ABSTRACT
 Currently, a subjective method is used to diagnose cough sounds, particularly wet and dry coughs, which can lead to incorrect diagnoses. In this study, novel emergent features were extracted using spectrogram methods and a parallel-stream one-dimensional (1D) deep convolutional neural network (DCNN) to classify cough sounds. The data of this study were obtained from two datasets. We employed the Mel spectrogram, chromagram constant-\(Q\) transform, Mel-frequency cepstral coefficient, constant-\(Q\) cepstral coefficient, and linear predictive code coefficient to conduct features analysis. The maximum, mean, variance, and standard deviation values of the original spectrogram as well as the maximum first and second derivatives of this spectrogram were extracted and fused to create a single-feature vector. We adopted two types of features: single features and combined features. Each design was restructured according to the magnitude of features with high discrimination power. A parallel-stream 1D-DCNN was developed for classifying cough sounds accurately. We compared the results obtained using the aforementioned network with those obtained using a single-stream 1D-DCNN. We found that the parallel-stream network outperformed the single-stream network for some feature sets. The developed network achieved \(F_1\) scores of 98.61% and 82.96% for the first and second datasets, respectively. The concatenation of layers at the flattening level resulted in an \(F_1\) score of 99.30% in dataset one. Moreover, layer merging strategies exhibited a better performance at the second convolutional layer level than at the flattening layer level in many cases.

INDEX TERMS
Classification, convolutional neural network, cough sounds, feature extraction, spectrogram methods.

I. INTRODUCTION
Because of the rise in respiratory diseases, increased research attention has been paid to cough sound classification. Coughing is a critical symptom of respiratory diseases [1], [2], and two types of coughs exist: wet and dry coughs [3]. Discriminating between these two types of coughs is crucial [4]; however, many hospitals in developing countries adopt inefficient approaches for diagnosing the cough type.

Advances in computer-assisted technology have enabled the use of audio tools and deep learning (DL) models for reliably classifying wet and dry cough sounds. An audio tool is an electronic device that records and stores sound. Audio tools are used to record sounds in cough research [5], [6] and other related fields. Various audio feature extraction methods have been proposed to detect, analyze, and classify cough sounds. Three types of audio features exist [7], [8], [9]:
time-domain features, including zero-crossing, root mean square, and energy envelope; frequency-domain features, including spectral centroid, bandwidth, roll-off, and power spectral density; and time–frequency features, including the Mel spectrogram and Mel-frequency cepstral coefficient (MFCC).

In the present study, time–frequency features were used because they can simultaneously represent signal properties in the time and frequency domains. These features have been used in many studies for classification application [10], [11], [12].

The following questions were addressed in the present study: (1) how are the emergent features extracted using different methods can be combined and input into a DL model? (2) which DL method is appropriate for classifying emergent features? and (3) how are the problems of a small dataset and varying cough signal dimensions overcome in cough research?

The output of the time–frequency method is a two-dimensional (2D) pixel matrix, which can be visualized, and this method is termed as the time–frequency spectrogram method [13]. Several types of features can be extracted from spectrograms to generate one-dimensional (1D) feature vectors. Emergent feature vectors can be extracted from spectrograms along the time axis (column) or frequency axis (row).

In our previous study [14], we used one spectrogram method and focused on extracting the maximum cepstral coefficient vector from MFCC row. In this study, we expanded the technique by including five spectrogram methods and their derivatives and then capturing numerous features from spectrograms and their derivatives. The extracted subfeatures include the maximum, mean, variance, and standard deviation. In each spectrogram method, the extracted subfeatures were fused to form a single-feature vector.

Feature vectors obtained in each adopted method were aggregated to obtain diverse feature combinations. Aggregating features and inputting them into a DL model is tedious. In general, a DL model [e.g., a convolutional neural network (CNN)] is affected by the relationships between features in space, especially when two or more features are integrated. In [15], the correlation matrix, clustering, and dendrogram techniques were used to restructure integrated features. A drawback of using the dendrogram technique is the long time required for processing dendrogram data, which leads to errors. Thus, in this paper, we propose methods for restructuring the position of combined features according to their discrimination power and mutual information value.

Studies have transformed cough signals into features such as Mel spectrograms and MFCCs [16], [17] and then have input these features directly into 2D DL models. Thus, cough sounds can be detected using attributes from a spectrogram. These attributes are one-dimensional features and are suitable inputs for 1D DL models, which are highly useful because of their low computational demand, time requirement, and cost.

To the best of our knowledge, a few studies have adopted a 1D DL model for cough detection, and most relevant studies have adopted a single-stream model for cough detection. For example, Baramulari et al. [18] classified cough sounds by using a bidirectional long short-term memory model. Hassan et al. [19] used a recurrent neural network to detect COVID-19. Amrulloh et al. [20] employed a neural network to classify pneumonia and asthma infections. In the present study, we examined the performance of a 1D-CNN, gated recurrent unit (GRU) model, and a neural network for cough detection. We found that the 1D-CNN model outperformed the other two models. Therefore, the 1D-CNN model was used for further analysis in this study.

Insufficient data are a challenge encountered in studies on cough sound [21], [22], as well as a class imbalance problem [23], [24]. A similar problem was encountered in this study. Of the two collected datasets, one contained 118 wet cough sounds and 170 dry cough sounds, and the other contained 389 wet cough sounds and 413 dry cough sounds. These datasets exhibited the class imbalance problem. Therefore, we used the weighted F1 score [25] and Matthews correlation coefficient (MCC) [26] as metrics for assessing model performance. Furthermore, the two datasets contained signals with different dimensions. We used a zero-padding system to address the varying dimensions of cough signals. The problem of insufficient data was addressed using the data enhancement technique.

The main contributions of this study are as follows:
1) Sounds of wet and dry coughs were classified using novel features extracted using spectrogram methods and a parallel-stream 1D deep CNN (DCNN).
2) The features extracted using spectrogram methods were analyzed using a novel method to classify wet and dry coughs.
3) Feature structures were designed, and two techniques were developed for restructuring the positions of combined features and were compared to determine the better technique.
4) A parallel-stream 1D-DCNN was developed, and the performance of this CNN was compared with that of a single-stream 1D-CNN. The developed model differs from existing related models [15], [36] in three ways: (1) it does not contain a maximum pooling layer, (2) layer concatenation occurs in its flattening layer, and (3) it contains a few layers as a small network might prevent overfitting [28]. Moreover, the performance benefits of concatenating layers at different levels were examined.
5) Model performance achieved with layer merging strategies at different levels in a parallel-stream network was examined.

The rest of this article is organized as follows. Section II provides an overview of the related research. Section III details the methodology used for constructing the designed system. Section IV describes the proposed DL models. Section V presents the experimental results and a discussion on the results. Finally, Section VI provides the conclusions of this study.
II. RELATED RESEARCH

Studies have reported that the cough type can be identified using audio recordings, feature extraction techniques, and DL models. Therefore, we reviewed research on feature extraction approaches and 1D DL models.

Islam et al. [29] employed a deep neural network (DNN) to detect COVID-19. They used time-, frequency-, and time–frequency-domain features for COVID-19 detection and obtained an accuracy of 97.5%. Zhao et al. [30] used pig cough sounds to differentiate respiratory diseases. They extracted 39 MFCC features and classified them using a hybrid DNN and hidden Markov model.

Lella et al. [31] used a 1D-CNN to detect COVID-19 on the basis of voice, breath, and cough sounds. They input MFCC data into an autoencoder to extract deep features, which were then classified using a single-branch 1D-CNN. The aforementioned authors achieved a classification accuracy of 90%. Amrulloh et al. [20] distinguished asthma and pneumonia by using three features: the MFCC, Shannon entropy, and non-Gaussianity score. They fed these features to a DNN and achieved a sensitivity of 89%.

Feng et al. [32] detected COVID-19 on the basis of recorded cough sounds. They obtained time- and frequency-domain features from each sound. They authors achieved a maximum classification accuracy of 99.56% with a recurrent neural network. Islam et al. [33] used the chromagram feature to detect COVID-19. They compared the performance of a CNN and DNN in COVID-19 detection and found that the CNN had higher accuracy than did the DNN.

III. METHODOLOGY

This section describes the methodology used in this study for constructing the designed system. The system design framework is illustrated in Fig. 1, and it contains seven key parts: dataset collection, data enhancement, zero padding, emergent feature analysis, feature structure design, restructuring of multiple features, and DL.

Two datasets were used in this study. The first dataset comprised 189 files of cough audio [34]. Cough signals were manually segmented using Audacity software [55] to obtain 170 dry cough sounds and 118 wet cough sounds for this dataset. Similarly, the second dataset comprised 222 recordings of cough audio [35]. Segmentation of cough signals identified 389 wet coughs and 413 dry coughs in this dataset. The details of data collection and enhancement are presented in Table 1. The two datasets were preprocessed using techniques that were similar to those performed in [14], with the only difference being that signals were not resampled in the present study.

A. DATA ENHANCEMENT

The basic concept of data enhancement in machine learning involves increasing the quantity of training data; however, data enhancement also can be performed to enrich data in a dataset [27]. Data enhancement can be performed using two approaches: image- and audio-based approaches. The audio-based approach was used in the present study. Two strategies were used in this study to enhance the quantity of data: time stretch and pitch shift. In the time stretch method, we stretched the duration of cough signals by factors of 1.07 and 0.5. The factor of 1.07 was used to accelerate a cough signal, and the factor of 0.5 was used to decelerate a cough signal. Pitch shift was performed using factors similar to those used in [27].

The results indicated that after data enhancement, the numbers of dry and wet cough signals in dataset 1 increased from 170 to 850 and from 118 to 590, respectively. Moreover, the numbers of dry and wet cough signals in dataset 2 increased from 413 to 2065 and from 389 to 1945, respectively. Overall, the total number of cough signals increased from 288 to 1440 for the first dataset and from 802 to 4010 for the second dataset.

B. PADDING SYSTEM

A padding system is used to overcome the problem of multivariable bit lengths of cough signals in a dataset. In this study, the bit lengths of the signals with short bit lengths were increased to the maximum value. Thus, a fixed bit length was achieved for all the cough signals (bit length is the size of a signal). Inspired by the random padding technique proposed by Dong et al. [36], we created a zero-padding system instead of a random padding system. The procedures for creating a zero-padding system are described in the following text.

Consider the example of dataset 2. First, we determined that the maximum bit length in this dataset was 45 982, approximately 2.08 s, when the sample rate was set as 22050 Hz. Second, we calculated the bit length of each

![FIGURE 1. System design framework.](image-url)
Essentially, a spectrogram is obtained after four steps: pre-emphasis, framing, windowing, and short-time Fourier transform (STFT). The spectrogram $S(n, k)$ is the squared magnitude of $X(n, k)$, which is expressed as follows:

$$X(n, k) = \int_{-T}^{T} x(\tau) \cdot w(\tau - k) \cdot \exp(-j2\pi nt) d\tau$$

where $x(t)$ is the cough signal, $n$ is the Fourier coefficient, $k$ is the time frame, $w(t)$ is the windowing function, and $X(n, k)$ is the STFT in the complex number.

$$S(n, k) = |X(n, k)|^2$$

### 1) MEL SPECTROGRAM

A Mel spectrogram (MELSPEC) is an auditory system derived by passing a cough signal through an STFT filter and a Mel filter bank [41]. A Mel spectrogram is expressed as follows [42], [43], [44]:

$$M(m, k) = \sum_m |X(n, k)|^2 \cdot \Delta(m)$$

where $M(m, k)$ is the generated Mel spectrogram, and $\Delta(m)$ represents a triangular Mel filter bank with $m$ Mel-frequency bands. The Mel frequency is calculated using the following formula:

$$\text{Mel freq} = 2595 \times \log_{10}(1 + \frac{f}{700})$$

In a Mel spectrogram, cough intensity bands are represented equally in Mel frequencies; thus, capturing different attributes from each frequency band will provide interesting results. Table 3 presents the code procedures used to obtain attributes from a Mel spectrogram.

### TABLE 3. Code for extracting emergent features from a Mel spectrogram.

| Input: cough signals, Output: a single feature vectors. |
|--------------------------------------------------------|
| 1. for $k$ in range of dataset shape:                 |
| 2. Compute Mel spectrogram                             |
| 3. Compute first and second derivatives of Mel spectrogram |
| 4. for $j$ in range of dataset shape:                  |
| 5. $\text{MEL} = M(m, k)[j]$                          |
| 6. $\text{MEL}' = M(m, k)'[j]$                        |
| 7. $\text{MEL}'' = M(m, k)''[j]$                      |
| 8. $\text{mx} = \text{np.max}(\text{MEL}(i) \text{ for } i \text{ in range(MEL.shape[0])})$ |
| 9. $\text{mn} = \text{np.mean}(\text{MEL}(i) \text{ for } i \text{ in range(MEL.shape[0])})$ |
| 10. $\text{var} = \text{np.var}(\text{MEL}(i) \text{ for } i \text{ in range(MEL.shape[0])})$ |
| 11. $\text{std} = \text{np.std}(\text{MEL}(i) \text{ for } i \text{ in range(MEL.shape[0])})$ |
| 12. $\text{mx}' = \text{np.max}(\text{MEL}'(i) \text{ for } i \text{ in range(MEL'.shape[0])})$ |
| 13. $\text{mx}'' = \text{np.max}(\text{MEL}''(i) \text{ for } i \text{ in range(MEL''.shape[0])})$ |
| 14. Fuse the results (8-13).                           |

In dataset 1, the Mel spectrogram $M(m, k)$ and its derivatives $(M(m, k)'$ and $M(m, k)''$) were computed for each cough signal. Subsequently, for each computed Mel spectrogram, the vectors of the maximum spectral intensity, mean spectral intensity, spectral intensity variance, and standard deviation...
of the spectral intensity were extracted from each frequency band. The aforementioned process was also used to extract maximum spectral intensity vectors from the derivatives of a Mel spectrogram. The results obtained from a Mel spectrogram and its derivatives were then fused. The fused feature was a single-feature vector. The resulting shape of a single-feature vector obtained from a Mel spectrogram for dataset 1 was (1440,384), where 1440 is the quantity of data in the dataset, and 384 is the length of a single-feature vector.

2) MEL-FREQUENCY CEPSTRAL COEFFICIENT

The MFCC is one of the most crucial features for speech recognition, and MFCC is based on the power spectrum. The MFCC is typically calculated after passing a cough signal through an STFT filter, a Mel filter bank, and a discrete cosine transform filter [45]. The MFCC is calculated using the following equation:

\[
MFCC(m, k) = \sum \log(\|X(n, k)\|^2 \cdot \Delta(m)) \cdot \cos\left(m(z - \frac{1}{2})\pi\right) \quad (5)
\]

where \(M(m, k)\) is a matrix in which the row \(m\) represents the MFCC and the column \(k\) represents the time frame. In this study, the attributes were acquired from each row of \(M(m, k)\) matrix. The following text describes how various attributes from the MFCC were captured. For each cough sound, the MFCC and its derivatives were generated.

Vectors of the maximum cepstral coefficient, mean cepstral coefficient, cepstral coefficient variance, and standard deviation of the cepstral coefficient were captured from each row of the MFCC. Moreover, the maximum cepstral coefficient was extracted from each derivative of the MFCC. The results obtained from MFCC and its derivatives were combined, and the shape of a single-feature vector obtained from the MFCC was (1440,240).

3) CHROMAGRAM

A chromagram (CHROMA) is a feature used to examine pitch characteristics in music. A chromagram is a pitch class profile and can be used to distinguish different types of cough sounds because the cough signals of different patients have different amplitudes; thus, transforming cough sounds into a chromagram can indicate how cough energy is distributed among different pitch classes. Three types of chromagrams exist [37]: the CHROMA-STFT, CHROMA-CQT, and CHROMA-energy normalized (CHROMA-EN). The CHROMA-STFT is generated through STFT, which includes a linear frequency scale. The CHROMA-CQT is generated using the CQT, which contains a logarithmic frequency scale [46]. The energy is normalized in the CHROMA-EN. The CHROMA-CQT was adopted in the present study.

A CHROMA [47] is usually a 2D matrix with pitch classes in the rows and the time frames in the columns. We intended to determine the features in the pitch classes; therefore, we employed a method similar to MELSPECT. First, the CHROMA-CQT and its derivatives were generated. Second, the maximum, mean, variance, and standard deviation of the CHROMA magnitude as well as the maximum magnitude of the derivatives of the CHROMA-CQT were generated. The overall shape of a single-feature vector developed using the CHROMA-CQT was (1440,120).

4) CONSTANT-Q CEPSTRAL COEFFICIENT

The CQCC was developed for automatic speaker verification. It has also been applied to distinguish between patients with asthma and healthy people [48]. The CQCC is determined using three steps: (1) the CQT is calculated, after which the amplitude of CQT is converted into decibels; (2) the MFCC is used to obtain a 2D CQCC; and (3) emergent features are extracted. The aforementioned steps are described in Table 4. The shape of a single-feature vector obtained from the CQCC was (1440, 240) in this study.

| TABLE 4. Code for extracting emergent features from the CQCC. |
|---------------------------------------------------------------|
| Input: cough signals,                                        |
| Output: a single feature vector.                             |
| 1. for \(k\) in range of dataset shape:                      |
| 2. Compute Constant-Q transform (CQT)                        |
| 3. Compute the magnitude of CQT                              |
| 4. Using results in (3) and transform to dB using amplitude to dB conversion |
| 5. Using results in (4), compute MFCC as a result CQCC       |
| 6. Compute the first and second derivatives of CQCC.         |
| 7. for \(j\) in range of dataset shape:                      |
| 8. \(CQ = CQCC(m, k)[j]\)                                    |
| 9. \(CQ' = CQCC(m, k')[j]\)                                  |
| 10. \(CQ'' = CQCC(m, k'')[j]\)                               |
| 11. \(m = [\text{np. max}(CQ(i)) \text{ for } i \text{ in range}(CQ, \text{shape}[0])]\) |
| 12. \(m' = [\text{np. mean}(CQ(i)) \text{ for } i \text{ in range}(CQ, \text{shape}[0])]\) |
| 13. \(m'' = [\text{np. var}(CQ(i)) \text{ for } i \text{ in range}(CQ, \text{shape}[0])]\) |
| 14. \(\text{std} = [\text{np. std}(CQ(i)) \text{ for } i \text{ in range}(CQ, \text{shape}[0])]\) |
| 15. \(m' = [\text{np. max}(CQ',(i)) \text{ for } i \text{ in range}(CQ', \text{shape}[0])]\) |
| 16. \(m'' = [\text{np. max}(CQ'',(i)) \text{ for } i \text{ in range}(CQ'', \text{shape}[0])]\) |
| 17. Fuse the results (11-16).                                |

5) LINEAR PREDICTIVE CODE COEFFICIENT

The LPC is a vocal tract feature used to characterize the spectral envelope of a speech signal. This coefficient has been used for classifying cough sounds [49], [50], with suitable results. After extracting the LPC [37], [51], its first and second derivatives are calculated. Subsequently, all the computed features are fused to obtain a single LPC feature. The shape of a single-LPC-feature vector generated in this study was (1440,81). Fig. 3 illustrates the features extracted using some spectrogram methods in this study.

D. PROPOSED FEATURE STRUCTURES AND METHODS FOR RESTRUCTURING COMBINED FEATURES

This section describes the proposed feature structures and techniques for restructuring combined features. The proposed
feature structures are single features and combined features. As described in section I, a single feature is a feature obtained after fusing the subfeatures extracted using different spectrogram methods. By contrast, a combined feature is obtained after combining the single features extracted using different spectrogram methods.

The structure of a single feature for dataset 1 is explained as follows:

- The length of a single feature of a Mel spectrogram is 384.
  \[ f_1 = \{a_1, a_2, a_3, \ldots, a_{384}\} \]  
- The length of a single feature of the MFCC is 240.
  \[ f_2 = \{b_1, b_2, b_3, \ldots, b_{240}\} \]  
- The length of a single feature of the CHROMA-CQT is 120.
  \[ f_3 = \{c_1, c_2, c_3, \ldots, c_{120}\} \]  
- The length of a single feature of the CQCC is 240.
  \[ f_4 = \{d_1, d_2, d_3, \ldots, d_{240}\} \]  
- The length of a single feature of the LPC is 81.
  \[ f_5 = \{e_1, e_2, e_3, \ldots, e_{81}\} \]  

Moreover, the feature combination \( F \) is expressed as follows:

\[ F = \{a_1, \ldots, a_{384}, b_1, \ldots, b_{240}, c_1, \ldots, c_{120}, d_1, \ldots, d_{240}, e_1, \ldots, e_{81}\} \]  

The overall structure of a feature combination is expressed as follows:

\[ F = \{k_1, k_2, \ldots, k_{1065}\} \]  

where; \( a, b, c, d, e, k \in \mathbb{R} \)

After determining a single-feature set \( f \) and feature combination \( F \), we restructured the position of multi-combining features in \( f \) and \( F \). The combined features were restructured according to their discrimination power (mean absolute deviation) and mutual information value. The two restructuring techniques are detailed in Table 5. These techniques were analogous, with the difference being that the mean absolute deviation was calculated using (13), whereas the mutual information [52], [53] was calculated using (14).

\[
MAD(t) = \frac{1}{n} \sum_{t=1}^{n} |x_t - x_{av}| \tag{13}
\]

\[
M(X, Y) = \iint p(x, y) \ln \frac{p(x, y)}{p(x)p(y)} \, dx \, dy \tag{14}
\]

where \( n \) is the number of data points, \( x_t \) is the value of each data point in a series, \( x_{av} \) is an average value of the data, \( MAD(t) \) is the mean absolute deviation of the data, \( p(x, y) \) is the joint probability of variables \( x \) and \( y \), \( p(x) \) is the probability of variable \( x \), and \( p(y) \) is the probability of variable \( y \).

IV. PROPOSED 1D-DCNN

The main DL architecture used in this study was a parallel-stream 1D-DCNN. The performance of this network was compared with that of a single-stream 1D-DCNN. Both the aforementioned networks exhibited the basic structure of a CNN, which comprises an input layer, a hidden layer, and an output layer. The parallel- and single-stream 1D-DCNNs were constructed using a Keras library and executed in TensorFlow-GPU. The aforementioned networks are described in the following text.

A. SINGLE-STREAM 1D-DCNN

As depicted in Fig. 4, the constructed single-stream 1D-DCNN contained one input layer, three convolutional layers, one flattening layer, one dense layer, and one output layer. The first convolutional layer of this network used the `regularizer` l2 (0.001) kernel. The rectified linear unit activation function was used in all the layers except the last layer, in which the `softmax` activation function was used. Each convolutional layer had a stride of 1 and the same padding. After the dense layer, a 50% dropout was used.

B. PARALLEL-STREAM 1D-DCNN

The architecture of the constructed parallel-stream 1D-DCNN was similar to that of the constructed single-stream 1D-DCNN;
however, in contrast to the single-stream 1D-CNN, the parallel-stream network included multiple streams in parallel. Each stream comprised a feature set (input layer), three convolutional layers, one flattening layer, one merged layer, one dense layer, and one output layer (Fig. 4).

When training the two networks, the number of epochs was set as 50, and the batch size was set as 32. The networks were optimized using the root mean squared propagation (RMSProp) optimizer; their loss function was the categorical cross-entropy function; and their performance was evaluated in terms of their accuracy.

C. EXPERIMENTAL SETUP AND EVALUATION METRICS

In the experiments, extracted spectrogram features were normalized using the z-score method. Subsequently, two steps were conducted to split the datasets. First, 80% and 20% of each dataset were randomly divided into a training set and testing set, respectively. Second, 80% and 20% of the training data were further divided into a training set and validation set, respectively. Finally, the F1 score and MCC were determined. The confusion matrix was used to evaluate the prediction for each cough category.

The weighted F1 score [25] is expressed as follows:

$$F_1 = \frac{TP}{TP + 0.5(FP + FN)} \times w_i$$  \hspace{1cm} (15)

The MCC [54] is expressed as follows:

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP + FP) \times (TP + FN) \times (TN + FP) \times (TN + FN)}}$$  \hspace{1cm} (16)

where $TP$ indicates the number of true positives, $TN$ indicates the number of true negatives, $FP$ indicates the number of false positives, $FN$ indicates the number of false negatives, and $w_i$ is the weight ratio of class $i$.

D. HARDWARE AND SOFTWARE

The hardware used in this study was a desktop with an Intel CoreTM i7-10700 CPU @2.9 GHz with 16 GB RAM, an Nvidia GeForce GTX 2060 graphics card with 6 GB VRAM, and a 1-TB hard disk drive. Audacity version 3.1.3 was used for signal segmentation in this study. Audacity is a multifunctional tool that enables users to import, edit, export, and record audio files [55]. A Librosa library [37] was used to analyze cough signals through processes such as audio wave loading and spectrogram extraction.

V. RESULTS AND DISCUSSION

A. COMPARISON OF DIFFERENT 1D DL MODELS

A simple exploratory study was conducted to compare the performance of a 1D-CNN model, 1D-DNN model, and GRU model. Each of these models comprised only one input layer and one output layer. The 1D-DCNN model comprised two convolutional layers and one flattening layer. For this model, the kernel size was 10, the number of filters was 32, and the number of units in the dense layer was 64. The 1D-DNN model contained two dense layers with 32 units each. The GRU model contained two recurrent neural network layers and a flattening layer. It had the same number of units as did the 1D-DNN model. As presented in Table 6, the 1D-DCNN, 1D-DNN, and GRU models achieved F1 scores of 97.21%, 96.52%, and 96.51%, respectively. Because the 1D-DCNN model exhibited the highest F1 score, this model was selected for further exploration.

B. COMPARISON OF THE METHODS USED FOR RESTRUCTURING COMBINED FEATURES

Two methods were used in this study for restructuring combined features, and the results obtained with these methods are presented in Table 7. The restructuring method based on discrimination power outperformed that based on the mutual information value. The F1 score obtained with the method based on discrimination power was 1.4% and 1.39% higher than that based on the mutual information value for two feature sets. Therefore, the restructuring method based on discrimination power was selected for further analysis.

C. RESULTS OBTAINED FOR THE SINGLE-STREAM 1D-DCNN FOR DIFFERENT DATASETS

Single-feature vectors extracted from all the spectrograms were aggregated, and the method based on discrimination power was used to restructure combined features. Subsequently, these features were input to a single-stream 1D-DCNN. The classification results of this network were...
TABLE 7. Results obtained for the two methods used in this study for restructuring combined features.

| Methods       | Feature sets                      | F1-score (%) | MCC   |
|---------------|-----------------------------------|--------------|-------|
| Discrimination power | CHROMA+LPC+MFCC                 | 97.57        | 0.949 |
|               | MFCC+LPC+MELSPEC+CHR OMA         | 98.26        | 0.964 |
| Mutual information | CHROMA+LPC+MFCC                 | 96.17        | 0.920 |
|               | MFCC+LPC+MELSPEC+CHR OMA         | 96.87        | 0.935 |

TABLE 8. Classification results obtained with the single-stream 1D-DCNN for different feature sets and datasets.

| Model/Dataset   | Feature sets                      | F1-score (%) | MCC   |
|-----------------|-----------------------------------|--------------|-------|
| Dataset 1       | MFCC+LPC                          | 97.22        | 0.942 |
|                 | MELSPEC+LPC                       | 95.82        | 0.913 |
|                 | CHROMA+LPC+MFCC                   | 97.57        | 0.949 |
|                 | MFCC+LPC+MELSPEC                  | 98.26        | 0.964 |
|                 | CHROMA+LPC+MELSPEC                | 95.48        | 0.906 |
|                 | MFCC+LPC+MELSPEC+CHROMA           | 98.26        | 0.964 |
|                 | MFCC+LPC+MELSPEC+CHROMA+CQCC      | 97.91        | 0.957 |
|                 | MFCC+LPC+MELSPEC+CHROMA           | 81.24        | 0.626 |
|                 | MELSPEC+LPC                       | 81.92        | 0.638 |
|                 | CHROMA+LPC+MFCC                   | 80.63        | 0.613 |
|                 | MFCC+LPC+MELSPEC                  | 83.53        | 0.67  |
|                 | CHROMA+LPC+MELSPEC                | 71.65        | 0.433 |
|                 | MFCC+LPC+MELSPEC+CHROMA           | 80.28        | 0.605 |
|                 | MFCC+LPC+MELSPEC+CHROMA+CQCC      | 80.02        | 0.601 |

For dataset 1, the best classification results were obtained for the MFCC + LPC and MFCC + LPC + MELSPEC + CHROMA feature sets. The F1 score and MCC for these feature sets were 98.61% and 0.971, respectively. An F1 score of 97.91% was obtained for the MFCC + LPC + MELSPEC feature set, with the F1 score being 93.37% and the MCC being 0.863. Fig. 5(a) shows the confusion matrix of the feature set for which the best classification results were obtained. Dataset 1 contained 170 dry cough sounds and 118 wet cough sounds. The classification results of the proposed parallel-stream network contained three false positives and one false negative. For dataset 1, the aforementioned network predicted 168 cough signals as dry coughs and 120 cough signals as wet coughs.

For dataset 2, the best classification results were obtained for the MFCC + LPC + MELSPEC + CHROMA + CQCC feature set. The F1 score and MCC for this feature set were 82.96% and 0.663, respectively. The worst classification results obtained for the inferior classification performance for dataset 2, we performed a quick review of previous studies conducted using this dataset. Poor classification results were obtained for dataset 2 in [56] and [57].

D. RESULTS OBTAINED FOR THE PARALLEL-STREAM 1D-DCNN FOR DIFFERENT DATASETS

In the parallel-stream 1D-DCNN, every single-feature vector was simultaneously fed to different inputs, and the features extracted from parallel streams were subsequently concatenated to form a merged layer. The resulting features were passed through a dense layer before being classified at the output layer (Fig. 4). The classification results obtained for the parallel-stream network are presented in Table 9.

TABLE 9. Classification results obtained with the parallel-stream 1D-DCNN for different feature sets and datasets.

| Model/Dataset   | Feature sets                      | F1-score (%) | MCC   |
|-----------------|-----------------------------------|--------------|-------|
|                 | MFCC+LPC                          | 98.61        | 0.971 |
|                 | MELSPEC+LPC                       | 95.12        | 0.899 |
|                 | CHROMA+LPC+MFCC                   | 97.22        | 0.943 |
|                 | MFCC+LPC+MELSPEC                  | 97.91        | 0.957 |
|                 | CHROMA+LPC+MELSPEC                | 93.37        | 0.863 |
|                 | MFCC+LPC+MELSPEC+CHROMA           | 98.61        | 0.971 |
|                 | MFCC+LPC+MELSPEC+CHROMA+CQCC      | 97.91        | 0.957 |
|                 | MFCC+LPC+MELSPEC+CHROMA           | 81.88        | 0.638 |
|                 | MELSPEC+LPC                       | 82.28        | 0.645 |
|                 | CHROMA+LPC+MFCC                   | 81.39        | 0.628 |
|                 | MFCC+LPC+MELSPEC                  | 81.27        | 0.625 |
|                 | CHROMA+LPC+MELSPEC                | 68.93        | 0.378 |
|                 | MFCC+LPC+MELSPEC+CHROMA           | 81.78        | 0.635 |
|                 | MFCC+LPC+MELSPEC+CHROMA+CQCC      | 82.96        | 0.663 |

The classification results obtained for dataset 2 were inferior to those obtained for dataset 1. To determine the reason for the inferior classification performance for dataset 2, we performed a quick review of previous studies conducted using this dataset. Poor classification results were obtained for dataset 2 in [56] and [57].
(results were obtained for the CHROMA + LPC + MELSPEC feature set, with the F1 score being 68.93% and the MCC being 0.378. Fig. 5(b) displays the confusion matrix of the feature set for which the best classification results were obtained. Dataset 2 contained 413 and 389 dry and wet cough sounds, respectively. The proposed network predicted 46 dry cough signals as wet cough signals and 90 wet cough signals as dry cough signals.

E. COMPARISON OF THE PERFORMANCE OF THE SINGLE-STREAM 1D-DCNN AND PARALLEL-STREAM 1D-DCNN

The performance, execution times, and number of parameters of the single-stream 1D-DCNN and parallel-stream 1D-DCNN were compared. For dataset 1, the parallel-stream network exhibited the best classification results for two feature sets, with the F1 score being 98.61% and the MCC being 0.971. Nevertheless, the single-stream network exhibited excellent classification results for most feature sets. In addition, when using all five features (MFCC + LPC + MELSPEC + CHROMA + CQCC), the single- and parallel-stream networks categorized cough sounds in 386.18 and 481.08 s, respectively. For dataset 2, the parallel-stream network exhibited superior classification results to the single-stream network for most feature sets. Moreover, when using all five features, the single and parallel-stream networks classified cough sounds in 864.21 and 1445.87 s, respectively (Fig. 6).

Overall, the single-stream network required fewer training parameters than did the parallel-stream network (3 866 954 vs. 3 998 042). The results presented in Tables 8 and 9 indicate that (1) training multiple parallel networks concurrently does not guarantee excellent classification results, but selection of input features are important, and that (2) the simultaneous aggregation of many features in a single-stream network does not result in high performance.

F. CLASSIFICATION RESULTS OBTAINED UNDER THE CONCATENATION OF LAYERS AT DIFFERENT LEVELS

We examined whether the classification performance of the constructed parallel-stream network could be improved by concatenating layers at different levels. We trained the proposed parallel-stream network [Fig. 4(b)] and then modified the network by performing concatenation at the second and third convolutional layers. The MFCC + CQCC feature set was selected as the input of the aforementioned network because of the similarities in the dimensions of these features. Better classification results were obtained when concatenating layers at the flattening level than when concatenating layers at other levels. When concatenating layers at the flattening level, the F1 score was 99.30%, and the MCC was 0.985 (Table 10).

G. CLASSIFICATION RESULTS OBTAINED WHEN USING DIFFERENT STRATEGIES FOR MERGING LAYERS

We compared the classification results obtained with the proposed parallel-stream network when using different strategies for merging layers, such as addition, multiplication, maximization, and concatenation. Layer merging involves combining two or more models or layers. Four layer merging strategies were adopted at different levels in this study (Table 11). At the flattening level, excellent classification

TABLE 10. Classification results obtained when concatenating layers at different levels using dataset 1.

| Level             | F1-score (%) | MCC  |
|-------------------|--------------|------|
| Flatting          | 99.30        | 0.985|
| Third convolutional| 97.57        | 0.949|
| Second convolutional| 98.26        | 0.964|

TABLE 11. Classification results obtained when adopting different layer merging strategies at different levels using dataset 1.

| Level             | Strategy   | F1-score (%) | MCC  |
|-------------------|------------|--------------|------|
| Flatting          | Add        | 95.50        | 0.909|
|                   | Multiplication | 96.15    | 0.922|
|                   | Maximum    | 97.23        | 0.944|
|                   | concatenation | 99.30        | 0.985|
results were obtained when using the concatenation strategy. Moreover, better classification results were obtained at the second convolutional level than at the flattening level for three of the four adopted strategies (i.e., the addition, multiplication, and maximization strategies). The maximization strategy exhibited the best results ($F_1$ score of 98.61%) at the second convolutional level, whereas the concatenation strategy exhibited the best results ($F_1$ score of 99.30%) at the flattening level.

VI. CONCLUSION

In this study, cough sounds were classified into wet and dry coughs through the analysis of the emergent features extracted from spectrograms and a parallel-stream 1D-DCNN. Two datasets were used in this study. Data enhancement was conducted to increase the quantity of data in each dataset, and each cough signal was then padded using a zero-padding system to generate cough signals with fixed dimensions. After using the zero-padding system, the cough signals of datasets 1 and 2 had fixed dimensions of 29952 and 45982, respectively.

Numerous attributes were extracted from each row of original spectrograms and their derivatives and then fused. The MELSPEC, CHROMA, MFCC, CQCC, and LPC spectrograms were used in this study. We obtained two types of attributes: single attributes and combined attributes. We then examined the performance of two techniques designed in this study to restructure combined attributes. One of these techniques was based on features with high discrimination power, whereas the other was based on features with high mutual information values. The approach based on discrimination power exhibited 1.4% and 1.39% higher $F_1$ scores than did the approach based on the mutual value when two feature sets were input to the proposed parallel-stream 1D-DCNN.

Before developing the proposed parallel-stream 1D-DCNN, we conducted a simple study on three models: 1D-DCNN, GRU model, and 1D-DNN. The 1D-DCNN outperformed the other two models; thus, this model was adopted for further analysis in this study. We compared the performance of the proposed parallel-stream 1D-DCNN with that of a single-stream 1D-DCNN.

We then compared the parallel-stream network and a single-stream network. For dataset 1, the highest $F_1$ score exhibited by the parallel-stream network was 98.61%. However, the parallel-stream network outperformed the single-stream network for only a few feature sets. Moreover, the confusion matrix of the feature set for which the best classification performance was obtained indicated that the numbers of false positives and false negatives were low.

For dataset 2, the best classification results were obtained for the MFCC + LPC + MELSPEC + CHROMA + CQCC feature set ($F_1$ score of 82.96% and MCC of 0.663). The confusion matrix of this feature set contained large numbers of false positives and false negatives. The number of false negatives was almost twice that of false positives. In some cases, the parallel-stream network exhibited excellent classification performance but required a long classification time and numerous training parameters. We also compared the classification performance achieved when concatenating layers at different levels. When the MFCC + CQCC feature set was used, better classification results were obtained when concatenating layers at the flattening level ($F_1$ score of 99.30%) than at other levels.

Finally, the classification performance of the proposed parallel-stream network was examined under four layer merging strategies: addition, multiplication, concatenation, and maximization. These strategies were implemented at two levels: the second convolutional level and flattening level. Better classification results were obtained for all the layer merging strategies, except the concatenation strategy, at the second convolutional level than at the flattening level. The best classification results were obtained with the maximization and concatenation strategies at the second convolutional and flattening levels, respectively.

In the future, we will develop a transfer learning algorithm that can execute the spectrogram methods used in this study. The performance of this algorithm will then be compared with the parallel-stream network designed in this study. Moreover, a novel method will be adopted to increase the quantity of data, and this method will be compared with the data enhancement method adopted in this study.

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