METHODS AND TOOLS FOR PROCESSING BIOSIGNALS: A SURVEY PAPER

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Abstract: **This paper examines the use of disciplines signal processing approaches for data pre-processing and feature extraction from biological signals. Then, it follows a discussion on AI methods for Classification such as Support Vector Machines, Decision Trees, K-Neural Networks. The application framework includes detecting ECG, EEG, and FHR events as case studies.**

Introduction.

Signal processing specialists are often confronted with the problem of recognizing a sequence of events corresponding to the signature of a particular process state. This difficulty may be even greater in biomedical domains where the model of the process is poorly known and consequently the related scenarios that must be recognized. This is the case in neurology, for instance, where the relation between EEG peaks (transient paroxysmal events associated to the pathology) and epilepsy crises is not well explained. The question is: "if a relation exists between signals and process states, how can it be automatically qualified?" Temporal dimension of biomedical signals is an important attribute of their processing. During the processing of biosignals we have to take into consideration their characteristics, namely:

- sampling frequency;
- number of variables (channels) being sampled;
- operation mode of the system (on-line vs. off-line);
- goal of the interpretation: real-time alarming, diagnosis, treatment planning, monitoring, etc.

Medical signal processing is a very complex problem. Data samples are usually acquired at regular time points but during the processing stage the course of the signal in specified intervals must be considered. Usually, the main objective is the identification of specific events in the biosignal, which represent a temporal interval over which the nature of the signal, in one or more channels, is characterized by the occurrence of a particular process. Moreover, another problem that may be successfully solved using automatic processing is the analysis of long-term signal recordings.

The outline of this paper includes a general discussion on biosignal processing and feature extraction methods and then the presentation of Fast Fourier Transform (FFT), Principle Component Analysis (PCA), Independent Component Analysis (ICA) and Wavelet Transform. Then, it follows a discussion on Artificial Intelligence (AI) methods for classification such as Support Vector Machines SVMs), Decision Trees, K-Neural Networks. Finally, an overview on ECG, EEG and FHR processing is presented along with the conclusions.

Signal Processing Methods

Biosignal processing results in the identification of events and successively methods from machine learning are utilized to classify the events. The signal-processing module cuts and divides the initial data samples into stationary segments and computes their basic characteristics. These values may be either used as inputs for cluster analysis to find the best division of all segments into clusters and subsequently the resulting clusters can be used as training and testing sets for various machine learning methods or may be used as inputs to a supervised classifier without the intermediate stage of cluster analysis. This work examines and presents existing different signal processing approaches for data extraction from biological signals. It aims to present and analyze the main characteristics, the advantages and disadvantages of discipline signal processing methods [1],[2] The application framework includes detecting events in ECG, EEG and FHR biosignals as case studies.

When evaluating the similarities among objects we resort to features or attributes that are of distinctive nature. Concerning the initial choice of features it is worth noting that it is more an art than a science, and as with any art, it is improved by experimentation and practice [3]. From each signal-pattern we extract information characterizing it, the features. Those features are expected to be adequate to categorize the pattern into different classes-categories. Usually (for simplicity reasons and not only) in pattern recognition tasks we use a limited number of features. For example from a ECG signal with 10000 samples it would be prohibitive to use all these samples as features due to the well known *curse of dimensionality* (even though newly developed learning paradigms such as Support Vector Machines are somehow ¨immune¨ to this problem). Prior knowledge of the problem at hand can be very helpful in extracting and selecting only a

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restricted number of features. In case of no prior knowledge a set of features from different domains may be gathered at first and then through a feature reduction or feature selection process the dimensionality of the feature-representation space may be reduced aiming at more efficient learning algorithms and increased generalization performance.

As it has been mentioned, features are measurements or values calculated from measurements, which maybe useful for the characterization of the pattern. In the case of biosignals the signal each self is the pattern. The dimension N of the pattern is usually too large, which increases computational complexity and may also decrease the performance of the classification system. Furthermore some of the information conveyed by the original pattern can be redundant or even irrelevant with respect to the classification process [4].

Since biosignals are time series signal, features can be extracted either from the time domain or the frequency domain as well as jointly from the time frequency domain. Moreover, statistical characteristics of the signal can be extracted (i.e. moments or central moments) and they are used as features as well features derived from nonlinear analysis of the time series. Moreover, the wavelet coefficients and measurements derived from the wavelet coefficients are also candidate features in a classification problem.

PCA and ICA

In case of multiple recordings Principle Component Analysis (PCA) and its generalization Independent Component Analysis (ICA) have both found application in biosignals. ICA have been used in ECG analysis for the elimination of the noisy components [5] the separation of heartbeat of a fetus from that of the mother [6] and in many other applications [7].

ICA was developed as a means to solve the so called “blind source separation“ problem. From a set of n observed signals, we seek for n statistically independent sources, which are linearly combined to produce the observed signal(s). Both the independent sources and their linear combination are unknown. The goal of ICA is to find a separating matrix which after multiplication with the observation vector will retrieve the source vector. Though this is not feasible, however it is feasible to retrieve an arbitrarily scaled and permutated “version” of the original set of sources. This transformation enables us to isolate the noise in the case of multuple recordings (as in the case of EEG and MEG).

Wavelet Transform

The analysis of nonstationary signals requires the use of a method which can provide good localization of signal discontinuities. Furthermore, even for stationary signals, it can be sometimes difficult to choose a good resolution to analyze the signal. This is the case when the signal contains various features and each of them contains a different resolution [8]. Wavelets are very appealing tools that are used in many biomedical applications [1], [9] due to the time-frequency localization they provide, as well as, due to the multiresolution analysis that they perform to a given signal (decomposition of a signal into a number of scales, each scale representing a particular “coarseness” of the signal under study [10]). Wavelets have been used with considerable success for the analysis of the inter-beat intervals of heart rate of adults [11], [12]. They have been also used for the analysis of FHR during the second stage of labour [13],[14].

Support Vector Machines

SVMs are a recently developed learning machine method and they have proved highly successful in a number of classification studies [15]-[17]. Due to their very appealing property of providing good generalization to unseen data they have found application to many demanding biomedical problems [14],[18].

The main idea behind SVMs, when dealing with a pattern classification problem, is to find an “optimal” hyperplane as the solution to the learning problem. By the term “optimal”, it is suggested that for a separable classification task, the hyperplane $(\mathbf{w}, b)$ with the maximum margin or distance from the closest data points belonging to the different classes is selected.

Formally speaking, having a set of points that each belong to one of two classes, for a binary classification or dichotomization problem, i.e. a training set $\{\mathbf{x}_i, y_i\}$, $i = 1, \ldots, n$, where each point $\mathbf{x}_i$ is a d-dimensional vector, and $y_i \in \{-1, 1\}$ is a label that specifies to which one of the classes the point $\mathbf{x}_i$ belongs, and if the two classes are linearly separable, then there exists more than one hyperplanes $(\mathbf{w}, b)$ which can perfectly separate the positive from the negative examples. The hyperplane that maximizes the margin of separation is the one for which the Euclidian norm of the weight vector $\|\mathbf{w}\|^2$ is minimum and at the same time satisfies the corresponding constraints.

This is a classical quadratic optimization problem with inequality constraints and can be solved using Lagrange multipliers. However, in real life problems the different classes are not linearly separable. Therefore, two actions usually need to be performed:

- nonlinear mapping of the input space into a potential much higher feature space,
- construction of an optimal hyperplane, allowing for some misclassifications.

After that again a quadratic optimization problem has to be solved, which has an additional constraint concerning the maximum value of the Lagrange multipliers, leading to the desired hyperplane in the feature space.

EEG Processing Methods

EEG signal belongs to stochastic signals. Stochastic signals can be divided into two basic groups, namely stationary and non-stationary signals. Stationary stochastic signals do not change their statistic characteristics in time. Non-stationary signals may have variable quantities in time, for example mean value, dispersion, or frequency spectrum. EEG signal is non-stationary as most of real signals. EEG signal processing represents a complex process consisting of several subsequent steps, namely data acquisition and storing, pre-processing, visualization, segmentation, extraction of descriptive features, and classification. We will briefly describe individual steps. We will focus on segmentation and classification as the most important steps that are decisive for the success of the whole process.

Data acquisition. EEG signal is recorded digitally and saved in defined format in files on a PC. The aim of **pre-processing** is to remove noise and thus prepare the signal for further processing. The operations include, for example removal of DC part of the signal, signal filtration, or removal of certain artifacts [19].

Segmentation. If we use signal divided to intervals of constant length for acquisition of informative attributes, non-stationariness of the signal may cause distortion of characteristics estimation. Segments defined in this way may contain mixture of waves of different frequencies and shapes. It is preferable to divide signal to segments of different interval length that are stationary. There exist several approaches to adaptive segmentation [20],[21], which divide signals to stationary segments.

Extraction of descriptive features is closely linked with segmentation. In automatic signal analysis, extraction of informative features with the greatest possible discriminative ability belongs to important tasks. Ordered set of features constitutes the feature vector. Values of individual features may differ in several orders and therefore feature normalization is performed. Output of this step is a vector of normalized features for each segment.

Classification means to assign class to unknown objects. A class is a group of objects with certain specific properties. In our case the objects are segments described by vectors of normalized features and classes correspond to different groups of graphoelements. Result of classification is signal divided into segments where each segment is assigned to a certain class. Methods, as for example neural networks, k-nearest neighbour, or decision trees, can be used.

In our study [22] we have decided to use for classification two methods, namely k-NN (nearest neighbour) [23] and fuzzy k-NN [24]. k-NN method is a relatively simple and frequently used method. However, it has several disadvantages. It is slow because the algorithm has to search the whole training set when classifying an unknown vector; it has high memory demands because the whole training set is stored in the memory. On the other hand, the classification error is in most cases comparable to classification error of neural networks. Fuzzy k-NN is similar to k-NN but it differs in the output information. It does not return number of class but class membership values. The class membership value can be determined in several ways. We have used two ways, namely plain determination of class membership and determination of class membership by nearest neighbours.

Plain determination of class membership values is based on the assumption that the vectors in the training set are characteristic vectors of the given class and thus they do not belong to the other classes. Plain learning keeps exactly information about the class. The vector has unambiguous membership to the given class and null to all other classes.

Determination of class membership by nearest neighbours is based on the assumption that the given value of class in the training set need not characterize exactly corresponding vector. Therefore the algorithm tries to find class membership according to distribution of neighbouring vectors in the feature space using k-NN algorithm. It tries to keep classes defined in the training set but at the same time it respects surrounding k nearest neighbours of the given vector in the feature space. In case of a representative vector of the given class (in its neighbourhood there are only vectors of the same class) the method corresponds to plain determination of the class membership.

The developed system has been tested using a real EEG signal containing epileptic graphoelements. Classification into two classes has been used. Based on individual experiments we can compare properties of applied methods for EEG processing. We have evaluated the impact of the value of constant k in k-NN algorithm and K in fuzzy k-NN with K-NN learning. The classifier reaches better results with higher value of k. However, if k exceeds a certain limit the classification error increases again. From the tests it has followed that the most suitable values of k are 5, 7 or 9. These values have been used for further tests when segmentation methods have been evaluated.

The system has reached very good results in detection of graphoelements. The whole processing has reached mean testing error of 6%. More exact results have been reached by mutually advantageous combination of setups of individual parts of the system.

ECG Processing Methods

Analysis of ECG records is performed by wavelet transform (WT) and the machine learning method of decision trees is used for classification. The wavelet transform allows good localization of QRS complexes, P and T waves in time and amplitude. The average accuracy of all events detection is above 87%. For learning and further classification we use the Quinlan's See5 application. ECG signal is decomposed into building blocks that are well represented in time and frequency. According to [25] dyadic WT is used for extracting ECG characteristic points. Our approach is based on the work of Mallat [26]and Li et al. [27]. The basic idea stems from the properties of the function derivatives that represent useful information about the analyzed signal in the time domain, i.e. the morphology of the signal. We can think of an ECG signal as a composition of basic elements. We detect significant points of a signal by using zero-crossing points of the first derivatives of the signal smoothed with the smoothing function Θ.

For numerical application we cannot compute the wavelet transform at infinitely fine scale. Parameters of the smoothing function determinate parameters of finite impulse response (FIR) filter that we use to obtain all details we use for ECG signal analysis. In this work we use the cubic spline smoothing function and the quadratic spline wavelet function with compact support, for details see [26].

After extraction of ECG features we have used ten extracted attributes for further learning and classification by a decision tree and fuzzy rules induction [28]. The attributes are: P-wave amplitude, P-wave duration, PR interval, QRS-complex duration, S-wave duration, T-wave duration, QT interval area, T-wave amplitude, R-wave amplitude, ST interval area. Since the ECG records consist of rows of ECG complexes we have had to extract attributes values. We have used either averages of each attribute or medians of each attribute in ECG record. We distinguish four different class sets – a set of five classes (Atrial Fibrillation, Malignant Ventricular Ectopy, Supraventricular Arrhythmia, Arrhythmia and Normal Sinus Rhythm), a set of three classes (Supraventricular Arrhythmia, Arrhythmia and Normal Sinus Rhythm), a set of two classes (Arrhythmia and Normal Sinus Rhythm) and a set of two classes where all records with pathological changes on ECG are in one class and all other records in the second one.

The best values have been acquired with attribute average values using all ten attributes for decision tree generation. In average the generated decision trees have ten rules. For fuzzy rules induction we have implemented our FURL derived algorithms in Prolog and C. The implementation uses Mamdani with min and max as T-norm and T-co-norm respectively. Aggregation is performed with the fuzzy union operator and the defuzzyfication method is center of area. With two datasets (the first one using 11 features of instances, the second one 4 features of instances), tests have been carried on at first using 3 triangular classes centered on points $a_0=0.0$ "Normal Sinus Rhythm, $a_1=0.5$ (Intermediate class), $a_2=1.0$ („All Diseases“). We have also made tests using classes whose fuzzy sets were approximating singletons (width of 0.000002) to partition the output space. In all the tests, we have used 10 partitions for each of the feature in the input space. Results have shown that we have achieved the best classification by using two narrow output classes with FURL with negated antecedents producing more compact rule bases. Comparing results of both approaches the FURL has reached lower classification error, on the other hand it generates greater number of rules than the decision tree.

FHR processing methods

For the processing of FHR signal many different approaches have been adopted [14]. The approaches can be divided into two main categories. The first one emphasized in the analysis of the FHR in a way similar to a doctor following specific guidelines and medical terminologies. Towards this approach a variety of methods have been proposed using specialized algorithms [29],[30][31][32],[33] and even more sophisticated methods derived from the field of artificial intelligence [34][35]. The second approach concentrates on the derivation of indices from the FHR signal that are able to characterize the condition of the fetus. Towards this approach many different approaches have been investigated ranging from simple measures such as the mean value and the standard deviation to more sophisticated such as the approximate entropy [36]and quantities calculated based on the analysis of the FHR using the wavelet transform [13][37].

For a quite descriptive bibliography concerning the FHR analysis the interested reader can see [14].

Results.

One of the most important aspects of the biosignals classification systems is reliable analysis, which enables significant values to be identified on the measured signal. The wavelet transform has proven to be a good tool for biosignal analysis. More specifically the detection of attribute values achieves a sufficiently high level of reliability – about 80% for ECG analysis, which is higher than manual reading from the signal. It enables to detect required values of selected attributes in few steps, which is important from the point of view of time required for processing. The extracted values are then used as input values for a classification system. The EEG signal is more complex, and thus it requires more steps of pre-processing. The first step is the adaptive segmentation that divides the EEG signal into stationary segments. When the signals are segmented, all attributes are calculated, some of them in time domain, some of them in frequency domain. The extracted values are used as input values of a classification system.

The Fetal Heart Rate (FHR) signal is also quite difficult to interpret especially during the intrapartum period. The usefulness of the FHR analysis as a means for fetal surveillance has been argued for quite a while and the association of FHR patterns to fetal outcome has been considered impossible. Using wavelet analysis and an adaptive scheme for feature extraction combined with a Support Vector Machine classifier we have managed to achieve high recognition rates. Furthermore using a combination of features derived form the time domain, the frequency domain as well as features that characterize the morphology of the signal satisfactory results has been also achieved using again Support Vector Machines for the classification task [5]. In this latter approach dimensionality reduction has been performed using PCA as well.

Discussion

It is necessary to stress that the selection of a pre-processing method is a very important step in data mining process, especially when working with continuous signals. Application of a certain method is usually very closely linked with the choice of attributes and thus requirements laid on extraction and calculation of values from the signal.

Conclusions

One of the main aims of a biosignal classification system is to help doctor to interpret biosignals records correctly, and then to propose the most appropriate treatment. Further applications of these systems can be useful in educating new doctors, in evaluating long-time ECG, EEG records, in ECG monitoring in intensive care units, in EEG monitoring at neurological clinics, or in labour units as a decision support system.

There are a number of algorithms and methods that may be employed to classify unknown biosignals. Proper selection of attributes plays a very important role in classification systems and significantly influences the success rate of classification. The goal of the search is to find the state with the highest value of the evaluation function that characterizes the success rate of classification with the corresponding attributes. It is obvious that such an evaluation function is only an estimation of the success rate of the classification, because the training set is limited.

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