UNIVERSITY OF
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MATHEMATICAL MODELLING PROJECT

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ABSTRACT

The deadly coronavirus is still spreading over the world, and mathematical models can be used to display suspected, recovered, and deceased coronavirus patients, as well as the number of persons who have been tested. Researchers are still unsure whether surviving a COVID-19 infection confers long-term immunity, and if so, for how long. We believe that this research will help us better predict the spread of the pandemic in the future. By combining isolation class into a mathematical model, we are able to depict the dynamical behavior of COVID-19 infection. The model's formulation is proposed first, followed by a discussion of the model's positivity. The suggested model's local and global stability, which are dependent on the basic reproduction, are presented. The suggested model is solved numerically using the SIR Model approach. Finally, several graphs of the results are shown.

Keywords: Covid – 19, Epidemic, Logistic Growth, Logarithmic Growth, Normalized Data, SIR Model, Stress theory, Kinetic Equations, Crowd Effect

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INTRODUCTION

Mathematical models are useful for understanding how an infection behaves when it enters a population and determining whether it will be eradicated or not. COVID-19 is currently causing enormous concern among researchers, governments, and the general public due to the high rate of virus transmission and the large number of deaths that have occurred. Coronavirus, which was first reported in Wuhan, China in December 2019, is an infectious disease caused by a newly discovered coronavirus. COVID-19 is spread mostly through droplets that are produced when an infected person coughs, sneezes, or exhales. These droplets are too heavy to float in the air and fall to the ground or other surfaces swiftly. Coronavirus swiftly spread across the globe causing millions of people to be infected and many people have lost their lives.

We have taken 3 Countries (Italy, Germany, and Turkey) to study how the virus spread across the population. Death, Recovery, and Infection rates are the essentials for SIR model.

We have downloaded the dataset from the website: https://covid19.who.int/info/ which contains the population of new cases, new deaths, cumulative cases, cumulative deaths.

CHAPTER 1

In the modelling of an epidemic, it is important to studying the underlying processes and factors that affect the behavior of the model. In this chapter, we study how the output of the model gives us an insight into the prevalence of the disease and its effects over time.

The countries chosen to be studied in this model are Italy, Germany, and Turkey.

Cumulative Cases

Figure 1.1 shows graphs of cumulative cases. We have represented cumulative cases in millions and observed a long interval up to the 70th day after which the cases rise drastically. The graph line of each country varies considerably. From the graph, we have noticed that Turkey started its first wave later, but the number of cases is higher when compared with Italy and Germany. Italy and Germany have similar wave until 300 days from the beginning of the pandemic. This data is demonstrated over an interval in time from 03.01.2020 till 20.09.2021.

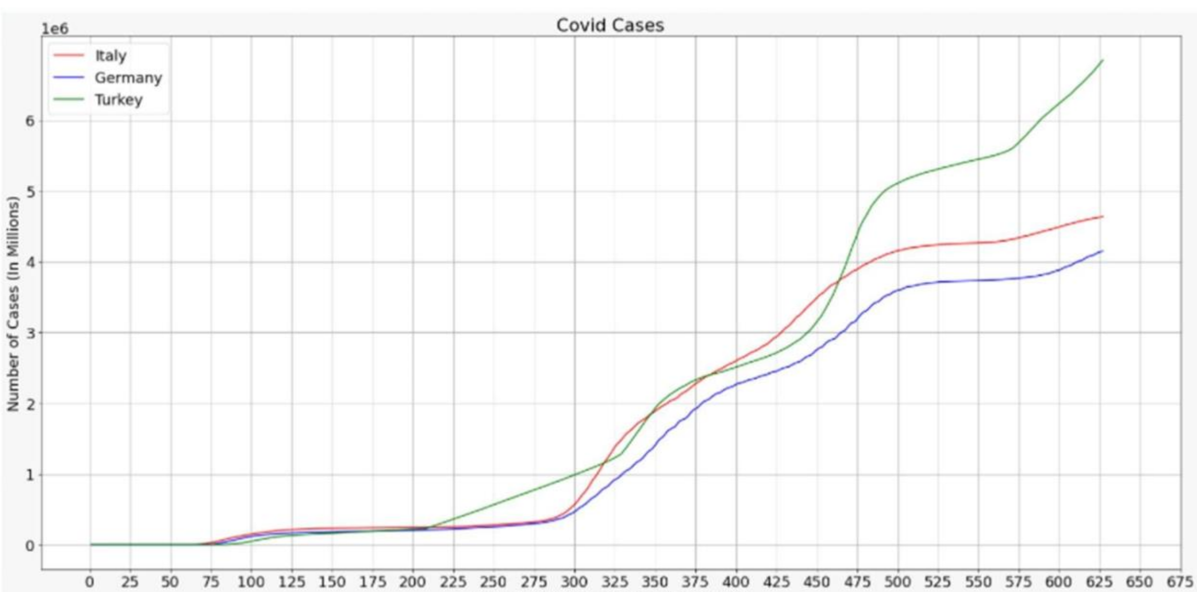

Figure 1.1. Raw Data of Italy, Germany and Turkey showing number of cases

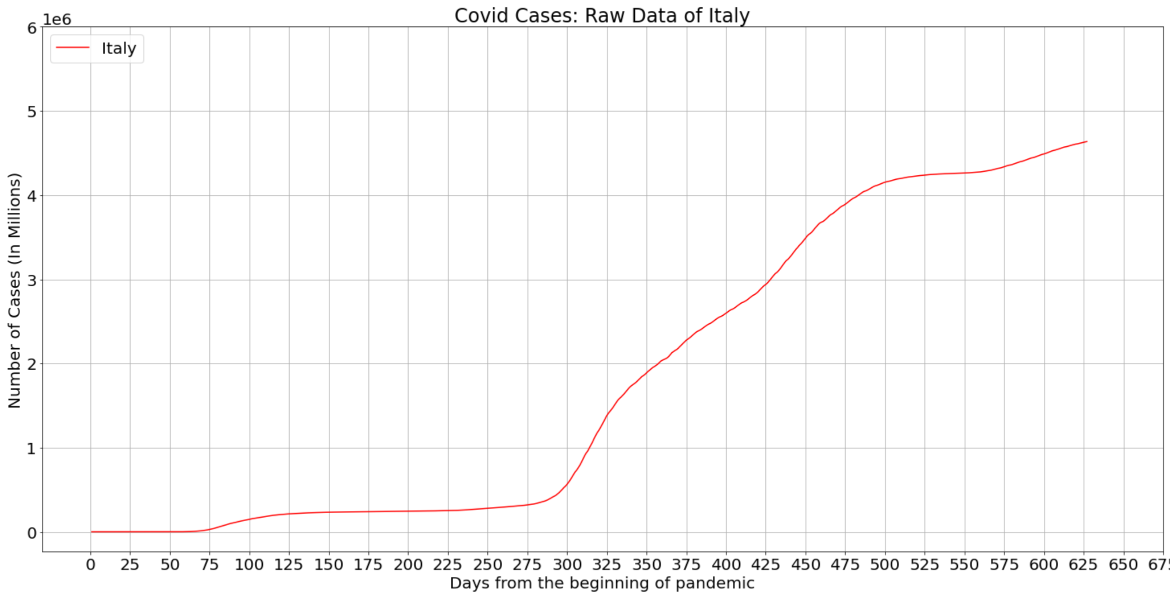

Figure 1.2. Raw Data of Italy

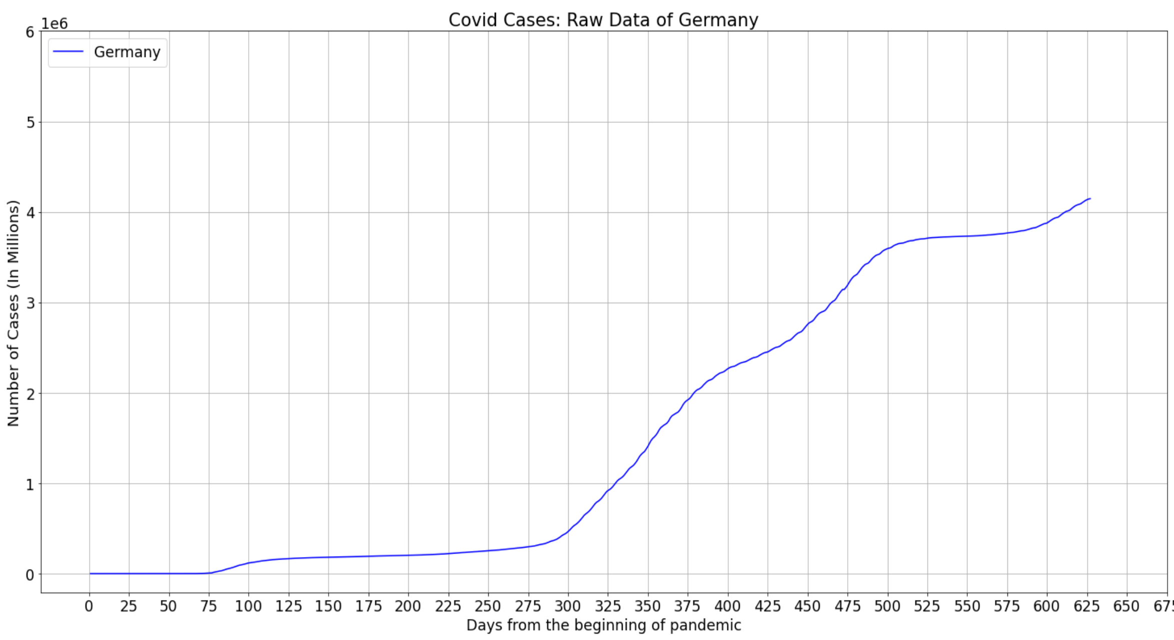

Figure 1.3. Raw Data of Germany

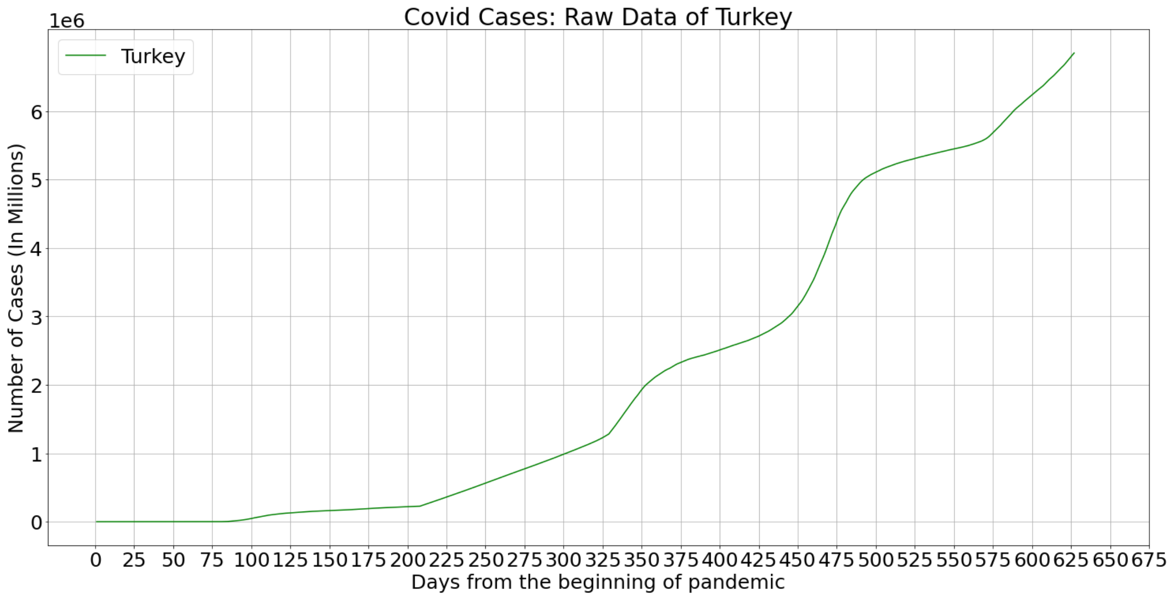

Figure 1.4. Raw Data of Turkey

We have decided to mark 50 cumulative cases as the beginning of Covid-19 for each country. The population of each selected country is significantly higher from this value but appears fair enough from zero to confirm it is not zero.

Based on this value, we have identified 23/02/2020 as beginning of epidemic in Italy with 79 cases, 29/02/2020 for Germany with 57 cases and 18/03/2020 for Turkey with 98 cases. The individual graphs of raw data for each country are demonstrated in Figure 1.2 – 1.4 above. The waves of each country are clearly visible and easy to understand, however we can truly understand and analyse them when compared with each other in a single graph (Figure 1.1).

We have found population of each country in 2020 through a Google Search and also, we have compared our search results with population available in the website: https://www.worldometers.info/world-population.

The Population of Italy is 59.55 million, the population of Germany is 83.24 million, and the population of Turkey is 84.34 million.

We will now consider cumulative fraction of infected population, we calculated cumulative fraction by dividing cumulative cases with Population of each respective country. Graphs of cumulative fractions are presented in Figure 1.5 below.

From the graph below we can clearly see that Germany has less cumulative fraction of population compared to other two countries, but however we can see that Germany and Italy do not have major difference in their infected population, but Turkey has significant raise in the cumulative fraction of infected population.

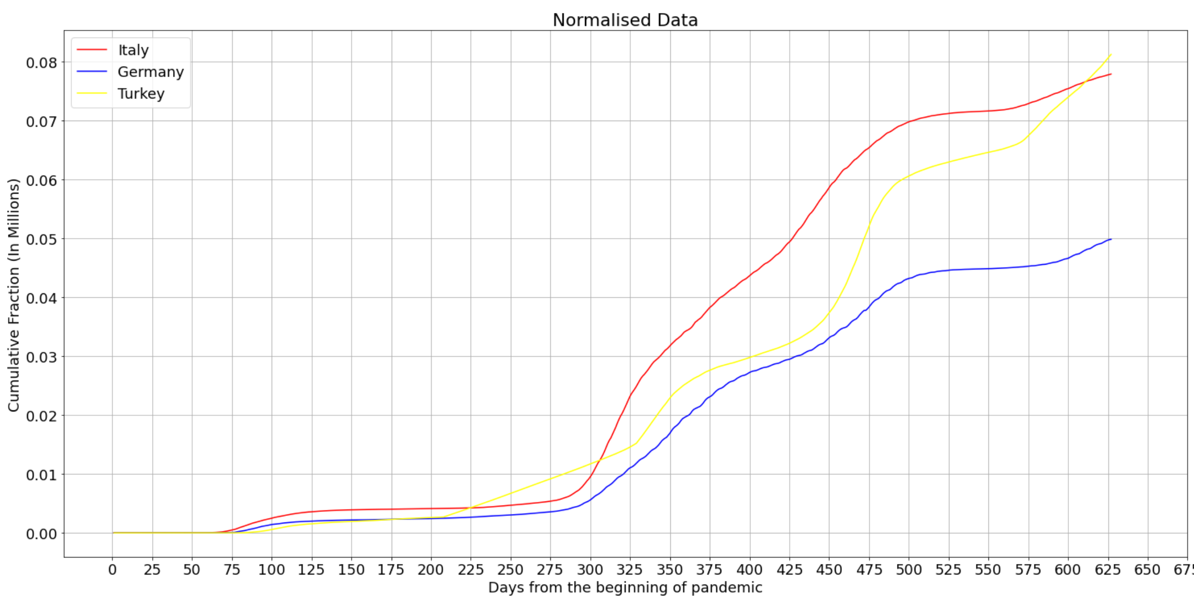

Figure 1.5. Cumulative Fractions (Normalization of Cumulative Case)

We have considered splitting of waves using one of the heuristics i.e., Straight line fragments on logarithm graph.

First, let us consider the logarithm graph of Italy (Figure 1.6 below)

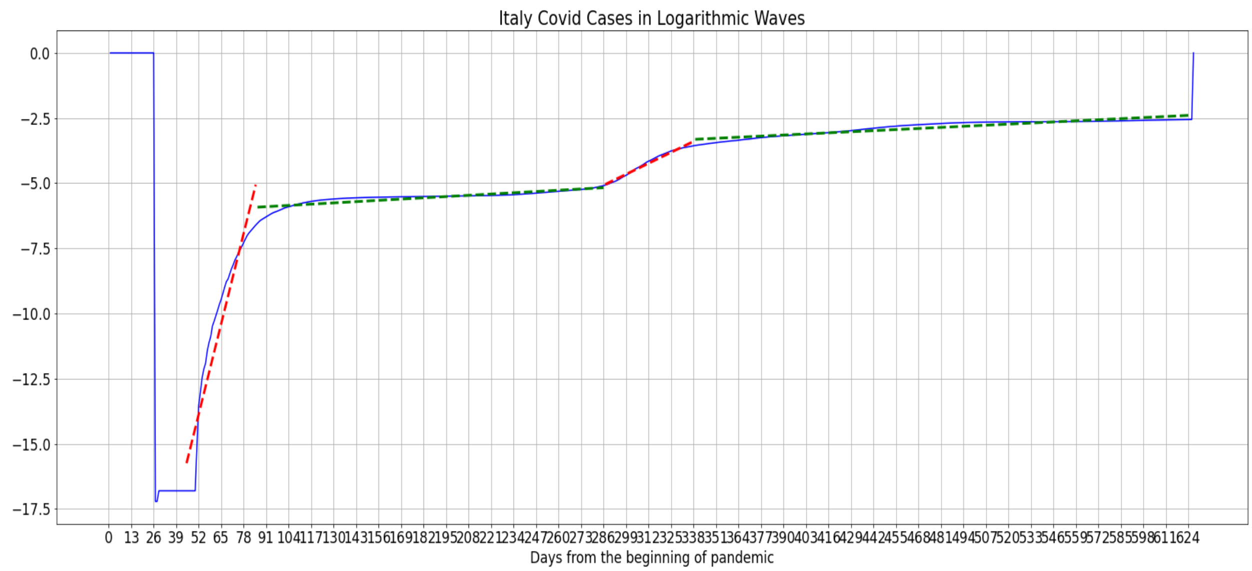

Figure 1.6. Straight line fragments of log graph of Italy's Data

In Figure 1.6, we observe a good approximation of the logarithmic data in four straight line fragments for the data from Italy. The first interval is exponential grows of the first wave from 51 to 85 (the first red line). The second interval from 81 to 286 (the first green line) is a fragment of the saturation of the logistic grows during the first wave. The third is a fragment of the exponential grows of the second wave from 287 to 330 (the second red line). Finally, the fourth interval from 331 to 620 (the green line at the end) is a fragment of the saturation of the logistic grows during the second wave.

Now let us consider the logarithm graph of Germany

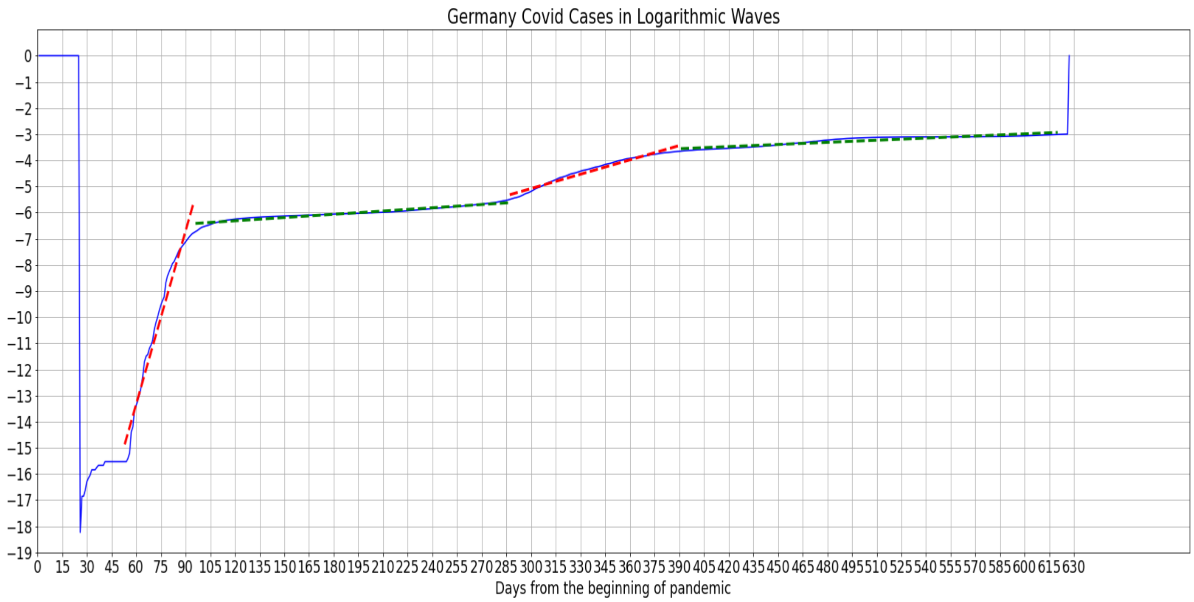

Figure 1.7. Straight line fragments of log graph of Germany's Data

In Figure 1.7, we again observe a good approximation of logarithmic data in 4 fragments each with the same depiction as Italy. For the best fit, we have found that the first "wave" is from 52 to 286 and the second wave is from 287 to 620. The exponential growth intervals and saturation of the grows are clearly visible in this graph. However, in the second wave we notice that the exponential growth has a slope smaller than its saturation fragment.

For Turkey, we have graph presented in Figure 1.8. We can see 5 fragments of the graph. The fragments are as follows:

1. 70 – 104 is the exponential growth of the first wave.
2. 105 – 207 is the fragment representing the saturation of the logistic grows.
3. 208 – 351 is the first fragment of exponential growth of second wave
4. 352 – 468 is the second fragment of the exponential growth of second wave.
5. 469 – 626 is the saturation phase of the second wave.

Therefore, we can select the first wave from 70 to 207 and the second wave from 208 to 626.

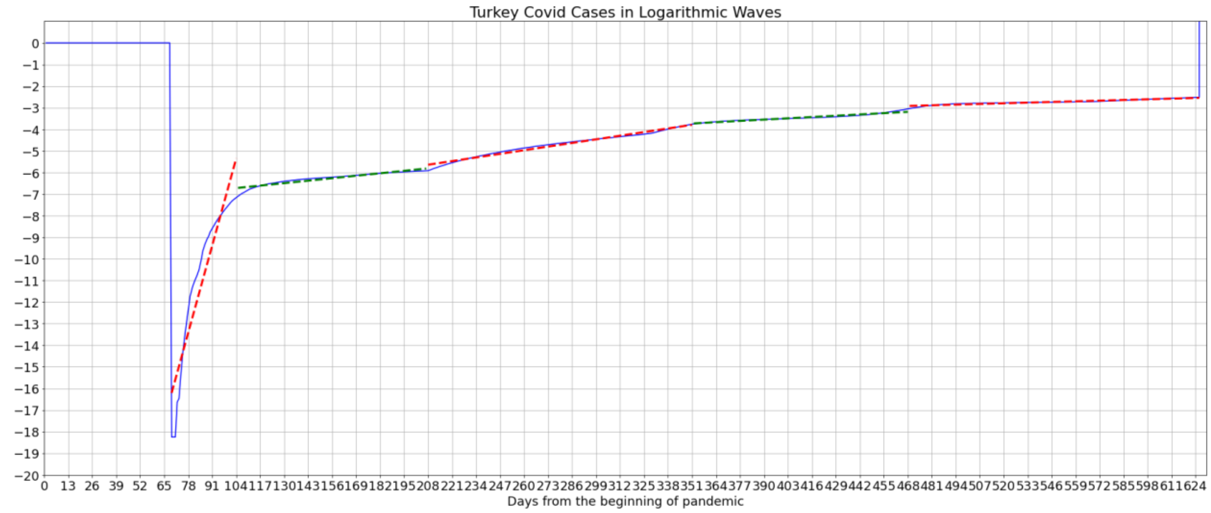

Figure 1.8. Straight line fragments of log graph of Turkey's Data

Italy

We have taken the data of first wave take as is. For the second and further waves, we subtracted the value at the last point of previous wave from the data. The graphical representation of logarithms of first wave and second wave is shown below:

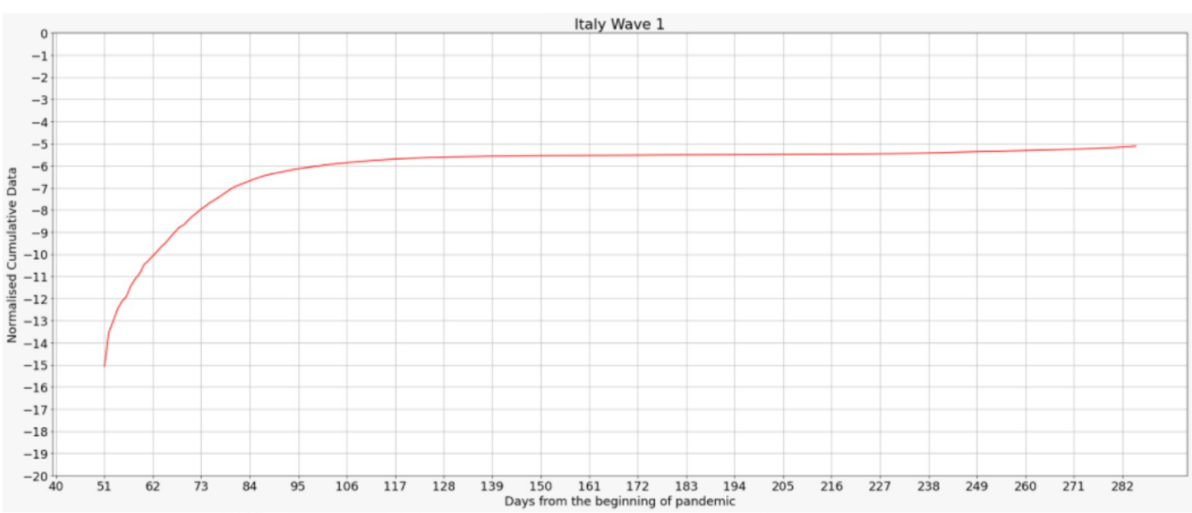

Figure 1.9. Logarithmic Graph of Italy's 1st Wave

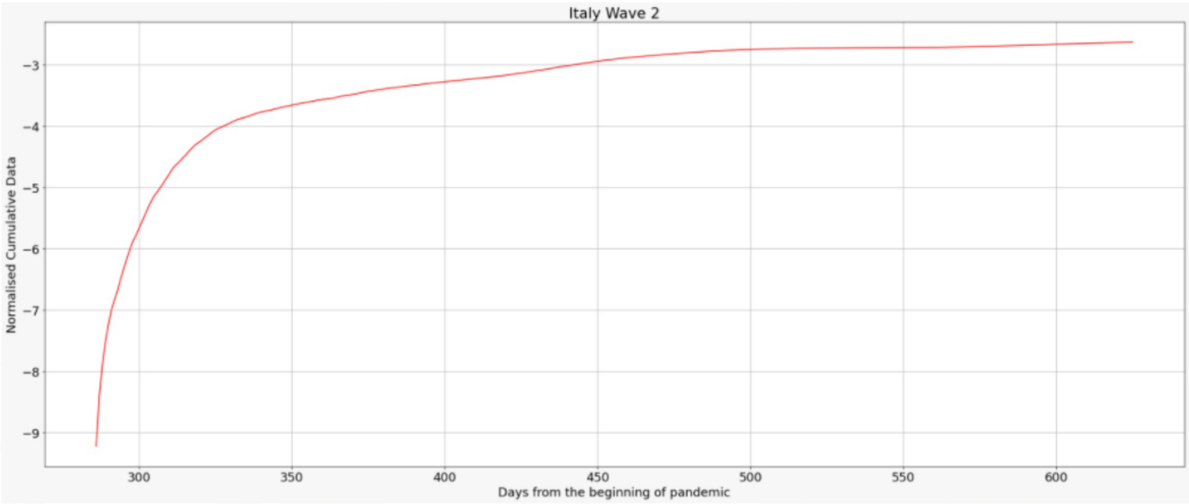

Figure 1.10. Logarithmic Graph of Italy's 2nd Wave

Germany

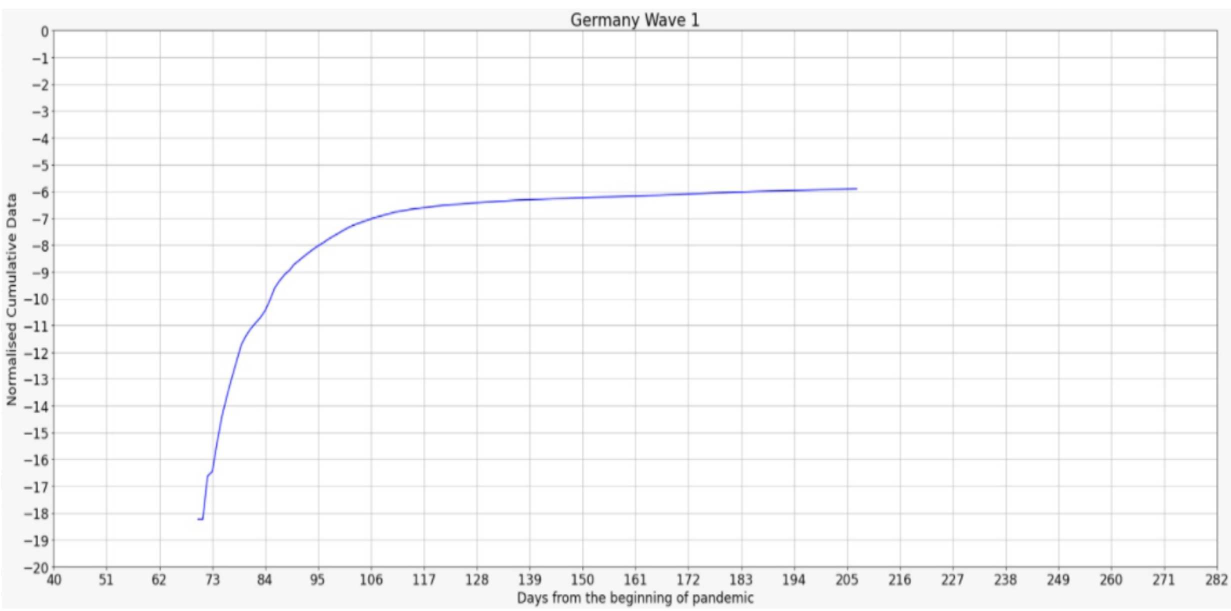

Figure 1.11. Logarithmic Graph of Germany's 1st Wave

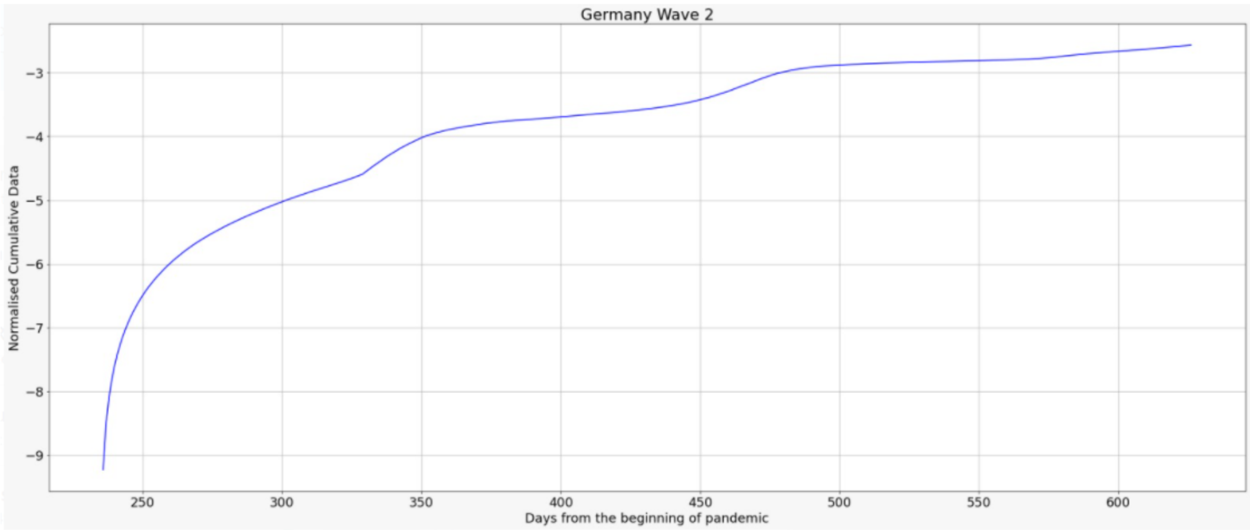

Figure 1.12. Logarithmic Graph of Germany's 2nd Wave

Turkey

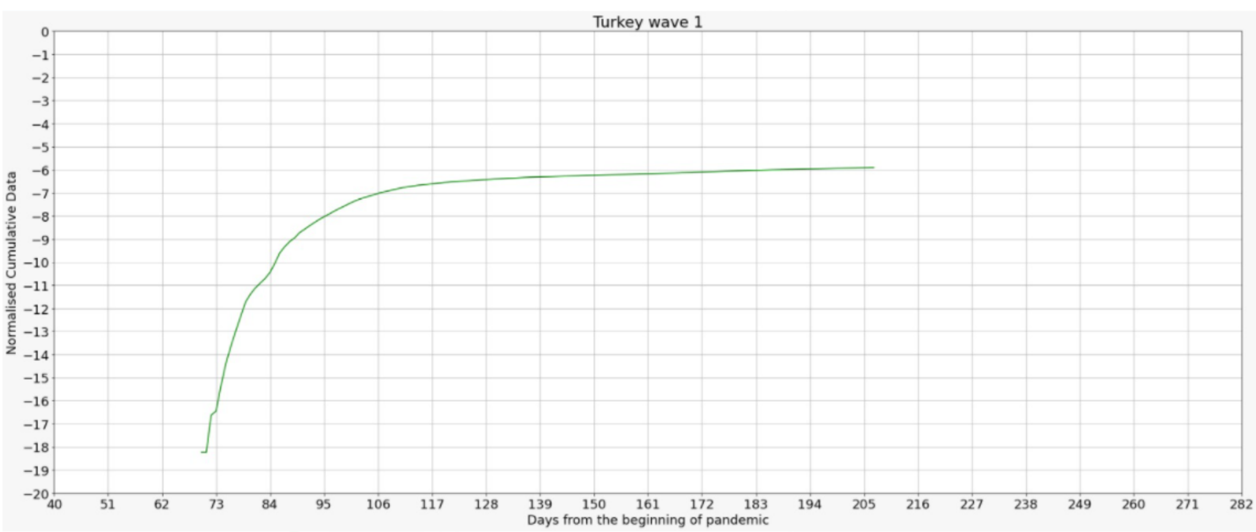

Figure 1.13. Logarithmic Graph of Turkey's 1st Wave

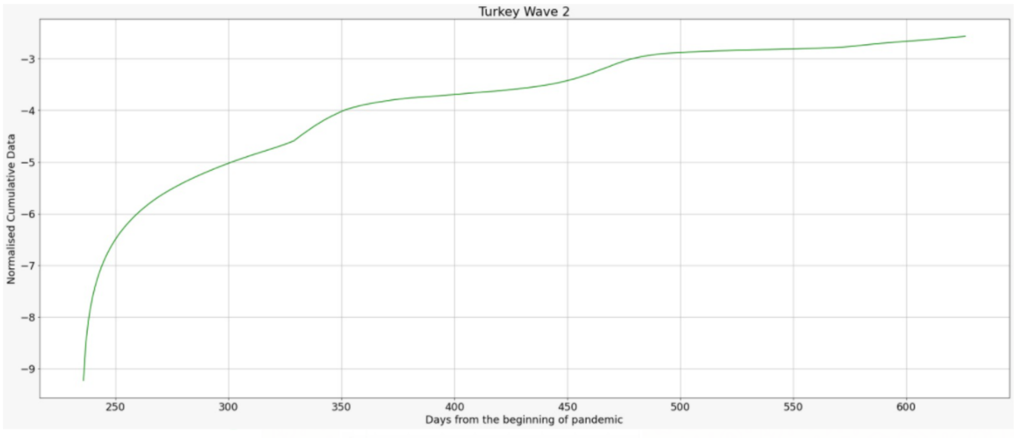

Figure 1.14. Logarithmic Graph of Turkey's 2nd Wave

Exponential Growth and Error

We have calculated the value of r and a using Polyfit function in Python which applies Linear Regression model on x and y values to give us the slope and intercept of the best fit line.

Italy:

First Wave: r = 0.01091888168966061, a = -7.008587461306366

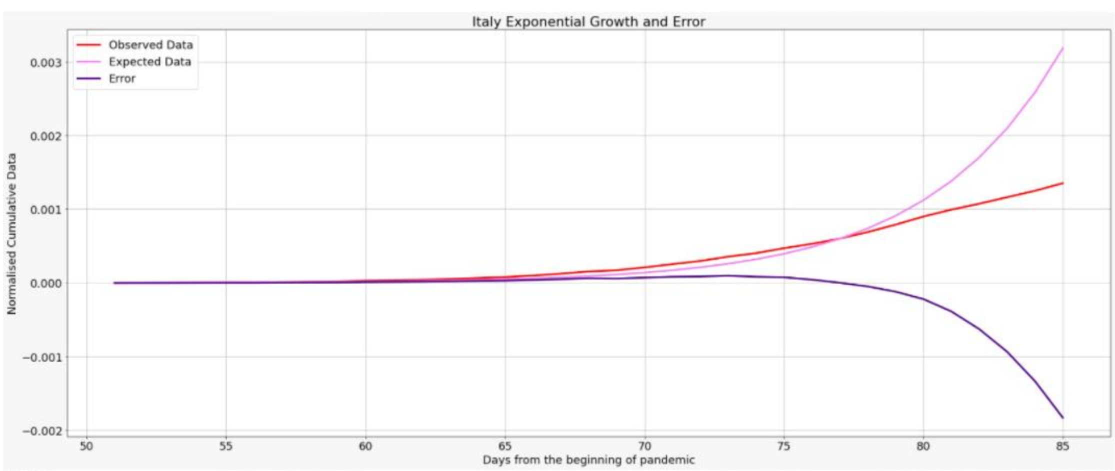

Figure 1.15. Italy's Exponential growth and Calculated Error for Wave 1

Similarly, a = -23.50340956721675, r = 0.20886596086806555 for second wave

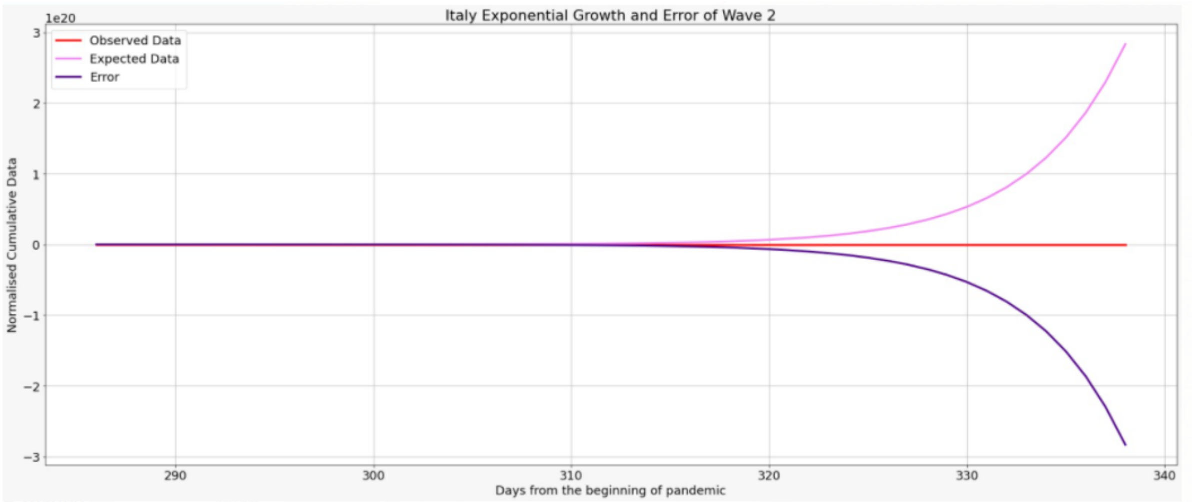

Figure 1.16. Italy's Exponential growth and Calculated Error for Wave 2

. ***Germany*:**

First wave: r = 0.2564971350815188, a= -28.902586472370114

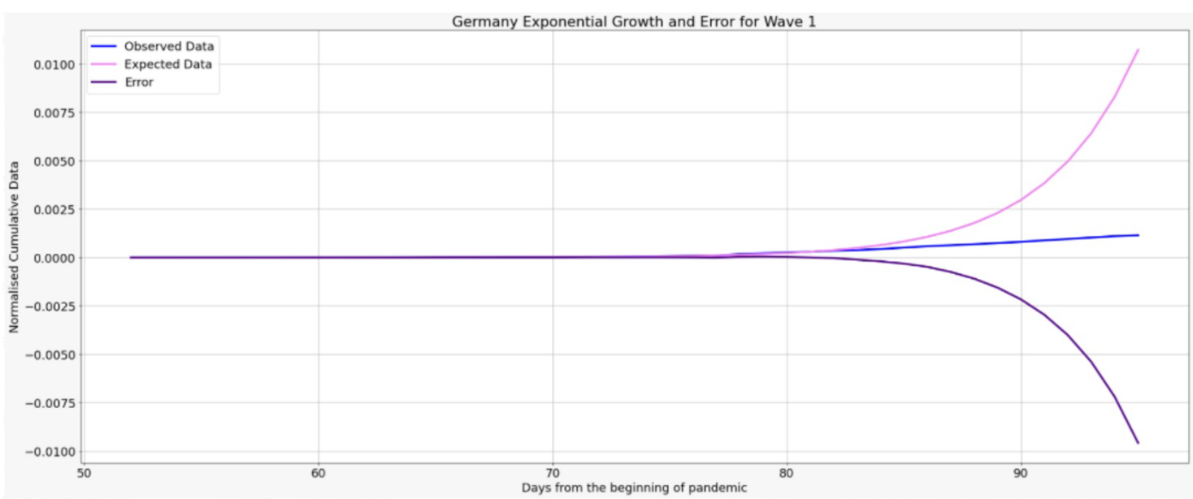

Figure 1.17. Germany's Exponential growth and Calculated Error for Wave 1

For Second wave, r = 0.011928612540211183 & a = -9.036841668012746

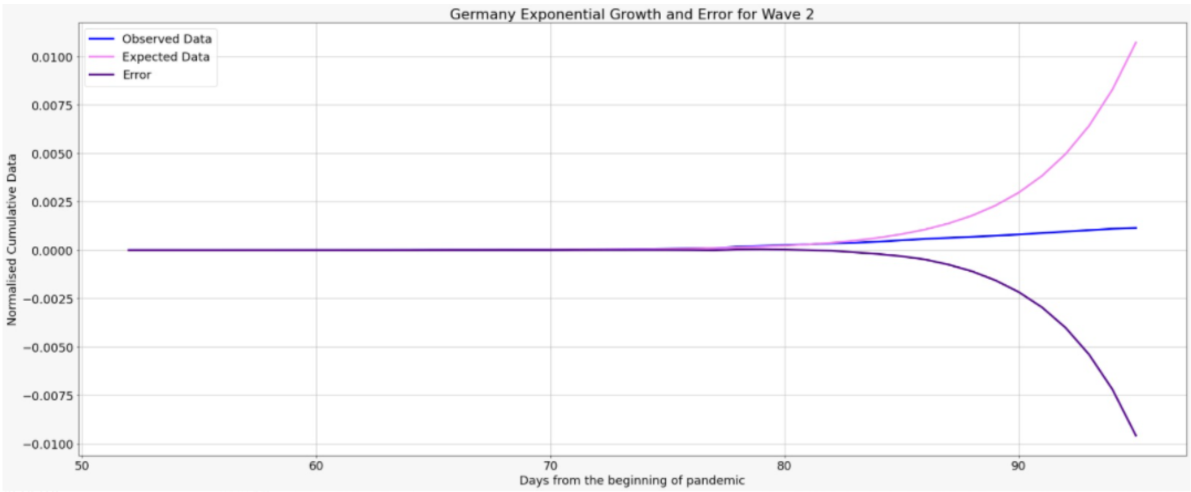

Figure 1.18. Germany's Exponential growth and Calculated Error for Wave 2

Turkey:

First Wave: r1 = 0.30909601512020407, a1 = -37.38870402286964

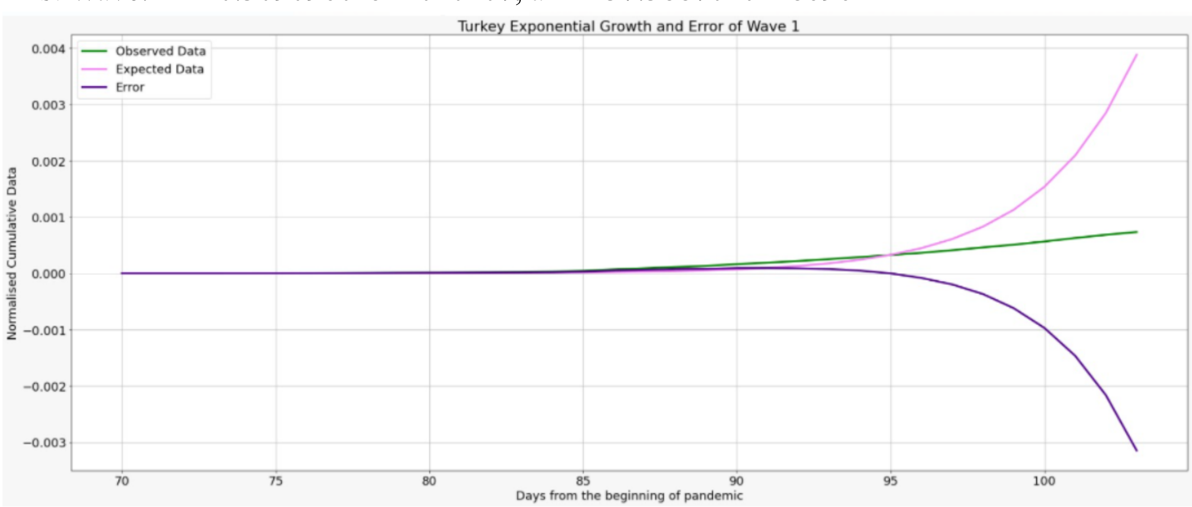

Figure 1.19. Turkey's Exponential growth and Calculated Error for Wave 1

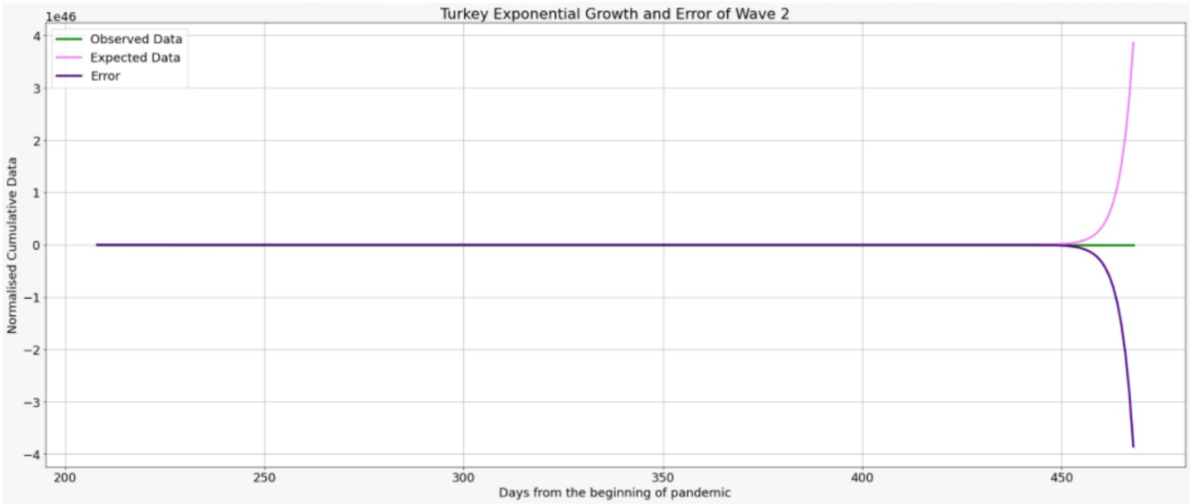

Figure 1.20. Turkey's Exponential growth and Calculated Error for Wave 2

Carrying Capacity

"Carrying capacity is the maximum population that a given area can sustain. The measures commonly used include the number of individuals or the total biomass of a population, which are each highly dependent on differences in physiology and age structure among species and across large taxonomic groups". [1]

Used the value of a and r from the exponential growth interval and plotted the approximation for K as function of time K(t) for Italy, Germany, and Turkey

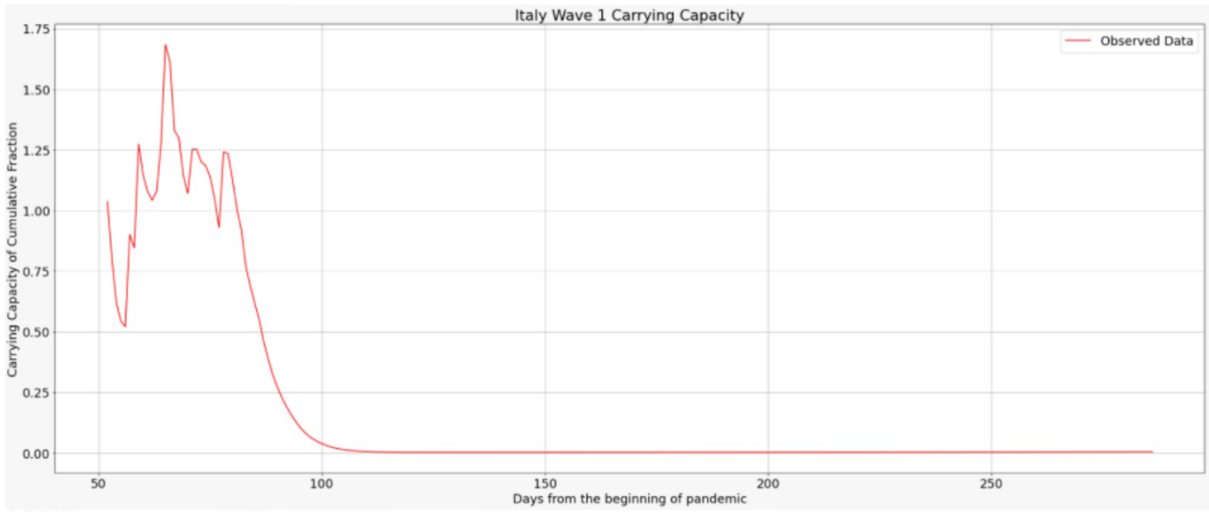

Figure 1.21. Italy's Carrying Capacity for Wave 1

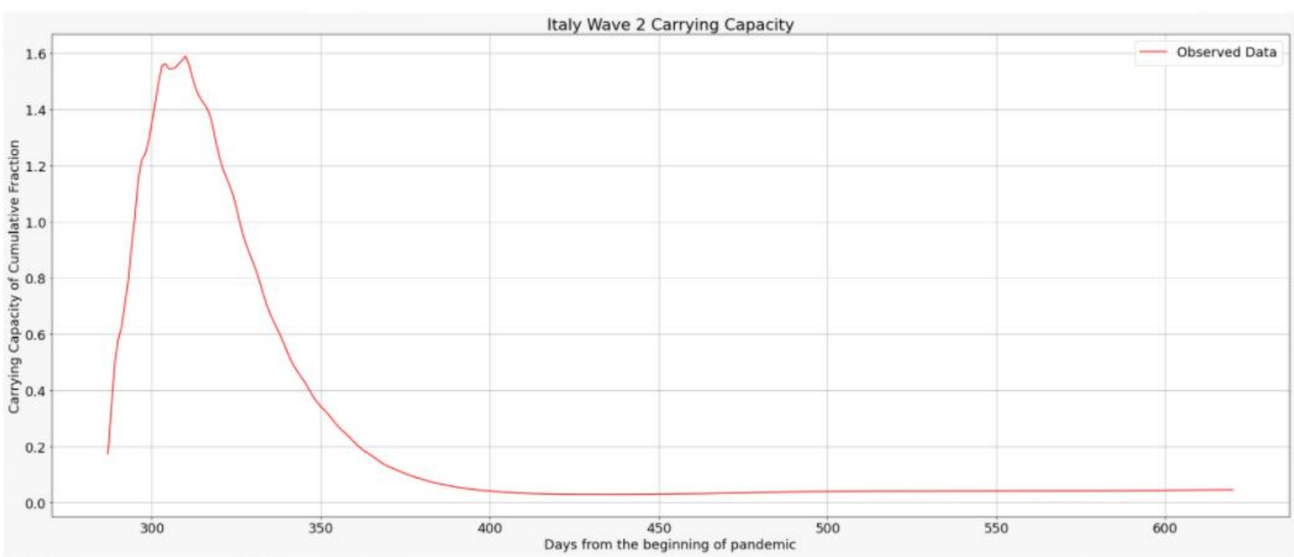

Figure 1.22. Italy's Carrying Capacity for Wave 2

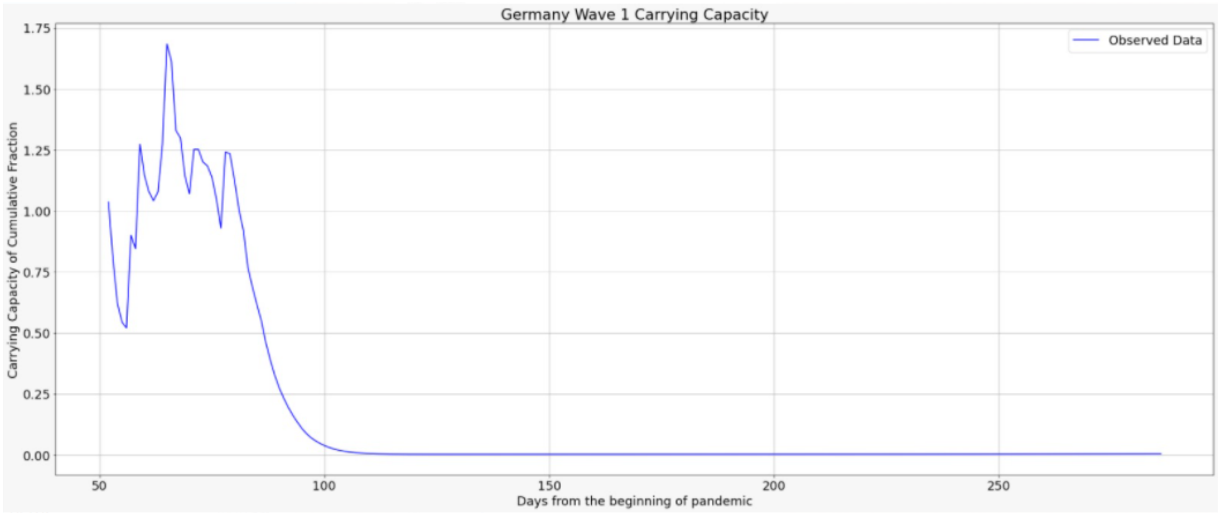

Figure 1.23. Germany's Carrying Capacity for Wave 1

Figure 1.24. Germany's Carrying Capacity for Wave 2

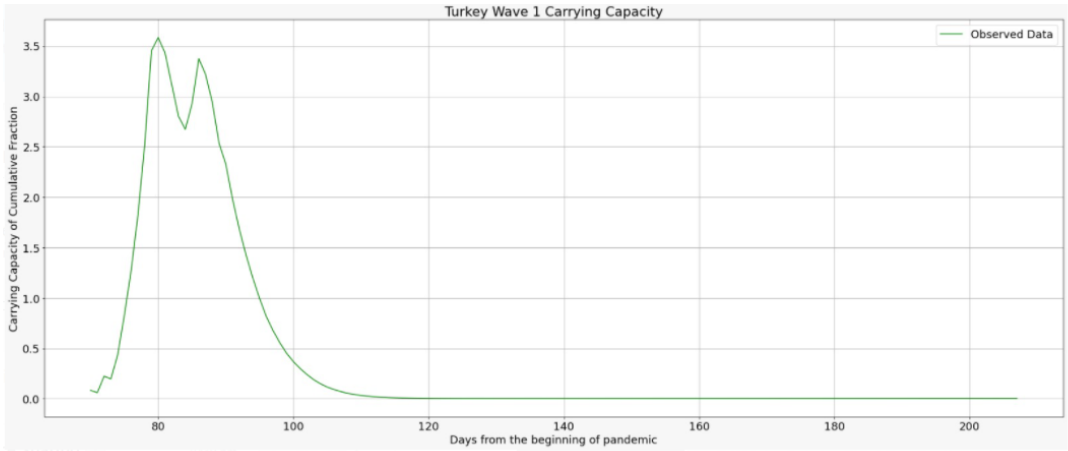

Figure 1.25. Turkey's Carrying Capacity for Wave 1

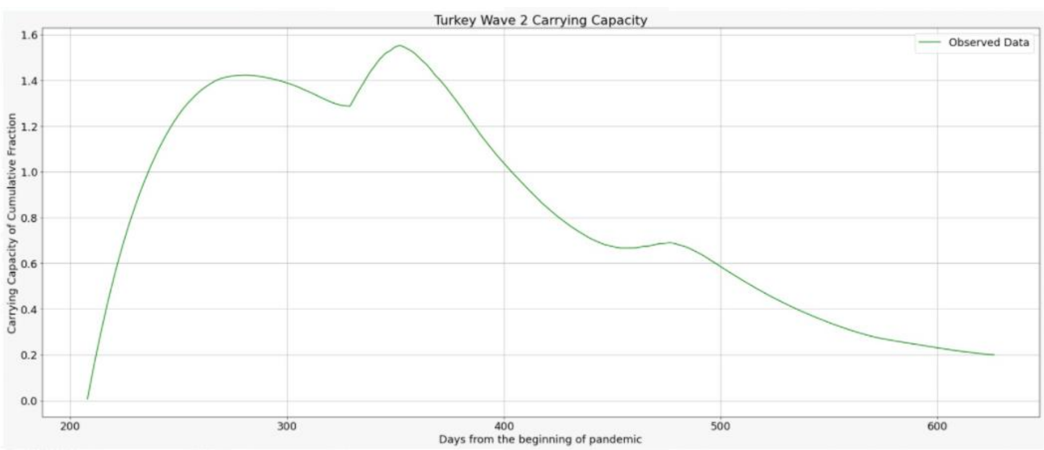

Figure 1.26. Turkey's Carrying Capacity for Wave 2

Logistic Regression

"Logistic regression is a statistical model that uses a logistic function to represent a binary dependent variable in its most basic form, though there are many more advanced variants. Logistic regression (or logit regression) is a technique for estimating the parameters of a logistic model in regression analysis (a form of binary regression)". [2]

Italy:

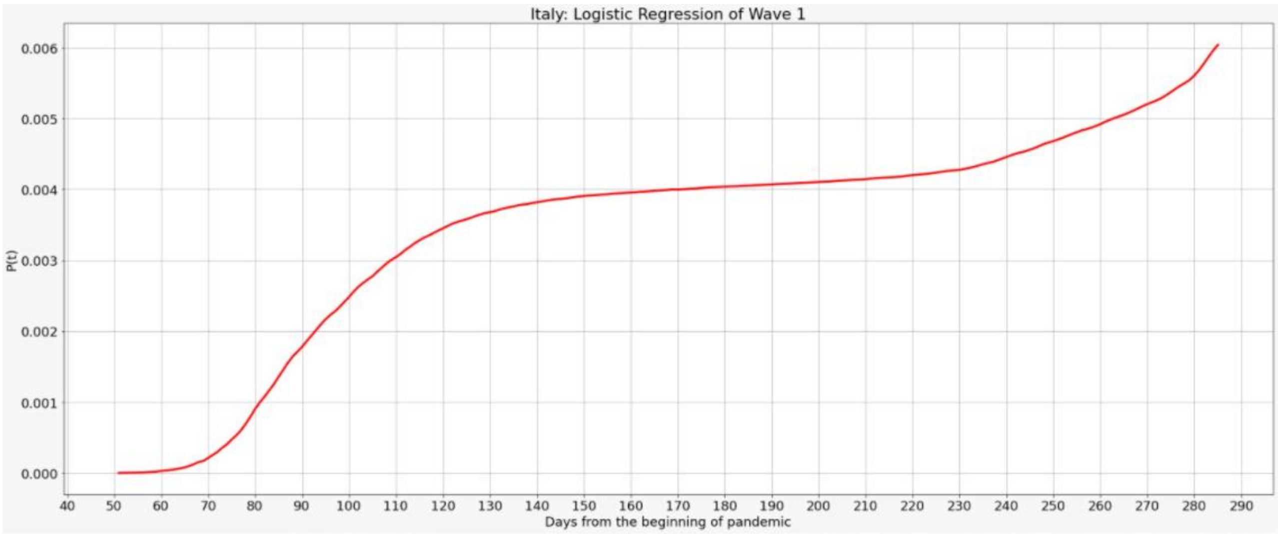

Figure 1.27. Italy's Logistic Regression for Wave 1

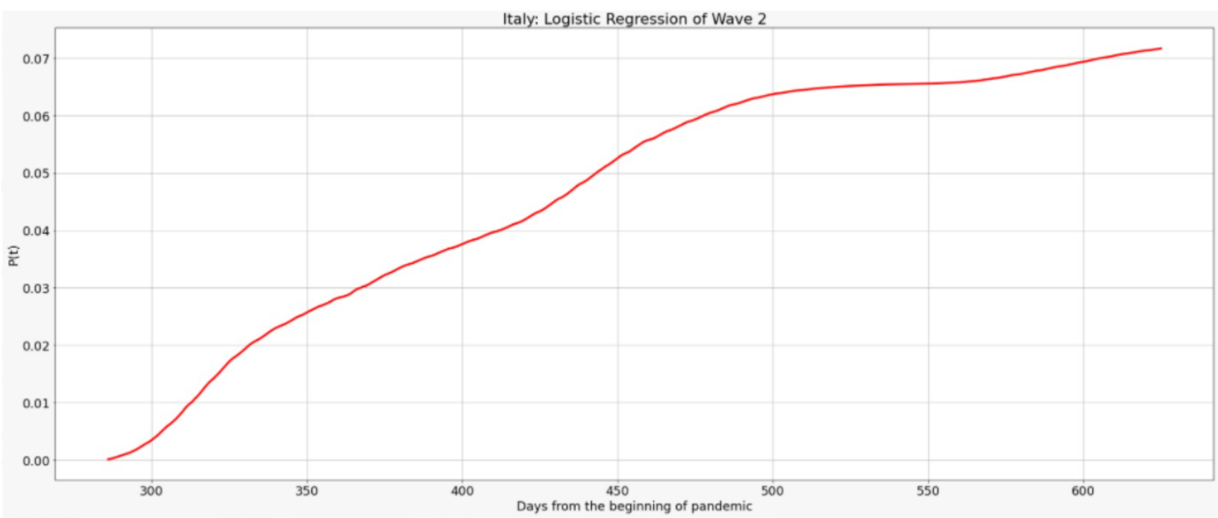

Figure 1.28. Italy's Logistic Regression for Wave 2

Germany:

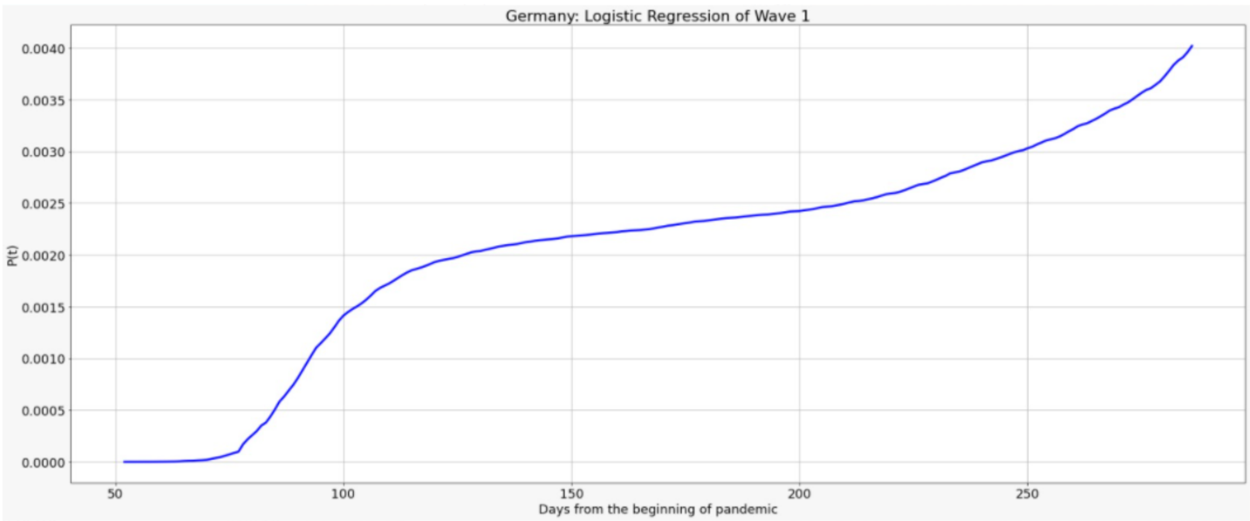

Figure 1.29. Germany's Logistic Regression for Wave 1

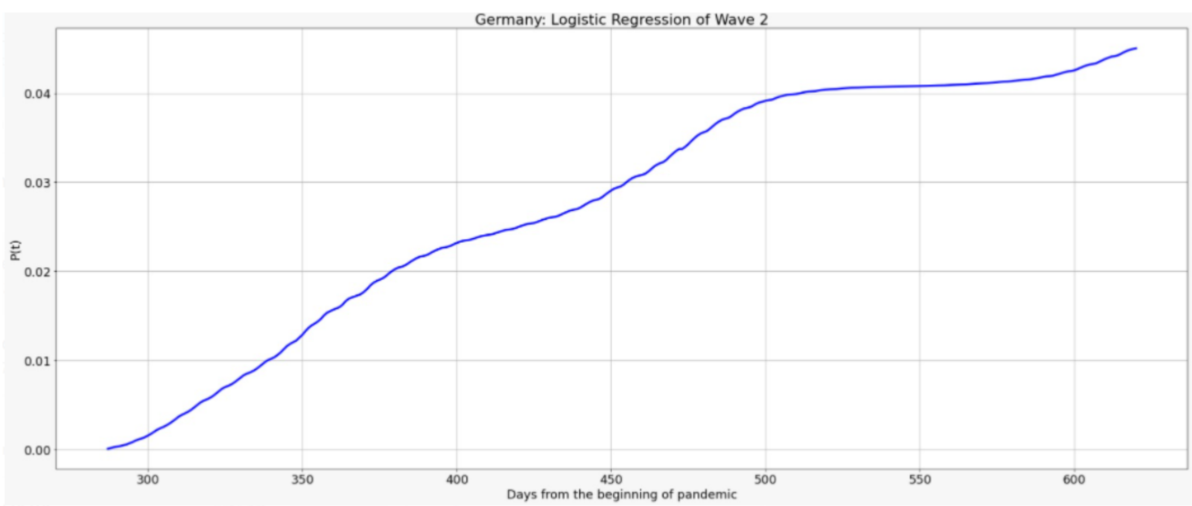

Figure 1.30. Germany's Logistic Regression for Wave 2

Turkey:

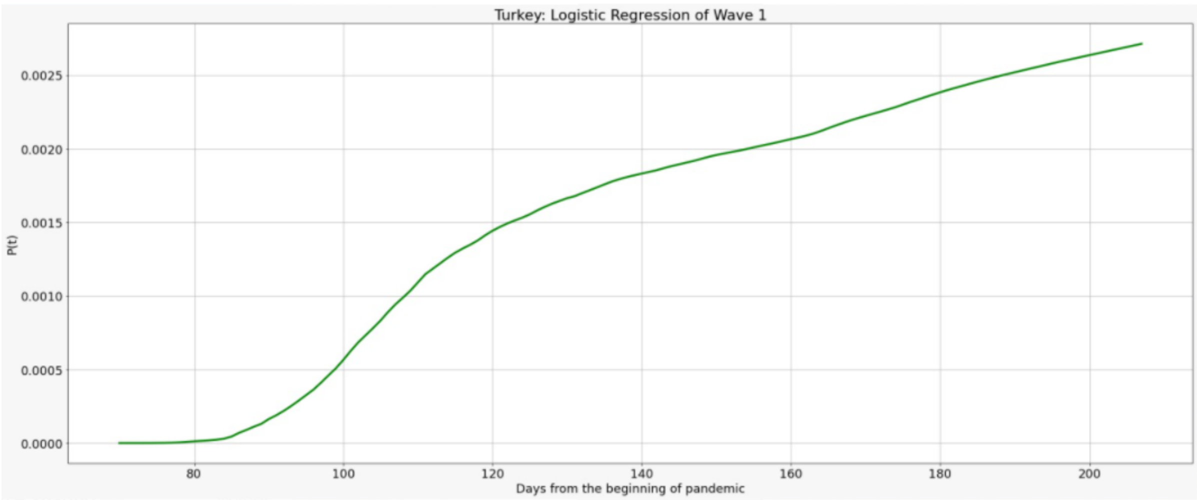

Figure 1.31. Turkey's Logistic Regression for Wave 1

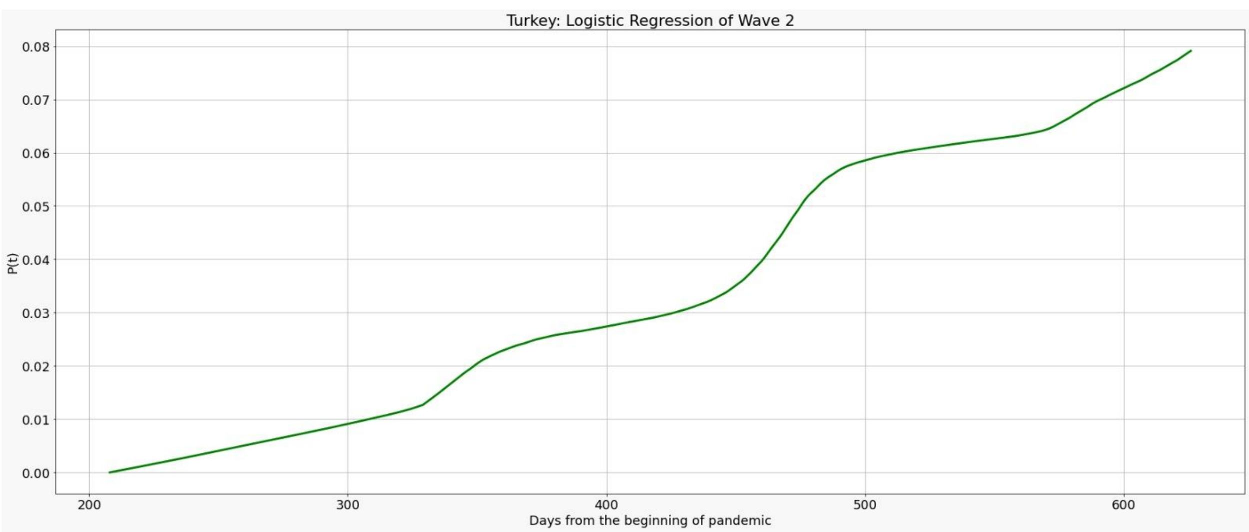

Figure 1.32. Turkey's Logistic Regression for Wave 2

- The three countries we selected do not have same number of waves, Italy has 4 whereas Germany and Turkey have two waves.
- The waves we observed for Turkey and Germany are almost synchronous but not Italy.

Italy has seen the cases at the very early-stage comparative to Germany and Turkey

CHAPTER 2

We have considered the normalized data for the countries Turkey, Italy and Germany from the first chapter.

We have chosen the day since at least 50 COVID-19 cases were confirmed. The initial fragments of the outbreak are eliminated where the COVID outbreak was negligible.

Normalized Data

Normalized data was calculated considering cumulative cases and population of the respective countries.

$$\boxed{Cumulative\ Fraction = \frac{Cumulative\ Cases}{Population}}$$

Below is the graph of Normalized data for three countries (Fig 2.1)

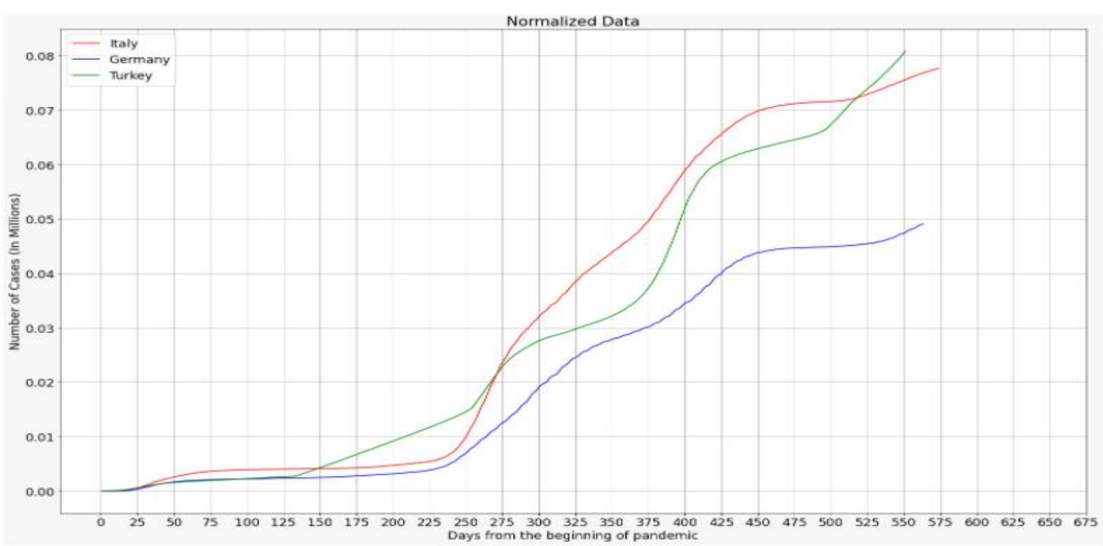

Figure 2.1. Normalized Data of Italy, Germany and Turkey

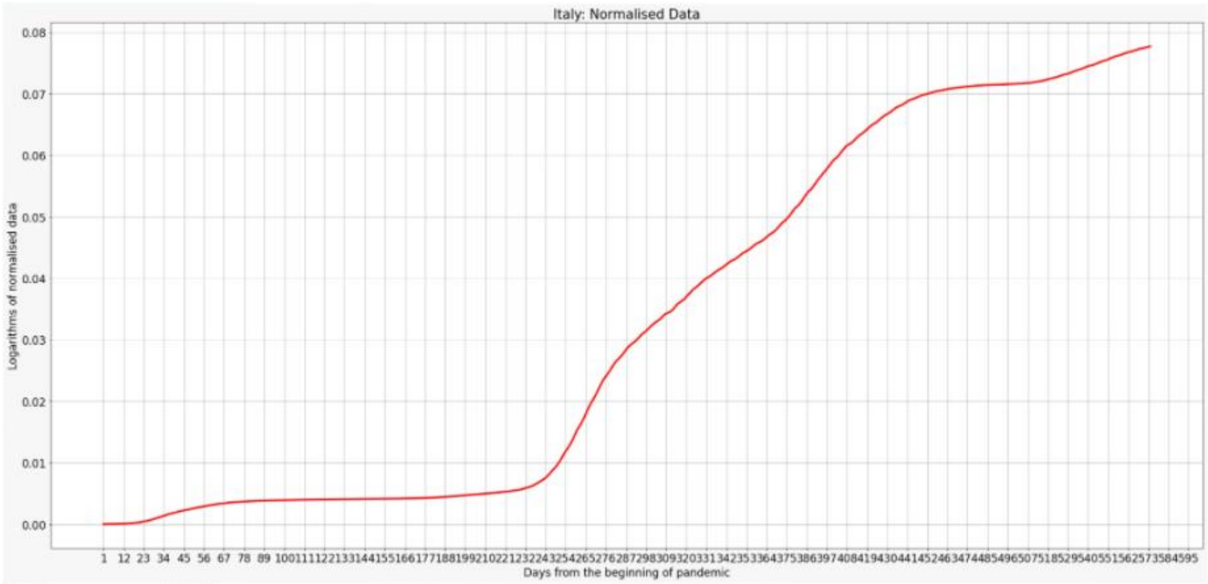

Figure 2.2. Normalized Data of Italy

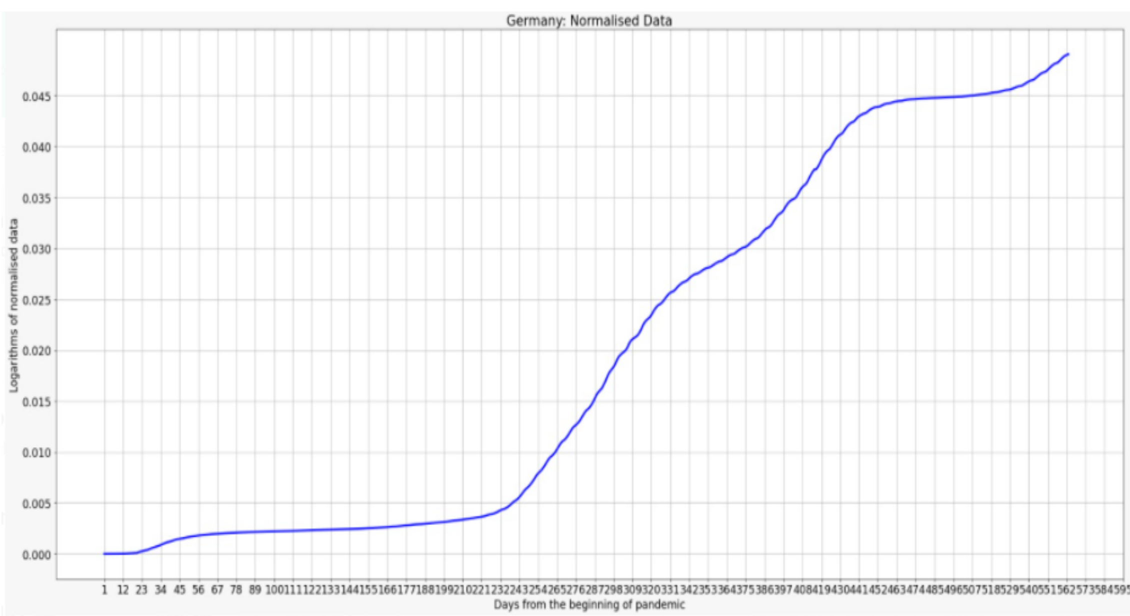

Figure 2.3. Normalized Data of Germany

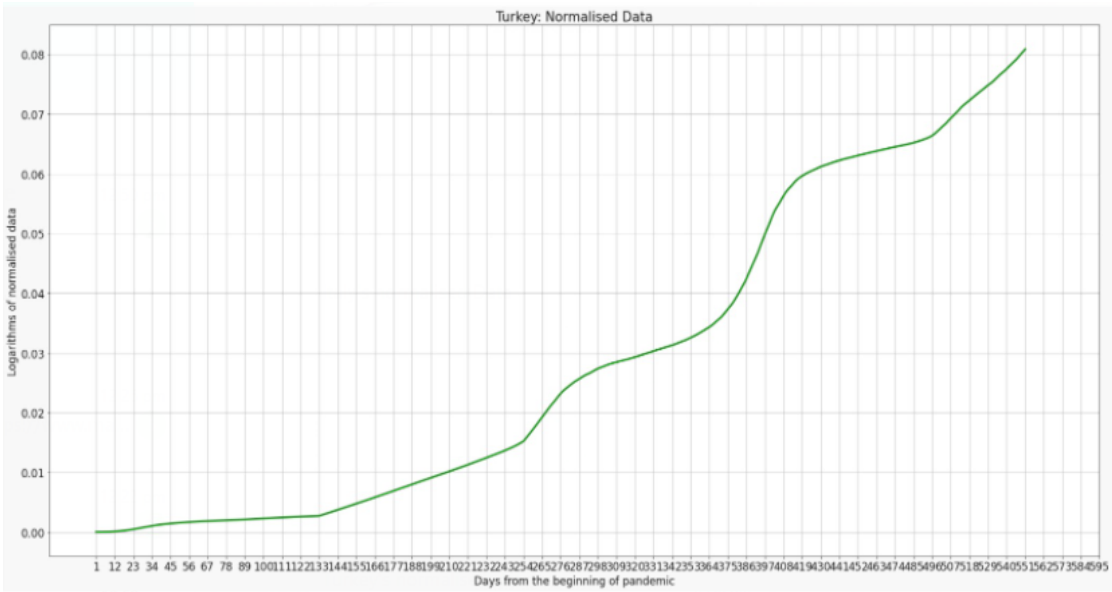

Figure 2.4. Normalized Data of Turkey

Considering the logarithms of the normalized data, we have obtained the below graph (Fig 2.5 – 2.7)

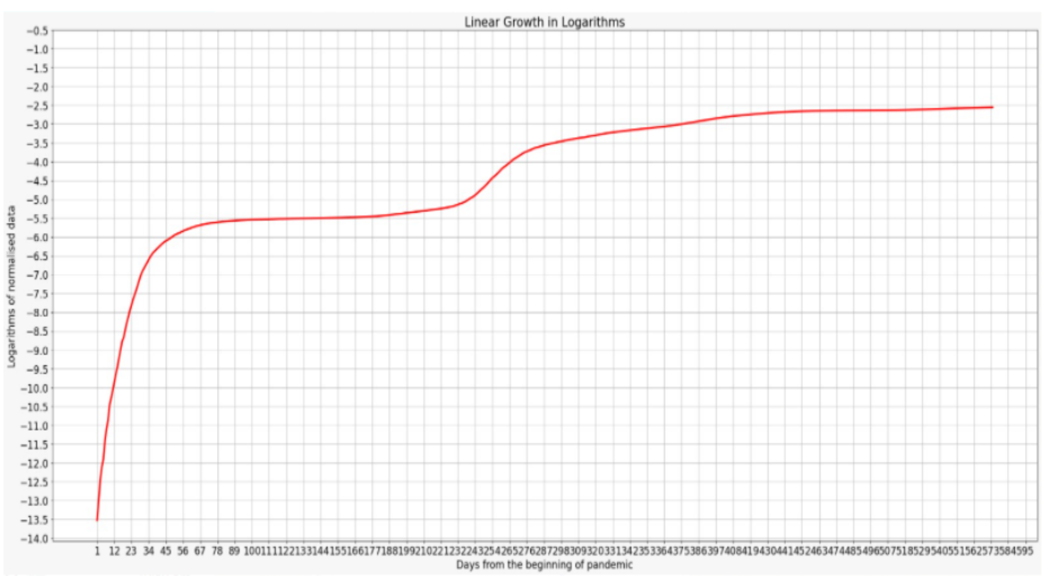

Figure 2.5. Logarithms of Normalized Data of Italy

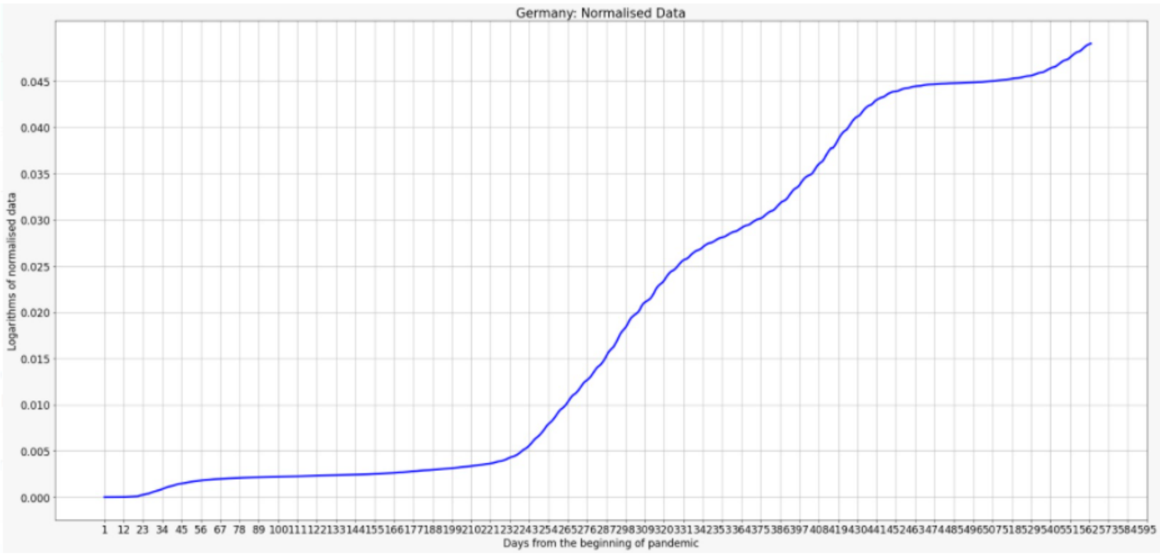

Figure 2.6. Logarithms of Normalized Data of Germany

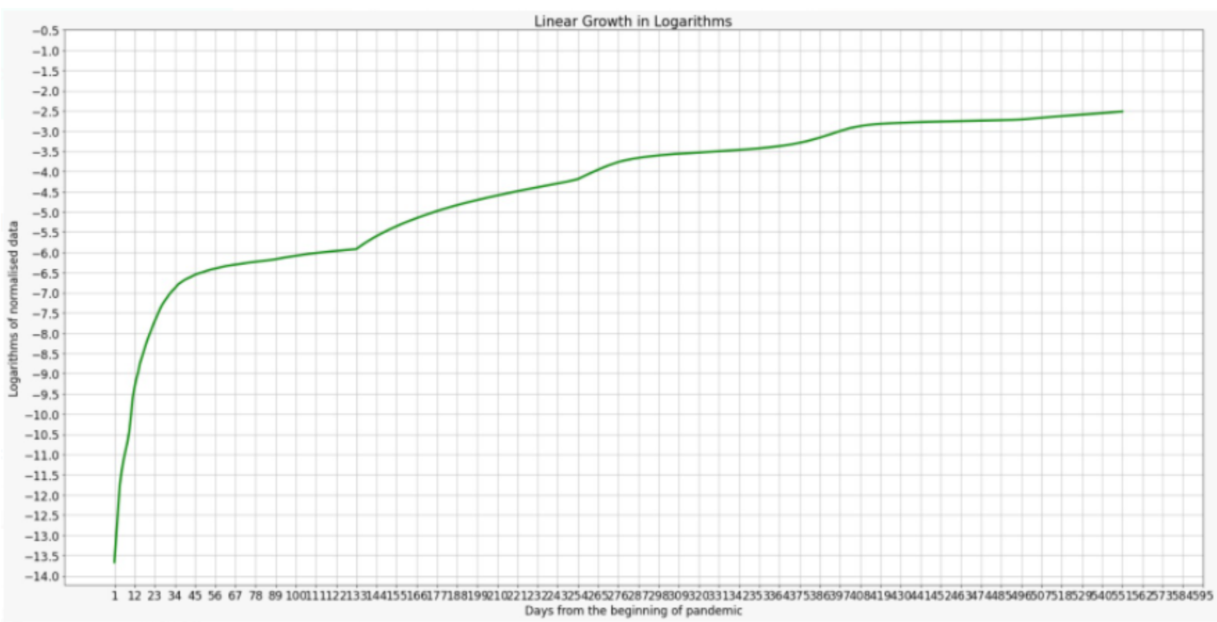

Figure 2.7. Logarithms of Normalized Data of Turkey

SIR Models for COVID

The total population is divided into three subsets: susceptible, infected, and recovered. There are transitions between these parts. Susceptible persons are derived by subtracting persons who are confirmed to be virus carriers via testing in hospitals from the total population.

S - Susceptible, I - Infected/infector, R - Removed (recovered or dead)

System of transitions: $\mathbf{S \rightarrow I \rightarrow R}$

For populations we used the same letters S, I, R.

We consider constant population size: $\mathbf{S+I+R = N = const}$. Further we use dimensionless variables:

$$\boxed{\mathbf{\{S, I, R\} = S+I+R = 1}}$$

Cumulative Cases, $\mathbf{C = I + R}$

Hence, we can find the population which are likely to be infected in the future,

Susceptible, $\mathbf{S = 1 - C}$

As the recovered number of patients are 0 in the beginning, we are considering 10 days earlier start date.

The r value obtained in Chapter 1

Italy

r1 = 0.20886596, a1 = -23.50340957]

r2 = 3.73405017e-03, a2 = -6.24022719e+00

Germany

r1 = 0.22068243, a1 = -26.56389637]

r2 = 4.15179659e-03, a2 = -6.81367255e+00

Turkey

r1= 0.28615977, a1 = -35.37681042]

r2 = 0.00877203 a2 = -7.63450307]

Comparing the r values, there is difference in values obtained through SIR and by Logarithmic Heuristics.

In SIR model, the initial fragments are removed from our data whereas in first chapter, we considered those data.

For log graph we can select two different intervals of initial exponential grows: from 1 to 34 and from 35 to 234. We also can try combination of these two intervals: from 1 to 235. Let us check all three versions. We consider the first 234 points

When S is close to 1, this exponent is **r ≈ a−b**, according to SIR model.

Taking b = 0.1 (time is measured in days; **b = 1/τ**, where τ is, approximately, the time of virus spreading by an infected person; we take here τ ≈ 10 days).

Thus, we know **b = 0.1** and **a = r +b**

Becoming infected depends on contact between S and I.

Therefore, assume that intensity of transitions S → I is aI and the flux S → I is aSI, a = const. Assume that the intensity of recovering (or death) is constant (b) and, therefore, the flux I → R is bI.

Now we have the following system of ODE,

$$\frac{dS}{dt} = -aSI,$$
$$\frac{dI}{dt} = aSI - bI,$$
$$\frac{dR}{dt} = bI.$$

Estimation of Parameters of SIR Model

All coefficients of SIR are tabulated below

Italy:

For b = 0.1

Interval	r	c	b	a	MSE
1 - 34	0.1970057044682587	12.57845966574984	0.1	0.1037340501732819	1.26675706906e-07
35 - 235	0.0037340501732819	6.049790635801064	0.1	0.1037340501732819	0.000127109004616
1 -235	0.014260261548827638	7.747109589659059	0.1	0.1142602615488276	1.40010788288e-05
1 -574	0.00963509192760245	7.0626126056141585	0.1	0.1096350919276024	0.001877497154771

Interval	R	I	S
1 - 34	5.0377833753148615e-08	8.863070132945156e-07	0.9999990633151529
35 - 235	0.0005290680100755667	0.0009234592779177162	0.9985474727120067
1 -235	5.0377833753148615e-08	8.863070132945156e-07	0.9999990633151529
1 -574	5.03778337531486e-08	8.863070132945156e-07	0.9999990633151529

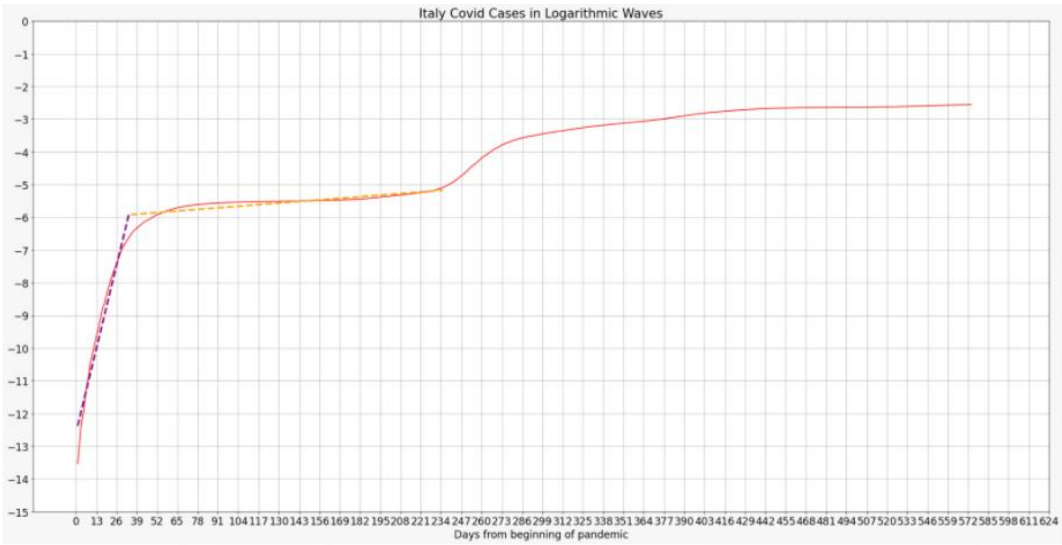

Figure 2.8. Italy Logarithmic Wave with two possible intervals of initial exponential grows

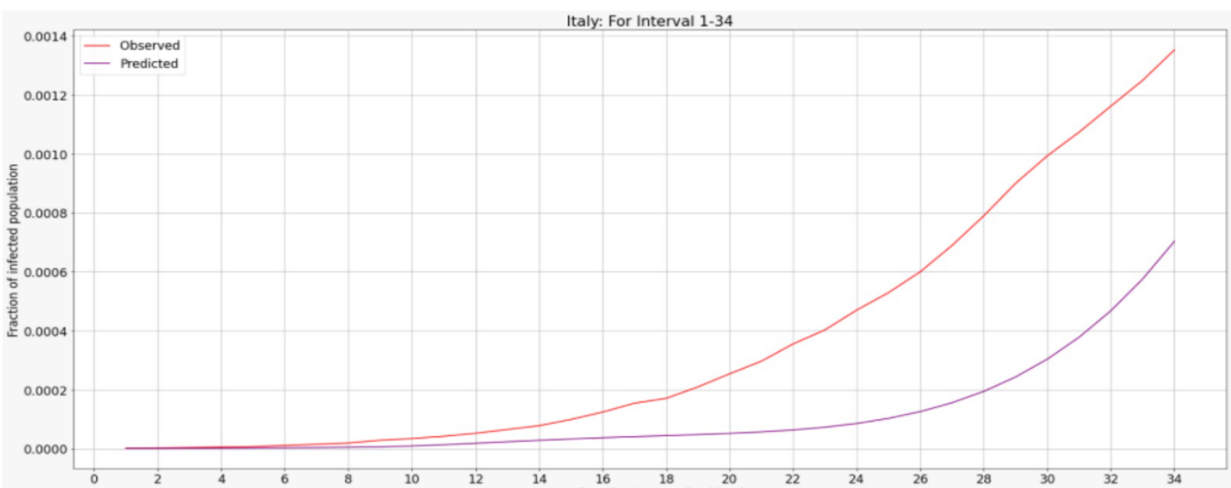

Figure 2.9. Italy's First Interval – Observed vs Predicted

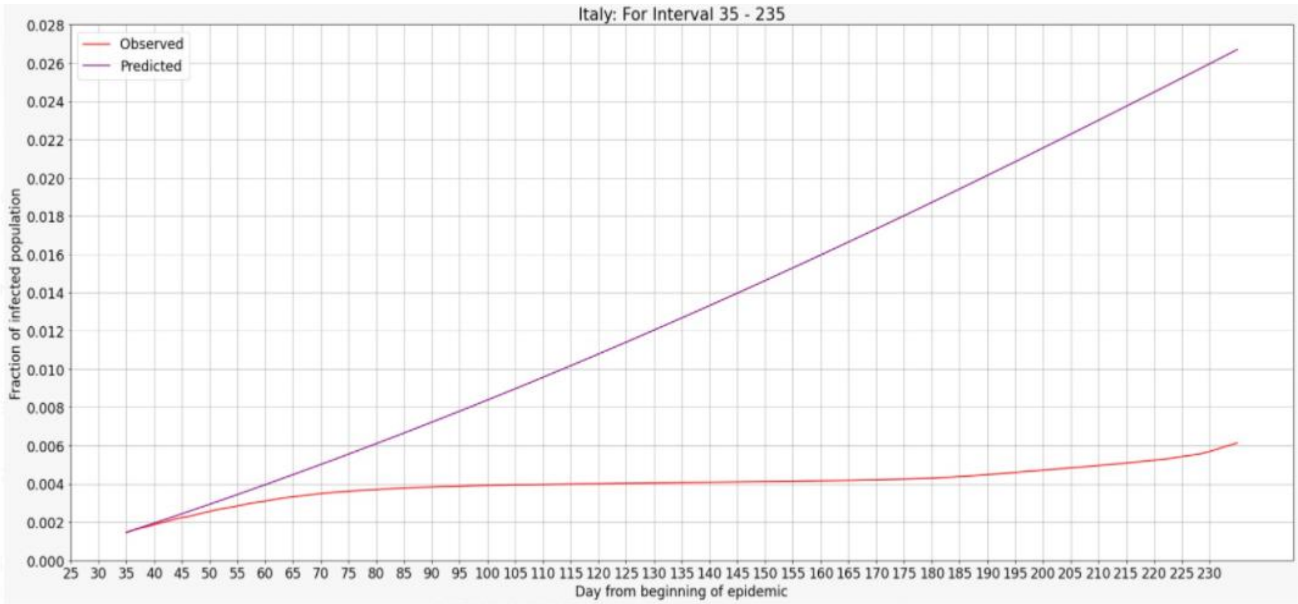

Figure 2.10. Italy's Second Interval – Observed vs Predicted

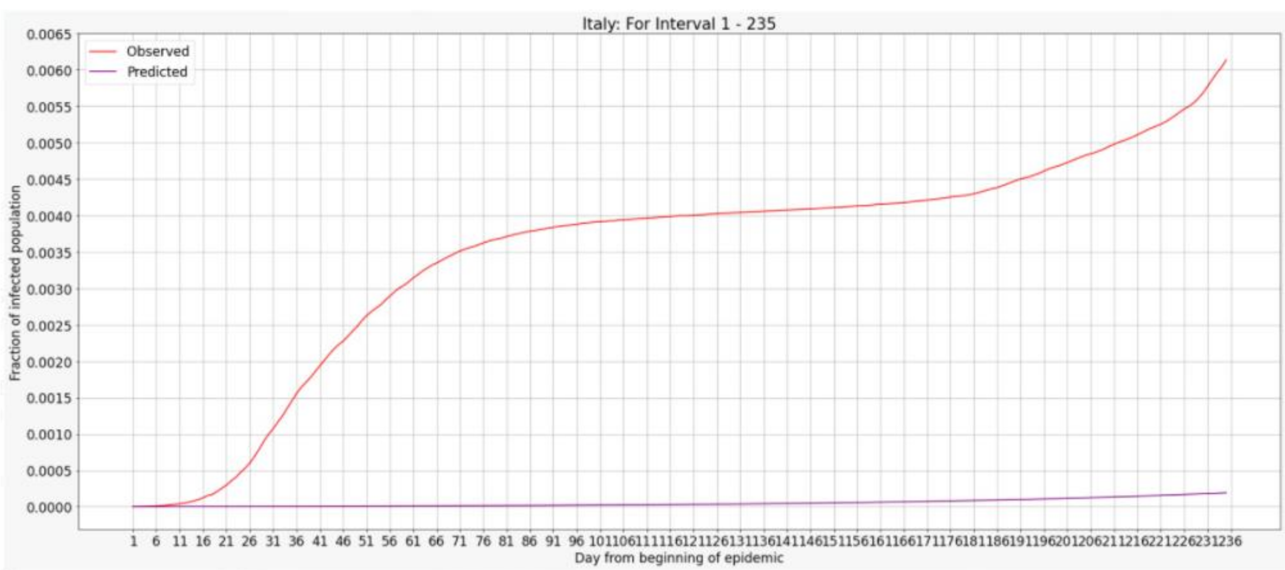

Figure 2.11. Italy's Third Interval – Observed vs Predicted

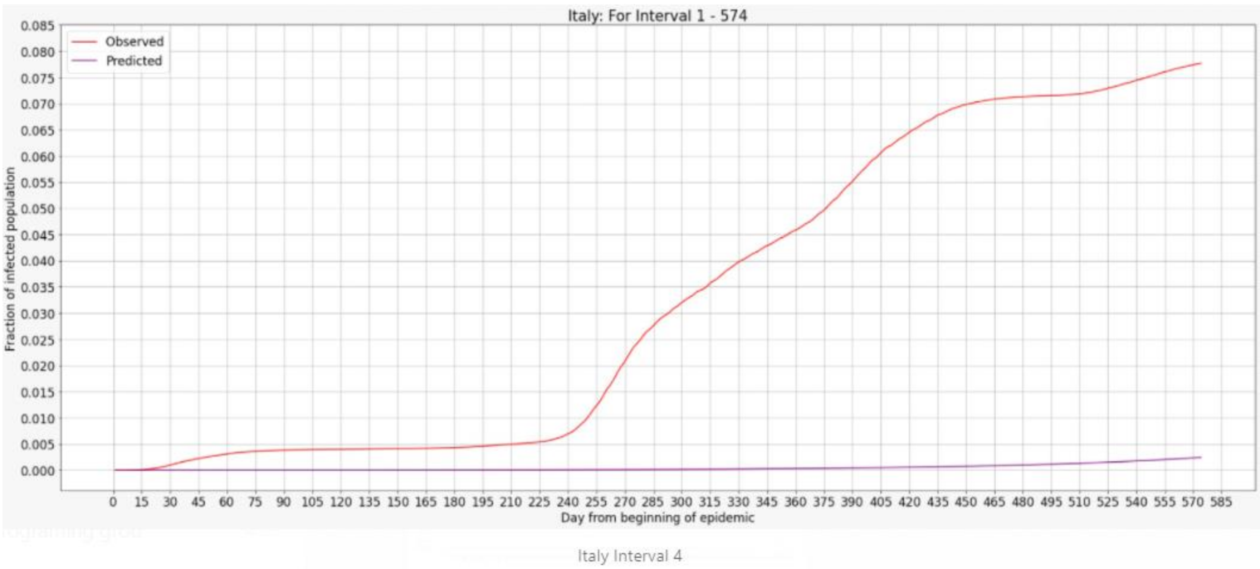

Figure 2.12. Italy's Fourth Interval – Observed vs Predicted

Germany:

For b =0.1

Interval	r	c	a	MSE
1-38	0.20219302192571031	13.52154885416230	0.3021930219257103	4.88171634301792e-08
39 - 229	0.00415179659396571	6.577020143269929	0.10415179659396571	4.00101175855258e-06
1-229	0.01623513349779421	8.47814774329356	0.11623513349779421	5.3123052875352e-06
1-563	0.01005244548368058	7.658247477538945	0.11005244548368058	0.000690983686752321

Interval	R	I	S
1-38	1.802018260451706e-07	5.045651129264776e-07	0.9999993152330611
39 - 229	0.0005836376741950985	0.0	0.9994163623258049
1-229	1.802018260451706e-07	5.045651129264776e-07	0.9999993152330611
1-563	1.802018260451706e-07	5.045651129264776e-07	0.9999993152330611

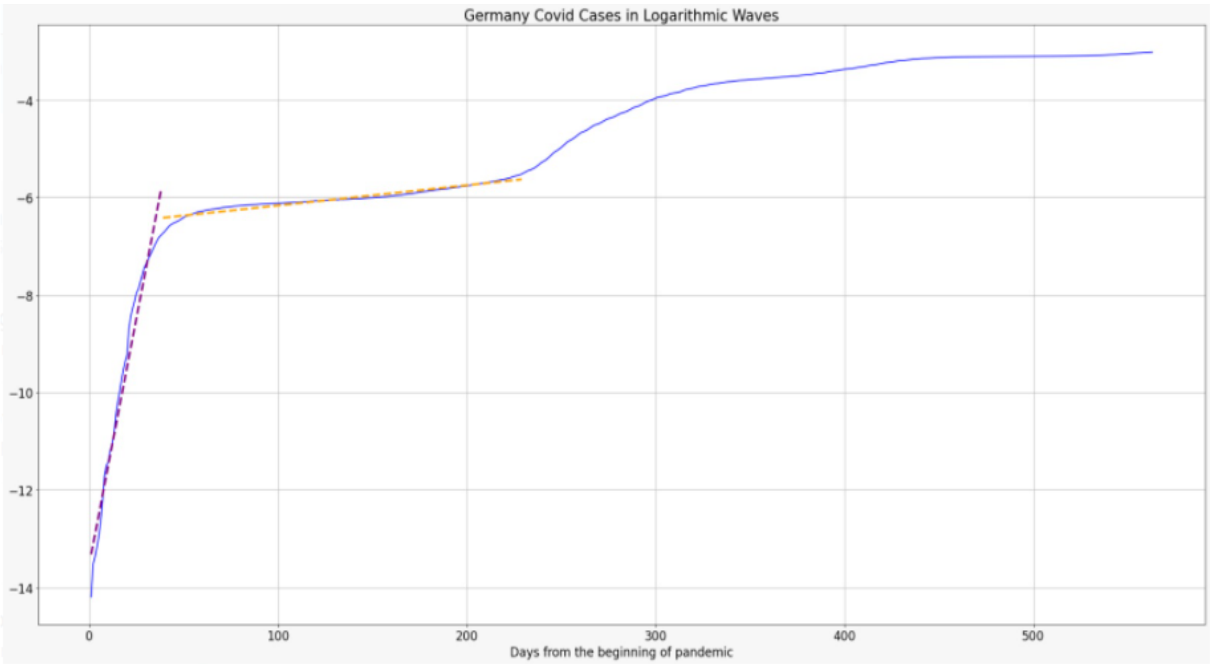

Figure 2.13. Germany Logarithmic Wave with two possible intervals of initial exponential grows

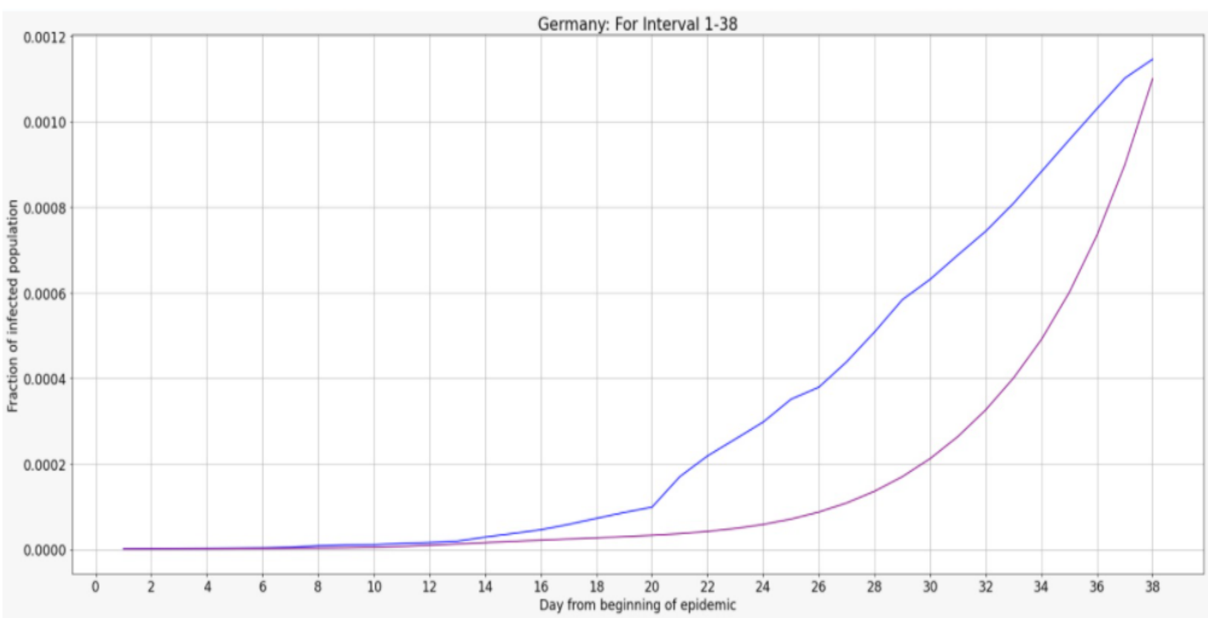

Figure 2.14. Germany's First Interval – Observed vs Predicted

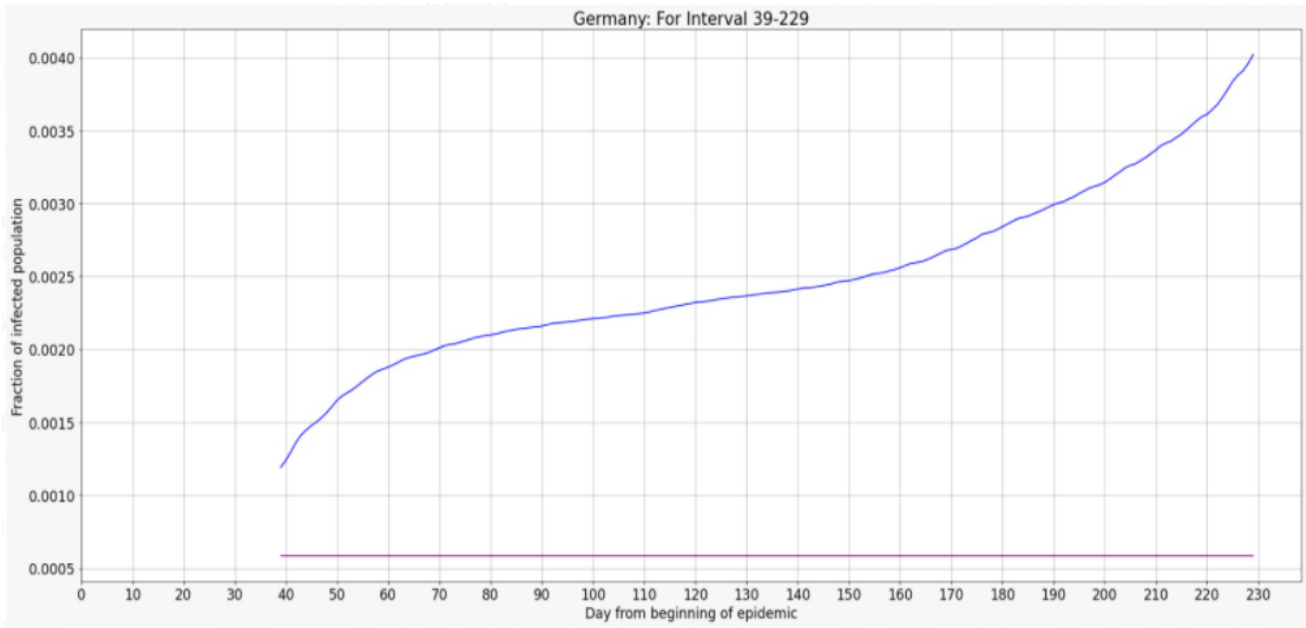

Figure 2.15. Germany's Second Interval – Observed vs Predicted

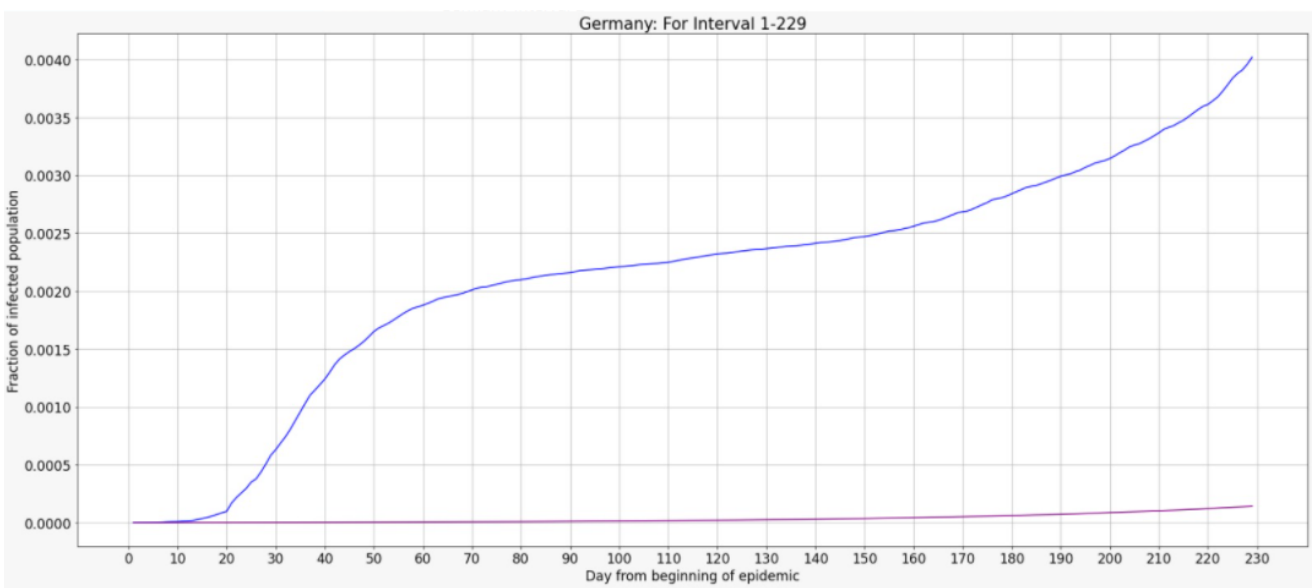

Figure 2.16. Germany's Third Interval – Observed vs Predicted

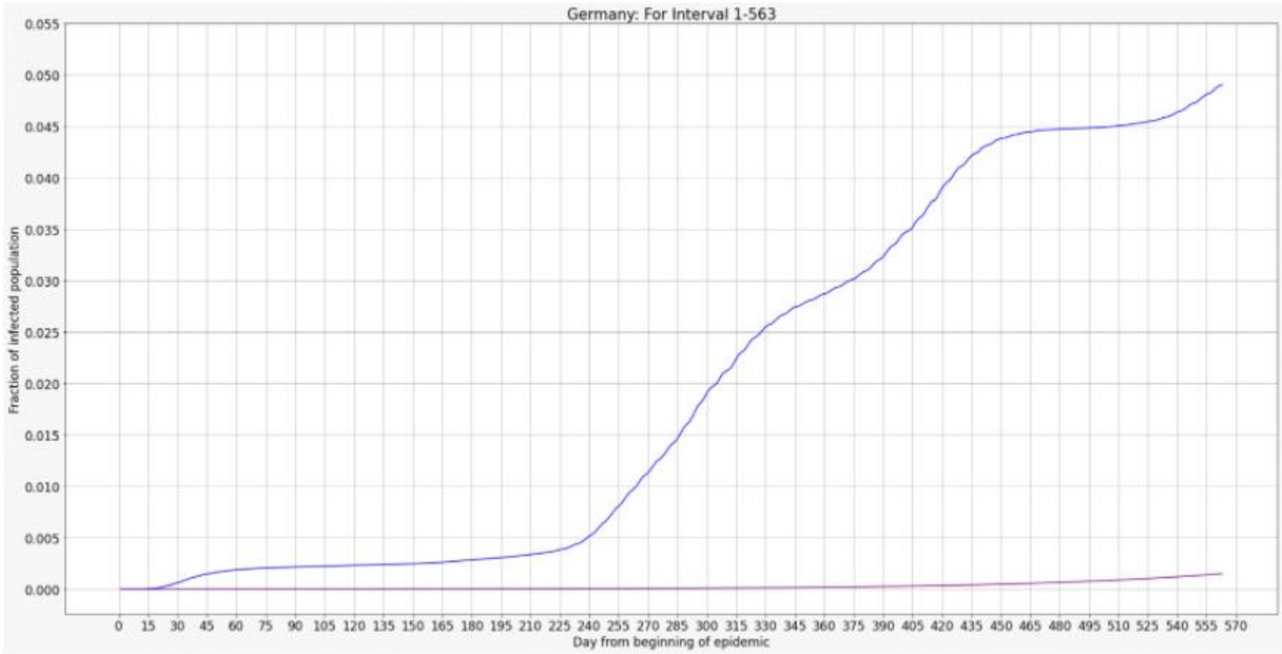

Figure 2.17. Germany's Fourth Interval – Observed vs Predicted

Turkey

For b = 0.1

Interval	r	c	b	a	MSE
1 - 29	0.2105025774435757	12.480853468315196	0.1	0.3105025774435757	3.652253218376e-08
29-132	0.0087720271144611	6.976601031911351	0.1	0.10877202711446118	1.03004493877e-05
1 - 132	0.03022144547571431	8.947461074620643	0.1	0.13022144547571432	0.0009892492458
1 -551	0.01019681561209958	7.227342429045574	0.1	0.1101968156120996	0.00264690292994

Interval	**R**	**I**	**S**
1 - 29	0.0	1.1619634811477353e-06	0.9999988380365189
29 - 132	0.00028377993834479 49	0.0004882262271757173 4	0.9992279938344795
1 - 132	0.0	1.1619634811477353e-06	0.9999988380365189
1 -551	0.0	1.1619634811477353e-06	0.9999988380365189

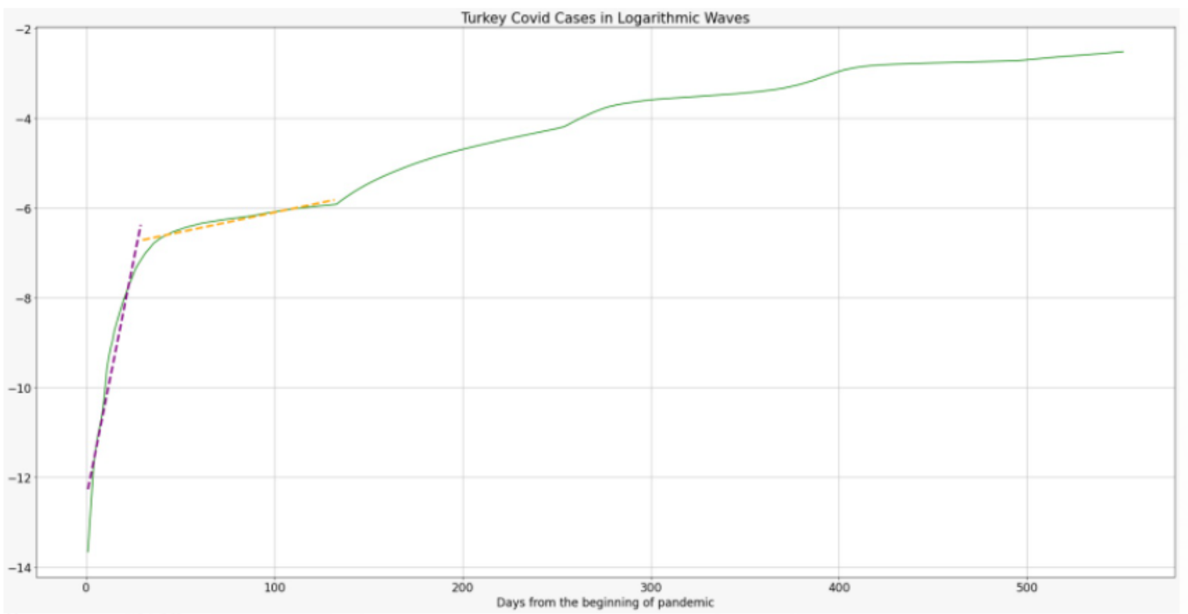

Figure 2.18. Turkey Logarithmic Wave with two possible intervals of initial exponential grows

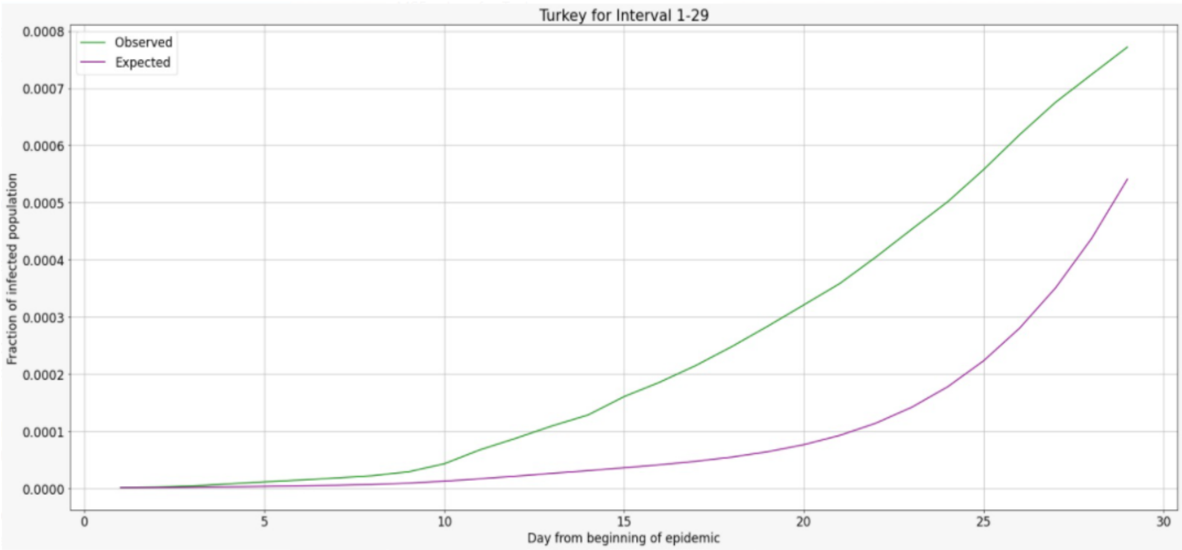

Figure 2.19. Turkey's First Interval – Observed vs Predicted

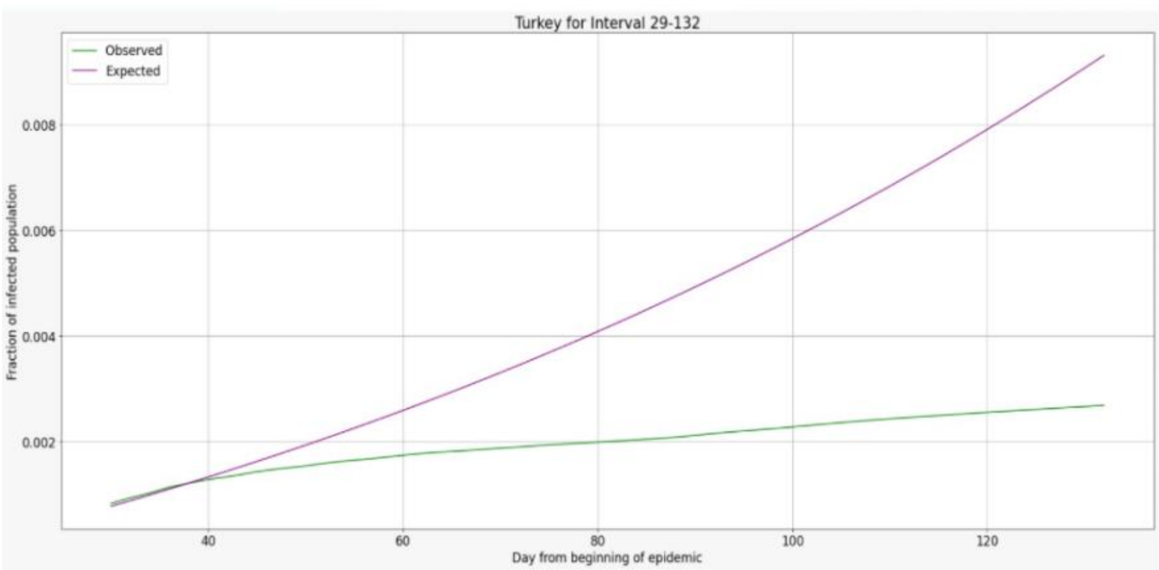

Figure 2.20. Turkey's Second Interval – Observed vs Predicted

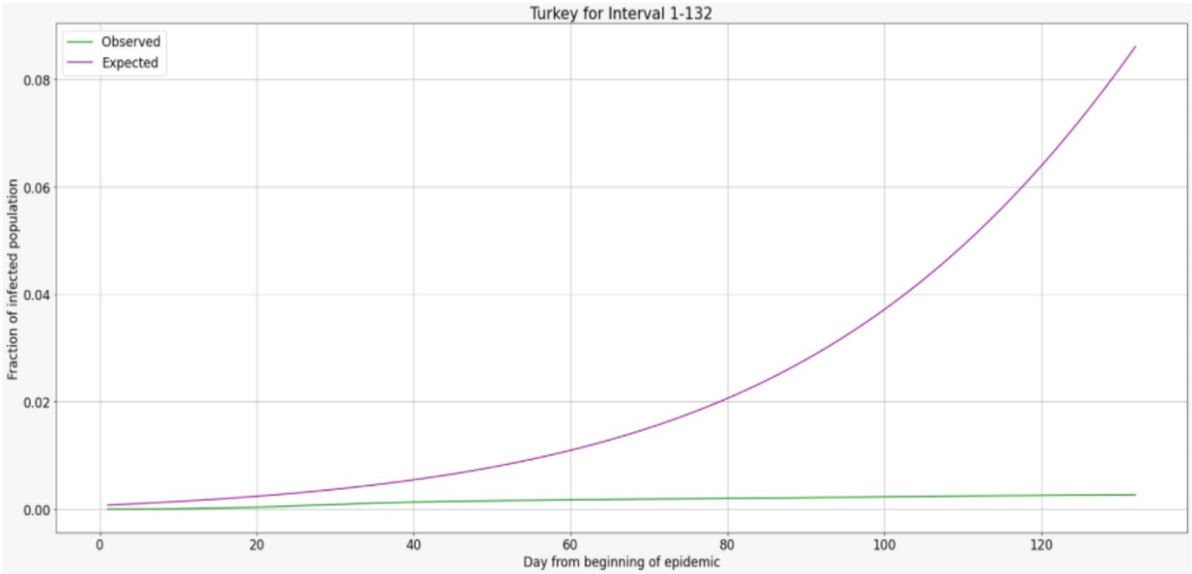

Figure 2.21. Turkey's Third Interval – Observed vs Predicted

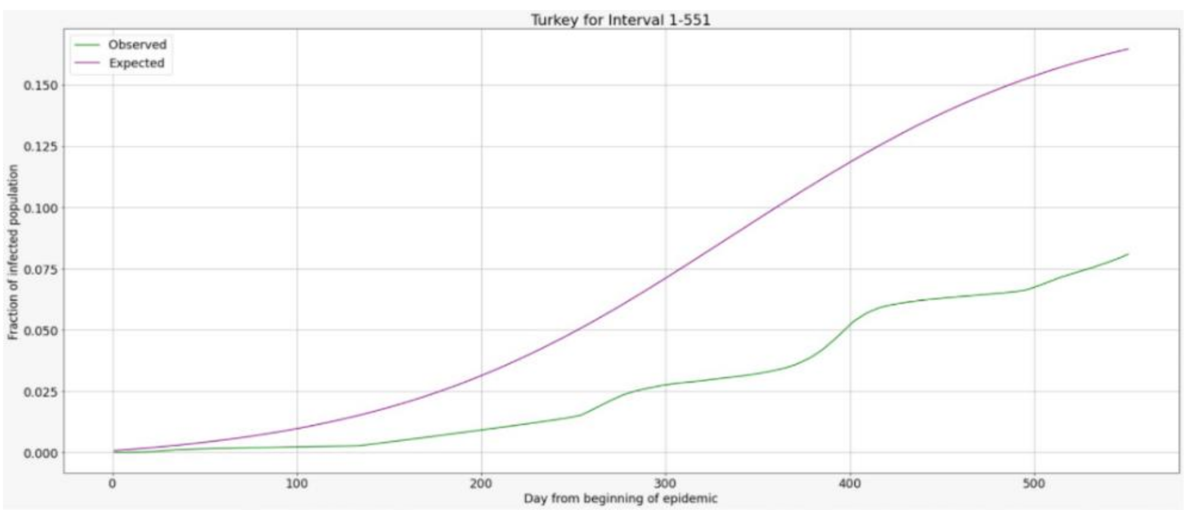

Figure 2.22. Turkey's Fourth Interval – Observed vs Predicted

Results and Discussion

The results obtained above are compared with the cumulative data about COVID patients.

$$\mathbf{P = 1 - S}$$

As the cumulative fraction increases, it means the number of COVID cases have raised and population of susceptible is decreasing.

In the first wave of Turkey and Germany, the COVID cases have raised exponentially, and the virus spread was high. The susceptible decreased exponentially and reached the saturation. But in Italy, Initially the raise of number of cases in the first wave is less but in the second interval, the virus outbreak had a major effect, so everyone was susceptible.

In each phase, the virus mutated and affecting different age groups. The rate of infected population raised again in the next intervals of the COVID outbreak.

The mathematical modelling methodology in building the new model by modifying the existing SIR model through incorporating assumptions that are more realistic. The existing SIR model give good analysis epidemic diseases but considering more realistic factors to the model will give better results.

The COVID-19 pandemic features are not coherent with the SIR modelling framework and the dynamics of this outbreak is under the influence of various parameters for most of which quantitative information is not yet available.

The “second wave” of COVID in each country is very much higher than the first wave, the COVID cases raised because of the dynamics of epidemics depend on how people's behaviour changes during an outbreak. At the beginning of the epidemic, people do not know about the virus, then, after the outbreak of epidemics and alarm, they begin to comply with the restrictions and the spreading of epidemics may decline. Over time, some people get tired/frustrated by the restrictions and stop following them (exhaustion), especially if the number of new cases drops down. After resting for a while, they can follow the restrictions again. But during this pause the second wave can come and become even stronger then the first one. Studies based on SIR models do not predict the observed quick exit from the first wave of epidemics. Social dynamics should be considered. The appearance of the second wave also depends on social factors. Many generalizations of the SIR model have been developed that consider the weakening of immunity over time, the evolution of the virus, vaccination and other medical and biological details.

Review of “The Mathematics of Infectious Diseases”

The most noticeable fact after reading the review of “The mathematics of Infectious Diseases” is the consideration of Age groups in the study. As we are certainly aware that the COVID-19 targeted each different age groups in each “wave”, considering Age Group in our study would make help us to improve our analysis.

Few of the limitations of SIR model is that they unrealistically assume that the population is uniform and homogeneously mixing, whereas it is known that mixing depends on many factors including age (children usually have more adequate contacts per day than adults). Moreover, different geographic and social-economic groups have different contact rates. Despite their limitations, the classic SIR models can be used to obtain some estimates and comparisons. Models with a variable total population size are often more difficult to analyse mathematically because the population size is an additional variable which is governed by a differential equation.

According to us, Age-structured MSEIR model would be well suited to improve agreement between SIR and empirical data. Because information on age-related fertilities and death rates is available for most countries and because mixing is generally heterogeneous, epidemiology models with age groups are now used frequently when analysing specific diseases. However, special cases with homogeneous mixing and asymptotic age distributions that are a negative exponential, or a step function are considered. These special cases of the continuous MSEIR model are often used as approximate models. For example, the negative exponential age distribution is used for measles in Niger. Also, MSEIR model does not depend on whether recovered people have no, temporary, or permanent immunity.

CHAPTER 3

Additions to SIR Model

In this Chapter, we have analyzed the data from the perspective of social psychology using SIR models. From SIR model used in previous chapter, we had presented 3 types of individuals, namely, Susceptible(S), Infected (I) and Removed (R). Now considering Hans Selye's classical theory of stress and general adaptation syndrome (GAS), have further divided susceptible state into 4 subpopulations which represent types of human behavior under epidemic stress.

Earlier representations of the states were:

- S - Susceptible
- I - Infected
- R – Removed (recovered/dead)

New representations of the states are:

- Sign – "Ignorant" people who lack awareness about the epidemic and remain unbothered.
- Sres – People who have adopted "Resistance" state to remain safe.
- Sexh – People who are in "Exhaustion" state and have stopped paying attention to resistance methods. They do not react to alarm stimuli.
- I – Infected
- R – Removed (recovered/dead)

During the pandemic, populations may have varying responses to an epidemic. These are influenced by culture, mass media, rumors and socio-economic conditions. Lower levels of behavioral changes may be due to the lack of a sense of crisis and people's lack of awareness or concern about their contribution to society.[1] Using these stress conditions, we assume that the population is majorly ignorant at the start of the epidemic. As the number of cumulative cases rise, a section of the population may be more alarmed towards the growing fear of the virus and adopt resistance techniques such as wearing masks, self-isolation, and medication. However, people who are uninformed and unaware remain ignorant towards epidemic information and will not show any method of resistance from being infected. If the resistance conditions are extended over long periods of time, populations may show exhaustion state, in which they behave in unsafe manner. We have developed several kinetic equations to represent interaction of these subpopulations throughout the epidemic.

Adopting a New Model

In chapter 2, we stated relationship between states of SIR model as:

- System of Transition: S -> I -> R
- Constant population size: S + I + R = N = const
- Sum of states: S + I + R = 1

For these states, we identified the following conditions:

1. The only way a person can leave the group of susceptible is by being infected. When a susceptible person meets an infected person, he/she gets infected as well. So, the intensity of this transition, S -> I is aI and its flux is aSI, where a is the infection rate
2. An infected person may only be removed from the group if they are recovered or dead. Both of which fall under the "removed" state. Hence, the intensity for the transition I -> R is b. The flux is bI, where b is the recovery rate.

We have developed several kinetic equations to represent interaction of these subpopulations throughout the epidemic. The variables we have considered to study the psychological effects on our data are:

The relation between these variables is:

$$S = S_{ign} + S_{res} + S_{exh}$$

Initially, we consider S(0) = $S_{ign}(0)$ and $S_{res}(0) = S_{exh}(0) = 0$.

The kinetic equations for interactions are as follows:

Reactions	Reaction rate	Stoichiometric vector (γ)
$S_{ign} + I \to 2I$	$r_1 = aS_{ign}I$	$(-1, 0, 0, 1, 0)^T$
$S_{ign} + I \to S_{res} + I$	$r_2 = k_2 S_{ign} I$	$(-1, 1, 0, 0, 0)^T$
$S_{res} \to S_{exh}$	$r_3 = k_3 S_{res}$	$(0, -1, 1, 0, 0)^T$
$S_{exh} + I \to 2I$	$r_4 = aS_{exh}I$	$(0, 0, -1, 1, 0)^T$
$I \to R$	$r_5 = bI$	$(0, 0, 0, -1, 1)^T$
$S_{exh} \to S_{ign}$	$r_6 = k_6 S_{exh}$	$(1, 0, -1, 0, 0)^T$

The Ordinary Differential Equations for our reactions are:

$$\boxed{\frac{dc}{dt} = \sum_{\rho=1}^{6} \gamma_\rho r_\rho}$$

$$\frac{dc}{dt} = \begin{bmatrix} -1 \\ 0 \\ 0 \\ 1 \\ 0 \end{bmatrix} r_1 + \begin{bmatrix} -1 \\ 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} r_2 + \begin{bmatrix} 0 \\ -1 \\ 1 \\ 0 \\ 0 \end{bmatrix} r_3 + \begin{bmatrix} 0 \\ 0 \\ -1 \\ 1 \\ 0 \end{bmatrix} r_4 + \begin{bmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 1 \end{bmatrix} r_5 + \begin{bmatrix} 1 \\ 0 \\ -1 \\ 0 \\ 0 \end{bmatrix} r_6$$

$$\frac{dc}{dt} = \begin{bmatrix} -aS_{ign}I \\ 0 \\ 0 \\ aS_{ign}I \\ 0 \end{bmatrix} + \begin{bmatrix} -k_2S_{ign}I \\ k_2S_{ign}I \\ 0 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ -k_3S_{res}I \\ k_3S_{es}I \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \\ -aS_{exh}I \\ aS_{exh}I \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \\ 0 \\ -bI \\ bI \end{bmatrix} + \begin{bmatrix} k_6S_{exh} \\ 0 \\ -k_6S_{exh} \\ 0 \\ 0 \end{bmatrix}$$

From this we get $\frac{dS_{ign}}{dt}$, which is change in the "ignorant" behaviour of the population,

$$\boxed{\frac{dS_{ign}}{dt} = -aS_{ign}I - k_2S_{ign}I + k_6S_{exh}}$$

We also get $\frac{dS_{res}}{dt}$, which is change in the "Resistance" behaviour,

$$\boxed{\frac{dS_{res}}{dt} = k_2S_{ign}I - k_3S_{res}}$$

The equation for $d$we get from $\frac{dc}{dt}$ represents change in "Exhaustion" state of population.

$$\boxed{\frac{dSexh}{dt} = k_3S_{res} - aS_{exh} - k_6S_{exh}}$$

The differential equation, $\frac{dI}{dt}$ represents change in “Infection” over a given population.

Similarly, $\frac{dR}{dt}$ represents change in “Removed” population.

$$\frac{dI}{dt} = aS_{ign} + \mathrm{a}S_{exh}\mathrm{I} - bI,$$

$$\text{and, } \frac{dR}{dt} = \mathrm{bI}$$

Reaction Rate

Reaction rate constant for a reaction A → B is the inverse lifetime of the particle A. We have chosen initial approximations for each.

Reaction rate constant for $S_{res} \rightarrow S_{exh}$ is 1/50 which indicates that people become tired of being in “resistance” state after 50 days and move to “exhausted” state. Reaction rate constant for $S_{exh} \rightarrow$

S_{ign} is 1/100 which indicates that people return to “ignorant” state from “exhausted” state after 100 days. We assume that reaction rate constant for $S_{ign} + I \rightarrow S_{res} + I$ is 1 by considering that if the proportion of I is close to 1 then ignorant people modify their behavior to “resistant”.

Therefore,

Reaction Rate	Value
k_3	1/50
k_6	1/100
k_2	1

Integrating ODE

Italy

Based on hypothesis that 50 cases are the start of the epidemic, we integrate our ODE to get values of S_{ign}, S_{res}, I, and R for each of the intervals defined in Chapter 2. These values are heavily dependent on the rate of every reaction.

k2=1

k3=1/50

k6=1/100

Following graphs are for the 4 different intervals.

The graphs below are for the interval 1-34, 35- 235, 1- 235, 1-574. We can see that the observed and predicted lines for the countries post calculations in the below graphs.

The below graphs are compared with modified values in later stages to see if our model fits the real life scenario.

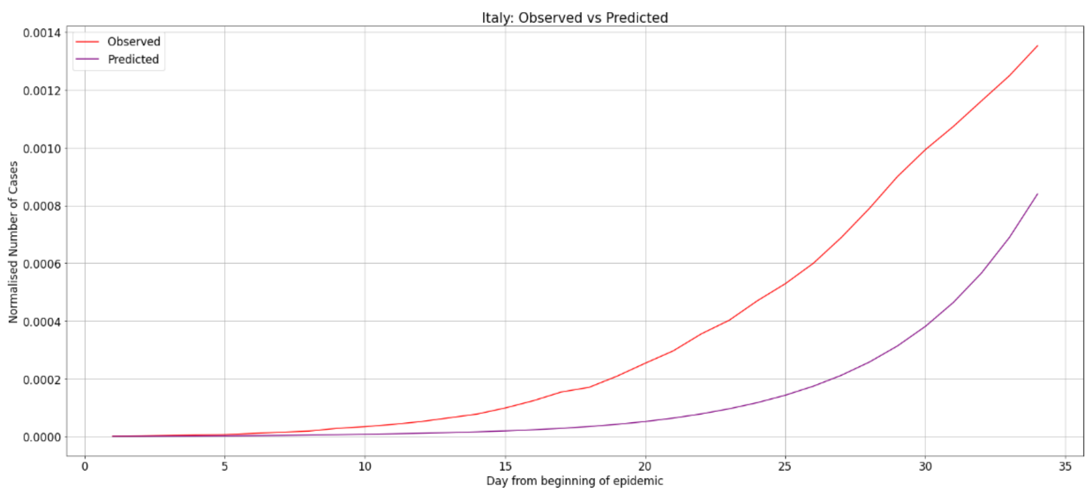

Figure 3.1. Italy’s Observed vs Predicted graph for Interval 1-34

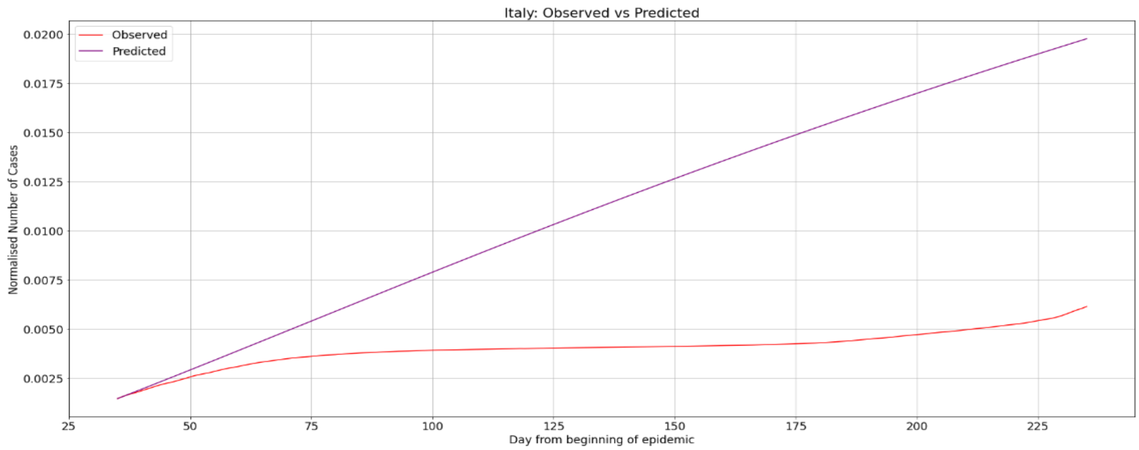

Figure 3.2. Italy's Observed vs Predicted graph for Interval 35 - 235

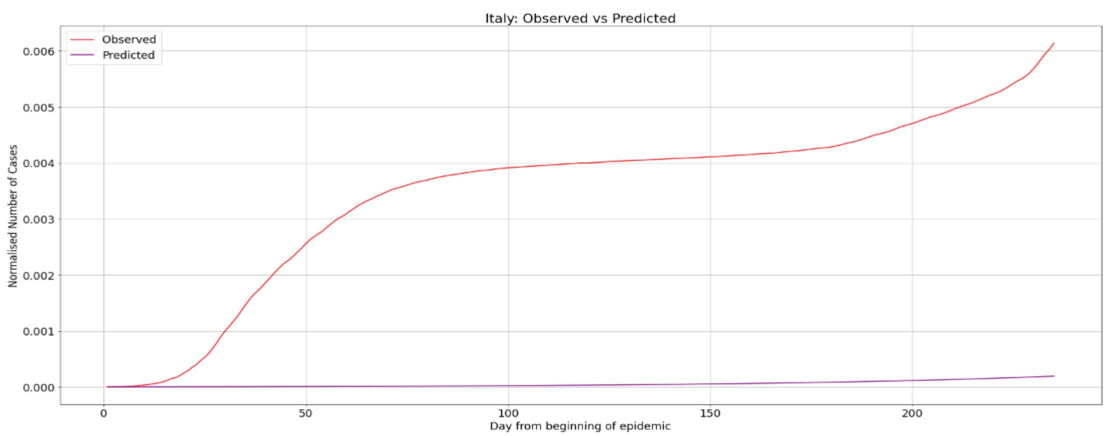

Figure 3.3. Italy's Observed vs Predicted graph for Interval 1 - 235

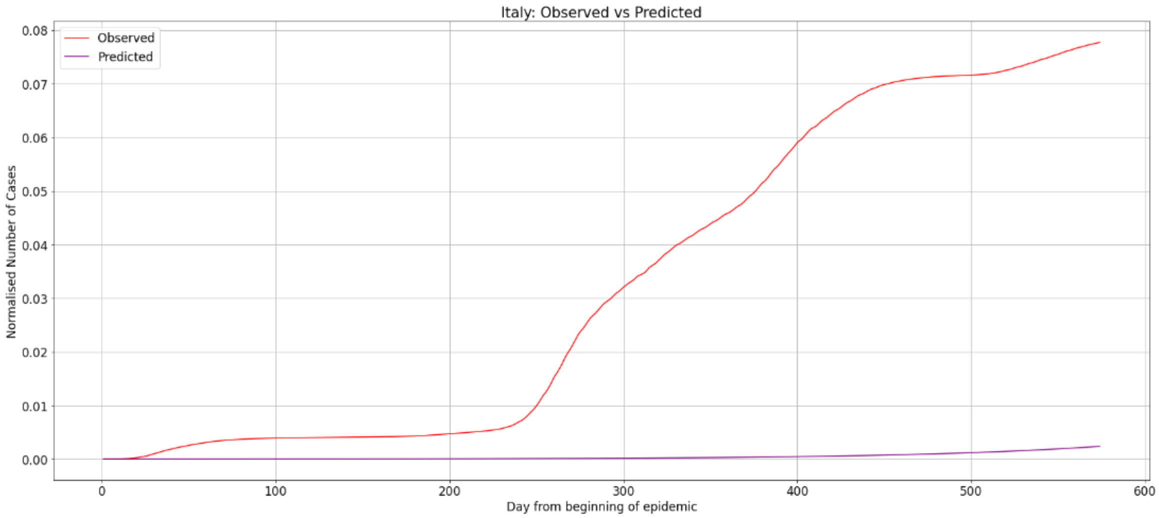

Figure 3.4. Italy's Observed vs Predicted graph for Interval 1-574

Italy	a	MSE	**a (Chapter 2)**	**MSE (Chapter 2)**
1^{st} Interval	0.2970057044682587	0.9263224548149729	0.1037340501732819	1.26675706906e-07
2^{nd} Interval	0.10373405017328197	1.1317017108177394	0.1037340501732819	0.000127109004616
3^{rd} Interval	0.11426026154882764	1.17481468297594	0.1142602615488276	1.40010788288e-05
4^{th} Interval	0.10963509192760246	1.5214301779364932	0.1096350919276024	0.001877497154771

Germany

Based on hypothesis that 50 cases are the start of the epidemic, we integrate our ODE to get values of S_{ign}, S_{res}, I, and R for each of the intervals defined in Chapter 2.

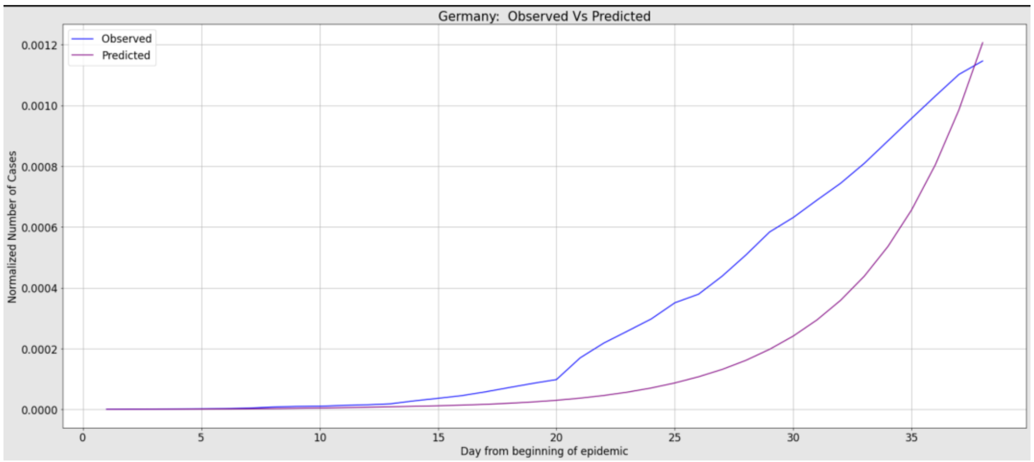

Figure 3.5. Germany's Observed vs Predicted graph for Interval 1-38

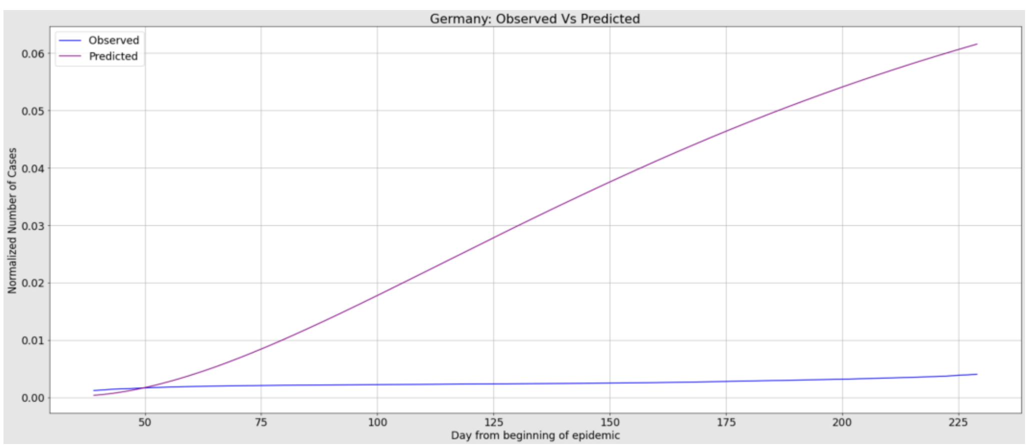

Figure 3.6. Germany's Observed vs Predicted graph for Interval 38 – 229

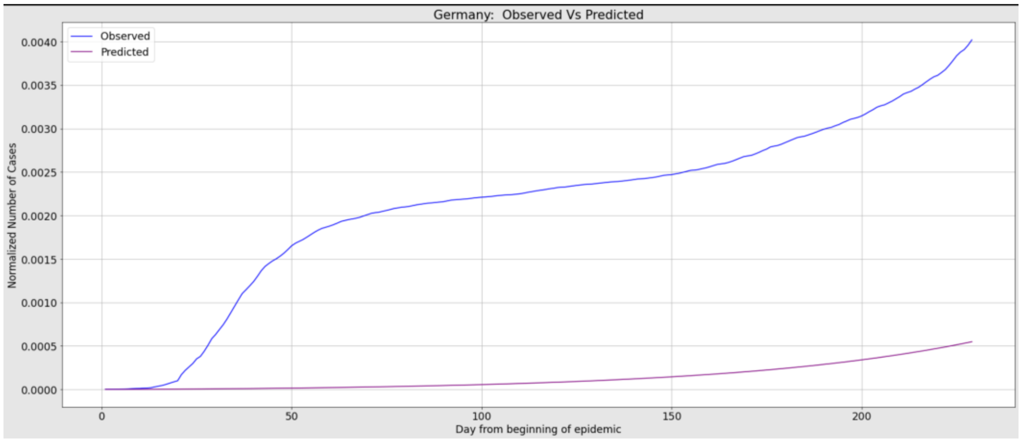

Figure 3.7. Germany's Observed vs Predicted graph for Interval 1 – 229

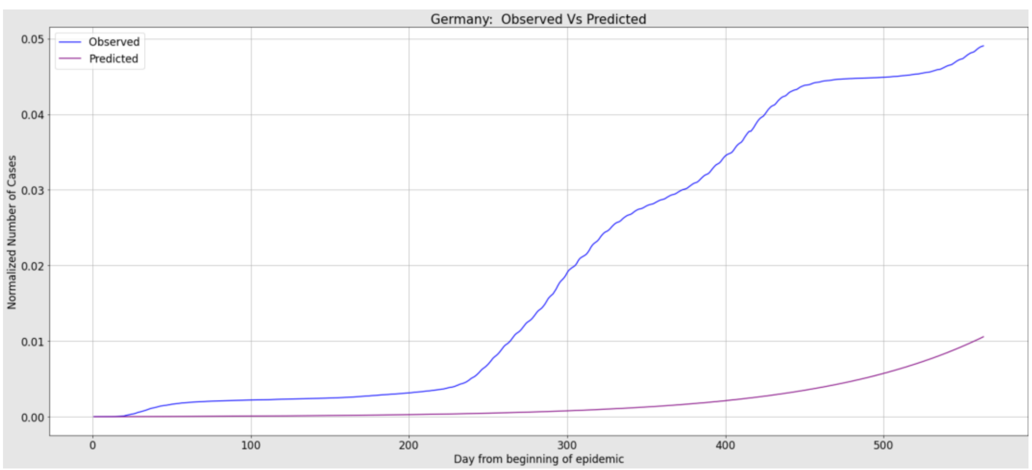

Figure 3.8. Germany's Observed vs Predicted graph for Interval 1 – 563

Germany	a	MSE	a (Chapter 2)	MSE (Chapter 2)
1st Interval	0.3021930219257104	0.9407350436165567	0.3021930219257103	4.88171634301792 e-08
2nd Interval	0.10415179659396571	1.1236492364742459	0.10415179659396571	4.00101175855258 e-06
3rd Interval	0.11623513349779421	1.171433410341442	0.11623513349779421	5.3123052875352 e -06
4th Interval	0.11005244548368058	1.5419447932383867	0.11005244548368058	0.000690983686752321

Turkey

Like Italy and Germany, we have plotted graphs using values S_{ign}, S_{res}, I, and R obtained from integrating the ODEs.

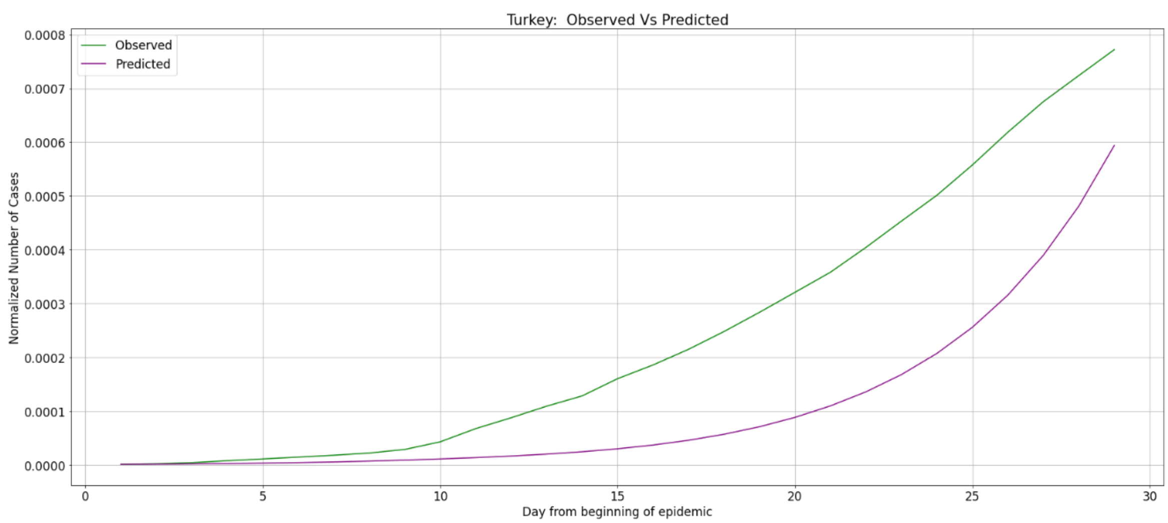

Figure 3.9. Turkey's Observed vs Predicted graph for Interval 1 – 29

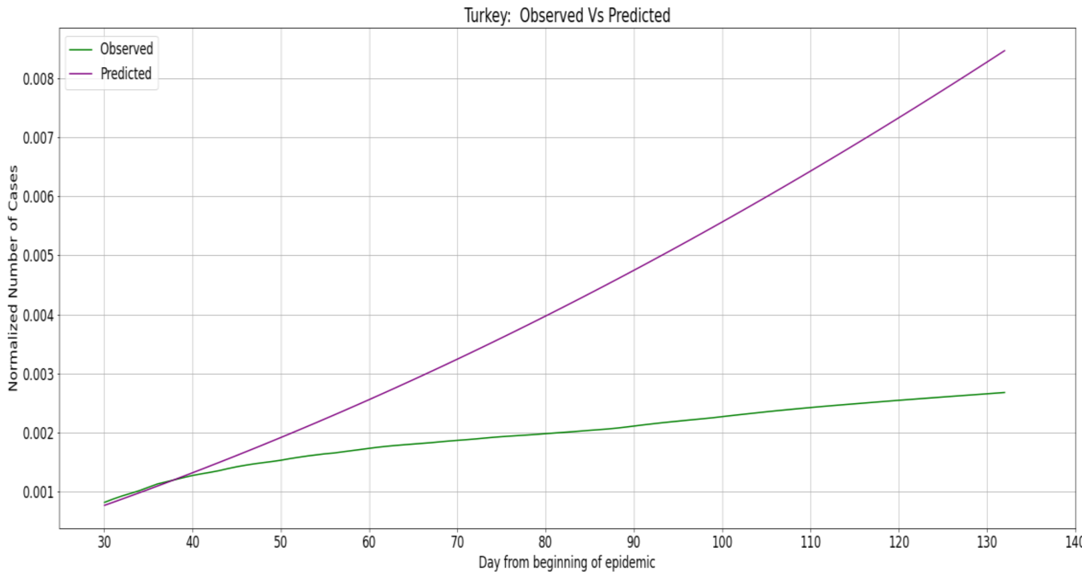

Figure 3.10. Turkey's Observed vs Predicted graph for Interval 30 – 132

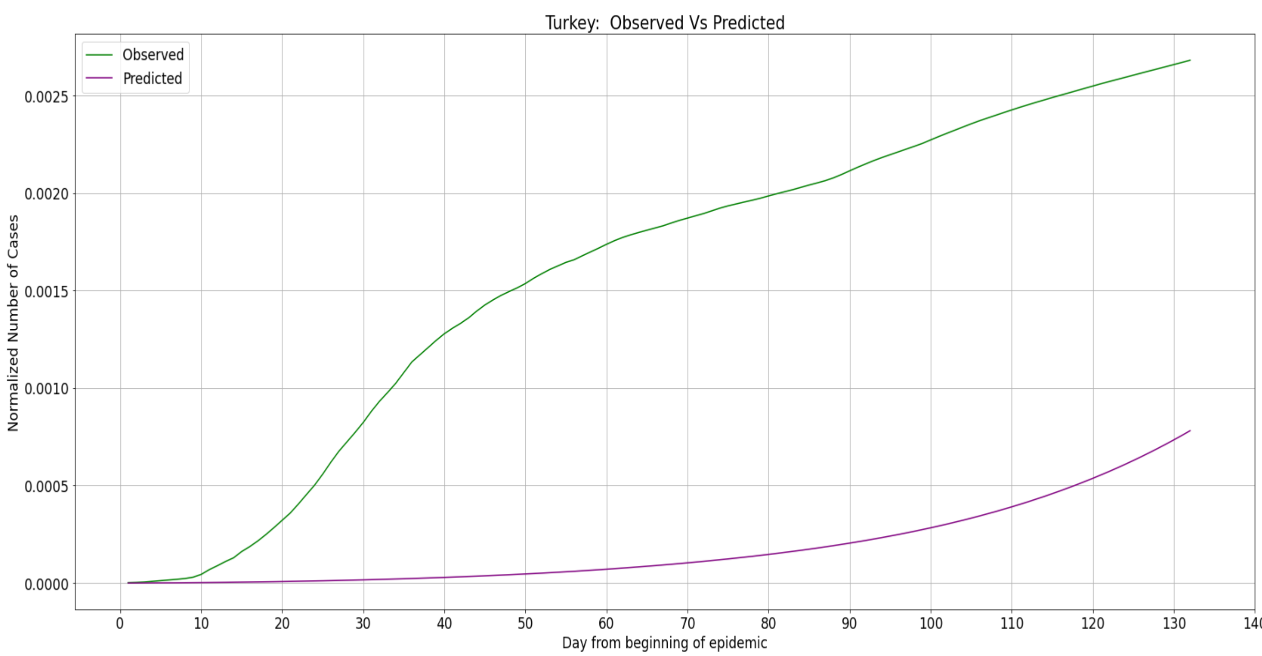

Figure 3.11. Turkey's Observed vs Predicted graph for Interval 1 – 132

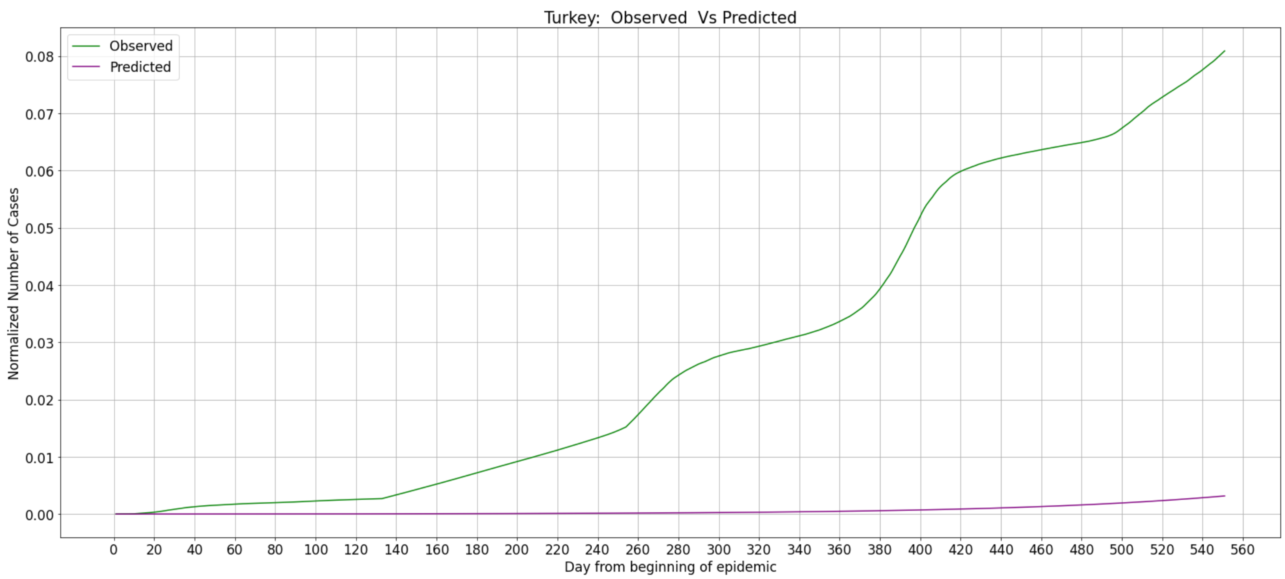

Figure 3.12. Turkey's Observed vs Predicted graph for Interval 1 – 551

Turkey	a	MSE	**a (Chapter 2)**	**MSE (Chapter 2)**
1st Interval	0.3105025774435757	0.9081243552928839	0.3105025774435757	3.65225321837 6e-08
2nd Interval	0.10877202711446118	1.0196150316998251	0.10877202711446118	1.03004493877 e-05
3rd Interval	0.13022144547571432	1.0578165998564693	0.13022144547571432	0.0009892492458
4th Interval	0.1101968156120996	1.5013374173482374	0.1101968156120996	0.00264690292994

Modified Model

To study the behavior of the model and to test the hypothesis, we have redesigned the reaction rate constant for states from "resistant" to "exhaustion". On changing the values, we have integrated the ODE to find modified values. Since our initial k2 value is 1, we have considered values close to this to study the change in behavior corresponding to it. The following are graphs for **k2 value 0.05.**

We have changed the k2 value to get the best output value.

We have considered 200 days based on the social behavior of the population where the maximum population is tired of following the government rules.

Italy

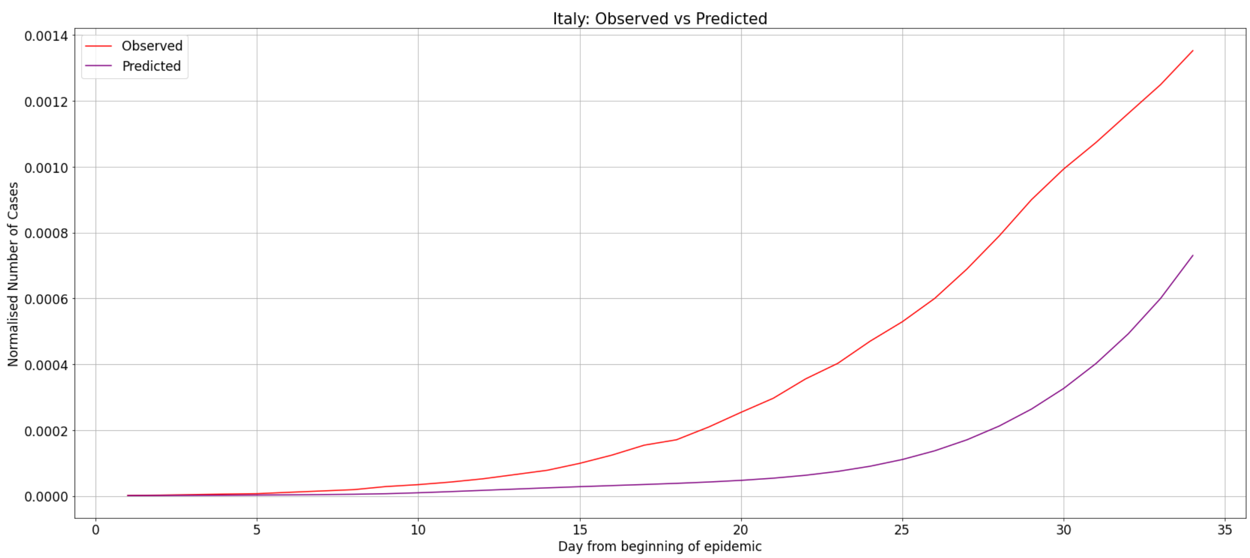

Figure 3.13. Italy's Observed vs Predicted when k2 = 0.05 for Interval 1

We can observe from the graphs that, after considering k2 value as 0.05, our predictions are better than the one by taking k2 value as 1.

Italy has suffered in the worst possible way, so we can say that after first wave, people were more careful and hence spread corona virus was comparatively less in other intervals.

Hence, we have observed better predictor.

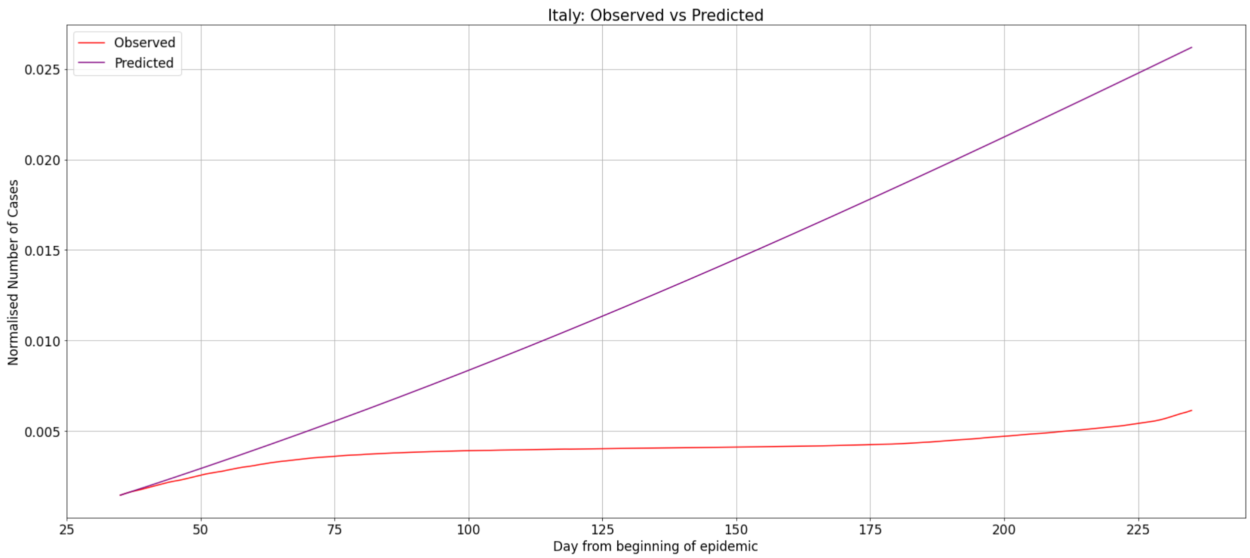

Figure 3.14. Italy's Observed vs Predicted when k2 = 0.05 for Interval 2

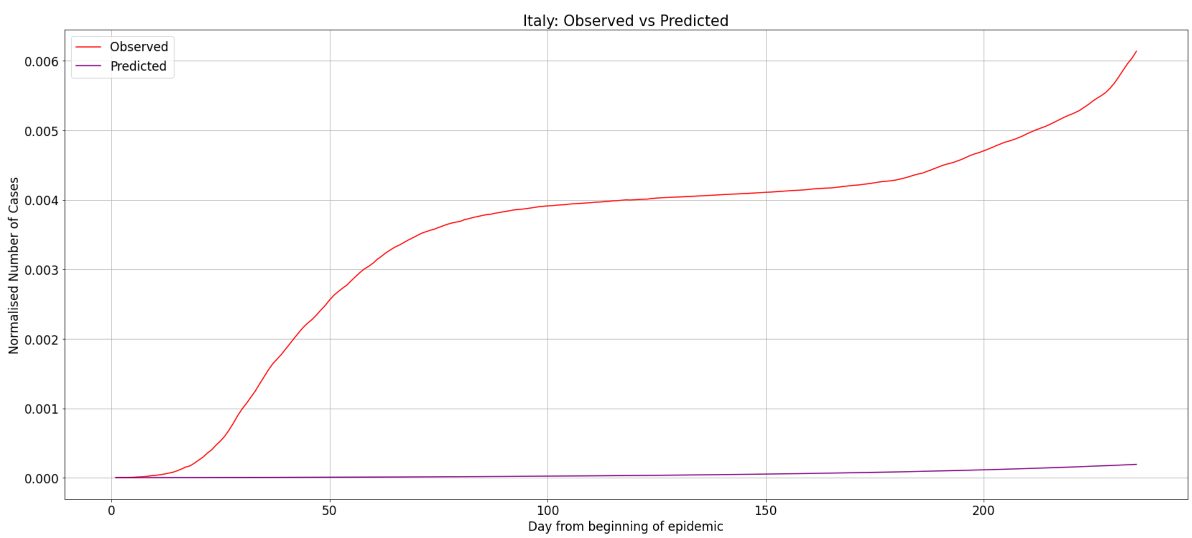

Figure 3.15. Italy's Observed vs Predicted when k2 = 0.05 for Interval 3

Our below graph clearly shows that the predicted value is not accurately matching with the observed graph. We can see that the observed and predicted graphs are slightly closer comparatively in the first 250 days and then we can see the observed value is increasing exponentially. Although, our observed and predicted values are not close enough but our predicted model accuracy has been improved.

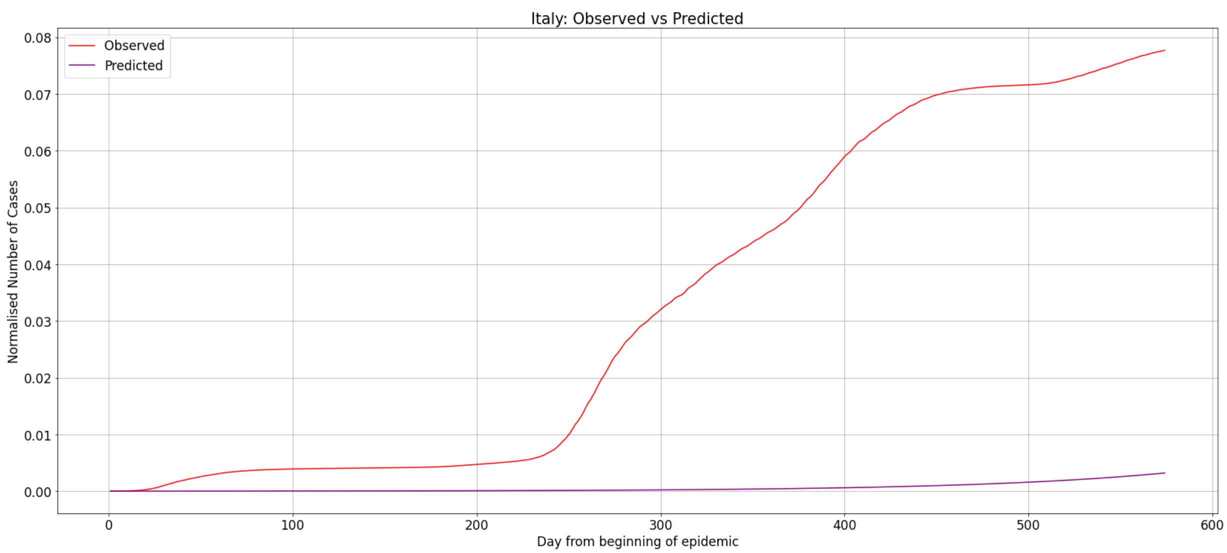

Figure 3.16. Italy's Observed vs Predicted when k2 = 0.05 for Interval 4

Germany

We have changed the k2 value to get the better output value.

We have considered 200 days based on the social behavior of the population where the maximum population is tired of following the government rules.

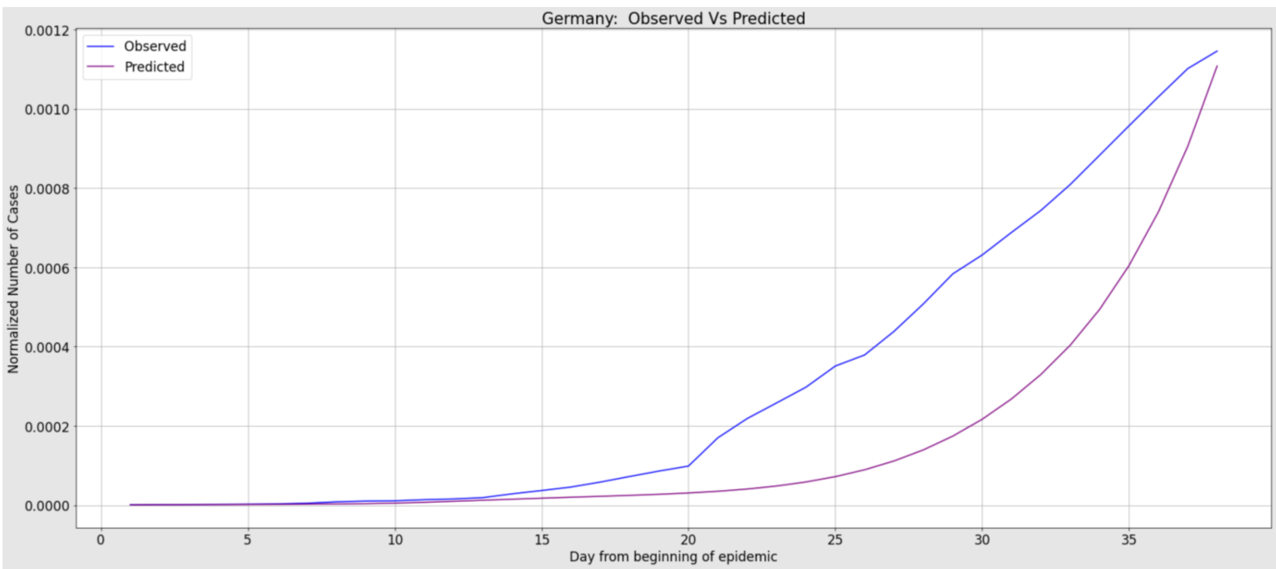

Figure 3.17. Germany's Observed vs Predicted when k2 = 0.05 for Interval 1

We can see that the wave is better for the value the above mentioned k2 value for the first interval. The observed and predicted graphs are almost similar but not accurate.

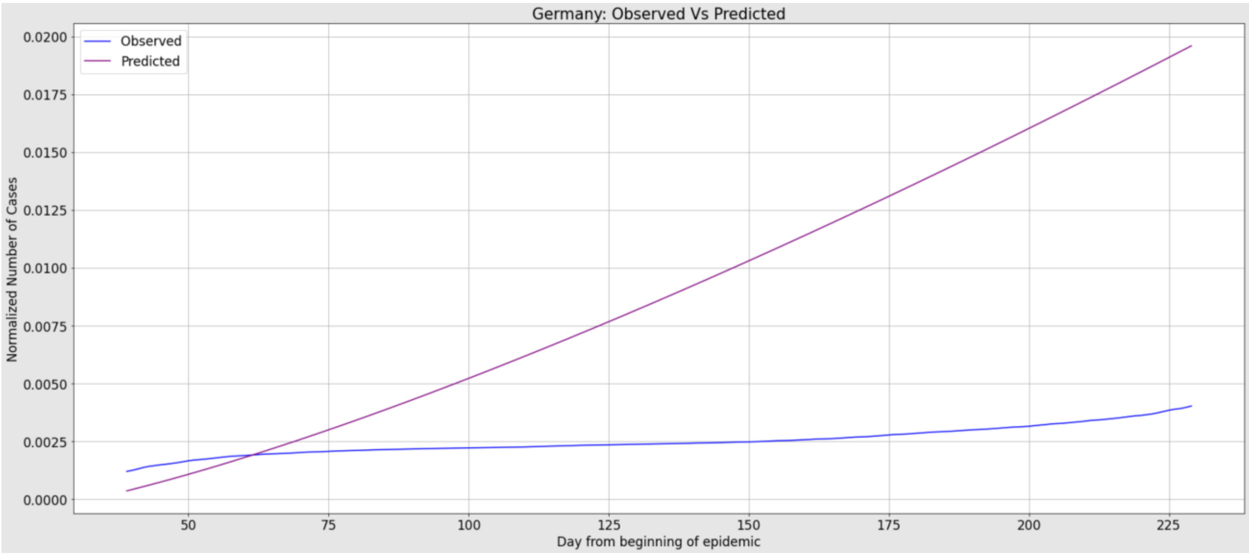

Figure 3.18. Germany's Observed vs Predicted when k2 = 0.05 for Interval 2

For the Second interval , we can see that the observed and predicted graphs are not coinciding with each other.

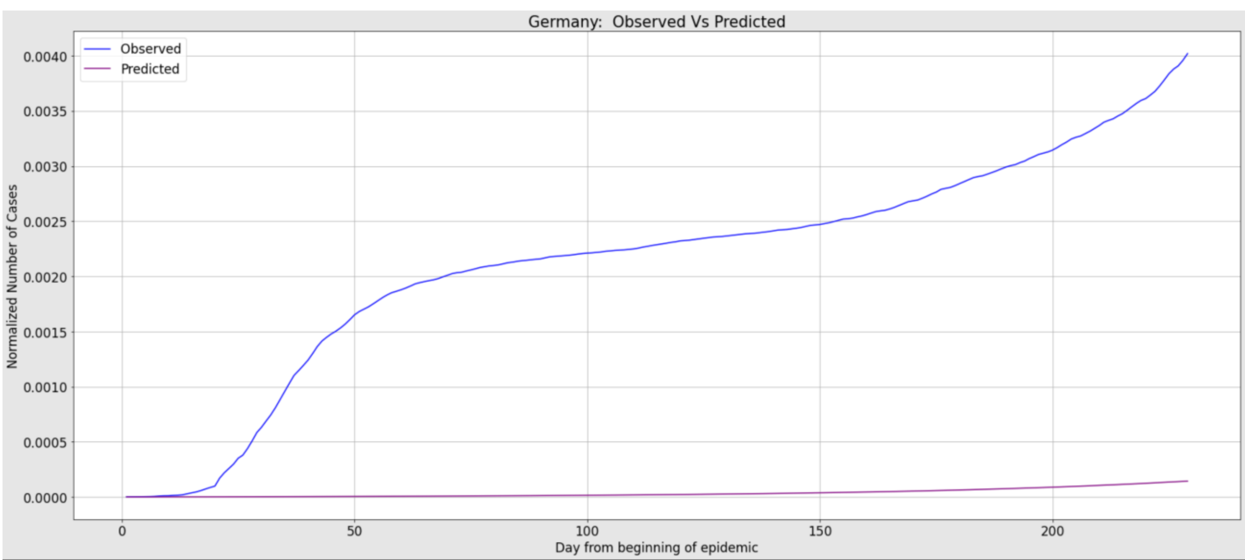

Figure 3.19. Germany's Observed vs Predicted when k2 = 0.05 for Interval 3

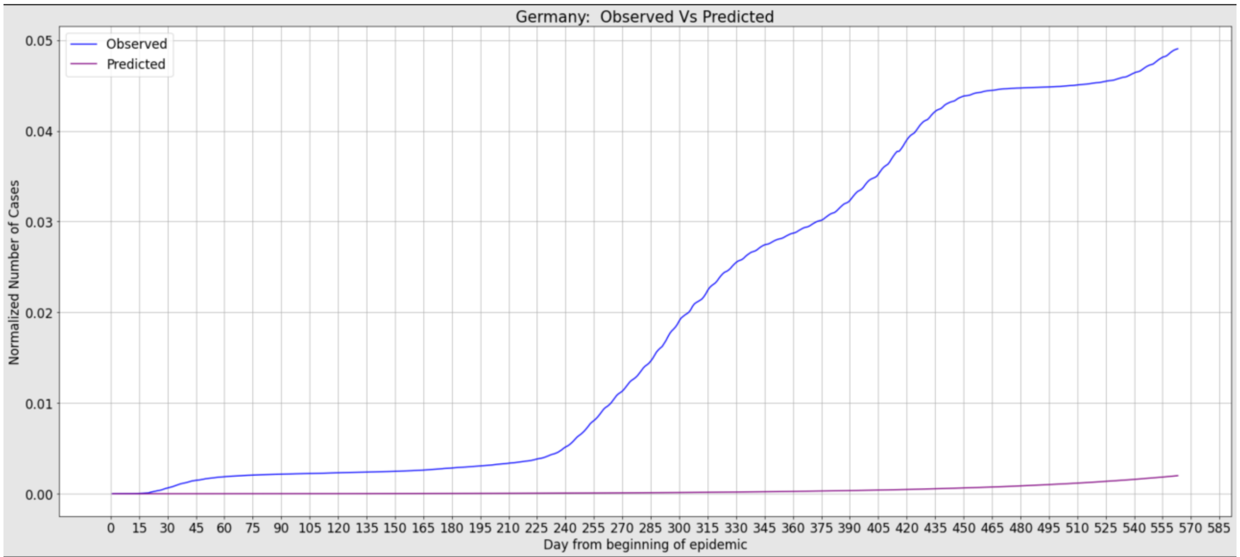

Figure 3.20. Germany's Observed vs Predicted when k2 = 0.05 for Interval 4

Our graph for Germany clearly depicts that the predicted values are slightly closer comparatively in the first 250 days and then we can see the observed value is increasing exponentially. Although, our observed and predicted values are not close enough but our predicted model accuracy has been improved.

Turkey

Following the same changes as we did for Italy and Germany, we have obtained the below graphs for all intervals of Turkey. We are drawing the same conclusion as that of other two countries i.e., our model accuracy is better with change in the value of reaction rate.

Although we haven't observed the best fit model for this data, but we can say that the decrease in reaction rate has improved the accuracy of model. Although we have not demonstrated the graphs for different k2 value, we can say that further accuracy in model can be obtained by lower reaction rate values.

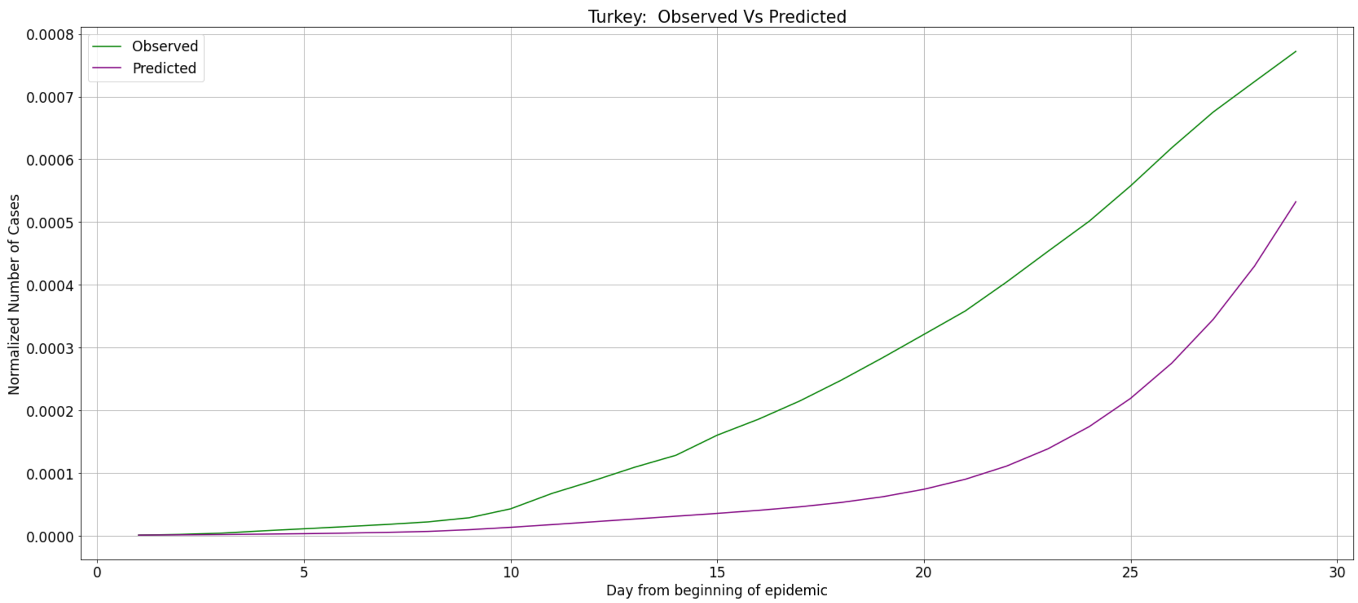

Figure 3.21. Turkey's Observed vs Predicted when k2 = 0.05 for Interval 1

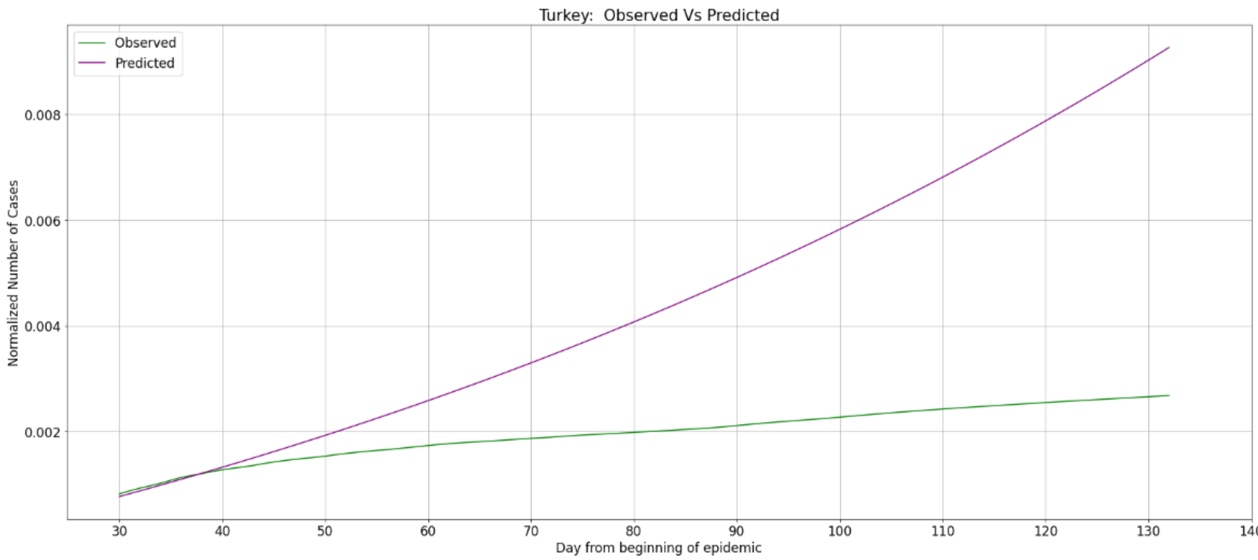

Figure 3.22. Turkey's Observed vs Predicted when k2 = 0.05 for Interval 2

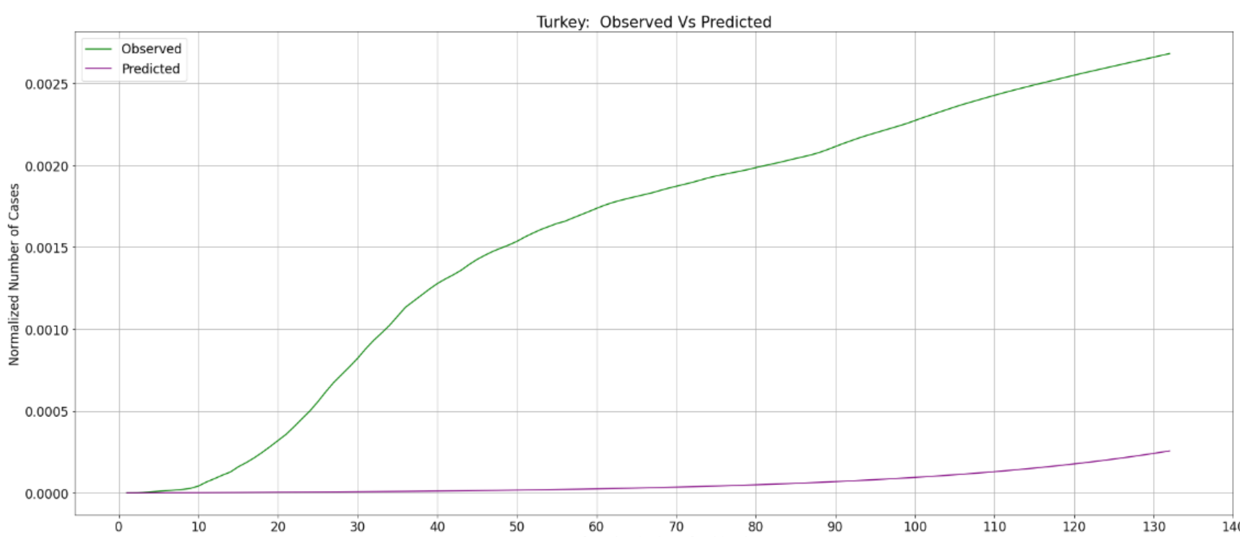

Figure 3.23. Turkey's Observed vs Predicted when k2 = 0.05 for Interval 3

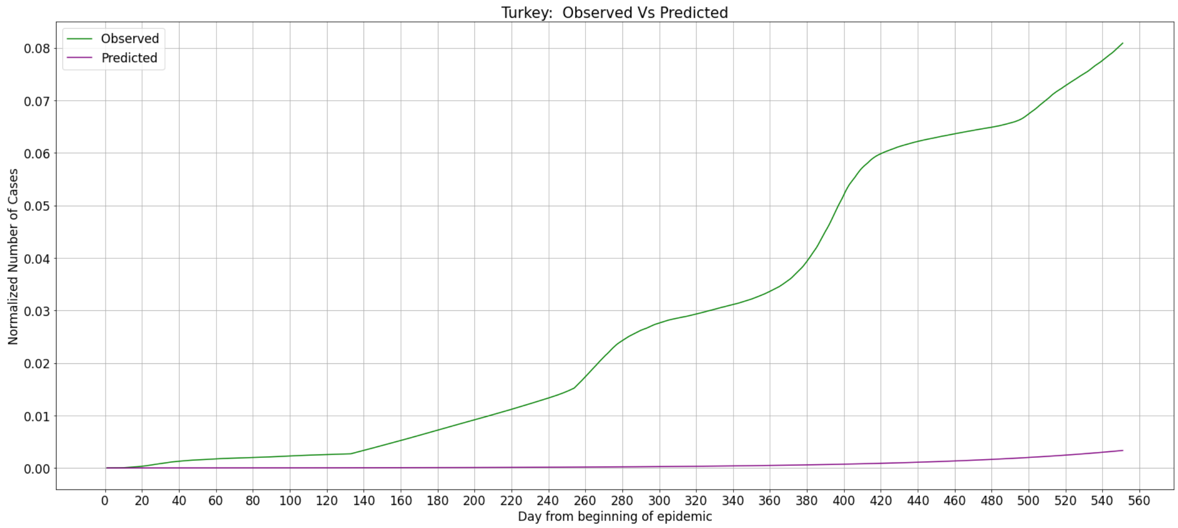

Figure 3.24. Turkey's Observed vs Predicted when k2 = 0.05 for Interval 4

Crowd Effect

By "crowd effect" we mean to represent how news spreads among people, resulting in a change in their behaviour. Factors that affect crowd effect in every human population are mass media, policies imposed by governments, medical infrastructure, like vaccinations and medications, and cultural influences such as festivals and traditions. Social dynamics are significantly modified by various stress factors. In modern times, information channels are TV, Internet, and social networking sites. Sometimes, these channels also serve as transmission source for false news and rumours that instigate fears and presumptions. Assume that the alarm increases super linearly because of these factors and the proper reaction form is,

$$S_{ign} + 2I \rightarrow S_{res} + 2I$$

This reaction signifies the consequences of an "Ignorant" person meeting "Infected" individuals. The reaction rate is

$$qS_{ign}I^2,$$

Where q is a new constant.

We evaluate q assuming that for some selected proportion of infected I the reaction rate is the same as for the linear reaction.

Say, let for $I = Ip = 0.02$ (2% of population)

$$qS_{ign}I^2 = kS_{ign}I_p$$

Then, $q = k/I_p$

The number I_p characterizes the "visibility" of epidemic and depends on activity of mass-media and corresponding influence on the masses.

While working with the crowd effect, we have tried to use the value of Ip and then used it in our code to get result.

Considering the graphs of Modified model, we can say that the below graphs are best fit. Hence, we can say that changing k2 to q has impacted on our predicted model in a better way.

Italy with Crowd effect

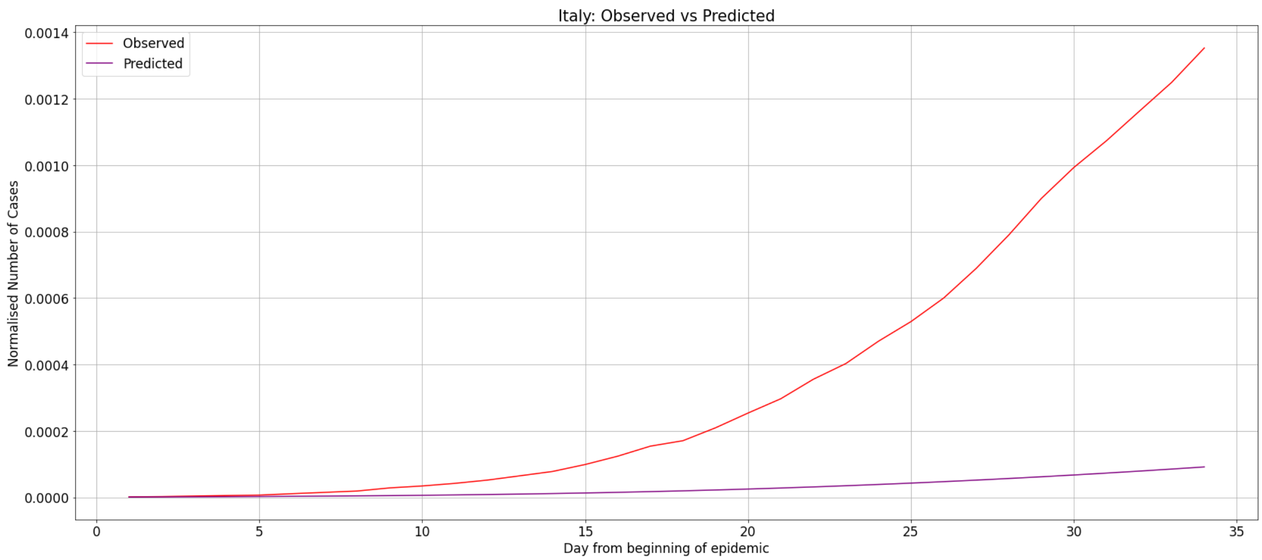

Figure 3.25. Italy: Interval 1 with Crowd Effect

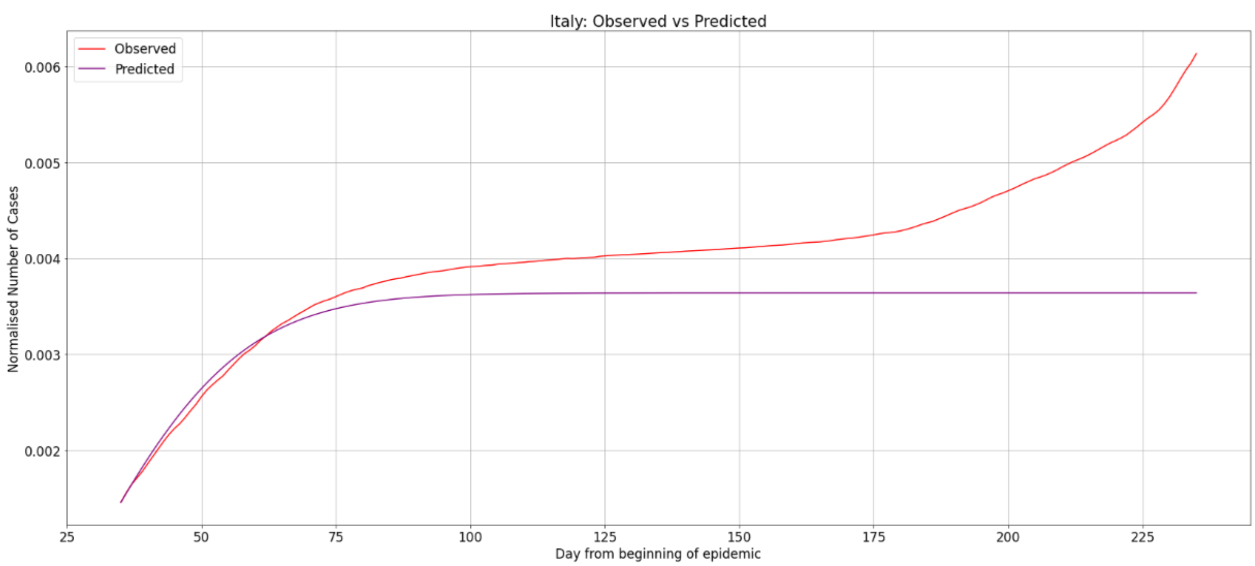

Figure 3.26. Italy: Interval 2 with Crowd Effect

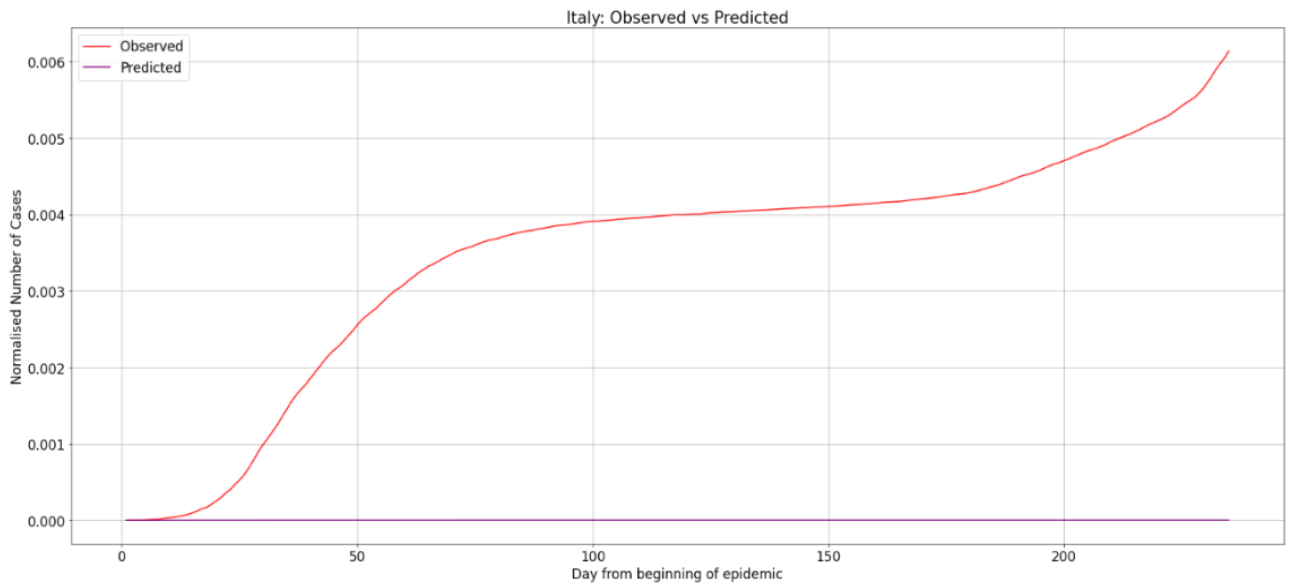

Figure 3.27. Italy: Interval 3 with Crowd Effect

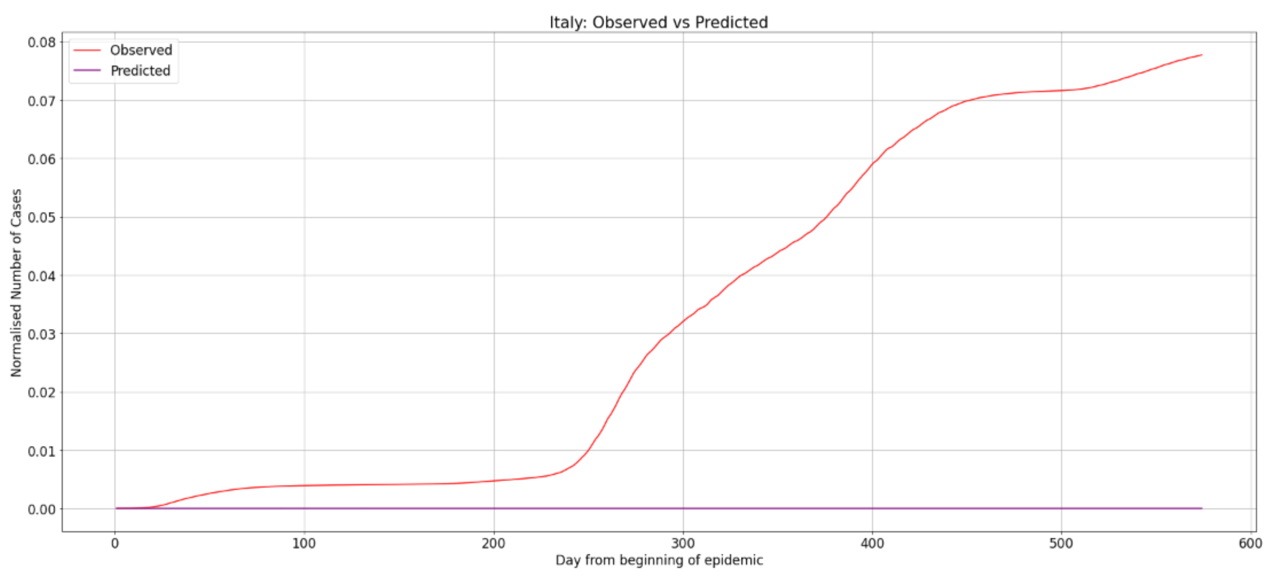

Figure 3.28. Italy: Interval 4 with Crowd Effect

Germany with crowd effect

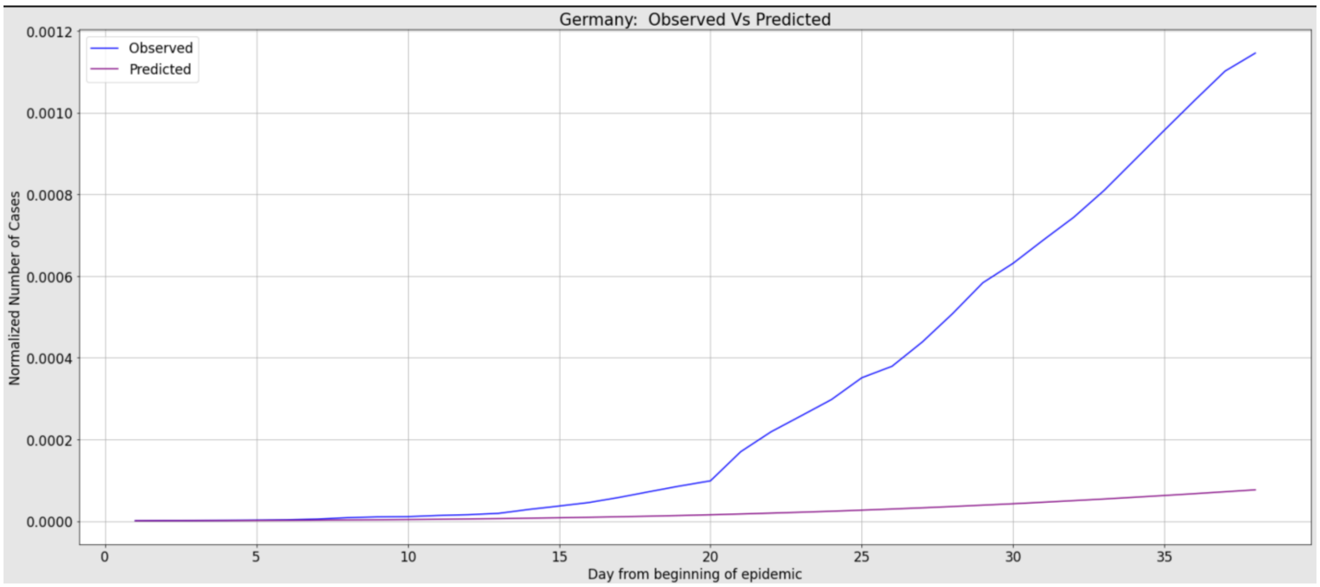

*Figure 3.29. German*y: Interval 1 with Crowd Effect

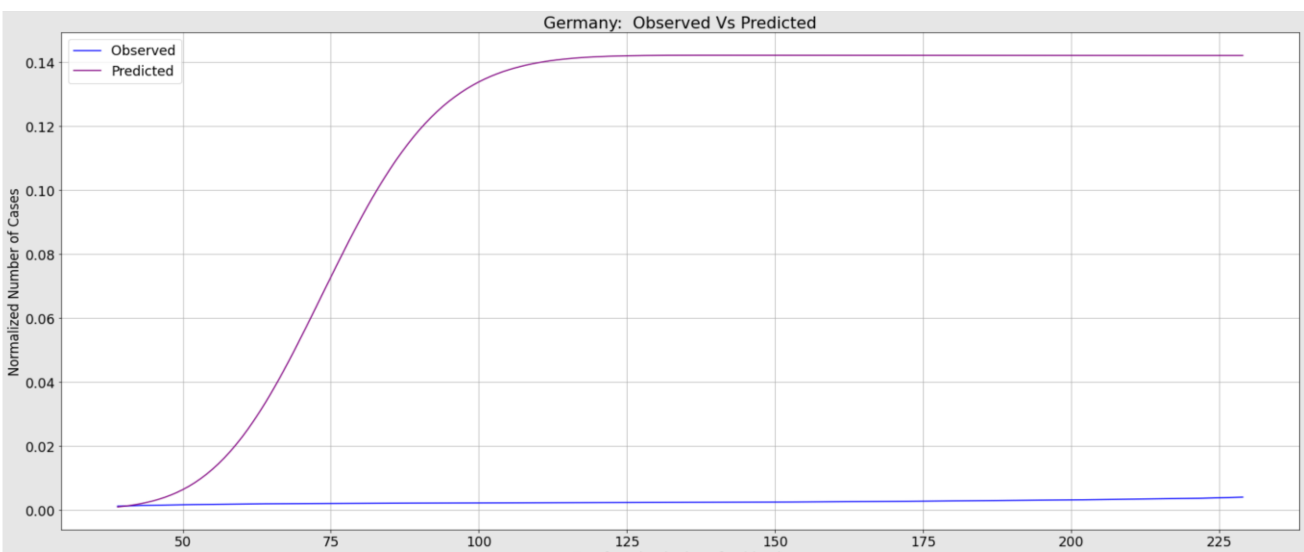

*Figure 3.30. German*y: Interval 2 with Crowd Effect

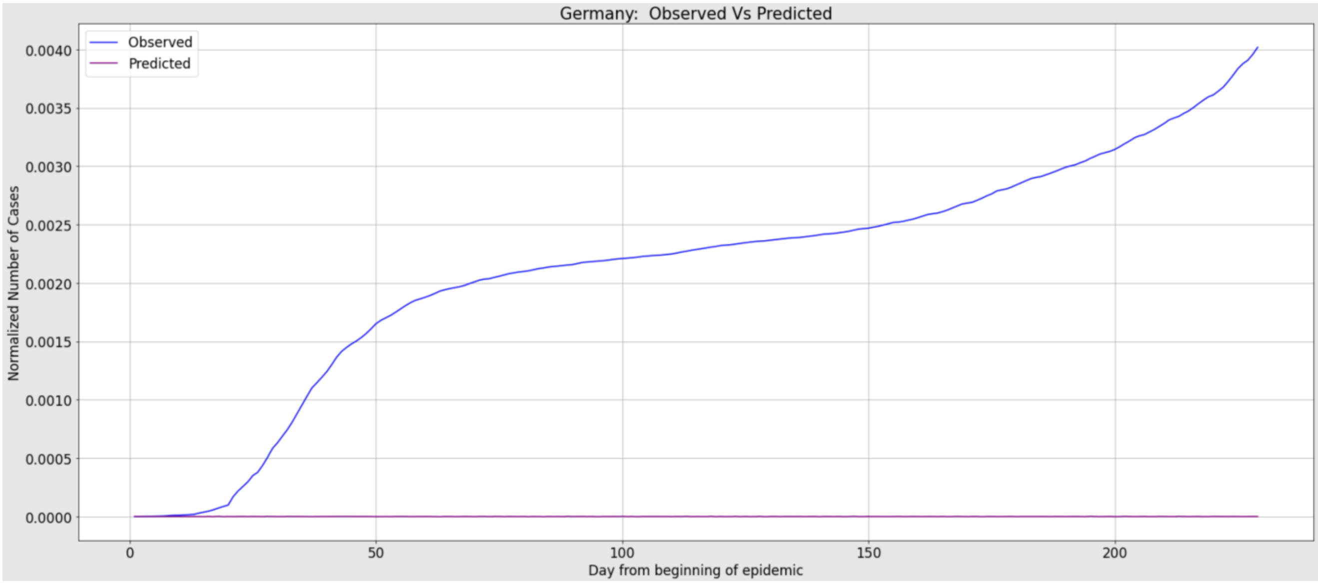

Figure 3.31. Germany: Interval 3 with Crowd Effect

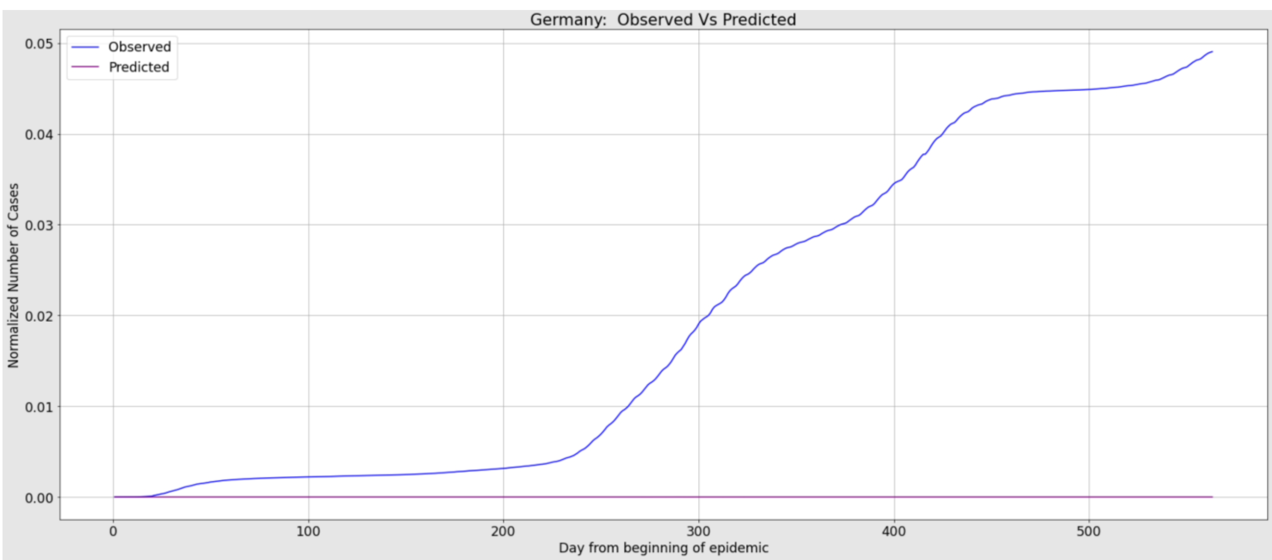

Figure 3.32. Germany: Interval 4 with Crowd Effect

Turkey with crowd effect

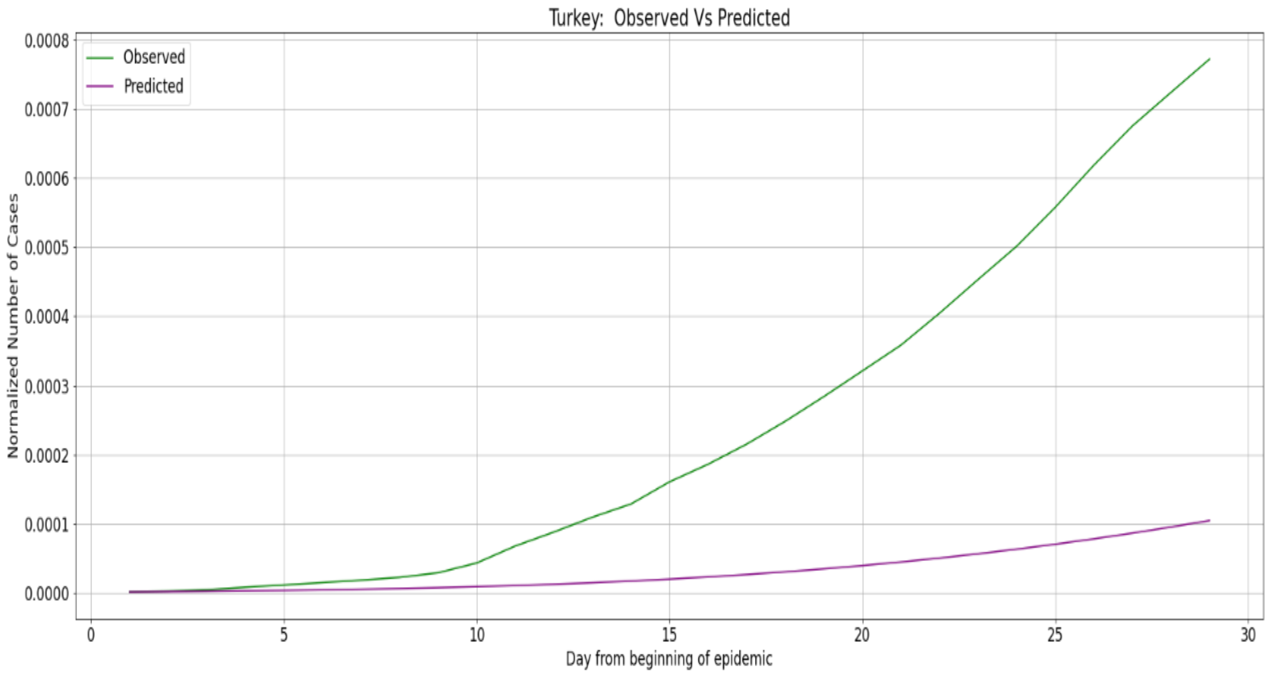

Figure 3.33. Turkey: Interval 1 with Crowd Effect

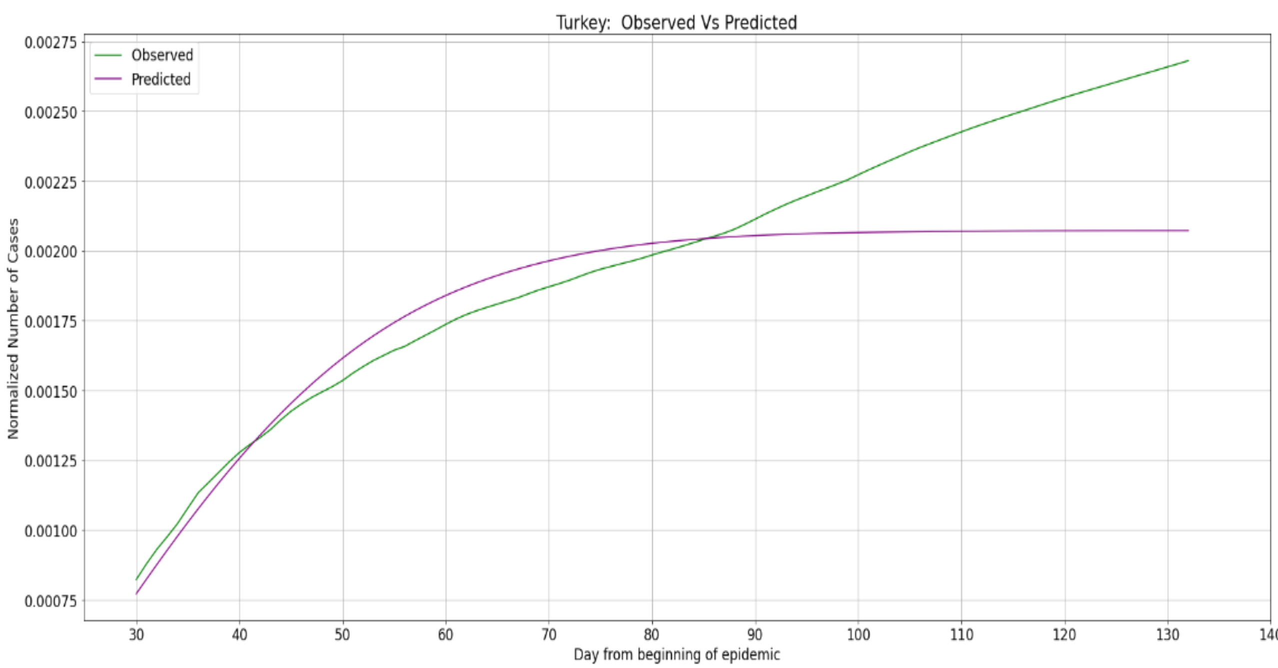

Figure 3.34. Turkey: Interval 2 with Crowd Effect

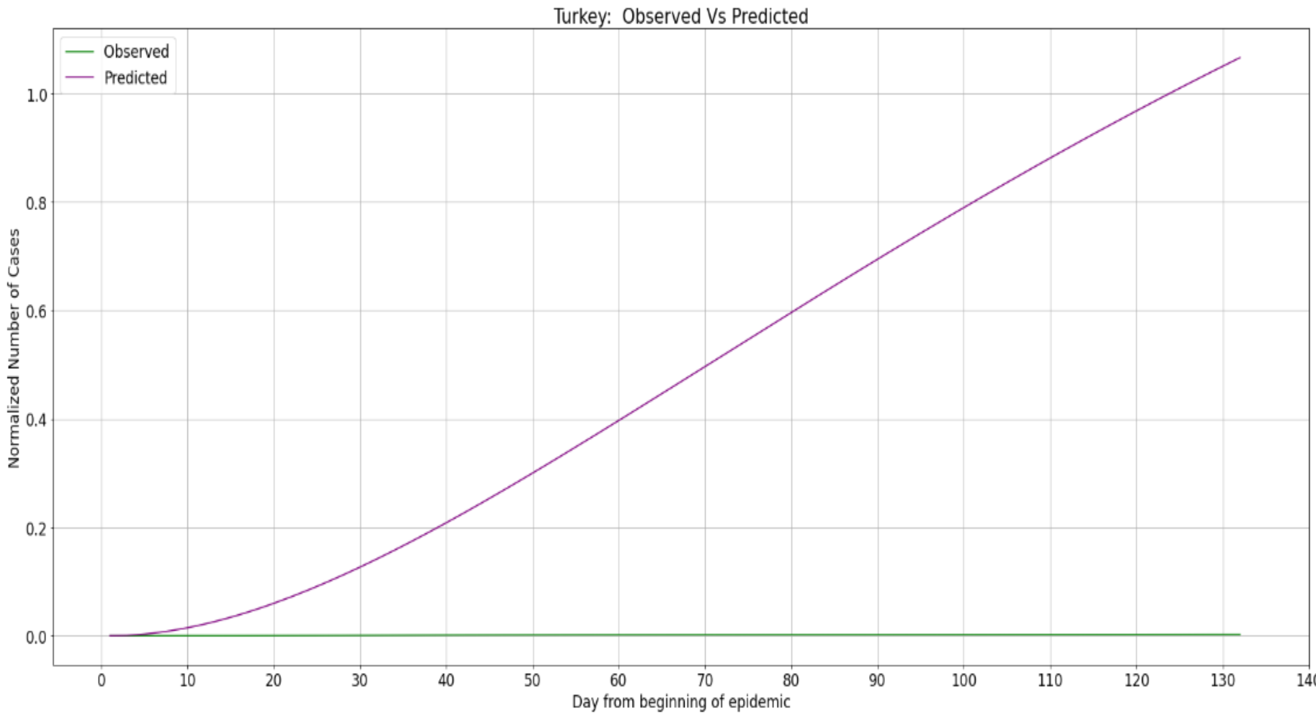

Figure 3.35. Turkey: Interval 3 with Crowd Effect

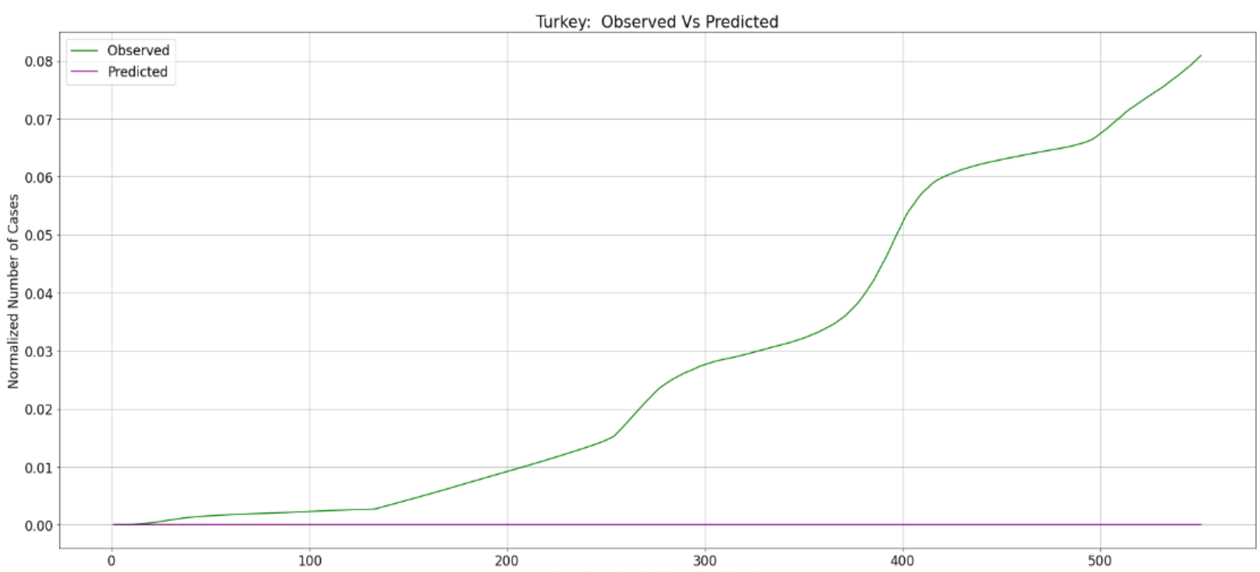

Figure 3.36. Turkey: Interval 4 with Crowd Effect

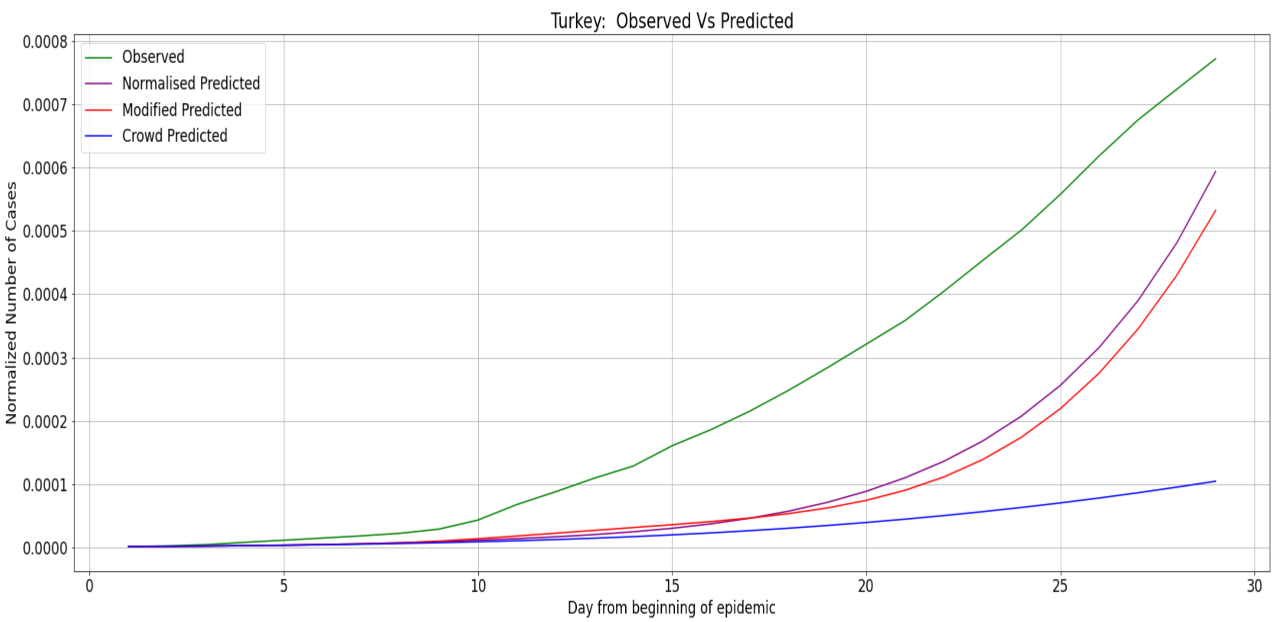

Figure 3.37. Turkey: Observed Infected Population vs All Predicted Infected Population for Interval 1

CONCLUSION

Modeling COVID in this course was a completely different experience. Based on COVID, we have seen different behavioral patterns as individuals in our home countries. But after a thorough investigation of patterns and behaviors, we can predict better about the global behavior of all people under pandemics and stress. In addition, how some countries dealt with this stress much better than others. It seems that stress and fatigue were high in the United States, Colombia, Iran, etc. Regarding the position of our group, when implementing this system for more realistic analysis in the field, there are several other things to consider when building this system. We know that this can complicate the model, but we also need to consider these factors, such as regional factors, age, religious beliefs, ethnicity, and immune system. Adding these to the vaccination process can build a much more powerful model. Otherwise, we'll talk about this SIR model. Grouping people in this way and identifying patterns between them was new to all of us, so this model is definitely a great model.

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