SPATIAL SHAPE VARIABILITY OF ECG WAVES

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Abstract: We present a method to measure spatial shape variability of ECG waves recorded, at a fixed time, from a Body Surface Potential Mapping (BSPM) device with 64 channels. Applications to P, QRS and T waves were made and evaluated on the ability to separate MI patients from healthy subjects. For each column of leads, the differences in shape between each couple of signals (P, QRS or T) associated to each couple of leads were computed using the Distribution Function Method (DFM). After selecting a reference signal in each column, all the shape distances were put in a vector of 61 components, for each person. The Karhunen Loève Transform (KLT) was applied to the data. It was observed that one eigen value was highly larger than the others leading to one eigen vector in each group. Finally, the numbers used for clustering were the differences between the two scalar products with these vectors. The results show a very good separation of the groups according to T wave shape analysis, a quite good according to QRS and also for the P wave with a lower specificity. The results are in agreement with the MI diagnosis for the patients.

Introduction

The heart electric activity is obviously affected by pathologies like Myocardial Infarcts (MI), but also its variability from beat to beat [1, 2]. This variability along time is currently measured on ECGs coming from one or several leads. On the other hand, Body Surface Potential Mapping (BSPM) may be used to characterize heart diseases. In this case, the value of some synthetic index, computed from a single or averaged ECG, is affected to each lead. The problem is then to build the index in such a manner that its distribution on the body surface is different for healthy subjects and for patients. For example, the symmetry of T-waves is reflected by the symmetry ratio [3] or the T-wave Shape Index (TSI) [4], and has been used to characterize MI patients. Generally, the values of the index are used directly, not their dispersion. Another remark is that the index value associated to a particular lead only depends on the signal recorded on this lead.

In our approach, dealing with spatial shape variability of ECG waves, the data (i.e. shape differences) are computed for all the leads in a same column, and then each column is represented by a parameter measuring shape variability in this column. To build such data, two points are important: how to measure shape differences, and how to choose a reference for these differences? Then the question is how to make use of the data in the decision problem of separating healthy subjects from patients.

In previous works [5, 6] we showed the advantage of T-wave shape variability, computed column by column, to distinguish a group of 12 MI patients from a group of 15 healthy subjects. In this paper our aim is to propose an improvement to the clustering problem, introducing a Principal Component Analysis (PCA) through the Karhunen-Loéve Transform (KLT) in the space of shape difference vectors. The results are compared on the same records.

Materials and Methods

Material: Both healthy subjects and patients underwent BSPM according to the same protocol [7]. The BSPM lead system contains a total of 64 leads: 3 limb leads and 61 unipolar leads placed around the torso according to the Amsterdam lead system (Fig. 1). The recordings were carried out in an electrically shielded room. The subjects where in supine position and had a normal sinus rhythm, apart from any episode of tachycardia or fibrillation. These data come from 15 healthy subjects being used as a control population and 12 patients after Myocardial Infarction of different natures. All measured signals were averaged over 100-150 cycles, imposing a correlation of 0.98.

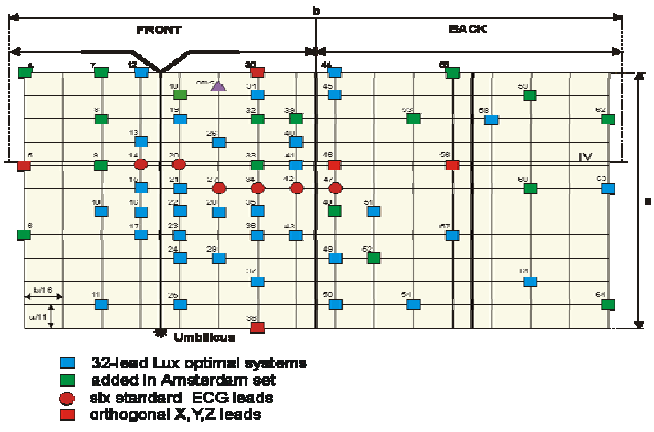

Figure 1: The 64 lead device

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Measuring shape differences: The difference in the shape between two signals, here two P-waves or two QRS complexes or two T-waves, is calculated using the Distribution Function Method (DFM) [8]. This method was initially conceived to compare signals that are positive on their supports. To compare positive functions of the different waves, we took into account the absolute value, after removing a base line joining the first and the last point of the chosen interval. To compare two signals s(t) and v(t), we defined the normalized integrals S(t) and V(t), which are increasing functions from zero to one. The difference in the shape between the two signals was characterized by a function φ defined by the relation:

$$S(t) = V(\varphi(t)) \quad (1)$$

In the case of equality of the shape between the two signals s(t) and v(t), φ is a straight line. The shape difference $D(s,v)$ corresponds to the distance between the φ function and the best fitted least mean square line Δ, using the Mean Square Error (MSE):

$$D(s,v) = MSE(\varphi,\Delta) \quad (2)$$

Reference signal: In order to attribute a data representing a shape difference to each lead it is necessary to define a reference. This reference is determined, for each lead, using all the leads of its column. Two possibilities have been investigated: (i) the reference signal is the signal which minimizes the mean shape difference over the column (real wave reference); (ii) the reference is a synthetic signal obtained by Integral Shape Averaging (ISA) [9, 10], which is a mean shape signal (ISA signal). When equal shape signals are averaged, the important property of ISA signal is to build a signal with the same shape. This property is obviously not verified by the classical signal averaging.

PCA using the KLT: The first idea, when we wanted to use the KLT to separate the MI patients from the healthy subjects, was to work on the set of the raw data that is the sampled records of the ECG waves, without including any shape parameter [6]. In terms of clustering, the results confirmed the study using shape dispersion in a column : only the T-wave was efficient. In the following we propose to combine shape analysis and the KLT approach.

- The data are composed by a set of vectors X_p, each of them being associated to one person p (healthy or non healthy). Each vector has 61 components corresponding to the 61 leads recording body surface potentials, connecting all the columns in a same sequence. Each component is the shape difference between the corresponding lead signal and the reference signal in its proper column.

- For each group (healthy subjects and MI patients) the covariance matrix is then estimated. Selecting the highest eigen values leads to a basis of eigen vectors.

In our application, the first eigen value was very higher than the others. So, there was only one vector, V_1, for the healthy group and one, V_2, for the MI patients group. For a person p, noting $\alpha_1(p)$ and $\alpha_2(p)$ the scalar products of X_p respectively with V_1 and V_2, we propose to separate the both populations looking at the parameter:

$$d(p) = \alpha_1(p) - \alpha_2(p) \quad (3)$$

Statistically, we are waiting for a positive value of d(p) if p is a healthy subject and a negative one if p is a patient.

Results

In the following we present results obtained using the ISA signal as reference, for they are slightly better than using the real wave reference.

First, the results concern the shape variability, column by column, for each group, and computed on P, QRS and T waves. Figure 2 shows that measuring the shape variability of the T-waves makes it possible to clearly separate MI patients from healthy subjects, specially looking at columns 4, 5 and 6. On the contrary the separation does not appear on the P-wave or QRS diagrams.

The second group of results is associated to data analysis using KLT. In Figure 3, the index d(p) is plotted for each person p, putting the healthy subjects on the left and the patients on the right, and this for each type of ECG wave.

It is obvious that the index d(p) perfectly separate the groups using T-wave. In addition the separation is quite good using QRS complex, and not so bad looking at P-wave. Table 1 gives the specificity and sensitivity for each wave.

Obtaining the best results with T-wave to characterize the patients is in agreement with the diagnosis of myocardial infarction. What is new is to observe an increased shape variability also on the other waves, and this due to a better analysis of shape variability through a PCA algorithm.

Table 1: Sensitivity and Specificity using KLT combined with shape difference measurements

ECG Wave	Sensitivity	Specificity
T-wave	100 %	100 %
QRS complex	100 %	92 %
P – wave	92 %	69 %

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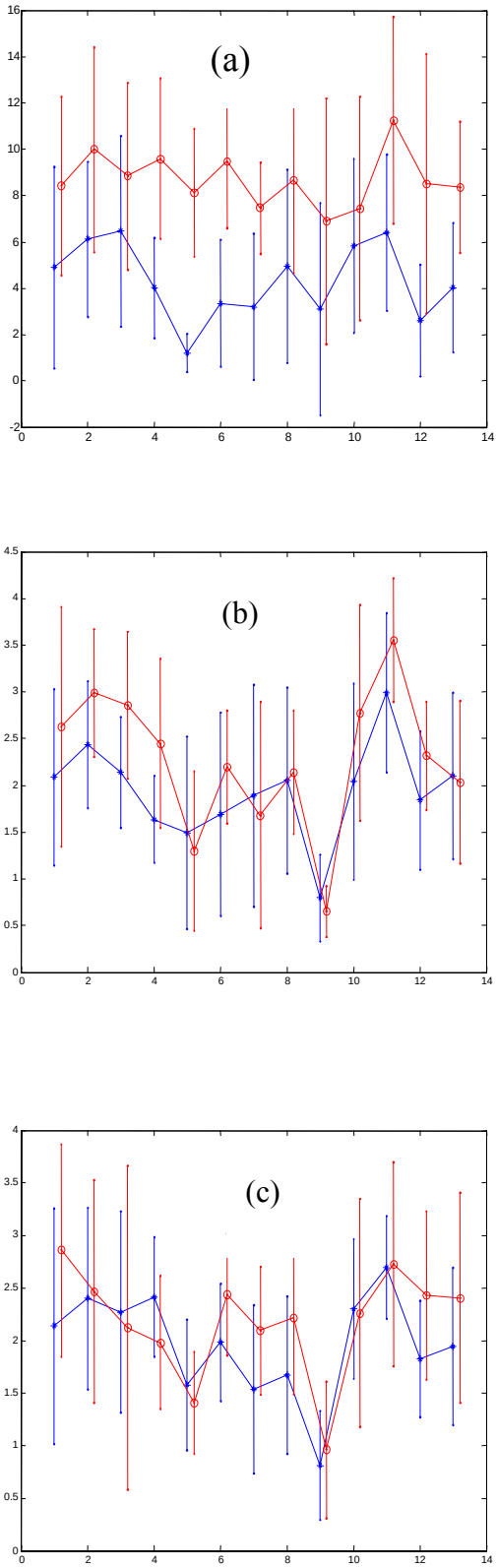

Figure 2: Shape dispersion using ISA as the reference in each column; (a) T-waves, (b) QRS complexes, (c) P-waves

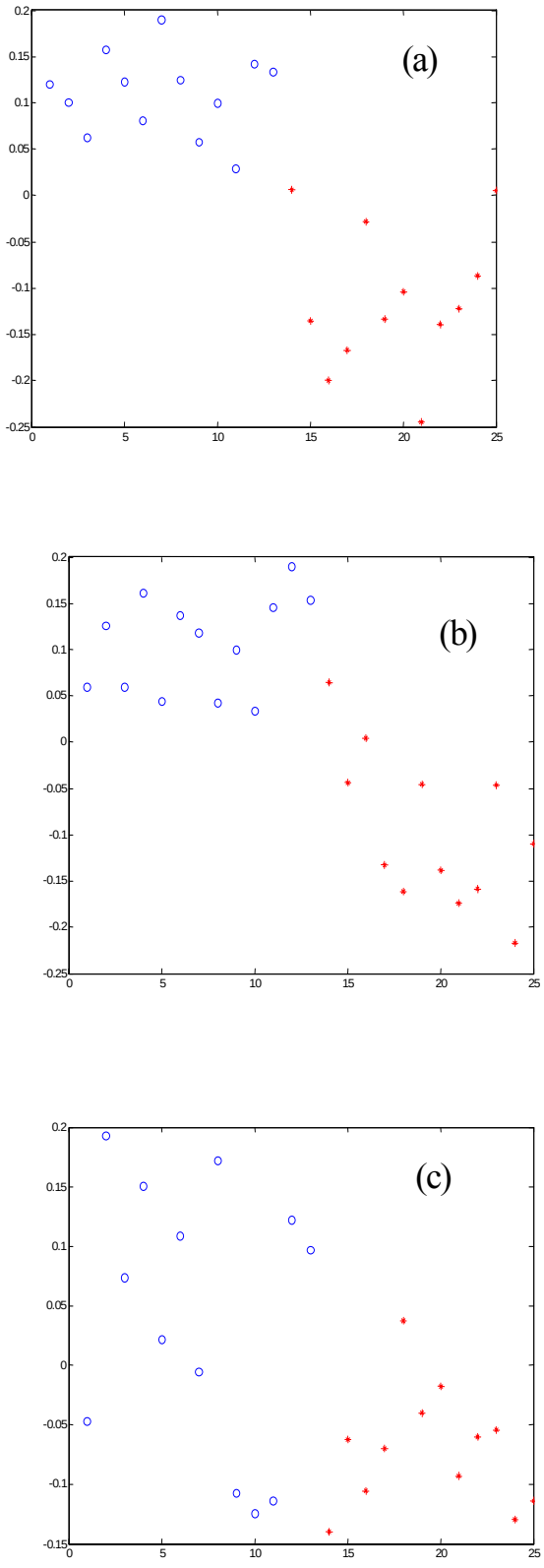

Figure 3: Separation using parameter d(p); (a) on T-waves, (b) on QRS complexes, (c) on P-waves. Healthy subjects on the left, patients on the right.

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Discussion

The first point addresses the measurement of the spatial variability of ECG wave shapes obtained from BSPM records. The proposed approach, using DFM as a similarity criterion between two signal shapes, proves the reliability of shape dispersion, computed on each column of leads.

Secondly, the main point of the paper was to show the improvement brought by KLT combined with shape difference measurement. In fact, applying directly the KLT algorithm on raw data, i.e. the sampled ECG waves and not the vectors containing the shape information, does not lead to significant results in our application, for QRS complex and P- wave.

Finally the same approach could be applied to estimate shape variability from beat to beat and compared to earlier results published in the literature.

Conclusions

In conclusion, even if the groups of healthy subjects and MI patients are rather small, the advantage of measuring the spatial shape variability of ECG waves from BSPM records combined with PCA has been established. The diversity of MI types in our example is an argument in favour of our approach. In fact, this diversity increases the uncertainty on the estimation of shape variability in the group of patients. Further applications on larger samples with more restricted diagnoses of MIs or other heart diseases are needed to study the ability of the method to characterize a particular pathology.

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