A Classification Framework to Detect Sars Covid-19 Disease Using Feature Selection and Variant-Based Ensemble Learning

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Abstract: The hazardous COVID-19 pandemic has caused millions of deaths worldwide which depicts the significance of an early screening of this infection in order to stop it from spreading. Real-time polymerase chain response (RT-PCR) test has been in use for detection of COVID-19 infection but it is time consuming and might generate results rather late as the test samples are required to be examined and tested at a suitably equipped lab. In contrast to this methodology, many deep learning strategies have been put forward to successfully identify this sickness by inspecting CT scan images and chest X-Ray images but doses of radiation, high cost and lack of specialized equipment do not allow these methods to be generally used for the prediction of COVID-19. In this research a classification framework is proposed which is inexpensive, readily available, and considerably fast and does not require specialized equipment or laboratories as it is based on complete blood count results. This proposed model uses machine learning techniques and routine blood results to predict COVID-19. It comprises of three stages 1) data preprocessing 2) hybrid feature selection (FS) 3) Ensemble learning classification.

Keywords: *Machine learning, COVID-19 Prediction, Hybrid feature selection, Ensemble learning, Classifier variants, CBC Test.*

1 Introduction

In December of 2019, the Chinese officials alerted people everywhere that a new viral infection was rapidly spreading among their people. Shortly it spread to various parts of the world with the number of infections multiplying in practically no time. This deadly sickness is known as COVID-19 which is caused by a virus named SARS-CoV-2. So far 524,339,768 confirmed cases have been reported globally with a total of 6,281,260 deaths, declaring COVID-19 as a first pandemic caused by a coronavirus [1]. Consequently, research has also been conducted worldwide for its fast and exact initial identification and appropriate treatment in order to stop the transmission of this disease. For the diagnosis of COVID-19 Reverse Transcription Polymerase Chain Reaction (RT-PCR) is considered as a gold standard [25, 26] but it has some drawbacks. It is very time taking, expensive, requires special laboratory tools and has approximately 20% false-negative rate [2]. In addition, RT-PCR test kits are scarce and not readily available internationally and low-income countries cannot afford to have these. Tests depending upon IgM/IgG antibodies have been utilized in diagnosing COVID-19 during its beginning stage but these tests have some downsides as they result in low values of sensitivity (18.8 %) and specificity (77.8%) [3]. consequently, other testing strategies are essential which are more affordable and more convenient. During the past couple of years, the area of artificial intelligence and machine learning has been getting popular across various areas and fields of study. A significant interest has been observed in investigating the capability of machine learning techniques to battle the COVID-19 pandemic by detecting, preventing, treating, managing, forecasting etc.

In this study, we shed light on the utilization of machine learning algorithms to help clinical experts in the exact and dependable early identification of COVID-19. In this unique situation, machine learning based clinical imaging CT scans and chest X-rays images [4], [31-34], [79-105] have exhibited positive outcomes accompanying the traditional diagnostic strategies of COVID-19 like RT-PCR and IgM/IgG tests. Despite all that CT scans cannot be of much help in COVID-19 prediction due to the doses of radiation, insufficient number of equipment and high expenses. Lately many clinical examinations have uncovered that blood samples of individuals infected with COVID-19 display significant change. Tracking down these blood parameters can assume a vital part in early diagnosis of COVID-19. Machine learning techniques can identify and separate different observed patterns in the standard routine blood exams. The machine learning model based on blood test samples for SARS-CoV-2 initial diagnosis provides a quick, convenient to utilize and more affordable option as compared to expensive and time taking tests like image-based tests and RT-PCR since it is based on CBC which is inexpensive, has a fast turn-around time and is readily available everywhere. This research presents a classification framework to detect COVID-19 from complete blood count results using feature selection and variant based ensemble learning. A framework like this will have a significant effect in under developed countries that do not have sufficient and adequate test kits and appropriately-equipped laboratory for PCR related tests. Other important benefits of a fast and simple framework incorporate quick test results for contaminated patients and slowing down of the infection rates.

2 Review of Literature

Machine learning algorithms have garnered considerable attention from researchers due to their ability to uncover hidden patterns and extract valuable information from raw data. They have been applied to various research fields, playing a crucial role in sentiment analysis [35-41], rainfall prediction [42-43], network intrusion detection [44-45], software defect prediction [46-55], health and medical data mining [56-63], Fraud detection [64-72], and stock market prediction [73-78]. Furthermore, machine learning techniques have been extensively explored for the detection of COVID-19 patients by analyzing patterns in complete blood count (CBC) test results. The following sections provide in-depth discussions on relevant studies in this area. Researchers in [10] developed a machine learning framework using XGBoost. This dataset consisted of 5333 blood specimens along with different bacterial and viral infections. After training, testing and cross validation the results depicted 97% AUC, 81.9% sensitivity and 97.9% specificity.

Researchers in [5] presented a machine learning framework known as ER-CoV which was based on routine blood tests [106]. The model used a fusion of three algorithms named as Support Vector Machine (SVM) [16], SMOTE Boost [17] and Ensemble [18] for prediction of COVID-19. This framework accomplished 86.78% AUC, 85.98% specificity and 70.25% sensitivity. Four models were developed by researchers in [6] based on routine blood exams for initial diagnosis of SARS-CoV-2 positive individuals. Lasso-Elastic-Net Regularized Generalized Linear Network (GLMNET), Random Forest (RF) [19], LR [21] and Artificial Neural Network (ANN) [20] are the four classification algorithms employed by these models. The frameworks resulted 87% Accuracy, 65% sensitivity, 91% specificity and an AUC of 86%.

Researchers in [7] explored various machine learning classification techniques for the prediction of COVID-19 from blood exams. Following algorithms were employed; LR, DT, SVM, K Nearest Neighbors (KNN) [23], Extremely Randomized Trees (ET) [22], RF and Naive Bayes (NB) [24]. The accuracy achieved by these models was 86% and a sensitivity of 95%. Research was reported by [8] to detect COVID-19 utilizing machine learning algorithms from emergency care blood tests. LR, ANN, RF, SVM and Gradient Boosting Trees were used for prediction. SVM showed the best results with 85% AUC, 85% specificity and 68% sensitivity. Researchers in [9] employed SVM and RF for initial screening of SARS-CoV-2 on the basis of blood samples. Three different predictions were made i.e., moderate vs viral, severe vs. viral and severe vs. moderate. A total of 15 key attributes were chosen. SVM performed better than the other classifiers. It showed 84% Accuracy, 88% sensitivity, 80% specificity and 92% precision.

3 Materials and Methods

The outbreak of COVID-19 has taken millions of human lives all around the world. An initial screening is required to stop this infection from spreading. To resolve this issue, a machine learning based classification framework is proposed in this research, which is considerably faster, cheaper and easily available as it is based on CBC results. CBC has many benefits [27] 1) it is the most common laboratory test that is requested very often in all clinical settings 2) medical experts order routine blood exams for the management of patients regularly 3) CBC is quite easy to perform 4) it is inexpensive [29, 30] 5) it is readily available in all healthcare centers. CBC has a fast turn-around time (TAT) which is 25 minutes for stat CBC results [28]. The proposed framework uses hybrid feature selection technique and ensemble classification to predict COVID-19 using CBC.

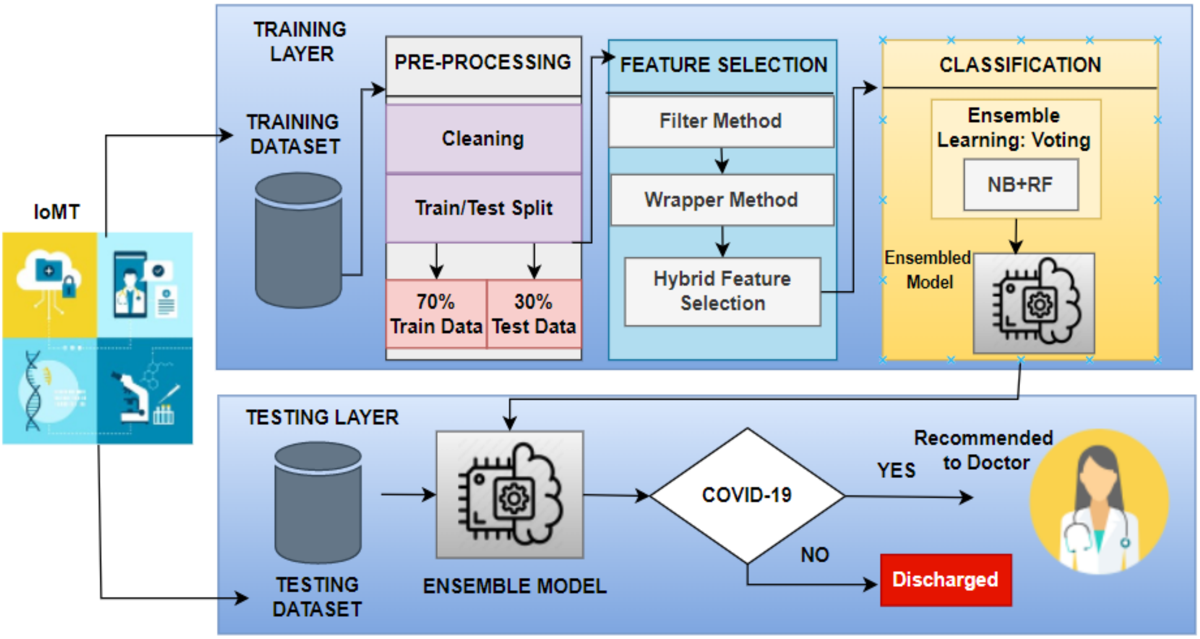

Fig.1. Detailed Framework Design

1.1 Framework Design

This research proposes a classification framework for the detection of COVID-19 disease using CBC test results. Fig. 1 presents a detailed design of the proposed model. The proposed framework includes two layers: training and testing. Both of the layers further include multiple stages. The working of the proposed framework initiates with the selection of relevant dataset from IOMT. After the selection of appropriate dataset, data is pre-processed then feature selection is employed. After FS next step is classification. The detailed working of the proposed framework is discussed below:

1.1.1 Dataset

The performance of the proposed framework is evaluated on COVID-19 dataset which is based on complete blood count. The dataset was taken from a public form, Kaggle [12], for the initial screening of COVID-19. The samples for this dataset were gathered from Israelita Albert Einstein Hospital, at São Paulo, Brazil which had also COVID-19 RT-PCR test performed on them along with other laboratory tests. All the data in this dataset has been anonymized. The original dataset when released contained records of 5,644 patients who were tested between March 28, 2020 and April 3, 2020. In this study only 598 records of complete blood count results were utilized. The rest of the 5046 patient records were not utilized as they did not contain full information of blood count results. The attributes selected for this research are the ones based on full blood count which include: "Red blood cells (RBC), hematocrit, mean corpuscular hemoglobin concentration (MCHC), mean corpuscular hemoglobin (MCH), basophils, lymphocytes, hemoglobin, platelets, mean platelet volume (MPV), monocytes, red blood cell distribution width (RBCDW), mean corpuscular volume (MCV), leukocytes and eosinophils". Neutrophils were excluded as they were not accounted for all 598 individuals. Along with these attributes it contains a target class which diagnoses COVID-19 positive cases. This output/target class is predicted by the framework on the basis of information given for the other attributes. The feature to be predicted is known as dependent feature and the rest of the features that are utilized in predicting the dependent feature are known as independent features.

1.1.2 Data Pre-Processing

The initial step of training layer in proposed model after dataset selection is data pre-processing. Firstly, cases of missing values were handled. Records with such cases were removed from our dataset. Secondly outlier analysis was performed to check for any abnormalities in the dataset and lastly the dataset was divided into 70% training and 30% testing data.

1.1.3 Proposed Feature Selection Technique

For the Feature Selection step, a Hybrid FS technique was employed. Fig. 2 describes the proposed hybrid FS technique in detail. For filter method we used "Correlation Attribute Eval" using 'Ranker' as a search method. In 'Correlation Attribute Eval' the value of a feature is evaluated by the measurement of Pearson's correlation between it and the class and Ranker method ranks the features according to their evaluation. Using this Filter Method, we selected top 10 attributes. We then proceeded with these 10 attributes and applied wrapper method. "Classifier subset evaluator" was used with Naïve Bayes with two search methods GA and PSO. In "Classifier subset evaluator" feature subsets are evaluated on training data or distinct testing set. A genetic algorithm (GA) is an adaptive heuristic search algorithm designed for solving search and optimization issues while PSO utilizes numerous particles which make up a swarm traveling around in the search space, searching for the optimal solution. 6 attributes were selected by GA and 5 by PSO. The Union of these two gave 7 attributes. These 7 attributes were taken further for classification.

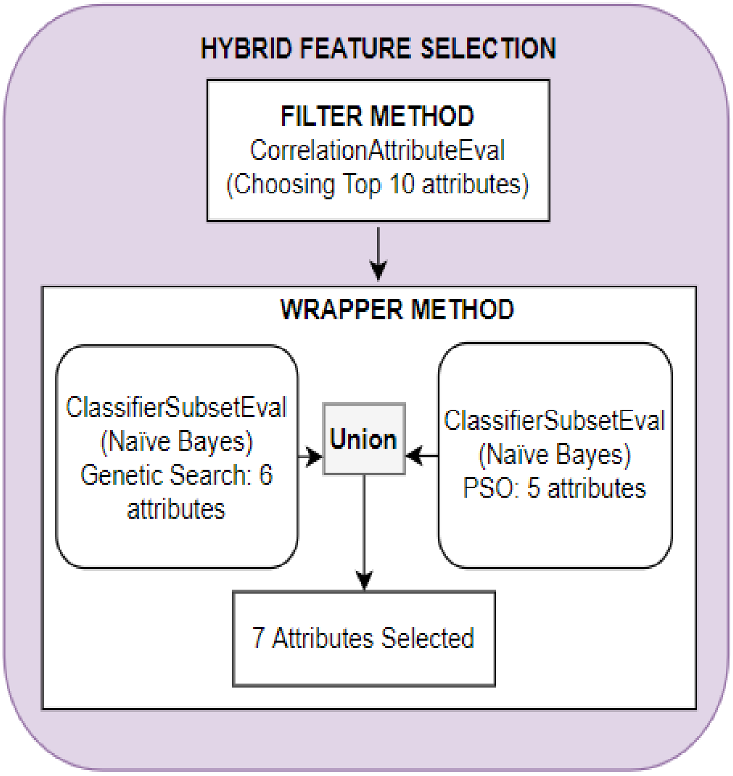

Fig.2. Hybrid Feature Selection

1.1.4 Classification

In this stage, first variants of different classifiers are produced by tuning their parameters. To create the variants, six algorithms are tuned. The classifiers chosen for variant selection are Multi-layer Perceptron, Naive Bayes, Random Forest, Decision Tree, K-Nearest Neighbor and Support Vector Machine. These algorithms are firstly applied with their default parameters and then multiple variants from every algorithm are produced by optimizing their parameters. Then all of these variants are employed for the prediction of COVID-19. The variants which give higher performance values are selected. One variant is selected from each classifier's family. For example, if NB has three different variants, then only that variant will be chosen which performs better than the rest of variants in that classifier family. Several Variants are produced of each base algorithm. The first variant of each algorithm is the one with its default parameters. The comparison of accuracy is performed with the base classifier, the first variant, and the rest of the variants produced from that family. If the variants of one classifier fail to giver higher accuracy than the base classifier then in that case the base classifier will be chosen for the comparison of accuracy with variants of other classifiers. After selecting the best performing variants, we use ensemble learning to integrate them. 'Voting' is used as the ensemble learning classifier. The detailed steps are given below:

1. Support Vector Machine is optimized to create three variants. The parameter considered for optimizing is the value of complexity. It controls the misclassification and defines the hyper-plan
2. In Multi-layer Perceptron there is a parameter which reflects number of hidden layers and number of neurons present in each hidden layer. This parameter is optimized to create variants of MLP. The

number of neurons is selected by a formula: $(attributes + Classes)/2$. We only used 1 hidden layer for all variants of this classifier with various numbers of neurons.

3. For Naïve Bayes two variants are produced. They are created by tuning two of its parameters. The first variant contains the default parameters and both “Kernel Estimator” and “Supervised Discretization” are not selected as true and for the other two variants these parameters are chosen one by one.
4. By optimizing the number of neighbors, three variants of K-Nearest Neighbor are generated.
5. For the classifier Random Forest, a parameter known as the ‘max depth’ is tuned to create two variants. The default value of this parameter is zero.
6. In Decision Tree algorithm there is a parameter called as confidence factor. This parameter controls pruning and by optimizing it four variants are generated.

1.2 Tools

For the experiments conducted in this research a tool created at the University of Waikato, New Zealand was utilized which is known as ‘Weka’. It is developed in Java and is an open-source tool for data mining tasks. Along with Weka, python programming language is also utilized for the implementation of this research for the fine tuning of algorithms.

1.3 Performance Evaluation

The performance measures which are utilized to evaluate the proposed framework in this research are “Precision, Recall, F-measure and Accuracy". Mostly the performance evaluation criteria can be easily deduced from 2x2 confusion matrix for binary class problems. It is used to measure performance of a machine learning classification problem where output class can be two or more. It is a specific table layout with four distinct combinations of actual and predicted values.

The parameters of a confusion matrix are as followed: -

True positive (TP): Dataset records which reflect the COVID-19 positive results and are also actually positive.

False positive (FP): Dataset records which reflect the COVID-19 positive results and are actually negative.

False negative (FN): Dataset records which reflect the COVID-19 negative results and are actually positive.

True Negative (TN): Dataset records which reflect the COVID-19 negative results and are also actually negative.

The performance of the classification is measured with “Precision, Recall, F-measure and Accuracy".

Precision:

The purpose of this performance measure is to identify that how many records are classified correctly as positive from the records which are classified as positive.

$$Precision = \frac{TP}{(TP + FP)}$$

Recall:

The purpose of this performance measure is to identify that how many records are classified correctly as positive from the actual number of positive records.

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

F-measure:

This performance measure reflects the average results of both precision and recall

$$F - measure = \frac{Precision \times Recall \times 2}{(Precision + Recall)}$$

Accuracy:

The performance measure of accuracy represents the ratio of the records which are correctly classified as positive and negative to the total number of records

$$Accuracy = \frac{TP + TN}{(TP + TN + FP + FN)}$$

4 Results and Discussion

This section presents the performance of the proposed framework in terms of multiple accuracy measures.

4.1 Feature Selection Results

Feature selection is a process that helps in selecting the relevant features. It is mandatory to make sure that only relevant features are being used in order to train an ideal model. All those features that are obtained after feature selection are represented in Table.1. First a filter technique with ranker search method is applied and top 10 attributes are selected for the next step. Then in the next step, wrapper method with two search methods PSO and GA is used. Six attributes are selected by GA and five attributes are selected by PSO search method. And finally, Union is taken of attributes obtained from these two search methods.

Table 1. Selected Features

FS Method		**Search Method**	**Attributes obtained**
Filter	CorrelationAttributeEval	Ranker	3,8,11,13,9,6,7,4,5,2
Wrapper-A	ClassifierSubsetEval (NB)	GA	1,2,3,4,7,8
Wrapper-B	ClassifierSubsetEval (NB)	PSO	2,3,6,7,8
Wrapper-A Union Wrapper-B		-	1,2,3,4,6,7,8

4.2 Variant Selection Results

For this study six classifiers were optimized to create several variants. One variant is chosen from all the variants created from every base classifier on the basis of higher performance in comparison with the rest of the variants of its family including the base classifier. The classification results of each variant are depicted in Table. 2. This table contains variants of six classifiers. These variants are created by tuning different parameters. Both testing and training accuracy of these variants is depicted in this table. After evaluation, it has been observed that on the basis of accuracy, mostly the variants with default parameters performed better. The variants chosen are SVM-1, RF-1, MLP-1, NB-1, KNN-3 and DT-1. These variants are used to create different ensembles with voting technique. All possible combinations of these variants are generated for classification with voting. Finally, the combination of NB-1 and RF-1 is chosen as it delivers accuracy of 91.06%.

Table 2. Performance of Variants

Classifier	**Optimized Parameter**	**Training Accuracy**	**Testing Accuracy**
SVM-1	(Default) Value of Complexity = 1	86.3962	86.5922
SVM-2	Value of Complexity = 10	86.3962	86.5922
SVM-3	Value of Complexity = 25	86.3962	86.5922
SVM-4	Value of Complexity = 50	86.3962	86.5922
MLP-1	(Default) No of Neurons = $(attributes + Classes)/2$	91.1695	88.8268
MLP-2	No of Neurons = 8	92.3628	87.7095
MLP-3	No of Neurons =10	91.6468	86.5922
MLP-4	No of Neurons = 12	91.4081	87.7095
MLP-5	No of Neurons = 14	91.4081	87.7095
NB-1	(Default) None	88.0668	90.5028
NB-2	Kernel Estimator	86.6348	86.0335
NB-3	Supervised Discretization	87.5895	84.3575
RF-1	(Default) Max depth= 0	100	87.7095
RF-2	Max depth= 10	99.7613	87.7095
RF-3	Max depth= 15	100	87.7095
KNN-1	(Default) No of Neighbors = 1	100	80.4469
KNN-2	No of Neighbors = 3	92.1241	86.5922
KNN-3	No of Neighbors = 5	89.7375	87.1508
KNN-4	No of Neighbors = 7	88.5442	86.5922
DT-1	(Default) Confidence Factor = 0.25	92.8401	88.2682
DT-2	Confidence Factor = 0.20	92.3628	87.7095
DT-3	Confidence Factor = 0.15	92.3628	87.7095
DT-4	Confidence Factor = 0.10	92.3628	87.7095
DT-5	Confidence Factor = 0.05	92.3628	87.7095

4.3 Performance Evaluation of Proposed Framework

Accuracy is used as a performance measure in this study. It shows the ratio of correctly classified instances. Accuracy is widely accepted as the parameter of performance evaluation of any machine learning classifier. Other useful performance measures that are employed by this study are Precision, Recall and F-measure. Ten supervised machine learning techniques are used as base classifiers in this research for an initial comparison with the proposed framework. The training results of the base classifiers and the proposed framework are depicted in Table 3.

Table 3. Training Results of Base Classifiers and Proposed Framework

Classifier	**Class**	**F-measure**	**Recall**	**Precision**	**Accuracy**
RF	Y	1.000	1.000	1.000	100
	N	1.000	1.000	1.000	
NB	Y	0.535	0.667	0.447	84.2482
	N	0.905	0.870	0.943	
RBF	Y	0.034	0.018	0.500	86.3962
	N	0.927	0.997	0.866	
SVM	Y	?	0.000	?	86.3962
	N	0.927	1.000	0.864	
MLP	Y	0.897	0.842	0.960	97.3747
	N	0.985	0.994	0.976	
kStar	Y	1.000	1.000	1.000	100
	N	1.000	1.000	1.000	
KNN	Y	1.000	1.000	1.000	100
	N	1.000	1.000	1.000	
OneR	Y	0.405	0.298	0.630	88.0668
	N	0.934	0.972	0.898	
DT	Y	0.887	0.825	0.959	97.136
	N	0.984	0.994	0.973	
PART	Y	0.835	0.930	0.757	94.9881
	N	0.970	0.953	0.989	
Proposed Framework	Y	0.808	0.702	0.952	95.4654
	N	0.974	0.994	0.955	

The results given by the testing of the base classifiers and the proposed framework are reflected in Table 4. Out of ten base classifiers OneR performs the best with 88. 2682 testing accuracy and it can be observed that the proposed model performs excellently in comparison with base classifiers. The training accuracy achieved by the proposed model is 95.47 % and the testing accuracy attained by the proposed framework is 91.06 %.

Table 4. Testing Results of Base Classifiers and Proposed Framework

Classifier	**Class**	**F-measure**	**Recall**	**Precision**	**Accuracy**
RF	Y	0.378	0.292	0.538	87. 1508
	N	0.928	0.961	0.898	
NB	Y	0.508	0.667	0.410	82.6816
	N	0.895	0.852	0.943	
RBF	Y	0.000	0.000	0.000	82. 1229
	N	0.902	0.948	0.860	
SVM	Y	?	0.000	?	86. 5922
	N	0.928	1.000	0.866	
MLP	Y	0.381	0.333	0.444	85.4749
	N	0.918	0.935	0.901	
kStar	Y	0.400	0.458	0.355	81. 5642
	N	0.891	0.871	0.912	
KNN	Y	0.255	0.250	0.261	80. 4469
	N	0.887	0.890	0.885	
OneR	Y	0.400	0.292	0.636	88. 2682
	N	0.935	0.974	0.899	
DT	Y	0.471	0.500	0.444	84. 9162
	N	0.912	0.903	0.921	
PART	Y	0.469	0.625	0.375	81. 0056
	N	0.884	0.839	0.935	
Proposed Framework	Y	0.600	0.500	0.750	**91.0615**
	N	0.950	0.974	0.926	

Table 5 shows the accuracy attained by our proposed model in comparison with the other classification models that were previously used to predict COVID-19. The results achieved by our proposed framework are compared with RF, LR, GLMNET, ANN [6], DT, ET, KNN, LR. NB, RF, SVM [7], SVM-based [9], RF [11], CNN with BGA [13], CR meta-classifier [14] and XGBoost [15].

Table 5. Accuracy Comparison of Proposed Framework with Published Techniques

Reference	Dataset source	Model Used	Dataset	Accuracy
[6]	Albert Einstein Hospital, Brazil	ANN, LR, RF, GLMNET	Blood samples	81%–87%
[7]	San Raffaele Hospital, Milan, Italy	SVM, ET, NB, LR, KNN, DT, RF	Blood samples	82%–86%
[9]	Hospitals in Wuhan, China	SVM-based classifier	Blood samples	84%
[11]	Veterans' Health Administration Sites, USA	RF	Blood samples, Laboratory data	83.3%
[13]	Albert Einstein Hospital, Brazil	CNN with BGA	Blood samples, Laboratory data	80%
[14]	Taizhou hospital, Zhejiang Province, China	CR meta-classifier	Blood samples, Laboratory data	84.21%
[15]	Sírio-Libanês Hospital and Israelita Albert Einstein Hospital	XGBoost	Blood samples	80%
-	Albert Einstein Hospital, Brazil	**Proposed Framework**		**91.0615%**

5 Conclusion

The life-threatening COVID-19 pandemic has been the cause of large number of deaths all around the world which goes to show the importance of an initial screening of this disease. For the detection of COVID-19, Real-time polymerase chain reaction (RT-PCR) test has been in use, however it is slow and tedious and time consuming as the tests are expected to be inspected at a laboratory that is properly equipped. As opposed to this technique, many machine learning systems have been developed by numerous researchers to effectively predict this ailment by examining CT scan images and Chest X-Ray images. Once more, the portions of radiation, significant expense and absence of particular equipment do not permit these techniques to be commonly utilized for the detection of COVID-19. This research proposes such a model which is simple, promptly accessible, and significantly quick and does not need specific equipment or research centers as it is based on complete blood count results. CBC has many benefits. It is the most common laboratory test that is requested regularly by medical experts. It is easy to perform and not costly at all. It is readily available in all healthcare centers and has a fast turn-around time (TAT) of 25 minutes for stat CBC results. The framework proposed in this research consists of three steps; 1) Data preprocessing 2) Hybrid Feature selection 3) Ensemble learning classification. In this research a unique hybrid FS technique is proposed. The proposed model with hybrid feature selection technique and ensemble classification produced results within a few seconds to few minutes which is very fast as compared to other conventional tests. The results of the proposed framework are compared with the results of other classification models with COVID-19 dataset from different published articles. Evaluation and comparison of these results show that our proposed framework performed better than previously published frameworks.

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