



## A Comprehensive Data Science Analysis of COVID-19 using Modern Tools and Techniques

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**Abstract:** COVID-19 (Coronavirus Disease 2019), a member of the Coronaviridae family, emerged as a global health crisis with no initial vaccine available, causing widespread disruption to human life, financial markets, and economic systems across the world. The virus brought society to a precarious standstill, affecting nearly every aspect of daily life. This study analyzes COVID-19 datasets to identify which age groups were most impacted by the disease. Several machine learning models were developed and evaluated for predictive performance.

**Keywords:** Linear regression, Decision Tree, SVM

### I. Introduction:

The COVID-19 epidemic began in December 2019 in Wuhan, China, and was caused by a novel virus identified as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) [30]. SARS-CoV-2 is responsible for the disease known as Coronavirus Disease 2019 (COVID-19) [30]. On January 30, 2020, the World Health Organization (WHO) declared the outbreak a global public health emergency, and it was subsequently classified as a pandemic [31]. The clinical symptoms of COVID-19 commonly include respiratory disorders, fatigue, dry cough, and tiredness [29]. Approximately 80% of infected individuals recover without requiring specialized medical treatment [29]. However, certain populations are particularly vulnerable to severe outcomes, including elderly individuals, children, and those with pre-existing conditions such as cardiovascular disease, obesity, and diabetes [30].

The most effective way to prevent and slow the transmission of COVID-19 is by maintaining social distancing. It is essential to protect oneself and others by practicing proper hand hygiene, using sanitizers, and avoiding touching the face. According to Worldometer data, as of May 11, 2020, India reported 67,161 confirmed COVID-19 cases and 2,212 deaths. Globally, the virus had infected approximately 4,180,305 individuals, resulting in 283,865 deaths. The availability of COVID-19 testing kits in hospitals was critically low, making it insufficient to meet the growing demand for testing. Consequently, there is a pressing need to implement automatic detection systems to help control the spread of COVID-19 among the population.



## **The Virus (SARS-CoV-2 )**

SARS-CoV-2 is an enveloped, spherical, single-stranded, positive-sense RNA virus with helical symmetry, classified under the Betacoronavirus genus of the Coronaviridae family [20]. The virus possesses peplomers composed of glycoproteins that project from its envelope in a crown-like arrangement, giving the virus its "corona" (crown) name. These spike proteins play a crucial role in facilitating the binding of the virus to host cells.

The spike proteins of SARS-CoV-2 facilitate the virus's binding to receptors present in the bodies of various animals, including bats, rodents, civets, cats, Malayan pangolins, camels, and other potentially competent hosts, as well as humans [21–23]. Modifications in the spike protein's receptor-binding domains are largely responsible for zoonotic spillover events and the crossing of species barriers. Based on high genomic similarity studies, it is suggested that SARS-CoV-2, the causative agent of COVID-19 in humans, originated from bats, which served as the natural ancestral host [24–28]. Advanced imaging techniques such as scanning electron microscopy, transmission electron microscopy, and cryo-electron microscopy have confirmed structural changes in the spike glycoprotein of SARS-CoV-2 compared to that of earlier coronaviruses.

## **The Disease (COVID-19)**

COVID-19 represents the third coronavirus (CoV) outbreak in humans over the past two decades, leading to clinical manifestations primarily affecting the respiratory, digestive, and systemic systems, most notably characterized by pneumonia [33,34]. The case fatality rate is estimated to be around 2–3%; however, severely affected patients may succumb to excessive alveolar damage, resulting in progressive respiratory failure, as observed in numerous countries, including Italy and China [35]. In cases of close contact transmission, some individuals may remain asymptomatic carriers, showing no clinical symptoms such as cold, fever, fatigue, or lung-related issues.

As competent carriers, asymptomatic individuals can shed the virus for up to 21 days, potentially infecting others who come into contact with them [36]. Initial symptoms of COVID-19 often include fever, mild chills, dry cough, fatigue, and shortness of breath. If not diagnosed and treated promptly, these symptoms can progress to severe respiratory distress and pulmonary pneumonia [37]. As lung inflammation worsens, hypoxemia can develop, which may trigger cardiac arrest as the body struggles to compensate for reduced oxygen levels, leading to fatal outcomes. Therefore, it is strongly advised that individuals consult a medical practitioner as soon as symptoms such as dry cough and fever appear, to prevent further pathological damage [38]. Histological examinations of biopsy tissues from the lungs, liver, and heart have provided detailed insights, revealing features such as pneumocyte



desquamation, hyaline membrane formation, bilateral diffuse alveolar damage, and the presence of cellular fibromyxoid exudates.

## II. Literature Review

In this section, we have studied few recent research articles that contributed their efforts on the research subject and made the detailed review below,

**(1) Furqan Rustam, Aijaz Ahmad Reshi, (member, Ieee), Arif Mehmood, saleem Ullah, Byung- won On, Waqar Aslam, (member, Ieee), and Gyu Sang Choi et al IEEE 2020**

In this Paper Demonstrates the capability of ML models to forecast the number of upcoming patients affected by COVID-19 which is presently considered as a potential threat to mankind. In particular, four standard forecasting models, such as linear regression (LR), least absolute shrinkage and selection operator (LASSO), support vector machine (SVM), and exponential smoothing (ES) have been used in this study to forecast the threatening factors of COVID-19. Three types of predictions are made by each of the models, such as the number of newly infected cases, the number of deaths, and the number of recoveries in the next 10 days. The results produced by the study proves it a promising mechanism to use these methods for the current scenario of the COVID-19 pandemic. The results prove that the ES performs best among all the used models followed by LR and LASSO which performs well in forecasting the new conformed cases, death rate as well as recovery rate, while SVM performs poorly in all the prediction scenarios given the available dataset.

**(2) Nita Madhav, Ben Oppenheim, Mark Gallivan, Prime Mulembakani, Edward Rubin, and Nathan Wolfe. et al (2017)** Pandemics are large-scale outbreaks of infectious disease that can greatly increase morbidity and mortality over a wide geographic area and cause significant economic, social, and political disruption. Evidence suggests that the likelihood of pandemics has increased over the past century because of increased global travel and integration, urbanization, changes in land use, and greater exploitation of the natural environment.

**)W.Qiu; S. Rutherford; A. Mao; C. Chu et al (2017)** In this Journal, the word “Pandemic” comes from the originates from the Greek pan meaning “all” and demos “the people”., and the word is commonly taken to refer to a widespread epidemic of contagious disease throughout the whole of a country or one or more continents at the same time. Nevertheless, in over the past 2 decades, the term has not been failed to be defined by many modern medical texts. Even authoritative texts about concerning pandemics do not list it in their indexes, including such resources as comprehensive histories of medicine, classic epidemiology textbooks, the Institute of Medicine’s influential 1992 report on emerging infections. Pandemics are for the most part disease outbreaks that become widespread as a result of the spread of human-to-human infection.



**(4) Prof. Chaolin Huang, Yeming Wang, Prof. Xingwang, Prof. Lili Ren, Prof. Jianping Zhao & Yi hu et al (2020)**

In this Article, both SARS-CoV and MERS-CoV were believed to originate in bats, and these infections were transmitted directly to humans from market civets and dromedary camels, respectively.<sup>35</sup> Extensive research on SARS-CoV and MERS-CoV has driven the discovery of many SARS-like and MERS-like coronaviruses in bats. In 2013, Ge and colleagues<sup>36</sup> reported the whole genome sequence of a SARS-like coronavirus in bats with that ability to use human ACE2 as a receptor, thus having replication potentials in human cells.<sup>37</sup> 2019-nCoV still needs to be studied deeply in case it becomes a global health threat. Reliable quick pathogen tests and feasible differential diagnosis based on clinical description are crucial for clinicians in their first contact with suspected patients. Because of the pandemic potential of 2019-nCoV, careful surveillance is essential to monitor its future host adaptation, viral evolution, infectivity, transmissibility, and pathogenicity.

**(5) R. Prasad, Bindu Shajan, Perappadan Jyoti Shelar & Jacob Koshy et al (2020)**

Coronavirus is one of the weakest family of viruses. The deaths caused so far or people affected could have been ones with less immunity like children or the elderly. Sometimes, the virus enters a person's lungs and causes pneumonia. People with vulnerable immunity like the elderly succumb to this. For young people with good immunity, the effects of the virus may not be too strong but if you are someone with comorbid conditions like diabetes or cardiac disease, or if you are on immune suppressive drugs, then the risk of infection is severe.

**(6) Ligui Wang, Hui Chen, Shaofu Qiu, Hongbin Song et al 2020**

In this Article, we used data released by the National Health Commission.<sup>5</sup> Since the data were not updated from January 1 to January 17, we used data from January 18 to February 13 to establish our model. Epidemic prevention and control in Wuhan can be divided into three stages: the first stage was the natural occurrence and spread of the epidemic from January 18 to January 23; the second stage was the blockade of Wuhan and the advocacy of residents going out less from January 23 to February 5; and the third stage was cabin hospitals put into use from February 6 to February 13 to ensure that all cases are admitted to hospitals and close contacts are under intensive medical observation. We used the susceptible-exposed-infected-removed (SEIR) dynamic model<sup>6</sup> to simulate the spread of the epidemic and Simulated Annealing (SA) algorithm to identify optimal parameters.

**Eili Klein, Gary Lin, Katie Tseng, Emily Schueller, Geetanjali Kapoor, Ramanan Laxminarayan et al (2020)**

In this Article, We fitted the model to available data from China and Italy. Key parameters include force of infection, age-specific infection rates, severe infection and case-fatality rates. We examine the potential for seasonality, based on the fact that most respiratory infections



decline in the summer, however to-date evidence for the magnitude of this effect, which is driven by changes in temperature and humidity is not well described, and there is potential for the virus to continue its rapid spread.

### III. Methodology, Tools & Techniques

In our Research work, we will be using the SIR model of an epidemic of an infectious disease in a large population. We assume the population consists of three types of individuals, whose numbers are denoted by the letters S, I and R (which is why this is called an SIR model). All these are functions of the time  $t$ , and they change according to a system of differential equations.

By fitting the model to data, estimates for the parameters  $\beta$  and  $\gamma$  can be obtained.  $\beta$ ,  $\gamma$  are the two most important elements in this model.

$\beta$  controls the contact rate or the average number of contacts that turn out to be infected for every infected individual per day

$\gamma$  controls the removal rate or the proportion of people recovering/dying/isolating on a daily basis Together, they give

$R_0 = \beta/\gamma \propto$  the number of secondary cases for every primary case

The reason I chose SIR approach, as compared to a more sophisticated model, is to limit the number of assumptions the system ends up making.

Data science is the process of deriving knowledge and insights from a huge and diverse set of data through organizing, processing and analysing the data. It involves many different disciplines like mathematical and statistical modelling, extracting data from its source and applying data visualization techniques.

Articles, reading material, look into reports, research papers, thesis, the web and other logical productions applicable to information will be utilized. For the classification purpose we will use any of the following classifier:

- a. A Decision Tree
- b. Analyzing Classification Reports
- c. Classification using Logistic Regression
- d. Random Forest Classifier
- e. Using Support Vector Machines

i.RBF Module

In this project, using the **Python libraries** scikit-learn, numpy, pandas, and RBF, we will build



a model. We will load the data, get the features and labels, scale the features, then split the dataset, build a model and then calculate the accuracy of our model

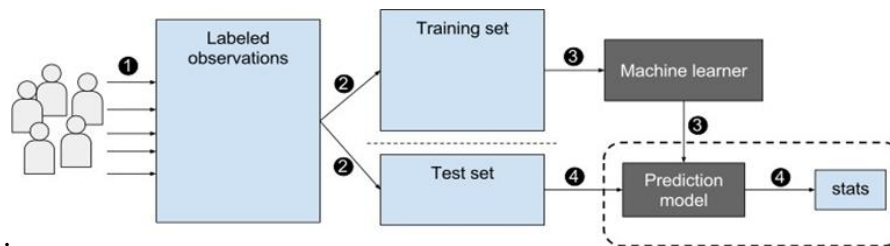


Figure 2: Steps

## IV. Data Collection and Preprocessing

### 4.1 Data Acquisition

The dataset used in this study contains COVID-19 case statistics, patient symptoms, and demographic data. The data is obtained from public health sources and loaded into Python using Pandas:

```
import pandas as pd  
df = pd.read_csv('covid_data.csv')
```

### 4.2 Data Cleaning

Handling missing values is essential for accurate predictions. We use:

- Drop missing values: `df.dropna(inplace=True)`
- Fill missing values: `df.fillna(0, inplace=True)`
- Handling categorical data: Convert categories using `LabelEncoder` or one-hot encoding.

### 3. Exploratory Data Analysis (EDA)

EDA helps in understanding data distribution and relationships:

- Summary statistics: `df.describe()`
- Correlation analysis: `df.corr()`
- Visualizations:

```
import seaborn as sns  
sns.histplot(df['cases'])
```



#### 4. Feature Engineering

Feature engineering enhances model performance by selecting and transforming relevant features: ● Scaling numerical data: StandardScaler() ● Selecting important features using correlation analysis.

#### V. Model Training

We implement multiple ML algorithms to predict COVID-19 trends:

##### 5.1 Machine Learning Models Used

- Linear Regression (for trend forecasting)
- Decision Trees (for classification tasks)
- Random Forest Classifier (for improved accuracy)
- Support Vector Machine (SVM) (for non-linear relationships)

##### 5.2 Model Implementation Example

```
from sklearn.ensemble import RandomForestClassifier
model = RandomForestClassifier()
model.fit(X_train, y_train)
```

#### VI. Model Evaluation

Model performance is assessed using:

- Accuracy Score
- Precision, Recall, and F1-score
- Mean Squared Error (MSE)

```
from sklearn.metrics import accuracy_score
y_pred = model.predict(X_test)
accuracy_score(y_test, y_pred)
```

The focus lies in identifying the most accurate classification model among several algorithms, thereby aiding in early diagnosis and intervention. COVID-19, caused by the SARS-CoV-2 virus, presents various symptoms that can overlap with other respiratory illnesses. Traditional testing methods can be time-consuming and resource-intensive. Machine learning (ML) offers a promising avenue for rapid diagnostics using accessible clinical data. This study utilizes a structured dataset to train and evaluate several ML models, aiming to detect COVID-19 cases accurately.



## VII. Covid-19 Algorithm Analysis:

This code performs several machine learning tasks on a dataset. The dataset contains information about COVID-19 statistics for various countries, including features like confirmed cases, deaths, and recoveries. The code demonstrates how to apply different algorithms to analyze and predict COVID-19 statistics.

### 7.1 Linear Regression

**Objective:** Predict the number of confirmed COVID-19 cases based on other features.

- **Libraries Used:**

- pandas for data handling.
- sklearn for modeling and evaluation.

- **Process:**

0. **Data Loading and Preprocessing:** Load the dataset and select relevant features and target.
1. **Splitting Data:** Split the data into training and testing sets.
2. **Model Creation and Training:** Create and fit a LinearRegression model.
3. **Prediction and Evaluation:** Make predictions and evaluate the model using Mean Squared Error (MSE) and R-squared ( $R^2$ ) score.

**Linear Regression:** This is a statistical method for modeling the relationship between a dependent variable (target) and one or more independent variables (features). It assumes a linear relationship between the variables. The model predicts the target variable by fitting a linear equation to the observed data.

### 7.2 Logistic Regression

**Objective:** Predict whether the number of confirmed cases exceeds 50,000.

- **Libraries Used:**

- pandas for data handling.
- sklearn for modeling and evaluation.

- **Process:**

0. **Data Preparation:** Create a binary target variable (HighConfirmed) based on a threshold (50,000 confirmed cases).



1. **Feature Selection and Data Splitting:** Choose features and split data.
2. **Model Training and Prediction:** Fit a LogisticRegression model and predict the binary outcome.
3. **Evaluation:** Use accuracy, classification report, and confusion matrix to evaluate the model.

**7.3 Logistic Regression:** This is a classification algorithm used to predict binary outcomes. It estimates the probability of a binary response based on one or more predictor variables. The output is transformed using the logistic function to predict the probability of the positive class.

```

LOGISTIC REGRESSION
ROC_AUC value : 93.23107490945218 %

Mean Squared Error : 3.035878564857406 %

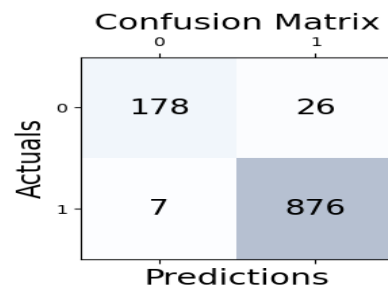
R2 score is : 80.08627006861634 %

Accuracy Score : 97.03243616287095 %

Classification Report :

```

	precision	recall	f1-score	support
0	0.96	0.87	0.92	204
1	0.97	0.99	0.98	883
accuracy			0.97	1087
macro avg	0.97	0.93	0.95	1087
weighted avg	0.97	0.97	0.97	1087



### 7.4 . Decision Tree Regression

**Objective:** Predict the number of confirmed COVID-19 cases.

- **Libraries Used:**

- pandas for data handling.
- sklearn for modeling and evaluation.
- numpy for numerical operations.

- **Process:**

0. **Data Cleaning:** Handle missing values and infinities.
1. **Feature Selection and Data Splitting:** Choose features and split data.
2. **Model Training and Prediction:** Fit a DecisionTreeRegressor model and make predictions.



3. **Evaluation:** Evaluate the model using MSE and R-squared score.

**Decision Tree Regression:** This model uses a tree-like graph of decisions and their possible consequences. It splits the data into subsets based on feature values and predicts the target variable based on the average value of the target in each leaf node.

## 7.5 . Random Forest Regression

**Objective:** Predict the number of confirmed COVID-19 cases.

- **Libraries Used:**

- pandas for data handling.
- sklearn for modeling and evaluation.
- numpy for numerical operations.

- **Process:**

0. **Data Preparation:** Select relevant columns and handle missing values.
1. **Feature Encoding:** Convert categorical variables to numerical using one-hot encoding.
2. **Feature Selection and Data Splitting:** Choose features and split data.
3. **Model Training and Prediction:** Train a RandomForestRegressor model and evaluate it.
4. **Feature Importance:** Print feature importances.

```
RANDOM FOREST TREE
ROC_AUC value : 96.94474052361602 %

Mean Squared Error : 2.2079116835326587 %

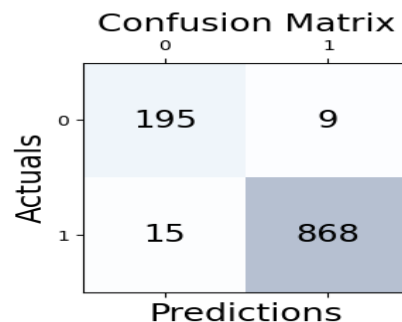
R2 score is : 85.51728732263008 %

Accuracy Score : 98.38969404186795 %

Classification Report :
precision    recall  f1-score   support

   0       0.93     0.96     0.94     204
   1       0.99     0.98     0.99     883

 accuracy          0.96     0.97     0.98     1087
 macro avg         0.96     0.97     0.96     1087
weighted avg         0.98     0.98     0.98     1087
```





**Random Forest Regression:** An ensemble learning method that uses multiple decision trees to improve prediction accuracy. It combines the results of multiple decision trees (built on random subsets of the data) to produce a more robust and accurate prediction.

## 7.6 . Gradient Boosting Regression

**Objective:** Predict the number of confirmed COVID-19 cases.

- **Libraries Used:**

- pandas for data handling.
- sklearn for modeling and evaluation.

- **Process:**

0. **Data Preparation:** Handle missing and infinite values.

1. **Feature Selection and Data Splitting:** Choose features and split data.

2. **Model Training and Prediction:** Train a GradientBoostingRegressor model and evaluate it.

**Gradient Boosting Regression:** An ensemble technique that builds models sequentially, where each model attempts to correct the errors of its predecessor. It combines the predictions of multiple weak learners (typically decision trees) to improve overall prediction performance.

## 7.7. Support Vector Machine (SVM)

**Objective:** Classify WHO regions based on COVID-19 features.

- **Libraries Used:**

- pandas for data handling.
- sklearn for modeling and evaluation.

- **Process:**

0. **Data Preparation:** Handle missing values and encode categorical variables.

1. **Feature Selection and Data Splitting:** Choose features and split data.

2. **Standardization:** Scale features using StandardScaler.

3. **Model Training with Hyperparameter Tuning:** Use GridSearchCV to find the best parameters for an SVC model.

4. **Evaluation:** Assess the model's performance using accuracy, classification report, and confusion matrix.



**Support Vector Machine (SVM):** A classification algorithm that finds the hyperplane which best separates classes in the feature space. SVM can handle both linear and non-linear boundaries through the use of kernel functions.

## Data Handling

- **Handling Missing Values:** Missing data is imputed with mean values or replaced with zeros.
- **Handling Infinite Values:** Infinities are replaced with a large number or NaN, which are then handled.
- **Feature Scaling:** Standardization is used to normalize feature values, which is essential for algorithms sensitive to the scale of features (e.g., SVM).

By following these steps, the code demonstrates how to apply and evaluate various machine learning models to analyze and predict COVID-19 data, each using different techniques suited for regression or classification tasks.

## Conclusion

The most efficient algorithm is the **Linear Regression Algorithm**. It has the highest R-squared value of 1.0, which indicates that the model perfectly fits the data. This means that the model can accurately predict the number of confirmed cases based on the given features. The Mean Squared Error is also very low, indicating that the model's predictions are very close to the actual values.

The other algorithms, such as Logistic Regression, Decision Tree, Random Forest, and Gradient Boosting Regression, also perform well, but they have lower R-squared values and higher Mean Squared Errors. This suggests that they are not as efficient as the Linear Regression Algorithm.

The Support Vector Machine algorithm has an accuracy of 0.50, which is not as good as the other algorithms. This suggests that it is not as efficient as the other algorithms.

Overall, the Linear Regression Algorithm is the most efficient algorithm for predicting the number of confirmed cases based on the given features. It has the highest R-squared value and the lowest Mean Squared Error, indicating that it is the most accurate and reliable model.

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