, C\geq 0.$$

Then, the set Λ below is biological feasible, that is, positive and invariant. Moreover, all of the solutions in $\mathbb{R}2+$ stay in π with respect to the proposed system.

$$\Lambda=\{(S,C) \quad \mathbb{R}2+: S+C\leq\pi\}.$$

Proof. Firstly, all terms of the equations in the system should be added. Then, we obtain

$$\frac{dN}{dt} =\pi-\mu(S+C).$$

As it is obvious from the above inequality $\frac{dN}{dt} \leq \pi$. Integrating both sides of the inequality with respect to t, we get

$$N(t)e\leq\pi e+k, \ ^{t}$$

for some arbitrary constant k. Applying Rota and Birkhoff stated in Birkhoff and Rota (1991) to the differential inequality, it is concluded that as t tends to infinity (∞), $0\leq N\leq\pi$ holds. As a result, all of the solutions of the proposed system enter the region π. Hence, it is concluded that the proposed model is biologically feasible, and it will be enough to consider the dynamics on the model in the set Λ.

Basic Reproduction Number and Equilibrium Points. As it is mentioned in Chapter II, existence of equilibrium points and their stability improves the strength of mathematical models. For the constructed model in Chapter III, 2 equilibrium points:

disease-free equilibrium point, denoted by $E_{0,1}$ and endemic equilibrium point, denoted

by $E_{*,1}$ are evaluated. For the presented model, one hand, $E_{0,1}$ is the point where cancer

does not exist in the population. On the other hand, $E_{*,1}$ is the point where the disease

is maintained with no need of external inputs. The basic reproduction number $R_{0,1}$ is

$$\left(\pi\left(b^2+b\,o+b\,\mu+o^2+o\,\mu+\mu^2\right)\right)\Big/\left(b^2\,c+b^2\,\eta+b^2\,\gamma+b^2\,\mu+2\,b\,c\,\mu+2\,b\,c\,o+2\,b\,\eta\,\mu+2\,b\,\eta\,o+2\,b\,\gamma\,\mu+2\,b\,\gamma\,o+2\,b\,\mu^2+2\,b\,\mu\,o+c\,\mu^2+2\,c\,\mu\,o+c\,o^2+\eta\,\mu^2+2\,\eta\,\mu\,o+\eta\,o^2+\gamma\,\mu^2+2\,\gamma\,\mu\,o+\gamma\,o^2+\mu^3+2\,\mu^2\,o+\mu\,o^2\right)$$

At the disease-free equilibrium point $E_{0,1}$ is unique and is obtained as

$$E_{0,1}=(S_{0,1},C_{0,1})=\left(\frac{\pi}{o+b+\mu},0\right).$$

It is obvious that $E_{0,1}$ attracts the region so that

$$E_{0,1}=\{(S_{0,1},C+0,1)\quad R2{:}C=0\}.$$

Endemic equilibrium point, denoted by $E_{*,1}$, consists of $S_{*,1}$ and $C_{*,1}$. That is,

$$E_{*,1}=(S*,1,C*,1),$$

where $S_{*,1}$ is the solution of

$$A(S_{*,1})^2+BS_{*,1}+F=0,$$

for

$$A=f1[(o+b)(1+\gamma+c)-(o+b+\mu)],$$

$$B=(\mu+\eta+\gamma+c)[(o+b)(1-\gamma-c)+\mu]-f1\pi,$$

$$F=-(\mu+\eta+\gamma+c)\pi,$$

and

$$C_{*,1}= \frac{(o+b)S_{*,1}}{\mu+\eta+\gamma+c-fS_{1*,1}}.$$

On the other hand, a real solution of the quadratic equation that depends on S_*,1 exists only if the coefficient A is positive. That is, if

$$(o+b)(1+\gamma+c)-(o+b+\mu)>0,$$

$$(o+b)(1+\gamma+c)>(o+b+\mu),$$

$$\gamma+c> \frac{\mu}{o+b}.$$

This inequality always holds since the value of natural death rate is very small.

Theorem 3.Disease Free Equilibrium, $E0,1$, is globally asymptotically stable whenever $\gamma+c>f1$.

Proof Consider the Lyapunov function

$$V(S,C)=S-S0,1-S0,1ln(\frac{S}{S0,1})+C.$$

The above function is always positive and at the point $E0,1$ it is equal to 0. So, for the stability, it is enough to show that $\dot{V}$ is a definite negative.

$$\begin{aligned}\dot{V} &= \dot{S}-\frac{S0,1}{S}\dot{S}+\dot{C}\\ &=\pi-(f1C+o+b+\mu)S+(\gamma+c)C\\ &-[\pi-(fC+o+b+\mu)S+(\gamma+c)C]+(fC+o+b)S\\ &-(\mu+\eta+\gamma+c)C.\end{aligned}$$

Since $\pi=S0,1(o+b+\mu)$,

$$\begin{aligned}&\pi-(f1C+o+b+\mu)S+(\gamma+c)C-\frac{S0,1}{S}[\pi-(f1C+o+b+\mu)S+(\gamma+c)C]\\ &+(f1C+o+b)S-(\mu+\eta+\gamma+c)C\\ &=\pi(2-\frac{S0,1}{S})+(f1-\gamma-c)C-S0,1.\end{aligned}$$

It is clear that $2 - \frac{S0,1}{S} < 0$. Hence, for the condition $\dot{V} < 0$, $f1-\gamma-c<0$ should hold. Therefore, $E0,1$ is globally asymptotically stable if $\gamma+c>f1$. □

Theorem 4. Endemic Equilibrium, $E*,1$, is globally asymptotically stable.

Proof. For the proof of the above theorem, the following Lyapunov function is constructed.

$$W(S,C)=S*,1g(\frac{S}{S*,1})+C*,1g(\frac{C}{C*,1}),$$

where $g(x)=x-1-lnx$. The function W is positive, and $W(S*,1,C*,1)=0$. So, it is enough to show that $\dot{V}<0$.

$$\begin{aligned}\dot{V} &= \dot{V}*\left(1-\frac{S}{S}\right)+\dot{V}-C*,1C\\ &=\pi-f1CS-(o+b)S-\mu S+\gamma C+cC\\ &-\left[\pi-f1CS-(o+b)S-\mu S+\gamma C+cC\right]+f\qquad 1CS+(o+b)S\\ &-(\mu+\eta+\gamma+c)C-\left[f1CS+\frac{C*,1}{C}(o+b)S-(\mu+\eta+\gamma+c)C\right]\\ &=\pi\left(1-\frac{S*,1}{S}\right)-\mu S-(\mu+\eta)C<0,\end{aligned}$$

Thus, $E*,1$ is globally asymptotically stable.

Parameter Fitting using Real Clinical Data. In mathematical epidemiology, deterministic models of illnesses depend considerably on statistics becoming to confirm that their predictions are in step with determined data. The capability to are anticipating the spread of illness is extra appropriate as it simplifies the estimation of model parameters like transmission and healing rates. By contrasting the version with the data, researchers can research extra approximate infection trends, remedy outcomes, and discrepancies, and adopt what-if analyses. If policymakers had extra religion inside the version`s projections, they may make extra knowledgeable choices. Improving the destiny version improvement is every other gain of increasing the medical knowledge base. The least squares approach has been considerably utilized in a huge kind of fields, from epidemiology to finance, to estimate parameters in mathematical models. When growing a deterministic model for infectious diseases, we first begin with differential equations that describe the dynamics of the disease. These equations can also additionally include vague values for parameters just like the rate of transmission or the rate of recovery. Model predictions produced with arbitrary settings for those parameters will now no longer fit the observed data. Finding those parameters` values that yield predictions as near the data as viable is the goal. To strike this equilibrium, the least squares method minimizes the squared differences (additionally recognized as "residuals") among the observed and predicted values. Once the parameter values are obtained, the squared deviations between the model's predictions and the data may be
effortlessly calculated. Finding parameter values that limit this sum is ideal because it
suggests that the model's predictions are near the data. The model's parameters are taken
into consideration to be "fit" to the data as soon as this constraint minimization is
complete. With those changed parameters, the model ought to seize the dynamics of the
infectious disease’s transmission and effect faithfully as located inside the actual world.
In epidemiology, becoming parameters to models the use of the ODE system in (1)
demonstrates an progressive strategy. Some of the complexity of the pandemic can be
better understood by using deterministic models, inclusive of people who use

parameters are derived from the fitted data, at the same time as others are taken from the mentioned evaluation in the available literature. Fig. 2 shows the outcomes of an evaluation among actual scientific data and model (1) simulations, along with residuals in Fig. 3 and the corresponding box plot in Fig. 4. Fig. 2 indicates that the curve of the simulated data agrees nicely with the real scientific data, and the scatter in the related residuals, as proven in Fig. 3. Lends credence to this conclusion. A similar declare is legitimate for the box plot in Fig. 4. The following preliminary conditions are used in the course of the simulations:

$$S(0)=88780, C(0)= 491.$$

The fitted parameters are acquired as follows:

$$f1=1.7576e-04, b=3.4756e-02, o=2.6415e-01,$$

$$c=5.9183e+01, and\ \eta=5.6503.$$

The rest of the parameters are taken to be fixed and given to be

$$\mu= \frac{1}{75.6 * 365}, \pi=36.855*\mu, \text{ and } \gamma=0.1.$$

It can be cited that the fitted R-squared value is 0.9987 displaying a greater degree of confidence inside the envisioned fitted parameters. With the above parameters, the least-squares curve becoming of the model is proven below to have an excessive degree of settlement with the actual clinical data.

Figure 2
The Comparison of Simulations of Model (1) with the Real Clinical Data

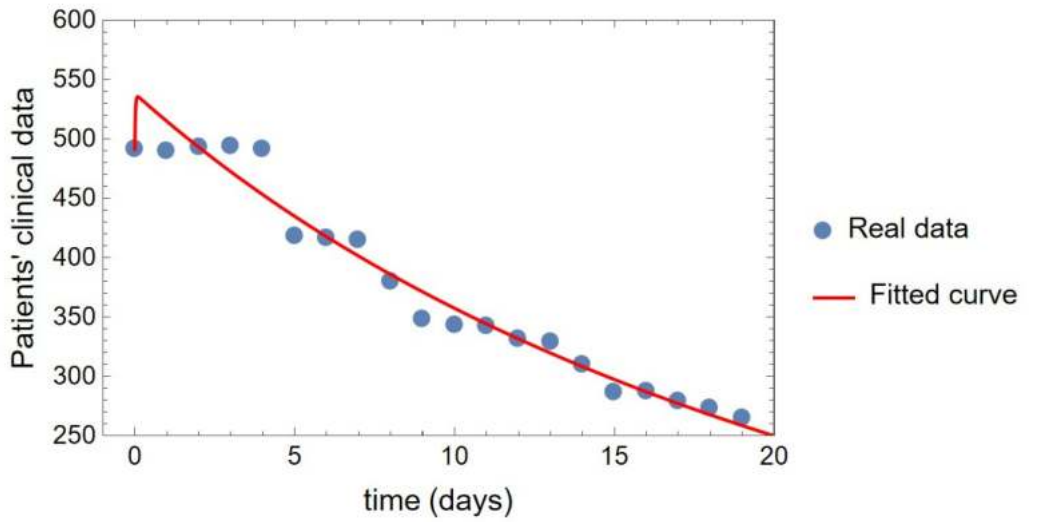


Figure 3:*Different Types of Residuals for the Curve Fitting of the Model (1)*

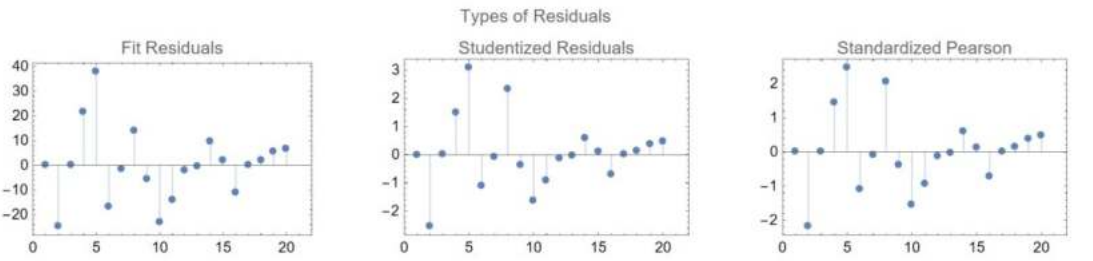
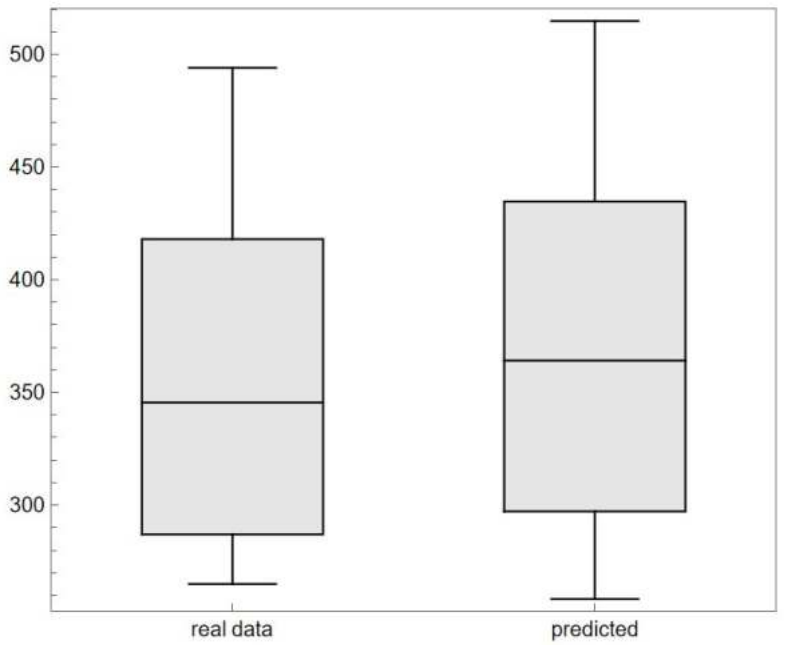


Figure 4:*The Comparison of the Box-plots for the Real Clinical Data and the Observed (predicted) data from Simulations of the Model (1)*



It might also additionally similarly be visible that the statistical measures (minimum, first, second, and third quartile (Q1, Q2, Q3), arithmetic mean, maximum, and standard deviation) computed in Table 3 also are in superb agreement with every other. This complements the validation and verification of model (1) due to the fact the standard deviation of magnitude 82.1, received under the simulations of model (1), is nearly sufficient to the standard deviation based at the real clinical data as proven in an ultimate column of Table 3.

Table 3:*Descriptive Summary of Statistical Measures for the Model (1)*

Summary	Min.	Q1	Q2	Q3	Mean	Max	SD
Real	2.45*10^(2)	2.87*10^(2)	3.43*10^(2)	4.18*10^(2)	3.74*10^(2)	4.94*10^(2)	8.33*10^(1)
Observed	2.58*10^(2)	2.97*10^(2)	3.57*10^(2)	4.35*10^(2)	3.74*10^(2)	5.15*10^(2)	8.21*10^(1)

In overall, Chapter III presents the research's framework and constraints, followed by an exposition of the acquired data. The verification of solution existence and equilibrium points is elucidated through diverse computational methods and theorems.

CHAPTER IV

Methodology

In this section, the evaluation of the number of diagnosed heart disease patients and diabetes patients are proposed through mathematical modelling. The aim of this section is to create a mathematical model between susceptible individuals to heart disease and diabetes and the number of heart disease and diabetes patients. In doing so, the aim is to assess the relationship between subcategories and find the most effective parameters on state variables or compartments using sensitivity analysis. For this purpose, first, the design and limitations of the research are provided. Following that, the obtained data is explained. Lastly, necessary theorems and proofs are presented in the analysis of the model, accompanied by numerical simulations. The model is built by using a system of ODEs.

Research Design and Limitations

A mathematical model has been constructed through ODEs to assess the relationship between susceptible individuals to heart disease and diabetes and the number of heart disease and diabetes patients. Subsequently, the proof of the existence of solutions and equilibrium points has been demonstrated and calculated using various computational techniques and theorems.

Data Collection

In this chapter, the data is obtained from the references.

Data Analysis

In this section of the thesis, analysis of the obtained data is given.

Mathematical Model and Its Analysis

While constructing the model, the whole population, denoted by $N(t)$ at time t, is divided into 3 compartments, that is, the model consists of 3 state variables. These are: susceptible individuals to he disease and diabetes ($S(t)$), heart disease diagnosed individuals ($H(t)$) and diabetes diagnosed individuals ($D(t)$), For determining the necessary parameters, the obtained data is analyzed. Hence, the model is constructed as follows:

$$\frac{dS}{dt} = \Lambda - (b+o)S - fHS - fD_1S + (c+\gamma)_2H + (c+\gamma_1 \quad _1 \quad _2 \quad 2)D - \mu S,$$

$$\frac{dH}{dt} = (b+ko)+_1 \quad S \quad f1HS - (c1+\gamma 1+\mu+\eta 1+a)H + eD,$$

$$\frac{dD}{dt} = (1-k1)oS + f2DS - (c2+\gamma 2+\mu+\eta 2+e)D + aH \quad .$$

In Table 1 and Table 2, descriptions of variables and parameters of the model are explained, respectively.

Table 4.

Description of Variables used in the Mathematical Model

Variables	Descriptions
S	Susceptible individuals
H	Heart disease patients
D	Diabetes patients

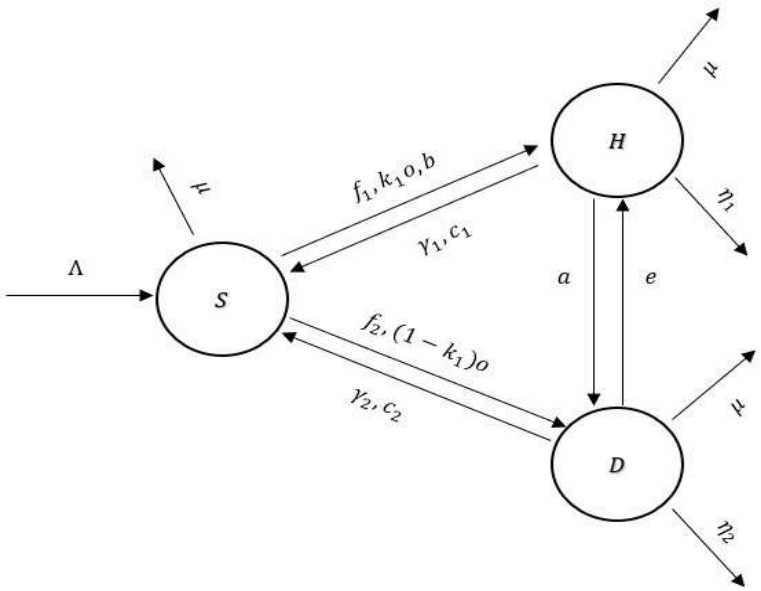
Table 5.

Description of Parameters used in the Mathematical Model

Parameters	Descriptions
Λ	Recruitment rate
b	Rate of smokers who are heart patients
$k1o$	Rate of obese individuals who are heart patients
$(1-k1)o$	Rate of obese individuals who have diabetes
$fi, i=1,2$	Transmission rate of hereditary
$ci, i=1,2$	Negative effect of COVID-19
$\gamma i, i=1,2$	Survival rate of diseases
μ	Natural death rate
$\eta 1$	Heart-disease-caused death rates
$\eta 2$	Diabetes-caused death rates

a	Transmission rate from H to D
e	Transmission rate from D to H

Figure 5: The flow diagram of the model (2)



For the proof of existence of solutions of the proposed model, the following theorem is stated an demonstrated.

Theorem 5. Assume that (S,H,D) is the solution of the constructed system above with the initial conditions $S\geq 0, H\geq 0$, and $D \geq 0$. Then, the following set

$$\pi=\{(S,H,D) \quad R3+: S+H+D\leq\Lambda\}$$

is positive, invariant, and the solutions in $R3+$ stay in π with respect to the constructed system.

Proof. The addition of all of the terms that are on the right side of the system gives

$$\frac{dN}{dt} =\Lambda-\mu(S+H+D)-\eta 1H-\eta 2D.$$

From the above equality, it is obvious that $\frac{dN}{dt} \leq \Lambda$. Integrating both sides with respect to t yields

$$N(t)et \leq \Lambda et + m,$$

For some constant m. Applying Rota and Birkhoff to the above differential inequality, it is obtained that as t tends to infinity, $0 \leq N \leq \Lambda$ holds. As a result, the solutions of the system enter the region π. Therefore, it is certain that the model is feasible by means of biology and it is enough to consider the dynamics on the model in π.

Basic Reproduction Numbers and Equilibrium Points. As it is mentioned in Chapter II, existence of equilibrium points and their stability improves the strength of mathematical models. For the constructed model in Chapter IV, 2 equilibrium points: disease-free equilibrium point, denoted by $E0,2$ and endemic equilibrium point, denoted by $E*,2$ are evaluated. For the presented model, one han $E0,2$ is the point where heart disease and diabetes do not exist in the population. On the other hand, E is the point where the diseases are maintained with no need of external inputs. The basic reproductio numbers $R0,2$ and $R0,3$ are computed.

At the disease-free equilibrium point, $E0,2$ is unique and is obtained as

$$E0,2=(S0,2,H0,2,D0,2)=\left(\frac{\Lambda}{o+b+\mu},0,0\right).$$

It is obvious that $E_{0,2}$ attracts the region so that

$$E_{0,2}=\{(S_{0,2},H_{0,2},D_{0,2}) \quad R_8^+ : H=D=0\}.$$

Endemic equilibrium point, denoted by $E_{*,2}$ consists of $S_{*,2}$ and $C_{*,2}$ That is,

$$E_{*,2}=(S_{*,2},C*,2,D*,2),$$

where $S_{*,2}$ is the solution of

$$A(S_{*,2})^4+B(S_{*,2})^3+E(S_{*,2})^2+FS_{*,2}+G=0,$$

for

$$A=(b+k1o)f22+f1f22(1-k1o-b+o+\mu),$$

$$\begin{aligned}B = {} & f1f2[\Lambda f2 + (c2 + \gamma 2)(k1 - 1)o + (o + \mu - k1o)(c2 + \gamma 2 + \mu + \eta 2 + e)] \\ & + f2\{f2(b + k1o)(-a - c1 - \gamma 1) \\ & +[(c1+\gamma 1+\mu+\eta 1+a)f2+(c2+\gamma 2+\mu+\eta 2+e)f1](b+\mu+k1o)-o\}(\mu+\eta \\ & +\gamma+c)[(o+b)(1-\gamma-c)+\mu]-f1\pi,\end{aligned}$$

$$E = \Lambda f2[-f1(c1 + \gamma 1 + \mu + \eta 1 + a)f2 + (c2 + \gamma 2 + \mu + \eta 2 + e)f1]$$
$$+f2(c1+\gamma 1-k1o-b-\mu)[(c1+\gamma 1+\mu+\eta 1+a)(c2+\gamma 2+\mu+\eta 2+e)-ea]$$
$$+ f2(b + k1o)[(c1 + \gamma 1)(c2 + \gamma 2 + \mu + \eta 2 + e) + a(c2 + \gamma 2)]$$
$$+ [(c2 + \gamma 2 + \mu + \eta 2 + e)(b + k1o) + eo(1 - k1)][(c2 + \gamma 2 + \mu + \eta 2 + e)f1 - af2]$$
$$+o(1-k1)(c2+\gamma 2)[(c1+\gamma 1+\mu+\eta 1+a)f2+(c2+\gamma 2+\mu+\eta 2+e)f1],$$

$$F=[(c1+\gamma 1+\mu+\eta 1+a)f2$$
$$+(c2+\gamma 2+\mu+\eta 2+e)f1][(c1+\gamma 1+\mu+\eta 1+a)(c2+\gamma 2+\mu+\eta 2+e)-ea](b$$
$$+o+\mu-c1-\gamma 1)$$
$$+\Lambda\{(c2+\gamma 2+\mu+\eta 2+e)[(c1+\gamma 1+\mu+\eta 1+a)f2+(c2+\gamma 2+\mu+\eta 2+e)f1]$$
$$+f2[(c1+\gamma 1+\mu+\eta 1+a)(c2+\gamma 2+\mu+\eta 2+e)-ea]\}$$
$$- (c2 + \gamma 2)\{o(1 - k1)[(c1 + \gamma 1 + \mu + \eta 1 + a)(c2 + \gamma 2 + \mu + \eta 2 + e) - ea]$$
$$+a[(c2+\gamma 2+\mu+\eta 2+e)(b+k1o)+eo(1-k1)]\},$$

$$G=-\Lambda(c2+\gamma 2+\mu+\eta 2+e)[(c1+\gamma 1+\mu+\eta 1+a)(c2+\gamma 2+\mu+\eta 2+e)-ea]$$

and so

$$S*,2=\Lambda(c2+\gamma 2+\mu+\eta 2+e)((c1+\gamma 1+\mu+\eta 1+a)(c2+\gamma 2+\mu+\eta 2+e)-ea),$$

$$H*,2= \frac{[(b + k1o)(c2 + \gamma 2 + \mu + \eta 2 + e - f2S*,2) + (1 - k1)eo]S*,2}{(c1 + \gamma 1 + \mu + \eta 1 + a - f1S*,2)(c2 + \gamma 2 + \mu + \eta 2 + e - f2S*,2) - ea},$$

$$D*,2 = \frac{(1 - k1)oS*,2}{c2+\gamma 2+\mu+\eta 2+e-f2S*,2}$$
$$+ \frac{[(b + k1o)(c2 + \gamma 2 + \mu + \eta 2 + e - f2S*,2) + (1 - k1)eo]aS*,2}{(c2+\gamma 2+\mu+\eta 2+e-f2S*,2)[(c1+\gamma 1+\mu+\eta 1+a-f1S*,2)(c2+\gamma 2+\mu+\eta 2+e-fS_{2*,2}) - ea]}.$$

Theorem 6. Disease Free Equilibrium, $E0,2$, is globally asymptotically stable when $f1<c1+\gamma 1$ and $f2<c2+\gamma 2$.

Proof. Consider the below Lyapunov function

$$T(S,H,D)=S(\frac{S}{S0,2}-1-ln(\frac{S}{S0,2}))+H+D.$$

Here, the constructed function T is always positive and equal to zero at $E0,2$. So, it will be enough to show that $\dot{T}<0$,

$$\dot{T}=S_{0,2}(\frac{S\dot{S}}{S0,2}-\frac{S0,2\dot{S}}{S0,2S})+\dot{H}+\dot{D}$$

$$=\Lambda-\Lambda\frac{S0,2}{S}+bS+oS-fHS+\gamma 1HS-fDS+\gamma 2DS-\frac{c1HS0,2}{S}-\frac{c2DS0,2}{S}-\frac{\gamma 1HS0,2}{S}$$

$$-\frac{\gamma 2DS0,2}{S}+\mu S-\mu(S+H+D)-\eta H-\eta D$$

$$=\Lambda(1-\frac{S0,2}{S})+(f-\frac{c1}{S}-\frac{\gamma 1}{S})HS+(f-\frac{c2}{S}-\frac{\gamma 2}{S})DS-\mu(S+H+D)-\eta H$$

$$-\eta 2D,$$

since $\Lambda=S0(o+b+\mu)$. It is obvious that $\frac{S}{S}-1-ln\frac{S}{S}<0$. For the rest, if

$$f1-\frac{c1}{S}-\frac{\gamma 1}{S}<0,$$

$$f1<\frac{c1}{S}+\frac{\gamma 1}{S}<c1+\gamma 1.$$

Similarly, if

$$f2-\frac{c2}{S}-\frac{\gamma 2}{S}<0,$$

$$f2<\frac{c2}{S}+\frac{\gamma 2}{S}<c2+\gamma 2.$$

Hence, $E_{0,2}$ is globally asymptotically stable if $f1<c1+\gamma 1$ and $f2<c2+\gamma 2$.

Theorem 7. Endemic Equilibrium Point, $E_*,2$, is globally asymptotically stable

If $\frac{D_*,2}{D} - \frac{H}{H_*,2} < 0$.

Proof. Consider the below Lyapunov function

$$X(S,H,D) = S_*,2\left(-1 - \frac{S}{S_*,2}\ln\left(\frac{S}{S_*,2}\right)\right) + H_*,2\left(-1 - \frac{H}{H_*,2}\ln\left(\frac{H}{H_*,2}\right)\right) + D_*,2\left(\frac{D}{D_*,2} - 1 - \ln\left(\frac{D}{D_*,2}\right)\right).$$

The constructed function X is positive for each value and equal to 0 at $E_*,2$. It is enough to show that $\dot{X} < 0$ is true.

$$\dot{X}(S_*,2, H_*,2, D_*,2) = \dot{X}\left(\frac{S}{S_*,2}, \frac{H}{H_*,2}, \frac{D}{D_*,2}\right) + \dot{X}\left(\frac{S}{S_*,2}, \frac{H}{H_*,2}, \frac{D}{D_*,2}\right) + \dot{X}\left(\frac{S}{S_*,2}, \frac{H}{H_*,2}, \frac{D}{D_*,2}\right)$$

$$= \Lambda - \mu S - \frac{\Lambda S_*,2}{S} + (b+o)S_*,2 + fDS_*,2 - (c+\gamma)_1 \frac{HS_*,2}{S} - (c2+\gamma 2) + \mu S_*,2 - (\mu+\eta)H_*,2 - \frac{DS_*,2}{S} - \frac{bS}{H}{}_1 H_*,2 - \frac{k1oS}{H_*,2}{}_1 H - fH\,S_*,2$$

$$+ (c1+\gamma 1)H_*,2 + (\mu+\eta 1)H_*,2 + aH_*,2 - \frac{eD}{H_*,2} H - (\mu+\eta)D - \frac{oS}{D_*,2}{}_2 D + \frac{k1oS}{D_*,2} D$$

$$- f2SD_*,2 + (c2+\gamma 2)D_*,2 + (\mu+\eta 2)D_*,2 - \frac{aH}{D} D + eD_*,2$$

$$= \Lambda\left(1 - \frac{S_*,2}{S}\right) + bS_*,2\left(2 - \frac{S}{S_*,2} - \frac{H_*,2}{H}\right) + oSS_*,2\left(2 - \frac{S}{S_*,2} - \frac{D_*,2}{D}\right) + ko\left(-2 - \frac{S}{S_*,2}\frac{D_*,2}{D}\frac{H_*,2}{H}\right) + 2_*,2DHD - \frac{H_*,2}{H} - \frac{D_*,2}{D}$$

$$+ f1S_*,2H_*,2\left(1 - \frac{H}{H_*,2} - \frac{S}{S_*,2}\right) + fS_*,2D_*,2\left(1 - \frac{D}{D_*,2} - \frac{S}{S_*,2}\right)$$

$$+ (eD+aH)\left(\frac{D_*,2}{D} - \frac{H_*,2}{H}\right) < (eD+aH)\left(\frac{D_*,2}{D} - \frac{H_*,2}{H}\right).$$

So, $\dot{X}$ is negative only if

$$\left(\frac{D_*,2}{D} - 1\right) < 0. \frac{H_*,2}{H}$$

According to the statistics proposed, there are more diabetic patients than heart patients in the world. Hence, for the stability of the endemic equilibrium point, this situation should be reversed and $\frac{D_*,2}{D} < \frac{H}{H_*,2}$.

As a summary, in Chapter IV, a mathematical model based on ODEs has been developed to examine the correlation between individuals susceptible to heart disease and diabetes and the prevalence of heart disease and diabetes patients. The verification of solution existence and equilibrium points has been established and computed employing a range of computational techniques and theorems.

CHAPTER V

Sensitivity Analysis and Numerical Simulations

Sensitivity analysis is a technique that can be used to determine how a mathematical model's parameters affect its compartments. This analysis aims to show how minor parameter changes might impact the emergence or extinction of a disease. A sensitivity analyses of the parameters for each of the two models are provided in this section. MatLab has completed all of the computations.

Sensitivity Analysis of the First Model.

This section carries out a sensitivity analysis to the first model's parameters.

Figure 6: Sensitivity Analysis of Parameter b in Compartment C

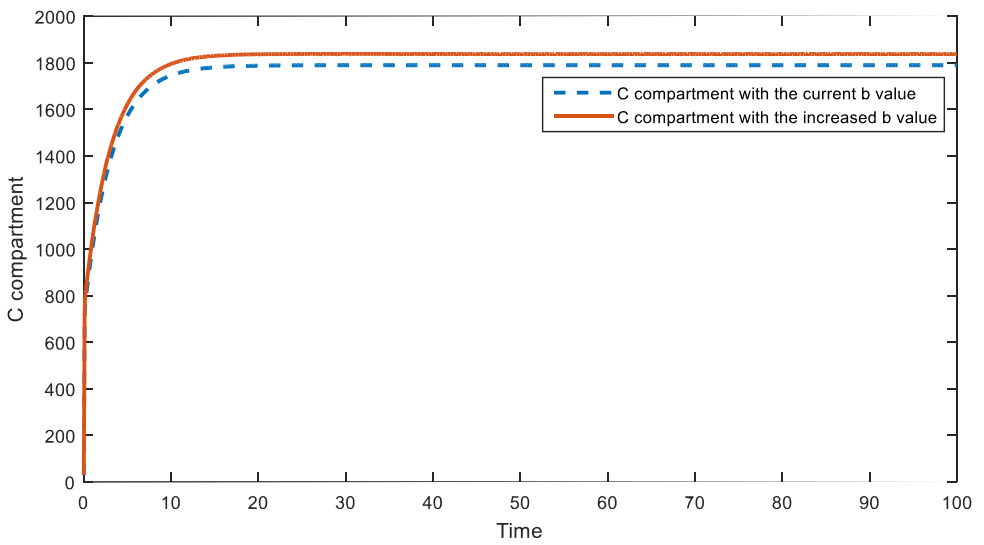
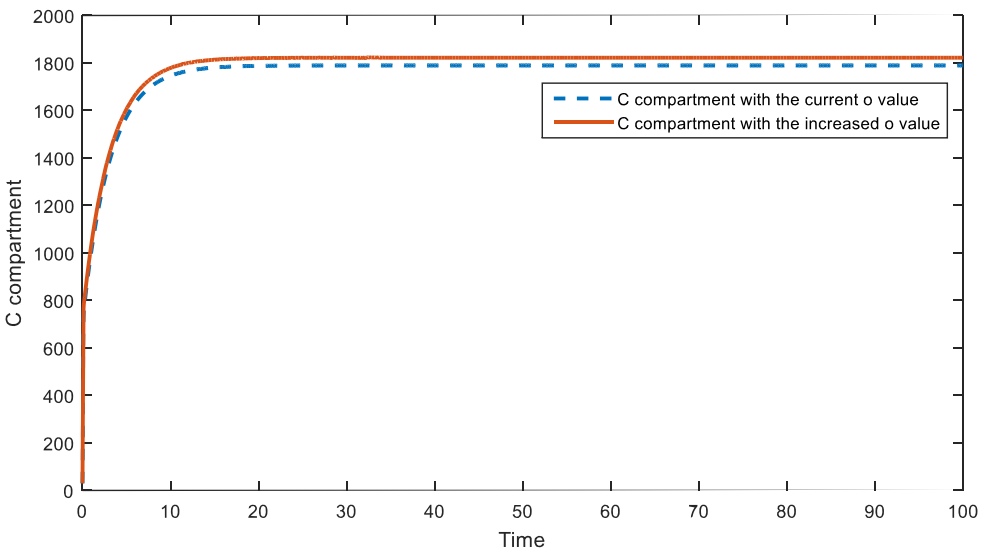


Figure 7: Sensitivity Analysis of Parameter o in Compartment C



As the b and o values are raised, respectively, Figures 6 and 7 depict the anticipated pattern for cancer patients. The C compartment will rise in both scenarios as a result of parameter increases. Therefore, it makes sense that as obesity (o) and smoking (b) rise, so will the number of cancer patients.

Figure 8: Sensitivity Analysis of Parameter c in Compartment C When It is Increased

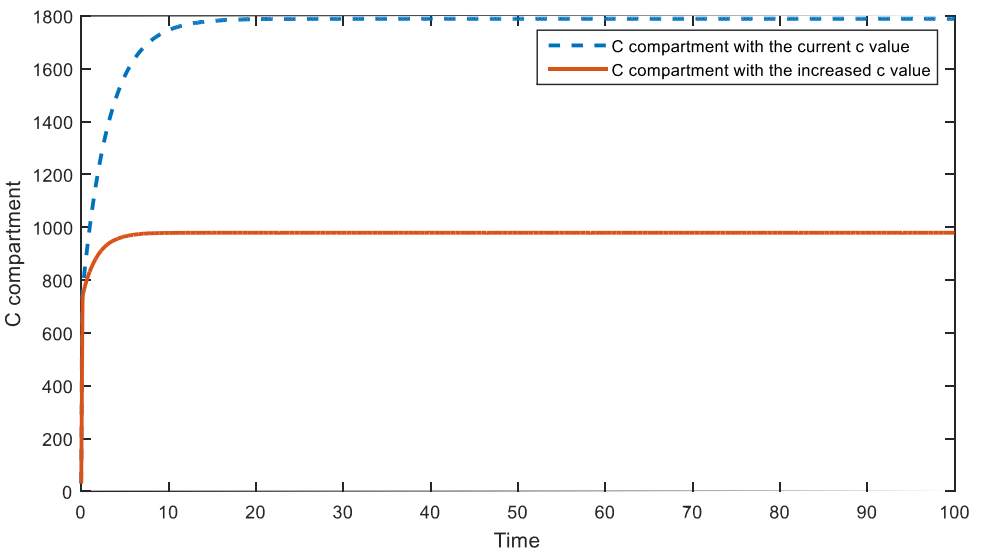
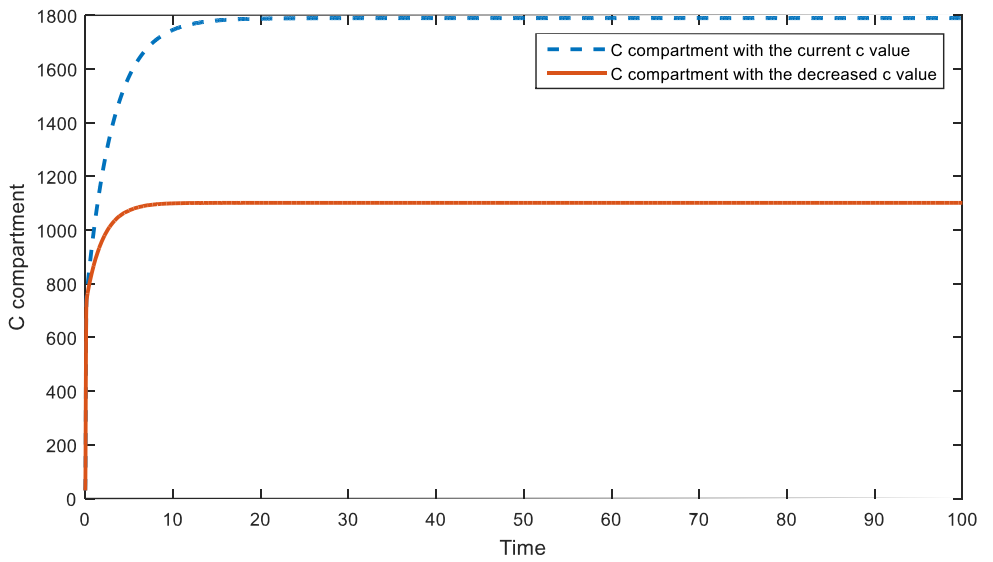


Figure 9: Sensitivity Analysis of Parameter c in Compartment C When It is Decreased



Figures 8 and 9 show the effects of increasing and decreasing parameter c, respectively. The two figures highlight the negative effect of the COVID-19 pandemic on cancer diagnosis.

Sensitivity Analysis of the Second Model.

This section carries out a sensitivity analysis to the second model's parameters.

Figure 10: Sensitivity Analysis of Parameter b in Compartment H

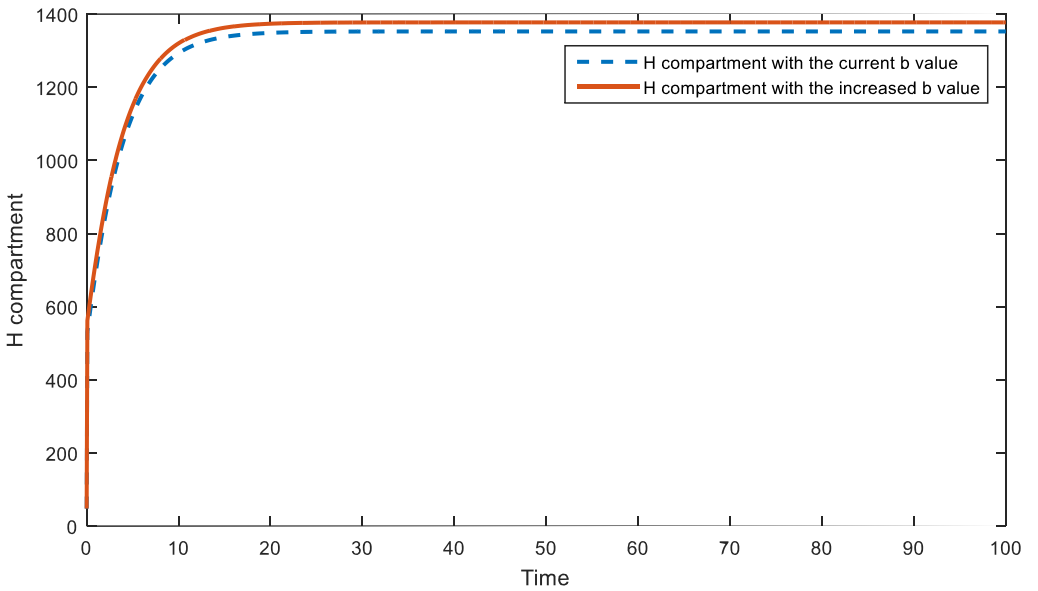
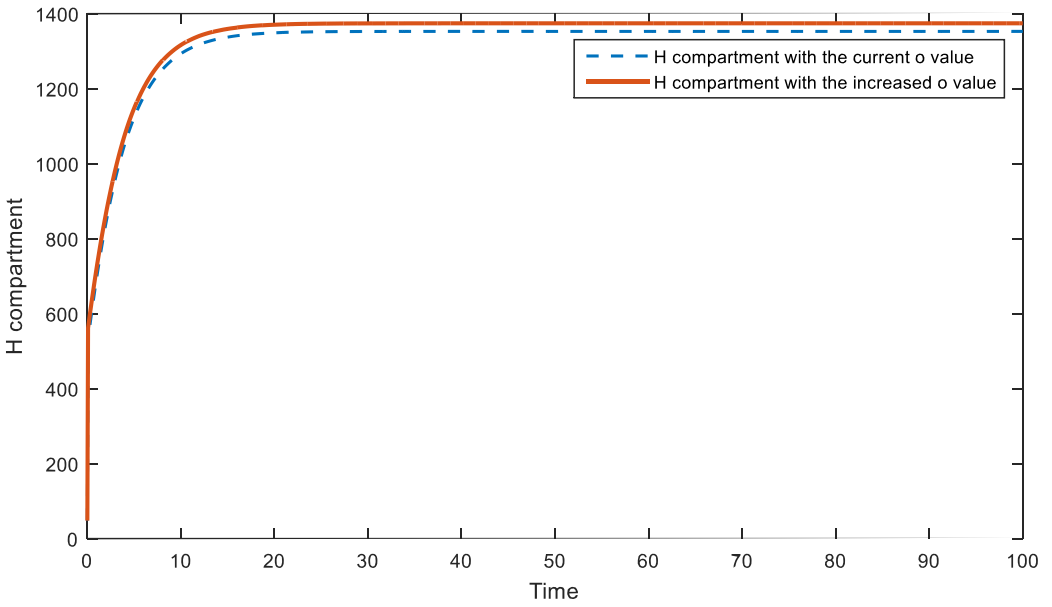


Figure 11: Sensitivity Analysis of Parameter o in Compartment H



The effects of parameters b and o on compartment H are shown, respectively, in Figs. 10 and 11. Compartment H will rise in response to increases in smoking and obesity, as the figures show.

Figure 12: Sensitivity Analysis of Parameter f1 in Compartment H

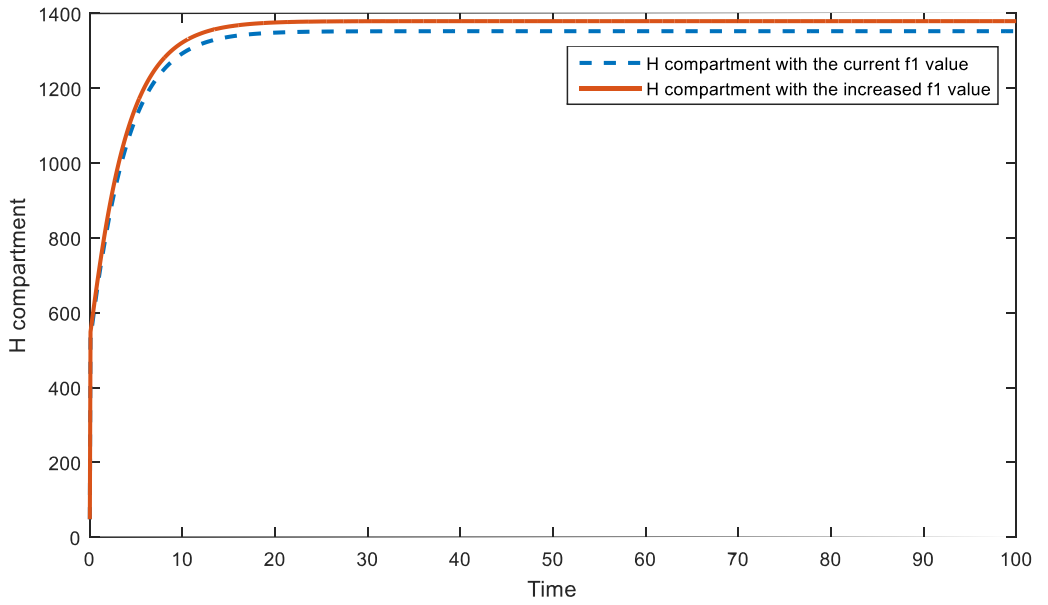


Figure 13: Sensitivity Analysis of Parameter c_1 in Compartment H When It is Increased

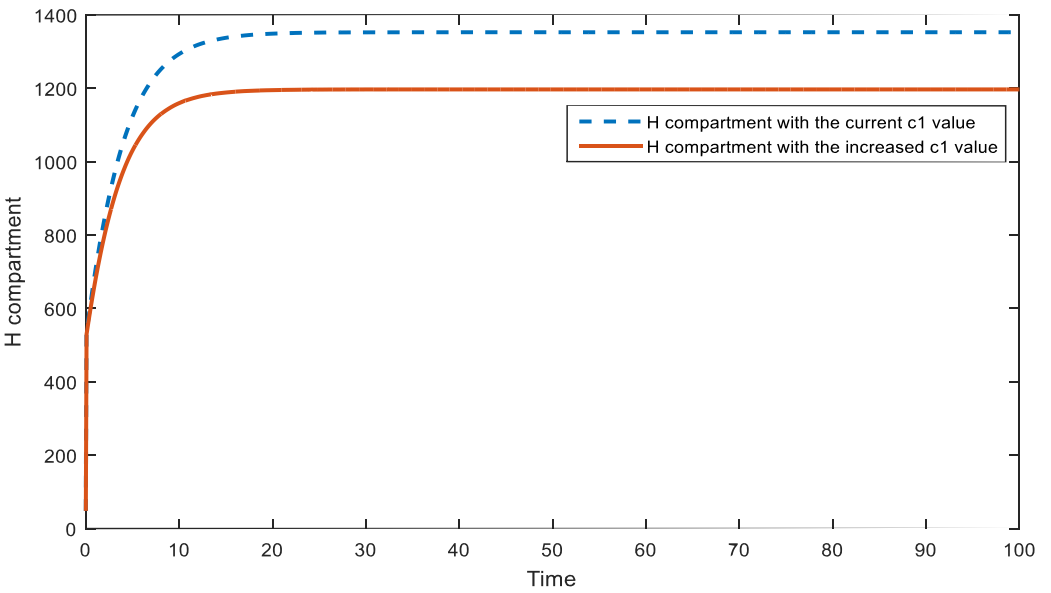
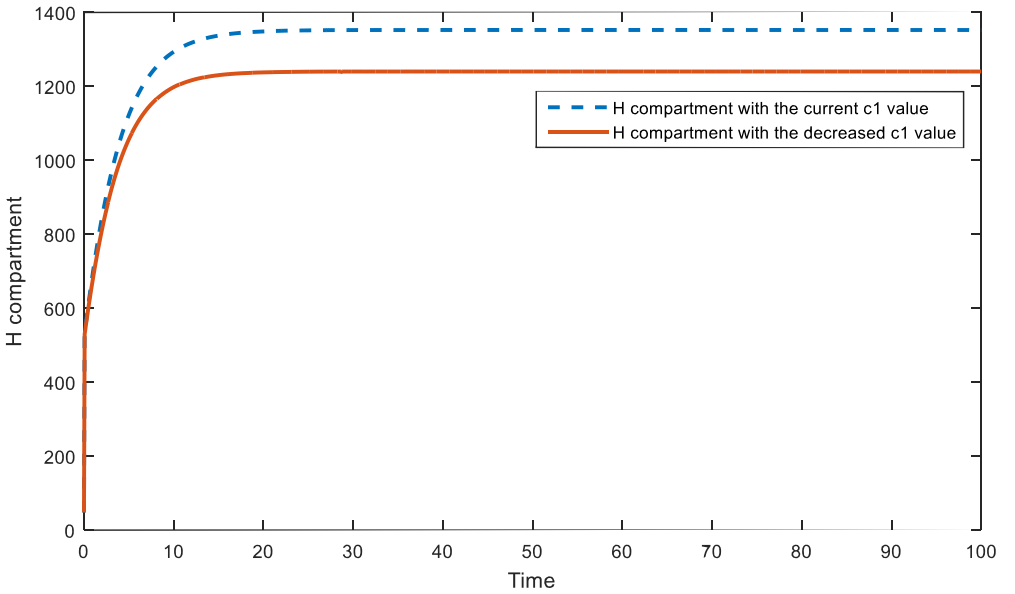
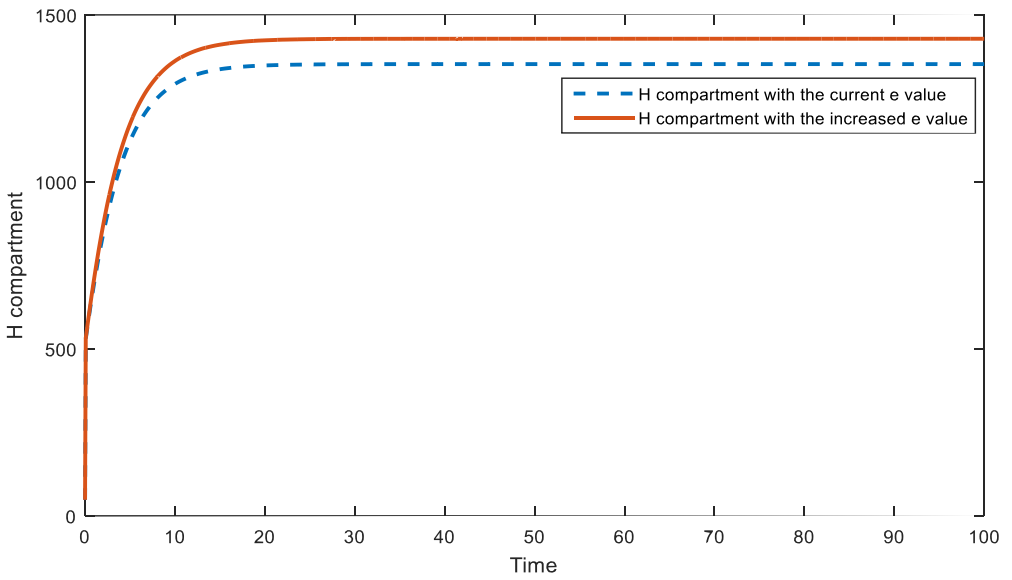


Figure 14: Sensitivity Analysis of Parameter c_1 in Compartment H When It is Decreased



As the percentage of inherited/family history, $f1$, rises, compartment H is predicted to experience the events shown in Fig. 12. The compartment capacity is displayed in Figs. 13 and 14 for both increases and decreases in parameter $e1$. The negative effect of the COVID-19 pandemic on heart disease diagnosis is highlighted by both figures.

Figure 15: Sensitivity Analysis of Parameter e in Compartment H



If diabetes rates rise, Fig. 15 shows the pattern of heart-diseased individuals. This is how heart-diseases are affected by diabetes.

Figure 16: Sensitivity Analysis of Parameter o in Compartment D

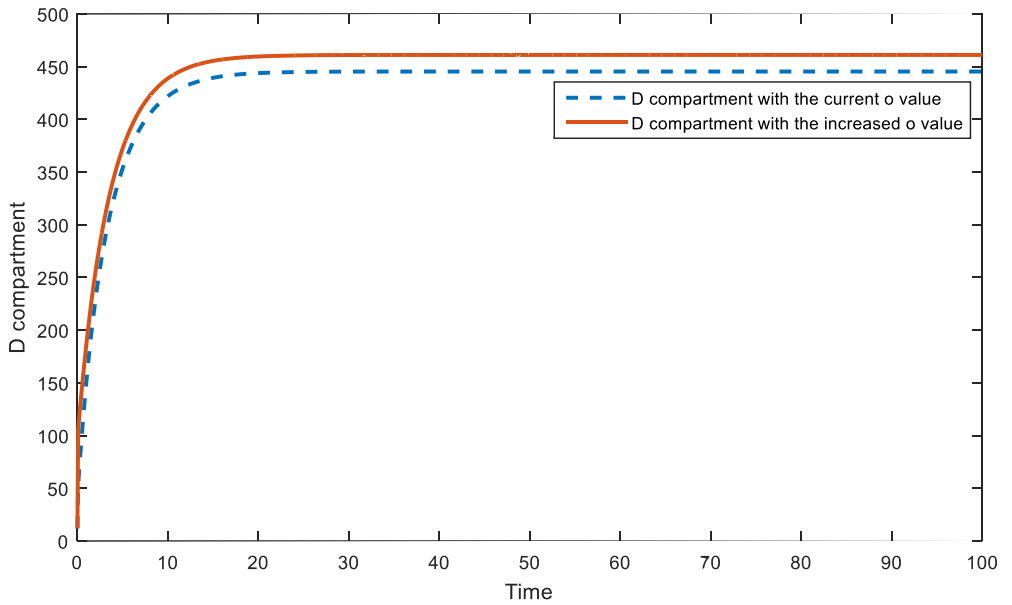


Figure 17: Sensitivity Analysis of Parameter $f2$ Compartment D

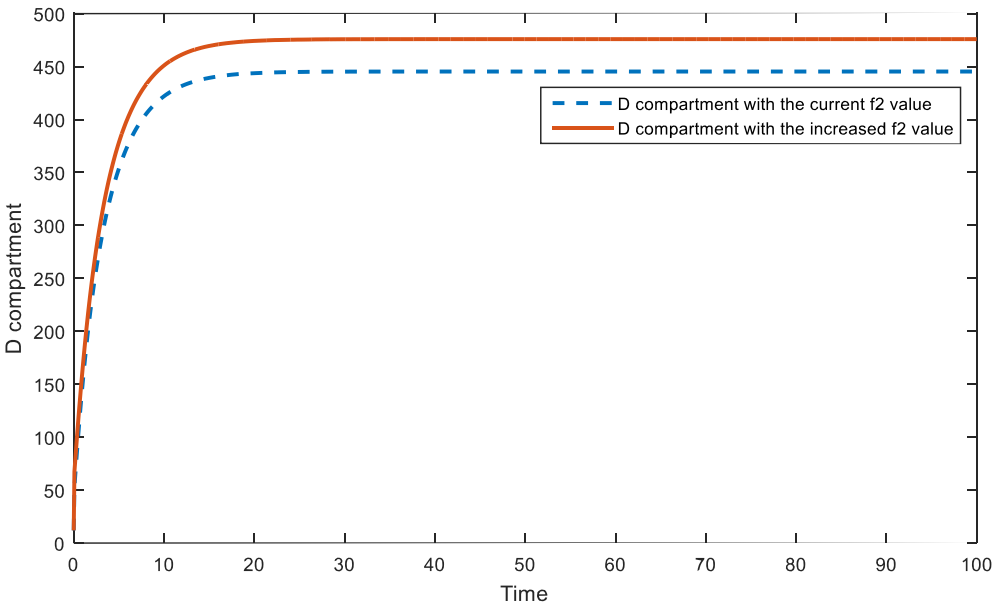


Figure 16 displays how the obesity parameter, o, affects compartment D, and Figure 17 illustrates how the hereditary/family history parameter, $f2$, affects the same compartment.

Figure 18: Sensitivity Analysis of Parameter $c2$ in Compartment D When It is Increased

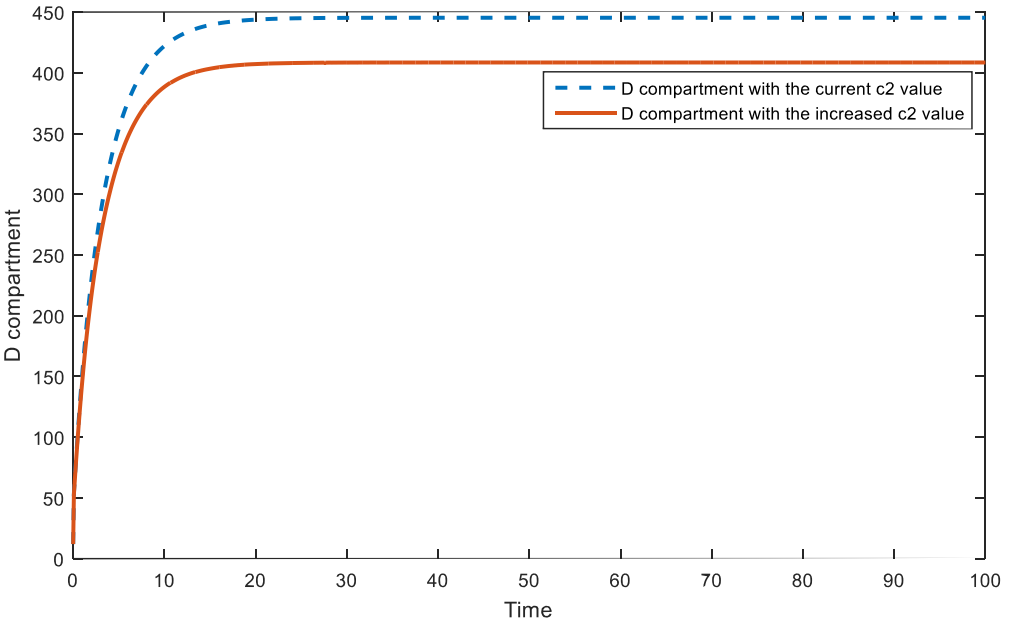
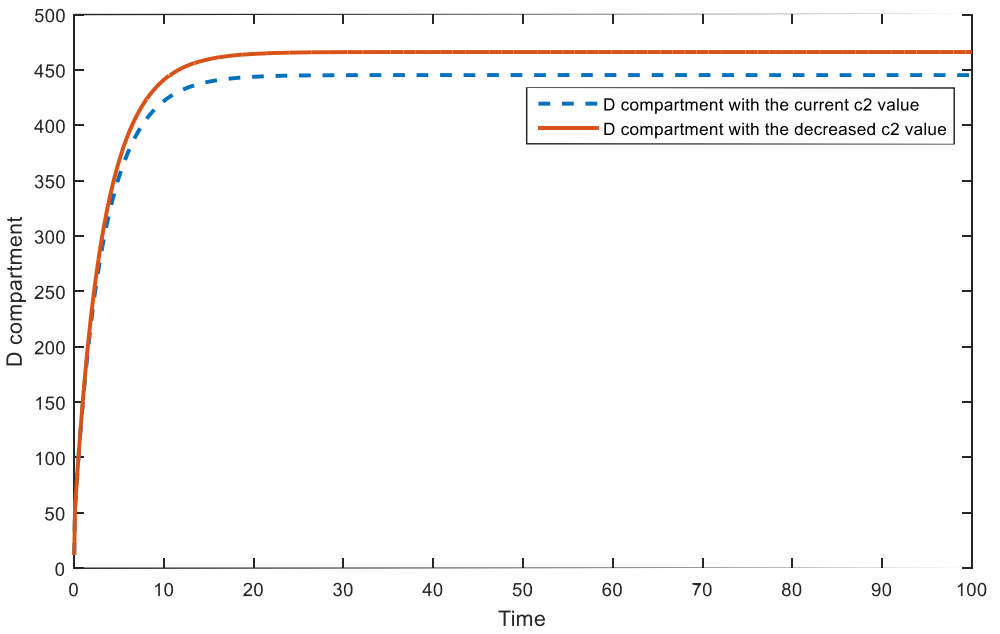
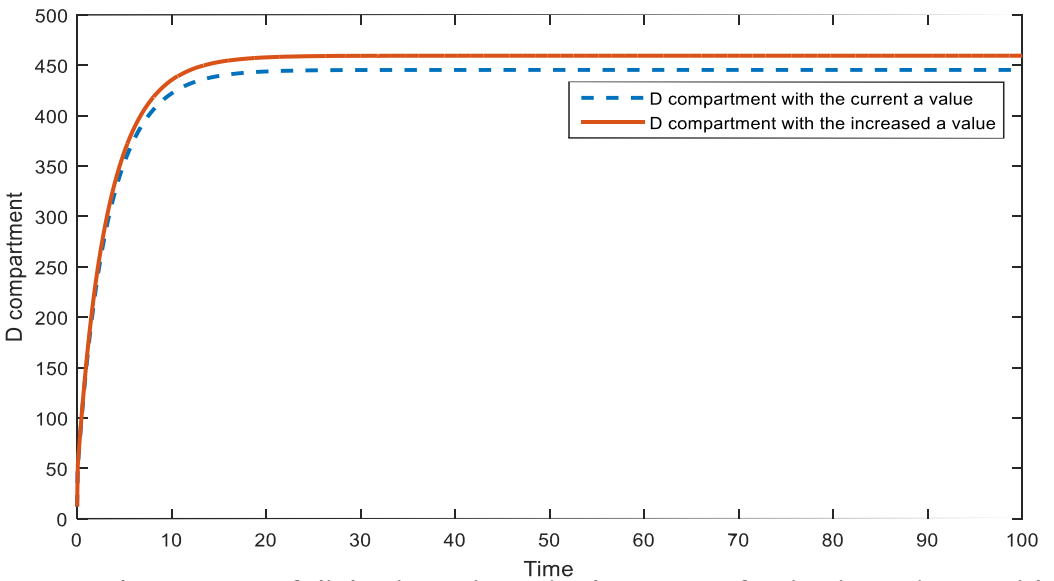


Figure 19: Sensitivity Analysis of Parameter $c2$ in Compartment D When It is Decreased



The purpose of revealing Figs. 18 and 19 is to demonstrate the importance of the COVID-19 parameter, $c2$, on compartment D. The two figures highlight the negative
effect of the COVID-19 pandemic on diabetes diagnoses.

Figure 20: Sensitivity Analysis of Parameter a in Compartment D When It is Decreased



The pattern of diabetic patients in the event of a rise in patients with heart-diseases is shown in Fig. 20. This is how diabetes is affected by heart diseases.

CHAPTER VI
Findings and Discussion

The main aim of this study was to illustrate the potential impact of COVID-19 on chronic illnesses like cancer, heart disease, and diabetes in the future. Two mathematical models were proposed in this regard and proved with the necessary theorems. The first model includes cancer-diagnosed and susceptible individuals, whereas the second model includes heart disease, diabetic, and susceptible individuals. The unconnected link between heart disease, diabetes and cancer is the cause for two different models.

Points and their existence proofs are identified in the analysis of the first model, which includes the disease-free equilibrium $E0,1$and the endemic equilibrium $E*,1$. Furthermore, under specific circumstances, the globally asymptotically stability quality of both points is proven. This suggests that there could be an endemic situation at point $E*,1$ and a population free of cancer disease at point $E0,1$.

Similar to the first model, the second model's analysis showed that there are two equilibrium points for it: the disease-free equilibrium point $E0,2$, and the endemic equilibrium point,$E*,2$. Given the required conditions, both points are globally asymptotically stable, indicating that the diseases could occur in either setting.

A sensitivity analysis was conducted on the parameters of both models in Section 5. The purpose of this analysis was to define how the parameters affected compartments C, H, and D. Figures 6 and 7 illustrate the impact of rising smoking and obesity rates, respectively. There will be a rise in the cancer compartment with increases in both parameters. Nevertheless, smoking has a greater impact in compartment C than obesity, even with a slight difference. Similar findings were also revealed and highlighted similar in papers Arnold et al. (2016) and Jacob et al. (2018). Since the model did not produce a significant result in this case, the figure shows $f1$, which illustrates the effect of hereditary transmission, is not provided. The population under study in this work could be the cause of this result. The effect was not visible because compartment C contains many cancer patients (rather than just one type of disease). There are a lot of research in the literature that outline the connection between a

hereditary/family history of cancer and certain cancer types. (Henrikson, et al., 2015; Murff, et al., 2004)

The expected result of increasing the effect of parameter c is displayed in Figure 8. As predicted, there will be a significant drop in cancer diagnoses as people's fear of visiting a doctor rises. Figure 9 presents the situation of the cancer compartment a with decreased *c* value. In this case, an increase is assumed again. But compared to the increase in Figure 8, this increase is substantially smaller. Figures 8 and 9 serve as global alerts regarding the COVID-19 pandemic. A greater knowledge of the issue and encouragement to schedule regular doctor's appointments are two ways to address it.

The effects on heart disease patients are shown in Figure 10 and Figure 11. The findings indicate that the H compartment will rise in response to increases in both parameters. The negative effects of smoking and obesity on heart diseases are also highlighted in papers Buttar et al. (2005) and Akbartabartoori et al. (2006).
As suggested in Fig. 12, hereditary is a significant in heart diseases. Impact of family history/hereditary on heart diseases are analyzed in papers Moonesinghe et al. (2005) and McCusker et al. (2006).

That being said, COVID19, $c1$, is the most important statistic for heart disease.
It is clear that $c1$ is an extremely important parameter for predicting future patterns in heart disease. A fall in compartment H is caused by both rises and falls in this parameter, highlighting the significance of knowledge regarding medical visits and COVID-19. Bugalia et al. discussed the spread of COVID-19 and the significance of lockdown and preventive measures. Conversely, Okyere et al. emphasized (2022) discussing the complications of COVID-19 disease on diabetes-diagnosed individuals. This study primarily focuses on how the COVID-19 lockdown affects people with cancer, heart-related diseases, and diabetes-diagnosed individuals in order to predict future outcomes for these conditions.

Figure16 and Figure 17 show the diabetes patient pattern at higher obesity and hereditary rates, respectively. Ahmad et al. examined (2023) the effects of smoking and obesity. Additionally, in this work, the authors stressed the significance of smoking and obesity in individuals with diabetes. The pattern of the D compartment rises when the

parameters are increased, but the effect of heredity, $f2$, is greater. Additionally, the

impact of COVID-19 in the D compartment is significant. Undiagnosed patients in

Figure 18 result in a fall in compartment D due to an increase in parameter

$c2$.Nonetheless, for compartment D, even with a slight fall in parameter $c2$, diagnosis

for those with diabetes will be higher (Figure 19). Figure 15 and Figure 20 serve as a warning, emphasizing the link between diabetes and heart diseases.

CHAPTER VII
Conclusion and Recommendations

Obesity is an effective parameter for the diseases under study, and a rise in it will have a negative effect on patients, according to the model's figures. Patients with cancer and heart problems suffer greatly when they smoke. For people with heart disease and diabetes, heredity is an important factor to consider. So, those who have a family history of these conditions need to make sure they attend their doctor's appointments. Furthermore, there exists a strong correlation between individuals with heart disease and diabetes. People with diabetes diagnoses should be more cautious and aware of heart diseases, as seen in Figure 15 and Figure 20.
Nonetheless, as a consequence of the COVID-19 pandemic, both models showed that the most dangerous parameter for the diseases is c, (the COVID-19 negative effect). Eventually, the research results demonstrated that a significant reduction in deaths depending on cancer, heart disease, and diabetes could occur from increased awareness of COVID-19 and its consequences. This in conjunction with regular medical visits may result in an earlier diagnosis and course of treatment for these illnesses.

The purpose of this study is to highlight how COVID-19 affects other critical illnesses. The main purpose is to show that more epidemics and even pandemics may occur in future in the case of insufficient control strategies. According to the study, one of the causes of this is avoiding routine checkups and doctor appointments due to the contagious nature of COVID-19. Being one of the strong models that addresses the COVID-19 pandemic's effects from a variety of serious perspectives, this study that is being presented has a significant role on the field of health sciences.

Healthcare institutions and policymakers should use the sensitivity analysis results to create control plans that will improve public health. Taking action against obesity is crucial because it is associated with a variety of health issues. Public awareness programs stressing the negative effects of obesity on one's health has to start right away. Furthermore, because smoking worsens cardiovascular disease and cancer patients' health, funding smoking cessation programs is essential. These campaigns could range from public awareness campaigns to providing free or inexpensive help for quitting smoking and access to local resources. Those with a family history of diabetes or cardiovascular disease may find genetic counselling to be of great assistance. During these meetings, people can find out more about the risks they face

and get advice on how to lessen those risks. Timely health checks are especially important because of the established association between diabetes and cardiovascular disease. Combining these checks with a comprehensive healthcare strategy that involves multidisciplinary teams can significantly enhance patient results. Some of the illnesses whose rates and outcomes have been greatly impacted by the COVID-19 epidemic and its aftermath are diabetes, heart disease, and cancer. Efforts to inform the public about the long-term consequences of the virus's spread are, therefore, crucial. Ensuring universal vaccinations and utilizing preventative measures can help decrease the spread of the virus and the associated health risks. However, in order to fully comprehend the extent of the virus's possible health impacts, further thorough research is desperately needed. The more precise development of public health treatments in the future depends on this knowledge. A comprehensive patient education framework that covers disease risks, symptom awareness, and the advantages of early diagnosis can help people become more ready for disease prevention and treatment. Mathematical modelling using fractional derivatives, which is anticipated to increase degrees of freedom in the choice of order of derivative, may also be a better way to characterize disease transmission that depends on memory attributes. (Zarin et al.,2023 ; Jamil et al., 2023) To effectively address the health risks and challenges that have been identified, it is necessary to foster collaborations among health organizations, government agencies, NGOs, and other relevant parties.

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Appendices

Appendix A

Turnitin Similarity Report

Thesis

ORIGINALITY REPORT

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SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

1	docs.neu.edu.tr Internet Source	5%
2	Submitted to Yakın Doğu Üniversitesi Student Paper	2%
3	Nezihal Gokbulut, Evren Hincal, Hasan Besim, Bilgen Kaymakamzade. "Reducing the Range of Cancer Risk on BI-RADS 4 Subcategories via Mathematical Modelling", Computer Modeling in Engineering & Sciences, 2022 Publication	2%

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Exclude bibliography	On		

Supervisor: Prof. Dr. Evren Hincal

18.01.2024

Appendix B

CV

AKADEMİK ÖZGEÇMİŞ

1. Adı Soyadı : Fatma Neşe Efil

2. Unvanı :

3. Öğrenim Durumu : Yüksek Lisans

Derece	Alan	Üniversite	Yıl
Lisans	Matematik	Celal Bayar Üniversitesi	Temmuz 2002
Y. Lisans	Matematik	Celal Bayar Üniversitesi	Şubat 2005
Doktora	Matematik	Yakın Doğu Üniversitesi	Şubat 2024

4. Yönetmekte Olduğu Yüksek Lisans ve Doktora Tezleri

6.1. Yüksek Lisans Tezleri: Closed Category Models of Simplicial Algebras, Doc.Dr. Ali Mutlu

6.2. Doktora Tezleri: Aggravation of Cancer, Heart Diseases and Diabetes Subsequent to Covid -19 Lockdown via Mathematical Modelling , Prof. Dr. Evren Hınçal

5. Yayınlar

7.1. Uluslararası hakemli dergilerde yayınlanan makaleler (SCI,SSCI,Arts and Humanities)

1) Hincal, E., Kaymakamzade, B., Suren, F. N., & Gokbulut, N. (2021). Estimating Covid-19 deaths by using binomial model. AIP conference proceedings, 2321(1). Doi: 10.1063/5.0040303

2) Efil, F.N., Qureshi, S., Hosseini, K., Hincal, E., and Soomro, A. (2023). Aggravation of Cancer, Heart Diseases and Diabetes Subsequent to COVID-19 Lockdown via Mathematical Modeling. Doi: 10.20944/preprints202309.1743.v1

6. Daha önce çalışılan kurum/kuruluş/şirketler

No	Kurum Adı	Görev Süresi	Ünvanı
1	The English School of Kyrenia	March 2018 – September 2023	Secondary Mathematics Teacher
2	TED İzmir College	August 2015 – March 2018	Head of the Mathematics Department
3	TED Bursa College	August 2013 – Ağustos 2015	IB Mathematics Teacher