# Forecasting of Covid-19 Virus Spread Using Machine Learning Algorithm

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Abstract: COVID-19 is an astoundingly infectious disease that has grabbed the eye of the general population across the globe. Modeling of such infections can be really significant in the forecast of their effect. While conventional models can give reasonable outcomes, it can likewise fail to understand the complexities contained inside the data. In this study, publicly available dataset (from Kaggle) is used, containing data on infected, recovered, and deceased patients in 625 regions more than 157 days (2nd April 2020 to 6th Sept 2020). This dataset, expected to be a time series dataset, is translated into a regression dataset and utilized in training a multilayer perceptron (MLP) and artificial neural network (ANN). The objective of training is to accomplish an overall model of the maximal number of patients over all regions in each time unit. Hyper-Parameters (HPs) of the MLP are shifted utilizing a grid search method, with an aggregate of 18614 HPs combinations. Utilizing those groups, an aggregate of 167526 ANNs are trained (55842 for every patient group—deceased-recovered-infected), and each model is assessed utilizing the coefficient of determination ($R2$). Cross-validation is performed utilizing K-fold method with 5-folds. Best models accomplished comprises of four hidden layers with four neurons in every one of those layers, and utilize a ReLU activation-function, with $R2$ scores of 0.979 for affirmed, 0.995 for decreased, and 0.989 for recovered patient models. At the point when cross-validation is applied, these scores drop to 0.95 for affirmed, 0.79 for recovered, and 0.97 for deceased patient models, demonstrating lofty robustness of the decreased patient model, great power for affirmed, and low for recovered patient model.

Key terms: COVID-19, ANN, MLP, Regression, Hyper Parameters

## 1. Introduction

COVID-19 is a tenderness infection from another virus. The infection causes respiratory sickness (like flu) with symptoms, for instance, fever, cough and cold, and in gradually severe cases, the issue in breathing. It is believed that the infection outbreak has creature origins, and it was first communicated to human beings in Wuhan area China, in Nov-2019 [1]. The first episode of COVID-19 pandemic in India was passed on 30th January 2020 affecting from the China. As of 25th April 2020, the Ministry of Health and Family Welfare has set up an aggregate of 24, 853 occurrences, 5, 123 recovery including 1 relocation, and 802 deaths in the republic. Earlier SARS (Severe Acute Respiratory Syndrome) pandemic in 2002 was controlled and halted by customary control measures, including travel limitations and patient isolation. At present, these measures are applied in practically all nations with the COVID-19 outbreak; nonetheless, their viability relies upon how thorough they are. It follows that the techniques empowering solid expectation of spreading of COVID-19 would be of extraordinary advantage in convincing general conclusion why it is critical to stick to these measures in the previous decade [2].

As of date (31st Oct-2020) affirmed COVID-19 cases over the globe are 45,140,131 and mortality around 2.6%. Progressively death rate is growing and it's an alarming element for

the entire world. Transmission is classified into four phases dependent on the method of spread and time. Each country forced various strategies beginning from stay-in home, utilizing masks, travel limitations, avoiding social meetings, habitually washing hands and cleaning the spots regularly on account of a typical exertion to battle the outbreak of this malady [3]. Almost all nations forced a lockdown express that prevents the movement of the residents pointlessly. Because of this social distancing component and movement limitations, the prosperity and economy of the different countries are being under risk. GPD of the whole world dropped radically. At the point when the individual is found infected, he is isolated and treatment is given for recovery [4]. Based on severity it will cause death and furthermore individuals left with a more elevated level of misery. In India, the outbreak of Covid-19 as upset the working of life all in all. All were pushed to remain back to protect from the horrible transmission. In the underlying stages, the affirmed cases are those gotten back from regulates followed by transmission through nearby transmission. More alert is given to the old and insusceptibility less individuals [5].

Modelling the spread and the impact of such an infection can be especially significant in understanding its effect. While conventional models, ML-based methods could be the way to discovering good forecast models. In this study, ML-based technique called MLP-ANN is designed to model spread of the virus, which anticipates the maximal number of individuals who gotten the virus per region in each time unit, maximal number of individuals who recovered per region in each time unit, and maximal number of deaths per area in each time unit [6]. MLP has been chosen for its straightforwardness in contrast with other AI strategies, due to limited preparing time related with such strategies, because the brisk generation of results is significant when demonstrating infections, due to the as-quick-as-

conceivable necessity for models with sufficient regression accuracy [7]. Modelling should be possible on existing data, utilizing statistical examinations. But, with regards to amazingly complex models, statistical examination can fail to fathom the complexities contained in the examined data. ML-based techniques can be utilized to "learn" the overall pattern, however the complexities of the data, which brings more precise results. Models got by ML strategies change their boundaries to accommodate their expectations to existing data, regardless of what it contains. This capacity to consider hard to watch complexities put away inside data ought to loan itself well, when utilized in an endeavor of regression an intricate model, for example, spread of COVID-19. Presently, existing models of COVID-19 spread have generally helpless outcomes or have made expectations which were demonstrated to not relate to genuine data [8].

The main objective this research is to accomplish a precise regression model through the use of a ML utilizing the data that existed during the time wherein this examination was performed. This was done so as to exhibit the chance of utilizing ML in early modelling of infective virus, for example, COVID-19, spread [9]. The goal of the model is to watch all the gathered data together, rather than isolating it into territories, as that method of perception could permit an ML technique to accomplish a superior worldwide model of viral spread. MLP technique is prepared utilizing a "Novel Corona infection (COVID-19) Cases", by John Hopkins CSSE. At the time of this investigation, the dataset contained 20706 data records and was divides in to training (80%—16564 records) and testing (20%—4142 records) sets. The hyper parameters of the MLP are resolved utilizing a grid search technique [10]. The power of the various models is tried utilizing K-fold cross-validation model. Accomplished outcomes are then assessed utilizing the R2 metric. The residue of the article is organized as follows. Related works of this study is summarized in

Section 2, Proposed Methodology is discussed in Section 3, Results and Discussions presented in Section 4 and Conclusions and Future works of the article are stated in Section 5.

## 2. Literature Review

In this section related works on spread of the decease prediction by machine learning techniques are presented. R O Ogundokun *et al.* [11] proposed a ML-based algorithm for COVID-19 prediction in India. Data collected for 3 –months (30th Jan-2020 to 22nd April-2020) from Ministry of Health and Family Welfare, India. Authors investigated the datasets using ARIMA time series model for prediction. The empirical results show that, the proposed model working good in prediction of COVID-19 cases. Sujatha et al. presented a technique for forecast the spread of COVID-19 cases utilizing regression, MLP and SVR. Dataset is collected form Kaggle. The experimental results illustrate that the proposed model working good in predict the spread of virus of future. Yang *et al.* [12] designed a dynamic SEIR approach for forecasting the COVID-19 spread. For this study, authors utilized ML-based model designed with to SARS dataset for future expectations. Velayan *et al.* [13] designed early phase location of COVID-19 by ML techniques realized actualized on stomach Computed Tomography pictures.

Elmousalami *et al.* [14] developed a correlation of day level estimation methods on COVID-19 impacted cases using time-series approaches. Rizk-Allah *et al.* [15] presented anticipating model with analyse and measure the spread of COVID-19 for the upcoming days subject to the declared data since 22nd Jan-2020. Rezaee *et al.* [16] presented a hybrid approach using Linguistic FMEA, FIS and FDEA model to discover new score for covering some RPN deficiencies and the prioritization of HSE dangers. Navares *et al.* [17] presented a solution for the issue of estimating daily medical clinical facility affirmations in Madrid due to circulatory and respiratory cases reliant on bio-meteorological markers. Torky *et al.* [18] presented a blockchain consolidated structure which research the opportunity of utilizing distributed, time venturing and decentralized capacity focal points of block-chain to develop another system for affirming and recognizing the dark sullied examples of COVID-19 contamination. Ezzat et al. [19] presented a novel procedure called GSADenseNet121-COVID-19 subject to a mixture CNN structure is proposed using a streamlining methodology.

## 3. Proposed Methodology

In this section MLP-ANN method is proposed to predict the COVID-19 spread. In this segment data collection and data description utilized in the study are discussed. The concept diagram of the proposed model is given in Figure 1.

### 3.1 Dataset Description

Dataset utilized in this examination is acquired from a freely accessible database by Kaggle. It contains the data for the COVID patients which depict the quantity of patients in a specific area, for every day since the beginning of the COVID-19 diseases (2nd April 2020) until 6th Sept-2020. Dataset is categorized to 3-clusters such as contaminated, recovered, and deceased. At the time of this exploration being planned, the dataset contained the data for 625 areas and 157 days [20]. The geological distribution of dataset is depicted in Figure 2, which shows the topographical distribution of tainted patients at different focuses as expected. Dataset, as published, is sorted out as time-series data demonstrating the spread of malady in different areas after over time. To train the MLP model, the dataset is sorted to make a group of input and outputs. The date is changed over into the quantity of days since the initial entry into the dataset. In this way, every data record contains data about the quantity of patients (confirmed, recovered, or dead) at a given region, at a given day since the initial

noted case [21]. Latitude, longitude, and the quantity of days since the first case are utilized as input data, with the output data being the quantity of patients in each cluster. Thusly, the time-series dataset is adjusted in a way that makes it fitting to train a regressive MLP. At last, the dataset, comprising of an aggregate of 20706 data records, is haphazardly divide into

five equivalent parts, or purported folds. Every one of these parts is utilized as a testing set, with the rest of the parts utilized as training set. This implies that training for every design is repeated five times, with a 20%:80% (16564haphazardly chose data records for training and 4142 data records for testing set) [22].
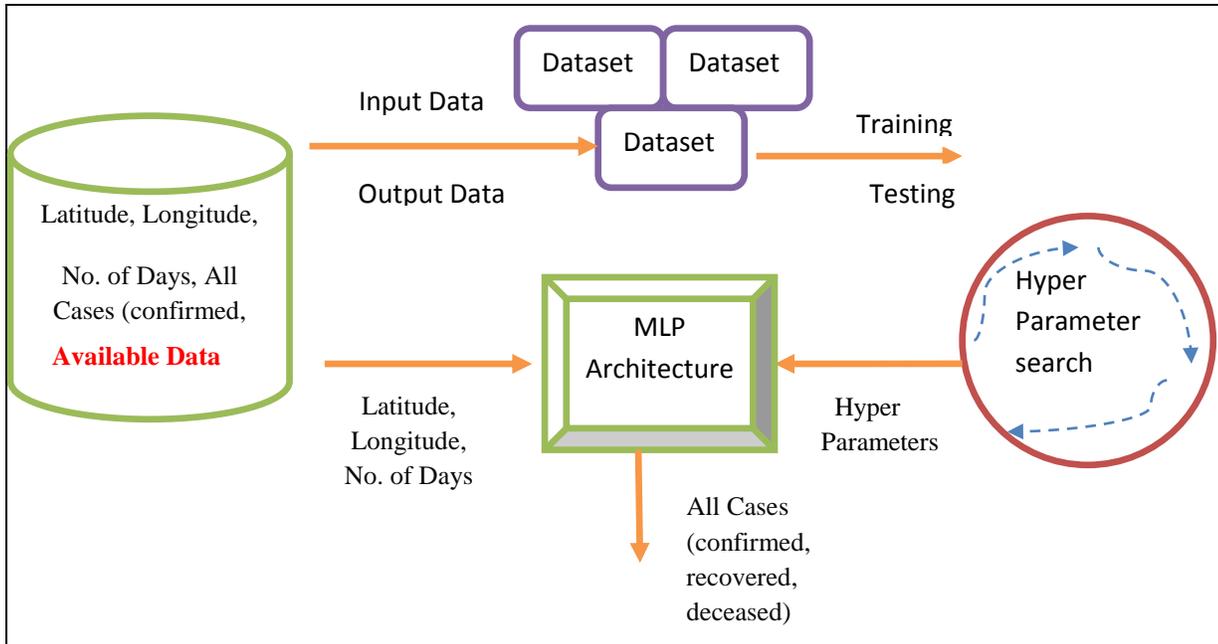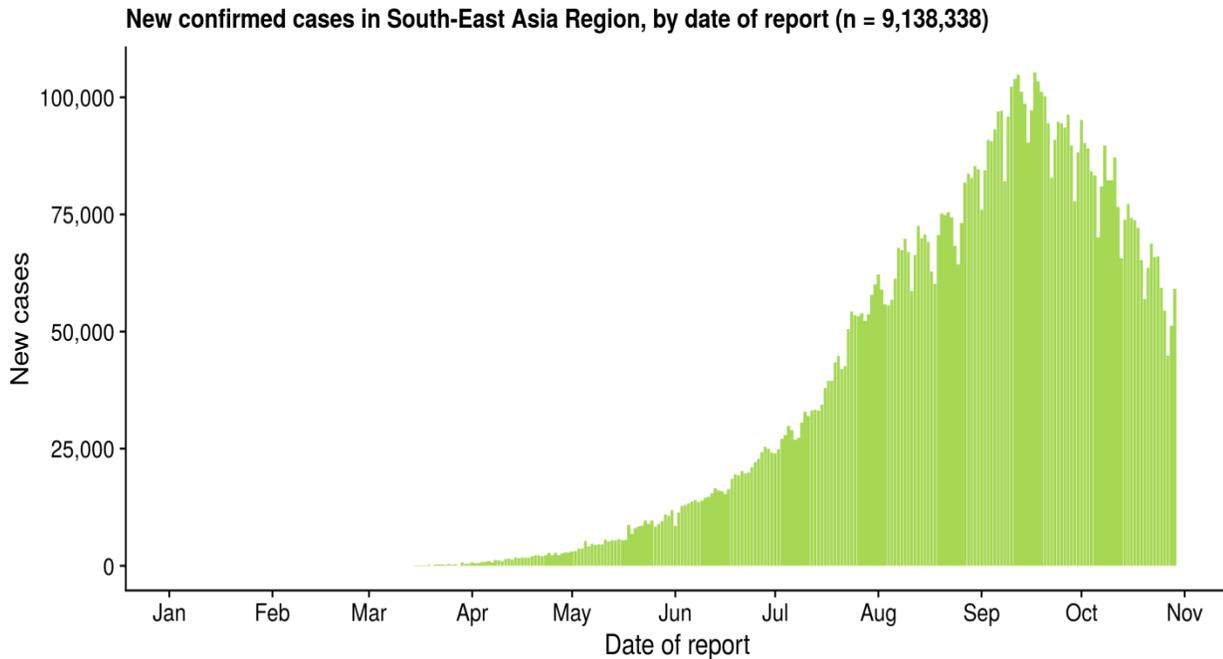


**Fig. 1:** Framework of MLP-ANN for COVID-19 Spread prediction

## 3.2 Multilayer Perceptron

Multi-Layer-Perceptron (MLP) is a kind of a completely connected, feed-forward ANN, comprising of neurons orchestrated in layers. Minimum of 3-layers formed MLP: an input, output, and hidden layers. The output layer comprises of a single neuron, the value of which is the output of the MLP-ANN. The input layer

comprises of the neurons in a similar number as the dataset inputs. MLPs utilized in this study will as such have three-neurons in the input. The purpose behind choosing MLP as the technique utilized in this exploration was the simplicity of execution of such strategies. MLP is likewise known to give top notch models, while keeping the training time moderately low contrasted with more intricate techniques [23].

**Figure 2:** Confirmed cases of Asia region as of 31-10-2020

MLP depends on computing the values of neurons in a current layer as the actuated summation of weighted outputs of neurons in a past layer, associated with the neuron. The weights of the neuron associations are at first random, yet then changed through the backward propagation method, in which the error for a forward spread of the MLP results gets back-proliferated through, and weights are changed relatively to the error. Because of the way that MLP-Regression can just regress a solitary value, if the issue comprises of different output values, a secluded model comprising of different models must be utilized [24]. While similarity is conceivable between models; training the models totally independently implies that all the designs will be tested, giving a higher opportunity to finding a superior forecast model for every objective. In the examination, 3-separate MLPs are trained—one for every one of the objectives—confirmed, recovered, and deaths patients. To affirm the legitimacy of the outcomes, the cross-validation process has been performed. The cross-validation strategy utilized in this exploration is the K-fold. During this method, the dataset is divide into k subsets (k = 5). At that point, every one of them is utilized as a testing set, while the rest of the k −1 subsets are utilized as a training dataset. The outcome is then displayed as the mean of accomplished scores, with standard deviation noted. The implementation of the proposed model is using Python [25].

**3.3 Hyper-Parameter Determination**

Hyper-Parameters (HPs) are values which characterize the design of the ANN model. Valid values of HPs are vital in accomplishing a quality model. To decide the best HP combination, the grid search method has been utilized. It takes a lot of potential parameters for each of the changed HPs. At that point, every conceivable blend of HPs is estimated. Every one of the blends is utilized to train the MLP. To keep away from the chance of poor answers because of the first random arrangement of the weights, each group of HPs is utilized for training 3-times. Every one of the accomplished models is then assessed. The HPs changed in this study are:

(i) Solver—the technique utilized for recalculating the loads of the MLP during BP method in training

(ii) Initial learning rate (α)—value of learning rate toward the start of training

(iii) Adjustment of LR—the manner in which the learning rate will change during the training, and if it will be changed relying upon the current estimation of cost-function or not

(iv) number of hidden layers and neurons— characterized as record, in which every integer

refers a solitary hidden layer and the integer value defines the quantity of neurons in that layer

(v) Activation Function—which utilized to change the input values of the neuron to the output value of the neuron, and

(vi) Regularization parameter L2—which restricts the impact of input parameters, to dodge the ANN being trained with an inclination towards a solitary input value which has a high relationship to the output; bigger the parameter, more is the impact brought down. Believable HP values are given in Table 1.

Table 1: Hyper-parameters used in training

| Name of the Hyper-Parameter | Possible values | Count |
|---|---|---|
| Solver Adam | LBFGS | 2 |
| Initial learning rate | 0.00001, 0.01, 0.1, 0.5 | 4 |
| Learning rate adjustment | Constant, adaptive, inv-scaling | 3 |
| Hidden layer sizes | (3), (6), (4, 4), (3, 3, 3), (6, 6, 6), (4, 3, 4), (12, 12, 12), (4, 4, 3, 3), (4, 4, 4, 4), (6, 6, 6, 6), (10, 5, 5, 10), (3, 3, 3, 3, 3), (10, 10, 10, 10, 10), (12, 12, 6, 6, 3, 3) | 14 |
| Activation functions | ReLU, identity, logistic, tanh | 4 |
| Regularization parameter | 0.00001, 0.001, 0.01, 0.1 | 4 |
| Total number of hyper parameter combinations | | 5376 |

## 3.4 Model Quality Estimation

Each obtained model is assessed utilizing the coefficient of estimation (R2). R2 characterizes how well is the fluctuation which exists in the real data clarified with the anticipated data. The output data, the actual number of patients, is contained in the vector x, while the anticipated data, gotten from the trained model, is set into the vector y. With that, R2 can be estimated as the coefficient between the residual difference and total fluctuation is calculated using Equation (1).

$$R2= 1- \frac{S_{residual}}{S_{total}}$$

Eq. (1)

Where, $S_{residual} = \sum_{j=0}^{n}(x - y)^2$, $S_{total} = \sum_{j=0}^{n}\left(x_j - \frac{1}{n}\left(\sum_{j=0}^{n} x_j\right)\right)^2$

Where, n being the quantity of evaluated tests. R2 is characterized in the reach $R2 \in [0,1]$, with the estimation of 0.0 implying that none of the fluctuations in genuine data is clarified in the anticipated data, and the estimation of 1.0 being the most ideal worth, which means the entirety of the changes is clarified in the anticipated data. Because of cross-validation being utilized, every design is trained 5-times on contrasting data. To depict the outcomes of cross-validation, the mean of R2(m)-scores is determined by Equation (2).

$$R2 \ (m) = \frac{1}{5}\left(\sum_{j=1}^{5} R_j^5\right)$$
Eq. (2)

To illustrate the variance between the scores on diverse folds, the Standard-Deviation (SD) of the $R2$-scores are estimated using Equation (3).

$$SD = \sqrt{\sum_{r=1}^{5} \frac{(R_t^2 - R2)}{5}}$$
Eq. (3)

## 4. Results and Discussions

In this segment, the complete discussions of the predicted outputs are achieved by proposed model are displayed.

### 4.1 Experimental Results

Finest models accomplished illustrate a top notch regression, with R2 scores of 0.987 for the affirmed model, 0.981 for the recovered model, and 0.995 for the deceased model. The best models accomplished for every one of the three objectives (number of affirmed, recovered, and deaths) have an equivalent essential ANN design. These models comprise of four hidden layers, and 16 neurons dispersed similarly among layers—4 neurons each. Best models for each of the three outputs additionally utilize the ReLU activation function and the LBFGS solver. The best model for affirmed cases has a steady LR of 0.1 and has a regularization boundary of 0.0001. For the recovered cases, MLP utilizes a consistent LR of 0.5 and a regularization boundary of 0.001. The model for foreseeing the quantity of deceased patients utilizes the versatile LR of 0.01, with the regularization boundary set at 0.1. The HPs of the best models are recorded in Table 2. Figure 3 shows the contrast of actual values to predicted values. Actual values, arranged by days, as well as trends for three model cases are displayed in Figure 3. Subfigures (a), (b), and (c) exhibit the contrast of actual values and predicted values by proposed models. Each bar presents various patients in a given gathering, per area. These envelopes show a guess of maximal malady spread per patient cluster, for both actual and predicted data, which shows that the displayed data follows the gathered data intently. Table 3 shows the cross-validation results accomplished for the best models appeared in Table 2.

**Table 2**. Hyper-Parameters of MLPs for best models achieved

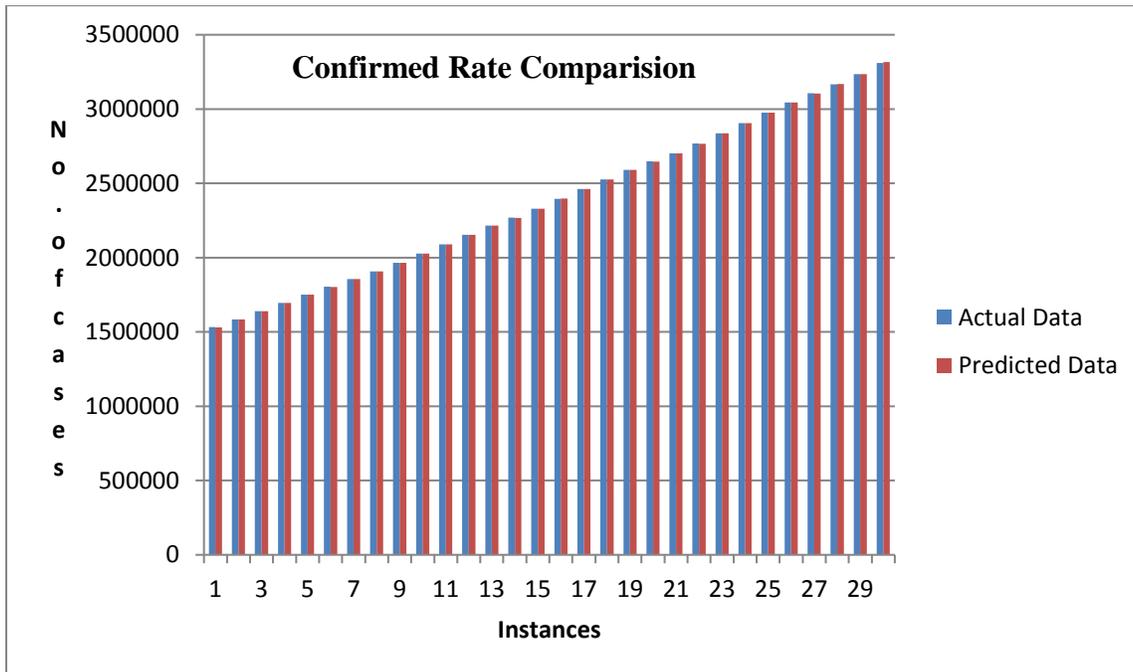| Hyper-Parameter | Confirmed model | Recovered Model | Deceased Model |
|---|---|---|---|
| Solver Adam | LBFGS | LBFGS | LBFGS |
| Initial learning rate | 0.1 | 0.5 | 0.01 |
| Learning rate adjustment | Constant | Constant | Adaptive |
| Hidden layer sizes | (4, 4, 4, 4) | (4, 4, 4, 4) | (4, 4, 4, 4) |
| Activation function | ReLU | ReLU | ReLU |
| Regularization parameter | 0.0001 | 0.001 | 0.01 |



**Fig. 3a.** Model trend of confirmed patients in comparison to real data

**Table 3.** Average scores for each goal and SD.

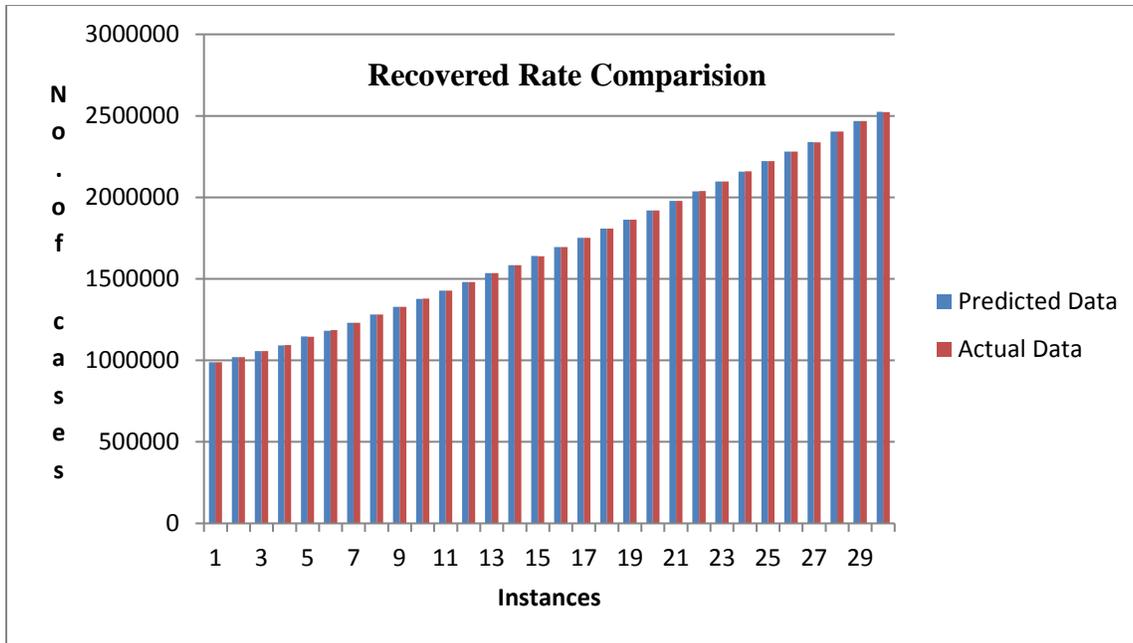| Goal | Average-$R2$ -score across folds | SD |
|---|---|---|
| Confirmed | 0.96 | 0.037 |
| Recovered | 0.792 | 0.072 |
| Deceased | 0.915 | 0.021 |

**Fig. 3b.** Model trend of Recovered patients in comparison to real data
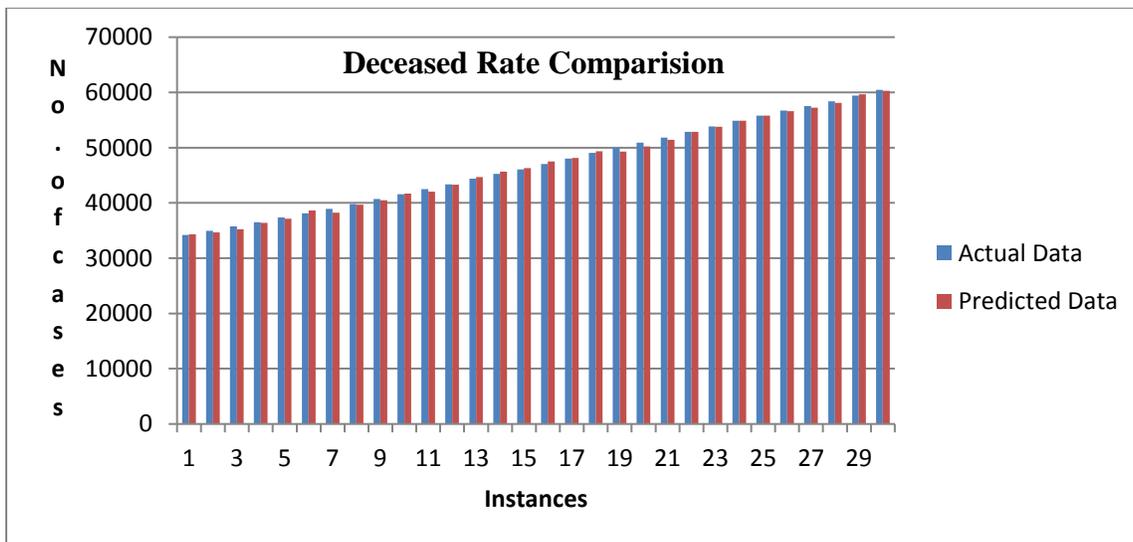


**Fig. 3c.** Model trend of dead patients in comparison to real data

## 4.2 Discussions

Results demonstrate that a alike design can be utilized for 3-models, recommending a same pattern between 3-objectives. The utilization of the ReLU-activation function isn't startling, as it removes the negative values; it is good for model and due to this model only predicts positive values only. LRs vary between techniques, both the approaches for confirmed and recovered utilize a moderately high steady LR, while the deceased model utilizes an altogether lower learning rate however adjusts over iterations. The regularization parameter is moderately low for the model of diseases however increased for the recovered and deceased models—highlighting the way that there is a higher impact of certain input

parameters on the output of those models which required to be concealed. Models prove helpless in tracking of abrupt and unexpected changes, for example, sudden jump in confirmed cases around day-22. Still, the model exhibits great following of overall model change, giving great forecasts even after such surprising jumps—whenever offered time to change. Because of the biggest number of cases being situated in Asia, the model is to a great extent fitted to that data. Future changes in the greatest number of contaminated, deceased, or recovered patients ought to be remembered for the models to additional test its power. Cross-Validation performed appeared over the solution-space shows a drop in R2-scores. The model for deceased patients shows the least drop in scoring utilized. The model of affirmed cases shows a huge drop from 0.987 to 0.96, however these outcomes are as yet satisfactory. The most elevated drop is appeared in the model of recovered patients where R2-score drops from 0.981 to 0.792, indicating the low vigor of the model for recovered patients. The designs of the models that show the best outcomes continue as before when cross-validation is applied.

The goal of this study, which was to produce a model of COVID-19 spread on a worldwide level utilizing ML strategies, was accomplished. The proposed models show a high constancy to existing data, except for the model for recovered patients. In contrast with existing studies, proposed models show a higher exactness, as well as tracking of recovery and death cases. Outcomes display a capable to numerically model a spread of an infective decease utilizing ML on a limited dataset, implying that nearly extensive stretches of data assortment are not carefully important to accomplish a decent model with AI models. Gotten outcomes point towards the capacity to utilize such models to show comparable phenomena in the future.

## 5. Conclusion and Future Work

The accomplished techniques illustrate that it is possible to get a quality approach of new viral diseases utilizing ML strategies, with geographical and data as inputs. In this study, high precision methods have been skilled for all regression goals. Accomplished results display the way that ML models can be utilized in illustrating issues, for instance, the spread and impact of infective deceases. This implies that the use of AI techniques ought to be endeavored in displaying the present and future spread of infective maladies, trying to anticipate the effect of such diseases on mankind. Model fitting to a great extent the Chinese patient populace shows that utilizing the quantity of patients per nation isn't really a decent measurement to use as a preparation objective; further examination ought to be put resources into testing how various sorts of measurements influence model quality. Future work ought to apply different strategies trying to discover far superior models or models that are more straightforward to utilize, or more straightforward than ones saw with MLP. Examination of models for various infective maladies would be intriguing. More information being procured should empower the utilization of different methods, for example, RNNs to be applied on the examinations of disease models utilizing time-series data.

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