

Analysis of COVID-19: An infectious disease spread

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Abstract

This study utilizes the Logistic Growth Curve (LGC) based forecast model to assess the effectiveness of Stay At Home (SAH) Order on COVID-19 pandemic spread in California while making comparisons and visualizations for multiple countries. In comparing results, previous work relied on confirmed or death cases which not scientifically valid due to the differences of population sizes of each country. We presented several methods being used in the past and how we utilize percentages, normalization and derivatives to help our evaluation and comparisons of several countries using our model. Our approach compared the spread of the virus considering the growth rate and developed a quantitative measure that can help compare quantitatively between multiple states or countries. In our analysis, we showed evidence to suggest that the forecast results correspond to the progress and effectiveness of the SAH Order in flattening the curve, which is useful in controlling the spike in the number of active COVID-19 patients.

Keywords: COVID-19, virus spread, Logistic Growth Curve, prediction, Stay At Home

1 Introduction

Infectious diseases that initially develop in a community or that may have existed earlier but are rapidly spreading are among the deadliest [1]. These types of diseases continue to pose a threat to human wellbeing [2]. It's been nearly two years since we began this difficult battle with the COVID-19 or Corona Virus Disease 2019. On December 31, 2019, Wuhan, China, became the first city to report coronavirus illness (COVID-19) [3] and on March 11, 2020, the World Health Organization (WHO) declared this virus as a pandemic [4]. A positive-sense single-stranded RNA virus is the source of this disease and is contagious in humans [5]. These rapidly spreading microscopic creatures are too small to be seen with the naked eye [6, 7].

The coronavirus pandemic is causing widespread fear, worry, and concern among the general population, as well as specific groups such as the elderly, caregivers, and people with underlying health difficulties, as it spreads around the world [8]. People over 65, as well as those with underlying medical disorders such cardiovascular disease, diabetes, chronic kidney disease, and cancer, are more likely to

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acquire serious illness [9]. The COVID-19 outbreak is also posing a significant economic danger to the world [10]. Almost all economic sectors have been affected by the closure and instability. Companies are shutting down as well as employees are losing their jobs [11, 12]. It is clearly obvious that any pandemic will have a significant negative impact on the global economy [13].

The COVID-19 pandemic has shaken the entire world and change the lifestyle of everybody [14]. People all over the world are fighting this epidemic around the clock, because of its aggressive nature of spreading ability [15, 16]. Health and infectious diseases experts suggested different measures to control or slow-down the spread of the virus. Such as, Stay At Home (SAH) order, quarantine, keeping six feet distance, mask for all while others are present [17]. The SAH was one of the most effective measures that helped to slow-down the spread of the virus rapidly. Different countries call this measure in different names, such as, in Malaysia it is known as Movement Control Order [18], and lockdown in the Netherlands [19]. The spread of the COVID-19 virus pandemic has caused millions of lives; it has impacted almost everybody socially and emotionally.

This type of pandemic is not something new to the world, and its measure to prevent the aggressive spread is also not new. For example, Spanish flu. This flu [20] began in March 1918 and is believed to have caused the death of over 50 million worldwide. At the time, the steps for lowering the affected rate were a copy of today's (masks, disinfection, and distance). Isolation measures were also similar to todays: restricting gatherings, closing borders, institutions and schools. It is not always that a counter-measure like SAH are welcomed by the general public. However, authors of researchers found that SAH is very effective to control the spread of a pandemic. Unfortunately, the world may experience a similar type of pandemic in the future and a detailed study to support the effectiveness of SAH could be beneficial to help people understand the importance of the counter-measure.

Purpose of the study The purpose of this study was to understand and compare the spread of the COVID-19 virus for different countries and see if SAH was helpful in slow-down the infection rate. This study focused on the following research questions.

- (1) What single mathematical model can help to model the virus spread for different countries?
- (2) How to compare virus spread in different countries?
- (3) How to measure the impact of SAH on virus spread in different countries?
- (4) How to compare the growth rate of viruses for different countries?

Our contributions to this paper can be listed as follows:

- Analyze the virus spread for more than one country using time segments. Time segment shows which portion had the most infection than the other.
- Present a way to show the aggressiveness of spread and visualize it by comparing with other countries.
- Show the intensity of the lockdown or SAH.
- Future projection of virus spread without the SAH.

2 Literature Review

The first infection of COVID-19 was reported in Wuhan, China [21]. Since then, it has rapidly spread throughout the world. The most-affected countries are the United States, Italy, and Spain. Researchers and medical professionals have been able to track the rate of growth of this virus in different countries, because of active research in the fields of computers and mathematics [22]. Researchers from across the world are attempting to evaluate the virus's impact and influence on our civilization. To assess its impact, researchers have gathered data and developed visual analytics and made their findings available to everybody. Different types of mathematical models helped to explain the nature of the spread of the virus.

2.1 Mathematical models to analyze infectious disease

Several mathematical models were presented from researchers to describe and predict the COVID-19 threat. For example, in [23], the authors demonstrated that the Logistic Growth Curve (LGC) Model can accurately predict the short-term picture of new cases for India and high-incidence states. They also demonstrated how Susceptible, Infected, and Recovered/Deceased (SIR) model may predict the maximum number of active cases and peak time, as well as how a Time Interrupted Regression model can be used to assess the impact of lockdown and other measures taken. In [24], the authors mentioned that LGC is a good fit for time-series data, which is the case for COVID-19 infection spread. The authors used LGC to explain the spread for China, South Korea, and Iran. According to their research, the model did not produce reasonable forecasts for countries that were in the early stages of outbreaks. A logistic framework for researching epidemics in places where the number of patients has already reached its maximum level, on the other hand, can produce reliable predictions.

For the projection of the epidemic spreading potential and pandemic cessation dates in China's mainland, Iran, the Philippines, and Taiwan, authors in [25] employed a Generalized Logistic Model (GLM). The short-term estimated number of COVID-19 cases matched confirmed reports of those infected throughout the four countries, while the long-term projections were able to appropriately assess the pandemic's spread in China's mainland and Taiwan. Likewise, the SIR Model is a well-known epidemiologic method for modeling the pandemic. Researchers [26] enhanced this model with the ability to accommodate surges in the number of susceptible individuals, and it was supplemented by recorded data from China, South Korea, India, Australia, the United States, Italy, and the state of Texas in the United States to provide insights into the spread of COVID-19 in communities.

Most existing studies used LGC to analyze the spread of the COVID-19 virus. Which indicates that LGC is a good mathematical model and appropriate to analyze infection of contagious disease. In this study we used LGC similar to [18] as well to model the virus spread in different states and countries. In addition, several other studies used machine learning to develop predictive models to analyze COVID-19 disease spread and related published studies[27, 28, 29, 30]. For example, Peng et al. [27] used support vector machine to predict COVID-19 cases for different countries. Elaziz et al. [29] used machine learning technique in X-ray image analysis to separate COVID-19 patients from other diseases. In this study, we mainly focused on use of machine learning technique to forecast analysis and comparison of spread to understand which place had the most aggressive spread.

2.2 Compare the spread of infectious disease

The distributions of COVID-19 in the United States of America, Spain, Italy, Germany, the United Kingdom, France, and Iran were compared and clustered using the fuzzy clustering technique by the authors in [31]. The distribution of spreading in Spain and Italy was roughly similar and distinct from

that of other nations, according to the clustering results. The data demonstrated a significant and positive link between total confirmed cases, total fatal cases, and the size of the countries' populations. As a result, comparing countries based on the number of confirmed or death cases was not scientifically valid because the number of cases was proportional to the population size.

To the best of our knowledge, no study tried to compare the spread of the virus considering the growth rate. But, developing a quantitative measure seems yet to be developed. To compare the spread it is important to develop a quantitative measure that can help to see which state or country has seen the most aggressive spread. In this study, we present a way to develop a quantitative measure to compare states and countries' infections. This model can be used in other studies where researchers could use it for comparison purposes. Therefore, this study could be a good reference study for those who are working to model and compare contagious diseases.

3 Methodology

3.1 The dataset/data collection/ data processing

For this study, we gathered epidemiological data for the Novel Corona Virus (COVID-19) from 22 January 2020 to 3 September 2021. As a result, the dataset contains data for 591 days, displaying the total number of confirmed COVID-19 positive cases on a daily basis. The data comes from a variety of sources, including the World Health Organization (WHO), the Ministry of Health Singapore (MOH), and others, and is produced by the Johns Hopkins University Center for Systems Science and Engineering [32].

3.2 Data Analysis

We used COVID-19 data from Malaysia, Spain, Italy, and California in this study. We used these countries data because of its availability and at the beginning these countries had the highest number of infection rates. The data for this investigation came from a variety of sources [32]. A list of the total number of positive COVID-19 cases is supplied in this dataset, however the positive number of cases on a specific day is absent. That's why we had to find out based on the information we had. Directly applying analysis to the dataset to compare the growth rate is not viable since it will not produce correct results and will have a significant risk of biasness because population sizes differ from country to country. Therefore, we begin by preparing the data. We examine percentage changes between two countries in this stage. But first, we normalized the data from 0 to 1 so that we could compare the results on the same scale. Thus, we thoroughly examined the data and arrived at a conclusion regarding our research questions.

Mathematical Model of the Virus Spread for Different Countries *What single mathematical model can help to model the virus spread for different countries?*

In this study, a logistic curve, rather than an exponential curve, was used to model the spread of infectious disease [33]. At first the growth begins exponentially, but it always slow down after a certain point known as the inflection point [34]. The inflection point is essentially the spread's midpoint. A logistic curve will be used to model the total number of new cases. In this study, we looked at the effectiveness of the SAH by comparing the total new cases of COVID-19 infections to the predicted total new cases and SAH orders in different time segments. LGC has been used in several previous studies to forecast growth in a variety of fields [35], [18].

An LGC is an S-shaped sigmoidal curve with three phases, as shown in Fig 1. In the first phase, growth is slow, in the second phase, growth accelerates, and in the third phase, growth slows down.

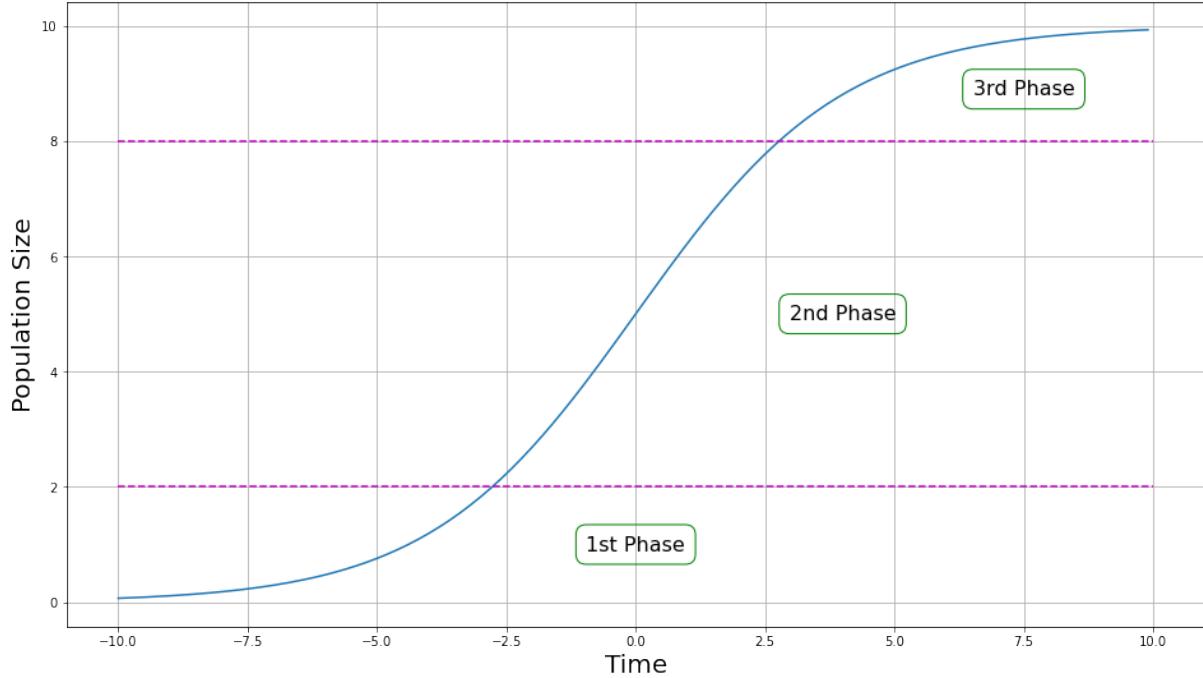


Figure 1: A Logistic Growth Curve (LGC) Structure

Equation to find the LGC can be written as,

$$y = \frac{K}{1 + \exp(a + b \times x)} \quad (1)$$

where y represents the total number of cases at a given time x . The parameters a and b aid in the shaping of the curve. K is known as the “Carrying Capacity”, which refers to the maximum size of a disease infection [36],[37]. The curve is fitted to the available data to determine the values for a and b for further forecasting. The Mean Squared Error (MSE) was used as the cost function (i.e., $J(\theta)$) in the process, which is defined as

$$J(\theta) = \frac{1}{n} \sum_{i=1}^n (h_\theta(x^{(i)}) - y^{(i)})^2 \quad (2)$$

The cost function $J(\theta)$ helped to adjust the parameters of the LGC (see Eq. 1 for more details about LGC). In Eq. 2 the θ is the parameter vector (a, b) to optimize, n is the number of data points that are available. At any particular moment $x^{(i)}$, the total number of infected cases is denoted by $y^{(i)}$, the total number of infected cases predicted for a particular θ using equation (1) is represented by $h(x^{(i)})$. The goal is to discover a θ that gives the lowest cost value, that is, when the curve’s projected values are very close to the actual data points. Our model is primarily applicable to infectious diseases with S-shaped growth, because the number of deaths is heavily influenced by a nation’s hospital management, population parameters, and a variety of other factors that do not meet the model’s assumptions and that could lead to a significant error.

Compare the spread of the disease *How to compare virus spread of different countries?* After that, we wanted to compare the growth rate among different countries. For this reason, we had to find out the percentage change on daily new cases of one country with respect to another country. But before that,

we normalized the data of two countries between the range of 0 and 1. As the amount of a country's population fluctuates, normalization was employed to compare two countries on the same scale. The formula for normalization is as follows:

$$z_i = \frac{d_i - \min(d)}{\max(d) - \min(d)} \quad (3)$$

The equation came from Amiruzzaman's [38] study. In this equation, z_i is the normalized value, d_i is the new number of positive cases on a day, $\min(d)$ is the minimum number of positive cases among all the cases and $\max(d)$ is the maximum number of positive cases among all the cases. Also d denotes all the positive number of cases recorded on a daily basis.

Measure the impact of SAH on virus spread *How to measure the impact of SAH for virus spread on different countries?* To accomplish this, we used time blocks to analyze the growth. This allowed us to compare different countries and states using the similar time blocks. Such as, 0 to 100 days, 101 to 200 days, etc.

Compare the growth rate of viruses *How to compare the growth rate of virus for different countries?*

After normalizing each day a new positive number of cases we then find out the percentage change among two different countries. The formula for percentage change is as follows:

$$\text{Percentage (\%)} \text{ change} = 1 - \frac{Y}{X} \quad (4)$$

In this equation, positive value indicates Y is more aggressive than X , whereas negative value indicates X is more aggressive than Y . On a given day, X indicates the number of new cases in one country and Y represents the number of new cases in another country.

Finally, we wanted to quantify the spread's increase across countries. That is why derivatives were utilized. We begin by drawing a trendline of polynomial order 4 and deducing an equation from it. We chose polynomial order 4 because it yielded the highest R2 value. On that equation, we then applied derivative.

4 Experimental Analysis

Forecasting COVID-19 total number of cases with a large number of accuracy was the main target of this analysis. The spread of the COVID-19 disease in California was another focus of our research. On January 26, 2020, the first two positive COVID-19 cases in California were reported. When the number of positive COVID-19 cases began to rise, the government imposed the SAH Order on March 19, 2020 for the very first time in California, which was followed by the Regional SAH Order on December 5, 2020 [39]. As a result, the Californian case fits perfectly with our work analyzing the effectiveness of the SAH Order. In this section, we describe the dataset we used in our analysis, followed by the experimental results and analysis of our approach to studying the effectiveness of SAH Orders in California.

On a scale of 100, we used time segment. The reason for this was to find the results on a smaller time scale rather than a larger scale, as larger scales can often produce incorrect results. The number of cases is dependent on the size of the population. As stated by the authors in [31], comparing countries based on the number of confirmed cases or fatal cases was not scientifically accurate. Hence we introduced the concept of normalization to reduce the effect of population sizes. Furthermore, we use derivatives to describe changes mathematically and to indicate quantitatively, how these changes differs. On a scale of 100, we calculated derivatives to quantify the growth of the mentioned countries.

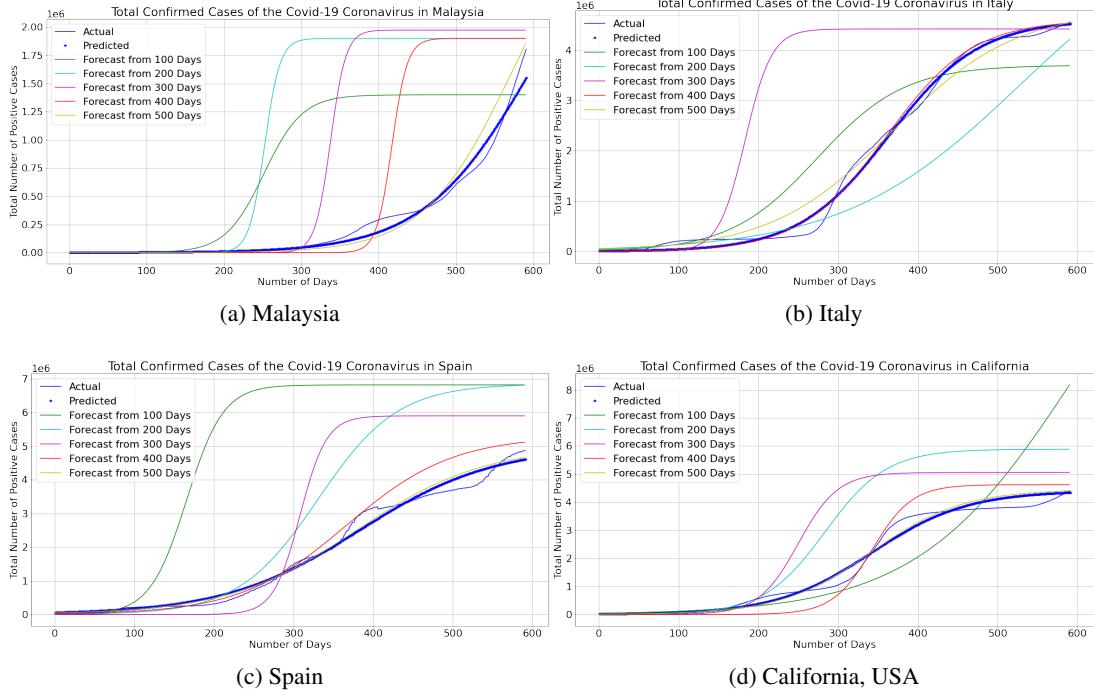


Figure 2: Forecasting using 100/ 200/ 300/ 400/ 500 days actual data on Malaysia, Italy, Spain and California.

5 Results, Analysis, and Discussion

Our forecasting relied on the use of a Logistic Growth Curve (LGC) fitted to the available dataset. As we have data for 591 days in total, we divide the total number of days into 100 days per grid and forecast data after every 100 days using the logistic growth curve.

Second, we looked at the consequences of California's SAH Order. Last year, California became the first state to issue a SAH Order, which went into effect on March 19, 2020, putting the state's 40 million inhabitants into the nation's largest experiment in preventing virus transmission. On June 15, the 15-month ordeal of public health restrictions, mandates, bans, and color-coded tiers to combat the COVID-19 pandemic came to an end [40]. We focused on the first 58 days of data, from January 22, 2020, to March 19, 2020, to assess the effectiveness of this strategy. To fit the LGC on this data, we used the iterative technique. We checked the R-squared value obtained from Equation 2 iteratively for different values of a , b , and K parameters. This procedure allows us to find optimal values for our desired parameters and increase the LGC's R-squared value. Fig 3 depicts the end result. The algorithm predicts that the total number of positive cases will be around 280000 in 150 days, as shown by the green line. This graph depicts the trend of infection growth in the absence of a SAH Order. However, because of the SAH Order, the actual infections are much lower, as shown by the blue line in Fig. 3. This demonstrates the power of the SAH Order (see Fig. 4).

The R^2 value expresses the goodness-of-fit. It is used to compare the similarity of a predicted and actual model. Generally, the R^2 value ranges from 0 to 1, with 0 indicating that the model is unable to explain the variances between actual and predicted values and 1 indicating that the model is the most accurate. The R-squared value for this forecast was 0.996.

California Governor Gavin Newsom announced a new Regional Stay at Home Order based on Inten-

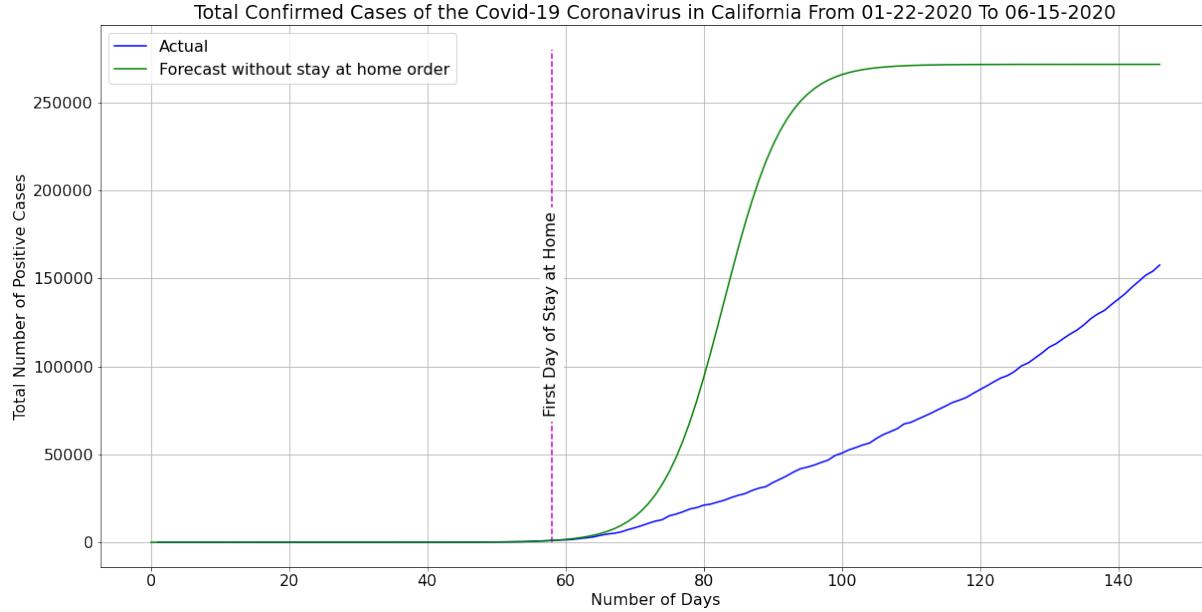


Figure 3: The actual positive cases of COVID-19 infection and the forecast positive cases based on the data before the first SAH Order.

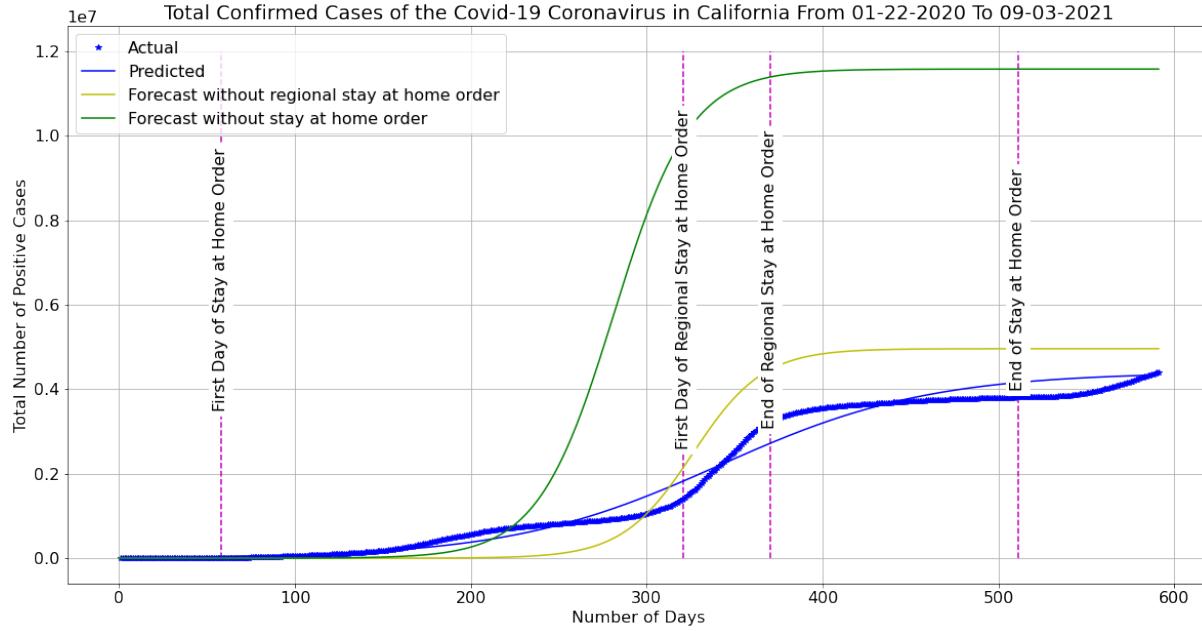


Figure 4: Forecast positive cases without SAH Order and Regional SAH Order.

sive Care Unit (ICU) bed capacity beginning in December 2020, in an effort to control the increase in COVID-19 cases and stabilize the overburdened hospital systems. The December Order went into effect on 5 December, 2020. This Order was terminated on 25 January, 2021 [41], as a result of improved ICU projections across California. We again forecast data to see the growth if there was no SAH Order and

Regional SAH Order in the 591 days data. The results are shown in Fig 5 where, the green line represents forecasting without the SAH order from March 19, 2020 with the R^2 value 0.996 and the yellow line represents forecasting without regional SAH order place from 5 December, 2020 with the R^2 value 0.951. The thin blue line represents curve fitting on the total actual no of positive cases with the R2 value 0.994, whereas the thick blue line is the Actual data.

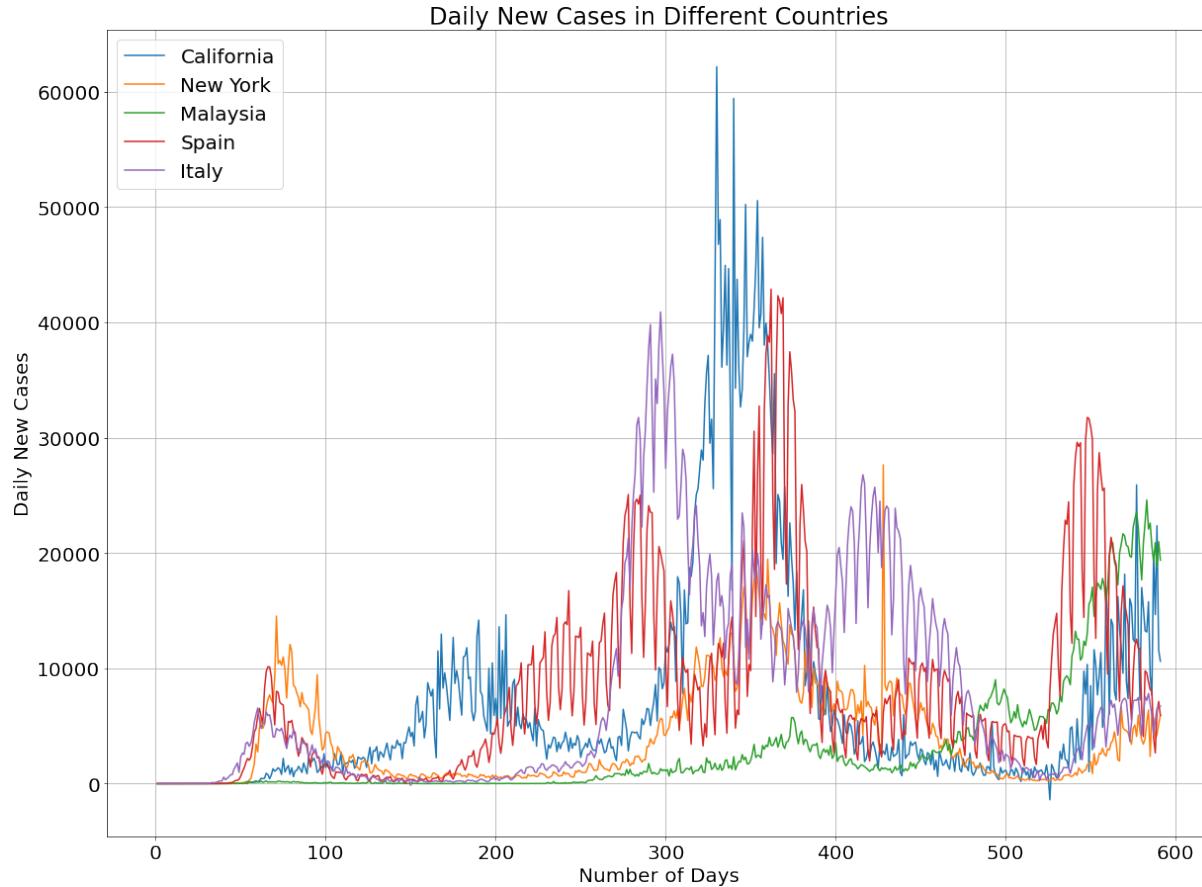


Figure 5: Daily new cases among different countries/ states.

Next, we wanted to quantify the growth behavior on a day so that we can compare and say on a day, which country is having more positive cases. So first we plotted daily new cases among different countries as shown in Fig 5. But it was way difficult to compare from this visualization as each country has varieties of number of population. The population size is not equal for each country or state.

Italy and Spain are seeing the greatest increase in COVID-19 positives in Europe [42]. In Fig. 6, percentage change between Spain and Italy and in Fig 7 percentage change between Malaysia and California are visualized from 21 March, 2020 to 31 March, 2020. Here, Italy is more aggressive than Spain only on 21 and 24 March, 2020. Remaining days Spain was more aggressive than Italy. On 24 March, 2020 the total number of positive cases in Spain was 5323 and in Italy the total number of positive cases was 5249. Despite Spain having a greater number of positive cases with respect to Italy, Italy was more aggressive on that day. Between Malaysia and California, California is more aggressive from 24 March, 2020 to 31 March, 2020. On the remaining days Malaysia was more aggressive than California. On 21, 22, 23 March, 2020 the total number of positive cases in Malaysia was 153, 123, 212 and the total number of positive cases in California was 169, 239, 462. Despite California having a greater number of

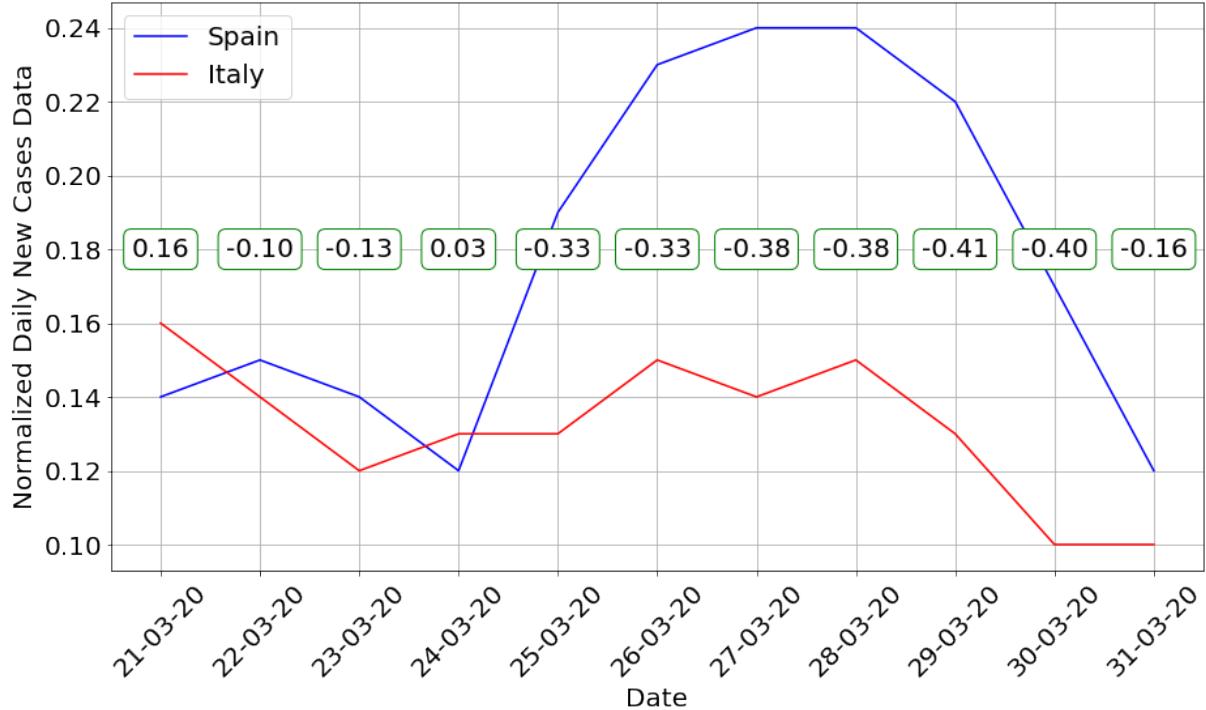


Figure 6: Percentage change of Italy with respect to Spain

positive cases with respect to Malaysia, Malaysia was more aggressive on these days.

We have also performed derivatives to quantify the growth of these countries on a range of 100. The results are shown in Fig 8.

6 Conclusion

In this study, we first used LGC to forecast the total number of positive cases based on real data from several countries over a period of time. The results have a precision of at least 95%. The impact of the lockdown or SAH in California was then shown. Without considering SAH, we forecast the total number of new cases, and it was proven that the SAH was beneficial and helped to flatten the curve. Then, we compared the data between two countries. Our approach involve a normalization process and percentage changes in the two countries compared. This approach was necessary to cater for the difference in population sizes between two countries. In making comparisons with more than two countries, our previous approach of normalization and percentages was no longer feasible and hence we took a different approach when comparing multiple countries more than two. This approach requires the use of derivative for better and faster visualization of data involving multiple countries (see Fig. 6,7 and 8). While using derivatives helped in many ways, there are also some limitations in this approach. The derivative findings in this case had some negative values, which makes comparisons difficult to comprehend. It is thus important to note that instead of creating a polynomial order of four trend-lines, an alternative method of obtaining the derivative can be utilized so that the derivative discoveries do not contain any negative values.

According to our findings, the LGC can be implemented to forecast the total number of cases in the future. SAH Order is one of the factors that aided in limiting the spread of COVID-19 infection in

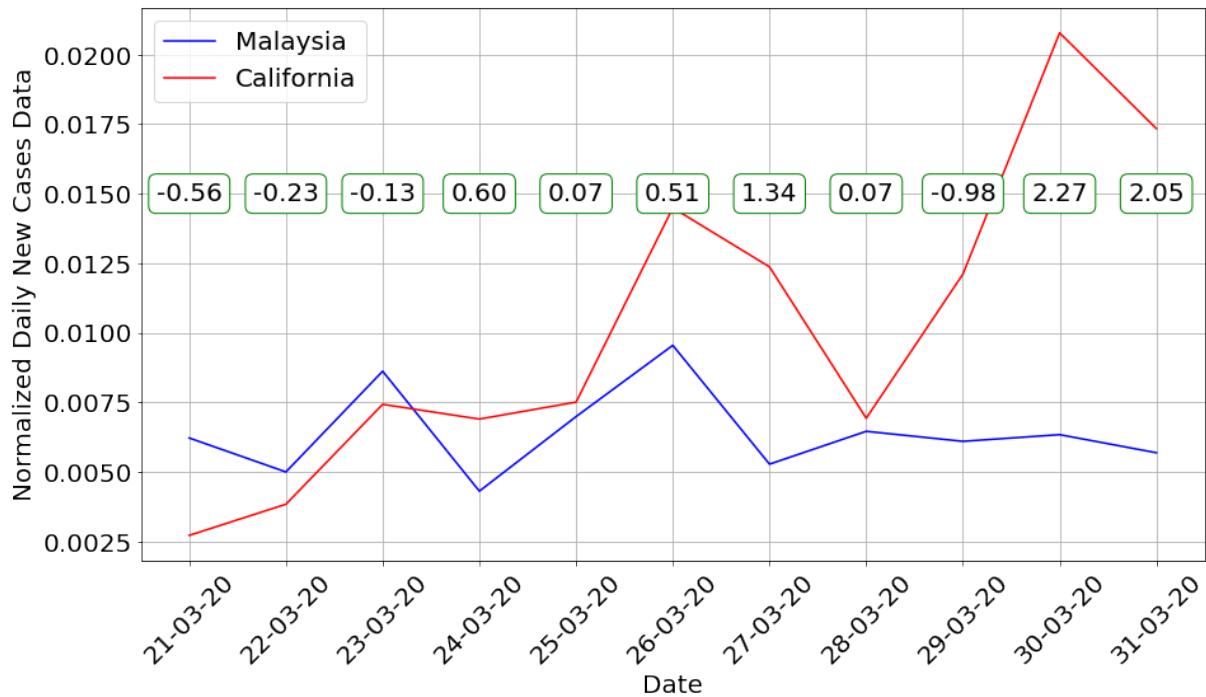


Figure 7: Percentage change of California with respect to Malaysia

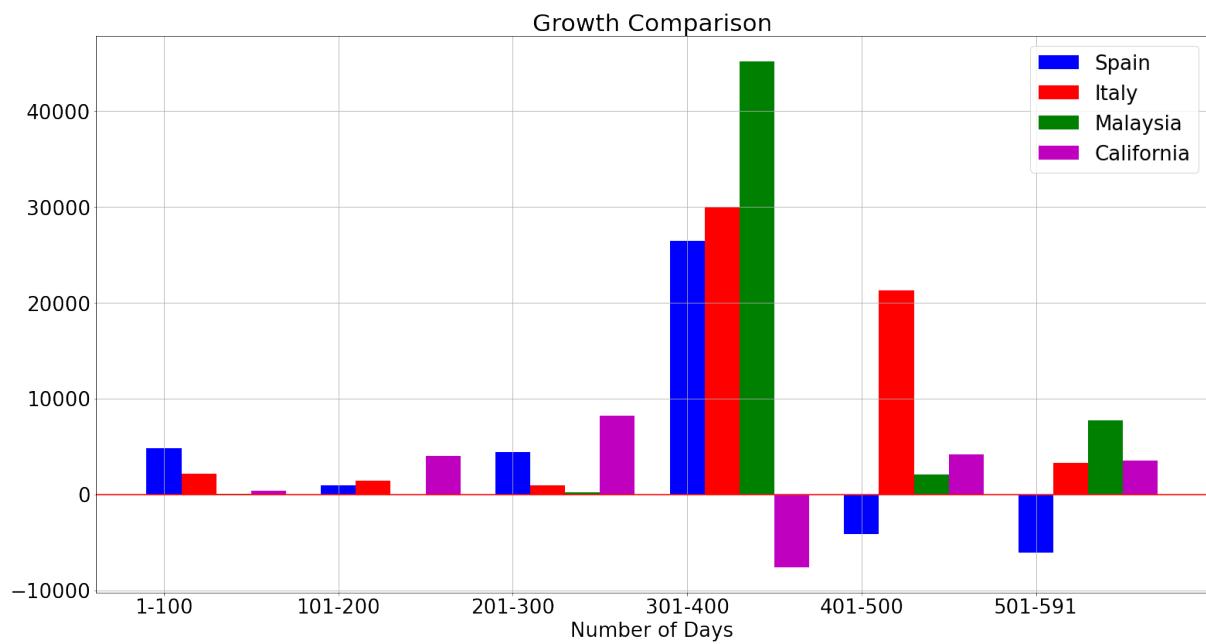


Figure 8: Growth Comparison among Spain, Italy, Malaysia and California

California. The implementation of both SAH Order and Regional SAH Order had prevented the worst-case scenario of the pandemic from occurring as well as stabilized the overburdened in hospital ICU capacity. It aided the Californian government in flattening the infection curve with the help of various agencies and the general public. It is important to note that the SAH Order is not intended to eradicate COVID-19 completely, but rather to flatten the curve and thus reduce new infections in comparison to the spread that would occur if the order was not in place. By the end of the Regional SAH Order in California, the curve had begun to flatten further, and the situation was under control. Hospitals had excess resource capacity, such as the number of beds for COVID-19 patients, including ICU. We believe that our approach can be easily adopted by others and will also be very useful for further planning.

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Author Biography



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