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Enriching Covid-19 prediction through CNN and LSTM Deep learning

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ABSTRACT

The pandemic that occurred very recently due to the Covid-19 virus has been very difficult to cope in terms of mental and physical problems faced by the sudden onset of virulent outbreak. The destruction through this pandemic has been seen in different walks of life which could considerably reduce if the ability of predict covid-19 outbreak or infection rate was available to combat the spread of the virus. The latest epidemic is proof of this; the Covid-19 infection has caused widespread mortality and damage throughout the globe. This outbreak was perhaps handled differently if the medical industry had a clearer understanding of the scope and potential consequences of the epidemic, allowing them to be adequately equipped in reaction to the mounting illnesses. A pandemic's evolution is exceedingly intricate and could only be anticipated via machine learning algorithms. This study employs Pearson correlation and K Nearest Neighbor clustering, as well as Convolutional Neural Networks and Decision Trees, for accurate Covid-19 forecasts. The experimental results demonstrated that the provided technique outperformed traditional approaches.

Keywords—Covid-19, Pandemic, Pearson Correlation, K-nearest Neighbor, Convolution neural network, LSTM,Decision making.

I INTRODUCTION

Humans now have a higher quality of life thanks to recent medical advances. Affordable healthcare and medical centers have made it possible to live a much better, pain-free existence. In comparison to earlier and medieval centuries, which have been plagued by different illnesses and maladies that decimated humans. Numerous illnesses have already been linked to large-scale mortality as a result of the healthcare system's incapacity to grasp the sickness and find a solution at the period. Mankind have gone a long way since then, and the medical system has changed dramatically. This has resulted in a large drop in newborn fatalities as well as an improvement in expected lifespan.

One of most crucial component of human life is wellbeing. Health is essential for humans to function at its peak productivity throughout all circumstances. This is only conceivable if humans have healthy lifestyle and diverse strategies for maintaining this condition for an extended period of time. Medical breakthroughs have made it possible to preserve one's wellbeing. All across historical events, there have already been significant advances in medical care. Years of scientific research and sustained effort have resulted in significant advances in health maintenance. Several contributions over the years have helped us to achieve the pinnacle of human wellbeing.

There were historically occurred epidemics that were successfully predicted to be extinction-level events for the humankind. Highly pathogenic outbreak, here as the current covid-19 epidemic, have demonstrated how well a condition may be life-threatening on a worldwide scale [1]. There are groups that monitor activities and warn of the possibility of an epidemic in ahead of time. This can assist in preparing the public for the breakout and avert a major disaster.

The current Covid-19 epidemic was not managed properly by the governments because they lacked the mechanisms to accurately determine the virus's transmission and discover strategies to limit it. These breakouts have already been extremely worrisome since they have resulted in a big number of deaths and a great deal of agony and distress for the afflicted. There had been a scarcity of integrated data and could be used to organize and manage the final result of real epidemiologists and other epidemiological authorities.

There were also studies that have been conducted for this goal in order to efficiently capture important data and develop algorithms for future projections of the proliferation. They have already been substantially developed in this study to accomplish our approach for delivering future forecasts of virus transmission. However, the majority of these techniques have already been determined to provide some form of constraint that has impeded a practical application [2]. As a result, there is a requirement for an effective approach that can offer precise estimates for prospective disease rates, allowing governments to plan ahead of time.

Epidemics are extremely difficult and troublesome circumstances because of the great deal of stress that everyone experiences throughout these periods. The most concerning aspect for healthcare personnel and individuals is the unpredictability of the future. There was a paucity of tools which could be used to successfully anticipate the transmission rate in the future during the current covid-19 infection outbreak. This has resulted in increasing ambiguity, which may be extremely difficult for medical practitioners and administrations in terms of planning. This research paper specifies the process for generating accurate and exact transmission rates for the covid-19 pandemic. The lack of an appropriate method for highly precise covid-19 infection rates and an adequate pandemic forecasting model resulted in massive fatalities and hardship for a lot of people worldwide.

This was a problem in both developing and mature economies. This is because the majority of these studies in the linked publications that we have investigated on this issue have suffered from a few of the shortcomings and constraints. This has resulted in erroneous forecasts for mistakes, lowering the overall predictive model's performance. An appropriate forecasting technique is required for this purpose in order to provide reliable estimates of future rates of infection. This study paper arrived at a powerful approach by analyzing previous studies on this issue, which have been mentioned in this article.

The description of relevant investigations is included in Section 2 of this publication. The third section discusses the proposed system's outline. Section 4 delves deeper into the experimental findings, while Section 5 wraps up the work and discusses future research directions.

II RELATED WORKS

Bowen Wang [3] investigated how to harness social interactions amongst smart phones in SIoT to assist decrease rates of infection by early detection of suspected COVID19 transmissions. The researchers then turned the optimization technique into a MWVC challenge for dynamic network design and devised a RAI approach for solving it. Using two actual datasets, they demonstrate that their strategy reduces the pandemic rate of infection dramatically across both huge and limited circumstances when contrasted to the references. Furthermore, by relying on early recognition of COVID-19 instances, the proposed strategy is ideal for research on the epidemiology.

Yi-Cheng Chen [4] provides the detailed application of mathematical study for the Covid -19 disease incidence. In compared to traditional Susceptible-Infected-Recovered approaches, the time varying Susceptible-Infected-Recovered framework can help and adaptable. Such SIR approaches are also comparable to direct estimating approaches, resulting in the SIR being much more resilient. To measure the influence of undiscovered infestations in COVID-19, the authors updated the SIR model by taking into account two groups of infected people: identifiable infected people and unknown infected people.

Ertugrul Karaçuha [5] described helpful information here about how to predict case statistics to build a successful strategic plan for redistributing health care services to patient populations in the picture of the existing disease outbreak. This simulations might be used not just for the current COVID-19 epidemic, but also for subsequent local or worldwide occurrences. This study models and forecasts the number of overall cases, mortality, and recovered from the COVID-19 outbreak for eight countries: the United States, the United Kingdom, Turkey, Spain, Italy, Germany, France, and China. First, the researchers used their recently reported Deep Assessment Methodology, which would be dependent on Fractional Calculus, to model the COVID-19 information from the very first confirmed instance. The Deep Assessment Methodology as well as Long-Short Term Memory have been then used to evaluate the efficiency of the Deep Assessment Methodology in a one-step projection. The final section of the study concentrated on short-term pandemic forecasting, utilizing the time-dependent SIR model as well as a Gaussian model predicting using elevation of the continuous incidence rates derived through Deep Assessment Methodology.

Ankit Ramchandani [6] presents a novel deep learning approach for evaluating multiple county-level factors and anticipating the spread of infected situations in the future. The proposed approach extracts comments using multivariate time series including multivariate spatial series data for the period in a novel way by utilizing both the temporal and spatial representation of the model. This integrated retrieval strategy might be used in other deep learning projects to evaluate similar sorts of data. Furthermore, in contrast to previous models, the presented model combines a large combination of multiple characteristics and establishes correlations between them. Even during COVID-19 epidemic, the model's accuracy in anticipating the surge in the prevalence of reported infections in counties across the United States were demonstrated.

Onder Tutsoy [7] develops a model of Suspicious-Infected-Death with completely unknown dynamics. Because suspected, contaminated, and death fatalities are all strongly dependent on each other and, the conventional Suspicious-Infected-Death paradigm is closely interrelated. Every Suspicious-Infected-Death sub-model adds 2nd degree internal dynamics to describe the spikes and fluctuations in COVID-19 fatalities. The precise bases pertaining to the model's dimensional space are created, and the input parameters are trained using just a batching style Least Squares estimation to educate the independent variables of the Suspicious-Infected-Death scenario. The model with the determined parameters was thoroughly studied using mathematical techniques, and potential COVID-19 fatalities for Turkey were predicted that use the built model.

Xingguang Chen [8] expresses that there has been an increase in the number of covid-19 cases that have been critical in realization of the reduction in the effect of the pandemic. This has been critical as it leads to a large number of cases which will be difficult to handle for an exponential amount of patients with the strained infrastructure. The lack of an effective strategy for the realization of an epidemic response is lacking. Therefore, for this purpose, the authors in this research article have proposed a framework for modeling infectious diseases by taking into consideration the asymptomatic infections which can be a significant contributor to the epidemic and the increasing numbers of covid-19 infections.

Sujata Dash [9] describes epidemic propagation through using best Forecasting methods for six higher complication countries around the globe and six heavily impacted states in India to anticipate future outcomes. Except in a few cases, the analysis shows values that are reasonably incredibly accurate. The ARIMA model that is most commonly used is not the best match. The expected BIC, AIC, and RMSE values are suitable for all Indian nations. Furthermore, ARIMA models developed for Indian states had large predicted BIC, AIC, and RMSE estimates. The effectiveness of the Model Parameters is shown by statistical outcome measures. The model's conclusions might have been utilized to develop potential ways to improve the health insurance system and supervision.

Michael Small [10] provided a framework with a small – maybe lowest – number of factors that captures the observed patterns of pandemic disease transmission. When interpreting data from the worldwide coronavirus pandemic, the model shows good subjective concordance with observational reality throughout large cities. Despite this, same experiments with varying starting conditions yield significantly different outcomes. The volatility in the reported model forecasts is significantly larger than the variation seen across other epidemiologic system parameters. As a result, following adequately characterizing interaction creating and developing a transmissions countermeasures, determining appropriate transmission speed becomes a secondary concern. Their findings imply that simulation results of models asserting predictive capability inside such a forecasting region may be susceptible to over-interpretation.

Hamdi Friji [11] introduces the concept of a mechanistic model that is being used for the purpose of achieving the forecasting of the covid-19 pandemic. This has been crucial for the development and handling of the presented approach to reduce the mortality in individuals. This is particularly concerning aspect as the large number of deaths that were recorded during the covid-19 pandemic have been highly problematic and unsettling. The realization of such a system has been facilitated through the implementation of the Levenberg-Marquardt algorithm which encounters a fitting problem. This problem is solved by the authors that have used 8 different states to achieve the characterization of the mechanistic model for precise forecasting of the epidemic.

Furqan Rustam [12] creates a system for evaluating the risk of a global COVID19 outbreak using machine learning. The system analyzes a collection containing day-by-day serious historical information and make recommendations for the upcoming days using machine learning techniques. The study's findings demonstrate that, given the kind and size of the dataset, linear regression works even better in the current forecasting arena. To some extent, linear regression, least absolute shrinkage, and optimization algorithm are reasonably good at forecasting incidence and mortality and establishing cases. According to the conclusions of these three examples, fatality rates will climb in the next occasions, whereas health outcomes will slow. Support vector machines produce inconsistent results in all circumstances because to the peaks and troughs in the dataset variables.

Nanning Zheng [13] creates a hybrid AI method for predicting COVID-19 that is based on the ISI framework and involves an NLP subsystem that encompasses essential intelligence obtained via national and local government efforts, as well as pervasive democratic engagement in the forecasting calculation method. The model's estimations are indeed very similar to the authentic epidemic cases, trying to demonstrate that the proposed scheme can more different assessment tools the virus's transmitting regulation and advancement trend than older designs, and that linguistic knowledge acquisition of similar news can significantly improve the performance of the models.

III PROPOSED METHODOLOGY

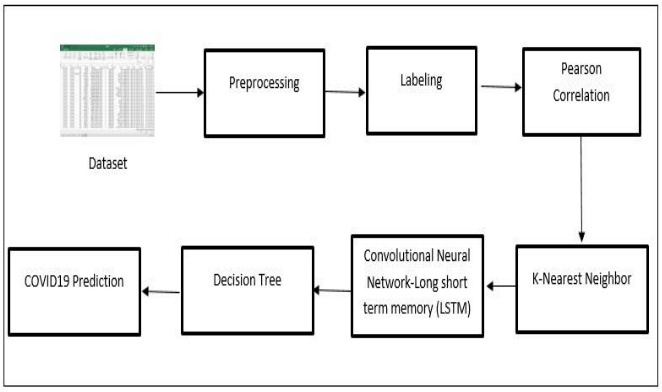


Figure 1: System Overview Diagram

The proposed methodology for the forecasting of Covid-19 cases has been realized using deep learning methodologies in the form of Convolutional Neural Networks and Long Short Term Memory. The prediction has been accomplished by means of a sequence of steps that have been demonstrated below.

Step 1: Dataset Collection and Data preprocessing – The proposed approach is initiated by providing the dataset as an input to this step of the procedure. A district-by-district dataset of India is provided as input into the system in .csv format at the start of the proposed model. The following URL was used to collect this data: https://api.covid19india.org/csv/latest/districts.csv. Date, State, District, Recovered, Deceased, Other, and tested are all included in this dataset. The dataset path is supplied to the variable in the application as a hard coded value. Following the path, rows and columns are separated to read the dataset as a double-dimensional list.

The dataset preprocessing is performed to condition the data and achieve improved execution performance of the proposed prediction model. The initial step for the preprocessing has been performed to identify the variable types in the dataset. Once these variable types are identified, the dataset is then used to find the correlation between the attributes through the implementation of the Pearson Correlation approach in the nest step of the procedure.

Step 2: Pearson Correlation – The Pearson Correlation determines the correlation between the attributes and the values of which are utilized to identify the attributes with the lowest correlation. This results in a correlation matrix which can be useful in determination of the combination of the attributes to be selected. Once this is determined, the attributes with lower correlation are dropped and a correlation values are calculated again. The Pearson correlation is performed through the equation 1 given below.

r ------- (1)

Where,

=values of x variable

= values of y variable

= mean of x variable values

= mean of y variable values

Some irrelevant columns, such as State, other, and tested, are removed from the list after the dataset is gathered in the double dimension list. Date, district, confirmed, recovered, and died are picked as preprocessed list elements in the Data segregation procedure, which is discussed in the following step.

Step 3: K nearest Neighbors – The data collected previously is being used for the purpose of achieving the effective clusters of the data. The K nearest neighbor classification clustering approach utilizes the dataset and finds the data points that are the closest to one another. This is done by calculating the distances and the deployment of appropriate centroids based on the value of K. This results in a list with the distances which is effectively sorted in the ascending order of the distances. The resultant list is divided into half and the uppermost list is then supplied to the next step for the infection rate prediction through the use of the CNN-LSTM approach. The Euclidean distance has been calculated using the equation 2 below.

ED ________ (2)

Where,

ED=Euclidian Distance

A_{Ti}=Attribute at index i

A_{Tj}= Attribute at index j

Step 4: Data segregation – This stage takes the preprocessed list and changes it into a district-specific segregated list. The date is converted into ordinal values using a data segregated list; this procedure changes the string type of data of the durations into Date type of data. This step allows for the model to easily sort or select the rows for the achieved list for the specified date intervals.

Step 3: Training and testing data Creation – Initially, the proposed model predicts the top ten districts for the given kind of case from the preprocessed list for creating the testing and training data list. This is accomplished using the sort values method, which takes two parameters: type and sorting value. Following the selection of the top ten districts, the train and test lists are created.

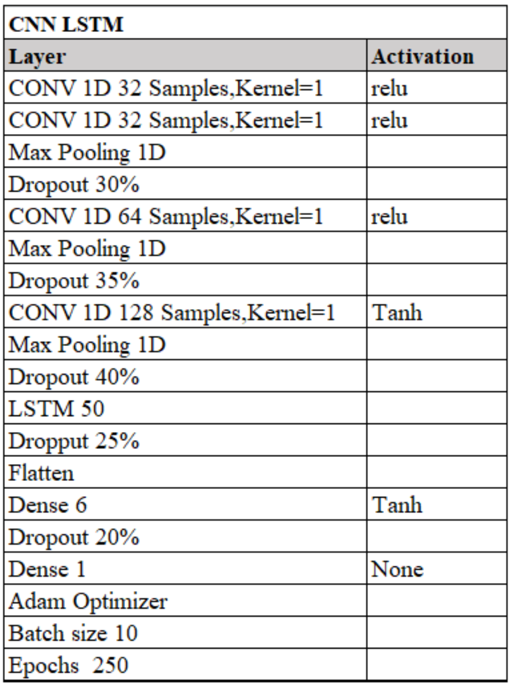
The data is picked from the preprocessed list between the two supplied date periods in a list. Then two lists are made, one for the date and the other for the specified district name. The test and train sets are then created using the function train test split(). Because the model is not rearranging the data according to date, this method takes the following parameters: X, Y, test size of 0.15, and rearranging Boolean value of false. The random train and test data is then generated and assigned to four lists: train x, train y, test x, and test y.

These train and test collections are translated to ordinal values, allowing them to assimilate all data kinds with ease. The MinMaxScaler() function is used to balance the test and training lists. This procedure normalizes the data by applying the upper and lower limits. Following normalization, the lists are reshaped into a single dimension through the implementation of the reshape function ( ). The reshaped data is supplied into several CNN-LSTM models to predict infection rates for the corresponding date intervals for the COVID -19 epidemic.

Step 4: Convolutional Neural Networks and Long Short Term Memory – This is the neural network, which takes train x, train y, test x, test y, and scalar object of normalization, test date, and case category as input parameters. Cases are capitalized using the capitalize() function. The conv1D is added with 32 filter with kernel size one and the activation function as ReLU. Another one dimensional layer is added with the similar parameters and the activation function as tanh. A max pooling one dimensional layer is deployed with a pool size of 1. In addition to the additional parameters, a dropout () is employed between the final hidden layer and the output layer at a rate of 30% (or 0.3).

Several layers of the model are constructed using different parameters, the subsequent second layer utilizes a filter of 64 and kernel size of 1, similar padding and tanh as the activation function. The max pooling is also realized with the pool size of 1 and a dropout layer of 35% or 0.35. Similarly a final one dimensional convolutional layer is deployed with 128 as the filter, keeping rest of the parameters same as the previous layers, along with the max pooling layer. Another dropout layer is added with a rate of 40% or 0.4.

The LSTM model is realized using 100 blocks with return sequences set as true as well as the activation function as tanh. The dropout layer of 25% or 0.25 has been added thereafter. The second layer of the LSTM utilizes 50 blocks and the rest of the parameters are unchanged and the dropout rate of 20% or 0.2 has been deployed. After this the model is flattened and a dense layer is added with the kernel size of 6 and the activation function as softmax, and another dropout layer of 20% and 0.2. A final dense layer is initialized with 1 as the kernel size with no activation function. The entire model is demonstrated in the architecture diagrams in Figure 2.



CNN LSTM	
Layer	**Activation**
CONV 1D 32 Samples,Kernel=1	relu
CONV 1D 32 Samples,Kernel=1	relu
Max Pooling 1D	
Dropout 30%	
CONV 1D 64 Samples,Kernel=1	relu
Max Pooling 1D	
Dropout 35%	
CONV 1D 128 Samples,Kernel=1	Tanh
Max Pooling 1D	
Dropout 40%	
LSTM 50	
Dropput 25%	
Flatten	
Dense 6	Tanh
Dropout 20%	
Dense 1	None
Adam Optimizer	
Batch size 10	
Epochs 250	

Figure 2: Architecture for CNN LSTM

The used tanh and ReLU activation function are depicted in equation 1 and 2.

______ (3)

Relu=max (0, x) _____ (4)

Where x is the input attributes values

The model is compiled with the adam optimizer and then trained on 1000 epochs with a batch size of 10. This results in a trained model file with the extension of .h5. This file is then used to perform the testing which is discussed in the next step of the procedure.

Step 5: Decision Tree – The testing is performed for the predictions for a specific test data. The model file is taken as an input along with the test data for a particular district in India with a specific time range. The trained model is being used for the purpose of achieving the effective realization of the prediction. The predict() method of the model object is used to identify predictions for a specific test list after establishing the CNN-LSTM neural network model. The predicted results are displayed in a graph created using the matplotlib API object.

IV RESULT AND DISCUSSIONS

The proposed approach for estimating Covid-19 infection rate was established using the Python computer language. The Spyder IDE was used to contribute to the formation of the suggested technique. The development computer has 4GB of RAM and 500GB of hard disk space, as well as an Intel Core i5 CPU. The Pandas API is being utilized to allow for the integration of the dataset in a spreadsheet form.

An experimental assessment was carried out to provide a thorough examination of the prediction technique for the possibility of any errors. The error evaluation generates the precision of the prediction, which may be quite valuable in defining the Covid-19 prediction system's reliability. The Root Mean Square Error (RMSE) performance metric was utilized to calculate the error of the proposed forecasting model.

To measure the error between these two parameters, the RMSE approach employs two constant and interrelated variables that are correlated. In our solution, the variables used are the predicted Covid-19 infection rate predictions and the actual Covid-19 infection rate predictions. The formula used to acquire the error is indicated in equation 5 below.

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}(x_{1,i} - x_{2,i})^2}{n}} \quad \_\ (5)$$

Where,

- Summation

$(x_1 - x_2)^2$ - Differences Squared for the summation in between the actual Covid-19 infection rate predictions and the predicted Covid-19 infection rate predictions

n - Number of samples or Trails

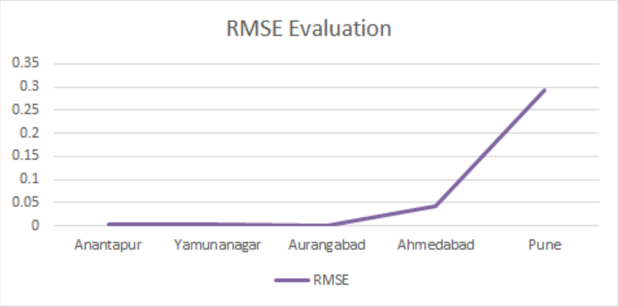
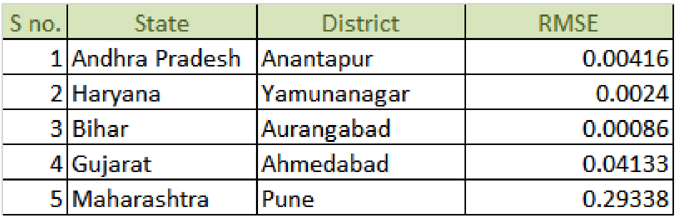


Table 1: RMSE evaluation in a district wise manner



S no.	State	District	RMSE
1	Andhra Pradesh	Anantapur	0.00416
2	Haryana	Yamunanagar	0.0024
3	Bihar	Aurangabad	0.00086
4	Gujarat	Ahmedabad	0.04133
5	Maharashtra	Pune	0.29338

Figure 2: RMSE values for specific districts

The empirical assessment and its results are listed in table 1 above. The data received from the table are utilized to create the line graph shown in figure 2 below. We may conclude from a comprehensive examination of the visual representation and the tabular numbers that the error achieved in this prediction procedure is negligible. A total of five tests with different districts were carried out in order to calculate the MSE or Mean Square Error.

The evaluation results demonstrate that the prediction system's error is reasonable and appropriate. The prediction error is generally evident in prediction models that operate with actual statistics. The RMSE value of 0.06842, obtained is quite good and demonstrate a reliable formulation of the Covid-19 infection rate prediction method. The suggested method outperformed the SIR, SEIR, eSEIR approaches defined in [14]. Our method achieves a lower RMSE. Table 2 below shows a tabular comparison of the SIR, SEIR, eSEIR based approach of [14] and the proposed CNN-LSTM Covid-19 infection rate prediction methodology.

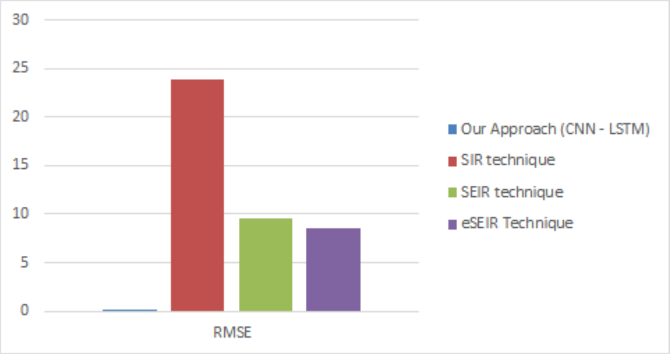
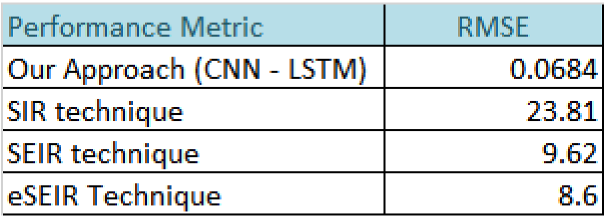


Table 2: Comparison with [14]



Performance Metric	RMSE
Our Approach (CNN - LSTM)	0.0684
SIR technique	23.81
SEIR technique	9.62
eSEIR Technique	8.6

Figure 4: Comparison with SIR, SEIR, eSEIR based approach in [14]

The novel CNN-LSTM technique utilized in this research considerably surpasses the SIR, SEIR, eSEIR based Covid-19 infection rate prediction approach described in [14], as seen in Figure 4. This is owing to the CNN-LSTM ensembling implementation, which dramatically reduces errors and improves prediction quality.

V CONCLUSION AND FUTURE SCOPE

The proposed methodology for achieving reliable and precise estimations for covid-19 infection rate was achieved using Convolutional Neural Network-Long Short Term Memory. Prior to actually passing the input dataset to the next component for segregation, it is preprocessed to remove redundant data. After that, the preprocessed data is divided into districts and delivered to the K Nearest Neighbors module. The KNN approach clusters a preprocessed and separated dataset based on the dataset's closest values. The CNN-LSTM module obtains segregated data by data normalization and Pearson Correlation, which is then divided into sections for training and testing. The CNN-LSTM module is trained using verified, recovering, and deceased cases. The

Deep Learning paradigm solves this problem in this scenario, enabling for the successful prediction of Covid-19 infection rates using an innovative combination of CNN and LSTM which is an ensembling technique that further enhances the accuracy of the predictions. The experimental results indicate that the infection rate estimations for Covid-19 are appropriate.

In the future, using a cloud-based Generative Adversarial Neural Network, the model might be deployed on massive amounts of data containing a high proportion of attributes from all over the world.

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