

A novel hybrid method for vocal fold pathology diagnosis based on russian language

V. Majidnezhad

United Institute of Informatics Problems, National Academy of Science of Belarus, Minsk, Belarus.

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*Corresponding author: vahidm@yahoo.com (V. Majidnezhad).

Abstract

In this paper, first, an initial feature vector for vocal fold pathology diagnosis is proposed. Then, for optimizing the initial feature vector, a genetic algorithm is proposed. Some experiments are carried out for evaluating and comparing the classification accuracies, which are obtained by the use of the different classifiers (ensemble of decision tree, discriminant analysis and K-nearest neighbours) and the different feature vectors (the initial and the optimized ones). Finally, a hybrid of the ensemble of decision tree and the genetic algorithm is proposed for vocal fold pathology diagnosis based on Russian Language. The experimental results show a better performance (the higher classification accuracy and the lower response time) of the proposed method in comparison with the others. While the usage of pure decision tree leads to the classification accuracy of 85.4% for vocal fold pathology diagnosis based on Russian language, the proposed method leads to the 8.5% improvement (the accuracy of 93.9%).

Keywords: *Ensemble of Decision Tree, Genetic Algorithm (GA), Mel Frequency Cepstral Coefficients (MFCC), Wavelet Packet Decomposition (WPD), Vocal Fold Pathology Diagnosis.*

1. Introduction

Early detection of vocal fold pathology by the use of non invasive methods and employing different techniques of speech processing has recently attracted scientists' attention. Their aim is to develop new techniques for processing the speech signals of patients in order to decrease the treatments expenses and to increase the accuracy of diagnosis.

Nowadays, medical specialists use different medical techniques based on the direct examination of vocal folds. But these methods have two main drawbacks. Firstly, they are invasive. They may cause patients to feel uncomfortable and to distort the actual signal. Secondly, they are expensive to buy and their maintenance fees are high. The best option, for overcoming the disadvantages related to the medical instruments is to employ acoustic analysis techniques. They let medical specialists examine vocal fold in short time with minimal discomfort. They also allow to reveal the pathologies on early

stages. In recent years, a number of methods based on acoustic analysis were developed for vocal fold pathology classification [1-3]. These methods usually have two phases, which are the feature extraction phase and the classification phase. The feature extraction phase involves the transformation of speech signal into some parameters or features. The second phase implies a choice including a variety of machine learning methods.

Traditionally, for the feature extraction phase, one deals with such parameters like as jitter [4-5], shimmer [6-7], signal to noise ratio [8-9], formants [10-11]. Also some of the well-known classifiers for the classification phase in the previous works were such as Support Vector Machine (SVM) [12-15], Gaussian Mixture Model (GMM) [16-18], Artificial Neural Network (ANN) [19-21], Hidden Markov Model (HMM) [22-24].

In [25], it is proved that the classification accuracy of vocal fold pathology detection systems extremely depends on the dataset and its characteristics such as volume of dataset. So, it is obvious that the reported accuracies of the pervious works are not comparable due to the lack of the same conditions such as dataset. Even it is possible that they use the same dataset but their train and test sets would be different and consequently their reported accuracies cannot be compared.

In fact the acoustic characteristics of vowels differ in different languages. There are some researches such as [26,27] in which the differences of vowels in the different languages have been investigated. That is why; each language needs its special technique for vocal fold pathology detection system. So, the existing methods for the other languages such as English or Arabic or Korean cannot be used for Russian language. Of course, our main aim is to develop a high efficient method for vocal fold pathology detection based on Russian language.

The rest of the paper is organized as follows: In the second section, the initial feature vector based on the combination of the MFCC and the WPD is presented. In the third section, optimizing of the initial feature vector by the use of feature reduction methods is investigated. Experimental results are summarized in the fourth section. The last section concludes the paper.

2. Initial feature vector

First, using cepstral representation of input signal, the 13 Mel Frequency Cepstral Coefficients (MFCCs) are extracted. Then, the wavelet packet decomposition in 5 levels is applied on the input signal to make the wavelet packet tree with the 63 nodes. Next, from the nodes of the obtained wavelet packet tree, the 63 energy features as well as the 63 Shannon entropy features are extracted. Finally, by the combination of these features, the initial feature vector with the length of 139 features is constructed.

2.1. Mel frequency cepstral coefficients (MFCCs)

MFCCs are widely used features to characterize a voice signal and can be estimated by using a parametric approach derived from linear prediction coefficients (LPC), or by the non-parametric discrete fast Fourier transform (FFT), which typically encodes more information than the LPC method.

The Matlab code to calculate the MFCC features was adapted from the Auditory Toolbox (Malcolm Slaney).

2.2. Wavelet packet decomposition (WPD)

The most important property of WPD is that it reveals more information than DWT or CWT due to its detailed sub-bands information. The hierarchical wavelet packet (WP) transform uses a family of wavelet functions and their associated scaling functions to decompose the original signal into subsequent sub-bands. The decomposition process is recursively applied to both the low and high frequency sub-bands to generate the next level of the hierarchy. WPs can be described by the following collection of basic functions [28]:

$$W_{2n}(2^{p-1}x-1) = \sqrt{2^{1-p}} \sum_m h(m-2l) \sqrt{2^p} W_n(2^p x-m) \quad (1)$$

$$W_{2n+1}(2^{p-1}x-1) = \sqrt{2^{1-p}} \sum_m g(m-2l) \sqrt{2^p} W_n(2^p x-m) \quad (2)$$

Where p is scale index, l the translation index, h the low-pass filter and g the high-pass filter with

$$g(k) = (-1)^k h(1-k) \quad (3)$$

The WP coefficients at different scales and positions of a discrete signal can be computed as follows:

$$C_{n,k}^p = \sqrt{2^p} \sum_{m=-\infty}^{\infty} f(m) W_n(2^p m-k) \quad (4)$$

$$C_{2n,l}^{p-1} = \sum_m h(m-2l) C_{n,m}^p \quad (5)$$

$$C_{2n+1,l}^{p-1} = \sum_m g(m-2l) C_{n,m}^p \quad (6)$$

For a group of wavelet packet coefficients, energy feature in its corresponding sub-band is computed as [28]

$$Energy_n = \frac{1}{N^2} \sum_{k=1}^n |C_{n,k}^p|^2 \quad (7)$$

The entropy evaluates the rate of information, which is produced by the pathogens factors as a measure of abnormality in pathological speech. Also, the measure of Shannon entropy can be computed using the extracted wavelet packet coefficients, through the following formula [28]

$$Entropy_n = - \sum_{k=1}^n |C_{n,k}^p|^2 \log |C_{n,k}^p|^2 \quad (8)$$

In this study, the mother wavelet function of the tenth order Daubechies has been used. It is reported to be effective in voice signal analysis [29,30].

3. Optimized feature vector

The discrimination power of the initial features can be evaluated by the use of T-test. It can be used to investigate whether the means of two groups are statistically different from each other or not. For this purpose, it calculates a ratio between the difference of two group means and the variability of two groups. The T-test is applied on each feature in our dataset to compare p-value for each feature as a measure of how effective it is at separating groups. The result is shown in figure 1.

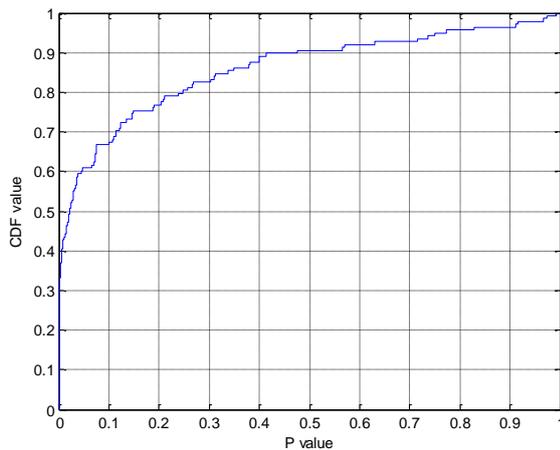


Figure 1. The P-value for the features.

There are about 40% of features having p-values close to zero and 60% of features having p-values smaller than 0.05, means that there are about 83 features among the original 139 features, which have strong discrimination power. Also, 40% of initial features (56 features) are not strong for the classification purpose. Therefore, feature reduction phase is necessary and important for our task.

Using every feature for the classification process is not good idea and it may cause to increase the misclassification error rate. Therefore, it is better to select proper features from the whole features. This process is called “Feature Reduction” or “Feature Selection”. In other words, the goal is to reduce the dimension of the data by finding a small set of important features, which can give good classification performance.

It is possible to categorize the feature reduction approaches into two categories: filter methods and wrapper methods. Filter methods focus on the general characteristics of the data to evaluate and to select the feature subsets without involving the chosen learning algorithm or the classifier. However, wrapper methods use the performance feedbacks of the chosen learning algorithm or the

classifier to evaluate each candidate feature subset. Wrapper methods search for a subset of features, which has better fitted for the chosen learning algorithm or the classifier, but they can be significantly slower than filter methods if the learning algorithm takes a long time to learn. The concepts of “filters” and “wrappers” are described in [31].

In this section, a well-known approach of the filter methods, which is called the Principal Component Analysis (PCA), is introduced. It is used frequently in the previous works such as [32-35]. Also a novel approach, the GA-based method, is proposed for the feature reduction phase. This method belongs to the wrapper methods.

3.1. Principal component analysis (PCA)

This method searches a mapping to find the best representation for distribution of data [36]. Therefore, it uses a signal-representation criterion to perform dimension reduction while preserving much of the randomness or variance in the high-dimensional space as possible [37]. The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. PCA involves the calculation of the eigenvalues decomposition of a data covariance matrix or singular value decomposition of a data matrix, usually after mean centering the data for each attribute.

In PCA, the optimal approximation of a random vector $X \in R^N$ in N -dimensional space by a linear combination of M ($M < N$) independent vectors is obtained by projecting the random vector X into the eigenvectors corresponding to the largest eigenvalues of the covariance matrix of vector X [37]. The main limitation of PCA is that it does not consider class separately, since it does not take into account the class label of the feature vectors.

3.2. GA-based feature reduction

GA is a heuristic optimization method, which acts on the basis of evaluation in nature and search for the final solution among a population of potential solutions. At the beginning of algorithm, a number of individuals (initial population) are created randomly and the fitness function is evaluated for all of them. If we do not reach to the optimal answer, the next generation is produced with selection of parents based on their fitness and the children mutates with a fixed probability and then the new children fitness is calculated and

new population is formed by substitution of children with parents and this process is repeated until the final condition is established.

In the proposed GA-based method, a fitness function f is defined which shows the misclassification error rate of the ensemble classifier for the train set.

$$f = \frac{\sum_{i=1}^n |a_i - r_i|}{n} \tag{9}$$

The a_i is the result of classifier and the r_i is the real class for i^{th} sample. The n is the number of samples in the train set. The aim of the proposed GA-based method is to find the subset of the initial features so that they minimize the f .

In the proposed method, the length of each chromosome is 139 (the length of the initial feature vector). Each gene in the chromosomes is related to one feature and can choose one of binary values (zero or one). These values show that whether the respective feature participates in the classification's process or not.

4. Experiments and results

Specialists from the Belarusian Republican Center of Speech, Voice and Hearing Pathologies created the dataset. The 75 pathological (vocal fold paralysis) samples and the 55 healthy samples, which are related to sustained vowel "a" have randomly been selected. All of the samples are the wave files in the PCM format and in a mono mode and the sample rate of 44100 Hertz and the bit-depth of 16 bit.

In this section, three experiments have been designed. These experiments are simulated in the Matlab. In all of the experiments, the 10 folds cross-validation scheme has been adapted to assess the generalization capabilities of the system and the obtained results [38]. The general scheme of the proposed method for the classification is illustrated in the figure 2.

In the first experiment, the classification has been done based on the initial feature vector, which contains all the 139 features. The results are shown in the table 1.

In the second experiment, the classification has been done based on the optimized feature vectors, which are obtained by the use of the PCA-based or the GA-based methods. The different feature vectors with different length are evaluated. The final optimized feature vector lengths and the obtained classification accuracies are shown in the table 2.

As it is obvious in the tables 1-2, both the PCA-

based and the GA-based methods can lead to the increasing of the classification accuracies. Of course, in terms of classification accuracy, the proposed GA-based method has a better performance in comparison with the PCA-based method. The main limitation of the PCA is that it does not take into account the class labels and it just focuses on the sample's value. In other words, the PCA searches for the features which their values have bigger variance in comparison with others and it does not collaborate with the classifier. But the proposed GA-based method uses a genetic algorithm in order to overcome this limitation of PCA. The GA-based method considers the misclassification error rate of the classifier in its fitness function and tries to minimize it.

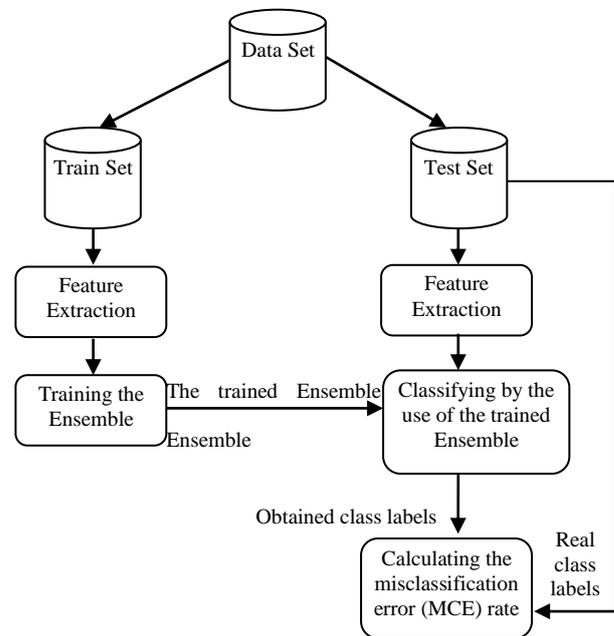


Figure 2. The general scheme of the proposed method for the classification.

Table 1. The obtained classification accuracies.

The classifiers	Ensemble of KNN	Ensemble of Discriminant Analysis	Ensemble of Binary Decision Tree
Classification Accuracy (%)	64.7	77	85.4

Table 2. The final feature vector lengths and the obtained classification accuracies.

The Classifiers/ Feature Reduction Methods	Ensemble of KNN	Ensemble of Discriminant Analysis	Ensemble of Binary Decision Tree
PCA-Based	77.7% (Feature vector length=22)	75.4% (Feature vector length=19)	86.2% (Feature vector length=11)
GA-Based	84.6% (Feature vector length=29)	78.5% (Feature vector length=3)	93.9% (Feature vector length=14)

Also, from the classifier point of view, the binary decision tree shows better results than the others. Finally, the experiment results show a better performance of the proposed method, which is based on the hybrid of the ensemble of decision tree as the classifier and the GA-based method as the feature reduction approach. It provides the best classification accuracy (93.9% of accuracy) in comparison with the others. It also leads to reduce the length of feature vector from 139 to 14 features. Therefore, the response time of the vocal fold pathology classification system based on the initial feature vector (with the length of 139) and the reduced feature vector (with the length of 14) should be different.

The third experiment is carried out to compare the response time of the vocal fold pathology classification system based on the initial feature vector and the reduced feature vectors. This experiment has carried out on a personal computer, which is equipped by the processor of Intel dual-core 2.13 Giga Hertz and the memory of 2 Giga Bytes. The response time in the case of the initial feature vector (139 features), 9.7 milliseconds is reported. The response time in the case of the reduced feature vector (11 features), which is obtained by the PCA-based method, 3.3 milliseconds is reported. Also, the response time in the case of the final reduced feature vector (14 features), which is obtained by the GA-based method, 3.6 milliseconds is reported. Therefore, using the reduced feature vectors leads to the decreasing of the response time of the program of vocal fold pathology classification in comparison with the non-reduced feature vector.

5. Conclusion

In this article, an initial feature vector based on the combination of the Wavelet Packet Decomposition (WPD) and the Mel Frequency Cepstral Coefficients (MFCCs) is proposed. The performances of the ensembles of three kinds of learners (KNN, discriminant analysis and binary decision tree) in the task of vocal fold pathology diagnosis are investigated. The experiments' results show the priority of the ensemble of decision tree in comparison with the others.

Also, the performance of three kinds of feature vector (the initial feature vector, the optimized feature vector by the means of the PCA-based method and the optimized feature vector by the means of the proposed GA-based method) is evaluated. The experiments' results show the priority of the optimized feature vector by the means of the proposed GA-based method in

comparison with the others. This better performance is due to taking into consideration of the ensemble classifier in the feature reduction phase. In other words, the proposed GA-based method tries to optimize the initial feature vector with the aim of decreasing the misclassification error rate of the ensemble classifier. But the PCA-based method just focuses on the data without any attention on the misclassification error rate of the ensemble classifier.

Finally, the proposed method is proposed based on the hybrid of the ensemble of decision tree as the classifier and the proposed GA-based method as the feature reduction approach. It is concluded that the proposed method has the higher accuracy (93.9% of accuracy) and the lower response time in comparison with the other ones.

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یک روش ترکیبی جدید برای تشخیص بیماری تارهای صوتی در زبان روسی

وحید مجیدنژاد

انستیتو انفورماتیک، آکادمی علوم بلاروس، مینسک، بلاروس.

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چکیده:

در این مقاله، ابتدا یک بردار ویژگی اولیه جهت تشخیص بیماری تارهای صوتی پیشنهاد شده است. سپس یک الگوریتم ژنتیک برای بهینه‌سازی این بردار ویژگی اولیه پیشنهاد شده است. تعدادی آزمایش برای ارزیابی و مقایسه دقت تشخیص، به هنگام استفاده از دسته‌بندهای مختلف (درخت تصمیم‌گیری تجمیعی، تحلیل تفکیکی تجمیعی، k-نزدیکترین همسایه تجمیعی) و بردارهای ویژگی مختلف (اولیه و بهینه)، انجام گرفته است. سرانجام یک ترکیب از درخت تصمیم‌گیری تجمیعی و الگوریتم ژنتیک برای تشخیص بیماری تارهای صوتی در زبان روسی پیشنهاد شده است. بطوریکه نتایج آزمایش‌ها نشان‌دهنده کارایی بهتر (دقت تشخیص بیشتر و زمان پاسخ کمتر) این روش پیشنهادی در مقایسه با سایر روش‌ها است. در حالیکه استفاده از درخت تصمیم‌گیری تجمیعی، به تنهایی به دقت تشخیص ۸۵.۴٪ منجر می‌شود، استفاده از این روش پیشنهادی باعث ۸.۵٪ بهبود (دقت تشخیص ۹۳.۹٪) می‌گردد.

کلمات کلیدی: درخت تصمیم‌گیری تجمیعی، الگوریتم ژنتیک، ضرایب فرکانسی مل کپستروم، تجزیه بسته‌های موجک، تشخیص بیماری تارهای صوتی.