# Continuous localization of ectopic left ventricular activation sites by means of a two-dimensional representation of body surface QRS integral maps

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Abstract— By means of Karhunen-Loève transformation it is possible to represent electrocardiographic body surface QRS integral maps using only two coefficients while retaining more than 80% of information. These coefficients are computed for a number of mean paced QRS integral maps, which were acquired from well-defined ventricular segments and are contained in a database used for localization of the origin of ventricular tachycardia. It is shown that these two coefficients are sufficient to compute the pacing site in a continuous fashion, without reference to a limited number of segments. These coefficients facilitate and improve the ventricular tachycardia localization procedure based on using the database of paced QRS integral maps, by establishing the relation between QRS integral map and corresponding site of origin.

## I. INTRODUCTION

An important application of multi-lead electrocardiography (body surface mapping) is the localization of endocardial sites of origin of ectopic ventricular beats and ventricular tachycardia (VT). The QRS integral map (QRSI) of a 62-lead ECG recording[1] is capable of predicting those sites accurately. SippensGroenewegen et al. created databases of 18 to 25 mean paced QRSIs covering most of the left ventricle (LV) in both normal and infarcted hearts[2], [3]. Each mean paced QRSI in the database corresponds to a known segment of activation onset on the endocardial surface. The site of origin of a VT can be predicted by comparing its QRSI with the paced QRSIs in the database. This method identifies the correct segment in 62%, and an adjacent segment in 30% of all cases [4]. It is a useful first step in the VT localization procedure, that further consists of catheter pace mapping and activation sequence mapping and can be followed by ablation.

A limitation of the method is that the localization result is expressed as just one out of 18 to 25 segments of origin. The localization accuracy may be improved if the QRSI distribution is modeled, to enable interpolation and extrapolation to any given ventricular site.

## II. Methods

Karhunen-Loève (KL) transformation can be applied to multi-lead ECG recordings in order to achieve datareduction[5]. A KL transformation matrix was obtained from 90 QRSIs recorded during sinus rhythm in 30 healthy subjects. With this matrix, a QRSI, which can be thought of as a vector, could be transformed to obtain another vector that is represented for 80–90% by its first 3 elements. This matrix was applied to the database of 25 mean paced QRSIs acquired in subjects without structural heart disease<sup>[2]</sup>. The distributions of the first 3 elements over the endocardial surface of the left ventricle were computed by spatial interpolation and visualized by contour plots in a LV polar projection (figure 1). This projection was used previously by SippensGroenewegen et al. to anatomically represent the pacing segments contained in the database[2], [3]. Subsequently the first 3 elements of each QRSI were transformed to spherical coordinates, i.e., two angles and a radius. Neglecting the amplitude by discarding the radius, two coefficients remain to describe each particular QRSI.

#### Localization

The results of SippensGroenewegen et al. show that there is a one-to-one correspondence between QRSI and site of origin/pacing site. We hypothesize that: 1) the two coefficients of the QRSI vary smoothly with the pacing site over the endocardial surface, and 2) the pair of these coefficients is unique for each possible QRSI. Then we may assume that these coefficients suffice to compute the site of origin of any given QRSI.

To test the hypothesis, two smooth parametric functions, each incorporating 3 parameters, were defined that relate the two coefficients to the ventricular coordinates of the corresponding pacing site. The function parameters were computed by fitting the functions to the data. The accuracy of fit was expressed as the mean distance between the computed locations and the measured locations of the 25 pacing segments. If the localization results are correct within the error bounds of the database, then the fit is succesful and our hypothesis is justified.

### III. RESULTS

The spatial distributions of the first 3 elements of the 25 KL transformed QRSIs are shown in figure 1a. These are very smooth and orthogonally looking distributions, which already suggests that together they may be well capable of identifying any given ventricular site.

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Figure 1. a: Distribution of the first 3 elements (left to right) of the KL transformed QRSIs over the endocardial surface, shown in a left ventricular polar projection as illustrated in b. The zero contour is indicated with a dotted line, and negative contour lines with dashed lines. b: The apex is in the middle of the diagram; the mitral valve ring (MVR) is represented by the circumference. Also indicated are the 4 quadrants (septum, anterior, posterior, lateral), the anterior and posterior papillary muscles (APM, PPM) and the direction of the aortic valve ring (AVR) [2], [3]. c: Differences between computed positions and measured (mean over several measurements) positions of segments. The computed positions are indicated by open circles, the measured positions by black dots. Two segments (posterior and postero-lateral) show relatively large differences, although the computed positions are still within the segments, possibly because these are large segments so that their location is not very well defined.

It was found that the localization algorithm based on these 3 elements was able to compute the coordinates of the pacing segments corresponding to the 25 QRSIs from the database with errors approximately equal to the segment size (see figure 1c).

# IV. DISCUSSION

The properties of the two coefficients that are used to describe QRSIs enable an algorithm to compute the location of the corresponding endocardial site of origin of the VT in terms of coordinates, instead of a limited number of segments corresponding to a fixed reference set of mean paced QRSIs contained in a database. Moreover, this algorithm uses information of all pacing segments in the database for the localization of a single site. This is likely to improve the localization accuracy. Besides localization of ectopic sites, the two-dimensional representation of QRSIs may be used for other tasks that require modeling of the QRSI distribution.

The accuracy of the method may be improved by using a larger database that uses a stimulus location distribution in terms of unique sites instead of segments. Further studies are required to provide a more extensive evaluation of the performance of the algorithm by using larger, and separate, training and test sets.

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