# Deep Learning for COVID-19 Prediction based on Blood Test

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Abstract: The COVID-19 pandemic is highly infectious and has caused many deaths. The COVID-19 infection diagnosis based on blood test is facing the problems of long waiting time for results and shortage of medical staff. Although several machine learning methods have been proposed to address this issue, the research of COVID-19 prediction based on deep learning is still in its preliminary stage. In this paper, we propose four hybrid deep learning models, namely CNN+GRU, CNN+Bi-RNN, CNN+Bi-LSTM and CNN+Bi-GRU, and apply them to the blood test data from Israelta Albert Einstein Hospital. We implement the four proposed models as well as other existing models CNN, CNN+LSTM, and compare them in terms of accuracy, precision, recall, F1-score and AUC. The experiment results show that CNN+Bi-GRU achieves the best performance in terms of all the five metrics (accuracy of 0.9415, F1-score of 0.9417, precision of 0.9417, recall of 0.9417, and AUC of 0.91).

## 1 INTRODUCTION

The Coronavirus Disease (COVID-19) is a global pandemic with high infectiousness and fatality rate. According to Johns Hopkins University (Johns Hopkins University, 2021), as of January 9, 2021, the worldwide COVID-19 death toll has passed 1.9 million, and the number of confirmed cases has exceeded 88.9 million. To make matters worse, the newly emerged COVID-19 variants are 70% more infectious than the original virus (World Health Organization, 2020). Facts have proved that "early detection, reporting, isolation and treatment" is the most effective way to prevent the rapid spread of the virus and minimize the infected number (World Health Organization, 2020). Therefore, frequent routine test plays a critical role in the battle against COVID-19.

Typically, there are two important ways of COVID-19 routine tests, i.e., the blood test and the nucleic acid test. The nucleic acid is currently widely used because of its simplicity. However, its false-negative rate can be as high as 20%. The blood test outperforms the nucleic acid test in that its false positives and false negatives are much smaller than those of the nucleic acid test (Ferrari et al, 2020). The blood test can not only effectively avoid missing true positive cases but detect seasonal coronaviruses patients with false-positive results, thereby avoiding unnecessary isolation (Peeling et al, 2020). However, pure medical approach for the blood test is confronted with two major problems. First, the blood test is time-consuming and usually takes several days to get the test result (World Health Organization, 2020). Second, the shortage of medical staff for COVID-19 blood test is very common (Wynants et al, 2020), especially in developing countries. As a result, patients usually have to wait a long time (sometimes as long as several weeks) after the blood is drawn to get the results (Amanda et al, 2020).

To address these issues, we adopt deep learning approaches for COVID-19 prediction based on the blood test. The objective is to relieve the medical staff from the heavy testing work and speed up the testing process. So far, artificial intelligence is becoming increasingly important in the area of medical diagnosis (He et al, 2019). However, the research of COVID-19 prediction based on deep learning is still in its preliminary stage. In 2020, Alakus et al. applied six deep learning models to the blood test data from Hospital Israelita Albert, among which the hybrid model of

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convolutional neural network (CNN) and Long Short-Term Memory (LSTM) achieved the best prediction accuracy of 92.3% (Alakus et al, 2020). Other proposed machine learning methods for COVID-19 prediction based on blood test include decision trees (DT), random forests (RF), support vector machines (SVM), logistic regression (LR). However, the prediction accuracies of these machine learning models are suboptimal (around 80-85%) compared with the deep learning methods (Jiang et al, 2020) (Batista et al, 2020) (Cabitza et al, 2020).

In this paper, we explore deep learning methods for COVID-19 prediction and propose a prediction system which contains four hybrid deep learning models including CNN+Gated Recurrent Unit (GRU), CNN+Bidirectional RNN (Bi-RNN), CNN+Bidirectional Long Short-Term Memory (CNN+Bi-LSTM), CNN+Bidirectional GRU (CNN+Bi-GRU). The blood test data are from Hospital Israelita Albert Einstein and have been used in the work of Alakus et al (Alakus et al, 2020). We evaluate the performance of the proposed system in terms of accuracy, precision, F1-Score, recall and AUC. And the experiment results show that the proposed hybrid model CNN+Bi-GRU outperforms the best model (CNN+LSTM) proposed by Alakus et al (Alakus et al, 2020) in terms of the five evaluation metrics. In summary, the main contributions of this paper are as follows:

- We design and implement four hybrid deep learning models including CNN+GRU, CNN+Bi-RNN, CNN+Bi-LSTM and CNN+Bi-GRU for COVID-19 prediction. And we use 18 attributes of blood test data from Hospital Israelita Albert Einstein for model training.
- We also implement two models proposed by Alakus et al (Alakus et al, 2020), i.e., CNN and CNN+LSTM, and conduct extensive comparisons among these six models in terms of accuracy, precision, F1-Score, recall and AUC. The blood test data used in this work are from Hospital Israelita Albert Einstein provided by Alakus et al (Alakus et al, 2020).
- The experiment results show that the values of accuracy, precision, F1-Score, recall and AUC of the proposed hybrid model CNN+Bi-GRU are 0.9415, 0.9417, 0.9417, 0.9417 and 0.91, respectively, which are better than those of the best model (CNN+LSTM) proposed by Alakus et al (Alakus et al, 2020).

The rest of this paper is organized as follows. Related work of our research will be given in Section 2. Section 3 describes the blood test data and the proposed deep learning models. We provide a thorough experiment study and performance comparison in Section 4. In Section 5, we give a conclusion of the paper.

## 2 RELATED WORK

Nowadays, AI plays an important role in assisting medical diagnosis. For example, CNN could be used for the early detection of cancer (Dlamini et al, 2020). Recurrent neural network (RNN) used for the diagnosis of Alzheimer's disease (Cui et al, 2020). For COVID-19 prediction, existing AI approaches can be classified into two categories, namely general machine learning methods and deep learning methods. Both machine learning and deep learning can be used to solve classification problems.

### 2.1 Machine Learning

In 2020, Jiang et al. proposed five machine learning models including LR, DT, RF, K-Nearest-Neighbor (KNN) and SVM for COVID-19 prediction. They applied the models to the data from Wenzhou Central Hospital and Cangnan People's Hospital. The data contain 53 blood samples from 53 hospitalized patients, each of which has 10 blood indicators (model features) (Jiang et al, 2020). The core idea of LR is to use existing data to establish a regression equation for the classification. DT is a model used to observe and realize the internal laws of data and to classify and predict results for new data. RF inherits the idea of DT. Differently, it uses the method of ensemble learning in which RF votes for the classification results of several weak classifiers to form strong classifiers. The idea of KNN is to calculate and compare the distances between the target point and the points of different categories in a given interval. And the category of the target point will be determined by its k nearest neighbors. SVM is a popular classification approach. In 0-1 classification, SVM calculates the maximum margin between two types of labeled data, based on which establishes a hyperplane for classification. The experiment results show that the best accuracy was 80% when using SVM. Besides the work of Jiang et al., Batista et al. applied SVM, RF, LR and gradient boosted trees for COVID-19 prediction based on the data from Hospital Israelita Albert Einstein at Sao Paulo Brazil (Batista et al, 2020). The number of patient samples is 235, and the number of blood indicators (model features) for each sample is 13. Specifically, gradient boosted trees use DT as the basis function, and the model is built in the direction of the gradient drop of the loss function for each time. The best accuracy of their proposed models was 84.7% when using RF. Another research team from Italy used the data from San Raffaele Hospital with 1,925 patients from February 2020 to May 2020. They selected 20 blood indicators as the model features in their study (Cabitza et al, 2020). Their proposed models were LR, Naïve Bayes, KNN, RF, and SVM, and the best accuracy rate achieved 88% when using RF model.

### 2.2 Deep Learning

To the best of our knowledge, the research for deep learning-based COVID-19 prediction is still in its preliminary stage. One typical work is the prediction system proposed by Alakus et al (Alakus et al, 2020). This system contains six deep learning models including artificial neural networks (ANN), CNN, RNN, LSTM, CNN+RNN and CNN+LSTM. ANN refers to the input layer, the hidden layer and the output layer are in the form of full connection. CNN is widely used in various scenarios such as image processing, text processing and speech recognition. It contains the convolutional layer, the pooling layer and the fully connected layer. The convolutional layer is used for extracting features, and the pooling layer can speed up calculation and prevent overfitting. In addition, shared weights and biases refer to the sharing of weight parameters in the process of convolution and pooling, which makes the model easier to optimize. In summary, the main idea of CNN is to learn the spatial hierarchies of features through backpropagation by using multiple building blocks. RNN is suitable for processing time series data, this model adds a hidden state for recording historical information, and the activation function uses Tanh to prevent the value from changing too severely. LSTM includes forget gate, input gate, output gate and the memory cell. The forget gate refers to the information that needs to be forgotten, the input gate refers to the information that needs to flow into the memory cell, and the output gate refers to the information that needs to flow into the hidden state. Memory cells are used to remember historical information. And the reason why the combination of CNN and other deep learning models can usually achieve better accuracy is that CNN has performed feature extraction on the data in advance. Alakus et al. used the blood test dataset including 600 patients from Hospital Israelita Albert Einstein at Sao Paulo Brazil, and selected 18 features for model training and testing. The best accuracy achieved 92.3% when using CNN+LSTM, which is higher than existing machine learning models.

## 3 COVID-19 PREDICTION USING DEEP LEARNING MODELS

Based on the work of Alakus et al., we propose and implement four hybrid models for COVID-19 prediction using blood test data. In this section, we introduce the four proposed models, which share the same general structure. This structure contains three convolution layers, two MaxPool layers, one recurrent neural layer and one fully connected layer. The major difference between the four models is that they have adopted four different variation of the recurrent neural layer, respectively, i.e., GRU, Bi-RNN, Bi-LSTM, Bi-GRU. We set the same parameters for the four models for the sake of fairness.

### 3.1 CNN+GRU

The first proposed hybrid model is CNN+GRU. GRU is a variation of RNN. The hybrid model of CNN and RNN was proposed in the work of Alakus et al. CNN and RNN are complementary to each other in modeling capabilities (Sainath et al, 2020). Specifically, CNN can extract features of different levels, while RNN can provide short-term memory. Therefore, combining them can improve the efficiency of diagnosis for COVID-19. However, one major problem of RNN is gradient disappearance or explosion caused by its iteration (Chung et al, 2014). To address this issue, we propose GRU to replace RNN in the hybrid model. The GRU network uses the cell to store information, and the gated mechanism controls whether the information needs to be retained in the cell. The internal structure of GRU is shown in Figure 1. GRU network has two gate control units, namely reset gate $r$ and update gate $z$. The reset gate controls whether the information of historical state needs to be forgotten. When the value of reset gate close to 0, the information of historical state is forgotten, and the candidate state is only related to the current input. This mechanism can discard some useless information to reduce computational complexity. The update gate controls whether the information of historical state needs to be sent to the current state. When the value of update gate value close to 0, the current state is only related to the current input; when its value close to 1, the current state is equal to the previous state.

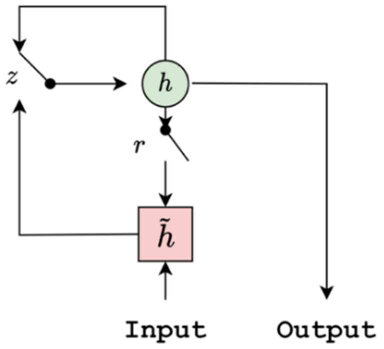

Figure 1: The Internal Structure of GRU.

## 3.2 CNN+Bi-RNN

The second proposed hybrid model is CNN+Bi-RNN. The basic idea is to adopt the Bi-RNN to extract the correlation between each different attributes of data. Bi-RNN can increase contents in the memory of future information (Schuster et al, 1997). This structure allows the model to better understand the correlation between current data and other data. The internal structure of Bi-RNN is shown in Figure 2. It shows that each training sequence has a forward network and a backward network, both of which are RNN. The two networks are connected with the output layer. This structure provides the output layer with complete data information about the past and future data.

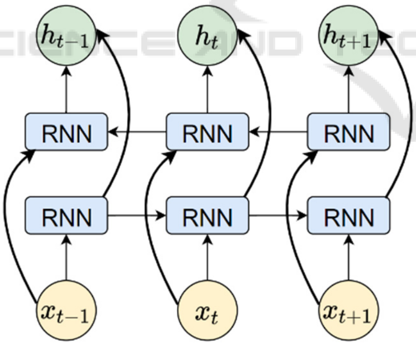

Figure 2: The Internal Structure of Bi-RNN.

## 3.3 CNN+Bi-LSTM

The third proposed hybrid model is CNN+Bi-LSTM. The basic observation is that, in order to simulate the memory characteristics of biological networks, neurons can use the current output information as the input of the next neuron to form a ring network structure, which is a neural network with short-term memory. LSTM is a good candidate to store short-term memory, and this memory can be retained for a long time.

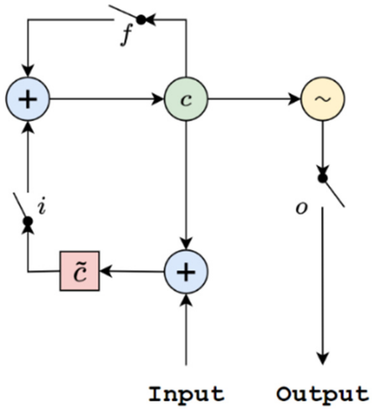

Figure 3: The Internal Structure of LSTM.

Specifically, LSTM uses the memory cell to store the information, and the gating mechanism helps the model determine how much information passes in the cell between a large time step (Sak et al, 2014). LSTM includes the forget gate, input gate, output gate and the memory cell, which are marked $f$, $i$, $o$, and $C$ in the Figure 3. Forget gate controls whether information from the long-time memory unit needs to be forgotten at the last moment; input gate controls whether input information is required to enter a long-time memory unit; output gate controls whether information from the long-time memory unit can be outputted; Cell is a storage unit for short-term memory. The Bi-LSTM model is to add a forward network and a backward network to a hidden layer of the traditional LSTM so that the correlation between the data can be extracted.

## 3.4 CNN+Bi-GRU

The fourth proposed hybrid model is CNN+Bi-GRU, which combines CNN and Bi-GRU networks. The CNN+Bi-GRU uses CNN to extract features at different layers from the data, and the Bi-GRU is used to construct the correlation between each attributes of blood test data. Figure 4 is the structure diagram of the CNN+Bi-GRU network. Specifically, the input to the network are the blood test data of each patient. First, CNN network extracts the characteristics of the blood attributes. Then, Bi-GRU extracts the correlation between the attributes. Finally, SoftMax function is adopted to predict whether COVID-19 is positive or not. As shown in Table 1, the network has eight layers: 1) three convolutional layers. The kernel size of the convolutional layer is 256, 128 and 64 respectively, after the first two convolutional layers, a dropout layer with 15% rate is used to prevent overfitting; 2) two pooling layers. The kernel size of the pooling layer is 3; 3) one Bi-GRU layer. The hidden state dimension is set to 256, and Batch Normalization is added to reduce the internal covariate offset. The objective is to speed up the deep network training; 4) one fully connected layer. A dropout layer with rate of 15% is used for reducing the risk of overfitting, and 5) one output layer with SoftMax function. The output value indicates whether the COVID-19 infection is negative or positive.

Table 1: The Summary of CNN+Bi-GRU.

| Layer | Type | Kernel | Stride |
|---|---|---|---|
| 1 | Convolution1D | 256 | 3 |
| 2 | MaxPool | 3 | 3 |
| 3 | Convolution1D | 128 | 3 |
| 4 | MaxPool | 3 | 3 |
| 5 | Convolution1D | 64 | 3 |
| 6 | Bi-GRU | 256 | - |
| 7 | Fully Connected | 256 | - |
| 8 | SoftMax | 2 | - |

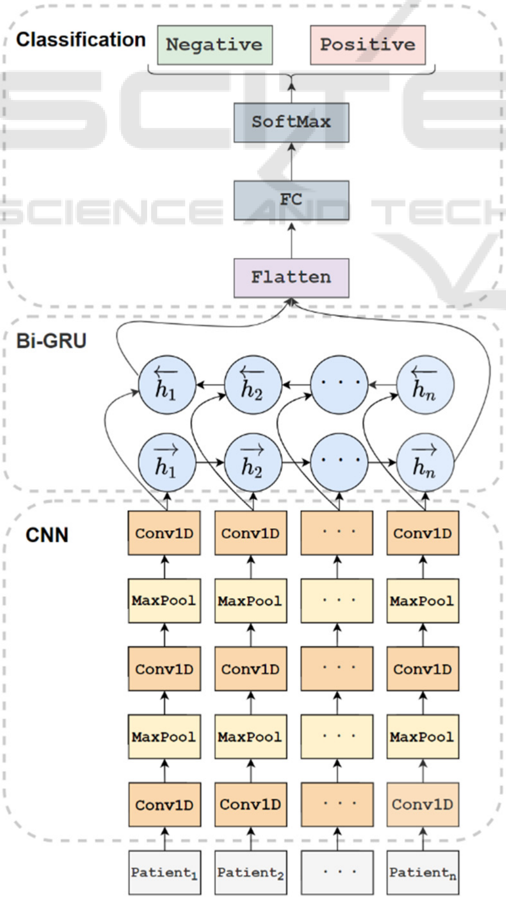

Figure 4: The Structure of CNN+Bi-GRU.

## 4 EXPERIMENT EVALUATION

In this section, we conduct experiments based on real data, which are produced by Hospital Israelita Albert Einstein in Sao Paulo Brazil. We first describe the dataset, the experiment environment and the evaluation metrics. Then we use five metrics to evaluate the performance of the six deep learning models. Finally, we compare the results with previous studies.

### 4.1 Data

We use the real data from Hospital Israelita Albert Einstein in Sao Paulo Brazil. The original data are provided by the research team from Schwab (Schwab et al, 2020), and include 111 laboratory results of 5644 different patients. These data were collected in 2020 from patients' blood samples for COVID-19 infection testing. The prevalence rate of the selected data was 13.3%. To protect the patients' privacy, all the personal information is abandoned. Each row of data represents the blood test information of an individual. According to previous research (Alakus et al, 2020), we select 18 attributes as the features of the proposed deep learning models. The attributes of the blood test are listed in Table 2:

Table 2: Attributes of Selected Attributes.

| | | |
|---|---|---|
| Hematocrit | Hemoglobin | Monocytes |
| Serum Glucose | Neutrophils | Platelets |
| Red blood Cells | Lymphocytes | Leukocytes |
| Basophils | Eosinophils | Urea |
| Sodium | Creatinine | Potassium |
| Proteina C reativa mg/dL | Alanine transaminase | Aspartate transaminase |

### 4.2 Experiment Environment

We design the deep learning models using Python and Keras package. The experiments are conducted using a desktop with an 8GB memory Intel Core i7-2.9GHz processor and a 4GB NVIDIA GeForce 940MX graphical processor. We set 80% of the data as the training set and 20% as the test set. The learning rate is 0.001, the batch size is 30 and the epoch is 200.

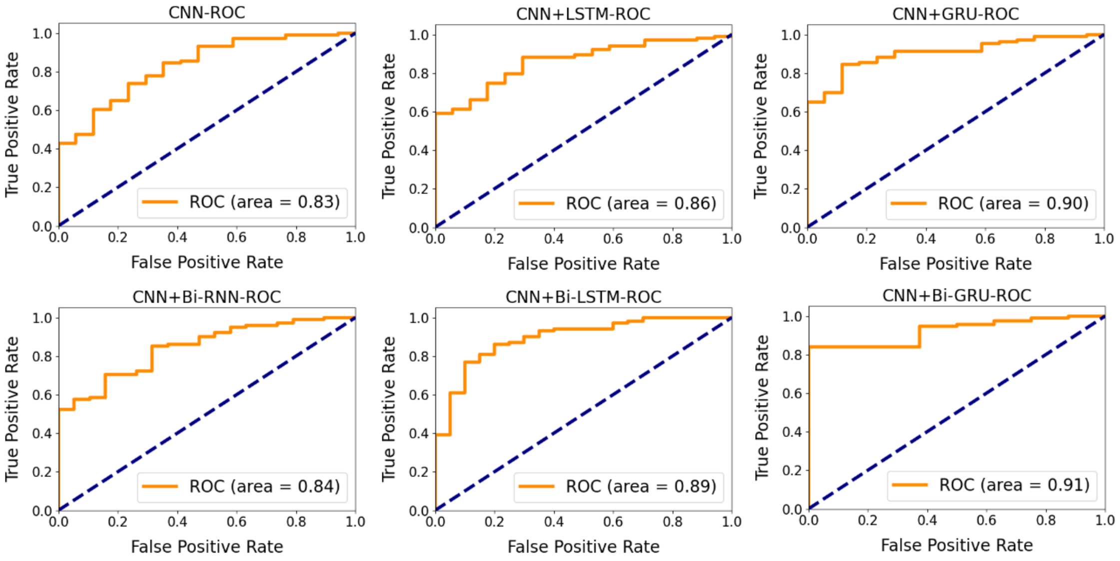

Figure 5: Deep Learning Models ROC Curves.

Table 3: Performance of Different Deep Learning Models.

| Model | Accuracy | F1-Score | Precision | Recall | AUC |
|---|---|---|---|---|---|
| CNN | 0.8843 | 0.8843 | 0.8843 | 0.8843 | 0.83 |
| CNN+LSTM | 0.8545 | 0.8545 | 0.8545 | 0.8545 | 0.86 |
| CNN+GRU | 0.9210 | 0.9209 | 0.9210 | 0.9210 | 0.90 |
| CNN+Bi-RNN | 0.8786 | 0.8786 | 0.8786 | 0.8786 | 0.84 |
| CNN+Bi-LSTM | 0.8885 | 0.8885 | 0.8885 | 0.8885 | 0.89 |
| **CNN+Bi-GRU** | **0.9415** | **0.9417** | **0.9417** | **0.9417** | **0.91** |

## 4.3 Evaluation Metrics

In this work, for the sake of fairness, we adopt the same five metrics as Alakus et al (Alakus et al, 2020) for performance evaluation, i.e., accuracy, F1-score, precision, recall and area under the receiver operating characteristic (AUC).

To calculate the metrics, the classification results of the models are summarized in the form of a confusion matrix. The matrix contains four different kinds of values: 1) True Positive (TP) which means positive classes are predicted to be positive; 2) True Negative (TN) which means negative classes are predicted to be negative; 3) False Positive (FP) which means negative classes are predicted to be positive, and 4) False Negative (FN) which means positive classes are predicted to be negative. These four values can be used to calculate accuracy, precision and recall. F1-score is calculated based on precision and recall (Hossin et al, 2015).

Specifically, accuracy refers to the proportion of the samples (TP+TN) which have been correctly classified among the total number of samples (TP+TN+FP+FN). It is the most common evaluation metric for the classification tasks. Precision is the ratio of the TP that belong to the predicted positives (TP+FP). It indicates whether the model has a good ability to discriminate between positive and negative samples. Recall refers to the TP among the sum of the TP and FN. It indicates the ability of the model to classify the relevant results correctly. F1-score refers to the harmonic average of the precision and recall. It is a comprehensive metric to judge the ability of the classification model. AUC is a method to evaluate the performance of classifier. If the AUC value exceeds 0.8, the classifier can be regarded as excellent classifier. If the AUC value is above 0.9, the classifier can be regarded as outstanding (Mandrekar et al, 2010). The calculation formulas of accuracy, precision, recall and F1-score are shown below.

$$Accuracy = \frac{TP+TN}{TN+FP+FN+TP} \tag{1}$$

$$Precision = \frac{TP}{TP+FP} \tag{2}$$

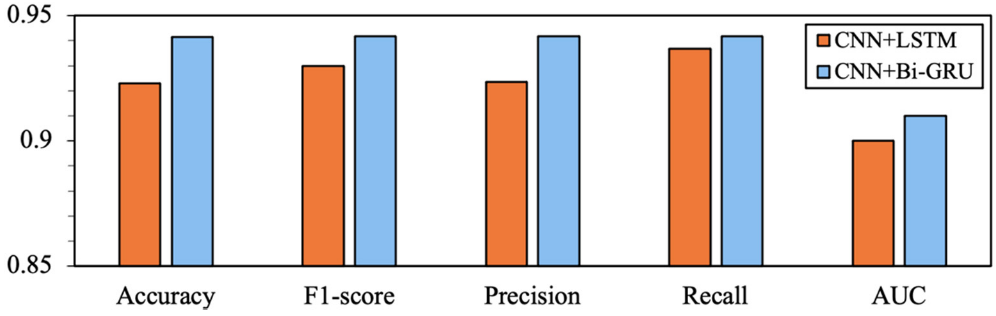

Figure 6: Comparison with CNN+Bi-GRU and CNN+LSTM.

Table 4: Comparison with Previous Studies.

| Dataset Location | Model | Accuracy | AUC | F1-Score |
|---|---|---|---|---|
| Hospital Israelita Albert Einstein | SVM, RF | - | 0.87 | 0.7200 |
| Hospital Israelita Albert Einstein | CNN+LSTM | 0.9230 | 0.90 | 0.9300 |
| Hospital Israelita Albert Einstein | CNN+Bi-GRU | 0.9415 | 0.91 | 0.9417 |

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (4)$$

## 4.4 Result Analysis

To make comprehensive comparisons, we implement the four proposed model as well as the two models (CNN and CNN+LSTM) proposed in the work of Alakus et al. (Alakus et al, 2020). Besides, we use five metrics to evaluate the six deep learning models, respectively.

The Receiver operating characteristic (ROC) curves of the six models are shown in Figure 5. Typically, the x-value of the ROC curve is the false positive rate (FPR), and the y-value of the ROC curve is the true positive rate (TPR). For the ROC curve, the area enclosed by the curve and the coordinate axis represents the classification performance of the model. The closer the area is equal to 1, the stronger the classification ability of the model is, and vice versa. In addition, we use the AUC value to describe the area under the ROC curve and the coordinate axis. AUC means that, if the sample is randomly selected, the probability of the model can classify it into correct category. Figure 5 shows that CNN+Bi-GRU model gets the best results among all the six models, whose AUC value achieves 0.91. It means that the model can effectively classify positive cases.

Table 3 presents the performances of different models in terms of different metrics. Specifically, it shows that the AUC values of all hybrid models are higher than the model CNN in the diagnosis of COVID-19. And the three proposed hybrid models CNN+GRU, CNN+Bi-LSTM, CNN+Bi-GRU outperform the model CNN in terms of the five metrics. For CNN+LSTM and CNN+GRU model, the experiment results show that the CNN+GRU model significantly improved the accuracy, F1-score, precision, recall and AUC over CNN+LSTM. The basic idea of GRU and LSTM is to reduce the problem of gradient disappearance while retaining long-term sequence information. But GRU has a simpler network structure than LSTM, which can accelerate the training and convergence of the network. So, the CNN+GRU model has achieved better results in our experiments. Comparing the experimental results of CNN+GRU and CNN+Bi-GRU models, we find that the values of the five metrics of Bi-GRU are all better than those of GRU. This is because the training data contain 18 attributes from blood test. The correlation between the data attributes is therefore a very important feature. The bidirectional structure of Bi-GRU can better model the correlations between each blood attribute. Therefore, CNN+Bi-GRU has better evaluation performances than CNN+GRU.

Figure 6 shows the detailed comparisons between CNN+Bi-GRU and CNN+LSTM. For the sake of fairness, we adopt the experiment results of CNN+LSTM from the paper of Alakus et al (Alakus et al, 2020), which are much higher than those of our CNN+LSTM experiment results. The comparison results show that our proposed model CNN+Bi-GRU outperforms CNN+LSTM in terms of all the five metrics.

Table 4 shows the comparison between CNN+Bi-GRU and the work of Batista et al and Alakus et al.

Batista et al used SVM and RF, and the best results are 0.87 of AUC and 0.72 of F1-score. According to Alakus et al, the best accuracy, AUC and F1-score of CNN+LSTM are 0.9230, 0.90 and 0.93, respectively. Our proposed CNN+Bi-GRU model provides the best performance whose accuracy, AUC and F1-score are 0.9415, 0.91 and 0.9417, both higher than SVM, RF and CNN+LSTM. Overall, the performance of CNN+Bi-GRU is better than the other existing models.

## 5 CONCLUSIONS

In this paper, four hybrid deep learning models are proposed to predict COVID-19 infection based on blood test, i.e., CNN+GRU, CNN+Bi-RNN, CNN+Bi-LSTM and CNN+BiGRU. Besides, 18 indicators from the blood test data are selected as features, and five metrics are adopted to evaluate the model performance, namely accuracy, F1-score, precision, recall and AUC. Experiment results show that CNN+Bi-GRU model outperforms the proposes models of Alakus et al in terms of all the evaluation metrics. We believe that CNN+Bi-GRU model will be an effective supplementary method for COVID-19 diagnosis based on blood test. In the future, we will continue explore deep learning models for COVID-19 prediction and design novel prediction models.

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