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PREPROCESSING METHOD FOR IMPROVING ECG SIGNAL CLASSIFICATION AND COMPRESSION VALIDATION

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Abstract

A method for improving electrocardiogram (ECG) signal classification in time domain is presented. The main idea is to preprocess the segmented waveforms in order to obtain an alignment of the ECG with respect to the maximum value of the R beat while keeping the information on its initial position as a feature.

We propose two simple preprocessing methods basically consisting in the alignment of the R-waves either by translation or by a slight nonlinear time scaling. It is shown that the methods significantly improve the classification rates obtained with two independent methods, one using a MLP artificial neural network and the other one based on the k-nearest neighbor (k-NN).

These techniques are also used to improve the validation of ECG compression by comparing the classification results obtained with original patterns and with reconstructed ones, a higher classification rate in the former case reflecting better compression results.

Key words

ECG, alignment, compression validation

1 Introduction

ECG signal classification is an important issue in clinical monitoring and has been thoroughly studied [Wei Jiang Kong, Peterson, 2005; AS Al-Fahoum, Qasaimeh, 2006; Addison et all, 2002; Povinelli et all, 2006; Roberts,Povinelli,Ropella, 2003]. The process involves extraction of attributes from ECG waveforms and subsequent comparisons with patterns characteristic to known diseases.

Even though much progress has been achieved in this area, it is unanimously agreed that the ultimate verdict concerning the correctness of the results falls under de competence of the cardiologist physician. However, since recognizing of deviation in the ECG trace is tedious and time-consuming when investigating long-term recording waves, improvements of automated classification results are of significant interest [Nyongesa, 2004; Graja, Boucher 2005; Jekova, 2000; Christov, Jekova, Bortolan, 2005].

After data segmentation, ECG heartbeat classification consists in using a comparison method to decide the class in which a heartbeat most probably belongs. No matter if artificial neural networks (ANN's), support vector machines (SVM), distance based methods etc. are used, either in the time domain or in the feature space, it is obviously important that similar waveform be classified in the same class. In all cases classification is related more or less to the concept of distance; distances between signals belonging to the same class are generally smaller than distances between signals belonging to different classes. (This statement is discussible for signals belonging to different classes but close to the delimitation zone between classes.)

The simplest way to segment ECG signals consists in taking samples between the middles of two successive RR periods so that the R wave will be placed somewhere about the middle of the signal support. The waveforms obtained in this way can be normalized to a constant number of samples (through interpolation, filtering and down sampling) to eliminate the influence of heart rate variability and to be easily compared using for instance the L2 norm, neural networks, etc. Such a technique has been used in [Fira, Goras, 2008] to validate the efficiency of a new compression method.

In this paper we propose two simple preprocessing methods basically consisting in the alignment of the R-waves either by translation or by a slight nonlinear time scaling. It is shown that the methods significantly improve the classification rates obtained with two independent methods, one using a MLP artificial neural network and the other one based on the k-nearest neighbor (k-NN). The above mentioned techniques are also used to improve the validation of ECG compression by comparing the classification results obtained with original patterns and with reconstructed ones, a higher classification rate in the former case reflecting better compression results.

2 Materials and methods

We start from the simple observation that, even after normalization to the same number of samples, the position of the R wave peaks for various frames containing normal or pathological beats generally does coincide neither as position nor as amplitude. In a standard normal beat the R wave has a peak about three times higher than any other maxima in the heart-beat. Even though the duration of the R beat is about 5% of the waveform support, due to its high amplitude the weight in the distance of the R wave contribution is significantly important. Thus, even though two or more waveforms are visually similar (`figure 1`), the distances between them might be high due to the un-alignment of the R waves.

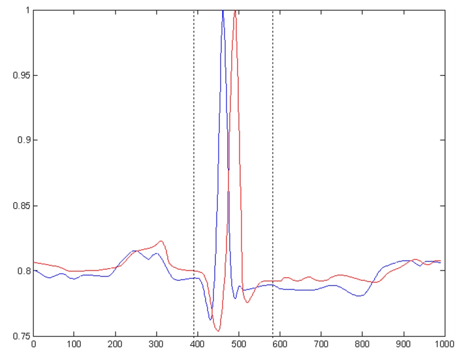

Figure 1. Superposed segmented and time normalized similar waveforms showing R-waves un-alignment

Thus the un-alignment of the R waves is a factor that might somehow artificially increase the distance between similar segmented waveforms when compared in the time domain by using the Euclidian distance, ANN's or other techniques. The main idea of this paper is based on the finally fully confirmed conjecture that aligning ECG waveforms with respect to the R wave will increase the time domain techniques classification rate.

To make an image on the contribution in the distance between two beats coming from the un-alignment of the R waves we have considered as a "toy" example two (highly) "stylized" R beats assimilated for simplicity with two isosceles triangles with the same basis width 2d and different heights A, A1 placed at different abscissas T/2 and aT respectively (a>T/2) as shown in `figure 2`.

Considering a value of d (`figure 2`) equal to 2.5 for a waveform with a normalized duration of 100 units (such that 2d represents 5% of the wave duration) and a maximum amplitude equal to unity for both triangles (A=A1=1), the maximum L2 distance between the two

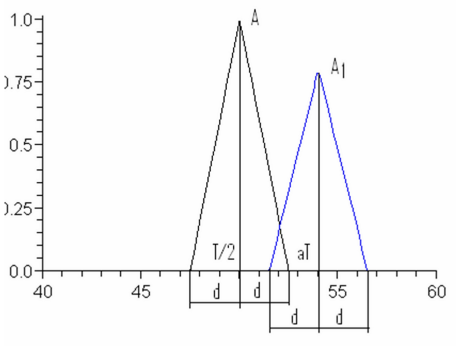

Figure 2. Stylized R-beats with different amplitudes and positions with details at another temporal scale

waves which corresponds to the case when the support of the triangles bases are disjoint (which happens for values of a higher than 0.55 or less than 0.45) is where $1.825 = 1.291\sqrt{2}$, a significant value, is the norm ("length") of each triangle. We have studied two R wave alignment techniques.

2.1 First method (R-wave centering through shifting)

The first and the simplest one consist in shifting the patterns to the left or to the right so that the R waves are placed just in the middle of the waveform interval. After shifting, the samples that leave out the interval at one end are discarded and the missing samples at the other end are replaced with the (same) rightmost/leftmost known value.

To make an image on the contribution in the distance between two waveforms coming only from the un-alignment of the R waves we will consider first the "stylized" R-waves described above. The distance between the two waves shown in `figure 3.a` varies with a and A1 for A = 1 and constant d = 2.5 as shown in `figure 3.b`. Obviously, the distance between the two functions vanishes for A1 = A and a = 1/2. Note that the previously mentioned value $1.825 = 1.291\sqrt{2}$ for the distance between two non-overlapping equal triangles can be found in (`figure 3.b`) for A1 = A = 1 and a>0.55 or a<0.45.

Coming back to real heartbeats, the distance between the two real R-waves selected between the two dotted lines in `figure 1` is 1.676 while the distance between the whole waves is 1.737. A typical value for the distance between two beats with completely non-overlapping R waves is 2.

2.2 Second method (R-wave centering through shrinking/stretching)

The second method consists in using a nonlinear time scaling to make the R waves coincide. An intuitive way to describe the method is the following. Imagine that the waveform already normalized to a specified duration T = 100 is drawn on an elastic sheet with width T

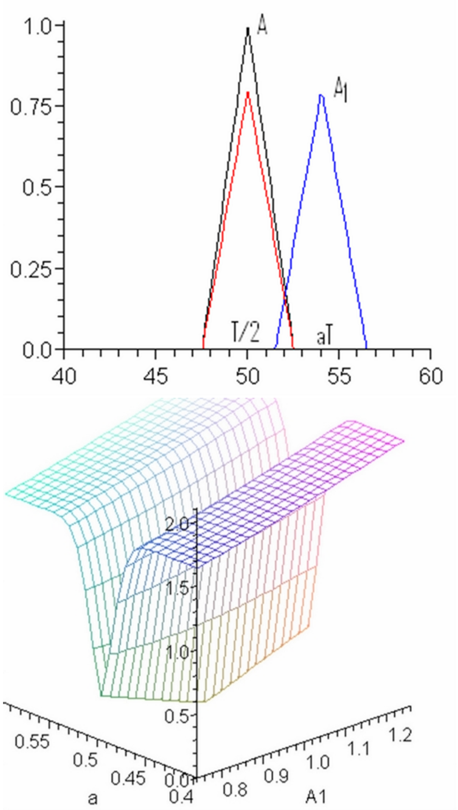

Figure 3. A. Alignment of triangle A1 with A (centered) B. Distance between the two triangles as a function of A1 and a (A=1, d=2.5)

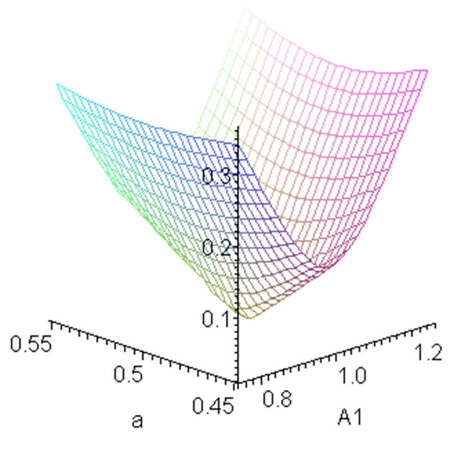

Figure 4. Dependence on a and A1 of the distance between triangles after alignment

and fastened lateral margins. Suppose that the waveform has the R peak placed to the right of T/2. Let us further imagine a rigid vertical line passing through the R wave peak fastened with the sheet. Now move the line to the left until its abscissa reaches T/2 thus slightly shrinking/stretching the left/right part of the waveform. In this way any waveform can be processed such that the peak has an abscissa of T/2. Moreover, the waveforms can be vertically (linearly) scaled as well to a normalized value of the peak equal to unity.
To make an image on how close the two "stylized" R-waves can get using the above procedure we have suggested in `figure 3.a` the aligning mechanism and sketched in `figure 4` the dependence of the distance between the two triangles on a and A1. We only mention that if the A1 triangle is translated and deformed until the abscissa of its peak reaches the value T/2, the abscissas of its bases become T/2-d/(2a) and T/d+d(2(1-a)). Let us note that, in this case, the A1 triangle is no more isosceles: in our example its left part has been slightly shrunk while it left part slightly stretched. This is why the distance between the two triangles vanishes only in the trivial case when A1 = A = 1 and a = 1/2. For any other value of a, even with a vertical scaling, the distance between the triangles will be not exactly zero. However, as it will be shown next, this very second technique proved to be *the most efficient* in preprocessing for improving classification.

The above consideration show that the un-alignment of the R waves is a significant factor that affects the distance between ECG signals - a fact that has been fully confirmed through simulations with real waveforms as shown below.

2.3 ECG preprocessing

The ECG signals used to illustrate the proposed method were taken from the MIT-BIH Arrhythmia database and consisted in ECG signals digitized through sampling at 360 samples/s, quantized and encoded with 11 bits. The segmentation was done by taking as heartbeats the waveforms between the middles of adjacent RR intervals. Since the segmented output patterns had different dimensions, each pattern was resampled to 100 samples by introducing extra samples through linear interpolation, filtering with a low-pass FIR filter with 90Hz cutoff frequency followed by decimation to 100 samples per pattern - a value which proved high enough to preserve the initial waveform.
The simulations used three classes of waveforms. The first class, denoted by **I (initial)** consisted of the above described resampled patterns which were used for classification with no extra processing. The second class, denoted by **S (shifted)** was obtained from the first one by shifting the pattern until the R wave reached T/2, discarding samples that left out the interval at one end and replacing the missing samples at the other end with the last known value. The last category, denoted by **S/S (stretch/shrink)** was obtained from the first one through resampling the patterns with 50 samples on each side of the R wave which is equivalent to a linear stretching/shrinking of the two sides of the pattern when the R wave was not in the middle of the interval.
Since the information about the period variability is surely a non-negligible aspect and should not be discarded, it can always be displayed in association to the processed waveforms. Moreover, it has been used as a feature in the classification scheme using ANN's as it will be further shown.

To make an image regarding the effect of the methods used for centering the R wave, we show in `figure 5`, several superposed patterns from the class ”right bundle branch block beat”.

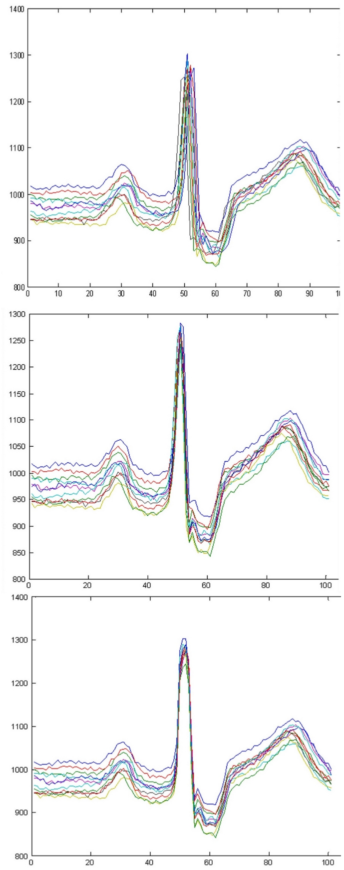

Figure 5. Patterns for the class right bundle branch block beat A. type I, B. type S, C. type S/S

An ANN consists of an interconnected group of artificial neurons that processes information using a connectionist approach to computation. In most cases an ANN is an adaptive system that changes its weights based on external or internal information that flows through the network during the learning phase [Haykin, 1998].
Compared to other methods, the MLP exhibits improved performances thus being widely used in cardiac pattern classification for its ability to learn from examples and for its very good generalization capability based on complex separation surfaces [Duda, 2001].
The k-NN is another method for classifying objects in the feature space being one of the simplest machine learning algorithms - an object is classified by a majority vote of its neighbors. The k-NN algorithm has the advantage of not requiring information on the class statistics, it can be easily implemented and has a small probability of error.
The performances of the k-NN algorithm are influenced by tree main factors: type of metric used for localization of the nearest neighbors, decision rule and number of neighbors used to classify the new example [Dasarathy, Belur, 1990].
Usually the metric is the Euclidean distance but other options as the overlap metric (or Hamming distance) can be used as well [Shakhnarovish, Darrell, and Indyk, 2001]. The number of neighbors, k, should be enough large to minimize the probability of wrong classification and enough small so that the k neighbors are really within the class to provide a correct estimation. In our case the best results were obtained with k=1.

3 Results

In order to verify the advantages of the proposed methods and to compare results, the two methods mentioned above have been used. Basically, the aim was to show the classification improvements for the above two methods. It is expected that the method would improve the results of other classification techniques as well, with even better recognition rates.
For the first method an ANN with a hidden layer containing 50 neurons has been trained with heartbeats from 8 classes (atrial premature beat, left bundle branch block beat, right bundle branch block beat, premature ventricular contraction, fusion of ventricular and normal beat, paced beat, fusion of paced and normal beat) taken from 23 records of the MIT-BIH Arrhythmia database.
For training the MLP network a back-propagation algorithm with gradient descent and cross-validation was used. From a total of 7500 patterns, 60% have been used for training, 20% for validation and 20% for testing.
The patterns used in the three sets above were distinct. The records no. 100, 101, 103, 104, 106, 118, 119, 200, 201, 207, 210, 213, 214, 217, 219 were used for training and records no. 102, 105, 202, 203, 208, 209, 212, 215 for testing and validation. From these last records, the validation and testing sets have been obtained through a random selection mechanism, each pattern being selected either in the testing set or in the validation set but never in both of them. The error function used was the mean square error and the stop criterion was the least error for the validation set.
The ANN was trained with the patterns alone from the classes I, S and S/S but also with patterns and features (which were either the initial length of the heartbeat for class I or the initial lengths of the left and right sides of the heartbeat for classes S and S/S). Additional results were obtained with patterns vertically scaled such that they have the same peak value of the R waves.
`Table 1` contains the results obtained with the MLP without and with features for the three classes of patterns (I, S and S/S) without and with vertical scaling. It can be observed that the classification results are better for the S and S/S classes and further improve when using features and vertical normalization.

It is also apparent that using features for comparing initial waveforms i.e., without centering and vertical

	MLP without features		MLP with features	
	No scaling	*vertical scaling*	*No scaling*	*vertical scaling*
(I)	90.9	91.4	90.4*	90.7*
(S)	91.7	92	93.23**	94.41**
(S / S)	92.8	93.1	94.9**	95.3**

Table 1. Results obtained with the MLP for the three classes of patterns (I, S and S/S) derived from original records of MIT BIH Arrhythmia database. Features: * initial length of the pattern, ** initial lengths of the left and right sides of the pattern.

scaling gives worse results. Thus the extra information contained in the initial length of the pattern is irrelevant for comparing waveforms if no other processing has been used. On the other side, the classification rate increased in the S/S case with vertical scaling with 4.4% compared to the un-processed situation (with or without features but with no vertical scaling).
Besides the ANN based classification, we have also used the k-NN algorithm for patterns, this time without features since the principle of the method is based solely on the concept of distance. The best results were obtained considering only the first neighbor and are presented in `table 2`. Since we have used the same database for both classification techniques, the results can be relevantly compared, both showing significant improvements when the preprocessing method has been used.

	k-NN	
	No vertical scaling	*vertical scaling*
(I)	93.36	93.84
(S)	94.48	93.68
(S/S)	95.60	95.76

Table 2. Results obtained with the K-NN algorithm for the three classes of patterns (I, S and S/S) derived from original records of MIT BIH Arrhythmia database

It is apparent that in case of k-NN classification using patterns with vertical scaling the results are better than those obtained using ANN, reaching 95.76% accuracy for the (S/S) segmentation method.
Since the number of papers dealing with classification of many classes is, to our knowledge, relatively small, it is rather difficult to make a comparison with other results (most authors classify only 2-3 types of cardiac pathologies) - the aim of the results presented here being that of showing the improvement of the classification. However, we mention here De Chazal [De Chazal, O'Dwayer, Reilly, 2004] who reports a classification accuracy of 97.4% for 5 classes (with a total of 15 pathologies) while Prasad [Krishna Prasad, Sahambi, Reilly, 2003] and Osowski [Osowski, Hoai, Markiewicz, 2004] using wavelets and SVM's respectively for 13 classes, report 96%.

3.1 Compression validation

In the following we make several comments regarding the possibility of using the classification rate for reconstructed signals to validate the quality of ECG compressed signals.
Indeed, the definition of the error criterion to appreciate the distortion of the reconstructed and original signal is of paramount importance for lossy compression techniques. For biomedical signals like the electrocardiogram (ECG), a slight loss or modification of information can lead to wrong diagnostics. Therefore, the measurement of these distortions is a very sensitive problem only partially solved for biomedical signals. In most ECG compression algorithms, the percentage root-mean-square difference (PRD) measure or normalization PRD, the root mean square error (RMS) and the signal to noise ratio (SNR) are used. In order to evaluate the relative preservation of the diagnostic information in the reconstructed signal compared to the original one, Zigel [Zigel, Cohen, Katz, 2000] introduced a new measure, not always easy to use, called Weighted Diagnostic Distortion (WDD), which consists in comparing the P and T wave, and QRS complexes features of the ECG signals.
Taking into account the need for relevant errors measures for the biomedical signal compression, but also that these measures should be easily calculated, we suggest that the classification error of reconstructed signals can be used as a distortion measure of the compression method, i.e., a higher classification rate of the reconstructed signals reflects a higher quality compression.
Based on the above considerations on preprocessing, we have tested the validation of the compression method proposed in [Fira, Goras, 2008] by comparing the classification results of a MLP trained with original waveforms and then with reconstructed ones. Using the procedures presented above the following results have been obtained.
The results in `table 3` show that using features always improve the classification rate while vertical scaling comes with little improvement (with an exception for class S when using features plus vertical scaling gives slightly weaker results). These results show that the suggested method for compression validation can be improved using the proposed preprocessing technique. The classification results using k-NN methods having the original waveforms as known patterns and the reconstructed ones as patterns to be classified are presented in `table 4`.
We remark that, in most cases the results are better

	MLP without features		MLP with features	
	No scaling	*vertical scaling*	*No scaling*	*vertical scaling*
(I)	78.2	81	83.5*	85.6*
(S)	84.7	86.5	89.89**	89.29**
(S/S)	86.4	88.9	90.05**	90.54**

Table 3. Results obtained with the MLP for the three classes of reconstructed patterns (I, S and S/S)

	k-NN	
	No vertical scaling	*vertical scaling*
(I)	77.71	79.30
(S)	90.80	90.39
(S/S)	93.16	93.98

Table 4. Results obtained with the KNN algorithm for the three classes of reconstructed patterns (I, S and S/S)

than those obtained with ANN, reaching a maximum of 93.98% for the (S/S) segmentation method.

4 Conclusion

We have presented an improved method for electrocardiogram (ECG) signal classification in time domain which takes into consideration the heart rate variability. By preprocessing the waveforms in order to obtain an ”alignment” of the R beats it has been shown that the classification results have been significantly improved for both tested methods (ANN and k-NN) and are expected to improve for other classification techniques as well.

A major advantage of the proposed method based on cardiac beat alignment consists in a reduced computational complexity and robustness. Last but not least, considering the results obtained for reconstructed signals after compression, the method can be used for compression validation as well.

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