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COVID-19 - Outbreak Prediction Using SIR Model

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Abstract: This paper deals with the trendy topic of coronavirus. The disease is causing severe damage to the entire population as well as to the nation's economy. Machine Learning algorithms like Support Vector Machines and SIR Models have been used to prepare good and valid predictions of this disease. Total cases, recovered cases, infected cases, and Deaths reported are there in the paper ahead represented beautifully in form of pie charts, bar graphs, and line plots. Predictions are there for the next 20 days and we all hope that the cases remain as low as possible, and we achieve the peak of the disease as early as possible. Also, it should be made clear that these are not clinically and globally accepted to be true, and these should not be used anywhere on a medical basis. This clearly gives us the right approach and a brief idea of how Machine Learning can be used in such pandemic situations.

Keywords: Coronavirus; SIR Model; Machine learning; Support Vector Machine

1. Introduction

1.1 What is Coronavirus (Covid-19) Outbreak

COVID-19 is an irreversible illness brought on by a new coronavirus as shown in Figure 1. In January 2020, during a pneumonia outbreak, the seventh human coronavirus, also known as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), was discovered in Wuhan, Hubei Province, China [1, 2]. According to COVID-19 epidemiology, since January the virus has spread worldwide as of May 20, 2020, it had infected 4,806,299 people and killed 318,599 of them [3]. Severe pneumonia is caused by SARS-CoV-2, SARS-CoV, and Middle East respiratory syndrome coronavirus (MERS-CoV), with fatalities ranging from 2.9% to 36% [4-6]. There are a few other types of coronaviruses namely, OC43, NL63, HKU1, and 229E, and they cause human illness that goes away on its own and shows minimal symptoms [7]. Since the beginning of the discovery of this novel coronavirus SARS-CoV2, there have been speculations concerning its origins among the scientific community [8]. It has been hypothesized that laboratory experiments resulted in the development of SARS-CoV-2. SARS-CoV-2 does not appear to have evolved from a previously identified virus backbone, as demonstrated by genomic data [9]. Every individual irrespective of age is susceptible to this virus and serious sickness. Patients over the age of 60, as well as those suffering from medical comorbidities like diabetes, chronic lung disease, heart disease, kidney disease, obesity, cancer, or patients having an organ or hematopoietic stem cell transplant history, have a greater risk of contracting a severe covid-19 infection. COVID -19 data based on gender distribution reveals that male patients are more prone to acquire severe disease and have a higher mortality rate due to COVID-19 than female patients [10]. Similar to other RNA viruses, SARS-CoV-2 is also susceptible to the phenomena o genetic evolution with frequent mutations over time. This results in variant forms of SARS-CoV-2 with distinct features from its original strains. Several SARS-CoV-2 variations have been described during the pandemic, however, only a handful are classified variants of concern (VOCs) by the WHO due to their impact on global public health. Since the start of the pandemic, five SARS-CoV-2 VOCs have been discovered.

As a result, SARS-CoV-2 variant strains with distinct characteristics emerge. During the pandemic, a number of SARS-CoV-2 variants were described; however, the World Health Organization (WHO) has only designated a small number of these variants as variants of concern (VOCs) due to their impact on global public health. Five

SARS-CoV-2 VOCs have been discovered since the pandemic began. These five strains based on the chronology were Alpha strain (also known as B.1.1.7) found in United Kingdom, Beta strain (B.1.351) found in South Africa, Gamma strain (P.1) identified in Brazil, Delta strain (B.1.617.2) identified in India and Omicron strain (B.1.1.529) in South Africa.

These variants are more contagious than the previous SARS-CoV-2 [11]. The Omicron variant is more transmissible than other variants. It has replaced Delta as the predominant variant of SARS-CoV-2 [12]. Despite the exceptional transmission and evolving speed of COVID-19, vaccines have been developed and extensive worldwide mass vaccination efforts, including vaccine boosters, have been undertaken. The significant progress made in containing these viral infections spread may be undone by the discovery of novel SARS-CoV-2 variants. A meta-analysis of 50 studies conducted by researchers in the United States and the United Kingdom found that people from Black, Hispanic, and Asian ethnic minority groups were more likely to get COVID-19 and die from it. Among these groups, Hispanics had the highest rate of COVID-19-related mortality [13, 14]. Large contamination contaminated with COVID-19 infection will meet with mellow to guide respiratory disease and recoup without requiring any unusual treatment [15-18]. Many experienced people, as well as those with hidden clinical problems such as heart disease, diabetes, respiratory illness, and physical injury, will inevitably create real illnesses. The best way to transmit wallets and prevent transmission everywhere is to learn about COVID-19 infection, the illness caused, and how it spreads. Protect yourself and other people by getting vaccinated and as a preventive measure wash your hands with soap or clean your hands with the use of alcohol-based sanitizer as often as you can and avoid making contact with your face.

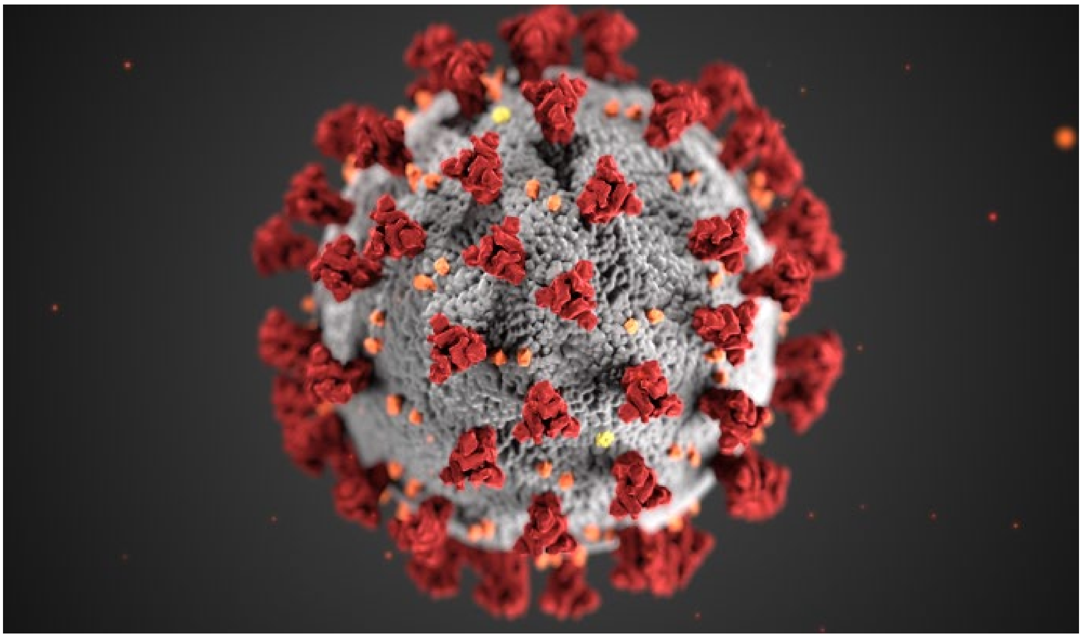

Figure 1. COVID-19 (Novel coronavirus)

1.2 How Does It Spread/ Covid-19 Transmission

SARS-CoV-2 infection can cause mild to severe symptoms in infected individuals, with a significant proportion of the population being asymptomatic carriers. The symptoms that are most frequently mentioned are shortness of breath, fever, and a cough. Pneumonia patients typically have numerous mottling and ground-glass opacity on their chest X-rays [19, 20]. SARS-CoV-2 has also been detected in the saliva of covid patients primarily due to the presence of cellular receptors known as the angiotensin-converting enzyme 2 (ACE2) receptor in the epithelial inning of the salivary gland ducts [21, 22]. The RNA of the SARS-CoV-2 virus was found in the patient's urine in some experimental settings. In spite of the fact that additional research is required to determine the duration of COVID-19 viral shedding in urine samples and the infection load [23], the average percentage of RNA positives during these investigations was approximately 5-6% [23]. The incubation period of SARS-CoV-2 infection must be evaluated in order to determine the duration of the isolation period, as well as to ascertain and calculate the efficiency of the entrance screening and contact tracing. The SARS-CoV-2 can also be transmitted vertically however there has been discord in this context. There was no mother-to-child transmission in a study of 9 pregnant women having confirmed COVID-19. Furthermore, the study indicated that the breast milk was not contaminated with any traces of SARS-CoV-2 resulting in no further transmission of the virus through nursing [24]. Most of the SARS-CoV-2 transmissions occur through droplet transmission from pre-symptomatic, asymptomatic, or symptomatic carriers of the virus or close contact with respiratory droplets containing the infectious virus. Aerosol-generating methods have also been linked to the spread of COVID-19 in the air. On the other hand, evidence of SARS-CoV-2 transmission via the air in the absence of aerosol-generating methods is emerging and is being investigated. However, this manner of communication is not widely accepted. Surprisingly, serology can assist in determining the transmission of SARS-CoV-2 because few individuals who were in close contact with COVID-19 patients tested positive for the virus despite having negative RT-PCR results and no symptoms [25].

COVID-19 infection is spread by the resemblance of spit beads or releases to the nose when individual hacks are attached or wheels, so it is important to rarely practice respiratory ornamentation (for example, by hammering on a changing part). Currently, there is no specific type of COVID -19 vaccine that can fight this virus. Nonetheless, there are several ongoing treatments exploring potential treatments. The WHO is always there to continuously update us with refreshing data when clinical findings are available [26, 27].

1.3 Measures That Were Undertaken to Control and Treat COVID-19

Different treatment facilities can be chosen to treat and isolate patients based on the severity of a patient's symptoms and the area's medical resources. According to Chinese regulations, the specific classification is as follows:

- ✓ No symptom cases: These individuals cannot be considered as new cases because they have no symptoms. The initial treatment is a 14-day quarantine period, after which the public health department conducts additional surveillance. Members of the household should remain in a separate room if these individuals are isolated in their home, or if the same is not possible, then, maintain a distance of at least one meter from the isolated individual [28].
- ✓ Suspected cases: Patients over the age of 65 who are capable of self-care and do not have primary conditions such as diseases related to respiratory function, cardiovascular function, or mental health disorder should voluntarily visit a healthcare facility [29, 30]. During the quarantine period, the suspected individual should not leave a single room at random.
- ✓ Mild cases: If a mobile cabin hospital is available, these cases are treated there, or at home, if hospitalization is not an option due to the high demand on the health care facility. Family members should keep an eye on and care for them in this situation. The distance between the beds should not be less than 1.2 meters if patients are housed in the same room, and each room should have its amenities. Avoid nursing and family visits at the same time.
- ✓ Severe Cases: The patients with severe symptoms should immediately be admitted to the Intensive Care Unit (ICU). After pre-screening at home or mobile cabin hospitals, patients whose condition changes from mild to severe should be moved to critical observation for treatment [31].

China used large-scale mobile cabin hospitals to control the spread and contain the COVID-19 pandemic, which had positive results [32].

The governance of healthcare systems and the management of public health catastrophes like the current COVID-19 outbreak may benefit from artificial intelligence (AI). AI may aid with the speedy analysis of large amounts of data during times of crisis, allowing health authorities to respond quickly [33]. The analysis of medical data, treatments, and test findings may accelerate the use of AI, quicken decision-making, and enhance patient care [34]. It has been hypothesized, for example, that AI may assist radiologists in interpreting images of CT scans. AI is capable of reading in a matter of seconds, whereas a manual read takes approximately 15 minutes. Thus, AI may be programmed in such a way that it can recognize coronavirus pneumonia-like lesions, assess density, volume, and form, and compare several lung lesions from one image. Clinicians should be able to make faster diagnoses with this information [35]. To pick out the people with probable SARS-CoV-2 infection, a mobile-phone-based survey consisting of an AI framework has been developed to capture travel history as well as frequent clinical signs. Based on the evidence gathered, the people under investigation ought to be categorized as having no risk, minimal risk, moderate risk, or high risk of contracting the virus. The identification of high-risk people should result in rapid quarantine to prevent the virus from spreading [36]. Remote patient monitoring and the transmission of clinical data to health authorities may both benefit from AI and blockchain technology. To prevent the virus from spreading, a patient who is positive for SARS-CoV-2 may be admitted to a quarantine facility for treatment and surveillance. In a similar vein, data from a specific area may be used to follow infected individuals or to quarantine that area to prevent viral spread. The Ministry of Electronics and Information Technology's National Informatics Centre developed the Indian COVID-19 contact tracing, syndromic mapping, and self-assessment digital tool known as Aarogya Setu. It is primarily a smartphone application [37]. This application is meant to inform people about COVID-19 and connect them to important health services in India that deal with the virus. By providing the most up-to-date information and best practices, this application adds value to the COVID-19 containment programs run by the Department of Health. It is a tracking app that tracks COVID-19 cases by making use of the smartphone's Bluetooth and GPS capabilities. The injection is the most common method of vaccine administration, there are also some novel methods. For instance, PittCoVacc, a vaccine developed by the University of Pittsburgh School of Medicine, injects spike protein fragments beneath the skin using (microneedle array) MNA delivery approach that leads to the production of antibodies against SARS-CoV-2 [38]. The growth of R&D, production cycle, and equipment requirements of various technology platforms are distinct.

Due to the unavailability of vaccines and effective antiviral medications, maintaining social distance will be essential during the second phase of covid-19. A significant reorganization of our society and way of life is implied by social distance. Smart working and telecommuting (working from home) [39] should be pursued whenever possible. When this is not feasible, the workplace must provide social seclusion in addition to protective measures like protective gear, hand sanitizer, and disinfectants. Restaurants, cafes, movie theaters, and other commercial enterprises will not be permitted due to the prohibition on large gatherings. will have to cut back on the number of employees, which will have a negative social impact and make poverty worse. For these workers, welfare will be very important. In order to provide students with education and safety, educational institutions will need to reorganize. All students will need access to the Internet in order to continue their education and, if necessary, take exams from home [40]. Lastly, staying in touch throughout this trying time will be essential. It will be necessary to send clear messages from national authorities in order to raise public awareness and encourage people to adhere to new norms.

1.4 Prevention

Face masks have been commonplace since the SARS-CoV-2 pandemic. Fear of being infected has compelled everyone who can use face masks to do so, contributing to the product's scarcity. Different nations made different policies related to the use of face masks. According to WHO facemasks are not recommended for healthy persons unless they are caring for someone with a suspected SARS-CoV-2 illness or respiratory symptoms. However, wearing a face mask is always advised since it may help to reduce illness transmission from asymptomatic carriers. According to Leung et al., wearing a face mask, significantly decreased the shedding of respiratory viruses like the SARS-CoV-2 and influenza [41].

To eliminate contamination and slow transmission of COVID-19, do the following:

1. Wash your hands frequently with cleansing water and water, or wash them with rub your hands.
2. You know in any event 1 split meter between you and individuals by hacking or Wheezing.
3. Avoid with-your-face contact.
4. Cover your mouth and nose when hacking or sniffling.
5. Stay at home if you feel uncomfortable.
6. Breaks out of various smokes and lungs.
7. Practice is the physical removal by keeping the technical distance from non-trivial movements and avoiding large crowds.

1.4.1 Symptoms

COVID-19 influences various individuals in various manners. Most tainted individuals will create mellow to direct sickness and recuperate without hospitalization. Most regular indications:

1. Fever.
2. Dry hack.
3. Tiredness.

1.4.2 Less regular indications

1. A throbbing painfulness.
2. Sore throat.
3. Looseness of the bowels.
4. Conjunctivitis.
5. Cerebral pain.
6. Loss of taste or smell.
7. A rash on skin, or discoloration of fingers or toes.

1.4.3 Genuine indications

1. Trouble breathing or brevity of breath.
2. Chest torment or weight.
3. Loss of discourse or development.

Look for sure fire clinical consideration in the event that you have genuine manifestations as shown in Figure 2. Continuously call before visiting your PCP or wellbeing office. Individuals with mellow indications who are in any case sound ought to deal with their side effects at home. On normal it takes 5-6 days from when somebody is contaminated with the infection for manifestations to appear, anyway it can take as long as 14 days [42].

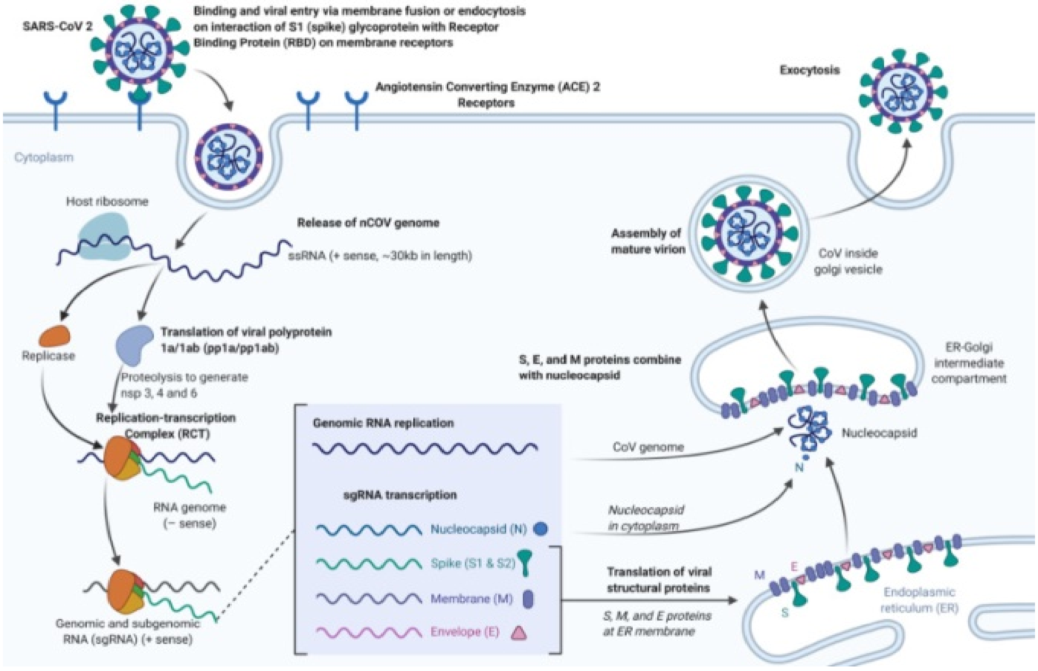

Figure 2. Replication pattern of COVID-19

2. Prerequisites for the Model

Support Vector Machines (SVM) [43] and SIR Models [44], two types of machine learning algorithms, have been used to make accurate predictions about this disease. Machine Learning is a way of exploring information that encourages computers to do what falls into place without clicking on humans and beings: to truly benefit. ML calculations use alignment techniques to "read" data directly from the data without having to go to a predetermined model for example. Mathematics improves their ability to work as the test value is obtained from reading ascents. Machine learning detects natural patterns in dataset that produce understanding and allows us to make better decisions and predictions. They are utilized daily to make critical decisions for medical diagnoses, trading in stock market, energy burden forecasts, and more. For example, media sites depend on machine learning algorithms to fetch out of ample number of options to give song or movie of recommendation. Marketers use these algorithms to get the insight of the customers' buying behavior and many other such examples. Machine learning is divided into two types of learning:

Schematic chart demonstrating the replication pattern of coronavirus and the phases wherein ER stress might be prompted during coronavirus disease. Contamination begins with receptor authoritative and section by film combination. After uncoating, the genomic RNA is utilized as a format to incorporate offspring genomes and a settled arrangement of sub genomic RNAs.

The replication translation centers are firmly connected with DMVs, which are proposed to be embraced from the changed ER, conceivably by the joined exercises of non-auxiliary proteins nsp3, nsp4, and nsp6. The S, E, and M proteins are integrated and moored on the ER, whereas the N protein is deciphered in the cytosol. Gathering happens in the ERGIC and develop virions are discharged by means of smooth-walled vesicles by exocytosis. The three phases that apparently prompt ER stress are featured with numbered star signs, to be specific:

1. Arrangement of DMVs.
2. Gigantic creation and alteration of basic proteins.
3. Exhaustion of ER layer during growing.

2.1 Supervised Machine Learning (ML)

The supervised ML [45], generates an impulse that creates expectations based on evidence within uncertainties. Monitoring of supervised learning takes the known classification of knowledge data and the known response to information (yield) and prepares the model to produce a reasonable prediction of the response to latest information. Use supervised reading if one knows the information about the harvest you are trying to foresee. Functional learning involves using symbols and then retransmitting processes to create learning models.

2.1.1 Classification techniques

These processes detect critical reactions - for example, whether the email is true or spam, or whether the tumor is cancerous or sensitive. The order models split the input information into classes. Intermediate applications include clinical imaging, speech recognition, and card scoring. Use visualization if your information can be written, edited, or split into explicit circles or classes. Classification algorithms include SVM, k-nearest neighbor, decision trees etc.

2.1.2 Regression technique

It predicts non-stop responses — for example, temperature alternate or energy demand fluctuations. Typical applications consist of electrical load prediction and algorithmic trading. Use return methods when working with a database or if your response popularity is a real variety, such as temperature or time till the system fails. Insert high-quality, non-linear lines, etc.

2.2 Unsupervised Machine Learning (ML)

Unsupervised studying detects hidden patterns or systems inside the information. It is used to tug several facts and factors that incorporate input information without categorized responses [46].

2.2.1 Clustering

It is the most normally used form of gaining knowledge that isn't broadly accepted. It is used for the evaluation of test information to locate hidden styles or clusters of statistics. Requests for collection analysis consist of gene sequencing, market research, and item recognition. For example, if a mobile enterprise desires to add locations wherein they build cell towers, they are able to use gadget getting to know to estimate the variety of corporations that humans depend on their towers. The telephone can talk about one tower at a time, so the team uses integration algorithms to build the high-quality placement of cellular towers to make brand recognition for teams, or teams, of their customers. Clustering's most famous algorithms are K-approach and imply shift clustering algorithms [47].

If you need to teach a version to make a prediction - for example, destiny price of a non-stop variable, together with temperature or inventory price, or category - for example, factor to the formation of automobiles from a webcam video show and then Supervised Learning is suggested and if you want to test your statistics and want to model schooling to get a good internal presentation, inclusive of dividing facts into companies and then unsupervised getting to know is suggested.

2.3 Support-Vector Machine (SVM)

A support-vector machine is a characterization-based approach or calculation. There are a few conditions where we can put it to use for relapse. In any case, there are uncommon times of utilization in unaided studying too. SVM in grouping is under studies for the unaided getting to know viewpoint. Here, we make use of unlabeled records for SVM. It is a solid records classifier. The assist vector gadget utilizes as a minimum marked training of information. It isolates two particular training of statistics with the aid of a hyperplane. The information focuses dependent on their state of affairs as indicated by way of the hyperplane will be placed in impartial classes. Furthermore, something crucial to observe is that SVM in Machine Learning consistently makes use of diagrams to plot the data. SVM is broadly classified into 3 parts:

- Support Vectors

Support vectors are unique information that focuses particularly in the dataset. They are responsible for the hyperplane's development and are the hyperplane's closest focus. The status of the hyperplane would be altered if these focuses were removed. The hyperplane is surrounded by choice restrictions. Furthermore, the support vectors aid in shrinking and growing the size of the constraints. They are the essential components of developing an SVM [48].

- Limits of Decision

The decision parameters in the SVM are the 2 traces we see next to the hyperplane. The distance between lines with a light tone is called the threshold. A true or notable hypertrane structure when the brink length is exceeded. The SVM algorithm adjusts the hyperplane and its edges in line with the aid vectors.

- Hyperplane

In this case, the hyperplane is a line in which the mild is 2-D dim. By the time we had a three-D aircraft, the aircraft would be a 2-D plane itself. There is a ton of science worried in studying the hyperplane. We could be taking a gander at that. However, to apprehend the hyperplane we want to see it first. Assume there is space for space (clean paper). In the meantime, visualize the road from the center.

2.3.1 Parameters of SVM

SVM parameters improve the quality of the Hyperplane and are included as standard parameters in the Python code. These parameters determine the composition of the hypertrane, the conversion of data between decision parameters, etc. There are four main types of parameters that we should be aware of these are:

Kernel Parameters

In the Kernel parameters, we likewise have four direct variables, RBF, polynomial and sigmoid. The fragment parameters determine the composition and composition of the hypertrane. For sewing, we will set the piece type and the corresponding mode.

Gamma parameters

The gamma parameter belongs to indirect hyperplanes. Here, the cost of an aspect is RBF, polynomial or sigmoid. This parameter tries to in shape all data.

C Parameters

The C parameter is slightly much like the penalty parameter. It famous to us that during case the C-scale is high, at that time, the ducts far away from the aircraft are also critical to us. This lets in us to add them in parallel and this results in an overload.

Degree parameters

Finally, the degree parameter. This parameter uses 'poly' as a degree of fee. The degree parameter helps in finding the hyperplane of the partition data. At that time the level of polynomial helpers in this. When the price of growth of a polynomial increase, the extra time of instruction takes over.

By tracking all of those attributes, one can manipulate Hyperplane because the SVM model.

3. Model Representation

The Results section may be divided into subsections. It should describe the results concisely and precisely, provide their interpretation, and draw possible conclusions from the results.

To create a notification for future use, we will use $x^i xi$ to represent the variable "inputs" also called input features, and $y^i yi$ to indicate "output" or target variables. pair $(x^i,y^i)(xi,yi)$ is called a training example, with the data that we will use to learn - a list of examples of 8 training (x^i,y^i), i=1,2, …, m=m, (xi,yi), i=1, ..., m is called the training set. that the text "i" in the text is simply a reference to the training set, and it has nothing to do with the description. We will also use X to define the input value space, and Y to specify the output value space. To describe the legally supervised learning problem, our aim is to be given a learning set, in order to learn the function h: $X \rightarrow Y$ so that $h(x)$ is a "good" prediction with a corresponding value of y. For historical reasons, this function h is called a hypothesis [49-53]. Seemingly symbolic, the process is as shown in Figure 3:

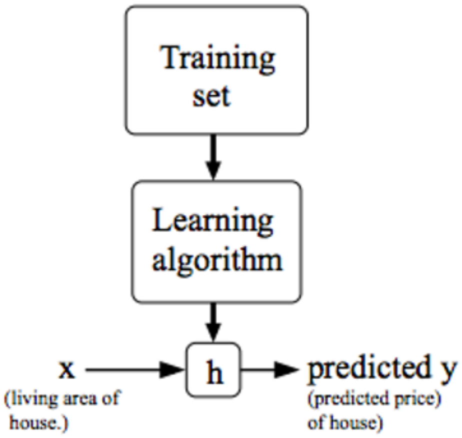

Figure 3. Process of learning algorithm (example)

When the target variable we are trying to predict continues, we call the learning problem as a thinking problem. When y assumes only a small number of discrete ones, we call it a separation problem.

4. SIR Model

A transcendent strategy for modeling the spread of irresistible ailment is to arrange people in the populace as having a place with one of a few unmistakable compartments, which speak to their wellbeing status concerning the disease. The rates of movement between these compartments would then allow for the investigation of the pandemic's components. The SIR model, as depicted in Figure 4, is one of the most important compartmental models, which shapes the premise of quite a bit of irresistible infection modeling [54, 55].

4.1 SIR Parameters

In the SIR model the populace is isolated into three compartments, *S* (suspected), I (infected), and *R* (recovered). People in the populace may exist in any of these three compartments at a given time. Susceptible: Susceptible people have never been tainted, yet are powerless to contamination. In the event that they become tainted they move into the Infected compartment. Infected: Infected people can taint powerless people. After a timeframe they move into the Removed compartment. Removed: Removed people have either recouped from the contamination and are resistant to reinfection, or have passed on.

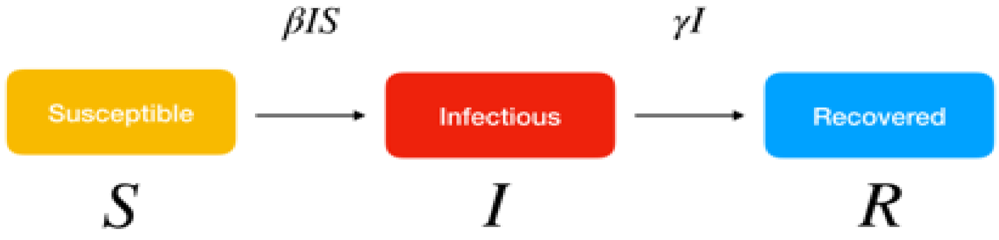

Figure 4. SIR model

4.2 SIR Differential Equations

The pace of move from the susceptible population to the Infected populace is βSI, where β is the per capita powerful contact rate (Ce/N). The successful contact rate (Ce) is the quantity of viable contacts made by a given individual for each unit time, where a viable contact is characterized as a contact adequate to prompt contamination if it somehow managed to happen between a vulnerable and an irresistible person. By rehearsing social separating, we are attempting to diminish the estimation of β. The rate at which Infected people move into the removed populace is I/r, where r is the recuperation delay. The recuperation delay speaks to the period of time an individual stays irresistible. The free factor of the model is the time *t*, and the paces of progress of the compartments are communicated as a lot of differential conditions.

$$\frac{dS}{dt} = -\beta IS$$

$$\frac{dS}{dt} = -\beta IS - \gamma I$$

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

The basic reproduction number (R0) is an indication of the transmissibility of a virus within a particular population. It represents the average number of new infections generated by an infected person in an entirely susceptible population. In this scheme R0 is given by:

R0=βNr=Cer

where, *N* is the total population:

N=S+I+R

This simple model predicts behavior similar to that observed in real-world epidemics.

5. Observation

Table 1. Confirmed cases worldwide

	Province/State	Country/Region	Lat	Long	1/22/20	1/23/20	1/24/20	1/25/20	1/26/20	1/27/20	…	5/4/20	5/5/20
0	NaN	Afghanistan	33.0000	65.0000	0	0	0	0	0	0		2894	3224
1	NaN	Albania	41.1533	20.1683	0	0	0	0	0	0		803	820
2	NaN	Algeria	28.0339	1.6596	0	0	0	0	0	0		4648	4838
3	NaN	Andorra	42.5063	1.5218	0	0	0	0	0	0		750	751
4	NaN	Angola	-11.2027	17.8739	0	0	0	0	0	0		35	36

Table 2. Deaths reported worldwide

	Province/State	Country/Region	Lat	Long	1/22/20	1/23/20	1/24/20	1/25/20	1/26/20	1/27/20	…	5/4/20	5/5/20
0	NaN	Afghanistan	33.0000	65.0000	0	0	0	0	0	0		90	95
1	NaN	Albania	41.1533	20.1683	0	0	0	0	0	0		31	31
2	NaN	Algeria	28.0339	1.6596	0	0	0	0	0	0		465	470
3	NaN	Andorra	42.5063	1.5218	0	0	0	0	0	0		45	46
4	NaN	Angola	-11.2027	17.8739	0	0	0	0	0	0		2	2

Table 3. Recovered cases worldwide

	Province/State	Country/Region	Lat	Long	1/22/20	1/23/20	1/24/20	1/25/20	1/26/20	1/27/20	…	5/4/20	5/5/20
0	NaN	Afghanistan	33.0000	65.0000	0	0	0	0	0	0		397	421
1	NaN	Albania	41.1533	20.1683	0	0	0	0	0	0		543	570
2	NaN	Algeria	28.0339	1.6596	0	0	0	0	0	0		1998	2067
3	NaN	Andorra	42.5063	1.5218	0	0	0	0	0	0		499	514
4	NaN	Angola	-11.2027	17.8739	0	0	0	0	0	0		11	11

The worldwide cases of corona virus are depicted below in a horizontal bargraph as shown in Figure 5. Each country is marked with their respective bars. This information might not be very clear to be able to gather information and deep insight into the graph so in later pages I will be plotting some more graphs to get better observation (Tables 1-3).

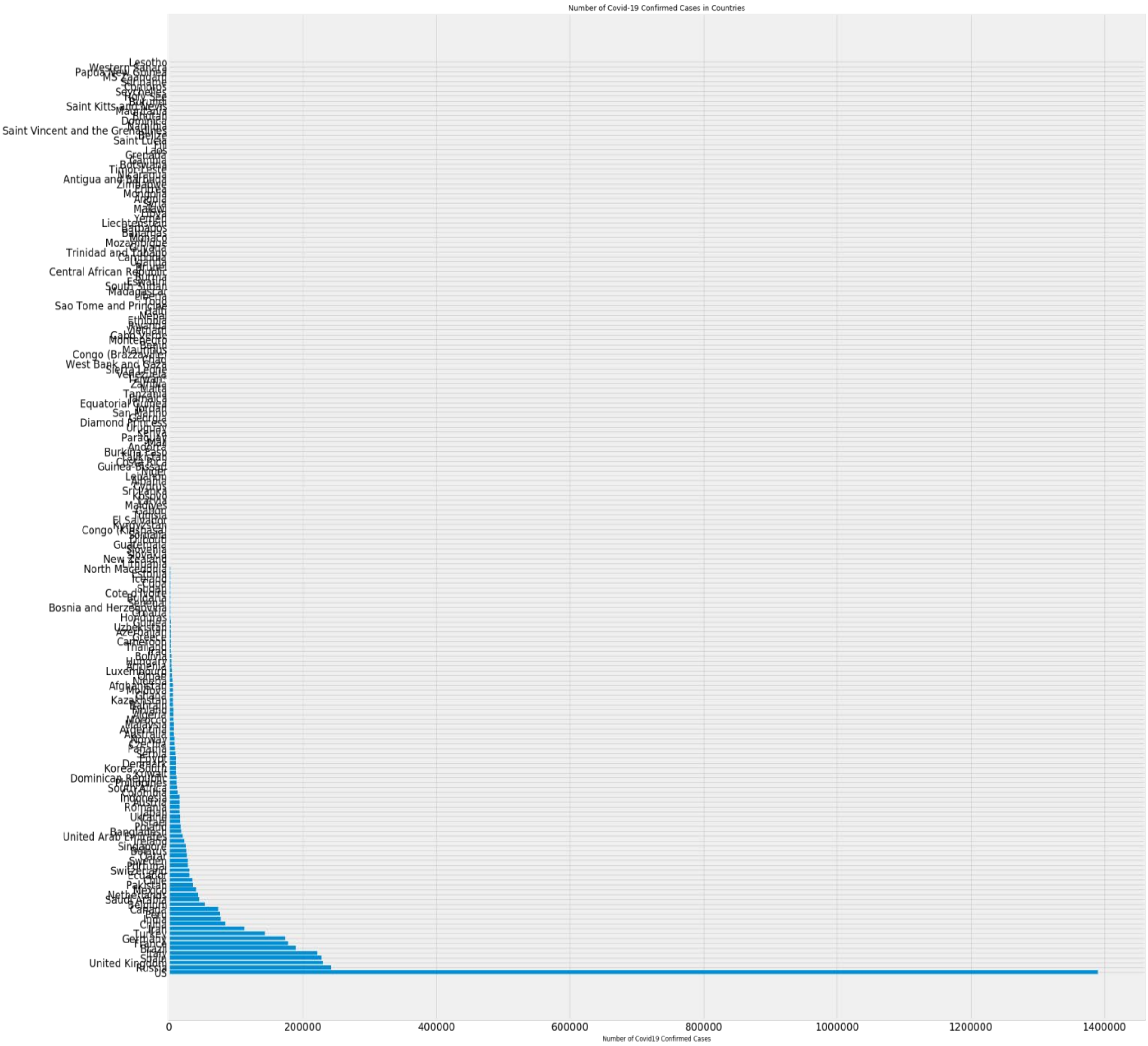

Figure 5. Worldwide cases on horizontal bar graph

It is expected that the origin of the coronavirus is in China.

The below graph depicts the top 10 countries with the maximum number of confirmed coronavirus cases as shown in Figure 6.

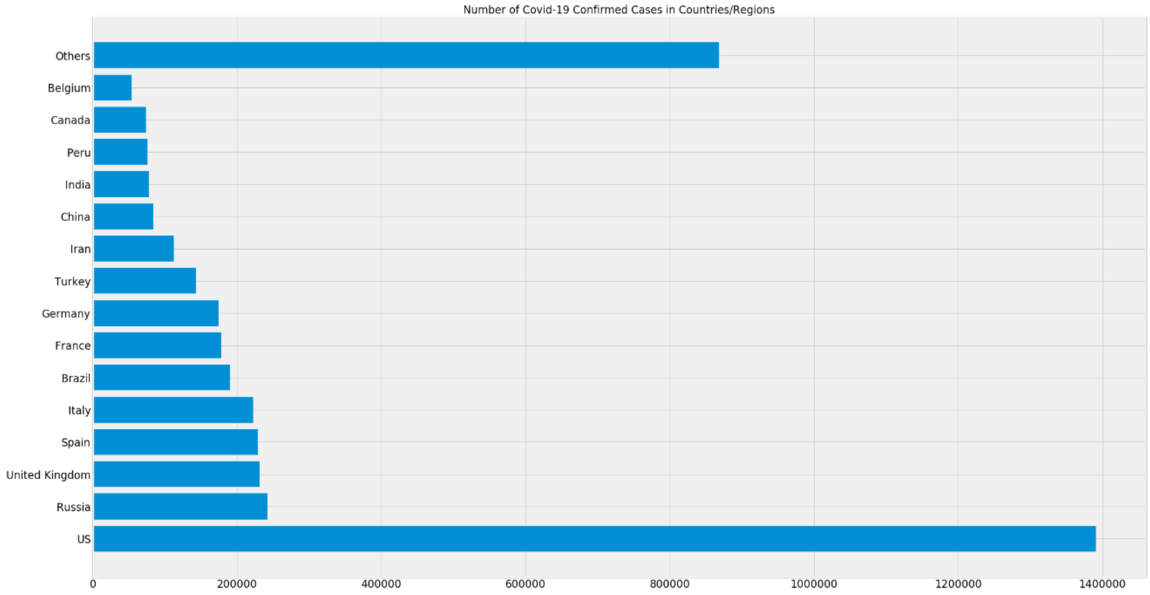

Figure 6. Confirmed cases in country/regions

6. Results for SIR Model

SIR Model trained over data of Italy as shown in Figure 7.

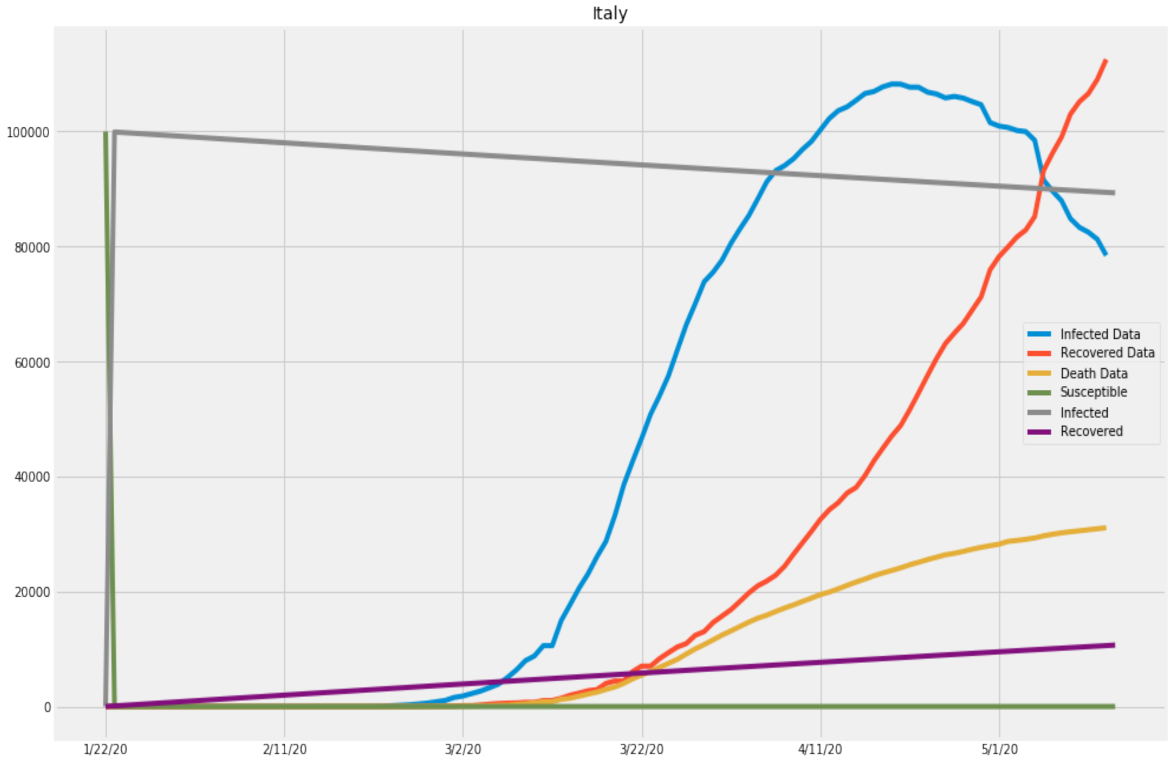

Figure 7. SIR Model for Italy

For a captured population of 1, 00,000, the trained model predicted the highest number of infected cases in Italy. The blue curve is the number of people infected with the virus. You touch the top and go down.

It can be seen that the model looks pretty good. The infected data and the infected curve are close. Data Received & Returned are very close.

Values read: country = Italy, beta = 0.000001233, gamma = 0.02875791, r_0: 0.00011435

Note: These results are N = 100,000.

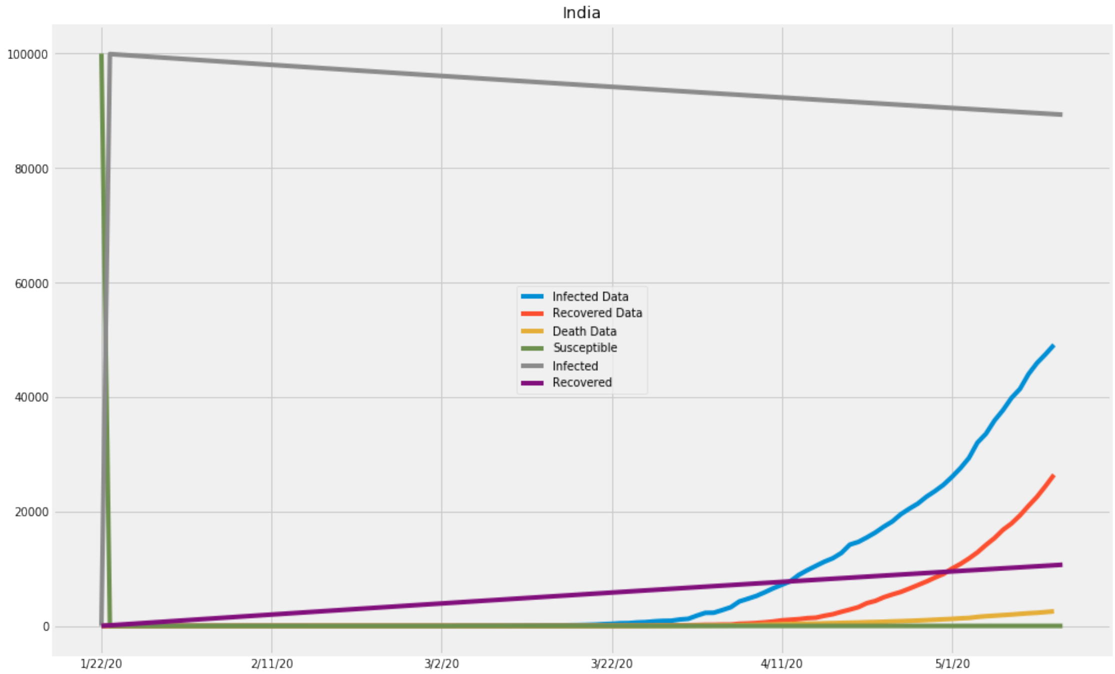

Figure 8. SIR Model for India

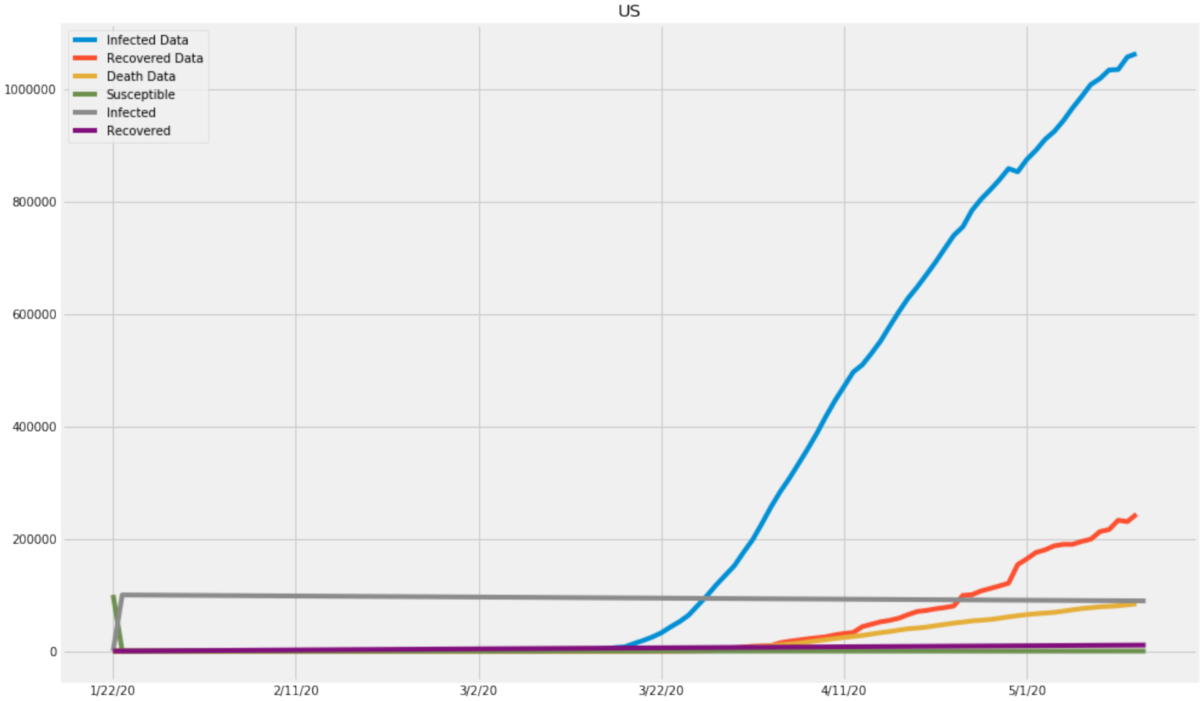

Figure 9. SIR Model for the US

It can be seen that the India model looks pretty as good as Italy shown in Figure 8. The infected data and the infected curve are close. Data Received & Returned are very close.

Values read: country = India, beta = 0.000001233, gamma = 0.02875791, r_0: 0.00011435

Note: These results are N = 100,000.

SIR Model trained over data of the USA.

It can be seen that the model looks pretty good. The infected data and the infected curve are close. Data Received & Returned very close. US as shown in Figure 9.

Values read: country = US, beta = 0.000001233, gamma = 0.02875791, r_0: 0.00011435

Note: These results are N = 100,000.

7. Conclusions

The COVID-19 pandemic has shown that even the most advanced healthcare systems were unable to handle a large number of coronavirus-infected patients in their emergency facilities. The COVID-19 pandemic has put an unprecedented strain on our healthcare systems, highlighting the significance of clinical medicine in the fight against new transmissible agents. The network topology of COVID-19 laboratories has been established almost everywhere to meet the special needs of people and patients. These networks will continue to be crucial until social and work activities resume. Because it accounts for 70% of clinical decisions, laboratory medicine has always been regarded as an essential component of decision-making [56]. Decisions regarding patient admission, isolation, and discharge are entirely based on laboratory results, this contribution may be even greater in the COVID-19 era—approximately 100 percent [57]. The COVID-19 pandemic revealed flaws in our healthcare systems, which were unable to accommodate a large number of covid-19 patients requiring respiratory support therapy in a shorter amount of time. The unanticipated circumstance necessitated the transformation of standard wards into intensive care units or sub-acute intensive care units and the suspension of all non-urgent medical treatments. The pandemic, on the other hand, has compelled the scientific community to collaborate in order to tackle this one-of-a-kind sickness. Several vaccination techniques have been developed or are in the works, with studies underway or about to begin to test their efficacy. The availability of a preventive vaccination is critical in the absence of efficient and targeted antiviral treatment against SARS-CoV-2. In the absence of effective and targeted antiviral treatment for SARS-CoV-2, the availability of a preventive vaccination is crucial. With 3.2 hospital beds per 1,000 people in Italy, as opposed to 2.8 in the United States, hospitals had significant difficulty accommodating critically ill patients who arrived quickly [58].

SIR is one of a mathematical model that is efficacious in predicting various scenarios involving epidemiologic factors and the potential outcomes to measure the epidemic spread of the disease. In the context of COVID-19, the SIR mathematical model is a useful tool for separately estimating disease transmission, recovery, deaths, and other important parameters for different nations, or distinct regions with high or low reported COVID-19 cases. To prevent the disease from spreading, numerous nations have already implemented specific and distinct measures. However, important factors like population density, insufficient evidence for various symptoms, the transmission mechanism, and the absence of a suitable vaccine continue to make it difficult to deal with such a highly infectious and fatal disease currently. This is especially true in nations with a high population density [59-61].

The SIR model generated the peak and flattening of the peak for various countries. This model is extremely beneficial in case of any epidemic in a country. Linear Regression Model and support vector model available in literature, that model did not fit well to the dataset. So, we had to go further in the analysis and generate new better models. The Linear Regression Model is good for other predictions but in case of epidemic it neglects many other features which need to kept in mind while training a model.

Author Contributions

Conceptualization, Vijay Khare and Rishabh Kaloni; methodology, Vijay Khare; software, Vijay Khare; formal analysis, Vijay Khare and Rishabh Kaloni; resources, Rishabh Kaloni; writing—original draft preparation, Vijay Khare and Rishabh Kaloni; writing—review and editing, Rishabh Kaloni; supervision, Vijay Khare. All authors have read and agreed to the published version of the manuscript.

Data Availability

The data used to support the research findings are available from the corresponding author upon request.

Conflicts of Interest

The authors declare no conflict of interest.

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