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Original Article

A Fully-Automated Method to Evaluate Coronavirus Disease Progression with COVID-19 Cough Sounds Using Minimal Phase Information

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Abstract—This paper focuses on an important issue of disease progression of COVID-19 (coronavirus disease 2019) through processing COVID-19 cough sounds by proposing a fully-automated method. The new method is based on time-domain exploiting only phase 1 data which is always available for any cough events. The proposed approach generates plausible click sequences consist of clicks for various cough samples from covid-19 patients. The click sequence, which is extracted from the phase slope function of an input signal, is used to calculate inter-click intervals (ICIs), and thereby a scoring index (SI) is derived based on coefficient of variation(CV) of the extracted ICIs. Moreover, probability density function (pdf) of the output click sequence is obtained. The method does not need to adjust any parameters. The experimental results achieved from real-recorded COVID-19 cough data using the medically annotated Novel Coronavirus Cough Database (NoCoCoDa) reveal that the proposed time-domain method can be a very useful tool for automatic cough sound processing to determine the disease progression of coronavirus patients.

Keywords—COVID-19, Coronavirus disease progression, Cough sounds/samples, Click sequence, Inter-click intervals, Automatic cough sound processing, NoCoCoDa database.

INTRODUCTION

The 2019 novel coronavirus, COVID-19 is one of the challenging global health crisis in this twenty-first century.[14] The virus is a strain of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2),[9] which affects the respiratory system and therefore causes symptoms such as coughing and breathing difficulties, fever, as well as ageusia and anosmia.[16] The cough is the second most common symptom for COVID-19 patients after the fever symptom.[1] During the investigation, it is found that the COVID-19 cough is initially dry or non-productive, similar to a cough which causes a tickle in our throat, but in more severe cases it can become more wet or productive, such as the type of cough one can get in case of cold or flu.[7]

On the acoustic viewpoint, cough can be described as a forced expulsive maneuver against a closed glottis that is associated with a characteristic sound.[17] Cough sounds can comprise up to three phases: explosive, intermediate and voiced (phases 1, 2 and 3, respectively).[19] They correspond to glottal opening, steady-state flow and interruption of airflow due to closure of the glottis, respectively. Phase 3 is not always present and in its absence the identification of the termination of phase 2 becomes difficult due to the gradual signal dissipation. Therefore, phase 1 (explosive phase) can be selected for primary analysis since it is always present and is most easily identifiable.

Various research efforts are going on to develop acoustic analysis and diagnostic tools for COVID-19 cough data and they are mainly based on frequency domain as well as machine learning and deep learning. In Ref. 8, the input recorded cough sounds possibly from smart phones/home devices are processed to classify them into binary classes to know whether they are COVID-19 or not by using MFCC images and CNNs (convolutional neural networks) and achieved high classification accuracy (97.5%). In Ref. 6, a COVID-19 cough type detection method is proposed based on frequency-domain features including power ratio between phases 1 & 2 and number of spectral peaks in the energy spectrum using NoCoCoDa database.[6] It is found in Ref. 6 that 77% of the recorded COVID-19 coughs are detected as more wet

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(productive) in nature, whereas the rest of the COVID-19 coughs are detected as more dry (non-productive) in nature. The work in Ref. 20 proposes a low-cost COVID-19 preliminary diagnosis approach utilizing covid cough data using deep learning in Mel frequency domain. Log-based Melspectrograms as well as filter banks are used to extract information for classification of four types of raw cough sounds including COVID, Pertussis, Pneumonia, and others by using deep learning LSTM (Long Short-Term Memory) multi-class classifier providing classification accuracies of 100%, 93.75%, 93.75% and 100%, respectively. Reference 11, proposes an AI-based preliminary diagnosis tool for COVID-19 (AI4COVID-19), using cough sound *via* a mobile app. This two-stage scheme has data collection and cough detection block followed by COVID-19 diagnosis block, which contains deep transfer learning-based multi-class classifier (DTL-MC), classical machine learning based multi-class classifier (CML-MC), and deep transfer learning-based binary-class classifier (DTL-BC). The cough detection is based on a deep CNNs classifier using MFCC (Mel Frequency Cepstral Coefficients) features. The results show that AI4COVID-19 app is able to diagnose COVID-19 with negligible misdiagnosis probability; for instance, the accuracies for the DTL-BC classifier as reported in Ref. 11, are 94.57% and 91.14% for binary classes, i.e. COVID-19 and No COVID-19. In Ref. 13 the proposed AI-based framework uses acoustics to pre-screen for COVID-19 from cough recordings. MFCC features are calculated from the recorded cough sounds and use as input to a Convolutional Neural Network(CNN) based scheme consist of one Poisson biomarker layer and 3 pre-trained ResNet50's in parallel, giving a binary pre-screening output of COVID-19 or No COVID-19. The detection results with high accuracy are obtained since the AI-model accurately identified 98.5% of coughs from people with confirmed COVID-19, and 100% of coughs from asymptomatic people who tested positive for the virus.

Moreover, the COVID-19 crisis initiates different new studies addressing various important issues. For instance, in Ref. 15, the study proposes a new design for a device called the patient particle containment chamber (PPCC) for COVID-19 airways management, together with a pragmatic evaluation of its efficiency. The following critical design criteria for the PPCC device are considered: reduction of aerosol transmission by at least 90% as measured by pragmatic testing; construction from readily available, inexpensive materials; easy to clean; and compatibility with common EMS stretcher. Thereby, the new device removes all limitations which make it effective and practical in out-of-hospital environments. The study in Ref. 4 introduces a computational model of pulmonary airway opening for acute COVID-19 patients and then investigates the effects of physical properties of lower airway secretions on airway reopening pressures and suction pressures. The experimental results show that the airway reopening pressure is dependent on surface tension of the air–liquid interface, consistency and yield stress of secretions, the volume of secretions, airway radius as well as airway opening velocity. On the other hand, the suction pressure varies with the surface tension of air–liquid interface and the viscosity of secretion. In Ref. 2, the authors, the two faculty members from one of the U.S. universities, examine the impact of coronavirus on higher education, or on education in general and talk of how social distancing brought the faculty members and others closer together as a disciplinary community through transitioning to online delivery during the COVID-19 outbreak. As a result of the challenges introduced due to the COVID-19 pandemic, a number of institutions within the Biomedical Engineering (BME) community compile an online repository to share knowledge and guidance to implement online learning curricula, as reported and recommended by the authors in Ref. 2 providing the perspectives of further new collaborations within and outside the BME community. In our study, we address the important issue of COVID-19 disease progression. To identify/quantify the disease progression is vital since it can assist in target treatment and resource allocation for the COVID-19 patients at different stages. For instance, the health care teams can find it an essential tool to assess the severity of each case so that outpatients/inpatients requiring oxygen/ICU patients treatments are provided as well as resources such as ICU beds and ventilators are correctly allocated and care priorities can be established for the high-risk patients based on the results of the disease progression.

In this paper, we report on the exploration of an automated time-domain method for cough sounds to evaluate the disease progression of COVID-19 patients. The proposed method is based on the time-domain and extraction of click sequence for phase 1 data in a cough sample utilizing phase slope function. Inter-click intervals (ICIs) are thereby obtained to derive a scoring index (SI) in terms of their coefficient of variation (CV). In addition, probability density function (pdf) of the output click sequence is found to quantify and qualify the COVID-19 cough data in order to determine the progress of the disease in COVID-19 patients.

The main contributions of this paper can be stated as follows: (1) The paper is addressing the challenging COVID-19 related problem. (2) We propose a new time-domain method for monitoring the progress of

COVID-19 disease with coronavirus patient's cough sounds using phase information. (3) Both the inter-click intervals (ICIs) and the distribution of the clicks for an output click sequence are exploited. (4) The method solely uses the information of phase 1 data, which is always available in any cough event and is easy to annotate being an initial phase. (5) There is no preprocessing involved for the raw input data. (6) The method is capable to process cough samples from various completing sources and is fully automated, since there is no need to adjust any parameters, as well as insensitive to the intensity of the input signal.

MATERIALS AND METHODS

The proposed scheme is based on extraction of a click sequence followed by retrieving ICIs (inter-click intervals) of the clicks. The phase 1 data of a COVID-19 cough sample is used as input to a click detector based on phase slope function. The extracted output click sequence is then analyzed to characterize the raw cough data in terms of an scoring index(SI) derived from ICIs. The probability density function (pdf) of the extracted click sequence is further obtained to evaluate (quantify and qualify) the disease progression of COVID-19.

Database Used

We have used the Novel Coronavirus Cough Database (NoCoCoDa),[6] which is one of the first available databases of COVID-19 cough sounds and medically annotated with time stamps unlike other available COVID-19 cough sounds databases, which are not annotated. The NoCoCoDa database currently contains 73 individual COVID-19 positive reflex cough sounds obtained from online interviews with COVID-19 positive individuals conducted from April to June 2020. As mentioned in Ref. 6, a total of 13 interviews have been conducted involving 10 individuals. For each interview, cough events have been manually segmented to assign a label (C19_subjectNumber_coughNumber). Each file are then saved as a WAV file with a sampling rate of 44.1 kHz. This resulted in 73 individual cough events. Since these cough events are extracted from media interviews, some of them contain speech or music as background noise. In addition, several cough events are found as a mix between a throat clear and a cough event, which are labeled in the supplementary file 'coughDescriptions.txt' that has nine columns (Name; Duration (s); Number of Phases; Phase Notes; Competing Sources; Sex; Age; Live vs. Home; Notes (including any self reported underlying conditions)), please see section IV in Ref. 6 for more details. For a more detail description of the database used, see the cited paper.

Proposed Scheme for Cough Sound Processing

The proposed automated cough sound processing scheme consists of the following click extraction with adaptive window-length selection.

Click Extraction

The clicks are extracted from the audio data (wav files) as positive zero-crossings of the phase slope function.[12] The phase slope function is generated from group delay, given by

$$\tau(\omega) = -\frac{d(\phi(\omega))}{d(\omega)} \tag{1}$$

where $\omega = 2\pi f$, f denotes the frequency and $\phi(\omega)$ refers the phase spectrum of the signal. Suppose a signal is delayed by n_o samples. Then the average over ω of $\tau(\omega)$ provides n_0, which corresponds to the negative of the slope of the phase spectrum for this corresponding signal. Here Fourier Transform has been computed considering the center of analysis window to be at $n = 0$. When the window center is moved to the right (closer to the instant $n = n_0$), the slope of the phase spectrum increases (the average of the group delay function decreases) reflecting the distance between the center of the analysis window and the position of the impulse. When the center of the analysis window is at $n = n_0$ then the slope is zero. Continuing moving the analysis window to the right the slope will continue to increase (while the average of the group delay will decrease). In this way, the slope of the phase spectrum is a function of n.

The steps for computing phase slope function as well as extracting clicks are as follows:

Step 1 Define an analysis window of length proportional to the period of the sequence (it can be referred to as long window), to perform a frame-by frame (short-term) analysis.

Step 2 In each frame, the slope of the phase spectrum of the windowed signal is calculated as the average of the group delay function and it is associated with the center of analysis window.

Step 3 By setting the analysis step size at one sample (moving the analysis window by one sample at a time), the phase slope function (sequence) is obtained which has the same time resolution as the original recording. The window length may have a duration shorter than the period of the signal (it can be

referred to as short window). Frame (step) size defines the resolution capability of the algorithm.

Step 4 Finally, clicks are detected by locating the positive zero crossings of the slope of the phase spectrum (referred to as phase slope function) computed as average of the group delay function. This makes the click extraction process insensitive to the variations of the sound source level.

To find the group delay of a signal or the average slope of the phase spectrum, we need to calculate the unwrapped phase spectrum. Usually phase unwrapping is performed by adding appropriate integer multiples of 2π to the principal phase values, as to remove discontinuity (jumps of 2π radians) in the phase function. For all simulations, a Hann analysis window with duration (length) determined by a pitch detection method described in "Pitch Detection and Window Length Selection," section is applied. To speed up the computation of the phase slope function, a step size of 2 samples is used. Undetermined values of the slope function are then computed by linear interpolation.

It is found that the method is capable of detecting clicks in raw data. The approach is insensitive to the intensity of the click source. By visual inspection, it is found that positive zero-crossings of the phase slope function correspond to clicks in most cases, whereas few erroneous clicks may appear from the occasional oscillations about zero of the phase slope function. As most of these erroneous clicks can be eliminated by subtracting a constant (dc component) from the phase slope function.

Pitch Detection and Window Length Selection

A time-domain algorithm, named as YIN algorithm,[5] is used to find pitch, i.e. the fundamental frequency (f_0), for the input cough data. YIN algorithm is based on the difference function, which while similar to autocorrelation, attempts to minimize the difference between the waveform and its delayed duplicate instead of maximizing the product (for autocorrelation). The difference function is given as

$$d_t(\tau) = \sum_{j=1}^{W} \left(x_j - x_{j+\tau}\right)^2 \tag{2}$$

where W is the length of the frame x_j since the algorithm is based on frame-by-frame calculation. In order to reduce the occurrence of subharmonic errors, YIN algorithm employs a cumulative mean function which de-emphasizes higher-period dips in the difference function:

$$d'_t(\tau) = \begin{cases} 1, & \tau = 0 \\ \dfrac{d_t(\tau)}{\frac{1}{\tau}\sum_{j=1}^{\tau} d_t(j)} & \text{otherwise} \end{cases} \tag{3}$$

Other improvement in the YIN pitch detection scheme include a parabolic interpolation of the local minima, which has the effect of reducing the errors when the period estimation is not a factor of the window length used (in this case, 25 ms). For a more detail description, see the cited paper. Lastly, the analysis window length (in s) for the phase slope function calculation in "Click Extraction," section is automatically set from the value of the detected pitch/estimated f_0 (Hz) as equal to or less than the pitch duration, $1/f_0$.

RESULTS AND DISCUSSION

We derive a scoring index(SI) based on inter-click interval (ICI) of the extracted click sequence for an input cough data. Similar to ISI (Inter-spike interval),[18] the variation in the ICI pattern can be quantified by using the coefficient of variation (CV), which is the standard deviation (SD) of ICIs divided by the mean of ICIs, given as

$$\mathrm{CV} = \frac{s}{\mu} \tag{4}$$

where s and μ are the SD and mean of ICIs. Small CV values close to 0 indicate regular clicks pattern, whereas large CV values close to or >1 indicate irregular clicks pattern of a click sequence.

The illustrative plots of some COVID-19 cough samples having different SI values, are shown in Fig. 1. The input raw cough data are presented in Fig. 1a, whereas the corresponding spectrograms of the 44.1 kHz data, are depicted in Fig. 1b which are calculated using a Hamming window of 256 samples (5.805 ms) with 86.3281% overlapping and 512-point FFT (frequency resolution 86.1328 Hz). Only phase 1 data of each cough samples are used as their time stamps are marked by vertical dotted lines in Fig. 1a, where the samples with data indices #63, #57, #45 #4 have 3 phases and the sample with data index #72 has 2 phases giving increasing SI (CV) values of 0.18029, 0.53246, 1.0045, 1.2581, 1.9423, respectively. By visual inspection of the spectrograms and their energy distributions at high frequencies in phase 1 and phase 2, it seems that the first two samples with lower SI values, are appeared more like dry cough, while the next three samples with higher SI values look more like wet cough.[3]

The phase 1 data for the cough samples in Fig. 1a are shown in Figs. 2a and 2e. The corresponding phase slope functions and the unit responses of the clicks

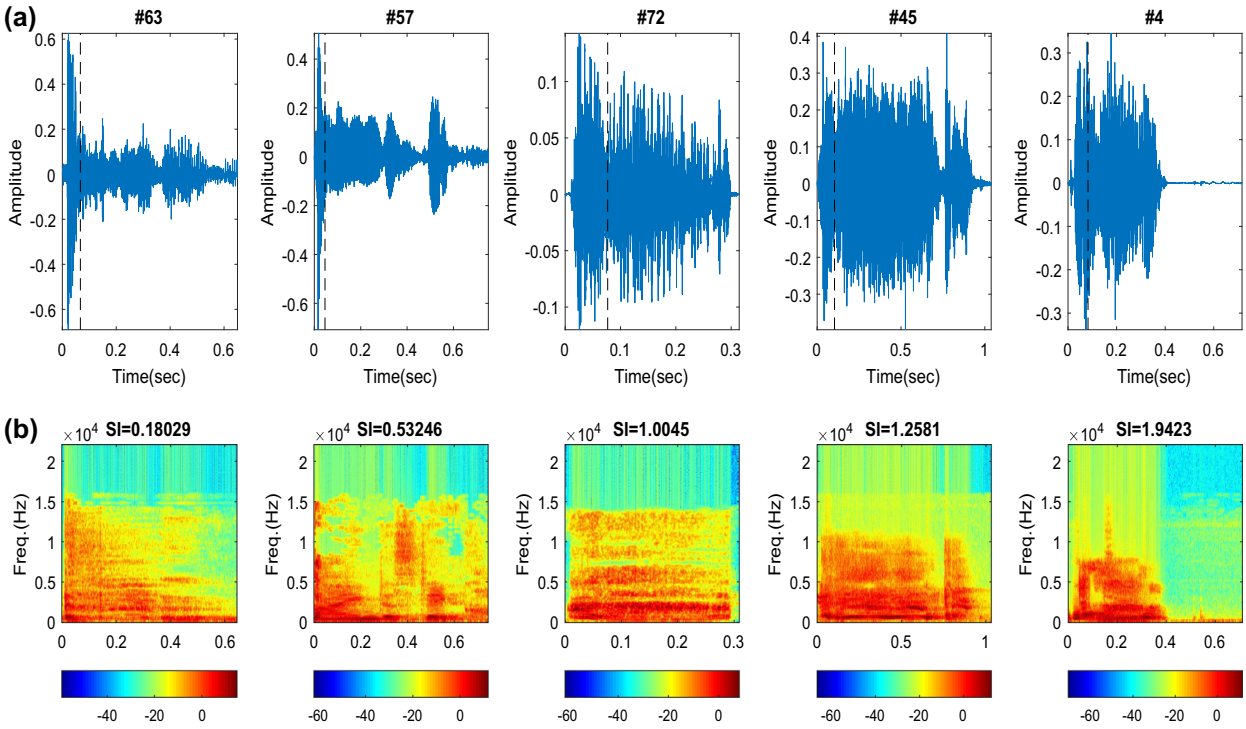

FIGURE 1. Illustrative plots are displayed for the COVID-19 cough samples having different values of SI within various SI intervals; (a) Raw COVID-19 cough data, (b) Spectrograms.

detected as positive zero-crossings of the phase slope function, are presented in Figs. 2b, 2f, 2c and 2g, respectively. The extracted output click sequences are displayed in Figs. 2d and 2h. As we can see, the click responses and click outputs are found rare for the first two samples and irregular (random/clumped) for the last three samples.

The probability density functions (pdfs) of the extracted output click sequences in Figs. 2d and 2h, are depicted in Fig. 3. The skewness of the respective pdfs are obtained as increasing values of 0.1523, 0.8037, 1.1772, 2.7373, and 4.3170, respectively. The more detailed analysis on the types of pdfs and their features will be followed in "Probability Density Function (pdf) of the Extracted Click Sequence," section.

In Table 1, both the SI and the skewness values are listed for all COVID-19 cough samples from the NoCoCoDa database together with the corresponding data indices and file names. It can be noted that the cough samples with indices #18 and #66 are not included in the list since their annotations are not available because they are overpowered by other sounds(speech/music). As we see in Table 1, the values of both parameters of CV and skewness show consistent results.

In Fig. 4, the scatter plot of the SI and skewness data is presented. All data points, listed in Table 1, are clustered into three groups shown by red, green, and blue colors. The group of data points having SI values within $0.9 \leq SI \leq 1.1$ interval as labeled in green, are highly dense around $SI = 1$. Next the data points with $SI < 0.9$ as labeled in blue, are grouped based on their moderate density. The third group containing the data points having $SI > 1.1$ which are marked in red, are highly sparse.

Table 2 shows the disease progression of COVID-19 as evaluated in three COVID-19 states: early state, moderate state, and severe state, based on the SI values and their intervals. In Table 3, the progress of COVID-19 disease is determined as early state, moderate state, and severe state with respect to their obtained probability density functions (pdfs).

It can be noted that the covid cough samples in the early COVID-19 state are more like dry coughs, whereas it is uncertain for the moderate COVID-19 state as it can be either more like dry cough or more like wet cough. For the severe COVID-19 state, the covid cough samples are more like wet coughs.

Figure 5 shows the stem plots of SI correspond to different COVID-19 states. As it can be seen in Fig. 5,

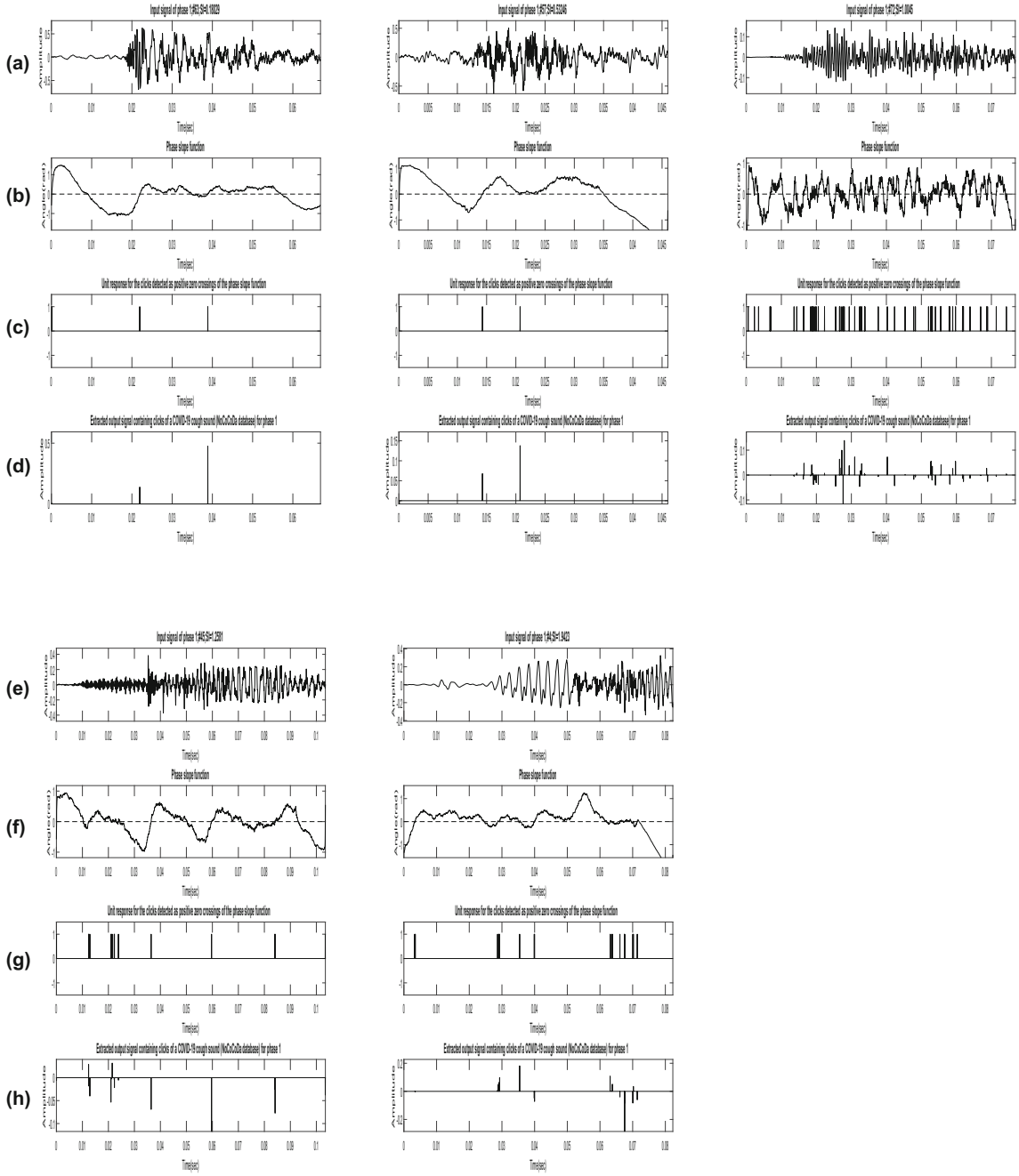

FIGURE 2. Illustrative results are shown for the phase 1 data of the COVID-19 cough samples, in Fig. 1a, at different SI values within various SI intervals; (a) and (e) Input raw cough data for phase 1, (b) and (f) Phase slope functions, (c) and (g) Unit responses of the clicks detected as positive zero-crossings of the phase slope functions, (d) and (h) Extracted output click sequences.

majority of the coughs are evaluated being more like wet (productive) coughs since there are some cough samples in the database as reported in Ref. 6, which have been recoded for serious covid patients who were admitted to hospital and/or to ICU. On the other hand, there are a small number of COVID-19 coughs which have been evaluated being more like dry (non-productive) coughs belong to early COVID-19 state (see Fig. 5a).

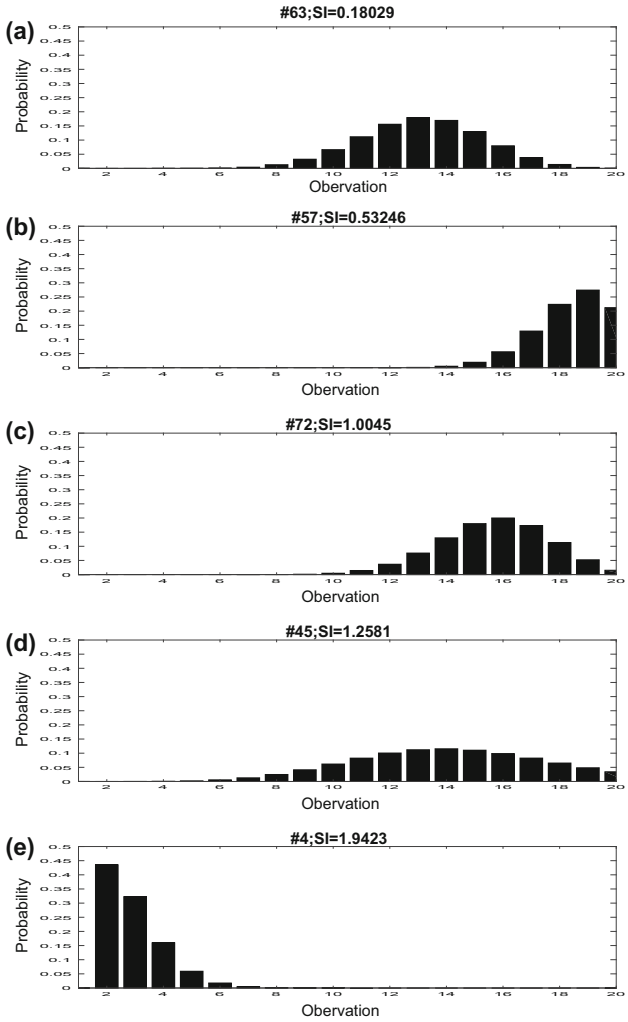

FIGURE 3. Illustrative probability density functions (pdfs) are depicted for the extracted click sequences in Figs. 2d and 2h of the COVID-19 cough samples for phase 1 data at different values of SI and its various intervals.

Discussion

Probability Density Function (pdf) of the Extracted Click Sequence

Regarding pdf of the extracted click sequence, we have considered the following three cases with the value of CV:

Case 1 When CV1 (or the standard deviation (SD) and the mean of ICIs are proportional and close to 1), then pdf of the corresponding extracted click sequence can be obtained as Poisson distribution.[10] The Poisson distribution can be expressed as $P(r) = \frac{e^{-m}m^r}{r!}$, where P is the fraction of samples that will occur r objects each, if an average of m objects per sample, i.e. the mean, is distributed at random over the collection of samples.

TABLE 1. The values of the scoring index (SI) (CV) and the skewness for the COVID-19 cough samples in the NoCoCoDa database.

Data Index(#)	File Name	SI(CV)	Skewness
1	C19-1-1.wav	0.9156	1.4026
2	C19-1-2.wav	1.4800	2.7777
3	C19-10-1.wav	1.2618	1.8015
4	C19-10-2.wav	1.9423	4.3170
5	C19-10-3.wav	0.9352	1.0516
6	C19-10-4.wav	1.1867	1.4436
7	C19-10-5.wav	1.7451	3.5572
8	C19-10-6.wav	1.1508	1.4416
9	C19-10-7.wav	1.4113	2.5521
10	C19-11-1.wav	1.0373	1.0010
11	C19-11-2.wav	1.1576	1.6584
12	C19-11-3.wav	1.1063	1.1321
13	C19-11-4.wav	0.7439	0.5667
14	C19-11-5.wav	0.9097	1.039
15	C19-11-6.wav	1.3989	2.5975
16	C19-12-1.wav	1.6169	2.7261
17	C19-12-10.wav	1.3737	1.7154
19	C19-12-13.wav	1.0282	1.2681
20	C19-12-14.wav	1.8604	3.8696
21	C19-12-15.wav	0.9471	0.9596
22	C19-12-2.wav	1.5539	3.9391
23	C19-12-3.wav	1.5179	2.9003
24	C19-12-4.wav	0.8122	0.7458
25	C19-12-5.wav	1.4669	2.4775
26	C19-12-6.wav	1.5417	2.7038
27	C19-12-7.wav	1.3655	2.6757
28	C19-12-8.wav	0.8111	1.0178
29	C19-13-1.wav	0.6293	1.0001
30	C19-13-2.wav	1.8185	3.2932
31	C19-13-3.wav	1.5232	2.2186
32	C19-2-1.wav	1.1343	1.1512
33	C19-2-10.wav	0.8391	1.0529
34	C19-2-11.wav	0.7251	1.1443
35	C19-2-12.wav	0.8195	1.0315
36	C19-2-13.wav	0.6375	1.1763
37	C19-2-14.wav	1.6993	3.7338
38	C19-2-15.wav	0.7622	3.2510
39	C19-2-2.wav	1.0085	1.0448
40	C19-2-3.wav	0.8884	1.1055
41	C19-2-4.wav	0.8363	1.0015
42	C19-2-5.wav	0.8932	1.6479
43	C19-2-6.wav	1.4446	2.6813
44	C19-2-7.wav	1.2187	2.2672
45	C19-2-8.wav	1.2581	2.7373
46	C19-2-9.wav	0.7753	1.6373
47	C19-3-1.wav	1.1246	1.7878
48	C19-3-10.wav	1.0405	1.0312
49	C19-3-11.wav	1.1897	1.7107
50	C19-3-12.wav	1.7592	2.6289
51	C19-3-13.wav	1.1415	1.7842
52	C19-3-14.wav	1.0435	1.0077
53	C19-3-2.wav	0.7717	0.5431
54	C19-3-3.wav	0.9668	1.0013
55	C19-3-4.wav	1.0370	1.0513
56	C19-3-6.wav	0.6610	0.7824
57	C19-3-7.wav	0.5325	0.8037
58	C19-3-8.wav	1.7518	3.0434
59	C19-3-9.wav	1.5390	2.8821
60	C19-4-1.wav	1.4482	2.2545

TABLE 1. continued

Data Index(#)	File Name	SI(CV)	Skewness
61	C19-4-2.wav	1.0809	1.0590
62	C19-4-3.wav	1.0197	2.2464
63	C19-5-1.wav	0.1803	0.1523
64	C19-5-2.wav	1.5131	2.5784
65	C19-6-1.wav	1.4649	2.3792
67	C19-7-2.wav	1.5070	2.1680
68	C19-7-3.wav	0.6868	0.5983
69	C19-7-4.wav	1.2210	2.2044
70	C19-7-5.wav	1.7782	3.8578
71	C19-8-1.wav	0.9406	1.9247
72	C19-8-2.wav	1.0045	1.1772
73	C19-9-1.wav	1.5114	2.5569

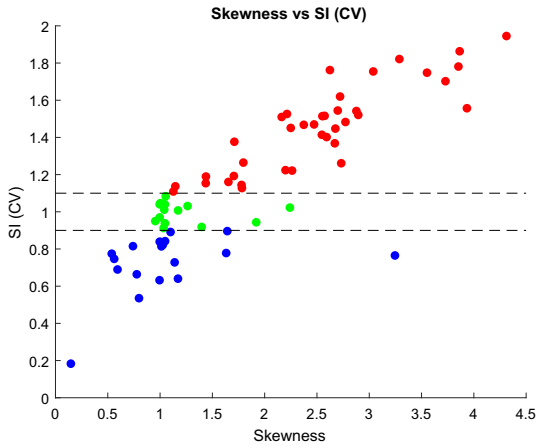

FIGURE 4. Scatter plot of SI vs skewness for the COVID-19 cough samples showing the disease progression of COVID-19 by grouping the respective cough data into three COVID-19 states as early state (blue), moderate state (green), severe state (red).

TABLE 2. Coronavirus disease progression with the COVID-19 cough samples based on SI values and their intervals.

Covid-19 progression state	Scoring Index (SI) (CV)
Early COVID-19 state	$0 < SI < 0.9$
Moderate COVID-19 state	$0.9 \leq SI \leq 1.1$
Severe COVID-19 state	$SI > 1.1$

TABLE 3. Coronavirus disease progression with the COVID-19 cough samples based on pdfs of the extracted output click sequences.

Covid-19 progression state	Probability density function (pdf)
Early COVID-19 state	Binomial distribution
Moderate COVID-19 state	Poisson distribution
Severe COVID-19 state	Negative binomial distribution

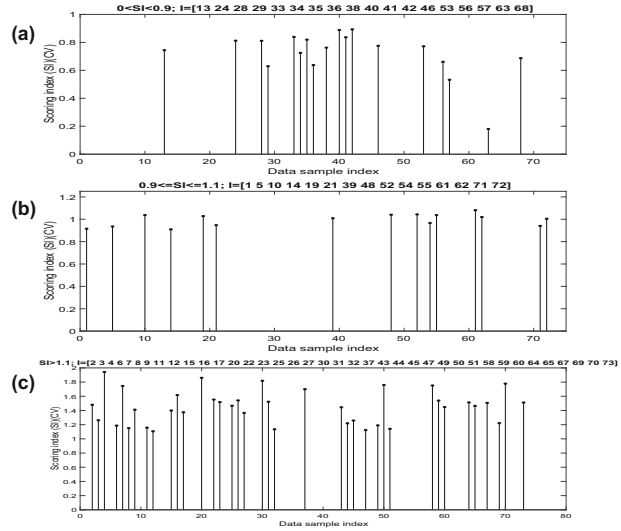

FIGURE 5. The values of scoring index (SI) (CV) are shown using the COVID-19 cough samples for different intervals of SI corresponding to different COVID-19 states; (a) 0<SI<0.9, (b) 0.9≤SI≤1.1, and (c) SI > 1.1.

Case 2 When CV $<$ 1, i.e. the SD decreases and less than the mean, the pdf of the corresponding output click sequence can have the Binomial distribution, expressed as $P(r) = (\frac{n!}{r!(n-r)!})p^r q^{(n-r)}$, where P is the fraction of samples that will occur r objects each, for the probability of success of p, the probability of failure of q and the number of samples of n when the mean is given by $m = np$ and SD $= \sqrt{npq}$.[10] The limiting value of the SD, as the Binomial distribution approaches the Poisson distribution, is the square root of the mean.

Case 3 When CV $>$ 1, i.e. the SD increases and higher than the mean, the pdf of the output click sequence can be found as Negative Binomial distribution $P(r) = (\frac{(r+k-1)!}{r!(k-1)!})p^k q^r$, with the mean $m = kq/p$ and SD $= \sqrt{m + m^2/k}$.[21] The expression $1/\sqrt{k}$ is a measure of the excess SD. As $1/\sqrt{k}$ approaches zero, the distribution converges to the Poisson. As $1/\sqrt{k}$ approaches infinity, the distribution approaches the logarithmic. The Negative Binomial distribution has a more important use for an overdispersed distribution, one with clumps of objects rather than a random distribution.

In Fig. 3, the results of pdfs are shown for the output click sequences in Figs. 2d and 2h which have different ICIs patterns (rare/random/clumped) providing Binomial distribution (SD $< m$) (rare or regular), Poisson distribution (SD m) (random), and Negative Binomial distribution (SD $> m$) (clumped/grouped), respectively.

Finally, we calculate the skewness of the distributions[22] as listed in Table 1.

Comparison with Another Method Using the Same Database

The results with the COVID-19 cough samples regarding their types (more like dry/wet cough) are found quite consistent with the results obtained in Ref. 6 using the same NoCoCoDa database. As reported in Ref. 6, 77% of the COVID-19 coughs in the database are found as wet (productive) type cough and 23% of the data samples are more like dry (non-productive) cough. We found 25.35%(i.e. (18/71)× 100) of the COVID-19 coughs are more like dry (non-productive) cough, while the rest of them (i.e. 74.35%(= (53/71) × 100)) are mainly more like wet (productive) type cough (see Fig. 5). It seems that our results are quite consistent with the results obtained in Ref. 6.

Statistical Analysis

The two-sample, two-tailed *t*-tests are performed on the SI (CV) and the skewness data whereas the corresponding results are presented below:

Early COVID-19 state → $t(34) = 2.18$, $p < 0.05$, CI [0.0236–0.6718], SD = 0.4776
Moderate COVID-19 state → $t(28) = 2.27$, $p < 0.05$, CI [0.0225–0.4242], SD = 0.2685
Severe COVID-19 state → $t(74) = 8.09$, $p < 0.05$, CI [0.8136–1.3454], SD = 0.5816

where CI: confidence interval.

Summary

Our fully-automated cough sound processing method as well as quantification and qualification strategy can assist physicians in evaluating the risk of disease progression of COVID-19 patients on-site or remotely. The preliminary results in terms of both the SI(CV) and the probability distribution of the extracted click sequence from phase 1 cough data are shown promising to use this method as an effective grading tool for COVID-19 patients. The benefits for using the proposed cough sound based method in evaluating the COVID-19 disease progression are as follows: It can be considered a simple method for quantifying/characterizing the COVID-19 disease progression as well as easy to perform with portable equipment, and inexpensive. As our future work, more detailed evaluation will be conducted with larger annotated COVID-19 cough dataset depending on its availability. In addition, we will investigate to derive other useful features, such as attention entropy[23] for the extracted click sequence and compare the results with the healthy persons as well as non COVID-19 patients data.

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CONFLICT OF INTEREST

Author declares there is no conflict of interest.

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