Telehealthcare and Covid-19: A Noninvasive & Low Cost Invasive, Scalable and Multimodal Real-Time Smartphone Application for Early Diagnosis of SARS-CoV-2 Infection

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ABSTRACT

The global coronavirus pandemic overwhelmed many health care systems, enforcing lockdown and encouraged work from home to control the spread of the virus and prevent overrunning of hospitalized patients. This prompted a sharp widespread use of telehealth to provide low-risk care for patients. Nevertheless, a continuous mutation into new variants and widespread unavailability of test kits, especially in developing countries, possess the challenge to control future potential waves of infection. In this paper, we propose a novel Smartphone application-based platform for early diagnosis of possible Covid-19 infected patients. The application provides three modes of diagnosis from possible symptoms, cough sound, and specific blood biomarkers. When a user chooses a particular setting and provides the necessary information, it sends the data to a trained machine learning (ML) model deployed in a remote server using the internet. The ML algorithm then predicts the possibility of contracting Covid-19 and sends the feedback to the user. The entire procedure takes place in real-time. Our machine learning models can identify Covid-19 patients with an accuracy of 100%, 95.65%, and 77.59% from blood parameters, cough sound, and symptoms respectively. Moreover, the ML sensitivity for blood and sound is 100%, which indicates correct identification of Covid positive patients. This is significant in limiting the spread of the virus. The multimodality offers multiplex diagnostic methods to better classify possible infectees and together with the instantaneous nature of our technique, demonstrates the power of telehealthcare as an easy and widespread low-cost scalable diagnostic solution for future pandemics.

Keywords: Telehealthcare, Covid-19, SARS-CoV-2, Noninvasive, Invasive, Low cost, Scalable, Diagnosis, Symptoms, Hematology, Cough sound, Ensemble machine learning, Smartphone application.

1. Introduction

Telehealth is the new paradigm in health care, integrating digital information and communication technologies, to remotely deliver medical services. Conventionally, it was limited to ambulatory care such as patient in rural areas, older adults, and people with limited mobility. It promises to connect people to in-demand specialists and provide affordable quality healthcare services. Recent study shows that around two-third of patient prefers the convenience of telemedicine and the need for rapid access to their health records by their practitioners.[1] Following the Covid-19 outbreak, a massive increase of 154% in telehealth users have been recorded.[2] This can solely be attributed to the general consensus of providing safe healthcare amidst the pandemic, and reducing the risk of exposure to the virus.

The rising popularity of telehealth brings the challenge of handling an enormous amount of data. To make the system more efficient Artificial Intelligence (AI) capabilities can be integrated to detect patterns, point out potential issues, and aid doctors to act quickly in case of an emergency.[3] Since the onset of the pandemic, Machine Learning (ML) has seen a plethora of wide range novel applications, such as real-time alert to users about false information during online health inquiries over a web search engine[4], COVID-19 drug discovery[5], and vaccine development[6]. The most popular work focused on identifying positive Covid-19 patients from the X-Ray images[7;8;9;10], with satisfying outcomes. Unfortunately, a recent extensive study demonstrated the lacking potential of this technique for clinical use, ascribing methodological flaws and/or underlying biases.[11]

Alternatively, Covid-19 diagnosis from biological parameters holds a great promise, as they are

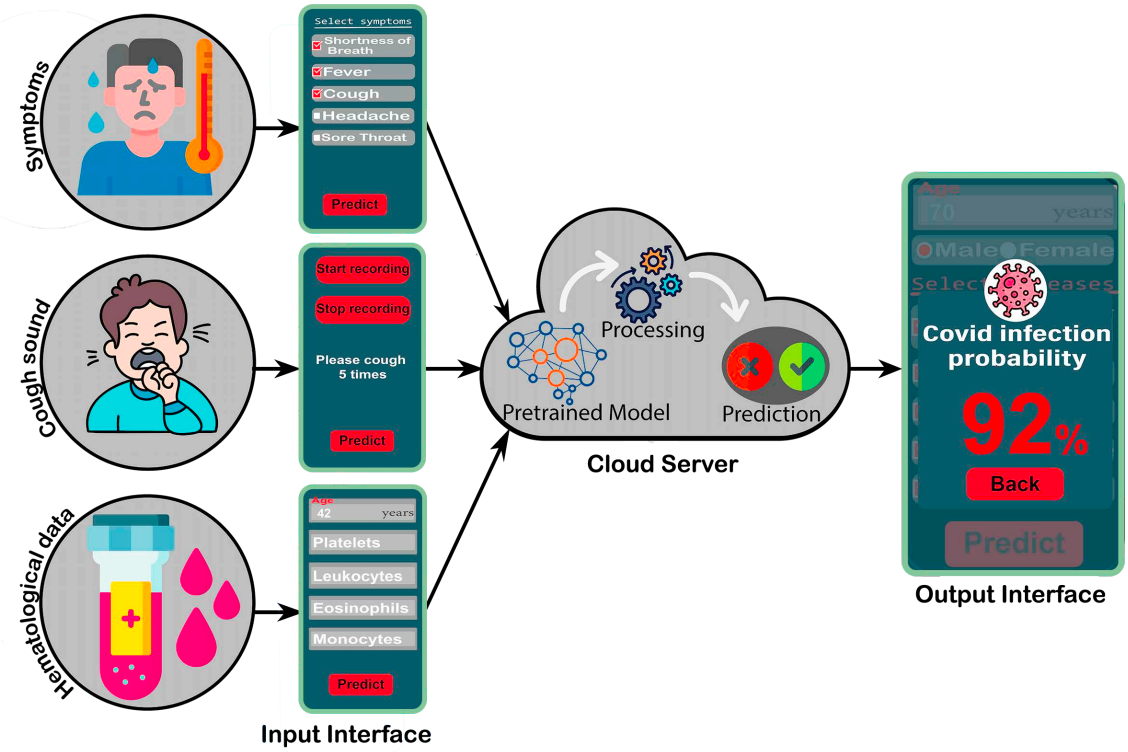

Figure 1. A Cloud based Multimodal Covid-19 diagnosis using Smartphone Application.

directly linked to the change in bodily function. Coronavirus infects people from mild to serious illness. The damage to multiple organs is associated with massive spike in inflammatory markers [12;13] and changes in other hematological parameters [14;15]. This is followed by the development of symptoms such as fever, loss of taste or smell, shortness of breath, sore throat, cough etc. Based on these clinical identifiers,

i. We propose and experimentally demonstrate a novel online framework to identify positive Covid-19 patients from the post infection symptoms, cough sound and the level of some hematological parameters. The concept is illustrated by Figure 1.

ii. The developed platform can be accessed through a Smartphone application, available for free from the *corresponding author website.*.

iii. All the attributes associated to symptoms, cough sound and blood parameters are optimized and only the most important features for accurate predictions are highlighted. This is significant to reduce the cost of Covid-19 detection from routine blood tests, which are available in most of the clinical and rural hospitalized settings. Therefore, our technique easily be integrated locally with available medical infrastructure in developed countries, where there is scarcity of Covid-19 PCR test kits [16], to provide an alternative feasible low-cost method of detection.

iv. The multimodal approach offers multiplex diagnostic methods to better classify possible infectees.

v. The online, scalable and real-time nature of our detection platform can be accessed by both non-ambulatory and hospitalized patients likewise. This can provide an additional fast and immediate screening method to limit the spread of the virus.

2. Related works

The contemporary studies with the most promising results are presented and compared in Table 1. It is important to note that, none of the studies achieved a sensitivity of 100% which is very important to correctly classify all the positive infectees. Also, different datasets than ours were used.

3. Methodology

Symptoms, cough audio data analysis, & hematological profile from routine blood test are identified as the key parameters for diagnosing Covid-19 patients. An online smartphone based application, Figure 1, can aid in the initial self-diagnostic assessment of contracting the infection. Symptoms & recorded cough audio are readily available to the individuals, and the blood profile can be obtained from any nearby pathological center.

3.1. *Dataset Collection & Feature Extraction*

Three distinct datasets for Symptom[24], Cough Audio[25;26] & Routine blood test[27] is considered in our study. For Symptoms based data, 21,235 samples was extracted, each with 7 features. Cough audio samples was collected from two different datasets, which were then merged together. Finally, a total of 586 audio samples were selected for further analysis. For the hematological study, 603 samples with 25 blood related attributes was considered.

3.2. *Data Pre-processing*

3.2.1 Missing Data Handling: The capability & great power of statistical estimation of a machine learning model is hampered due to missing values in a dataset that may occur even in a controlled & well-scrutinized study. Until this time, several data imputation techniques have been invented among which the KNN imputer has been used in this study with k=5 number of neighbors to handle null data in the dataset.[28]

3.2.2 SMOTE Analysis: Imbalanced distribution of target class in the dataset poses challenge to develop an effective model irrespective of var-

Table 1. Algorithm and performance metrics of contemporary studies.

Diagnostic method	Reference	Algorithm	Performance
Symptoms	Martinez et al.[17]	DT & RF	Accuracy: 68.1%, Sensitivity: 75.2% & Recall: 60.9% & F1-Score: 67%
	Hashmi et al.[18]	Statistical analysis (P, χ^2, Corr)	Sensitivity: 48.11% (Proposed Hashmi-Asif Chart)
Cough sound	Mouawad et al.[19]	XGBoost	Accuracy: 97%, Sensitivity: 83%, Recall: 100% & F1-Score: 91%
	Laguarta et al.[20]	CNN	Accuracy: 88%, Sensitivity: 98.5% & Recall: 94.2%
	Laguarta et al.[20]	CNN	Accuracy: 77%, Sensitivity: 80% & Recall: 71% & F1-Score: 75%
Blood test	Mohammed et al.[21]	RF	Accuracy: 95.95%, Sensitivity: 95.12%, & Recall: 96.97%
	Wu J et al.[22]	RF	Accuracy: 88%

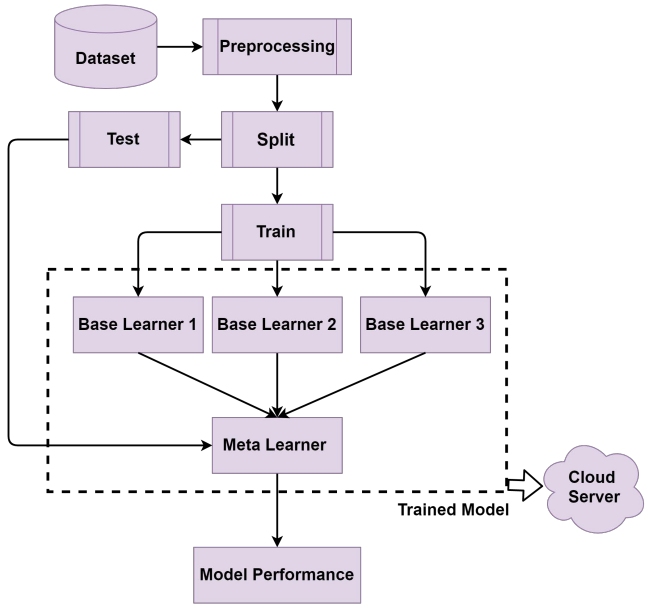

Figure 2. Overall methodologies represented as block diagram.

ious classifiers since the predictive model tends to bias more along the target class of high frequency. To ameliorate this raised concern, one of the most popular data oversampling algorithms known as 'Synthetic Minority Over-sampling Technique (SMOTE)' has been employed in our analysis that performs synthetic data point fabrication grasping the working principle of k-nearest neighbors .[29]

3.2.3 Data Splitting: All of the datasets had been splitted maintaining 70:30 ratio where 70% data were being used to train stacked ensemble model & 30% data used for overall model (1^{st} & 2^{nd} layer) evaluation.

3.2.4 Feature Scaling: Extracted features from cough audio signal, features from symptoms & blood sample analysis lies in a range of different numerical values. To work with these data stemmed from real world problems, it's imperative to bring all the data in a certain range in order to save computation power & make the calculation faster. Therefore, standard scalar (sklearn.preprocessing.StandardScaler)[30] method is used in all of our datasets to standardize the features.

3.2.5 Feature Correlation: Pearson Correlation Coefficients of the three datasets had been computed & plotted (Figure 3) in order to explore the relationship between attributes & target variable, multi-collinearity analysis & feature selection.

Since blood test for too many parameters will cost excessive test fee, we analyzed the blood dataset using both 25 & 5 features. These 5 features were being selected upon scrutinizing the correlation coefficients from 25 features.

3.3. Stacked Ensemble Machine Learning

Many researchers nowadays are using this technique to push their model performance to epitome. In stacked model, this study used double layer namely weak-learner (1^{st} layer) & meta-learner (2^{nd} layer). Weak-learner makes preliminary predictions having relatively less performance but merging few weak learners' prediction as training dataset for meta-learner improves the overall system.[31]

3.4. Machine Learning Algorithm

Short description of the algorithms used in the experimental process are given below:

3.4.1 Logistic Regression (LR): A logistic function called sigmoid function takes a set of attributes as input & classifies them as positive or negative class based on the position of output against the threshold line.[32]

Default hyperparameters were being used for LR with random_state = 0.

3.4.2 K-Nearest Neighbors (KNN): It's a lazy learning algorithm that computes statistical distance of a test datapoint from each of the training datapoint. The algorithm predicts the class of the test data based on the target class of k-nearest distant training datapoints.[32]

Following parameters were selected for KNN: n_neighbors = 5, metric = 'minkowski', p = 2.

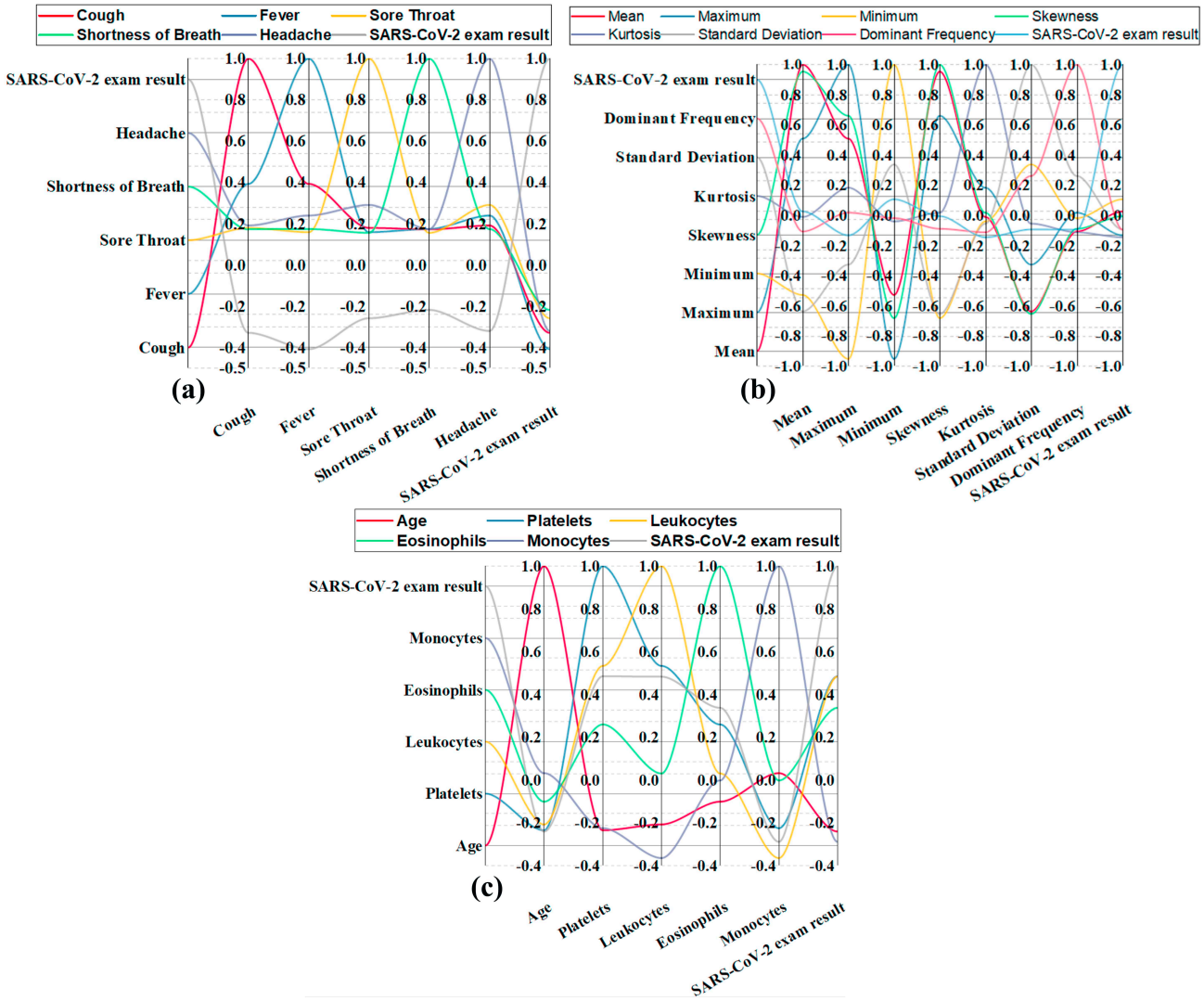

Figure 3. The Pearson Correlation Coefficient Parallel plot of - a. Symptoms, b. Cough Audio, and c. Blood profile (05 features)

3.4.3 Support Vector Machine (SVM): SVM classifier groups the training datapoints in n-dimensional space according to their target class & finds the critical edge points called support vectors. Then it draws hyperplanes touching the support vectors & gets the line separating the hyperplanes at maximum distance. The algorithm predicts the target class of a test datapoint based on the area that falls in.[33]

'rbf' kernel with random_state = 0 were being used for SVM.

3.4.4 Naïve Bayes (NB): Exploiting Bayes theorem, this classifier measures the probability of each target class assuming all the features are not correlated with each other & finally predicts the class with highest probability.[4]

GaussianNB( ) with default parameters were being used for this case.

3.4.5 Decision Tree (DT): Starting from the root node it calculates information gain & entropy of each feature and selects the feature corresponding largest information gain or smallest entropy. That's how the algorithm forms a 'tree-structured flow chart' and finally predicts target class via top-down attribute search approach.[34]

Following parameters were being selected for DT: criterion = 'entropy', max_leaf_nodes = 300, random_state = 0.

Table 2. Optimized attributes for patient symptoms, cough sound and blood test parameters.

Dataset	Number of features	Attributes
Symptoms	5	Headache, Fever, Cough, Sore throat, & Shortness of breath
Cough sound	7	Minimum, Maximum, Mean, Standarad deviation, Skewness, Kurtosis & Dominant Frequency
Blood test	25	Age, Hematocrit, Hemoglobin, Platelets, MPV, RBC, Lymphocytes, MCHC, Leukocytes, Basophils, MCH, Eosinophils, MCV, Monocytes, RDW, Neutrophils, Urea, Potassium, Creatinine, Sodium, Aspartate transaminase, INR, Albumin, Alanine transaminase & C-reactive protein
Blood test	5	Age, Platelets, Leukocytes, Eosinophils & Monocytes

3.4.6 Random Forest (RF): This classifier combines multitude of Decision Trees using 'bagging' method for eliminating the pitfalls (data overfitting & low variance) associated with DT.[29]

Following parameters were being selected for RF: n_estimators = 1500, criterion = 'gini', random_state = 0.

3.4.7 AdaBoost (AdB): Individual use of weak-learners give some misclassification but together their learning strength gets improved since their weakness is covered by the strength of the other fellow. That's how the AdB employes boosting technique for dealing with both bias-variance trade-off by combination of weighted sum of few weak-learning classifiers.[28]

Following parameters were being selected for AdB: n_estimators = 200, learning_rate = 1.

3.4.8 XGBoost (XGB): This library performs distributed & parallel computing exploiting ensemble of various classifiers using distributed & optimized gradient boosting technique. Parallel computing makes the process more efficient & faster.[29]

Following parameters were being selected for XGB: n_estimators = 25, max_depth = 15, subsample = 0.7.

3.5. Compute Statistical Metrics

Overall system performance was compared using the statistical metrics: Accuracy, Precision, Recall & F1-score. These were calculated using confusion matrix values such as true negative (TN), true positive (TP), false negative (FN) and false positive (FP).

3.6. Working Principle of the Smartphone Application

As mentioned earlier, the smartphone application provides three diagnostic options, as discussed below.

i. Symptoms: A list of possible symptoms are presented as checkboxes. The checked symptom is marked as 1 and the unchecked symp-

tom as 0. All the values are then accumulated into an array of binary values.

ii. Cough audio: This option allows the prediction of Covid-19 affection from the recorded audio of cough-sound of the patient. It provides a start and stop recording button and the application requires the patient to voluntarily cough loudly for 5 times. When user selects the predict button, the application encodes the sound of cough to base64 string and sends the encoded audio to remote server which is then reverted back to the original audio format and processed for prediction.

iii. Hematological parameters: A list of input parameters with their respective units are displayed on respective input fields, which takes numeric values.

Once the input parameters of a particular option are completed, the predict button can be pressed. The application then collects the values from input fields/check boxes/encoded audio and convert them to a JSON file, which is sent to the pre-trained ML model on a remote cloud server. The server continuously listens for a JSON file from the application. After receiving a JSON file, the ML model predicts the probability of Covid-19 infection, which is sent back to the application and displayed in a popup dialogue box. This procedure in chronological order is illustrated by Figure 1 & 5.

4. Result & Discussion

This research work leveraged the opportunity to utilize the novelty of double layer (base and meta learners) stacked ensemble algorithm for the diagnosis of SARS-CoV-2 from Symptoms, Cough sound and Hematological parameters to classify among COVID positive or negative patients. Our study swept through all the machine learning classifiers, described in Section-3.4, to propose the best possible model according to the promising performance metric values.

At first, we discuss the prediction of Covid-19 infection from the possible symptoms of a patient. The features are optimized and the five most important attributes are selected for prediction, as shown in Table 2. It can be observed from Figure 3(a) that none of the attributes have strong significance in predicting SARS-Cov-2 correctly. This is expected because, these symptoms are not specific to Covid-19 and may arise due to other diseases or physical complications. Nonetheless, an ensemble ML model with RF, XGB and SVM as the base learners and NB as the meta learner achieved the highest overall accuracy of 77.59%, as shown in Table 3, and could uniquely identify Covid-19 positive and negative patients with 74.06% and 84.15% respectively. To make the prediction risk free, 100% of an algorithm is desired. A recall score of less than 100% means that some Covid-19 negative patients would be falsely classified as positive, which upon quarantine poses no further threat. But, if sensitivity is less than 100% then the virus would persist in the community and depending on the reproduction number (R_0), may spread the virus, as demonstrated by Figure 4.[35]

A common symptom of SARS-CoV-2 is cough and it may initiate because of a reflex action to irritants or inflammation from the lungs and windpipe. Windpipe and lungs are a closed air system. Such a pathway resembles a resonating structure with a distinct fundamental frequency. Inflammation from Covid-19 may alter this dominant frequency, which can be identified from signal processing, and served as the motivation for the diagnostic method from cough sounds. We extracted seven parameters for our prediction as listed in Table 2, and Figure 3(b) shows dominant frequency, from the cough sound, to be the most significant parameter for Covid-19 diagnosis. The performance of the ML models are highlighted in Table 3. In-

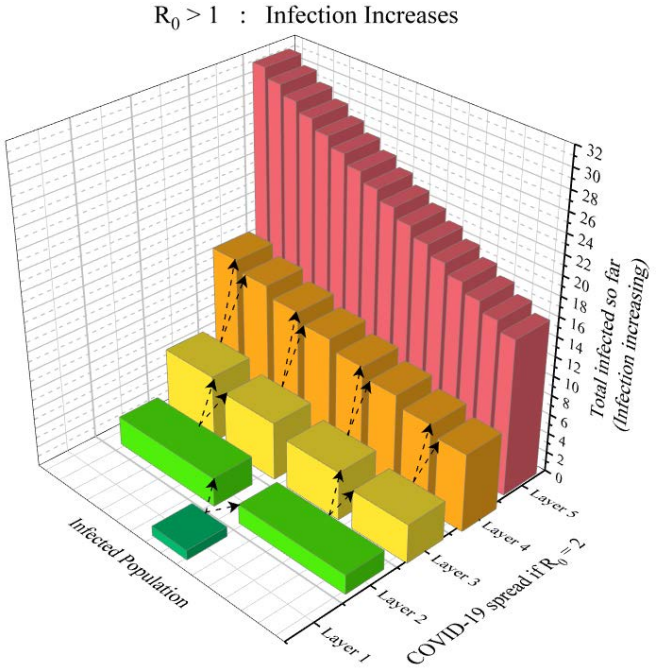

Figure 4. Effect of Basic Reproduction Number (R_0) on transmissibility/contagiousness of infectious diseases.

dividually, RF algorithm has the best performance with an accuracy, precision, recall and F1 score of 87.72%, 85.25%, 91.23% and 88.14% respectively. After thorough investigation, we design an ensemble ML model with RF, XGB and DT as the base learners and LR as the meta learner. It can be observed that the ensemble ML model has a significant gain in accuracy and F1 score to 95.65% and 96.3% respectively. This can be mainly attributed to an increase in the precision of the model as the recall score did not improve notably. A precision score of 100% signifies that our ensemble model can correctly identify all the Covid-19 patients, which is important for any diagnostic procedure to limit the virus spread as mentioned earlier.

Using hematological parameters from routine blood tests, showed the most promising results, when a total of 25 parameters are used for prediction. In this case also, for an individual algorithm, RF demonstrated the highest accuracy, precision, recall and F1 score of 97.12%, 99.32%, 94.81% and 97.01% respectively. Furthermore, we designed an ensemble model to attain the desired performance metrics of 100%, as shown in Table 3. This is significant in terms of correctly classifying between the Covid-19 positive and negative patients. This diagnostic method is noninvasive and the only technique associated with cost which scales up with the number of parameters to be measured from routine blood tests. To reduce the cost, we heuristically minimized the number of parameters to five, as listed in Table 2. The low cost solution comes at the expense of a reduced accuracy to 95.24% for the ensemble model. This is because, now with a reduced number of parameters, the ML model can correctly identify negative patients, with a veracity of 90.32%. Nonetheless, the model can successfully diagnose all the Covid-19 positive patients, which can be related to high correlation values of these parameters, seldom seen for other diagnostic approaches. Therefore, the five parameter proposal can be a low cost and risk free diagnostic approach.

Figure 5(a-c) illustrates the user interface of the mobile application for symptoms, cough sound and blood test parameters respectively. In the latter case, the unit of the input parameters are shown when a specific input field is selected. The prediction results are demonstrated using a separate dialog box, which shows Covid-19 infecion probability, Figure 5(d-e).

The Smartphone based diagnostic approach presented here offers a real-time, scalable, low cost multimodal detection of Covid-19 infected people. The authors believe such rapid intervention method can not only help control the spread of the virus, also can assist to sustain people's business and maintain the stable economic balance of a country by reducing the lockdown period.

Table 3. Performance metrics of the Proposed ML models.

Dataset: Symptoms	**Base Learners**			**Meta Learner**	**Ensemble**
	RF	XGB	SVM	NB	
Accuracy	76.83%	76.83%	76.83%	77.59%	Yes
Precision	74.13%	74.13%	74.13%	74.06%	
Recall	82.77%	82.77%	82.77%	84.15%	
F1 Score	78.21%	78.21%	78.21%	78.78%	

Dataset: Cough Sound	**Base Learners**			**Meta Learner**	**Ensemble**
	RF	XGB	DT	LR	
Accuracy	87.72%	85.09%	83.33%	95.65%	Yes
Precision	85.25%	81.25%	80.65%	100%	
Recall	91.23%	91.23%	87.72%	92.86%	
F1 Score	88.14%	85.95%	84.03%	96.30%	

Dataset: Blood Test (25 features)	**Base Learners**			**Meta Learner**	**Ensemble**
	RF	XGB	SVM	NB	
Accuracy	97.12%	96.19%	92.95%	100%	Yes
Precision	99.32%	97.28%	96.48%	100%	
Recall	94.81%	92.86%	88.96%	100%	
F1 Score	97.01%	95.02%	92.57%	100%	

Dataset: Blood Test (5 features)	**Base Learners**			**Meta Learner**	**Ensemble**
	RF	XGB	KNN	NB	
Accuracy	92.31%	88.46%	87.18%	95.24%	Yes
Precision	97.10%	88.82%	95.24%	100%	
Recall	87.01%	87.66%	77.92%	90.32%	
F1 Score	91.78%	88.24%	85.71%	94.92%	

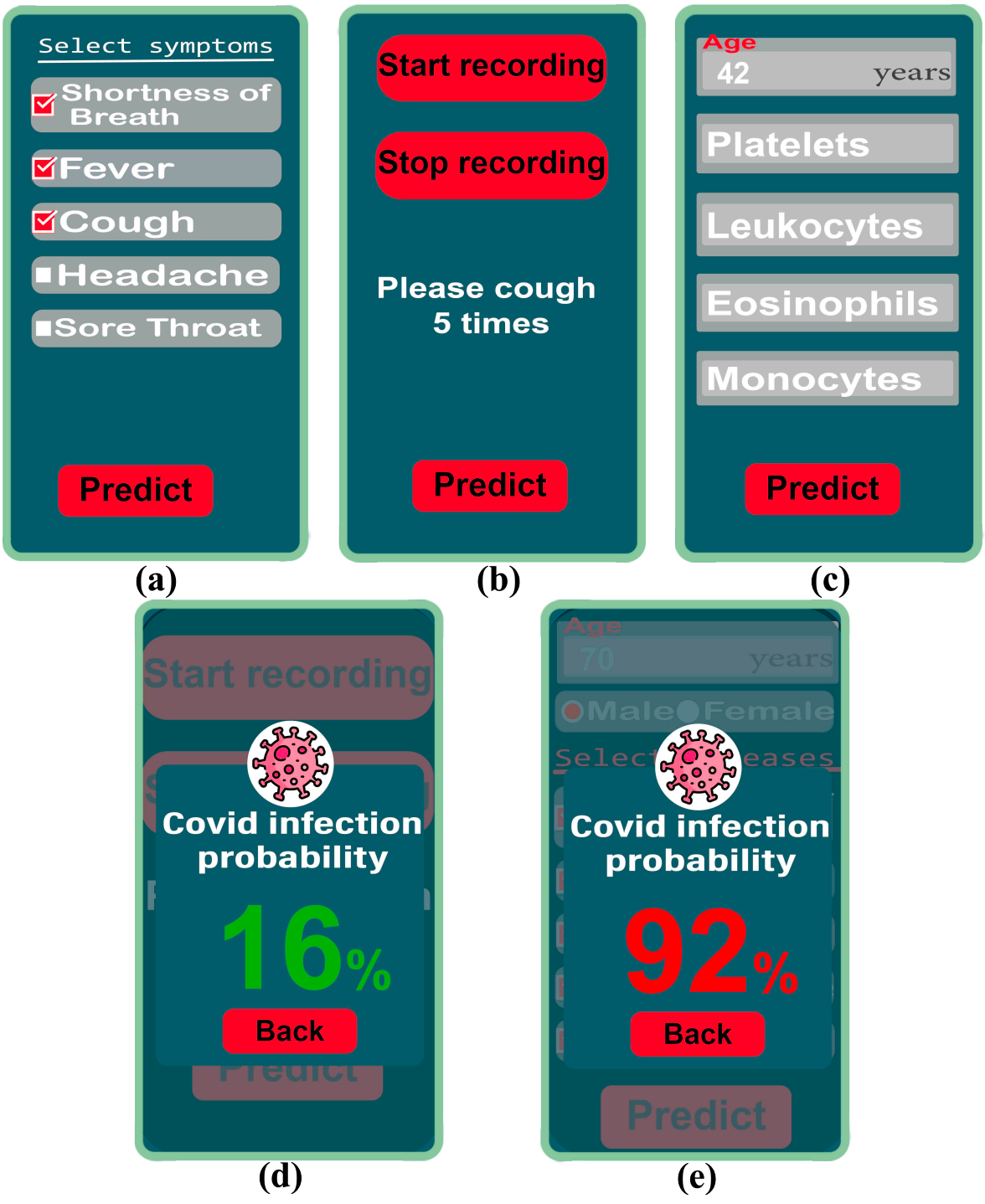

Figure 5. Cloud-based Multimodal Covid-19 diagnostic Smartphone Application: User Input Interface - (a) Symptoms, (b) Cough Sound and (c) Blood test parameters; Sample Output Interface - (d) Not Covid affected, (e) Covid affected.

5. Conclusion

This paper proposes and experimentally demonstrates a novel online framework to identify positive Covid-19 patients using machine learning. It can be accessed through a Smartphone application by both non-ambulatory and hospitalized patients and provides three modes of diagnosis using symptoms, cough sound and hematological biomarkers with an accuracy of 77.59%, 95.65% and 95.24% (for 5 blood features, but 100% for 25 blood features) respectively. The algorithms had a sensitivity of 100% for blood and sound, which indicates correct identification of Covid-19 positive patients. The multimodal diagnosis helps to better classify possible infectees. Also, the attributes required for the predictions are optimized and minimized. This is imperative to reduce the cost of Covid-19 detection, especially from routine blood test, which is available in most of the clinical and rural medical infrastructure in even underdeveloped & developing countries to provide an alternative feasible low-cost method of detection, when there is scarcity of Covid-19 PCR test kits. The online, scalable and real-time essence of the diagnostic platform can provide an additional fast and immediate screening method of the continuous mutating virus and control the future potential waves of infection. The authors hope that the proposed technique herein demonstrates the power of telehealthcare as an easy and widespread low-cost scalable diagnostic solution for future pandemics.

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