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Title: MULTI-SCALE TWO-DIRECTIONAL TWO-DIMENSIONAL PRINCIPAL COMPONENT ANALYSIS AND ITS APPLICATION TO HIGH-DIMENSIONAL BIOMEDICAL SIGNAL CLASSIFICATION

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MULTI-SCALE TWO-DIRECTIONAL TWO-DIMENSIONAL PRINCIPAL COMPONENT ANALYSIS AND ITS APPLICATION TO HIGH-DIMENSIONAL BIOMEDICAL SIGNAL CLASSIFICATION

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Abstract: Time-frequency (TF) analysis including the wavelet transform (WT) offers simultaneous interpretation of the biomedical signal in both the time and frequency domains for analyzing signals such as electromyography (EMG), electroencephalography (EEG), electrocardiography (ECG), and Doppler ultrasound. In this paper A novel multi-scale two-directional two-dimensional principal component analysis for high-dimensional signal classification is proposed for efficient extraction of essential feature information from high dimensional signal. Spatial-time frequency discriminate information from high-dimensional EMG electrode array can be effectively extracted and reduced using this method. Multi-scale matrices constructed in the first step incorporate the spatial correlation and physiological characteristics of sub-band signals among channels The efficiency and effectiveness of the method can be further validated by using high-dimensional EEG, MEG, fMRI signals. Although the present study focuses on high-dimensional signal pattern classification, based on the PCs obtained at multiple scales, it is relatively straightforward to expand MS2D2PCA for high-dimensional signal compression, denoising, component extraction, and other related tasks. Results are presented from an experiment, which illustrates the efficiency and effectiveness of the proposed method for high-dimensional biomedical signal analysis

Index Terms—time-frequency analysis, wavelet transform

1. INTRODUCTION

Simultaneously preserving the most original Most biomedical signals are typically nonlinear and non stationary. Time-frequency (TF) analysis including the wavelet transform (WT), offers simultaneous interpretation of the biomedical signal in both the time and frequency domains, allowing the elucidation of local, transient or intermittent components at various scales [1]. However, there are typically a large amount of wavelet

coefficients generated from such a two-dimensional analysis. In addition, noise artifacts as well as redundant information may be present in these time-frequency coefficients. Principal component analysis (PCA) decomposes the covariant structure of the dependent variables into orthogonal components by calculating the Eigen values and eigenvectors of the data covariance matrix. It linearly projects the original data from a high-dimensional space to a set of uncorrelated components in a low-

dimensional feature space, while simultaneously preserving the most original information. Therefore, WT combined with PCA (WT-PCA) has been one of the most powerful approaches for simultaneously extracting discriminative features and reducing the dimension for bio signals classification tasks. The basic algorithm for this hybrid method consists of decomposing biomedical signals into the time-frequency plane, re-arranging the time-frequency elements into a row vector, and reducing the dimension using PCA. Examples of application of this algorithm in the area of electromyography (EMG) signal analysis include Engle hart et al. [2, 3], who decomposed four channels of transient EMG signals using short-time Fourier transform (STFT), WT, and wavelet packet transform (WPT) methods to discriminate six hand motions for prosthetic hand control. They

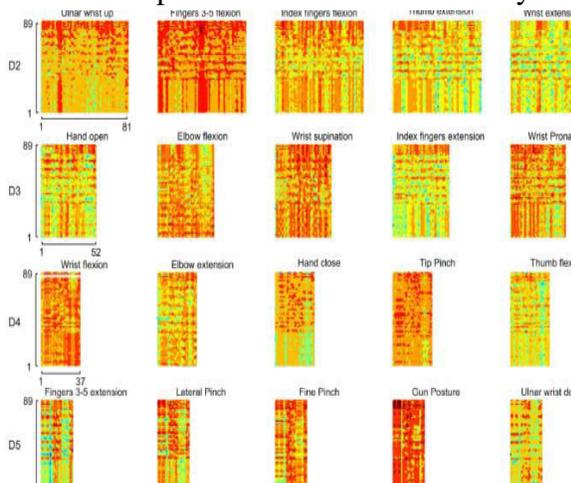


Fig.1 Contour plots of multi-scale matrices for 89-channel EMG traces of 20 hand movements

Compared the performance of PCA feature reduction against the Euclidean distance class separability (CS) criterion. The results indicated TF-PCA was vastly

superior to TF-CS in classification accuracy, as well as a significant improvement of all TF-based methods compared to time domain feature extraction when using a linear discriminant analysis (LDA) classifier.

II. LITERATURE SURVEY:

TOPIC: Real-time intelligent pattern recognition algorithm for surface EMG signals Electromyography (EMG) is the study of muscle function through the inquiry of electrical signals that the muscles emanate. EMG signals collected from the surface of the skin (Surface Electromyogram: semg) can be used in different applications such as recognizing musculoskeletal neural based patterns intercepted for hand prosthesis movements. Current systems designed for controlling the prosthetic hands either have limited functions or can only be used to perform simple movements or use excessive amount of electrodes in order to achieve acceptable results. In an attempt to overcome these problems we have proposed an intelligent system to recognize hand movements and have provided a user assessment routine to evaluate the correctness of executed movements.

We propose to use an intelligent approach based on adaptive neuro-fuzzy inference system (ANFIS) integrated with a real-time learning scheme to identify hand motion commands. For this purpose and to consider the effect of user evaluation on recognizing hand movements, vision feedback is applied to increase the capability of our system. By using this scheme the user may assess the correctness of the performed hand movement. In this work a hybrid method for training fuzzy system, consisting

of back-propagation (BP) and least mean square (LMS) is utilized. Also in order to optimize the number of fuzzy rules, a subtractive clustering algorithm has been developed. To design an effective system, we consider a conventional scheme of EMG pattern recognition system. To design this system we propose to use two different sets of EMG features, namely time domain (TD) and time-frequency representation (TFR). Also in order to decrease the undesirable effects of the dimension of these feature sets, principle component analysis (PCA) is utilized This study shows that ANFIS real-time learning method coupled with mixed time and time-frequency features as EMG features can provide acceptable results for designing semg pattern recognition system suitable for hand prosthesis control.

TOPIC: Signal processing of the surface electromyogram to gain insight into neuromuscular physiology A surface electromyogram (semg) contains information about physiological and morphological characteristics of the active muscle and its neural strategies. Because the electrodes are situated on the skin above the muscle, the semg is an easily obtainable source of information. However, different combinations of physiological and morphological characteristics can lead to similar semg signals and semg recordings contain noise and other artifacts. Therefore, many semg signal processing methods have been developed and applied to allow insight into neuromuscular physiology. This paper gives an overview of important advances in the development and applications of semg signal processing methods, including spectral estimation, higher order statistics

III.EXISTING SYSTEM

3.1.Discrete wavelet transform

The foundations of the DWT go back to 1976 when Crosier, Esteban, and Galand devised a technique to decompose discrete time signals. Crochiere, Weber, and Flanagan did a similar work on coding of speech signals in the same year. They named their analysis scheme as sub band coding. In 1983, Burt defined a technique very similar to sub band coding and named it pyramidal coding which is also known as multi resolution analysis. Later in 1989, Vetterli and Le Gall made some improvements to the sub band coding scheme, removing the existing redundancy in the pyramidal coding scheme. Sub band coding is explained below. A detailed coverage of the discrete wavelet transform and theory of multi resolution analysis can be found in a number of articles and books that are available on this topic, and it is beyond the scope of this tutorial. S is the number of channels the D_{ij} represents discrete wavelet detail coefficients vector for channel i at scale j and the A_{iL} denotes the corresponding approximation coefficients vector for channel i

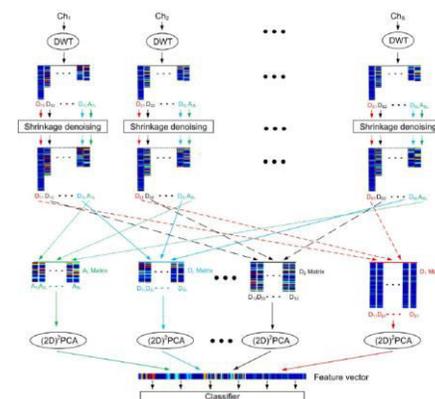


Fig2 .Multi-scale

two-directional two-dimensional principal component analysis method for high-dimensional biomedical signal classification.

3.2.D²PCA

One of the important technique of recognition is template matching in which a template to recognize is available and is compared with already stored template. In our approach PCA method for feature extraction and matching is used. Principal Component Analysis: PCA is used to reduce the dimensionality of the image while preserving much of the information. It is the powerful tool for analyzing the data by identifying patterns in the dataset and reduces the dimensions of the dataset such that maximum variance in the original data is visible in reduced data.

3.2.1 ALGORITHM FOR PCA

Training Stage: Calculation of Eigen vectors

1. Obtain the database containing N training images of dimensions $M \times M$: $I_1, I_2, I_3, \dots, \dots, I_N$.
2. Convert these N images into vectors Z_i , N of dimension M^2

$$\Psi = \frac{1}{N} \sum_{i=1}^N Z_i$$

3. Obtain mean image vector
4. Obtain the difference image by subtracting the mean image vector from the training image. $\Phi_i = Z_i - \Psi$
5. Obtain the covariance Matrix C having dimensions $M^2 \times M^2$

$$C = \frac{1}{N} \Phi_n \Phi_i^T = AA^T$$

$$A = [\Phi_1, \Phi_2, \Phi_3, \dots, \dots, \Phi_N.] \text{ Dimension } M^2 \times N$$

6. Compute the Eigen vectors V of AA^T
As the dimensions of AA^T $M^2 \times M^2$ Are

very large so computation of eigenvectors is impractical.

7. Obtain Eigen vectors u_i Of AA^T [dimensions $N \times N$. AA^T Has M^2 Eigen vectors and Eigen values. AA^T Has N Eigen vectors and Eigen values
8. Obtain the best N eigenvectors of AA^T By following equation. $u_i = AA^T$ Take only V Eigen vectors corresponding to V largest Eigen values

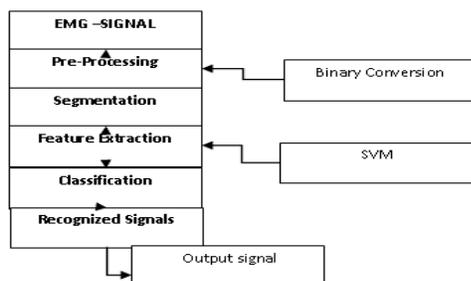
IV. Spatial Multi-Scale Muscle Activity Patterns

Using the proposed multi-scale spatial matrix technique, the spatial EMG activity at each scale was obtained. Since approximate coefficients at level 5 contained considerable low-frequency artifact, whilst the detail coefficients for level 1 corresponded to high-frequency components greater than 500 Hz, both of these were discarded in the analysis. Fig. shows the typical contour plots obtained for the twenty movements for subject 5 at scales D2-D5 of Coif let 4 mother wavelet. The five panels from left to right in the first row corresponded to the spatial-time-frequency activities of intended movements corresponding to ulnar wrist up, fingers 3-5 flexion, index-finger flexion, thumb extension, and wrist extension. With each intended movement, a significant difference between the intensity of the surface EMG signals at D2 over the upper limb muscles can be readily discerned in these contour plots. The second row of Fig. 3 indicates the STF distributions of hand open, elbow flexion, wrist suppiration, index-finger extension, and wrist pronation at scale D3.

The third row displays EMG activities corresponding to wrist flexion, elbow extension, hand closing, tip pinch, thumb flexion at scale D4. The final row of Fig. below displays the specific characteristics of the five remaining movements, namely fingers 3-5 extension, lateral pinch, fine pinch, gun posture, and ulnar wrist down. Similar to the panels in the top row, there was significant discrepancy in the intensity distributions of the remaining contour plots, indicating useful discriminate information in the multi-scale matrices.

V. PROPOSED SYSTEM

i) structured learning for emg signal segmentation Segmentation of handwritten document images into text-lines and EMG signals is an essential task for optical character recognition. However, since the features of handwritten document are irregular and diverse depending on the person, it is considered a challenging problem. In order to address the problem, we formulate the EMG signal segmentation problem as a binary quadratic assignment problem that considers pair wise correlations between the gaps as well as the likelihoods of individual gaps. Even though many parameters are involved in our formulation



Scheme, removing the existing redundancy in the pyramidal coding scheme. Sub band coding is explained below. A detailed coverage of the discrete wavelet transform

and theory of multi resolution analysis can be found in a number of articles and books that are available on this topic, and it is beyond the scope of this tutorial.

i) For the EMG signal segmentation some of the features map selection and the adopted structured learning techniques are discussed as follows: 1) Normalized distances of the neighboring super pixels: The most important property of the EMG signal separators are their distances between two EMG signals. As compared to the intra-EMG signal gap, width between the two EMG signals are large. In this paper four measures are used to represent the width of gaps. They are boundary distances between rectangles/ ellipses and center-to-center distances of them. All these distances are normalized to find the mean width W .

ii) Features of projection profiles: The projection profile of a text-line shows the number of pixels for each horizontal position. The length of consecutive zeros of projection profile has been formulated for the EMG signal segmentation of machine printed documents [13].

Hard-margin

If the training data are linearly separable, we can select two parallel hyper planes that separate the two classes of data, so that the distance between them is as large as possible. The region bounded by these two hyper planes is called the "margin", and the maximum-margin hyper plane is the hyper plane that lies halfway between them. These hyper planes can be described by the equations

$$\vec{w} \cdot \vec{x} + b = 1$$

and

$$\vec{w} \cdot \vec{x} + b = -1.$$

Geometrically, the distance between these two hyperplanes is so to maximize the distance between the planes we want to minimize. As we also have to prevent data points from falling into the margin, we add the following constraint: for each either. These constraints state that each data point must lie on the correct side of the margin. This can be rewritten as: We can put this together to get the optimization problem: "Minimize subject

$$\vec{w} \cdot \vec{x}_i + b \geq 1, \text{ if } y_i = 1$$

or

$$\vec{w} \cdot \vec{x}_i + b \leq -1, \text{ if } y_i = -1.$$

To for "The and that solve this problem determine our classifier, An easy-to-see but important consequence of this geometric description is that max-margin hyper plane is completely determined by those which lie nearest to it. These are called support vectors.

Soft-margin

To extend SVM to cases in which the data are not linearly separable, we introduce the hinge loss function, This function is zero if the constraint in (1) is satisfied, in other EMG signals, if lies on the correct side of the margin. For data on the wrong side of the margin, the function's value is proportional to the distance from the margin. We then wish to minimize where the parameter determines the tradeoff between increasing the margin-size and ensuring that the ie on the correct side of the

margin. Thus, for sufficiently small values of, the soft-margin SVM will behave identically to the hard-margin SVM if the input data are linearly classifiable, but will still learn a viable classification rule if not

Feature Extraction Stage

Feature extraction is the process of getting useful information from the EMG signal/character image. The information will be used to generate modules to train the classifier and to be used for classification purposes. In general there are two categories of features extracted, structural and statistical features. Choosing the Wright feature extraction method might be the most important step for achieving a high recognition rate. However, in some cases the combination of several features extraction types could be a wise decision to enhance the overall recognition performance. Structural features are the character/EMG signal image geometrical and topological information. Those obtained information include the number of PAWS, descenders', ascenders, dot below the baseline, above the baseline, etc. Figure shows a structural features example. Statistical feature are numerical measures computed over the signals

2.Gaussian Mixture Model

A Gaussian Mixture Model (GMM) is a parametric probability density function represented as a weighted sum of Gaussian component densities. Gmms are commonly used as a parametric model of the probability distribution of continuous measurements or features in a biometric system, such as vocal-tract related spectral features in a speaker recognition system. GMM parameters are estimated from

training data using the iterative Expectation-Maximization (EM) algorithm or Maximum A Posteriori (MAP) estimation from a well-trained prior model

A Gaussian mixture model is a weighted sum of M component Gaussian densities as given by the equation,

$$P(x|\lambda) = \sum_{i=1}^M w_i g(x|\mu_i, \Sigma_i)$$

Where x is a D -dimensional continuous-valued data vector (i.e. Measurement or features), $w_i, i = 1, \dots, M$, are the mixture weights, and $g(x|\mu_i, \Sigma_i), i = 1, \dots, M$, are the component Gaussian densities. Each component density is a D -variate Gaussian function of the form,

$$G(x|\mu_i, \Sigma_i) = \frac{1}{(2\pi)^{D/2} |\Sigma_i|^{1/2}} \exp - \frac{1}{2} (x - \mu_i)' \Sigma_i^{-1} (x - \mu_i)$$

With mean vector μ_i and covariance matrix Σ_i . The mixture weights satisfy the constraint that $\sum_{i=1}^M w_i = 1$. The complete Gaussian mixture model is parameterized by the mean vectors, covariance matrices and mixture weights from all component densities. These parameters are collectively represented by the notation

$$\Lambda = \{w_i, \mu_i, \Sigma_i\} \quad i = 1, \dots, M.$$

There are several variants on the GMM shown in Equation (3). The covariance matrices, Σ_i , can be full rank or constrained to be diagonal. Additionally, parameters can be shared, or tied, among the Gaussian components, such as having a common covariance matrix for all components, The choice of model configuration (number of components, full or diagonal covariance matrices, and parameter tying) is often determined by the amount of data available for estimating the GMM parameters and how the GMM is used in a particular biometric application. It is also important to

note that because the component Gaussians are acting together to model the overall feature density, full covariance matrices are not necessary even if the features are not statistically independent. The linear combination of diagonal covariance basis Gaussians is capable of modeling the correlations between feature vector elements. The effect of using a set of M full covariance matrix Gaussians can be equally obtained by using a larger set of diagonal covariance Gaussians. Gmms are often used in biometric systems, most notably in speaker recognition systems, due to their capability of representing a large class of sample distributions. One of the powerful attributes of the GMM is its ability to form smooth approximations to arbitrarily shaped densities. The classical uni-modal Gaussian model represents feature distributions by a position (mean vector) and an elliptic shape (covariance matrix) and a vector quantizer (VQ) or nearest neighbor model represents a distribution by a discrete set of characteristic templates [1].

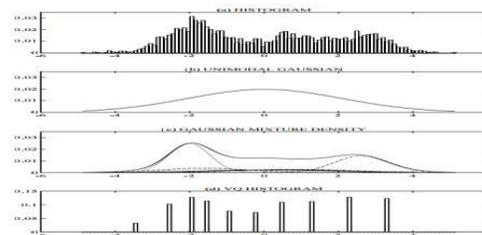


Fig 3. Comparison of distribution modeling. (a) histogram of a single cepstral coefficient from a 25 second utterance by a male speaker (b) maximum likelihood uni-modal Gaussian model (c) GMM and its 10 underlying component densities (d) histogram of the data assigned to the VQ centroid locations of a 10 element codebook

The use of a GMM for representing feature distributions in a biometric system may also be motivated by the intuitive notion that the individual component densities may model some underlying set of hidden classes. For example, in speaker recognition, it is reasonable to assume the acoustic space of spectral related features corresponding to a speaker's broad phonetic events, such as vowels, nasals or fricatives. These acoustic classes reflect some general speaker dependent vocal tract configurations that are useful for characterizing speaker identity. The spectral shape of the i th acoustic class can in turn be represented by the mean μ_i of the i th component density, and variations of the average spectral shape can be represented by the covariance matrix Σ_i . Because all the features used to train the GMM are unlabeled, the acoustic classes are hidden in that the class of an observation is unknown. A GMM can also be viewed as a single-state HMM with a Gaussian mixture observation density, or an ergodic Gaussian observation HMM with fixed, equal transition probabilities. Assuming independent feature vectors, the observation density of feature vectors drawn from these hidden acoustic classes is a Gaussian mixture. The proposed two-directional two-dimensional principal component analysis was then used to reduce the dimension of each matrix. Fig. 4 shows the contour plots of each matrix in Fig. 3 following dimension reduction using 2D2PCA when the energy conservation rate and total energy preserved were 98% and 88% respectively. Compared with Fig. 3, the intensity difference between certain sub-panels in Fig. 4 is further enhanced, including, Table I summarize the

matrix sizes at all scales before and after 2D2PCA for 93%, 88%, and 83% total energy conserved for subject 5. It would be obviously problematic to compute such a high dimensional covariance matrix containing more than 8×10^3 elements. However, the use of multi-scale matrices followed by 2D2PCA resulted in the size of all covariance matrices being less than 100×100 , avoiding the Curse of dimensionality and small sample issue as well as improving the numerical stability.

Method	Technique	Error rate	Accuracy
PCA	DWT	0.2	
2DPCA	PCA	0.5	
2D ² MS PCA	SVM	0.6	
	GMM	0.66	

Table I. Multi-scale matrix size at various threshold values of total energy conserved for subject 5

Recognition of Intended Movements

Pattern recognition analysis was performed using the optimal number of PCs previously determined and SVM and classifiers with the fivefold cross-validation scheme. summarizes the subject-specific classification accuracy for all 20 intended upper-limb movements. A high average classification accuracy above 95% could be achieved for most subjects. Across all subjects, there was no significant difference in the accuracy of SVM and ELM ($p > 0.05$), although the average accuracy for ELM was slightly lower. Compared with a previous study on the same EMG dataset using PCA reduction in the time domain feature [30], 2D2PCA yielded higher average accuracy

with much fewer PCs for the same SVM classifier, indicating the efficiency and effectiveness of 2D2PCA. Although the PCs needed for ELM was higher than SVM, ELM exhibited better computational efficiency due to its unique learning scheme. In addition, the average accuracy of MS2D2PCA-ELM was also higher than GMM, LDA, and SVM classifiers used in conjunction with PCA in [30]. This further suggested that MS2D2PCA was more effective than PCA for high-dimensional EMG classification. It should be emphasized, however, that EMG activity is subject-dependent for both healthy subjects and stroke survivors. Therefore, the structure and information distribution in the multi-scale matrices varied between subjects, which led to different reduced sizes with MS2D2PCA. Ultimately, this subject-specific spatial time- frequency distribution of EMG feature information led to inconsistent classification errors among different stroke subjects. The subject-specific EMG activity and classification performance suggested that optimal myoelectric pattern-recognition control system parameters should be individually customized for stroke survivors.

CONCLUSION:

In this paper we studied biomedical signals in Time-frequency coefficients at various scales were usually transformed into a one-dimensional array using only a single or a few signal channels. The steady improvement of biomedical recording techniques has increasingly permitted the registration of a high number of channels. Time-frequency analysis incorporating the wavelet transform followed by principal

component analysis (WT-PCA) has been a powerful approach for the analysis Biomedical signals .However, WT-PCA is not applicable to high-dimensional recordings due to the curse of dimensionality and small sample size problem. In this paper, we present a DWT based Technique and SVM based method for the efficient and effective extraction of essential feature information from high-dimensional signals.. Results are presented from an experiment to classify 20 hand movements using 89-channel EMG signals recorded in stroke survivors, which illustrates the efficiency and effectiveness of the proposed method for high-dimensional biomedical signal analysis.

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