Optimized Selection Of Features For COVID-19 Diagnosis Using Cough Sound Datasets In Health-Care System

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ABSTRACT

Several studies have investigated the use of CT or X-ray images and diagnostic reagents to diagnose COVID-19 infection. However, these methods are time-consuming, labor-intensive, and less effective given the high transmission rate of COVID-19. Therefore, a fast and accurate diagnostic method is essential to prevent its spread. Recently, research has focused on pre-screening for COVID-19 using acoustic biomarker features derived from cough sound datasets. This paper proposes an optimal feature vector for rapid and accurate COVID-19 diagnosis using easily acquired cough sounds. Bhattacharyya distance was employed to calculate the degree of separation for each feature vector, and vectors with high degrees of separation were combined to create the optimal feature vector. As a result of the experiment, using 12 feature vectors, 79% accuracy and 85% AUC (Area Under the Curve) were achieved. Notably, when using a subset of seven feature vectors with high degrees of separation, the performance improved to 81% accuracy and 86% AUC. The selected seven key feature vectors are as follows:

Spectral Contrast, Spectral Flatness, RMS Energy, Spectral Bandwidth, Δ-MFCC (Delta Mel-Frequency Cepstral Coefficients), Δ^2-MFCC (Delta-Delta MFCC), MFCC (Mel-Frequency Cepstral Coefficients), This study demonstrates the potential of leveraging specific acoustic biomarkers for quick and reliable COVID-19 pre-screening, which could significantly contribute to controlling the spread of the pandemic.

Keywords: COVID-19, Audio Analysis; Coughing; Preprocessing; Feature extraction; Bhattacharyya distance

INTRODUCTION

Several studies have investigated the diagnosis of COVID-19 infection using CT or X-ray images and diagnostic reagents. However, these methods are time-consuming, labor-intensive, and inefficient in addressing the high transmission rate of the disease. Therefore, a quick and accurate diagnostic method is essential to prevent its spread. Historically, audio signals generated by the human body, particularly cough sounds, have been used as indicators to assess disease progression. Cough sounds are also much easier to collect than diagnostic reagents. This paper proposes an optimal feature vector for detecting COVID-19 based on deep learning, using easily obtainable cough data as input. The experimental dataset consisted of 1,120 cough samples from COVID-19-negative patients and 560 cough samples from COVID-19-positive patients. From these cough samples, 12 feature vectors were extracted: spectral contrast, spectral flatness, spectral centroid, spectral bandwidth, spectral roll-off, zero-crossing rate, Chroma STFT, MFCC, Δ-MFCC, Δ^2-MFCC, RMS energy, and onset. To select the optimal feature vectors, the separability of the 12 features was calculated using Bhattacharyya distance. The feature vectors with high separability were combined, and a binary classification experiment was conducted using SVM (Support Vector Machine). Performance evaluation was carried out using binary classification metrics, including accuracy, precision, recall, F1-score, and AUC. The training results showed that the best performance was achieved using seven high-separation feature vectors: spectral contrast, spectral flatness, RMS energy, spectral bandwidth, Δ-MFCC, Δ^2-MFCC, and MFCC. These features achieved superior scores across all evaluation metrics, demonstrating their effectiveness for COVID-19 detection.

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RELATED WORKS

Lange [1] conducted a COVID-19 detection study using four types of characteristics: general information such as age and gender, symptoms, respiratory status, and cough data. The 94 samples are classified into 74 training data and 20 experimental data, and each sample is represented by a 43-order feature vector. The 43rd order feature vector contains 26th order feature vectors extracted from 2 general information, 5 respiratory status, 10 symptom and cough data. The cough data for the experiment went through a preprocessing section to remove non-cough sections and a preprocessing process to remove noise, and three types of classification models were used: logistic regression, SVM, and neural networks. When the Fully Connected NN classification model was used, the accuracy of 70% was obtained and the best experimental results were obtained.

Brown [2] conducted a COVID-19 detection study using crowdsourced cough and breath sounds as experimental data. All experimental data were resampled at 22050Hz, and the experiment was performed by extracting 10 feature vectors using the librosa [3] library. Audio feature vectors are extracted from cough and breathing sounds recorded through a smartphone or website, and the extracted feature vectors are combined with the output of a pre-trained audio neural network. The training data and test data are divided in an 8:2 ratio, and the model is trained with the training data to detect COVID-19 and evaluate the accuracy through the test data. Brown conducted the experiment using the SVM model and divided the experimental data into three methods to proceed with the experiment. The first experiment was conducted using the cough sounds and breathing sounds of COVID-19 positive and negative patients, and the second experiment was conducted using only the cough sounds of COVID-19 positive and negative patients. Finally, an experiment was conducted using the cough sound of a COVID-19 positive patient and the cough sound of a COVID-19 negative patient with asthma. In all three experiments, AUC of 80% or more was achieved.

Laguarta [4] conducted an experiment to prescreen for COVID-19 using an acoustic biomarker feature extractor using 5320 cough data. Cough data is converted to MFCC and input into a single CNN-based architecture. A biomarker layer and three pre-trained RestNet50s are placed in parallel to output binary pre-screening diagnostics. The CNN-based model was trained with 4256 training data and tested with 1064 test data. The COVID-19 discrimination architecture proposed by Lagurata uses four biomarkers used to detect Alzheimer's disease [5]. The four biomarkers [6][7][8][9][10] are muscle weakness, vocal fold changes, emotional/mood changes, and lung and respiratory changes. The model validated as COVID-19 positive patients through official testing achieved a specificity of 94.2% and a sensitivity of 98.5%. For asymptomatic patients, a specificity of 83.2% and a sensitivity of 100% were achieved.

Dataset

A. Experimental data

The experimental data in this paper consists of the data set of COUGHVID [11] and the data set of Cambridge [12]. In the COUGHVID dataset, 441 cough data from COVID-19 positive patients and 162 cough data from negative patients were used, and in the Cam-bridge dataset, cough data from 119 positive patients and 398 negative patients were used. The experimental data consists of 560 cough data from COVID-19 positive patients and 560 cough data from negative patients, a total of 1120 cough data. All cough data were sampled at 22050 Hz. Table I shows the composition of the experimental data.

Table I. Experimental data composition

	COVID-19 positive	**COVID-19 negative**	**Total**
COUGHVID	441	162	603
Cambridge	119	398	517
Total	560	569	1120

The Cambridge data set was collected via the COVID-19 Sound app in April 2020 and aims to collect data primarily for COVID-19 diagnosis based on voice, breathing and cough. Participants provided audio samples along with COVID-19 test results through various platforms (webpage, Android app, iOS app). The original crowdsourced audio data varied in sampling rate and format. All data were resampled at 16kHz. In this paper, experimental data were constructed using the CCS (COVID-19 COUGH) data set. Cough data from 119 COVID-19 positive patients and cough data from 398 COVID-19 negative patients were used. The app called COUGHVID is a simple web app that you can run on any web browser, any device that has a microphone. The COUGHVID dataset provides over 25,000 crowdsourced cough data representing different ages, genders, geographic locations, and COVID-19 status. The COUGHVID data set consists of two files with the same cough data name but different extensions. One of the files contains audio data. All audio data is sampled at 48kHz. The .json extension file contains metadata encoded in plain text in format 23.

In this paper, only data with a cough detected score of 0.9 or higher was selected to construct experimental data, and a total of 603 data of 441 COVID-19 positive cough data and 162 COVID-19 negative cough data were used to construct experimental data. In an experiment to diagnose COVID-19 using cough, if the non-cough section is included in the experimental data, unnecessary information may be included and interfere with the experimental results. For more accurate experimental results, preprocessing is performed to remove non-cough sections from cough data. The cough section has a higher energy value than the non-cough section. An Integral Absolute Value (IAV) feature vector, which means an energy magnitude value, is used so that the cough section and the non-cough section can be numerically distinguished. The IAV feature vector is the integral of the absolute value of the signal for a certain time, and the equation is as follows.

$$\bar{X} = \sum_{i=1}^{N} |X(i\Delta t)| \qquad (1)$$

To define the criteria for the non-cough section, the maximum and minimum values of the IAV feature vector are calculated, and 10% of the difference is added to the minimum value and set as a threshold value. If the minimum value is greater than 70% of the maximum value, the threshold value is selected as 20% less than the maximum value. An example of the process of selecting a threshold is shown in Figure 1.

The signal magnitude threshold can be obtained by dividing the IAV threshold by the frame size. Since the IAV feature vector is the sum of the absolute values of all signal values in the frame, dividing by the frame size gives the average value of the frame signal. This value becomes the value obtained by replacing the IAV threshold with the signal magnitude threshold. To extract the cough sound section, the start index and end index of the cough sound are obtained. If a section larger than the IAV threshold is found in units of frames, the cough start index is set at a point greater than the signal energy threshold within the frame and a point where the IAV threshold becomes smaller is set as the end index to extract a cough sound section. [13]. Figure 2 and Figure 3 show the results before and after extracting the cough section.

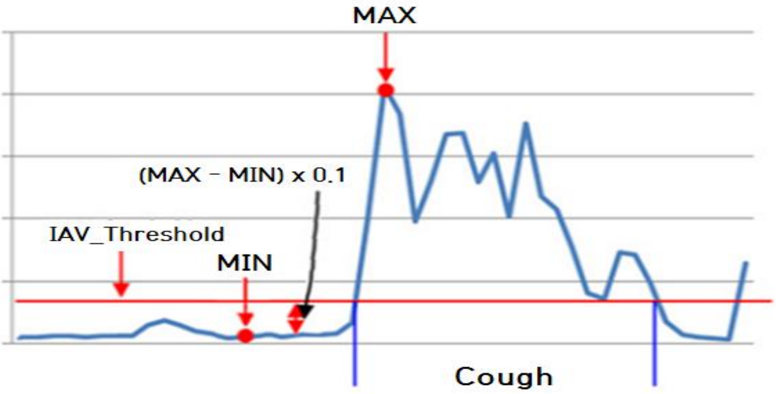

Figure 1. IAV Threshold Setting Process

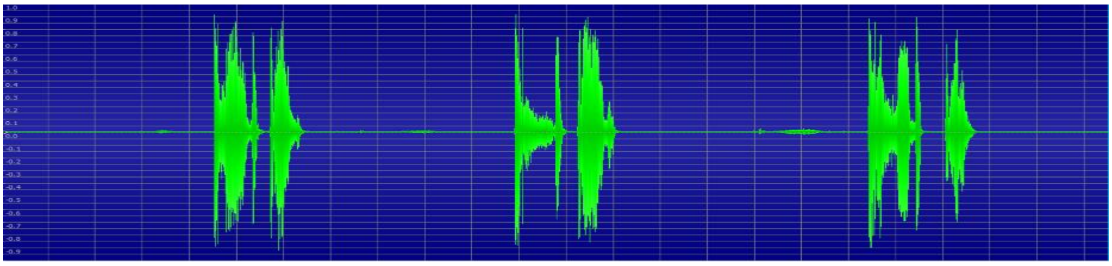

Figure 2. Before extraction of cough

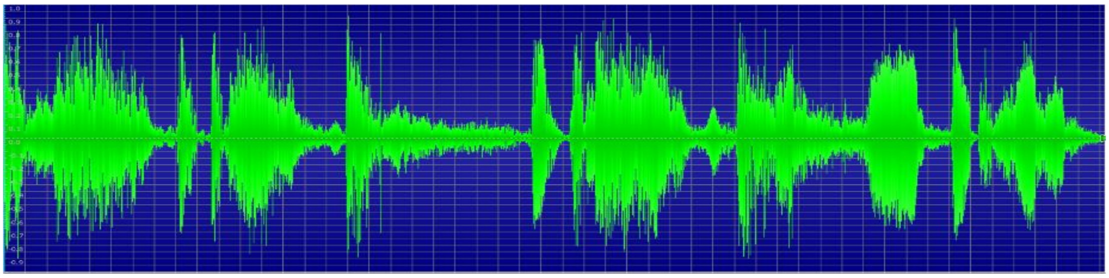

Figure 3. After extraction of cough

B. Feature Extraction

Twelve feature vectors are extracted from cough data that has undergone a preprocessing process to remove non-cough sections. The 12 feature vectors used in this study are as follows.

- Chroma: Chroma features obtained by combining the normalized sub-band energies of 12 pitch classes to represent the tonal information of audio signals [14]
- Spectral centroid: the mean (centroid) extracted per frame of the magnitude spectrogram.
- Spectral bandwidth: computes the order-p spectral band width.
- Spectral contrast: Spectral contrast considers the spectral peak, the spectral valley, and their difference in each frequency sub-band.
- Spectral flatness: Spectral flatness (or tonality coefficient) is a measure to quantify how much noise-like a sound is, as opposed to being tone-like [15].
- Spectral roll off: the center frequency for a spectrogram bin so that at least 85% of the energy of the spectrum in this frame is contained in this bin and the bins below.
- Zero-crossing: the rate of sign-change of the signal.
- MFCC: Mel-Frequency Cepstral Coefficients obtained from the short-term power spectrum, based on a linear cosine transform of the log power spectrum on a nonlinear Mel scale. MFCCs are amongst the most common features in audio processing [8]. We use the first 20 components.
- Δ-MFCC: the temporal differential (delta) of the MFCC.
- Δ2-MFCC: the differential of the delta of the MFCC (acceleration coefficients).
- RMS Energy: the root-mean-square of the magnitude of a short-time Fourier trans-form which provides the power of the signal.
- Onset: the number of pitch onsets (pseudo syllables) is computed from the signals, by identifying peaks from an onset strength envelope, which is obtained by summing each positive first-order difference across each Mel band [16].

EXPERIMENTS AND RESULTS

A. Separation of Features

To select an effective feature vector for detecting COVID-19, we use the Bhattacharyya distance, a method of calculating the degree of separation between each class [17]. The degree of separation between the two classes, the cough data of a negative patient and the cough data of a positive COVID-19 patient, is calculated and compared with the average value for each feature vector. A large Bhattacharyya distance value means that the distance between classes is large, which means that the corresponding feature vector is effective in detecting COVID-19. The average value of the Bhattacharyya distance for each feature vector can be seen in Table II. Spectral Contrast was the highest at 0.11834 and Spectral Rolloff was the lowest at 0.01495. The degree of separation has a large value in the order of Spectral Contrast, Spectral Flatness, RMS Energy, Spectral Bandwidth, Δ-MFCC, Δ2-MFCC, MFCC, Onset, ZCR, Chroma, Spectral Centroid, and Spectral Roll off. Equation 2 is the Bhattacharyya distance equation.

$$\mu(1/2) = \frac{1}{8}(M_2 - M_1)^T \left\{\frac{\Sigma_1 + \Sigma_2}{2}\right\}^{-1} (M_1 - M_2) + \frac{1}{2} ln \frac{\left|\frac{\Sigma_1 + \Sigma_2}{2}\right|}{\sqrt{|\Sigma_1||\Sigma_2|}} \qquad (2)$$

Table II. Separation degree calculation result

Feature Vector	**Bhattacharyya Distance**
Chroma	0.01552
Spectral Centroid	0.01512
Spectral Bandwidth	0.04109
Spectral Flatness	0.10997
Spectral Contrast	**0.11843**
Spectral Roll off	0.01495
Zero-crossing Rate	0.0268
MFCC	0.03047
Δ - MFCC	0.0347
Δ^{2} - MFCC	0.03067
RMS Energy	0.04667
Onset	0.02802

B. Binary Classification Evaluation Feature Extraction

In order to check whether the selected feature vectors are effective in diagnosing COVID-19, learning is carried out with SVM and the experimental results are evaluated using Binary Classification Evaluation. The confusion matrix is a matrix that evaluates the performance of classification on the test data set. Table III is an example of the error matrix of the binary classifier. Based on this value, five indicators are calculated and used for model evaluation: Accuracy, Recall, Precision, F1-Score, and AUC.

Table III. Confusion matrix

		Predicted Class	
		TURE	**FALSE**
Actual Class	**TURE**	TP (True Positive)	FN (False Negative)
	FALSE	FP (False Positive)	TN (True Negative)

TP = True Positive, FP = False Positive, TN = True Negative, FN = False Negative. The number of what the classifier actually identified as COVID-19(+) and COVID-19(+) is TP, the number of people mistaking it as COVID-19(−) is FN, actually COVID-19(−) and the number of what the classifier identified as COVID-19(−) is TN, FP is when those with COVID-19(−) are mistakenly classified as COVID-19(+) [18].

Accuracy refers to the ratio of the number of samples correctly predicted among all samples. Recall refers to the ratio of the number of samples printed as belonging to the positive class among samples belonging to the actual positive class. The higher the model, the better it is. Precision refers to the ratio of the number of samples belonging to the positive class to the number of samples outputted as belonging to the positive class. The high-er the model, the better it is. The weight harmonic average of Precision and Recall is called F1-score. The ROC (Receiver Operator Characteristic) curve is a visualization of the change in fall-out and recall according to the change in the class discrimination reference value. Area under the curve (AUC) means the area of the ROC curve. The closer to 1, the better the model.

Accuracy, Precision, Recall, F1-Score, TPR, and FPR can be expressed by Equations (3), (4), (5), (6), (7), (8).

$$Accuracy = \frac{TP + TN}{TP + FN + FP + TN} \quad (3)$$

$$\mathrm{Precision} = \frac{TP}{FP + TP} \quad (4)$$

$$Recall = \frac{TP}{FN + TP} \quad (5)$$

$$F1 = 2 \times \frac{\mathrm{Precision} \times Recall}{\mathrm{Precision} + Recall} \quad (6)$$

$$TPR = \frac{TP}{TP + FN} \quad (7)$$

$$FPR = \frac{FP}{FP + TN} \quad (8)$$

C. Experimental Performance Evaluation

Table IV shows the results of binary classification performance evaluation when binary classification experiments are performed for each feature vector. The higher the degree of separation, the higher the AUC value. Binary classification experiments were conducted by combining feature vectors with high resolution and performance was evaluated. Table V is a table evaluating the performance of a binary classification experiment using 8, 7, 6 feature vectors with high separation and Spectral Contrast with the highest resolution and 6, 5 feature vectors with low separation. High 8; Spectral contrast, Spectral flatness, RMS, Spectral bandwidth, Δ-MFCC, Δ2-MFCC and MFCC, Onset. High 7; Spectral contrast, Spectral flatness, RMS, Spectral bandwidth, Δ-MFCC, Δ2-MFCC and MFCC. High 6; Spectral contrast, Spectral flatness, RMS, Spectral bandwidth, Δ-MFCC, Δ2-MFCC. Low 6; Spectral roll off, Spectral centroid, chroma, ZCR, Onset, MFCC. Low 5; Spectral roll off, Spectral centroid, chroma, ZCR, Onset.

Table IV. Binary classification performance evaluation result by feature vector

Feature Vector	**Accuracy**	**Precision**	**Recall**	**F1-Score**	**AUC**
Chroma	0.76	0.8	0.72	0.76	0.8103
Spectral Centroid	0.49	0.48	0.97	0.65	0.6895
Spectral Bandwidth	0.57	0.55	0.88	0.67	0.6726
Spectral Flatness	0.6	0.56	0.76	0.64	0.672
Spectral Contrast	0.63	0.62	0.68	0.65	0.666
Spectral Roll off	0.53	0.63	0.25	0.36	0.6475
Zero-crossing Rate	0.6	0.58	0.9	0.7	0.6372
MFCC	0.56	0.54	0.85	0.66	0.6219
Δ- MFCC	0.59	0.6	0.37	0.46	0.6184
Δ^{2-}MFCC	0.5	0.67	0.12	0.21	0.5883
RMS Energy	0.47	0.48	0.9	0.63	0.5813
Onset	0.52	0.6	0.21	0.31	0.5527

Table V. Binary classification performance evaluation result

	Accuracy	**Precision**	**Recall**	**F1-Score**	**AUC**
ALL	0.79	0.8	0.78	0.79	0.8544
High 1	0.76	0.8	0.72	0.76	0.8103
High 8	0.79	0.81	0.75	0.78	0.8475
High 7	**0.81**	**0.81**	**0.8**	**0.8**	**0.8608**
High 6	0.76	0.8	0.7	0.75	0.829
Low 6	0.69	0.65	0.8	0.71	0.7936
Low 5	0.73	0.76	0.76	0.76	0.7487

As a result of performance evaluation using binary classification performance evaluation, the results of binary classification experiment using 7 feature vectors with high spectral contrast, spectral flatness, Rms energy, spectral bandwidth, Δ-MFCC, Δ2-MFCC and MFCC separation were 12 When all of the feature vectors were used, the

Accuracy, Precision, Recall, F1-Score, and AUC Score all showed better performance than the results when 8 or 6 were used.

CONCLUSIONS

To enhance the diagnostic rate of COVID-19 using cough sounds, it is essential to employ feature vectors that are effective in detecting the disease. In this study, effective feature vectors were selected for diagnosing COVID-19 using cough sounds. The experimental dataset consisted of 560 cough samples from healthy individuals and 560 samples from COVID-19 patients, totaling 1,120 samples. To improve the accuracy of the experimental results, non-cough sections were removed through IAV (Instantaneous Amplitude Variation) threshold-based preprocessing. From the preprocessed cough data, 12 feature vectors were extracted: Spectral Contrast, Spectral Flatness, Spectral Centroid, Spectral Bandwidth, Spectral Roll-Off, Zero-Crossing Rate, Chroma STFT, MFCC, Δ-MFCC, Δ^2-MFCC, RMS Energy, and Onset. After determining the degree of separation for each feature vector, those with high separation were selected for further analysis. A binary classification experiment was conducted by implementing a classification system using SVM (Support Vector Machine). When binary classification experiments were performed using all 12 feature vectors, the results showed an Accuracy of 0.79, Precision of 0.80, F1-Score of 0.79, Recall of 0.78, and an AUC of 0.8608. For Spectral Contrast, the feature vector with the highest degree of separation, the performance was as follows: Accuracy of 0.76, Precision of 0.80, F1-Score of 0.76, Recall of 0.72, and an AUC of 0.8103. When binary classification was performed using seven feature vectors with high separation—Spectral Contrast, Spectral Flatness, RMS Energy, Spectral Bandwidth, Δ-MFCC, Δ^2-MFCC, and MFCC—the results improved. The model achieved an Accuracy of 0.81, Precision of 0.81, F1-Score of 0.80, and an AUC of 0.8608. These results outperformed both the experiment using only the single best feature vector and the experiment using all 12 feature vectors. This study demonstrates that using the proposed feature vectors along with an effective binary classification algorithm can significantly improve the diagnostic performance of COVID-19 in the future.

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