# Modeling an Activation of Heart Ventricular Segments

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## Abstract

*Background: Knowing activation times of specific myocardium segments can help to identify conduction disturbances which may, consequently, result in more targeted treatment of patients. Here, we present a 2D activation model evaluating activation of specific myocardium segments.*

*Methods: Precordial six-lead ECG signal was measured with a 5kHz sampling frequency. A total of 10 left bundle branch block (LBBB) and 5 right bundle branch block (RBBB) recordings were analyzed. The analysis includes following steps: 1) QRS complexes detection, 2) QRS complexes morphology clustering, 3) averaging of 150-1000 Hz envelopes (16 frequency bands) of dominant QRS complexes, 4) a genetic algorithm (GA) produces artificial envelopes from (initially random) timing of myocardium segments. The task for GA is to produce envelopes the most similar to measured; then final timing should reflect real activation of myocardium segments.*

*Results: Presented activation model determined activation of left ventricular segments before right ventricular segments in all RBBB patients (mean 61.4 ± 13.7 ms) and activation of right ventricular segments before the left ventricle segments in all LBBB patients (mean 87.8 ± 15.8 ms). Computed activation of segments corresponds to the expected activation for the LBBB and RBBB record.*

*Conclusion: We introduced a new method determining activation times of myocardium segments; this is achieved non-invasively using only high-frequency ECG signal from chest leads.*

## 1. Introduction

Determining activation times of heart ventricles from signals sensed on the body surface is a frequently solved problem in recent years [1, 2, 3]. This problem is called the inverse problem of electrocardiography and procedure for imaging electrical activation time of the heart is called electrocardiographic imaging (ECGI) [1]. Current methods allow the determination of activation times with high resolution. However, it is necessary to sense signals from many electrodes on the patient's torso (often over 100 electrodes) [1, 4].

This article describes a method for determining activation times of only 11 heart ventricular segments: 3 in the right ventricle, 3 in the left ventricle, 3 in the septum and 2 in the apex. However, the ECG records were sense with only 6 standard chest leads. ECG records were sensed with a sampling frequency 5 kHz and 24-bit resolution [5]. Magnetic resonance imaging was also performed for each of the analyzed subject to determine heart geometry. A total of 10 subjects with LBBB and 5 subjects with RBBB were tested.

## 2. Method

The block diagram of the proposed algorithm is shown in Figure 1. The presented method is based on a genetic algorithm. The inputs to this algorithm are heart geometry and amplitude envelopes measured from 6 chest leads. The genetic algorithm aims to determine a timing of heart segments activation that will generate amplitude envelopes as close as possible to the measured amplitude envelopes.

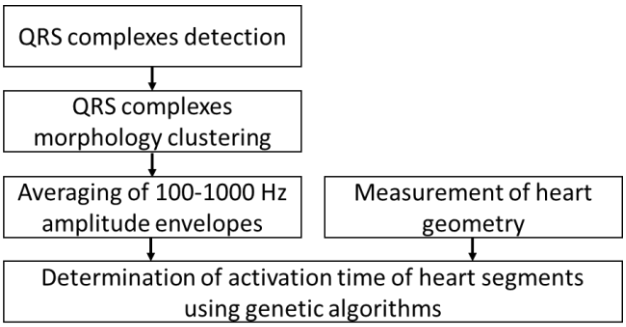


Figure 1. Block diagram of the proposed algorithm

## 2.1. Detection and morphology clustering of QRS complexes

Robust multichannel QRS detector [6] was used for QRS complex detection. The presented method uses high frequency (HF) components of QRS complex. These components are very weak. Averaging several QRS complexes will suppress noise and allow analysis of these weak HF components. This is necessary to divide the detected QRS complexes into morphological groups before averaging so that the average is not influenced by significantly noisy QRS complexes or pathologies, e.g. premature heart beats. The algorithm used for morphology clustering is described in [7].

## 2.2. Calculation of envelopes

Amplitude envelopes were computed in 16 frequency bands with width 100 Hz from 150 Hz to 1000 Hz with step 50 Hz. It was computed for all QRS complexes with dominant morphology in all chest leads. The amplitude envelopes of QRS complexes were then averaged and normalized in each frequency band. Normalization ensures that each frequency band has the same weight. Finally, all 16 normalized amplitude envelopes were averaged. This averaged envelope is the input to the genetic algorithm.

## 2.3. Measurement of heart geometry

Magnetic resonance scan was performed for each of the analyzed subject to determine heart geometry. The heart ventricles were divided into 11 segments - 3 in the right ventricle, 3 in the left ventricle, 3 in the septum and 2 in the apex. The distance of each segment from each sensing electrode and the size of each segment were manually measured. These values are necessary to subsequently generation of amplitude envelopes from the specified activation times of each segment.

## 2.4. Determination of activation times of heart segments

Determination of activation times of heart ventricular segments was performed using genetic algorithms. Each individual in the population represents one realization of the timing of activation of all heart segments.

One individual in the population is represented by an 11 × 48 matrix. Each row of the matrix represents one heart segment and each column is a time point at which we determine the activation of the segment. The distance of two adjacent time points is 5 ms, so we analyze a total of 240 ms.

The size of the population is 60 individuals. The initial population consists of random individuals. The sum of each row of individual is always the same.

The quality of each individual is evaluated according to the degree of similarity between the measured and generated amplitude envelopes.

Amplitude envelopes are generated for each lead according to the formula:

$$y(t) = \sum_{i=1}^{11} \frac{SS(i) \times Ac(t,i)}{SE(i)^2}$$

where y(t) is the value of the envelope amplitude at time t, SS(i) is the segment size of the i-th segment, Ac(t, i) is the value of activation of the i-th segment at the time t, and SE(i) is the distance between the heart segment and the electrode sensing the currently calculated lead. Thus, Ac is a matrix described above optimized by a genetic algorithm.

Creation of a new population (reproduction) is performed after the assignment of quality to each individual. The algorithm uses the principle of elitism, the two best individuals are automatically in the new population. The other offsprings are generated by randomly selecting pairs of individuals from the old population, from which 3 offsprings are generated according to the following formulas:

$$offspring1 = 0.5 \times parent1 + 0.5 \times parent2,$$
$$offspring2 = 1.5 \times parent1 - 0.5 \times parent2,$$
$$offspring3 = -0.5 \times parent1 + 1.5 \times parent2.$$

The worst of the generated offsprings is deleted and the other two are part of the new population.

Single-point and three-point mutations occur further in new individuals. A single point mutation means that each value of each individual can be increased or decreased by 0.1 with a probability of 10%. The three-point mutation means that three consecutive values of heart activation in one heart segment are set to zero. Thus, this mutation ensures faster optimization. Multipoint mutation occurs in each offspring with a probability of 20%.

The genetic algorithm is stopped after 5 million iterations.

The output of the genetic algorithm is the activation of each segment at any time. It is sometimes necessary to determine one time point of maximum activation of individual segments. This activation is determined at a point where half of the area under the curve is to the right and half to the left of the designated point (center of gravity of the curve).

# 3. Results and discussion

The results of the proposed algorithm were tested on the fifteen records, of which 10 were LBBB and 5 were

RBBB.

Presented activation model determined activation of the left ventricular segments before the right ventricular segments in all RBBB patients (mean 61.4 ± 13.7 ms) and activation of the right ventricular segments before the left ventricle segments in all LBBB patients (mean 87.8 ± 15.8 ms). The calculated activation of the segments corresponds to the expected activation in LBBB and RBBB.

We do not have data for which the activation times are known. The results will be further shown in selected cases – one LBBB and one RBBB.

Determination of segment activation in a patient with LBBB will be shown in a record with a QRS complex duration of 182 ms with typical LBBB morphology – qS in V1 and V2; slurr or notch in I, aVL, V2, V5 and V6. In total, 379 QRS complexes of dominant morphology were detected.

Determination of segment activation in a patient with RBBB will be shown in a record with a QRS complex duration of 184 ms with typical RBBB morphology – rSR' with negative T wave in V1 and qRS in I and V6. In total, 275 QRS complexes of dominant morphology were detected.

The envelopes calculated from the measured data and the corresponding envelopes generated by the segment activation timing selected by GA are shown in Figure 2 and Figure 3.

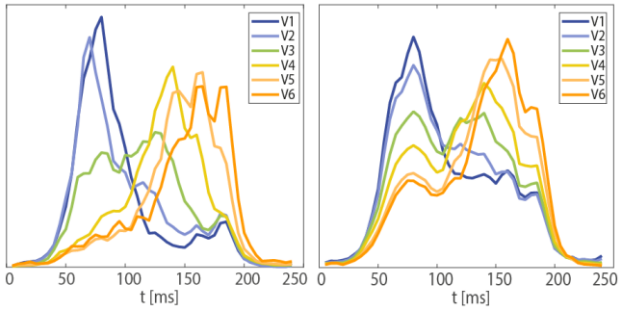


Figure 2. Envelopes of LBBB record; envelopes generated from determined activation times of heart segments (right) and envelopes of measured QRS complex (left).

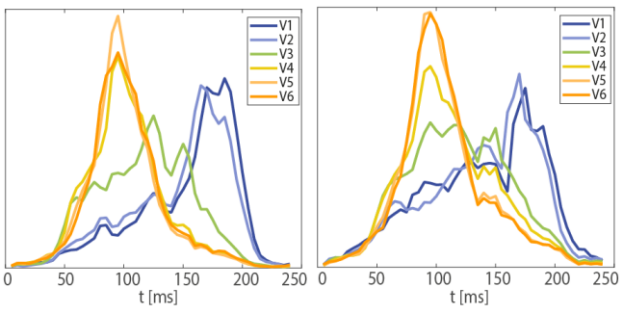


Figure 3. Envelopes of RBBB record; envelopes generated from determined activation times of heart segments (right) and envelopes of measured QRS complex (left).

It can be seen that the chronological sequence of extremes in individual leads remains the same. The biggest inaccuracies are that our method does not allow to generate activity only in the left ventricle sensing electrodes with minimal activity in other electrodes and vice versa. At the time when the right ventricle is activated, higher than measured amplitudes are also generated in the leads sensing mainly the left ventricle and vice versa.

Signals showing the activation of all segments are shown in Figure 4 and Figure 5.

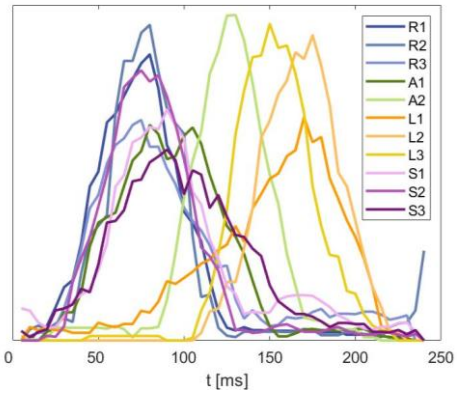


Figure 4. Activation of individual segments over time; LBBB record (the positions of the segments in heart ventricle are shown in Figure 6).

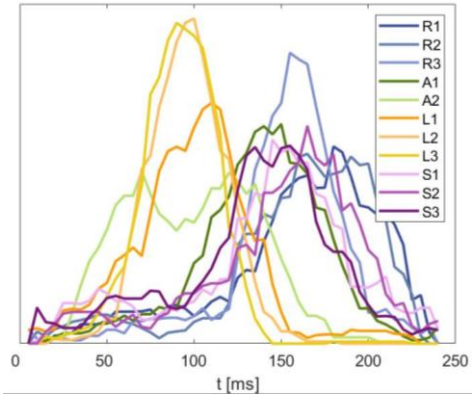


Figure 5. Activation of individual segments over time; RBBB record (the positions of the segments in heart ventricle are shown in Figure 6).

After determining the center of gravity of each curve, the resulting activation map of heart ventricle was created (Figure 6). Obviously, the determined segment activation distribution corresponds to the expected activation for the LBBB and RBBB record.

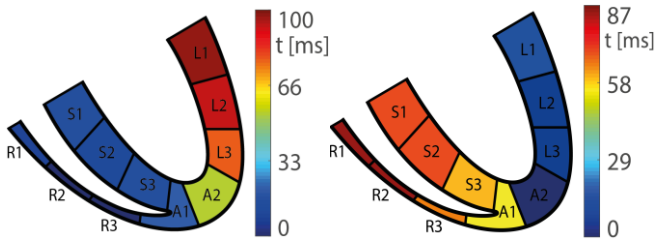


Figure 6. Heart ventricle activation map of the record with LBBB (left) and RBBB (right); segments R1, R2 and R3 are in the right ventricle; L1, L2 and L3 are in the left ventricle; S1, S2 and S3 are in the septum; A1 and A2 are in the apex.

## 4. Conclusion

A method for creating activation maps from only 6 standard chest leads and knowledge of heart geometry was introduced. All calculated activation maps correspond to the theoretical expectation about the propagation of depolarization in LBBB and RBBB records. It is necessary to test the algorithm on data with known segment activation times for a more detailed evaluation. This data is not yet available.

Our method is not affected by low-frequency noise because we only use high-frequency components to create envelopes. Resistance to high-frequency noise is given by the accumulation of more QRS complexes.

The proposed algorithm can be useful for selecting the right therapy targeted individually to each patient. Although patients have the same diagnosis (for example LBBB or RBBB), they do not always have the same sequence of activated segments. This method may also better describe activation of heart in patients with nonspecific intraventricular conduction delay.

## Acknowledgments

This work was supported by grant Czech Science Foundation with grant number GA17-13830S and by Internal grant Brno University of technology with grant number FEKT/FIT-J-19-5800.

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