

Understanding the Spread of Coronavirus (COVID-19) in Ireland using S-I-R Model and Logistic Growth Function



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Declaration

I hereby declare that except where specific reference is made to the work of others, the contents of this dissertation are original and have not been submitted in whole or in part for consideration for any other degree or qualification in this, or any other university. This dissertation is my own work and contains nothing which is the outcome of work done in collaboration with others, except as specified in the text and Acknowledgements.

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Abstract

The novel coronavirus, formerly called 2019-nCoV, or SARS-CoV-2 by ICTV (severe acute respiratory syndrome coronavirus2, by the International Committee on Taxonomy of Viruses) caused an outbreak of atypical pneumonia, now officially called COVID-19 by WHO (World Health Organization) first in Wuhan, the capital city of Hubei province in December, 2019 and then rapidly spread out in the whole country of China [1].

This research aims at exploring the propagation of COVID-19 using S-I-R model and the mathematical Logistic Growth Function and to understand the spread and propagation of COVID-19 in Ireland, from the date of the outbreak, i.e. 29th of February 2020 [2]. The purpose of this research is to analyse the propagation of COVID-19 in Ireland and Sweden through the compartmental S-I-R model and to forecast the same using a general growth model based the Logistic Growth Fuction, as it varies over a period.

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Chapter 1

Introduction

1.1 What is COVID-19, how did it start?

The first case of COVID-19 was found in Wuhan province of China and later spreading to Hubei and eventually it has propagated worldwide. It was declared a pandemic by WHO on 11th of March 2020 [3]. The virus spread rapidly due to its asymptotic nature and initially it was very difficult to trace the spread of the virus.

1.2 What is Epidemiology?

Epidemiology is defined as the scientific, systematic and data driven study of the distribution and determinants of health-related states and events in a specific population. One of the primary applications of epidemiology is to study and control health problems of a population [4].

To study any outbreak, it is necessary to understand how it propagates through a population. The following things need to be considered about the outbreak:

1. The time trends of the outbreak and how is the distribution of cases over time [4].
2. The general outliers or cases that are unusual compared to the overall pattern [4].
3. The magnitude of the outbreak [4].
4. The mode and pattern of the spread of the disease and its inferences [4]

1.3 Mathematical Epidemiology around COVID-19: The S-I-R Model

To better understand the spread of the novel Coronavirus, various mathematical and statistical models are being developed. The most common among these are the mathematical compartmental models.

The S-I-R model is a mathematical compartmental model used to simulate and predict the outbreak of an disease or an infection in a closed set of population. It consists of three basic components [5]-

1. Susceptible(S) - The number of people in a population who're susceptible to the virus or the infection
2. Infected(I) - The number of people already infected by the virus
3. Recovered(R) - The number of people who've either recovered or died from the virus (removed)

The model was implemented for understanding the spread of COVID-19 Ireland and is discussed in further detail in Chapter 4, the Methodology section.

1.4 The Basic Reproductive Number R_0 and What it Means

It is an important parameter for quantifying the rate of spread of virus. During the early stages of the outbreak, it is important to calculate the R_0 as it helps in determining how quickly the virus will spread throughout the population assuming there is no pre-existing immunity and every individual is susceptible to the virus [6]. It is not a rate and is just a ratio or a number to quantify how the virus is propagating [7].

In epidemiology, R_0 is defined as the mean the number of people infected by a single infected individual during his or her entire infectious period, in a population which is entirely susceptible to the infection [7].

There are three possible scenarios depending on the value of R_0 (threshold property)-

- If $R_0 = 1$, then it means that one infected individual will infect one another susceptible individual. The number of cases in this scenario will remain constant over time[8].
- If $R_0 > 1$, then it means that the infection is going to spread exponentially, and the number of cases will keep increasing over time [8].

- If $R_0 < 1$, then it means that the infection will spread very slowly and die out eventually[8].

There are many factors that influence the reproduction number. The infectiousness of the virus, the contact rate of the individuals (how many people are coming in contact with an infected individual on an average), the mode of transmission of the virus (shedding-potential of the virus), the density of the population and the initial proportion of susceptible people and the recovery or mortality rate during the time of infectivity. If the population density is higher, there will be more susceptible people, thus increasing the chances of high infectiousness of the virus, thereby leading to higher R_0 [7].

According to a study by Ying Liu and Albert Gayle, in case of COVID-19, the R_0 ranges from 1.49 to 6.49, with mean R_0 being 3.28, median being 2.79 and inter-quartile range was at 1.16 [9]. Hence, to stop the spread of virus, R_0 should be less than 1.

1.5 How is R_0 calculated?

Estimating the R_0 during for any disease outbreak is a challenge for epidemiologists. It is easier to measure the approximate R_0 during the initial stages of the outbreak provided that the data captured about the outbreak is accurate during the onset of the disease. But the initial data is often incomplete and is not recorded accurately due to lack of proper data collection systems and tools. Hence, R_0 is generally estimated in retrospect using various methods or mathematical models. Some of the approaches of determining R_0 are by using Survival Function in a non-spatial deterministic model, Next Generation method which is based on dividing the population into discrete and disjoint classes and is most commonly used in compartmental models like S-I-R and S-I-E-R. The main difference between these two methods is that while survival function gives us the total number of infected people in a same class produced by a single infected individual of that class, the next generation method gives us the mean number of new infectives per infective in any class [9].

Other methods include estimating R_0 from epidemiological data based on incidental data [7]. However, it is difficult to estimate the transmission rate. Hence it is necessary to simplify the assumptions basis the available data, thereby reducing the number of unknown parameters.

1.6 Mathematical Epidemiology around COVID-19: The Logistic Growth Model

A Belgian mathematician, Pierre François Verhulst devised the logistic function which is an important tool to model population growth and is used for binary decision making by epidemiologists, economists and statisticians [10].

Besides the above S-I-R model, the Logistic Growth Model based on the logistic function was implemented to predict and forecast the count of COVID cases in Ireland and in Dublin. The same will be further discussed in more detail in methodology section.

The main aim of this research is to explore the propagation dynamics of the novel Coronavirus in Ireland and to predict and analyze the trends using real world data, so that effective measures could be taken to curb the spread of the virus.

Chapter 2

Literature Review - Study of Existing Models

2.1 Existing Research Based on Mathematical Models

In his study, Dhanwant and Ramanathan studied the spread of COVID-19 in India using the S-I-R model. The research did a comparative analysis of Hubei and Italy, based on the hidden parameter α , which is the period between which a person gets infected and is confirmed positive. It was seen that the number of reported cases kept increasing even after the actual cases had stopped rising. The S-I-R model was developed using Python and Scipy and using a custom loss function, the value of β was calculated as 0.1 and was later used to predict the test data. Also, two additional values of β were estimated for when the lock-down was not imposed and when it was imposed by the government. The β values were found to be 0.3536 and 0.2627. It was later concluded that imposing a lock-down does help, reducing the exponential growth in controlling the spread of the virus [11].

The study also estimated the death rate related to the virus using the data of Italy. However, the model was found to have a high bias. The model concluded that despite imposing a lock-down, which slowed the growth of cases, it is necessary to observe strict social distancing measures to stop the virus from spreading [11].

In their research, Iglesias and Juez considered the outbreak of COVID-19 in Madrid, which started on 20th February 2020. The research aimed at building an experimental and mathematical simulation model to analyze the spread of the disease. It was built using the S-I-R epidemiological model and Monte-Carlo simulations were implemented to estimate the R_0 value over a period. For the analysis, the first 15 days of the outbreak were taken into consideration for building the stochastic model [12].

For calculating R_0 , sequential Monte-Carlo method was used, basis the number of infected and diagnosed during the initial phase of the outbreak. The estimated cases were then compared with the real cases and the probability of each R_0 value was calculated with 95% confidence interval and 90% confidence interval. The R_0 values were regressed against each day of the outbreak. By this method, the R_0 was estimated around 2.22(+/-1.21 S.D) and an increase of 0.093 (+/- 0.037, $p=0.025$) was estimated. The research concluded that if no PHM measures are implemented, the cases will continue to rise and the situation will be like that of Wuhan, with the R_0 increasing over time [12].

In a research related to calculating the basic reproductive number, S. Kucinkas uses the SIR model in combination with Kalman Filter to estimate R_0 from data based on new cases. The research uses the fact that in S-I-R model, the reproductive number R is linearly related to the growth rate of infected individuals. The method used in the research first used the data on new COVID-19 cases to build a time-series to estimate how many people are infected at a given time. After that, the growth rate of the same was calculated using Kalman Filter. And once the growth rate was obtained, the study uses the theoretical relationship provided by the S-I-R model to measure the reproductive number from estimated growth rate [13]. Using the baseline assumption that the serial interval for COVID-19 is seven days, the research estimated the R_0 to be 2.67(95% confidence interval, 1.96-3.44). It was also found that implementing social distancing measure and imposing lock-downs have statistically significant impact on reducing R_0 . The data used to estimate R_0 was only after the cumulative number of cases reached 100. The effective reproduction numbers (R_t) were estimated first for the worldwide data and using these estimates, the basic reproduction number R_0 was calculated. R_0 was estimated by the average value of R_t in the first week of epidemic [13].

The study found that upon imposing a lock-down, the estimated values of R_t declined substantially from 2.18 to 1.31. The research concluded that the developed real time estimator may be used to track COVID-19 dynamics [13].

In this research, J. Valentin used the Kermack and McKendrick model[14], in a two-step manner to estimate the basic reproduction number using the data of Denmark. The data included for the study consisted of the number of deaths, the number of patients in ICU and the number of in-patients. The model focused on modelling the number of infected individuals, the number of susceptible people and the number of recovered individuals. The period of infection was assumed to be 6.5 days. The research also assumed that all patients are hospitalized for 10 days. Age-stratified percentages obtained by recovered patients were used to estimate the cumulative number of deaths[15] .

Using the above assumptions, the basic reproduction number was estimated by implementing a three-parameter model. The parameters consisted of basic reproductive number in the initial step, basic reproductive number in the second step and the time of switch. The model was fit to the number of beds needed. After fitting the model, it was later projected on number of in-patient and ICU beds required and the number of cumulative deaths. It was then compared with observed data [15]. The study found the basic reproductive number was found to be 2.65 in the initial step and 1.99 in the second step. The time of switch was estimated to be 18th March 2020 (13th February 2020 was the model origin). The mean absolute error was found to be between 8.3 to 9.4 in-patient beds. The model however had some limitations regarding its assumptions. The assumed period of stay in hospital of 10 days and the assumption that 50% of the cases are asymptomatic is debatable [15].

In a similar study conducted by Aravind Lathika Rajendrakumar, the growth rate and doubling time of COVID-19 was studied in India, using crowd sourced time series data. The research also estimated the basic reproduction number R_0 using serial intervals and dependent reproductive number R_t using the data. The estimated R_0 was then compared with five different methods [16]. The research utilized the S-I-R model and modified it to S-I-R-D to consider the number of deaths basis R_0 with Sequential Bayesian Method [16]. To account for the number of deaths, the existing S-I-R model was modified as follows-

$$\frac{dS}{dt} = -\beta SI \quad (2.1)$$

$$\frac{dI}{dt} = \beta SI - (1 - \alpha) - \alpha \rho I \quad (2.2)$$

$$\frac{dR}{dt} = (1 - \alpha) \gamma I \quad (2.3)$$

$$\frac{dD}{dt} = \alpha \rho I \quad (2.4)$$

In the above set of equations, β is the rate of transmission, γ is the recovery rate, α is case fatality rate and ρ is the rate at which death occurs. For calculating β , the estimated R_0 was used. γ was estimated from infectious period – (1/infectious period). ρ was estimated as

inverse of time to death based on the available WHO reports between the range of 2-8 weeks [16].

It was observed that on an average, 2.8 individuals were infected by an index case. The average serial interval was found to be at 3.9 days. The estimated range of R_0 was between 1.43 to 1.85. The research also estimated the mean recovery time of 14 ± 5 days. The model estimated that the growth rate of India was at 0.16 and the doubling time was of 4.30 days. From these results, the research predicted that 12.5% of the population will be infected during the peak of COVID-19 cases in India, which was forecasted to be in July and early August [16].

2.1.1 Model Based on Exponential Growth

The research conducted by B. Rai, A. Shukla and L.K. Dwivedi utilized an exponential growth model to predict the cases of COVID-19 regarding to confirmed cases, recovered cases and deaths respectively. In the study, the data for a period of 21 days was considered. The developed model was later used to calculate the average reproduction number. The model predicted the number of cases to reach up to 2,49,635 till the end of April and the estimated reproduction number was found to be 2.56, with the herd immunity of around 61%. Along with this, the cumulative cases predicted by the model was 1,20,203 [17].

The research used the basic exponential growth model given by the equation, $N(t) = \alpha * \exp(r * t)$, where $N(t)$ is the number of cases at given time t , α is constant, r is growth rate and t is time of the day. The Herd immunity was estimated by the equation $HI = [1 - (1/R_0)] * 100$. The serial interval was considered as 4.4 based on earlier studies [17].

2.1.2 Model Based on Machine Learning

In this research, Ashis Kumar Das, Shiba Mishra, Saji Saraswathy Gopalan, performed prediction of community mortality risk owing to COVID-19 by using standard machine learning techniques and algorithms. Their main objective of the research was to predict the mortality of confirmed COVID-19 patients in South Korea and to deploy the algorithm that gave the best performance as on open-source online decision-making tool. The dataset used was from January 20, 2020, to April 07, 2020, and five algorithms were implemented on the dataset. The algorithms applied were: Logistic Regression, Support Vector Machine,

K Nearest Neighbour, Random Forest, and Gradient Boosting. Upon implementation and comparison of these algorithms, it was found that the Gradient Boosting algorithm gave the best performance with the area under the ROC curve at 0.966, the accuracy of 98.7%, and Matthews Correlation Co-efficient at 0.656 and Brier Score of 0.013 [18].

This algorithm was then deployed as an online tool titled CoVID-19 Community Mortality Risk Prediction tool named CoCoMoRP¹ in R-Shiny [18].

2.1.3 Model Based on Logistic Growth

In this research Bliznashki predicts the spread of COVID-19 in New York using the Bayesian Estimation method for Logistic Growth Model. The research used the Bayesian Estimation method based on posterior distributions, which was used to make predictions based on probability. To sample the four parameters of the Logistic Growth Equation model, the Random Walk Metropolis algorithm was used. The research considered three simulations using the data for New York [19].

For the first simulation, the period of first 28 days was considered starting from 4th March 2020 to 31st March. The data was standardized and was re-transformed back to the original scale, after calculating the posteriors [19].

However, the predictive distributions fail to capture the immediate true value in the first simulation, hence in the second simulation, weights were added to the data points similar to a Rectified Linear function, which linearly increases the weights being added to the data. Despite this, the results were not satisfactory as the simulation could not predict the third data point after two successive data points. For the third simulation, two new parameters were introduced called scale and df, to describe the distribution of the model's errors. This model had a relatively good convergence as compared to the previous two simulations. The third model simulation was able to make accurate predictions for short term and had much accurate interval estimates [19].

The research concludes that the model would be more accurate if provided with an extensive dataset based on new observations [19].

¹<https://ashis-das.shinyapps.io/CoCoMoRP/>

2.1.4 Similar Existing Research Models

In this work, J Guadalupe Reyes Victoria, Julio E. Solis Daun, and Leonardo D. Herrera Zuniga tried to understand and monitor the Covid-19 pandemic. The research implemented a simple, stable, and low-cost, discrete compartmental model. This model is based on a non-linear differential equation, where the parameters concerned are potential for contagion, population recovery, and percentage mortality. Their proposed equation is a modification of the classic discrete logistic method, and the conditions for deriving the results are relevant to the theory of qualitative systems. The research has used the SIR (Susceptible–Infected–Removed) deterministic model, which is based on a non-linear differential equation. The primary aim of the research was to control the spread of an epidemic. Since the research focuses only on the health and economic aspect, only the economically active population sample has been considered [20].

Although the population is closed and immigration is not permitted to prevent a resurgence of the epidemic, the discrete model predicts the presence of the epidemic's 'cyclical decreasing' rebounds until it reaches its equilibrium for some parameter values. In the case of the Covid-19 pandemic in Italy, this activity was predicted. Using the methods of non-linear dynamic systems, it was observed that a chaotic behavior existed at the beginning of the epidemic in Wuhan, China [20].

In their research on Coronavirus epidemic prediction and controlling measures, Mohammad Mehdi Pejman and Armaghan Fereidooni followed a similar approach and utilized the SIR model for the same. First, in containing the virus in different countries, the research explored the value of important factors such as quarantine, isolation, face mask, social distancing, etc. Later, a mathematical model was proposed to forecast the spread of the virus in countries viz. China, Germany, Iran, Italy, S. Korea, Spain, the UK, and the US [21].

Likewise, in this research Rajneesh Bharadwaj, a faculty of Indian Institute of Technology, developed a data-driven extrapolation model, using an exponential function to fit the growth of the virus instead of a linear fit which does not effectively fit the growth rate. Initially, the model was implemented based on three countries, Italy, Spain, and Germany, where the pandemic had reached its peak, and the growth was declining. Secondly, countries like the USA and Brazil were considered, where the peak was yet to occur. Lastly, the model was implemented in India. Upon implementation, the model was validated with the data of China and South Korea. However, the model had limitations as it assumed the population as

constant with uniformity in people's interaction. It could not predict the number of deaths or recoveries. Also, the mitigation measures were not considered by the model [22].

Tom Britton of Stockholm University, in his research, developed a simple estimation and prediction-based method. The focus of the research was to predict the number of infected people over a period. It was a general SIR based epidemic model that utilized the basic reproduction number and doubling time in the initial stage of the epidemic [23].

In their research, Darcett, Q. Wang and D. Sornette implemented a logistic growth model and did a comparative analysis of the outbreak in China and its 29 provinces. For the comparative analysis, the classical Logistic Growth Model, the Generalized Logistic Growth Model, and the Generalized Richards Model was used to predict and analyse the spreading behaviour of the virus. The study was divided into four phases based on the different stages of the outbreak. The research identified a strong co-relation between the early stage confirmed number of cases and the total number of cases with the travel index which was for quantifying the mobility aspect of the outbreak [10].

The research did a comparative analysis of countries where the outbreak was in a middle stage with that of China. It was found that the growth trajectory of the spread of the virus was much slower as compared to that of China, owing to early lockdowns and stringent health and social distancing measures in place. However, the research does not account for the re-emergence of second wave of outbreak [10].

Chapter 3

Research Introduction

3.1 Research Aims

The recent outbreak of COVID-19 across the globe has turned into a pandemic. The number of daily cases keeps on increasing with the overall count of confirmed cases standing at 10,185,374 infected cases and 503,862 deaths as of June 30, 2020, and the global number keeps on growing every day [24]. Over time, the virus has affected human life and well-being severely and is now even impacting the global economy. This research focuses on forecasting and predicting the spread of the novel Coronavirus using S-I-R Model and Logistic Growth Function.

The main aim of this research is to analyze and understand the spread of the COVID-19 outbreak using the epidemiological S-I-R model and the mathematical logistic growth function, which can help suggest necessary public health and control measure to curb the spread of the virus and assist the government in allocating the needful health and economic resources accordingly.

3.2 Research Objectives

- To identify the patterns in COVID-19 virus spread behaviour in Ireland using the S-I-R model and the Logistic Growth Model based on the logistic growth function for developing relevant control measures and strategies accordingly

- To simulate and forecast the propagation and transmission dynamics of the virus
- To compare the results obtained from both these models and analyse and better understand these models in terms of epidemiology and data analytics

3.3 Research Questions

1. How is the virus going to propagate in future and how is it going to grow in Ireland?
2. What is the number of infected people in Ireland at any given time in future?
3. At what given time in future will the curve of spread of virus flatten?
4. Does relaxation of travel restrictions affect the growth of virus and the cumulative number of cases at a given time in future?
5. Can the model predict the impact of lockdowns, quarantine and social distancing measures taken by the public health department?
6. Can the model predict the infection spread/reproduction rate basis the measures implemented?

Chapter 4

Methodology

4.1 Introduction

The research focuses on analyzing and studying the spread of novel COVID-19 virus in Ireland. A comparative study has been done considering Ireland and Sweden by implementing the S-I-R model. Furthermore, on a county level, the same model was applied to Dublin and Kildare, to understand how the virus propagated on a local level. Also, a logistic growth model was applied to study the flattening of the curve which is not considered in existing exponential models.

4.2 Data Collection and Pre-Processing

Data from multiple sources was considered for this research. For the S-I-R model, the data of daily confirmed, recovered and death cases provided by the John Hopkins University¹ was considered.

For data regarding Dublin county, the daily reported dataset provided by the Irish Government Health and Protection Surveillance Protection Centre(HSPC)² was used.

¹<https://github.com/CSSEGISandData/COVID-19>

²<https://data.gov.ie/dataset/covid19countystatisticshpscireland>

For the Logistic Growth Model, the COVID-19 public dataset was taken from Our World In Data³

The necessary data cleaning was performed by removing NaN values and the data pre-processing was done in Microsoft Excel, where a custom subsets were prepared for Ireland and county level data of confirmed cases, using the above data sources. The data sets have been included in the artefact.

4.3 Data Exploration

The initial data exploration was performed using Plotly⁴ in Python and the initial trends were observed around the propagation of the virus in Ireland. This is covered ahead in the implementation part.

4.4 The S-I-R Model

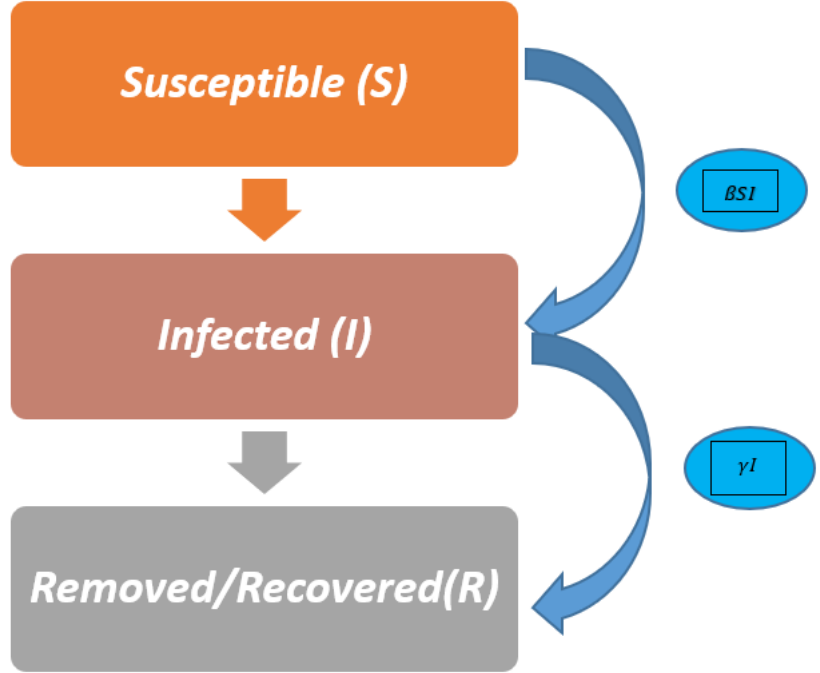
The S-I-R model was first introduced by Kermack and McKendrick in 1927 and it remains a powerful model to understand the spread and propagation of diseases and viruses in a large population [25]. It is a compartmental model in which the population is divided into three primary components, denoted by S(Susceptible), I(Infected) and R(Recovered/Removed). These three components are dependent on time and are denoted by a system of differential equations [26].

S (Susceptible) is the number of people in the population who are not yet infected. I (Infected) represent the people who are infected and are now the carriers of the disease, thereby helping in transmission of the same [26].

R (Recovered or Removed) represent the individuals who have recovered from the disease and are no longer the transmitters or carriers of the disease. This can happen if the develop a natural immunity or have lost their lives to the disease [26].

³<https://github.com/owid/covid-19-data/tree/master/public/data>

⁴<https://plotly.com/>



In the S-I-R model, after compartmentalizing the population into Susceptible, Infected and Recovered, they are described as differential equations based on time and the equations are given as follows:

$$dS/dt = -\beta SI \quad (4.1)$$

$$dI/dt = -\beta SI - \gamma I \quad (4.2)$$

$$dR/dt = \gamma I \quad (4.3)$$

In the above equations, dS/dt represents the rate of change of Susceptible individuals over time, dI/dt represents the rate of change of infected people over time and dR/dt represents the rate of change of recovered over time. The population of the region N at any given point t is $N = S(t) + I(t) + R(t)$. [26]

The parameter β is the transmission rate and is given by the average number of people one infected person will infect over a period. The underlying assumption being that the infected individual only contacts susceptible individuals. The transmission rate different for different diseases and viruses. The more infectious the disease, the higher is its transmission rate [26].

Similarly, γ is the rate of recovery. This way, we can calculate the average period during which an infected person will be infectious to the population as $1/\gamma$. The rate of infection for per unit time t can thus be given by the product of $\beta S(t) \cdot I(t)$ [26].

For the implementation, as per the above equations, the rate of transmission is given here by β , a parameter which depends on the contact that every infected individual has with a susceptible person and the probability of that individual infecting a susceptible individual.

The rate of recovery γ is the other parameter that forms the basis of the S-I-R model.

There are certain initial implicit assumptions related to the S-I-R model, which are as follows-

- The population is well-mixed, and every individual is equally likely to encounter other individual. It does not consider geographical or social proximity
- The population is homogeneous in nature and that every person in the population is like the other person, in terms of transmission of the virus
- The model does not consider birth rates and immigration of the population, and every individual of the closed population is susceptible. The only way a susceptible individual can not be in that compartment is by being infected
- The spread of the disease is exponentially distributed during the period of infection
- The population is assumed to be large enough to be articulated in terms of fractions hence it is easier to use differential equations to model

Besides this the initial conditions were defines as well. The initial conditions of the outbreak are given by $S(0)$, $I(0)$ and $R(0)$, where $S(0)$ is the number of susceptible individuals at the beginning of the outbreak, $I(0)$ is the initial number of infections and $R(0)$ is the initial number of recovered or removed individuals [27].

It is a ratio of β/γ and is known as basic reproduction number, denoted by R_0 . It is defined as the average number of susceptible individuals infected by an infectious person during the infectivity period of the disease [26].

After estimating the values of β and γ based on the real world data, along with the initial values the epidemic curve of a COVID-19 in Ireland is predicted using the S-I-R model.

4.5 The Logistic Growth Model

The Logistic Growth Model is a mathematical model that uses historical data to fit the prediction curve and depends primarily on the growth rate and the population dynamics. It describes the dynamic evolution of a population P which is the number of infected people based on the growth rate ' r ' and the capacity of the population ' K ' [28].

The rate of change of P with respect to time is given by the equation-

$$dP/dt = rP(1 - P/K) \quad (4.4)$$

During the initial stages of the outbreak, the growth of the population tends to follow an exponential curve as the term $(1-P/K)$ tends to be close to 1. But as the population increases, the growth rate slows down as it becomes effective instantaneous growth and is given as-

$$r_e = r(1 - P/K) \quad (4.5)$$

In more general term, this is also known as the 'flattening of the curve', in case of COVID-19 [29]. The above equation has time as a continuous quantity. However, in real world, the number of infected cases for COVID-19 are recorded daily. This makes time as a discrete quantity, hence we need to modify the above equation as follows-

$$P(t+1) = R_0 * P(t)[1 - P(t)/K] \quad (4.6)$$

Here, $P(t)$ and $P(t+1)$ are populations on each successive day. R_0 is the growth rate, which is like the basic reproduction number as discussed earlier and it is estimated at the initial stage of logistic growth. K is the population limit.

Upon plotting the above equation as a function of time t , the above equations display a sigmoidal curve which can be denoted by the equation –

$$R_e = R_0 [1 - P(t)/k] \quad (4.7)$$

where R_e is the effective reproduction rate at given time t [7].

As it has been discussed earlier in the literature review, the exponential models are not suitable for prediction and forecasting in later stages of the outbreak, as the growth tends to slow down, and the curve flattens. Hence to tackle this, the logistic growth model was implemented to forecast the eventual decline in the count of cases when the curve flattens.

4.6 L-BFGS-B Algorithm for Optimizing Parameters of S-I-R model

It is an extension of the BFGS algorithm for solving non-linear optimization problems with bounds. Based on the gradient projection method and related closely to the BFGS method, it is a very efficient algorithm for huge scale problems unlike the BFGS algorithm. L-BFGS-B is a Quasi-Newton method of optimizing a function and is based on approximation of inverse Hessian of the objective function $F(x)$. The main advantage of Quasi-Newton methods is that it is not necessary to adjust all hyper-parameters of the function [30].

It is an affordable algorithm for computing very large-scale problems as it is very efficient in terms of memory requirement and solves large scale optimization problems in a short span of time. However, it does get computationally expensive for larger datasets [31]. L-BFGS-B is an iterative algorithm which iterates through stages to minimize the function x in R^n which is bounded by constraints $l \leq x \leq u$, where l is the lower bound and u is the upper bound [31].

This algorithm was used to estimate the parameters for the S-I-R model and the implementation was done using the `Scipy.Optimize`⁵ function in Python.

4.7 Minimizing Mean Squared Error for Calibrating The Logistic Growth Model

For calibrating the Logistic Growth Model after fitting it to the real data, the mean squared error was minimized to estimate the parameters of the Logistic Function.

It is used to quantify the errors. The deviation of values predicted by the model to the actual values is squared, since there is a possibility that the positive and negative error values might cancel each other out. Hence then the mean of the squared errors is used to evaluate how well the model has fit the data.

4.8 R2 Score for Evaluating The Model Performance

R2 score is used to measure how co-related two variables are. It is a statistical value that depicts the ratio of variance of the dependent variable to that of the independent variable. While co-relation is used to measure the relationship between two variables, R2 score of a model gives the measure of how the variance of one variable will explain the variance of other variable. It is calculated by the following formula [32].

$$R2Score = 1 - \text{UnexplainedVariation} / \text{TotalVariation}$$

Generally, R2 score of 100% is considered to be a good. But it depends on the model and in what context the score is calculated [33].

⁵<https://docs.scipy.org/doc/scipy/reference/optimize.minimize-lbfgsb.html>

Chapter 5

Implementation and Results

5.1 Data Exploration using Plotly

After importing and loading the global data from John Hopkins University, a new dataframe was created using Pandas to create a subset of data related to confirmed cases, recovered cases and death cases in Ireland. The same was aggregated to plot and visualize the trends. After doing an initial observation of the confirmed cases curve, it can be seen that the curve is sigmoidal in nature, and hence the decision of using a Logistic model to forecast and fit the curve for prediction was considered.

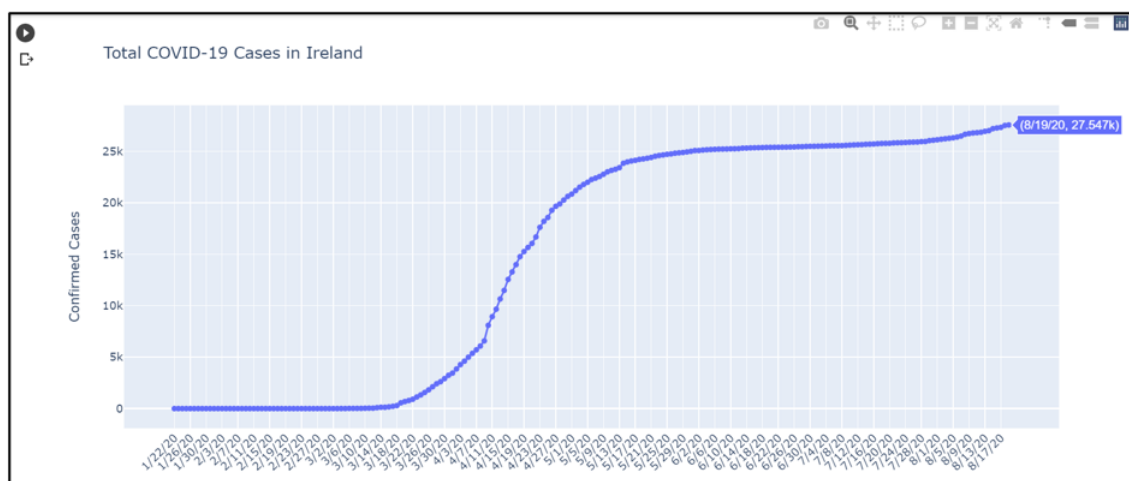


Fig. 5.1 Total Confirmed Cases in Ireland

A similar visual analysis was done for recovered and death cases. It can be seen from the graph of recovered cases that there had been an initial delay in the recording the number of recovered cases.

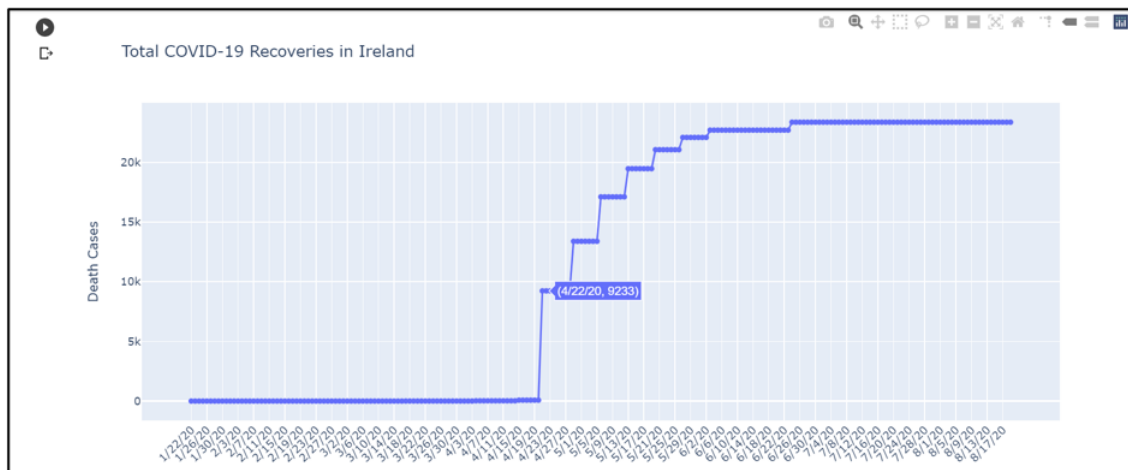


Fig. 5.2 Total Recovered Cases in Ireland

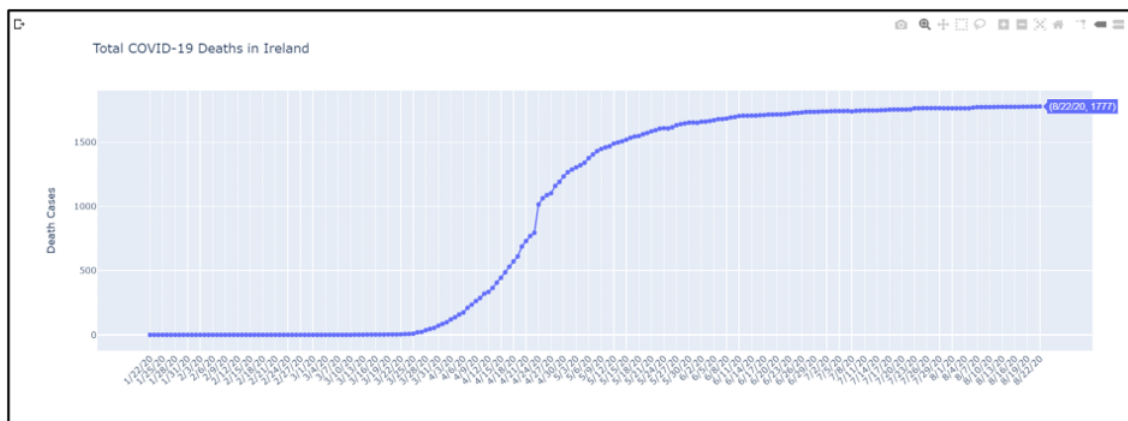


Fig. 5.3 Total Covid Deaths In Ireland

The mortality rate of Ireland is 6.367, with a total of 1777 people succumbing to the virus as of 22nd of August.

To understand the total active cases, the actual death cases and recovered cases were subtracted from the total number of confirmed cases and the same was plotted as shown in the figure below.

Confirmed	Deaths	Recovered	Active	Incident_Rate	People_Tested	People_Hospitalized	Mortality_Rate
27908	1777	23364	2767	565.191			6.36735

Fig. 5.4 Exploratory Analysis For Ireland

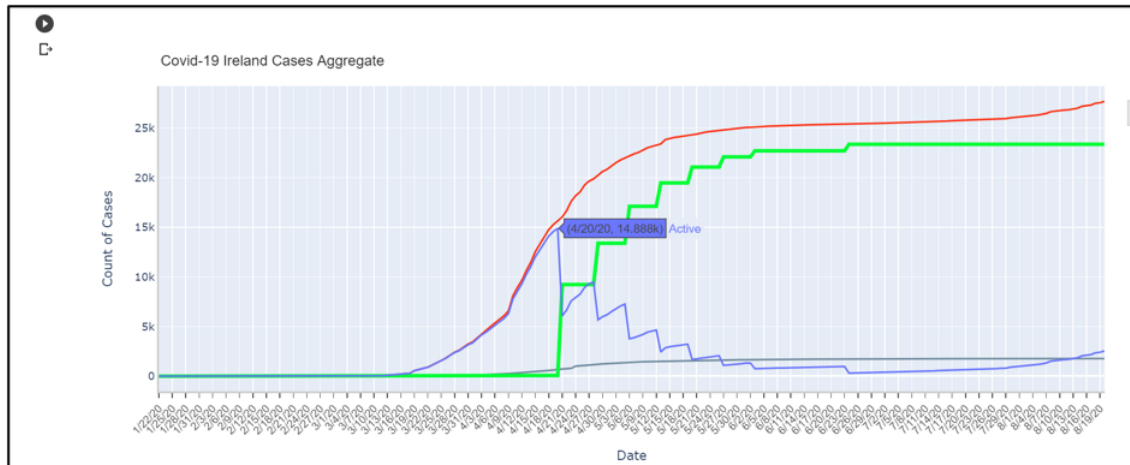


Fig. 5.5 Aggregate Plot of COVID-19 cases in Ireland

5.2 Implementing S-I-R Model for Ireland and Comparing it with Sweden

To further visualize and simulate the spread of Coronavirus in Ireland, the S-I-R model was implemented for Ireland. To estimate the parameters β and γ the data of actual cases was used. After estimating the β and γ values, to train the model, it was then fit to the count of confirmed cases to using the 'L-BFGS-B' optimizer method.

Root Mean Squared Error was used to reduce the loss function and while simulating the model, the initial susceptible was population of Ireland was set at 10000. The reason for setting the initial population at 10000 was that for higher populations, the simulation took longer time to execute. The following figure shows the results generated by the simulation-

It can be seen that the simulation model performed well during the initial phase of the outbreak but during the later stages it didn't give satisfactory results as the actual cases kept rising. The reason for this might be because the initial susceptible population was set at 10000. The following graph depicts the model simulation for first 40 days of the outbreak-

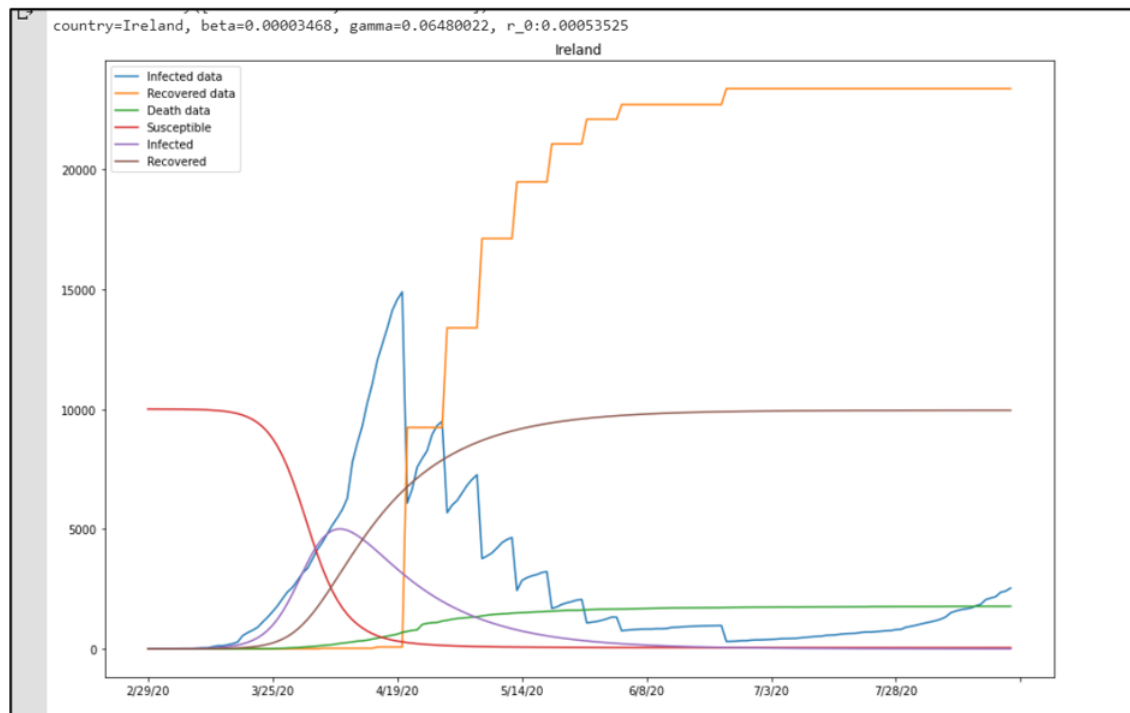


Fig. 5.6 SIR Model Simulation for Ireland

The model was fairly good in approximating and predicting the confirmed case numbers for first 40 days and upon calculating its R^2 score, it was 0.9695 (for the first 40 days)

However, the R_0 value of 0.000512 calculated by the model was much smaller than that of real world value of the reproduction number in Ireland, which is close to 1.

This may be due to the optimizer not being able to find the global minima and satisfactorily estimate the initial transmission rate parameter β and the recovery rate γ . Also, in case of Ireland, there has been an initial delay in reporting the number of daily recovered cases, as it was seen above from the graph.

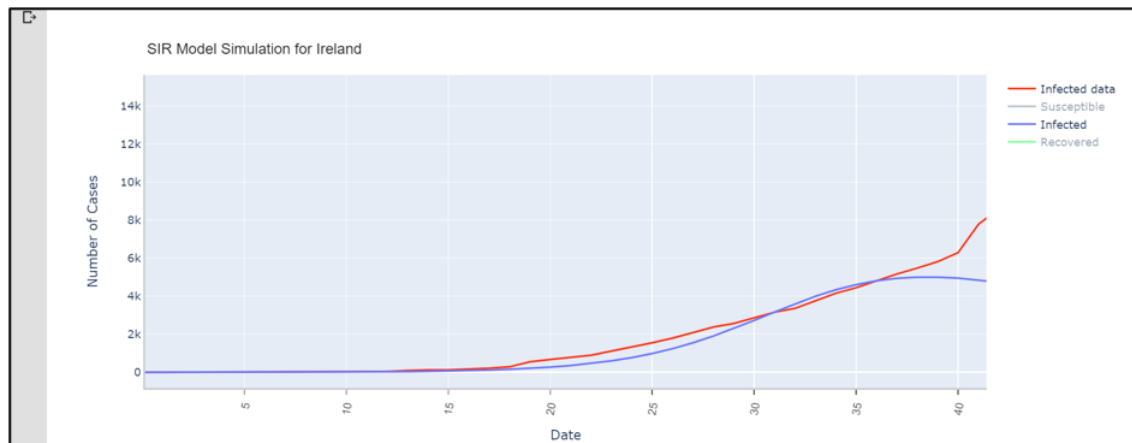


Fig. 5.7 SIR Model Simulation for Ireland for first 40 Days

5.3 Simulating the S-I-R Model for Sweden for Comparison

Unlike Ireland, Sweden did not impose a public lockdown during the course of the outbreak [34]. Upon simulating the S-I-R model for Sweden, the model gave a very high R_0 value of 15.87. The initial susceptible population was kept the same at 10000, however, the date of outbreak was changed to match the actual recorded date of the first infected case. The following figure shows the same.

Similar to Ireland, the model was fairly successful in predicting the trends of the initial stages of the outbreak. The following figure shows the model visualization during the first 80 days of the outbreak in Sweden.

Sweden's policy of no-lockdown has negatively affected their economy and even led to more people getting infected [35]. This shows that imposing a lockdown and necessary social distancing restrictions do play a crucial role in curbing the growth and spread of the virus and reducing the basic reproduction number of the virus.

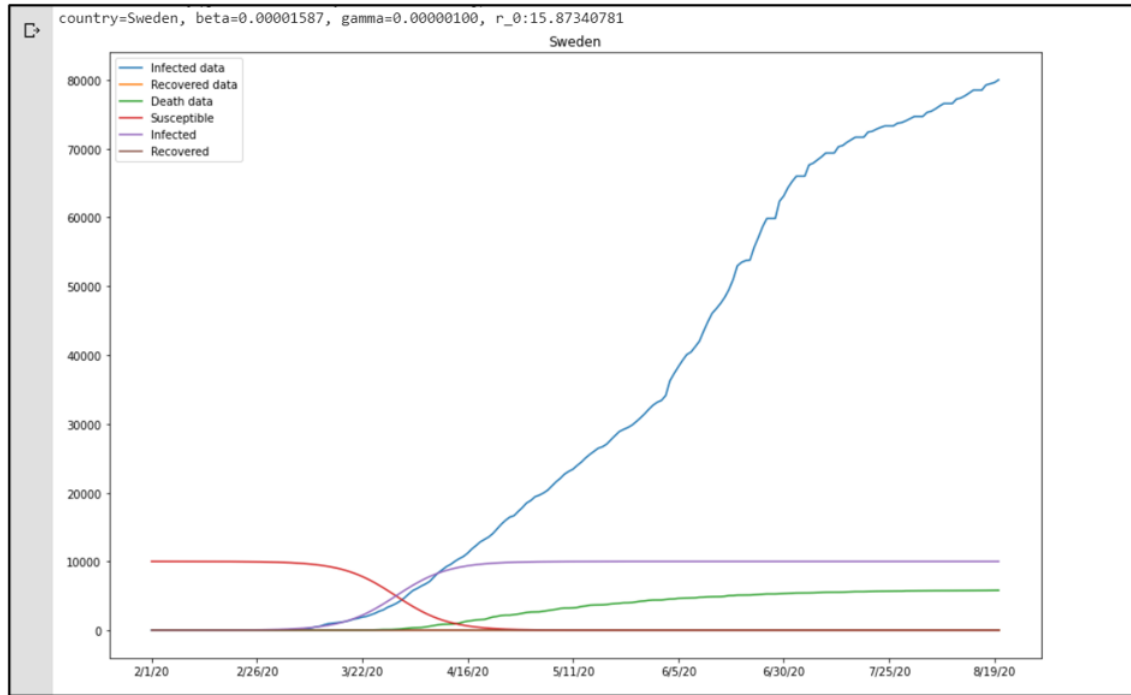


Fig. 5.8 SIR Model Simulation for Sweden

5.4 Implementing Logistic Growth Model for Ireland

To further analyze and forecast the propagation behaviour of the virus in Ireland, the Logistic Growth Model was implemented for Ireland to forecast the growth of the outbreak and to further predict the spread of the virus.

As discussed earlier in equations (1.4), (1.5) and (1.6), the logistic function has a sigmoid curve and the total number of cases at a certain time ' t ' can be denoted by $C(t)$. Social interaction among the people in a given population has been a driving force behind the rapid spread of the virus. Social actions such as shaking hands or being in close proximity of infected individuals of a population, lead to the rapid transmission of the virus from those infected individual to the healthy individuals. The encounters between infected individuals and healthy individuals of a population can be denoted by ' r '. There is a possibility that every encounter with an infected individual might turn out to be risky and lead to the healthy individual contracting the virus. This probability of this encounter infecting a healthy individual is given by ' P ', the proportion of population which will be infected.

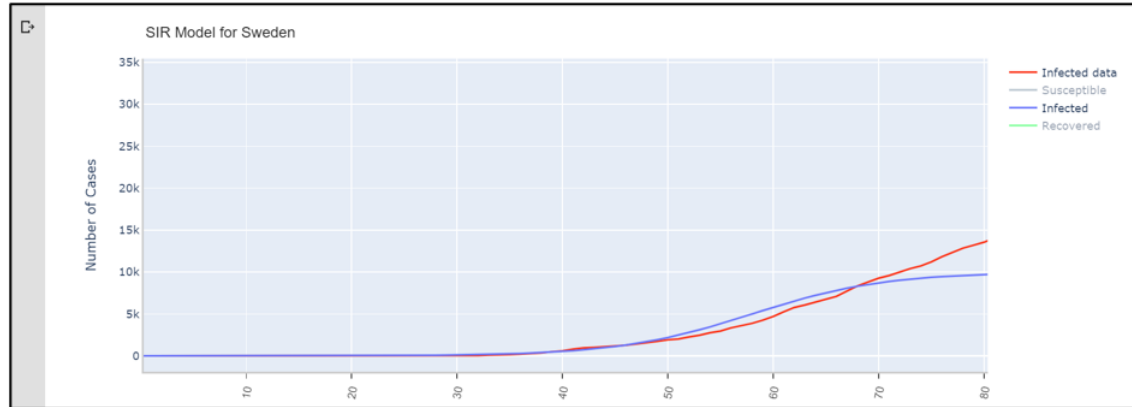


Fig. 5.9 SIR Model Simulation for Sweden for the first 80 days

So, according to this model, the total number of new confirmed COVID-19 cases on any given day ' t ' is denoted by the product of the expected contacts between infected individuals with people, the probability of contracting the virus during contact with an infected individual and the total number of cases . i.e. $r * P * C(t)$

Thus, the total count of confirmed cases on the following day will be $C(t + 1) = C(t) + r * P * C(t)$

For the implementation, the model considers some initial assumptions. The first assumption is that the population of the region is fixed and doesn't consider new births or influx of the population. Also, as the count of cases increases, the probability of contracting the virus will gradually decay. It can be given as $P = (1 - C(t)/K)$

Thus, upon implementing the Logistic Growth Model for Ireland, the logistic growth model was fit by minimizing the squared mean of errors. The population of Ireland was considered as 4.86 million and the dataset of confirmed cases up to 23rd of July, 2020 was taken into account while fitting the model. The following figure shows the model fitted using the dataset-

It can be seen from the above graph that the model fitted to the actual data gave a good R2 score of 0.9992.

The model predicted that the number of total confirmed cases and new cases will decrease in the month of August. The following plots visualize the same.

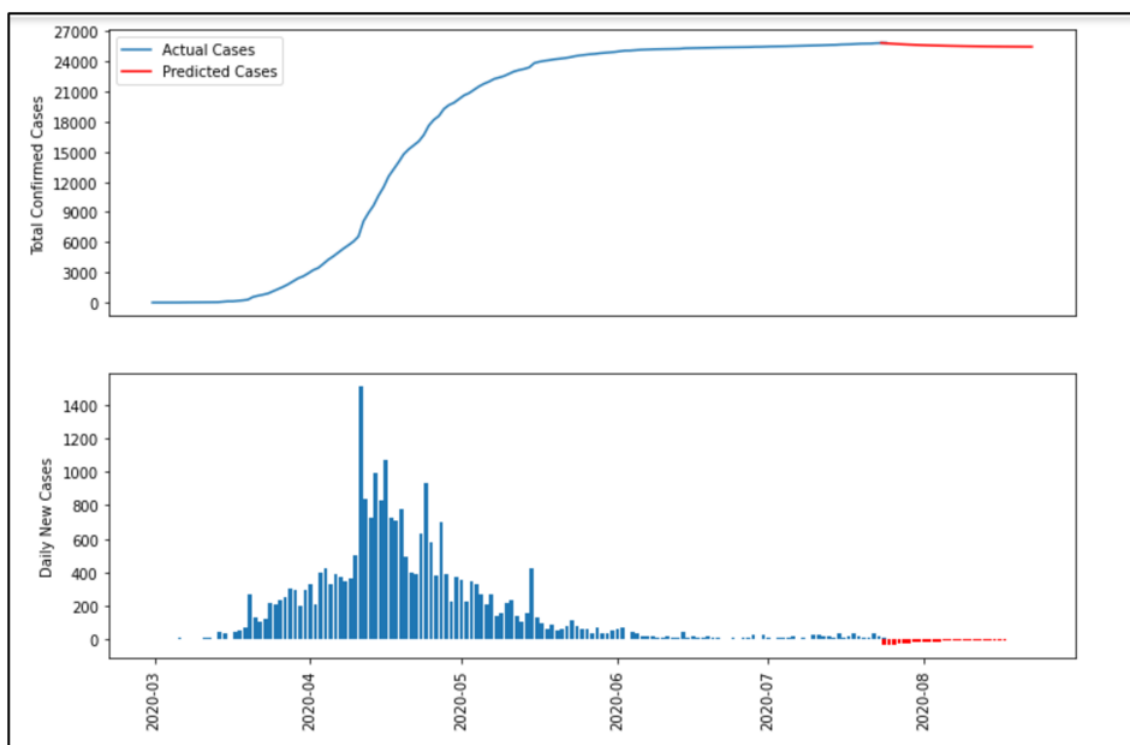


Fig. 5.10 Logistic Model Simulation for Ireland for Total Cases and New Cases

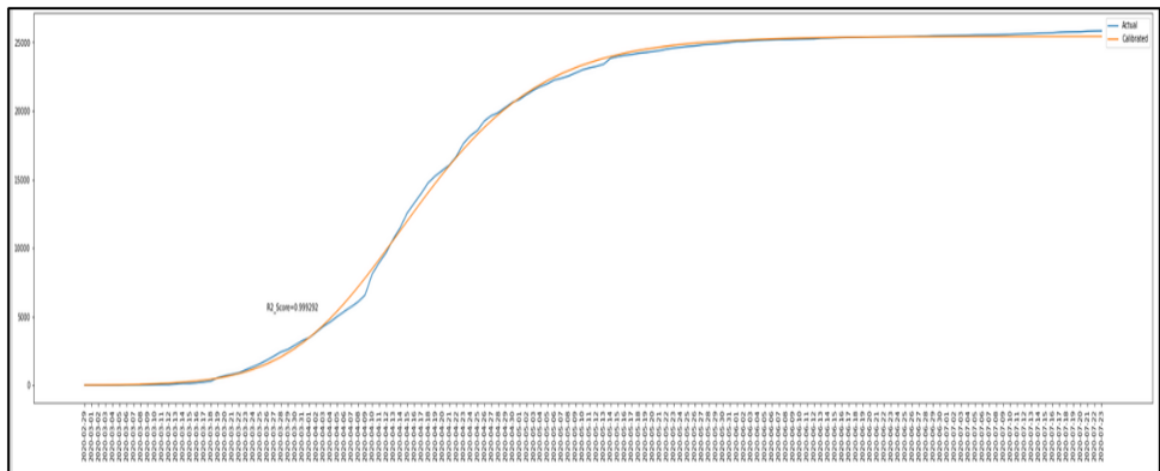


Fig. 5.11 Logistic Model Simulation for Ireland

It is evident from the above figures that Ireland reached the peak number of confirmed COVID-19 cases in mid April. However, the cases started to decline in the following months owing to an efficient lockdown and social-distancing measures in place. The model predicts that the trend will continue and the number of cases will continue to drop, if the current restrictions are in place and people continue following the basic hygiene etiquettes and social distancing protocols.

5.5 Implementing The Models For Dublin and Kildare

To further analyze and forecast the spread of COVID-19 on a local level, the above logistic growth model was applied to Dublin and Kildare counties, respectively.

For Dublin, the R2 score was 0.9826 and the model was a good fit for actual data. Also, the model predicted an overall drop in total cases and new cases.

Similarly, the model was applied to Kildare and the following graph shows the overall propagation trend of the same- It can be seen that the model has predicted an overall decrease in the number of total confirmed cases and new cases.

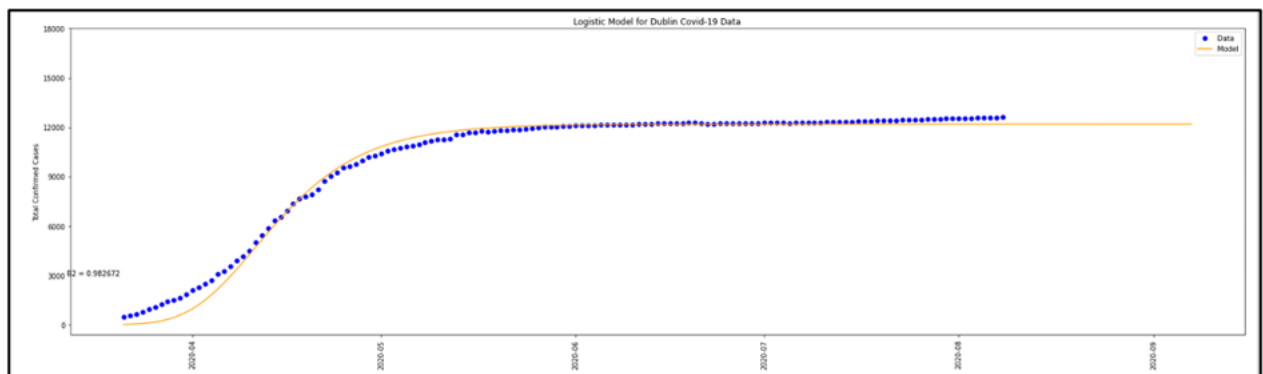


Fig. 5.12 Logistic Model for Cases in Dublin

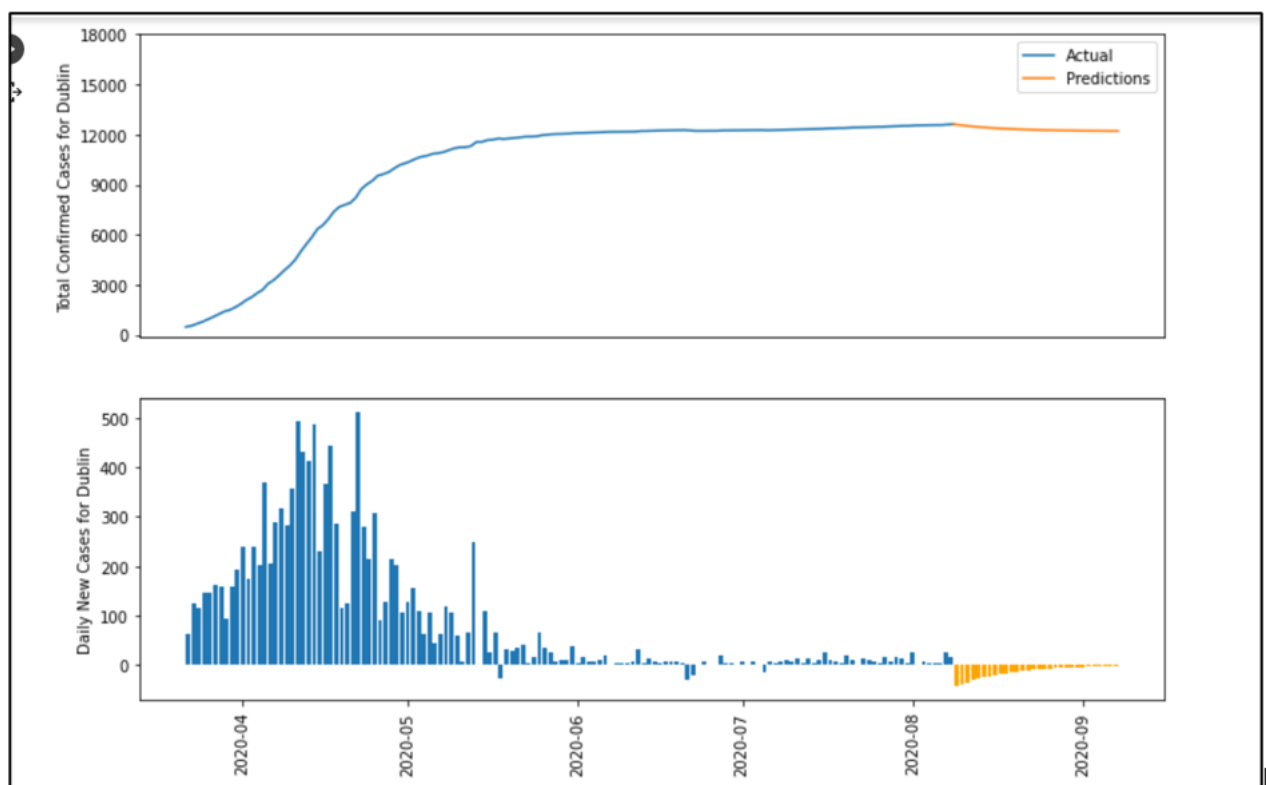


Fig. 5.13 Model Predictions for Total and New Cases in Dublin

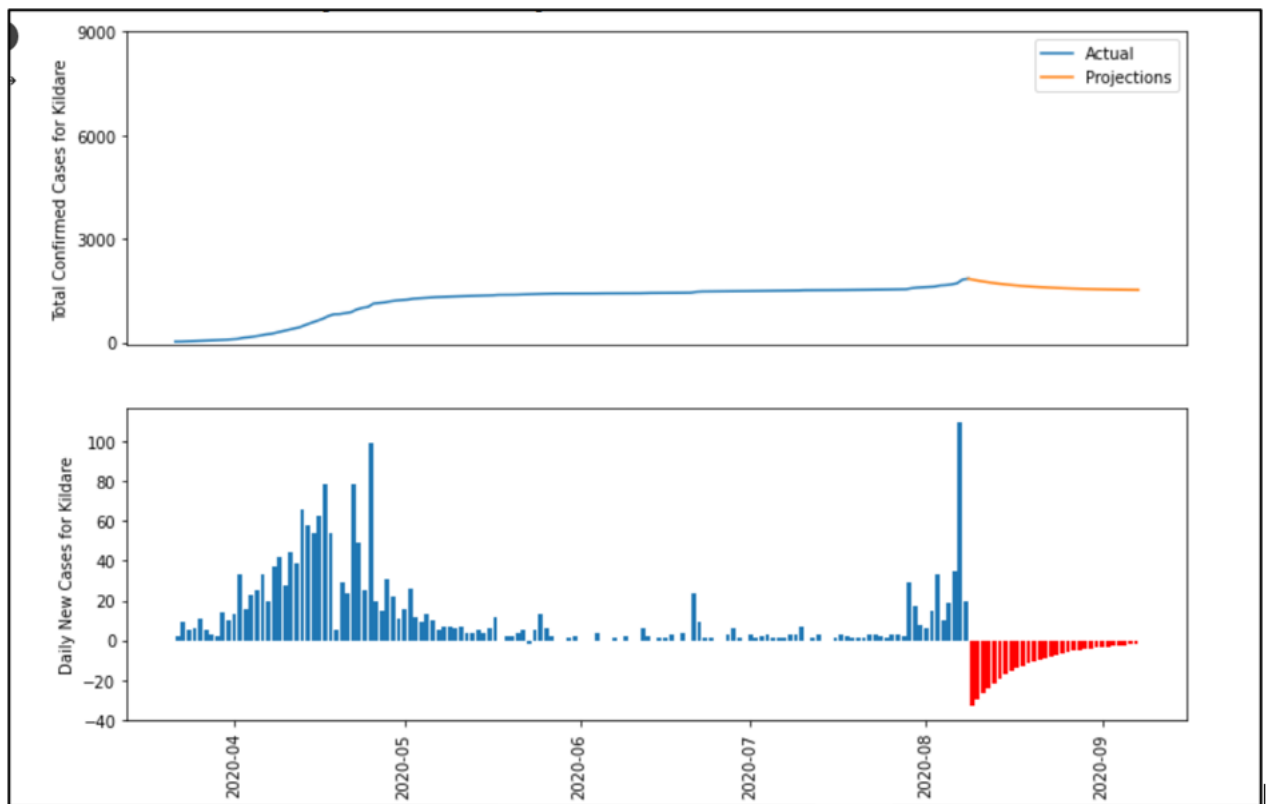


Fig. 5.14 Model Predictions for Total Confirmed Cases and New Cases in Kildare

Chapter 6

Conclusion

The primary purpose of this research was to analyse and understand the spread and behavioural trend of the novel COVID-19 virus in Ireland. Basis the implemented S-I-R model and the Logistic Growth Model, it can be concluded that both these models have been able to simulate and predict the propagation trend of the virus at various stages of the pandemic.

The S-I-R model performed well during the initial phase of the outbreak and successfully identified and simulated the beginning phase of the virus (from 29th February 2020 to mid-April, when the cases started to rise in Ireland, and the epidemic curve was at its peak). However, in later stages of the outbreak, the model did not give satisfactory results. This reason for this might be that only a proportion of population was considered during the simulation (10000 people) and due to data limitations and delay in reporting of recovered cases, the recovery rate parameter was impacted, thereby affecting the estimation of the basic reproduction number estimated by the model.

To overcome this issue, I implemented the Logistic Growth Model, calibrating it on the actual data, to understand the nature of the virus during the advanced stages of the outbreak. The Logistic Growth Model was more successful in fitting the model to Ireland data accurately with an R2 score of 0.992. The same model was implemented for Dublin and Kildare, to examine the transmission of the virus on a more localized level and to understand the later stage of the outbreak, which involves the curve flattening stage of the virus.

It can be concluded that imposing lockdowns and social distancing measures do play a vital role in slowing down and curbing the spread of the virus. The comparative analysis of Ireland as compared to Sweden is evident that relaxing restrictions can lead to a higher

reproduction number R_0 and thereby leading to a steep increase in the total number of confirmed cases. The Logistic Growth model predicted an overall decrease in the cumulative number of confirmed cases and new cases.

Chapter 7

Discussion and Future Scope

Modelling an outbreak or an epidemic is a challenging and interesting task for epidemiologists and data scientists alike. For a model to make accurate predictions, it is necessary that it is good at estimating the parameters of the function. And most of the times, they are very dynamic in nature. For example, the rate of transmission β for the S-I-R model may determine the approximate number of individuals an infected individual may encounter in a population of susceptible people. However, to quantify it accurately as per the real-world dynamics is very difficult. The transmission rate continues to change in real world during the pandemic however while modelling a deterministic model like S-I-R, it is constant. The data limitations do affect the performance of the model. The enhanced versions of the S-I-R model do consider for factors like exposure rate and re-infectivity of recovered individuals, but even they have their own limitations basis the assumptions.

To overcome this problem and to examine the virus behaviour in later stages of the pandemic, the Logistic Growth Model was implemented to visualize and predict how the virus will spread in Ireland. Also, the existing research around exponential models depict that these models are not able to approximately forecast the flattening of the curve, during the later stages of the virus outbreak.

At the time of writing this thesis, the number of cases in Ireland have started to rise again with some new clusters being formed and counties like Kildare and Offaly going back into lockdown [36]. Despite the model having predicted an overall decrease in the number of total confirmed cases and new cases, it does not satisfactorily quantify for the various human and environmental factors involved in the spread and that is a huge challenge in any

epidemic modelling. The period for the data on which the model was calibrated for Ireland was from 29th February 2020 to 23rd July 2020. Ireland had started reopening phases of lockdown from 8th of June 2020. And by the start of first week of July, majority of travel and commercial restrictions were lifted [37]. This explains the model's inability to account for the re-emergence of cases (second-wave) and the spike in the reproduction number of the virus.

Therefore, it can be concluded from the research that is necessary for governments to continue their efforts to ensure that proper social distancing protocols and hygiene measures are followed by the people in order to slow down the spread of the virus and to keep the reproduction number in check, i.e. it should be less than 1, to put an eventual end to the spread of COVID-19 virus in Ireland. The primary purpose of epidemic modelling is to understand the initial trends about the spread of the virus or a disease in a population, so that effective decisions about health measures and precautions can be taken by the governments and the important decisions related to allocation of public healthcare and economic resources can be taken rationally for the welfare of the people.

Furthermore, the further road-map for this research would be to explore the non-linear dynamics of the spread of the virus can be explored to identify if the propagation displays a chaotic behaviour. And if so, what impact does it have on the existing deterministic and stochastic models related to studying the transmission behaviour of the virus.

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