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Research Article

"A Deep Learning Approach for Forecasting COVID-19 Patient Outcomes"

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ABSTRACT

"Deep learning" is a subfield of artificial intelligence that uses artificial neural networks, a machine learning technique, to comb through massive amounts of data in quest of patterns and predictions. In recent years, it has been characterised by rapid advancement and broad, successful application across numerous domains. Healthcare transformation faces a major challenge in extracting actionable insights from complex, multi-dimensional, and varied biological data. An overview of deep learning research on COVID-19, a summary of recent advances in the field, and a look at some practical uses of deep learning algorithms for COVID-19 diagnosis, prognosis, and treatment management are the goals of this study. Deep learning (DL) has the ability to improve the efficiency and accuracy of drug development by evaluating medical imaging data, laboratory test results, and other relevant data to diagnose, evaluate the progression and prognosis of diseases, and even provide treatment recommendations and medication use regimens. Furthermore, it could help legislators develop efficient control and prevention measures. Furthermore, we assess the current capabilities and limitations of deep learning in relation to the accuracy of COVID-19 treatments. This evaluation covers topics such as the lack of phenotypically abundant data and the need for deeper learning models that are more user-friendly. We conclude by discussing ways to overcome the current barriers that prevent deep learning from being fully utilised in future clinical applications.

Keywords: COVID-19, deep Learning, Clinical Route, Prognosis, Mortality risk prediction

I. INTRODUCTION

A high number of pneumonia cases were reported in Wuhan, China in December 2019. The unique coronavirus that caused that strain of pneumonia in 2019 was designated as COVID-19. It was a subtype of SARS-CoV-2 virus. On January 30, 2020, the disease was declared a pandemic by the World Health Organisation (WHO) as it rapidly spread to other regions. Government statistics show that nearly 5 million people perished from COVID-19 infections between then and February 2022, with an estimated 380 million people infected [1].

Chlamydia coronavirus causes respiratory disease. Characteristics seen in the vast majority of pneumonia patients (e.g., fever, chills, cough, sore throat, dyspnoea, etc.) are shown in Figure 1. Their opacity makes them hard to spot. Thus, a rapid diagnosis is the first and most critical step in treating a COVID-19 infection. Diagnostic tools for this virus often employ molecular biology techniques, such as the Real-time RT-PCR [2]. However, real-time polymerase chain reaction has many issues. Incorrect diagnoses owing to lack of sensitivity are one possible outcome. Another is that it may show that the majority of patients experience pulmonary symptoms, such as ground-glass opacity of the lungs on chest x-rays [3]. CT employs high radiation doses, which restricts its usage in pregnant people and children [4]. CXRs, on the other hand, are great for lung imaging and could be a suitable way to identify COVID because they use low radiation doses and are inexpensive.

Early detection and prompt treatment are the only ways to prevent the illness from worsening. In order to achieve this goal, methods such as illness severity prediction models have been developed. Using these models can improve

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clinical decision-making, patient triage, and the establishment of priorities. By evaluating the seriousness of the disease and the probability of death, predictive algorithms can identify patients at high risk early on. Care for those at high risk should be prioritised in order to reduce the COVID-19 mortality rate. Algorithms developed for this purpose often incorporate medical imaging, clinical and laboratory data, and other similar sources to forecast death rates [5].

The high expense and elevated radiation risk of computed tomography (CT) scans, especially in children, make more accessible data a top priority for the development of prognostic models. According to the World Health Organization's guidelines for the treatment of COVID-19, imaging should only be considered if the test is unavailable. A COVID test, however, can be inconvenient to schedule and may return negative results even in cases where symptoms are present [6]. So, more patient-related data is needed for prediction models to be built and to help with clinical decision-making. When patients are led to a health centre that offers inexpensive costs, they have simpler access to their lab reports. In order to estimate the severity of the illness, this data source is vital. It is convenient, inexpensive, and safe when compared to other data sources like images or CT scans of the lungs [7].

Several studies in screening, prediction and forecasting, and contact tracing have focused on machine learning algorithms and deep learning approaches, even if the COVID-19 conversation is still in its early phases. An attempt to predict the life expectancy of COVID-19 patients has also been made by researchers using three or more pieces of patient data, such as demographics, vital signs, symptoms, comorbidities, treatment, and laboratory results [8].

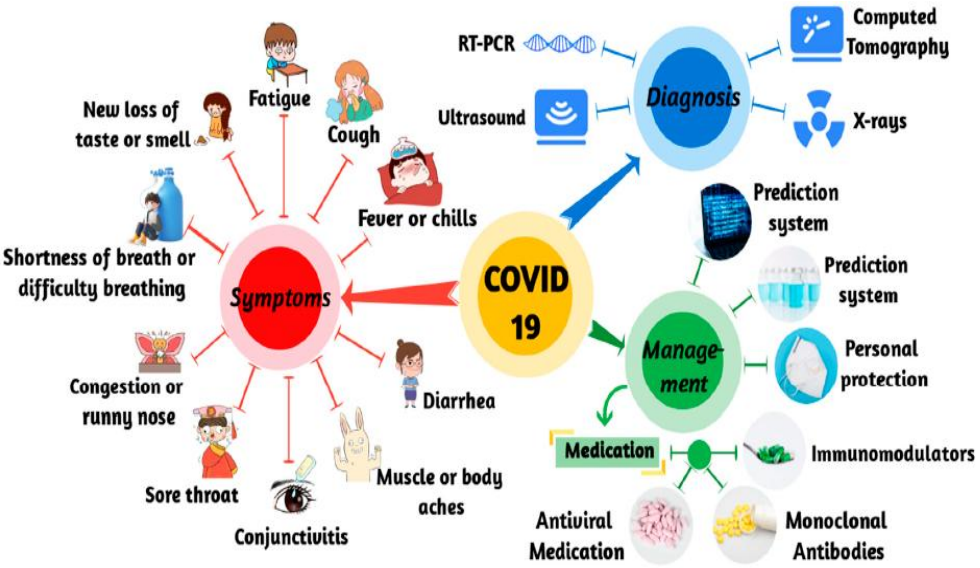

Fig.1. Representation of COVID19 (symptoms, diagnosis, &management).

In addition, there have been many recent studies aimed at understanding and diagnosing COVID-19 patients. These studies have used various methods. The severity of the danger can be reduced with early patient identification using COVID-19. Early detection of high-risk individuals is more important than late detection of low-risk people for this life-threatening illness. Furthermore, not all hospitals have the means to perform a battery of complex tests prior to determining the risk, including the necessary personnel, funding, time, and equipment. A COVID-19 mortality risk calculator is developed with utmost precision and employs a minimal set of characteristics to get a satisfactory prediction rate. The survival rate of the patient can be more accurately predicted with the use of the suggested methods. Many Machine Learning (ML) methods have been developed for COVID-19 patient prediction, but few have achieved ideal results. This might be due to a lack of relevant data or an extreme bias towards a certain demographic.

The subsequent are the key benefits of this research:

1. The trade-off amid efficiency characteristics and sample-space, as well as biomarkers for predicting the transience risk of COVID19 patients, is among the forty-eight critical elements that are taken into account.

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2. A data imputation methodology is presented that utilizes a combination of the SMOTE and K-Nearest Neighbor methods.

3. The suggested DL model was developed using an AWS web application with the goal of assisting frontline clinicians in making time-sensitive therapeutic decisions for COVID-19 patients with limited resources.

4. By comparing DL models' prediction performance with that of specialized features, we find that basic features perform better.

II. RELATED WORKS

The purpose of this review does not permit comprehensive discussion of all deep-learning techniques. Rather, we offer a synopsis of the DL strategy used in COVID19. In recent years, DL has achieved remarkable strides in solving the problems that have impeded the advancement of artificial intelligence for a long time [9]. Many scientific, commercial, and governmental domains can benefit from its exceptional ability to unearth intricate structures in high-dimensional data. When it comes to estimating the activity of possible therapeutic compounds, it outperforms existing machine-learning algorithms and even breaks records in picture recognition [10].

The initial use of neural networks was as a prominent connectionist model [11]. While later models shifted their focus to the modeling of certain cognitive capacities like object identification and language understanding, earlier models emphasized biological reason. An early example of a basic neural network without feedback and with signals flowing unidirectionally from input to output layers was the feed-forward neural network (FNN), sometimes called a multilayer perceptron (MLP). The biological receptor field mechanism served as inspiration for CNNs, which are DNNs that share weights and have local connections [12]. Although MLPs are effective for broad prediction, they may easily become overfit. RNNs possess strong computational and representational skills that allow them to approach. The most popular models in computer vision, on the other hand, CNNs are somewhat invariant with respect to translation, scaling, and rotation [13]. Non-image data, such as genetic data in vector, matrix, or tensor forms, may also be analyzed using CNNs. Clinicians and researchers in several fields of biological science have suggested using MLPs, RNNs, and CNNs to aid in diagnosis, epidemiology, and therapeutic therapy, among others [14].

To make DL-based strategies for COVID-19 more interpretable, researchers have employed a number of visualization techniques, the most direct of which is deep-network visualization, which allows one to easily investigate hidden visual patches in neural units. The attention maps may aid in locating the borders of the trained network, both of which are useful means of explaining network choices [15]. The Grad-CAM is a popular tool for debugging deep neural networks; some researchers use it to make sure their models are interpretable [16]. Medical biometric pictures can also benefit from the semantic segmentation method's interpretability and classification capabilities. Segmentation, the process of dividing the input image into regions from which data can be extracted, is an essential evaluation step in medical image processing and analysis for separating ROIs from irrelevant pixels or unwanted background area. For semantic segmentation, generative adversarial networks (GANs) stand out [17]. GAN pictures of lung nodules can enhance radiologists' diagnosis efficiency, and GANs can offer a data-augmentation strategy to fight the destruction of most accessible datasets. Researchers initially used the CNN architecture for picture semantic segmentation in 2015, when they also presented the idea of a fully convolutional network [18].

A famous model in medical image processing, U-Net adds additional layers to the standard contract network by extending fully CNNs for FCN. To get better segmentations with fewer training photos, an up-sampling operator is used instead of a pooling operator. When it comes to medical picture-segmentation, U-Net performs better than other methods. This, in turn, may make the optimizer's job easier [19] and lead to better segmentation overall, particularly for lesions that manifest at different sizes. When it comes to medical picture analysis, the U-Net-based design is revolutionary and useful. Clinicians and software developers may learn about DL-strategies throughout their maturity &deployment processes because to the variety of methodologies and DL-interpretable strategies used in biomedical imaging [20].

III. PROPOSED METHODOLOGY

Deep learning's core tenet is that, as the network depth increases, a more abstract representation of data may be obtained by stacking several shallow multilayer algorithms. Lately, DL has been all the rage, especially in computer

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vision, but it's quickly expanding into other domains, like medical diagnosis and prognosis. The ANN is the most basic DL algorithm. ANNs are a subset of ML-strategies that take cues from the structure and function of the brain's neurons and how they communicate with one another to acquire knowledge of abstract concepts. This study makes use of a DL model that optimizes the network's weights using the Adam method and uses binary cross-entropy as the loss function. There are three hidden layers in the model, and each one has 17, 10, and 5 neurons. A method called minibatch optimization was employed. The suggested DL model were all used in its development. Figure 2 depicts the suggested model.

A. Pre-processing dataset

We used a pre-processing approach to make more training data available. It's a greedy-like technique that, at iteration, chooses the feature column with the most available rows to maximize the number of samples. A smaller sample is required for each additional feature since there are many missing cells in the original dataset [22]. Since it is not possible to predetermine the subset using highly differentiated information, the learning method was performed to all eight sub-datasets, which provide a trade-off amid the amount of features and the quantity of samples. The remaining numerical characteristics were rescaled utilizing the min-max normalization approach since normalizing data typically speeds up the learning rate and leads to quicker union. It was divided into eight sub-datasets with distinct characteristics after analyzing the datasets [23].

B. Training and testing data splitting

A training sample including 90% of the datasets and a testing sample comprising 10% allowed for an accurate evaluation of the suggested model's efficacy. It was common practice to choose test samples that were just big enough to account for statistically significant population variation. For each dataset, the K-fold cross-validation(CV) technique was employed. Before dividing the dataset into K-equally sized portions (folds), the dataset was randomly mixed to remove bias [24]. The dataset was utilized as the testing set iteration of the K-fold training iteration of the proposed model, with training occurring every other fold. Summing together all of the assessment metrics across all of the folds yielded the final, objective outcome. Every layer maintained the fraction of the distribution of label classes. The sole purpose of this was to prevent the model from being trained with either positive/negative class trends. We accomplished this by employing the sci-kit-learn tool, which maintained the label feature proportion throughout all folds [25].

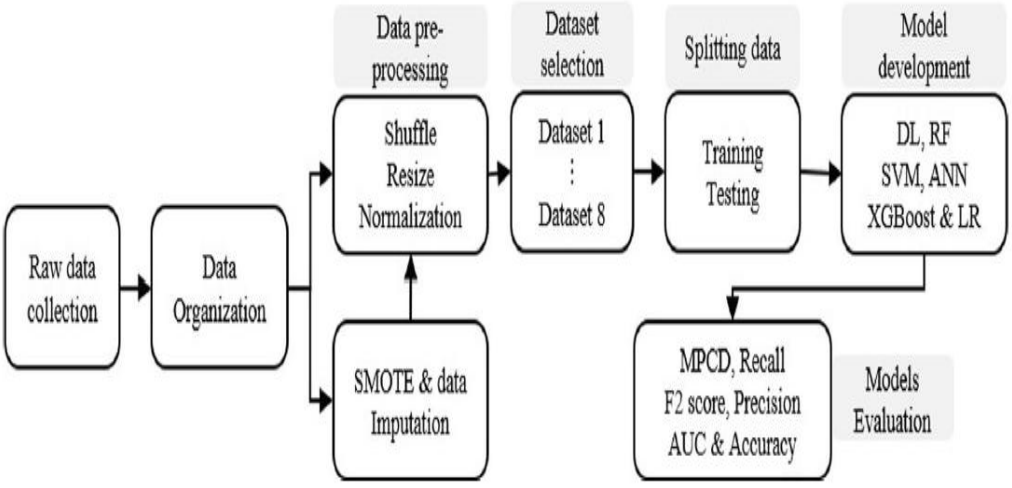

Fig.2. Workflow diagram of the proposed model

IV. RESULTS AND DISCUSSIONS

Numerous performance indicators, including the confusion-matrix with its true-positive(TP), false-positive(FP), true-negative(TN), and false-negative(FN) values, precision(P), recall(R), area-under-the-curve(AUC), F-measure, accuracy, alpha, beta, and maximum-probability-of-correct-decision(MPCD), were employed to test the suggested

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methods. For any given test, the precision (P) is the ratio of the number of correct results to the total number of results, including both true and false positives. You may express the P as

$$P = TP/(FP+TP) \quad (1)$$

The sensitivity or recall (R) is determined by dividing the total number of TPs by the addition of the TP &FN counts. It is also possible to express it as the proportion of all relevant outcomes that are appropriately labeled. It is possible to posture the R as

$$R = TP/(FN+TP) \quad (2)$$

Predicting a machine learning model's perfection is what accuracy (ACC) is all about. The precision may be determined via

$$Acc = (TN+TP)/(FP+FN+TP+TN) \quad (3)$$

When examining data structures with a large degree of imbalance, one possible metric to use is the MPCD, which is based on probability. One possible design for the MPCD is

$$MPCD = (1 - alpha)(1 - beta) \quad (4)$$

Where alpha = FP/(FP+TN) , beta = FN/(FN+TP)

The most effective outcomes of the deep learning approach are displayed in Figure 3. Substituting values for missing data is known as data imputation. Findings from the NEU%m and LIN%M biomarkers' imputation approach. With and without imputation, we compared the boxplot graph of all performance metrics. The imputation method created an error, which is expected, and we can see it in the increased variance of each assessment metric. There was no introduction of incorrect information during the imputation procedure, as the model's mean performance values were consistent throughout. There appears to be decent imputation performance here, as the variances of the imputation and actual value models are comparable.

From one dataset to another, the suggested model's performance varies. This is to be anticipated given the increased utilization of features, as additional data is required to enhance the system's behavior. More characteristics were added and more samples were eliminated, which increased the variability in the findings. On one side, we can see the distribution of classes in the original database, while on the other, we can see the distribution that was predicted by DL. That the suggested model captures the essence of the dataset's distribution is evident from this. Even with the imbalanced dataset, the suggested DL model can produce a reliable prediction. The distributions of the projected DL results, when compared to the dataset's actual outputs, are also quite similar.

While the SMOTE method's recall distribution is closer to 1, the accuracy metric shows higher fluctuation, according to the comparison data. This is evident on the MPCD expenditure, which hovers around 0.95, suggesting that adding more training data can potentially enhance the model's performance. The same holds true for the final sample; although there is more variation in the MPCD score, there are still some extremely high-scoring outliers. As a result of the close proximity of the class proportions, the SMOTE approach's threshold value approaches 0.50. The substantial imbalance in the dataset explains why we saw such a wide range of results for each assessment parameter.

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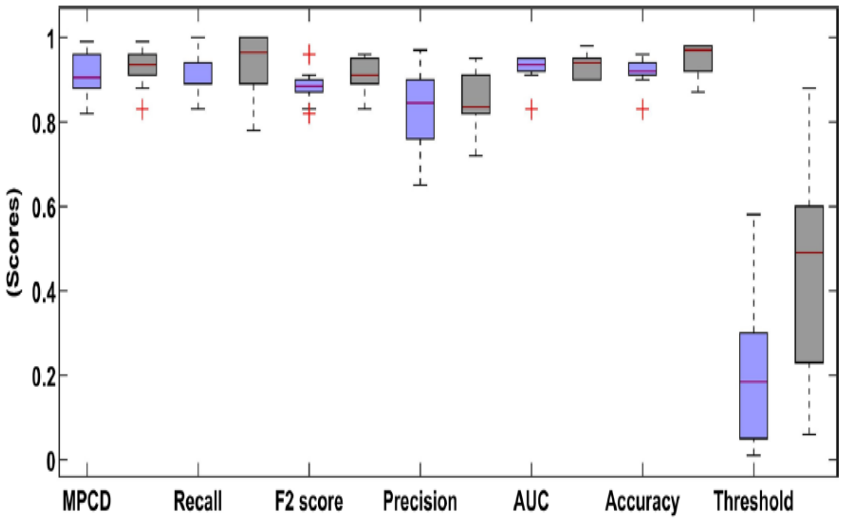

Fig. 3. Performance assessment of the proposed model

V. CONCLUSIONS

Successfully classifying high-risk individuals and improving pertinent features are essential for a mortality risk calculator. As a result, healthcare facilities can evaluate the benefits of collecting more complex biomarkers in the future while making early predictions using simple biomarker characteristics. On average, the proposed DL model's MPCD score was 0.75 when trained with few features. The proposed DL model performs admirably on all datasets. Data imputation and oversampling were methods used in the analyses. The performance of MPCD was enhanced through the application of KNN-based data imputation. Even with just two characteristics imputed, the proposed method improved both recall (0.92) and MPCD (0.75). It is more important to incorrectly anticipate a patient's reduced chance of mortality than the reverse. It follows that false negatives are better than false positives. Biomarker imputation enhances model performance, as seen by both imputation results. With an average value of 0.90, the recall measure achieved 0.95, which was better than the 0.87 achieved by the models that did not use imputations. Next, you should evaluate data imputation for complex biomarker datasets. Alternate statistical representations for biomarkers time series data should be added by standardising the sample frequency of vital signs and lab tests. Put RNNs, ARMA models, and other time series algorithms through their paces in order to predict how a patient will progress over time. Carefully evaluate the efficacy of data imputation for each biomarker-feature.

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