2021 IEEE Asia-Pacific Conference on Computer Science and Data Engineering (CSDE) | 978-1-6654-9552-3/21/$31.00 ©2021 IEEE | DOI: 10.1109/CSDE53843.2021.9718501

CovidEnvelope: An Automated Fast Approach to Diagnose COVID-19 from Cough Signals

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***Abstract*—COVID-19 pandemic has a devastating impact on human health and well-being. Numerous biological tools have been utilised for COVID detection, but most of the tools are costly, time-extensive and need personnel with domain expertise. Thus, a cost-effective classifier can solve the problem where cough audio signals showed potentiality as an screening classifier for COVID-19 diagnosis. Recent ML approaches on cough-based covid-19 detection need costly deep learning algorithms or sophisticated methods to extract informative features. In this paper, we propose a low-cost and efficient envelope approach, called *CovidEnvelope*, which can classify COVID-19 positive and negative cases from raw data by avoiding above disadvantages. This automated approach can select correct audio signals (cough) from background noises, generate envelope around the informative audio signal, and finally provide outcomes by computing area enclosed by the envelope. It has been seen that reliable data-sets are also important for achieving high performance. Our approach proves that human verbal confirmation is not a reliable source of information. Finally, the approach reaches highest sensitivity, specificity, accuracy, and AUC of 0.96, 0.92, 0.94, and 0.94 respectively to detect Covid-19 coughs. Our approach outperformed other existing models on data pre-processing and inference times, and achieved accuracy and specificity of 0.91 and 0.99 respectively, to distinguish COVID-19 coughs from other coughs, resulted from respiratory diseases. The automatic approach only takes 1.8 to 3.9 minutes to compute these performances. Overall, our approach is fast and sensitive to diagnose the people living with COVID-19, regardless of having COVID-19 related symptoms or not. In this connection, the model can be implemented easily in mobile-devices or web-based applications, and countries with poor health facilities will be highly beneficiary for covid diagnosis and measuring prognostication.**

***Index Terms*—COVID-19, Envelope, Cough, Audio Signals, Diagnosis**

I. Introduction

COVID-19 is a respiratory disease caused by SARS-CoV-2 virus – a novel Coronavirus of family Coronaviridae. Coronaviruses of this family, especially viruses of genus Betacoronavirus (e.g. Middle East Respiratory Syndrome Coronavirus, aka MERS-CoV, Severe Acute Respiratory Syndrome Coronavirus, aka SARS-CoV etc) are highly pathogens of respiratory tract diseases, and their characteristics of highly variable genetic diversity and diverse host adaptability make them deadly and devastating around the world [1]. Current COVID-19 pandemic and its widespread infection and mortality rate has made SARS-Cov2 virus a hot topic for diverse research communities. Beside developing vaccines to cure COVID-19, substantial effort is being made to develop tools to diagnose COVID-19.

COVID-19 diagnoses tools can be widely divided into two categories. Firstly, biological tools, which are involved in viral nucleic acid-based detection (e.g. RT-PCR, LAMP etc.) and protein-based detection (e.g. rapid antigen-based detection and serological tests). Among the available tools, RT-PCR based nucleic acid detection is being considered as "gold-standard" for COVID-19 diagnosis because of its high specificity, sensitivity, and ability to detect at initial stage of infection [2]. Due to substantial similarity with other sister species of coronavirus, two-targeted multiplex RT-PCR is adopted to detect SARS-CoV2 virus, where 'first target' broadly detects presence of any members of coronavirus, and the 'later target' further narrow down to SARS-CoV2. Although this technique is rapid and highly reproducible, it is labour-extensive, time-consuming, and need molecular biology expertise with sophisticated laboratory facilities to do certain steps [3]. Different modifications of RT-PCR techniques have been proposed, like one-step Loop-mediated iso-thermal amplification reaction (LAMP), Microarray-based methods, barcoded bead assays [4], which need sophisticated instruments and are not as sensitive as RT-PCR. On the other hand, protein-based detection tests are simple and fast alternatives, utilises host immune response to viral antigens. Currently, numerous serological tests (e.g. Enzyme-linked immunosorbent assay-ELISA, Indirect immunofluorescence- IIFT) are under development for COVID-19 diagnosis with variable specificity. Even though host antibodies, generated in response to viral infection, can be useful tool for COVID-19 diagnosis, there is a potential chance of producing similar antibodies (cross-reactive antibody response), in response to other coronaviruses – resulting in false positive detection [5]. Besides, antibody-based serological tests are also prone to viral lag-period of 4 to 7 days, where they does not show any responses, and also show poor response up to 6 days of infection, which is alarming for public health [6].

Beside biological tests, several clinical feature-based tests are being proposed and analysed. The initial mild symptoms of the COVID-19 include cough, fever, fatigue, followed by headache, dyspnea, myalgia, and gastrointestinal complications with nausea and watery diarrhoea [7], which are being considered during these tests. Severe COVID-19 infection

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manifested by pneumonia with acute respiratory distress syndrome, severe cough, and infiltrates on chest image. Based on the features, fever, cough, and dyspnea are considered as potential indicator of suspicious COVID-19, and numerous machine-learning (ML) algorithms are being developed as a pre-screening diagnostic tool for COVID-19 detection.

Different ML methods have been used to diagnose various diseases [8]–[11] and similar principle has been adopted for diagnosing COVID-19 from chest computed tomography (CT scan) images in [12]. On the other hand, audio signals have been successfully utilised in diagnosis and therapies of various diseases [13]. Cough detection from the audio signals is a very important and promising process to detect pathology severity of the people, infected with COVID-19. The audio-based screening tool could be implemented in residential environments to track individuals who are suffering from COVID-19 as a subsystem of remote health monitoring systems.

ML has been found as a useful method to design the audio-based screening tool to diagnose coughs [14]. Convolutional Neural Network (CNN) and Recurrent Neural Network (RNN) models were used to detect cough sounds by varying hyper-parameter values manually in [15]. A real-time cough detection method was designed, by combining Gaussian Mixture model and Universal Background model [16], that requires four steps to complete the process: sound pre-processing, segmentation, feature / event extraction, and cough prediction. Wavelet decomposition and statistical parameters were used to detect pneumonia cough [12]. Logistic regression was considered to detect tuberculosis cough from short-term spectral features [17]. Further, Brown et al. [18] used logistic regression, gradient boosting trees (GBT) and support vector machines (SVM) to distinguish COVID-19 cough sound from large-scale crowdsourced respiratory sound dataset. Laguarta et al. [19] considered CNN for diagnosing COVID-19 cough from extracted features. Moreover, Fakhry et.al [20] used deep neural networks to diagnose COVID-19 by considering clinic records and mel-frequency cepstral coefficients and mel-frequency spectrograms of cough audios. However, they [18], [20] used ”verbal” confirmed cough sounds, which can lead to false-positive or negatives in COVID-19 detection. Both of these models are computationally expensive, require heavy data prepossessing and inference time.

Finding a reliable and well-balanced dataset is pre-requisite to build and test ML model, but there is a scarcity of COVID-19 cough audio dataset. Most of the existing models [20], [21] used Coughvid, Cowsara, Sarcos and Virufy dataset, which lack proper annotation and corresponding confirmation. Coughvid dataset mostly contains cough audios from verbal confirmation, and for PCR verified audios, it only contains COVID-19 positive samples. Cowsara dataset [21] contains 236 audios, verified with PCR tests but most of them contain either one or repeated cough audios, which substantially decreases the audio quality. Virufy and Sarcos dataset contain PCR-tested cough audios, but the number of audios (20 and 50 respectively) is insufficient to test ML algorithms. The most reliable, well-balanced and publicly available dataset used in current study, was collected by the Medina Medical Group[1] in Russia. we called it ”Russian dataset” from hereafter. It is a freely available representative dataset for developing low-cost AI tools for developing countries as they are suffering heavily on Covid diagnosis. For example, there are only 8000 pests per million population in Africa [22] that urge to present a more cost-effective and reliable method to help with the Covid-19 diagnosis.

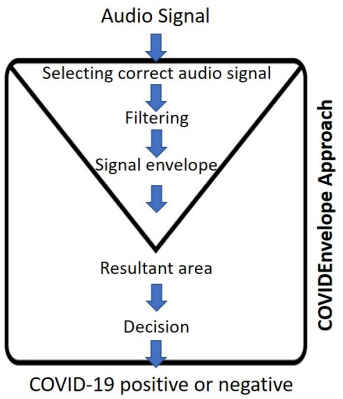

Figure 1. A flowchart of the *CovidEnvelope Approach*.

In this paper, we propose a fast and low-cost envelope approach, which can detect COVID-19 coughs from other coughs. our approach needs minimal time for prepossessing and extracting features from raw cough signals. In addition, it can distinguish COVID-19 coughs from other diseased coughs with high performance. *CovidEnvelop* is a computationally inexpensive approach, which will be useful to design real-time cough-screening tool for diagnosing COVID-19 immediately.

II. Methods

We developed an automated approach, namely *CovidEnvelop*, which is capable of diagnosing COVID-19 from the raw cough signals. We tested its performance on the reliable and publicly available Russian dataset. A flowchart of our approach is illustrated in Figure 1.

A. CovidEnvelope approach

We designed an envelope approach[2] for computing area of cough sounds which take raw cough audio signals as input and provide outcomes as COVID-19 positive or negative from the computed resultant area (see Figure 1). Correct cough-based audio signals were selected from the raw audio signals and then, filtering was performed to get rid of background noises. A “signal envelope” was generated over the filtered audio signal, and the envelope-enclosed resultant area was calculated. Based on the resultant area, decision was made to identify COVID-19 positive or negative. Each step of this automatic approach is described accordingly and a resultant signal is illustrated in Figure 2.

[1] https://fkthecovid.ru/en

[2] Code Availability: https://github.com/ZakirANU/CovidEnvelope

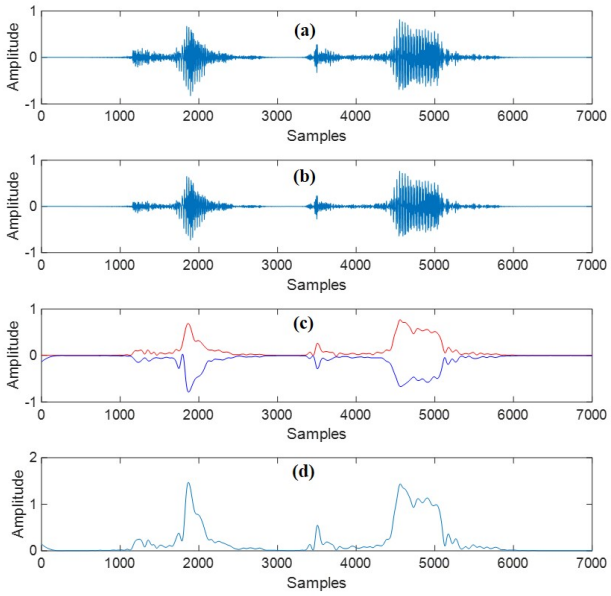

Figure 2. Generating envelope from cough audio signals.

Audio signal, as depicted in Figure 2(a), was taken as input to the algorithm. In addition to the original audio signal, the recording may often contain additional high frequency noisy signals. Correct audio signal was selected by comparing the sum of variances of the recorded signals, and then filtered using a three-point moving average filter to remove random fluctuations between samples of the audio signal as illustrated in Figure 2(b). An envelope of the filtered audio signal was generated as shown in Figure 2(c), where the upper and lower boundaries of the audio signal are shown by the red and blue lines, respectively. The resultant signal was generated by applying equation 1.

$$R_i = \mid U_i - L_i \mid \tag{1}$$

where R_i, U_i, and L_i are the amplitudes of the resultant, upper, and lower boundaries for the i_{th} sample. A sample resultant signal is depicted in Figure 2(d). The absolute difference between the upper and lower boundaries was taken to produce positive amplitude enclosed by the signal envelope. The area enclosed by the envelope was calculated by summing up the sample amplitudes of the resultant signal by applying equation 2.

$$A = \sum_{i=1}^{n} R_i \tag{2}$$

where *'A'* and *'n'* are the area enclosed by the envelope and number of samples in the resultant signal, respectively. The resultant area of the COVID-19 positive cough was often different from the COVID-19 negative cough. To distinguish COVID-19 positive and negative coughs, we analyzed the resultant area with varying thresholds. An optimized threshold of 5000 was found effective as explained in section III. Applying the optimized threshold, COVID-19 positive cough records were diagnosed with highest performance.

B. Testing cough dataset

There is a number of COVID-19 cough data-sets available online, namely Coughvid, Cowsara, Sarcos, Virufy and a Russian dataset, but due to lack proper annotation and corresponding PCR-based confirmation, we only considered the Russian dataset to test our model. The Russian dataset contains acoustic cough sound data of 1324 subjects, collected during October-November 2020, where 2 sound data were corrupted. Thus, total number of readable sound data was 1322 as mentioned in Table I.

The dataset contains two types of records – *Verbal Positives*: where subjects confirmed their COVID-19 presence verbally, *Verbal Negatives*: where subjects confirmed their COVID-19 absence verbally. Further the verbal confirmations were verified using laboratory-based PCR tests, generating two types – *Verified Positives*: where the records had been further confirmed to the presence of COVID-19 by laboratory-based PCR tests and *Verified Negatives*: where the records confirmed for the absence of COVID-19 by PCR tests. Verified positives dataset further divisible into two specific groups – *Symptomatic*: where the subjects exhibit COVID-19 specific symptoms and *Asymptomatic*: where the subjects did not show any COVID-19 specific symptoms. In this study, regardless of COVID-19 presence or absence, we formed another type of dataset, namely *'Matched'*: where verbal confirmation data matched with the laboratory confirmations. This study found 819 *'Matched'* records, where the number of *'Matched Positives'* (*i.e. Verbal Positives = Verified Positives*) and *'Matched Negatives'* (*i.e. Verbal Negatives = Verified Negatives*) were 381 and 438 respectively. The *'Matched Positive'* records are further divided into *'MatchedSymp'* and *'MatchedAsymp'* based on the observed COVID-19 related symptoms. There are 201 and 108 records who showed (*'MatchedSymp'*) and did not show (*'MatchedAsymp'*) COVID-19 symptoms, respectively. We further constructed another dataset, namely "combined", to test the capability of our approach on distinguishing between COVID-19 and coughs from other diseases. We combined 381 COVID-19 positive coughs from the Russian dataset (confirmed by both verbally and PCR-testing) and 40 cough audios from other audio dataset [23] (cough audios of patients of dry cough, wet cough, croup, pertussis and bronchitis). The COVID-19 coughs were assigned with positive labels and the other coughs are assigned with negative.

C. Performance evaluation

To compare among different models, we compared our *CovidEnvelope* approach with the state of art models [18], [20]. For COVID-19 cough detection, we used Russian dataset, including different conditions of "Verbal", "Verified", "Matched", "MatchedAsymp" and "MatchedSymp". To detect COVID cough from coughs resulted from other respiratory tract diseases, we evaluated our approach on our combined dataset. Results are reported based on 10 fold cross validation.

Table I
DATA SPECIFICATIONS WITH THE NUMBER OF RECORDS IN PARENTHESES

COVID-19 cough records **(1322)**	Verbal Positives **(681)**	Verified Positives **(381)**	Asymptomatic **(180)**
			Symptomatic **(201)**
		Verified Negatives **(300)**	
	Verbal Negatives **(641)**	Verified Negatives **(438)**	
		Unverified **(203)**	

We use sensitivity, specificity, accuracy, kappa coefficient, areas under ROC curve (AUC), and time to measure the performances of our approach. They measure the proportion of each class / whole samples been predicted as ground truth labels, inter-rater reliability and the classifier ability on distinguishing classes. We executed and tested our *CovidEnvelope* approach performance on Intel(R) Xeon(R) CPU @ 2.30GHz, 12 GB of RAM machine, with python3.7.

III. RESULTS AND DISCUSSION

Selecting threshold values play a vital role before computing the overall performance. We considered the *Matched* cough audios from the Russian dataset and computed various evaluation matrices against three thresholds for determining optimised threshold values as shown in Figure 3. For threshold 4,000, sensitivity (0.99) was found highest but other matrices were found lowest compared to other two cases. For threshold 2,000, specificity (0.96) was found highest but other matrices were found lowest compared to threshold 3,000. On the other-hand, for threshold 3,000, accuracy, Cohen's kappa coefficient (k), and area under ROC curve (AUC) were found highest compared to other two thresholds, which are 0.94, 0.88, and 0.94 respectively. Sensitivity (0.97) and specificity (0.92) are also found reasonable for threshold 3,000. It is worthwhile to note that the accuracy and AUC of the *CovidEnvelope* approach were calculated from the sensitivity and specificity. Thus, we selected threshold 3,000 for further analyses.

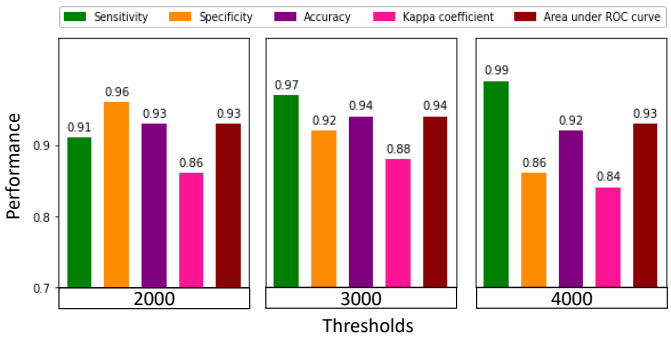

Figure 3. Determination of the optimum threshold value.

To compare data processing and inference times across different models, we used verified and matched contidions of Russian dataset in our CovidEnvelope approach and two other state of art methods [18], [20]. Our approach is significantly faster in data preprocessing and inference time which is shown in Figure 4. The explanation of the lags of the later two models

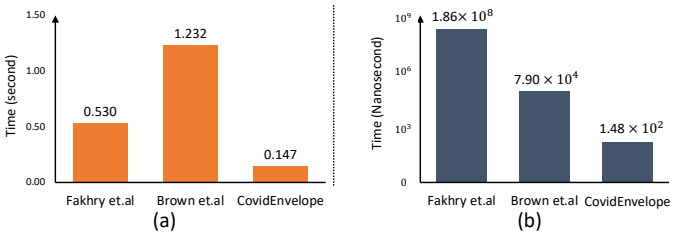

Figure 4. Comparison of **(a)** data preprocessing time and **(b)** inference time.

is their sophisticated ML algorithms. Both of the models utilise numerous parameters, which made their model costly for deployment, portability and hinders to develop standalone mobile softwares. On the contrary, we have reduced the model complexity in our approach by retaining a reasonable prediction accuracy. Our approach can be extended as a reliable and portable application for any smartphones (even with poor computation resource) for screening COVID-19 within short time.

Table II
PERFORMANCE EVALUATION OF THE DESIGNED ALGORITHM WITH DIFFERENT CONDITIONS.

Conditions	**N [a, b]**[1]	**Sensitivity**	**Specificity**	**Accuracy**	**kappa coefficient**	**Area under ROC curve**	**Execution time (min)**
Verbal	1322 [681, 641]	0.00	1.00	0.48	0.00	0.50	3.9
Verified	1119 [381, 738]	0.90	0.82	0.84	0.68	0.86	3.3
Matched	819 [381, 438]	0.96	0.92	0.94	0.88	0.94	2.4
MatchedAsymp	618 [180, 438]	0.90	0.96	0.94	0.86	0.93	1.8
MatchedSymp	639 [201, 438]	0.93	0.93	0.93	0.84	0.93	1.9

[1]Number of records where a and b represent COVID-19 positive and negative records

Table II shows the overall performance of our approach on Russian dataset. We analysed five conditions as explained in Table II, namely *'Verbal'*, *'Verified'*, *'Matched'*, *'MatchedAsymp'*, and *'MatchedSymp'*. The lowest performance (Accuracy = 0.48, AUC = 0.50) was found for *'Verbal'* condition where the dataset consisted of verbal confirmation - verified or unverified with PCR tests. Verbal confirmations are not often correct, prone to miscommunications or fraudulence among participants, and it could be a reason for the lowest performance. The null sensitivity and kappa coefficient further validate the above statement. When *'Verified'* condition was considered for the dataset, our approach performed better (Accuracy = 0.84, AUC = 0.86) than the previous *'Verbal'*

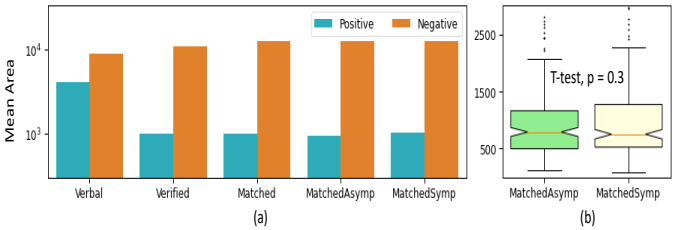

Figure 5. Mean areas **(a)** captured by CovidEnvelope Approach (log-transformed y-axis) and **(b)** for COVID-19 positive cases (Asymptomatic vs Symptomatic).

condition. *Verified* records are the reliable records, where COVID-19 positive or negative cases were confirmed by laboratory PCR-tests. Performance was improved further, when the verbal confirmation was matched with the verified condition (*'Matched'* condition). Sensitivity, specificity, accuracy, kappa coefficient and AUC were observed 0.96, 0.92, 0.94, 0.88 and 0.94, respectively for the *'Matched'* condition. For matched asymptomatic (i.e. *'MatchedAsymp'*) and matched symptomatic (*'MatchedSymp'*) conditions, the *CovidEnvelope* approach reaches up to accuracies of 0.94 and 0.93 respectively, which is very similar to the *'Matched'* condition. Our approach takes only 1.8 to 3.9 minutes for diagnosing COVID-19 cases depending on an applied condition.

A t-test was performed on computed resultant mean areas for measuring significance tests considering each conditions separately. The computed mean areas are illustrated in Figure 5 (a). For *'Verbal'* condition, mean areas of COVID-19 positive cases were found significantly different ($p<0.001$) than COVID-19 negative cases. For other conditions (*'Verified'*, *'Matched'*, *'MatchedAsymp'*, and *'MatchedSymp'*), mean areas of COVID-19 positive cases were found highly significantly different ($p<0.001$) than COVID-19 negative cases. The results indicate that *'Verbal'* confirmation is less reliable than verified and matched conditions for designing an efficient and automatic COVID-19 diagnosis tool.

In addition, the mean areas of asymptomatic COVID-19 positive and symptomatic COVID-19 positive cases are illustrated in Figure 5 (b) and the mean areas of these cases were not statistically significantly different ($p = 0.3$). The results alternatively indicate that the performance of our approach is independent of the symptoms of COVID-19.

Moreover, CovidEnvelope has 0.91 accuracy on our combined dataset. We are bias on high sensitivity instead of specificity as Covid disease is more fatal than other respiratory diseases. Our approach has 0.99 sensitivity and can distinguish positive COVID-19 coughs from other diseases, which could assist in managing limited resource during the pandemic.

The main challenge of this study was to identify trustworthy and reliable dataset, which is available online. There are several publicly available datasets [13], [18], which were verbally confirmed, but can introduce false-positives and false-negatives in our approach, we have seen anomaly in verified and unverified dataset from present study. Till date, MIT Open Voice dataset is the largest COVID-19 cough audio dataset, comprising 5,320 subjects, resulted in highest sensitivity and specificity of 0.98 and 0.94 respectively, but unavailability and confidentiality of such type of dataset hinders us to utilise it in our present approach [19]. Using similar datasets to validate our approach will enhance both sensitivity and specificity of present study.

Further, our study has shown a compact machine learning approach, which only needs raw audio signals, do not need to extract any features, and can be recorded easily using available devices like cell phones. Unlike existing approaches, it is computationally inexpensive and requires only less than 4 minutes to screen the whole COVID-19 cough audio signal. Our approach can distinguish COVID-19 positive coughs from COVID-19 negative cough, regardless the patients show symptoms or not. While current approach is similar with a linear classifier, the future direction of this study can be to develop more complex model, incorporating data with annotations for covid severity.

The *CovidEnvelope* approach can also be utilised to study other respiratory tract diseases in human, such as tuberculosis, asthma, pneumonia etc. As an extension of current study and potential application in public health sector, real-time low-cost software is possible to design in near future. Such a sophisticated, end-to-end encrypted application will need considerable amount of verified COVID-19 records to validate our approach. While benchmarking our model with Russian dataset, in future we will explore this *CovidEnvelope* approach with other avenues including international, national, and regional bodies.

IV. Conclusion

We developed a fast, low-cost, and reliable COVID-19 cough detection approach, which can diagnose COVID-19 with the highest sensitivity, specificity, accuracy and AUC of 0.96, 0.92, 0.94, and 0.94, respectively. COVID-19 positive and negative coughs are significantly different in terms of area enclosed by envelope and highly effective regardless of symptomatic or asymptomatic COVID-19 patients. Further, verbal confirmation is not a reliable source of information. Our approach is fast, capable of processing cough audios in a limited time and can be implement as diagnosis tool to detect the COVID-19 coughs. Our approach achieved an accuracy of 0.91 to distinguish COVID-19 cough from other coughs, resulted from respiratory diseases. Our future work will focus on collecting more reliable datasets by collaborating with relevant authorities, and developing a model with high accuracy and low computation cost and a reliable, standalone mobile application for screening COVID-19 within short duration of time while at home or outside. In addition to Covid diagnosis, our model can serve in insect-pests surveillance [24] and human mental health monitoring [25].

Acknowledgment

The authors would like to thank *Medina Medical Group* to make the dataset available for research community, and

Shlomo Berkovsky from Macquarie University for introducing to the dataset.

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