MODIFIED LOCAL DISCRIMINANT BASES AND ITS APPLICATIONS IN SIGNAL CLASSIFICATION

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ABSTRACT

One of the major challenges in classification problems based on signal decomposition approach is to identify the right basis function and its derivatives that can provide optimal features to distinguish the classes. With the vast amount of available libraries of orthonormal bases, it is hard to select an optimal set of basis functions for a specific dataset. To address this problem, pruning algorithms based on certain selection criteria is needed. Local Discriminant Bases (LDB) algorithm is one such algorithm, which efficiently selects a set of significant basis functions from the library of orthonormal bases based on certain defined dissimilarity measure. The selection of this dissimilarity measure is critical as they indirectly contribute to the performance accuracy of the LDB algorithm. In this paper, we study the impact of the dissimilarity measures on the performance of the LDB algorithm with two classification examples. The two biomedical signal databases used are 1. Vibroarthographic signals (VAG) - 89 signals with 51 normal and 38 abnormal, and 2. Pathological speech signals - 100 signals with 50 normal and 50 pathological. Classification accuracies of 76.4% with VAG database and 96% with pathological speech databases were obtained. This modified method of signal analysis using LDB has shown its powerfulness in analyzing non-stationary signals.

1. INTRODUCTION

The Local Discriminant Bases (LDB) [1] algorithm is recently being used successfully in many classification problems. The optimal choice of LDBs for a given dataset is driven by the nature of the dataset and the dissimilarity measures [2] used to distinguish between classes. The choice of the dissimilarity measure for a particular dataset depends on knowledge of the data, computational complexity, and the classification accuracy requirements. For example probabilistic dissimilarity measures such as relative-entropy needs prior knowledge of the dataset distribution, whose accuracy depends on the size of data, on the other hand simple dissimilarity measures such as Euclidean distance is only suitable for numeric data sets. A combination of multiple dissimilarity measures with varying complexity can be used to achieve high classification accuracies.

In this paper we analyze two biomedical signal databases using LDB algorithm with 3 different dissimilarity measures. The LDB algorithm is based on the wavelet packet decompositions with 3 different wavelets namely Daubechies (db4), Coiflet (cf4) and Symlet (sy4) [3]. This gives us 9 different combinations for each of the databases. A two group (class1 and class2) classification was performed for the 9 combinations. Linear discriminant analysis (LDA) based classifier was used to compute the classification accuracies. The classification accuracies were verified using the leave-one-out method [4]. The paper is organized as follows: In Section 2 on Methodology, Local Discriminant Bases algorithm, dissimilarity measures, feature extraction and pattern classification are covered. Results and discussions are covered in Section 3, and Conclusions in Section 4.

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2. METHODOLOGY

2.1. Local Discriminant Bases Algorithm

In the LDB [1] algorithm with wavelet packet bases, a set of training signals x_i^c for all C classes are decomposed to a full tree structure of order N. We restrict our analysis to binary wavelet packet trees. Let $\Omega_{0,0}$ be a vector space in R^n corresponding to the node 0 of the parent tree. Then at each level the vector space is spilt into two mutually orthogonal subspaces given by $\Omega_{j,k} = \Omega_{j+1,2k} \oplus \Omega_{j+1,2k+1}$ where j indicates the level of the tree and k represents the node index in level j, given by $k = 0, ..., 2^j - 1$. This process repeats till the level J, giving rise to 2^J mutually orthogonal subspaces. Our goal is to select the set of best subspaces that provide maximum discriminant information between the classes of the signal. Each node k contains a set of basis vectors $B_{j,k} = [\mathbf{w_{j,k,l}}]_{l=0}^{l=2^{no-j}-1}$, where 2^{no} corresponds to the length of the signal. Then the signal x_i can be represented by a set of coefficients c as:

$$x_i = \Sigma_{j,k,l} c_{j,k,l} \mathbf{w_{j,k,l}} \qquad (1)$$

Basically the signal x_i is decomposed into 2^J subspaces with $c_{j,k,l}$ coefficients in each subspace. With the training signals decomposed into wavelet packet coefficients we need to define a dissimilarity measure (D_n) in the vector space so as to identify those subspaces, which have larger statistical distance between classes. This dissimilarity measure is used in an iterative manner to prune the tree in such a way that only a node is split if the cumulative discriminative measure of the children nodes is greater than the parent node. The resulting tree contains the most significant LDBs, from which a set of K significant LDBs are selected to construct the final tree. The testing set signals are then expanded using this tree and features are extracted from the respective basis vectors for classification.

In the proposed method we use a similar approach with some modification. Instead of the selective splitting of the nodes, which basically helps in removing the redundancy in the LDB selection, we used all the nodes from the full decomposition tree and ranked them in decreasing order of their dissimilarity measure values between classes. The first 5 nodes that exhibit high dissimilarity measure values between the classes are selected for each trial. Among these nodes, based on the frequency of occurrence in all the trials, the 5 most occurring significant LDBs are selected. The redundancy within these 5 LDBs is later removed in the feature evaluation process in the LDA classifier. This is basically done to reduce the computational complexity of the LDB algorithm implementation. The whole process is repeated for three different wavelets (db4, cf4 and sy4) and the wavelet, which provides maximum dissimilarity measures among all the tested wavelets, is chosen to be the best basis for expansions.

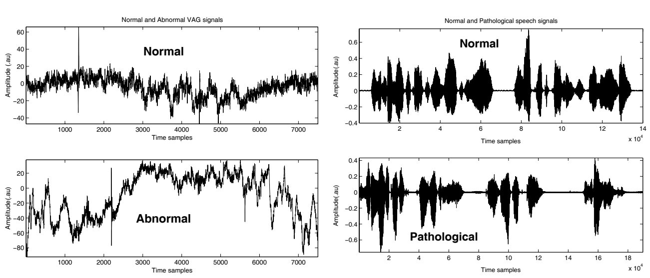
2.2. Databases

2.2.1. Vibroarthographic (VAG) signals

These are the vibration signals emitted from the human knee joints during an active movement of the leg. The VAG signals can be used to detect the early joint degeneration or knee defects that are reflected in knee movements. Extensive work [5] has been done using time-frequency approach in classifying these signals into multiple groups. Few important characteristics of the VAG signals which make them difficult to analyze are as follows: (i) Highly non-stationary in nature, (ii) Varying frequency dynamics, and (iii) Multi-component signal. The database consists of 89 signals with 51 normal and 38 abnormal signals. A normal and an abnormal VAG signal are shown in Fig. 1a.

2.2.2. Pathological speech signals

These are speech signals recorded from the pathological and normal talkers in a sound-proof booth at the Massachusetts Eye and Ear Infirmary. The normal talkers exhibited no abnormal vocal characteristics and indicated no history of voice disorders. All signals were sampled at 25 kHz. The signals were the first sentence of the rainbow passage, 'when the sunlight strikes rain drops in the air, they act like a prism and form a rainbow', as spoken by the subjects. More details about the database and the classification problem can be found in authors previous work [6]. The database consists of 100 signals with 50 normal and 50 abnormal signals. A normal and pathological speech signal are shown in Fig. 1b.



(a) VAG signals (b) Pathological speech signals

Fig. 1. An Example of normal and abnormal/pathological signals for both the databases.

2.3. Dissimilarity measures

In this study we used three different dissimilarity measures and performed a two group (class1 and class2) classification on the databases. In general most of the biomedical signals can be characterized by one or more of the following, (i) Their average energy distribution pattern over frequency bands, (ii) Event based temporal structures, (iii) Periodicity, and (iv) The amount of randomness. These rationales were used in arriving at the following dissimilarity measures.

The first dissimilarity measure D_1 is the difference in the normalized energy between the corresponding nodes of the training signals from class1 and class2. This gives the difference in the energy distribution of the signals on the time-frequency plane.

$$D_1 = E^1_{j,k} - E^2_{j,k}, \tag{2}$$

where $E^1_{j,k}$ and $E^2_{j,k}$ are the normalized energy of the corresponding nodes for class1 and class2 signals.

The second dissimilarity measure D_2 is the correlation index between the basis vectors at corresponding nodes. This measure emphasizes those nodes that can detect the difference in the temporal characteristics of the signals between class1 and class2.

$$D_2 =< B_{j,k}, F_{j,k} >, \tag{3}$$

where B and F are the corresponding basis vectors of class1 and class2 at node (j, k)

The discriminant measure D_3 is a measure of estimating the randomness or non-stationarity of the basis vectors. It is computed as the set of variances along the segments of the basis vector coefficients. The ratio of this variance measure between the signals from class1 and class2 indicate the amount of deviation observed in the non-stationarity between the classes.

$$D_3 = \frac{var(var(p))_{j,k})}{var(var(q))_{j,k})}, \tag{4}$$

where p and q are the index of the L segments obtained by segmenting the basis vectors at node (j, k) for class1 and class2.

2.4. Feature extraction

Once the LDB nodes for each of the three dissimilarity measures are identified using the training sets (in our study 10 randomly selected signals for each class were used to form the training set) as explained in Section 2.1, all the 89 VAG signals and the 100 pathological speech signals were decomposed using the corresponding sets of LDB tree structures. Figs. 2 and 3 show the sample LDB tree structure obtained for the VAG and pathological speech databases respectively.

The basis vectors from each of the nodes (LDBs) can be directly used as feature vector, however, considering the dimension of the basis vectors, we extract the same features from the basis vectors of LDBs using the dissimilarity measures (D_1, D_2, and D_3) [1]. That is, from each of the LDB nodes of the corresponding tree structures, the normalized node energy, correlation index and the variance measure were calculated. In short, each signal in the database is used to compute 15 features, 5 from each dissimilarity measure. As for the correlation index calculation we use a random choice of normal signal as a template to correlate with the signals from respective test databases. The above procedure was

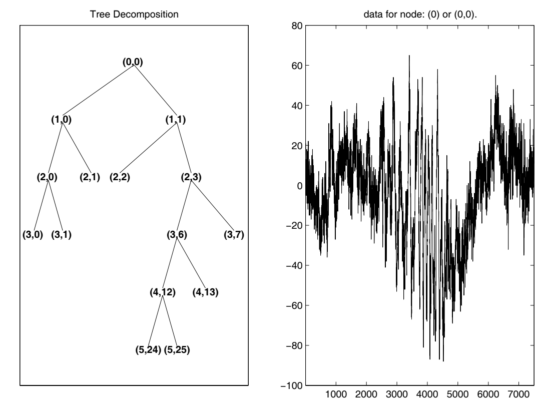


Fig. 2. A sample LDB tree decomposition for VAG database (db4 wavelet and D_3 dissimilarity measure)

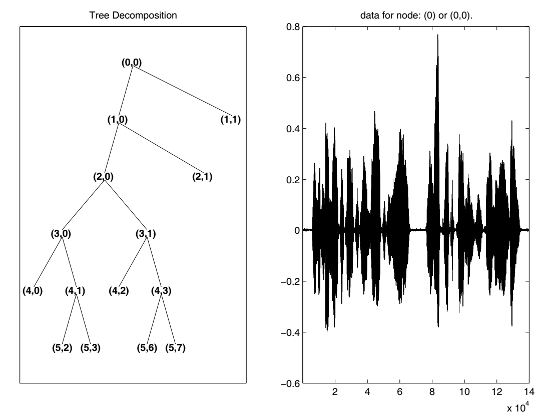


Fig. 3. A sample LDB tree decomposition for pathological speech database (cf4 wavelet and D_3 dissimilarity measure)

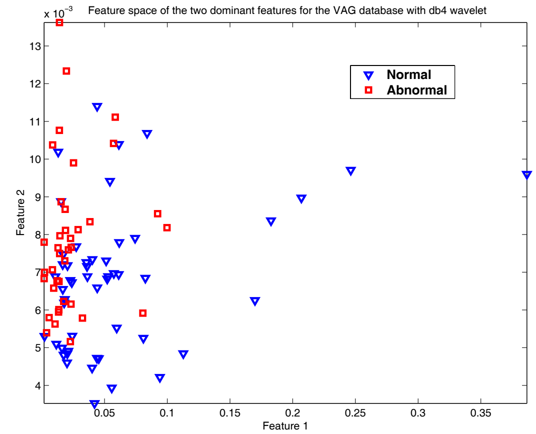


Fig. 4. Feature space with the first two dominant features - VAG database, db4 wavelet

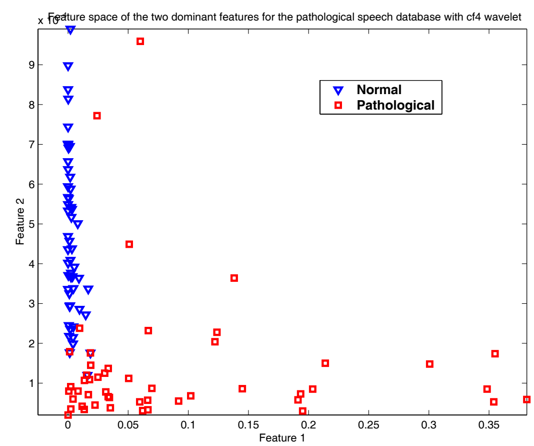


Fig. 5. Feature space with the first two dominant features - Pathological speech database, cf4 wavelet

repeated for all the three wavelets. So, in total, for each wavelet, a set of 15 feature vectors was extracted from each of the signal in the test database.

Figs. 4 and 5 demonstrate the feature space with the first two dominant features of the VAG and pathological speech database respectively. From the figures of the feature space plots, the discriminatory boundaries can be visualized between the signals of class1 and class2. These extracted features were then fed to a linear discriminant based classifier as will be explained in next section.

2.5. Pattern Classification

The motivation for the pattern classification is to automatically group signals of same characteristics using the discriminatory features derived as explained in the previous section. Pattern classification was carried out by linear discriminant analysis (LDA) technique using the SPSS software [7]. In discriminant analysis, the feature vector derived as explained above were transformed into canonical discriminant functions such as

$$f = x_1 b_1 + x_2 b_2 + \ldots\ldots + x_{42} b_{42} + a, \qquad (5)$$

where $\{x\}$ is the set of features, $\{b\}$ and a are the coefficients and constant respectively estimated and derived using the Fisher's linear discriminant functions [7]. Using the chi-square distances and the prior probabilistic values of each group the classification is performed to assign each sample data to one of the groups.

The classification accuracy was estimated using the leave-one out method which is known to provide a least bias estimate [4]. In leave-one-out method, one sample is excluded from the dataset and the classifier is trained with the remaining samples. Then the excluded signal is used as the test data and the classification accuracy is determined. This is repeated for all samples of the dataset. Since each signal is excluded from the training set in turn, the independence between the test and the training set are maintained.

3. RESULTS AND DISCUSSIONS

All the signals from both the databases were decomposed using their corresponding LDB tree structures. Features were extracted as explained in Section 2.4 and fed to the LDA based classifier. Classification accuracies were computed for the 9 combinations of the wavelet and the dissimilarity measures as shown in Table

Wavelet	LDA type	D_1	D_2	D_3
db4	Regular	65	64	67
	Cross.V	61	57	64
cf4	Regular	70	61	61
	Cross.V	65	57	48
sy4	Regular	67	63	57
	Cross.V	61	60	45

Table 1. Classification table for VAG database. Regular - Normal LDA, Cross.V - Leave-one-out method LDA, Classification accuracies are in percentage (%)

Wavelet	LDA type	D_1	D_2	D_3
db4	Regular	84	64	77
	Cross.V	84	60	72
cf4	Regular	85	52	92
	Cross.V	84	37	91
sy4	Regular	87	53	86
	Cross.V	84	32	84

Table 2. Classification table for pathological speech database. Regular - Normal LDA, Cross.V - Leave-one-out method LDA, Classification accuracies are in percentage (%)

1 and Table 2 for both the databases. It can be observed from Table 1 that even though there are little variations, on an average all the three dissimilarity measures perform equally for the VAG database. However from Table 2 for the Pathological speech database it can be seen that the dissimilarity measures D_1 and D_3 provide high classification accuracies, whereas D_2 performs poorly. In overall for VAG database we observe that the db4 wavelet in combination with all the three dissimilarity measures provides the highest classification accuracy. Similarly we observe for pathological database that the cf4 wavelet in combination with D_1 and D_3 provides the highest classification accuracy. Using these combinations we computed the highest possible classification accuracies for both the databases as shown in Table 3 and Table 4.

For the VAG database an overall classification accuracy of 78.7% using regular LDA and 76.4% using leave-one-out method were achieved. This is higher than the reported classification accuracy in [5]. For the pathological speech database an overall classification accuracy of 97% using regular LDA and 96% using leave-one-out method were achieved. This is higher than the reported classification accuracy in [6]. The above results demonstrate the performance optimization of the LDB algorithm using the right choice and combination of the dissimilarity measures to achieve high classification accuracies for non-stationary signal analysis.

4. CONCLUSIONS

The importance of the dissimilarity measure in the performance optimization of the LDB algorithm was discussed with two classification examples. Classification accuracies were analyzed for different combinations of wavelets and the dissimilarity measures. Improvement in the classification accuracies by using a combination of multiple dissimilarity measures was demonstrated. High classification accuracies were achieved for the databases under study, thus proving the success of the modified LDB in analyzing non-stationary signals. Future work involves in automating the choice of dissimilarity measures based on the nature of the databases and applications.

Method	Groups	Normal	Abnormal	Total
Regular	Normal	39	12	51
	Abnormal	7	31	38
%	Normal	**76.5**	23.5	100
	Abnormal	18.4	**81.6**	100
Cross.V	Normal	39	12	51
	Abnormal	9	29	38
%	Normal	**76.5**	23.5	100
	Abnormal	23.7	**76.3**	100

Table 3. Table showing the highest classification accuracy achieved for the VAG database(db4 wavelet and selective combination of D_1, D_2 and D_3) . Regular - Normal LDA, Cross.V - Leave-one-out method LDA, % = Percentage of classification

Method	Groups	Normal	Pathological	Total
Original	Normal	48	2	50
	Pathological	1	49	50
%	Normal	**96**	4	100
	Pathological	2	**98**	100
Cross.V	Normal	48	2	50
	Pathological	2	48	50
%	Normal	**96**	4	100
	Pathological	4	**96**	100

Table 4. Table showing the highest classification accuracy achieved for the pathological speech database (cf4 wavelet and combined D_1 and D_3). Regular - Normal LDA, Cross.V - Leave-one-out method LDA, % = Percentage of classification

5. REFERENCES

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