Pathological Voice Classification Using Mel-Cepstrum Vectors and Support Vector Machine

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Abstract—Vocal disorders have affected several patients all over the world. Due to the inherent difficulty of diagnosing vocal disorders without sophisticated equipment and trained personnel, a number of patients remain undiagnosed. To alleviate the monetary cost of diagnosis, there has been a recent growth in the use of data analysis to accurately detect and diagnose individuals for a fraction of the cost. We propose a cheap, efficient and accurate model to diagnose whether a patient suffers from one of three vocal disorders on the FEMH 2018 challenge.

Index Terms—vocal disorder, neoplasm, nodule, polyp, mfcc

I. INTRODUCTION

The human standard of life can be severely affected by their individual pathological voice condition. This has also financially burdened several patients, organizations, and societies [1]. Some of the common impairments to the voice are structural lesions, neoplasms, and neurogenic disorders [1]. One of the most frequently utilized tools to diagnose these vocal disorders is through a laryngoscope [2]. Laryngoscopy is an expensive time-consuming process, that requires trained personnel to perform the test [3]. In addition, vocal disorders must also be detected and treated at an early diagnostic stage when they are faced with several symptomatic challenges to properly detect, as in the case of larynx cancer [4]. Therefore, patients who do not have easy access to advanced technology or those who cannot afford expensive medical treatments are in a derogatory position to receive effective treatments. To alleviate these issues, it has become very popular to utilize non-invasive techniques for detecting vocal disorders through eliminating subjective biases [5]. In this paper, we propose an algorithm to accurately and quickly classify voice disorder using cheap diagnostic tools.

In the past 60 years, a significant amount of work has been developed in the field of automated speech pathology, which has assisted physicians to diagnose vocal disorders accurately. In 1960s, the detection of voice quality was measured by the widespread shimmer, jitter and harmonic-to-the-noise ratio technique (HRN) [6]. Subsequently, linear discriminant analysis (LDA) was used to discriminate pathological voices from normal ones [7]. In another study, glottal noise parameter was measured primarily to identify vocal disorder [8]. Another common technique extracted the Mel-frequency cepstral coefficient features (MFCC) and fed into a Gaussian mixture model (GMM) [9]. More recently, the F-Ratio and Fisher’s discriminant ratio was used for feature selection of acoustic analysis [4]. Little et al., used recurrence and fractal scaling to quadratically analyze disordered vowels. These samples were then bootstrapped to distinguish normal and disordered voices [10]. In the early 2000s, Arias-Londoó et al. combined the information obtained from MFCC and Modulation spectra (MS) to input into a GMM and support vector machine (SVM) classifier [11]. Arjmandi and Pooyan et al. focused their study on Short-Time Fourier Transform (STFT) and Continuous Wavelet Transform (CWT) to discriminately analyze voice impairments as they used Linear Discriminant Analysis (LDA), Principle Component Analysis (PCA) and an SVM classifier [12]. In May 2014, Muhammad and Melhem et al. employed MPEG-7 features to differentiate pathological voice from normal voice [13].

Deep learning approaches are becoming more commonly used to categorize voice disorders. One such study utilized convolutional layers with Long Short Term Memory (LSTM) recurrent layers on raw audio signals as an end-to-end model classifier [14]. Another deep learning approach used the VGG-16 and CaffeNet models for voice disorder classification [15]. Successively, Tsao et al. compared deep neural networks (DNN), GMM, and SVM models that apply MFCC, MFCC+delta and MFCC(N)+delta features from the raw signals [1].

In this study, we develop a supervised classification model on a range of given voice data samples (obtained from the 2018 Far Eastern Memorial Hospital Voice Disorder Challenge) to detect the pathological defects and classify them into one of the three commonly identified vocal disorders, Neoplasm, Vocal Palsy, and Phonotrauma. The voice samples included samples of 50 normal voice and 150 voice disorders which were characterized by vocal nodules, polyps, and cysts (mutually related to Phonotrauma), glottis neoplasm, and unilateral vocal paralysis [1]. Our model utilizes MFCC and MFCC delta features from the raw signals as an input to an SVM classifier. The hyperparameters of the SVM classifier is tuned via a state-of-the-art algorithm developed by researchers at Google (sequential, halving, and classification algorithm [16]). In this study, we compare our model with a deep learning model (Long Short-Term Memory Fully Convolutional Network [17]) and a classical model (XGBoost) to show how our proposed model can perform similarly to more complicated models on the FEMH dataset [18]. We propose our model be utilized as

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a baseline for which physicians can diagnose vocal disorder accurately, and other researchers can compare their results against.

The remainder of the paper is structured as follows: Section II contains the background work on which this work is based. Section III describes the methodology we use to train our proposed models. In section IV, we discuss the results obtained on our experiments. Finally, in Section V, we conclude and describe potential future work that needs to be performed.

II. BACKGROUND WORK

A. Mel-frequency Cepstral Coefficients

Mel-frequency Cepstrum is a representation of a sound signal, based on the linear cosine transform of a log power spectrum on a nonlinear mel scale of frequency [19]. The coefficients that collectively comprise the Mel-frequency Cepstrum are called MFCC features. In contrast to the linearly-spaced frequency bands obtained from the cepstrum of a sound signal, in a mel-frequency cepstrum, the frequency bands are uniformly spaced on the mel scale. This frequency warping allows for better representation of sound and voice data.

B. Temporal Derivatives

In order to extract the dynamic features of speech, auxiliary delta and delta-delta features must be computed as input features for the model, which are calculated as the temporal derivatives of the original MFCC features [20]. In order to estimate smooth derivatives \( f_{l,n} \), we often simply compute the local least squares polynomial fit to the data samples, so as to minimize the cost function

\[
C_{l,m}^{p} = \sum_{m=-M}^{M} \left( \sum_{k=0}^{p} a_k m^k - f_{l,n+m} \right)^2
\]

with respect to the MFCC coefficients \( a_k \) where \( f \) is the spectrum-based feature vector, \( L \) being the number of coefficients, \( N \) being the number of frames, \( p \) is the order of the polynomial and \( M \) is the number of samples used to fit the polynomial.

We compute the delta features via the local estimate of the derivative of the input data, computed using Savitsky-Golay filtering [20] as we utilize the Librosa [21] package to preprocess the dataset.

III. METHODOLOGY

Voice samples were obtained from a voice clinic in a tertiary hospital (Far Eastern Memorial Hospital (FEMH). The dataset is comprised of voice samples of 50 individuals who do not exhibit a pathological abnormality in their speech, and voice samples 150 individuals who exhibit one of three different voice disorders, including vocal nodules, polyps, and cysts (collectively referred to Phonotrauma); glottis neoplasm and unilateral vocal paralysis. Table I describes the demographics of the dataset, and Table II provides the number of samples available for each of the three vocal disorders, stratified by gender.

Each voice sample is a recording of a 3-second sustained vowel sound of the letter "A", under a background noise of amplitude between 40 and 45 decibels, and a microphone-to-mouth distance of approximately 15-20 centimeters. The recordings were obtained using a Shure SM58 microphone and a Shure X2u digital amplifier, with a sampling rate of 44,100 Hz at 16-bit resolution, which was saved in uncompressed waveform-audio format.

| TABLE I | DEMOGRAPHICS OF NORMAL AND PATHOLOGICAL SAMPLES |
|---------|-----------------------------------------------|
| Gender  | Count | Mean Age | Age Range | Standard Deviation |
|         | M     | F        |           |                  |
| Normal  | 20    | 30       | 30.9      | 34.5             | 10.9 12          |
| Pathological | 78    | 72       | 53.8      | 44.6             | 15.3 13.5        |

| TABLE II | DISEASE CATEGORIES OF THE 150 PATHOLOGICAL VOICE SAMPLES |
|---------|--------------------------------------------------------|
| Neoplasm Phonotrauma Vocal Palsy | M | F | M | F | M | F |
| Neoplasm | 32 | 13 | 33 |
| Phonotrauma | 8 | 47 | 13 |

A. Data Processing

Each audio waveform is processed to derive MFCC features using the Librosa [21] library, using a sampling rate of 22050 Hertz. We compute the temporal derivatives (delta) of these MFCC features, of which we compute the mean and maximum across all samples, and concatenate all three vectors into a single vector of size \( \mathbb{R}^{3d} \), where \( d \) is the number of extracted MFCC coefficients. We select the number of MFCC coefficients \( (d) \) computed to be 15, which we find via grid search over the space of \( \{10, 15, 20, 25, 30, 40, 50, 100\} \).

When assessing the performance of any model, we compute a weighted average of the sensitivity and specificity of the model on the binary task of predicting whether the sample is normal or pathological, and the average recall of the model on the multitask objective of classifying the sample as one of four classes. We assign the weights for the above scores as 40%, 20%, and 40% respectively.

B. Hyperparameter Tuning

As the dataset comprises of a mere 200 samples, we perform 5 fold cross validation for every model using the same global seed across all models. We utilize the sequential halving and classification (SHAC) algorithm from Kumar et al. [16], as an efficient alternative to exhaustive grid search to sample hyperparameter settings in continuous search spaces. To avoid overfitting the data distribution in the 5 folds used for evaluation of the models, we train and evaluate the SHAC algorithm on 5 different folds of the dataset using a different random seed. This preserves the generalization properties of
the parameters sampled from the SHAC algorithm while also providing robustness to random seed overfitting. For better robustness, we round off all floating point values to the 3rd decimal place, and find that performance is not impacted.

When training the classifiers of the SHAC algorithm, we compute a maximum of 10 classifiers, with a batch of 100 hyperparameter samples per classifier and a total budget of 1000 hyperparameter samples evaluated. It is to be noted that once we obtain a sample from the SHAC algorithm, we use the same parameters for all 5 folds. Therefore, the sampled parameters are more robust and generalize better, as they must perform well across all 5 folds. We then obtain 100 hyperparameter samples, compute the mean and standard deviation of this batch, and select those candidates which obtain a score greater than the mean plus one standard deviation. We use a publically available implementation of the SHAC algorithm 1.

C. Proposed Model

Our proposed model is comprised of a feature selection stage followed by a multi-class classification stage. We utilize a set of Random Forest models, each trained on the training data of a given fold, to compute the feature importance of the 45 dimension input vector. We then determine a threshold value sampled from the SHAC algorithm, which is used to select only those features which are above that threshold. These features are then supplied to a Kernel Support Vector Machine, which utilizes the Gaussian Radial Basis Function as its kernel. We utilize the One-vs-One strategy for multi-class classification, which builds \( N \times (N-1) \) classifiers. Such a strategy is applicable here due to the small amount of data available and relatively fast training, but we observe that One-vs-All strategy is nearly identical in performance. We utilize the excellent Scikit Learn [22] package for all models described in this section. Figure 1 details the various stages of the proposed model pipeline.

We construct a search space consisting of the number of trees in the Random Forest \( \{10, 20, 50, 100\} \), depth of the tree \( \{3, 4, 5, 6, 7, 8, \text{no limit}\} \), selection threshold \( (U \in (0, 0.5)) \), penalty parameter \( C \) for the SVM \( (U \in (0, 25)) \), gamma parameter for the RBF kernel \( (U \in (-1, 1)) \), where we resolve negative values to be \( 1 / \text{(number of features)} \). We then search over this space using the SHAC algorithm and sample its best parameters as described in Hyperparameter tuning III-B.

D. Baseline Models

All baseline models utilize the same input features and 5 fold training as described in the proposed model, to ensure a consistent training methodology. Random Forest based feature selection is performed, but the hyperparameters for the baseline models are searched via SHAC to ensure we obtain unbiased hyperparameters. The search space for the Random Forest and the selection threshold remain consistent across all models.

1) XGBoost: We compare against XGBoost [23], a powerful Gradient Boosting Tree model which obtains state-of-the-art results on multiple structured and unstructured datasets and is a standard baseline model to compete with. While XGBoost has a large number of hyperparameters that can be tuned, we find that only three of these parameters significantly impact the final score, and therefore construct a search space only over those three parameters. We search over the number of estimators \( \{10, 25, 50, 100, 200\} \), the maximum depth of the tree \( \{3, 4, 5, 6, 7, 8\} \), and the learning rate \( U \in (0.01, 0.2) \).

2) Long Short Term Memory Fully Convolutional Networks: We also compare this dataset on a hybrid deep neural network, called the Long Short Term Memory Fully Convolutional Network (LSTM-FCN) [17]. It comprises of two branches, one with Convolutional blocks comprised of a Convolutional Layer, followed by Batch Normalization [24] and then the Relu activation function. Another branch is comprised of a

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1https://github.com/titu1994/pyshac
SHAC the FEMH 2018 Challenge. As discussed in III-B, we use models, and how we selected the best model to submit to the 5 fold cross validation score obtained by each of the significant enough to be comparable to the proposed model.

Upon inspection of the results, we find that the proposed model and XGBoost perform quite similarly. However, the standard deviation of the XGBoost model is much higher than that of the proposed model, albeit the mean of the score is marginally higher. It is for this reason that we state that the proposed model performs similarly and in a case outperformed more complicated models, such as XGBoost and LSTM-FCN. We recommend using this approach to provide a fast yet simple baseline to diagnose the vocal disorder in clinical practice. We leave the extension of this model to automatically diagnose larynx cancer as future work.

V. Conclusion

In this study, we present a model that classifies vocal disorders using a range of voice data samples obtained from the 2018 FEMH Voice Disorder Challenge. The proposed model extracts MFCC and MFCC delta features from raw input signals and applies them on a SVM classifier. We utilize the SHAC algorithm to tune the parameters of the classifier for optimal performance. Our results of the proposed model perform similarly in a case outperformed more complicated models, such as XGBoost and LSTM-FCN. We recommend using this approach to provide a fast yet simple baseline to diagnose the vocal disorder in clinical practice. We leave the extension of this model to automatically diagnose larynx cancer as future work.

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Long Short Term Memory Recurrent layer [25] followed by a dropout [26] layer (with a probability of 80%).

We utilize the same FCN and LSTM branch structure as provided by Karim et al. to be consistent, and only modify the number of LSTM cells in the LSTM branch, which we find using grid search [17]. All aspects of initialization and training methodology are kept consistent with the paper to provide the best results.

IV. Results

Due to the lack of a distinct test set, we instead discuss the 5 fold cross validation score obtained by each of the models, and how we selected the best model to submit to the FEMH 2018 Challenge. As discussed in III-B, we use the SHAC algorithm to randomly sample the best parameters which it determines can obtain strong scores on the overall validation sets of the 5 folds. For each of the models, out of the 100 hyperparameter settings sampled, we found one or more hyperparameter settings which scored above the mean + 1 standard deviation threshold we had set. We then train and evaluate each of these models on those candidates, and rank each of them. We find that we need to train fewer than 3 candidates in all cases as the candidates all score very close to each other. All code employed in this paper is available online. 2

The scores of each of these models has been provided in Table III. The final column contains the weighted score of the Sensitivity, Specificity and Recall scores with the weights 40%, 20% and 40% respectively.

| Model          | Sensitivity | Specificity | Recall  | Scores | Std. Dev |
|---------------|-------------|-------------|---------|--------|----------|
| Proposed Model| 0.8860      | 0.7823      | 0.5900  | 0.7469 | 0.0160   |
| XGBoost       | 0.8747      | 0.7561      | 0.6150  | 0.7470 | 0.0710   |
| LSTM-FCN      | 0.8539      | 0.6624      | 0.5550  | 0.6960 | 0.0401   |

2https://github.com/houshd/FEMH
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