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Methodology for Automated Detection of Fragmentation in QRS complex of Standard 12-lead ECG

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Abstract— **Fragmented QRS (f-QRS) has been found to have higher sensitivity and/or specificity values for several diseases including remote and acute myocardial infarction, cardiac sarcoidosis etc, compared to other conventional bio-markers viz. Q-wave, ST-elevation etc. Several of these diseases do not have a reliable bio-marker and hence, patients suffering from them have to undergo expensive and sometimes invasive tests for diagnosis viz. myocardial biopsy, cardiac catheterization etc. This paper proposes automation of fragmentation detection which will lead to a more reliable diagnosis and therapy reducing human error, time consumption and thereby alleviating the need of enormous training required for detection of fragmentation. In this paper, we propose a novel approach to detect the discontinuities present in QRS complex of standard 12-lead ECG, known as fragmented QRS, using Discrete Wavelet transform (DWT) targeting both hospital-based and remote health monitoring environments. Fragmentation Detection Algorithm (FDA) was designed and modeled using PhysioNet's PTBDB and upon reiterative refinements it successfully detected all discontinuities in the QRS complex. The QRS complexes of 31 patients obtained randomly from PhysioNet's PTBDB were examined by two experienced cardiologists and the measurements obtained were compared with the results of our proposed FDA leading to 89.8% agreement among them.**

I. INTRODUCTION

In last 5 years, presence of fragmentation in QRS complexes of standard 12-lead (S12) system has gained clinical significance in diagnosis of various cardiologic disorders [1-6] (e.g. remote and acute myocardial infarction, cardiac sarcoidosis, nonischemic cardiomyopathy etc). It has been found to be an important bio-marker for detection of several diseases resulting in higher sensitivity and/or specificity than other conventional markers (e.g. ST-elevation, Q-wave, etc). However, detection of fragmentation in QRS complexes requires training and involve human error which, despite of enormous clinical significance, will inhibit its widespread acceptance and application. In this paper, we propose a novel method to detect fragmentation in the QRS complex using Discrete Wavelet Transform (DWT) with 'haar' wavelet.

Computerized ECG interpretation and feature extraction is being successfully used in a hospital-based environment [7]. Automation of QRS detection and extraction of other features viz. R, S, P, Q waves, their duration and peaks, ST elevation/depression, PT interval and (non) inverted T wave, targeting hospital-based, ambulatory and remote health monitoring services have been performed previously by several researchers [8-10]. However, beside being one of the potential bio-marker no work exist as of now, upto the best of our knowledge, to detect fragmented QRS in an automated way. It has been found that f-QRS can be used as selection criteria for implantation of ICD devices [12,13]. A long-term monitoring is required for this purpose and an automated system will considerably reduce the effort and time required for verification of the signals. Recently, Selvester QRS scoring system [11] was automated for the accurate calculation of QRS score for reliable disease diagnosis and therapy.

This paper introduces, for the first time, a novel methodology to detect fragmentation present in QRS complexes using DWT with Haar function as the wavelet, which has been shown to be low in complexity and power consumption [8], targeting ambulatory and remote health monitoring as well as hospital-based environments. Moreover, the proposed methodology can be implemented either by software or hardware or by adapting hardware-software co-design strategy. The paper has been organized in the following manner. Section II presents the proposed methodology for fragmentation detection, section III presents the experimental results and section IV concludes the paper.

II. PROPOSED METHODOLOGY

First, we introduce the database used in the study (section II A) which is then preprocessed using a wavelet transform based preprocessing module comprising of baseline wandering (BW) removal and denosing (section II B). Then the nature of detailed DWT coefficients is discussed (secion II C) followed by the extraction of QRS complex using TDMG algorithm and preconditioning (section II D). This QRS complex is then fed as an input to the Fragmentation Detection Algorithm (FDA) (section II E).

A. Material

PhysioNet's PTB database (PTBDB)[18,19] was used for designing and verification of the proposed FDA algorithm. PTBDB is a raw 15 lead database consisting of standard 12 leads and 3 Frank leads digitized 1 kHz frequency. The patients were categorized on the basis of cardiologic disorders and 12-lead ECG of more than 50 patients from various categories were used in the designing of the algorithm.

B. Preprocessing Module

Wavelet based preprocessing module was used to remove BW and noise. BW removal was based on Discrete Wavelet

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```
[c,t] = wavedec(x,9,'sym10'); %Decomposition of signal
signal = wrcoef('a',c,t,'sym10',9); %Reconstruction of signal
BW_removed_signal = x − signal;
qmf = MakeONFilter('Symmlet',8);
denoised_signal = recTI(BW_removed_signal,'H',qmf);
```

Fig. 1. Snippet of MATLAB code for implementation of preprocessing module.

Transform (DWT) [14] and denoising was based on Translation Invariant Wavelet Transform (TIWT) [14,15]. Fig. 1 provides the snippet of the MATLAB code for implementation of the preprocessing module. Other denoising methods [16,17] can be used, however, TIWT appears to outperform the rest and therefore we used it in the proposed methodology. The implementation of TIWT requires the input number of samples to be in the power of 2. For example, if a patient's ECG was recorded for about 38s the number of samples obtained at a sampling rate of 1 kHz was 38399, out of these we have taken $2^{15} = 32768$ samples i.e. first 32768 samples for the algorithmic need and rest were excluded from the study. For every patient the denoised signals were used for all further processing. For baseline wandering the level of decomposition was down to level 9 and wavelet used was Symmlet 10. For denoising the level of decomposition was self determined by the code, wavelet used was symmlet 8 and hard thresholding was used.

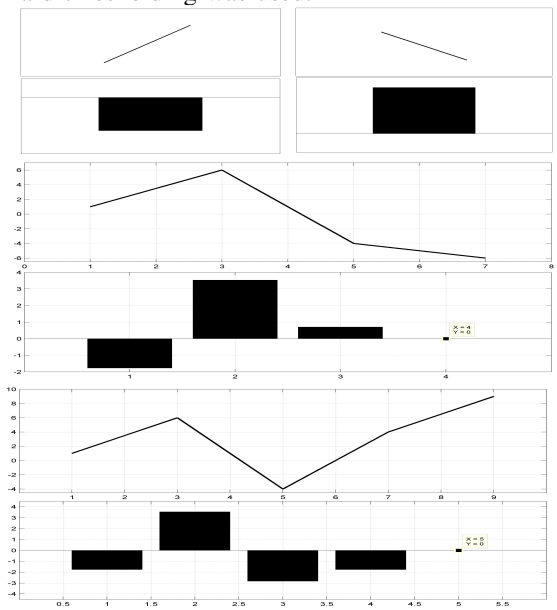


Fig. 2. Patterns observed in detailed DWT coefficients corresponding to the morphology of wave encountered

C. Nature of Detailed Coefficients

Consider the line segment joining two point with a positive slope as shown in Fig. 2-A1. Fig. 2-A2 shows the bar plot of its one level detailed DWT coefficients using haar wavelet. It can be observed that in an increasing part of the curve the detailed coefficients are negative. Similarly, from Fig. 2-B1,B2 it can be noted that in a decreasing part of the curve the detailed coefficients are positive. Let's consider Fig. 2-C1,C2, it shows four consecutive points joint together by line segments, which may represent a portion of the curve, along with the bar plot of their detailed DWT coefficients. With the help of Fig. 2 A,B and C, we hypothesize that if in a digitized signal a pattern similar to Fig. 2-C1 appears (an extremum) then there will be a change in sign of two consecutive detailed coefficients. We test aforementioned hypothesis on Fig. 2D and found that whenever an extremum is encountered there is change in the sign of detailed coefficients. It should also be observed that the magnitude of coefficients depend on the slope of the line segment joining two consecutive points. Greater the slope greater is the magnitude. This phenomenon has been used in modeling and designing of the algorithm.

```
LINEAR INTERPOLATION and DWT
L = length(qrs);z = 1;Interpolated_qrs = zeros(1,2∗L − 1);
for k = 1:1:L
if k < L
w = [qrs(k),mean([qrs(k),qrs(k+1)]),qrs(k+1)];
interpolated_qrs(z) = w(1); interpolated_qrs(z+1) = w(2);
z = z+2; end end
interpolated_qrs(z) = qrs(k);
[C, D] = dwt(interpolated_qrs,'haar');
```

Fig. 3. Snippet of MATLAB code for interpolation and DWT to obtain the detailed coefficients.

D. QRS Extraction and Interpolation

Our recently proposed TDMG algorithm [9] was used to extract the QRS complex from all the leads of preprocessed ECG of every patient. This QRS complex was then preconditioned using simple linear interpolation, $Y_{interpolated} = (Y_k + Y_{k+1})/2$, to increase the number of samples. It was observed that on increasing the number of samples detailed DWT coefficients were accurately capturing all the discontinuities and hence, was applied to all the QRS complexes. Fig. 3 shows the MATLAB (ver. 7.10.0−2010a) code snippet for linear interpolation and DWT to obtain the detailed coefficients from preprocessed and preconditioned QRS complex. Interpolation does not affect the shape of the QRS complex but only inserts an extra sample between two consecutive samples.

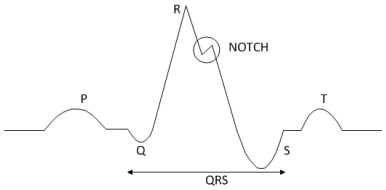


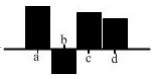
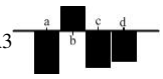
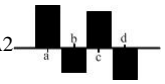
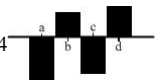
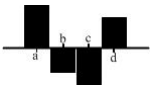
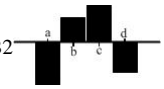
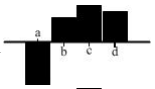
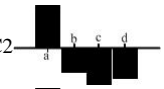
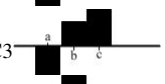
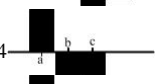
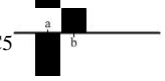
Fig. 4. PQRST complex with fragmented QRS

E. Fragmentation Detection Algorithm (FDA)

Fig. 4 shows the PQRST complex having a fragmented QRS with the presence of a notch on the R wave. The peaks and/or nadirs of QRS complex i.e. Q, R and S wave will be hereafter known as extrema. Discontinuities will be defined as notches along with the extrema. Following from our previous argument in section III A. Detailed DWT coefficients respond in a particular fashion to discontinuities. Notches lead to two consecutive changes in sign of the coefficients as local maxima and minima occur in very close proximity. Extrema, on the other hand, leads to change in sign only once. The conflict arises when an extremum notch pair occur in close proximity where it becomes difficult to recognize the difference between extremum of a notch or a peak. Upon reiterative refinement of the algorithm the criteria of discontinuity detection were framed considering

TABLE I

RULES FOR DETECTION OF DISCONTINUITIES

PATTERN	DESCRIBTION†		POINT OF OCCURRENCE
	NOTCH		
A1  A3 	$A1 - a > 0; b < 0; c > 0; d > 0$ $k = k + 2$	$A3 - a < 0; b > 0; c < 0; d < 0$ $k = k + 2$	A3 and A4 $Peak - a + b$ $Nadir - b + c$
A2  A4 	$A2 - a > 0; b < 0; c > 0; d < 0$ $\|b\|^* < \|c\|;\ k = k + 2$ If $\|b\| > \|c\|$ then C6	$A4 - a < 0; b > 0; c < 0; d > 0$ $\|b\| < \|c\|;\ \ k = k + 2$ If $\|b\| > \|c\|$ then C5	A1 and A2 $Peak - b + c$ $Nadir - a + b$
	NOTCH		
B1  B2 	$B1 - a > 0; b < 0; c < 0; d > 0$ $max(\|b\|, \|c\|) < \|d\|$ $k = k + 3$	$B2 - a < 0; b > 0; c > 0; d < 0$ $max(\|b\|, \|c\|) < \|d\|$ $k = k + 3$	B1 $Peak - c + d$ $Nadir - a + b$
	If $max(\|b\|, \|c\|) > \|d\|$ then C4	If $max(\|b\|, \|c\|) > \|d\|$ then C3	B2 $Peak - a + b$ $Nadir - c + d$
	EXTREMA		
C1  C2 	$C1 - a < 0; b > 0; c > 0; d > 0$ $k = k + 3$	$C2 - a > 0; b < 0; c < 0; d < 0$ $k = k + 3$	For all C1−C6
C3  C4 	$C1 - a < 0; b > 0; c > 0$ $k = k + 2$	$C2 - a > 0; b < 0; c < 0$ $k = k + 2$	Peak or Nadir $-a + b$
C5  C6 	$C1 - a < 0; b > 0$ $k = k + 1$	$C2 - a > 0; b < 0$ $k = k + 1$	

†Pointer 'k' initially starts at 'a'. 'a', 'b', 'c' and 'd' are the values of four consecutive detailed coefficients shown in the form of bar plot and also denote the corresponding bars. Incrementing 'k' shifts it from box 'a' to box 'b', then to 'c' and so on.

*|.| - denotes magnitude of the detailed DWT coefficient at a particular point.

all conflicts that may occur. Table I shows the rules for detection of all forms of discontinuities. The figures shown (A - C) in table I present the pattern that are observed when a discontinuity is encountered. These patterns were selected upon careful observation of QRS complex and its detailed coefficients for more than 50 patients taken from various categories. FDA algorithm works in the following way. DWT, with one level of decomposition, is applied on preprocessed and preconditioned QRS complex using haar wavelet to obtain the detailed coefficients which are then observed starting from first to the last coefficient using a pointer(k) and patterns are identified using the criteria given in table I. The pointer is incremented by one in every turn if no discontinuity is encountered or else it is incremented in accordance to the criteria mentioned in table I. It is necessary to increment the pointer accordingly so as to prevent a discontinuity to be detected more than once. The pointer traverses through the array of detailed coefficients noting all the extrema and notches in the form of their position and point of occurrence and their magnitudes. The complete information about the discontinuities obtained after traversing through the detailed coefficients is used to detect fragmentation in a particular lead on comparison with the morphologies discussed in the literature [1-6].

III. EXPERIMENTAL RESULTS AND DISCUSSIONS

For the better understanding of FDA algorithm we present case study of four fragmented QRS complexes (section III A) and then present and discuss the results (section III B,C).

A. Case studies

To provide more insight into the working of FDA algorithm we present four cases as shown in fig. 5. The 'A' part of the sub-figures show the preprocessed and interpolated QRS complex and 'B' part of the sub-figures shows the bar plot of detailed DWT coefficients. On the beginning of traversal the pointer(k) is placed at the start of the array of coefficients and then it increments either by one or according to the criteria in table I depending on pattern observed. It keeps on traversing until the end and takes note of peaks, nadirs and magnitudes of discontinuities. From the results, presence of fragmentation in a particular can be verified with the help of number of notches, maximum and minimum and comparing these with the morphologies discussed in the literature. All the cases shown in fig. 5 have fragmentation present in the QRS complex. Cases 1 and 2 have no notch while cases 3 and 4 have one notch (circled) present in the complex. The point and position (above (> 0) or below (< 0) the horizontal axis) have been pointed out using text arrows and the same index has been used to denote the points of their occurrence in the corresponding bar plots of detailed coefficients.

B. Results

40 patients were randomly selected from various categories and were examined by the cardiologists. 9 patients were removed from the study owing to their extreme artifacts and paced rhythm. The measurements for 31 patients obtained from the cardiologists were compared with those obtained using the FDA algorithm. The results were compared lead-wise and were found to have 89.8% agreement among them.

C. Discussion

BW removal and denoising is necessary to smooth the complex so that no extra notches are appearing. For accurate detection of fragmentation it is important that accurate QRS

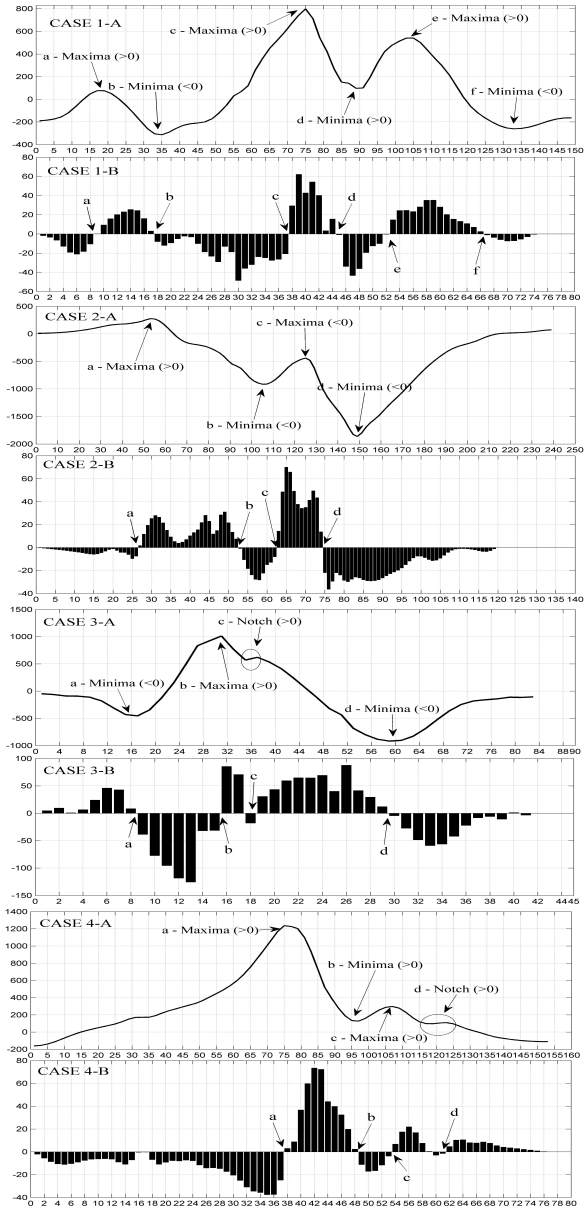


Fig. 5. Patterns observed in detailed DWT coefficients corresponding to the morphology of wave encountered

complex is extracted from a heart beat. In some cases the length of QRS complex was found to be longer than the actual length and was modified to its actual length in consultation with the cardiologists. Case-3 shown in fig. 5 presents a conflicting case as was mentioned in section III C, it can be seen that maxima and notch occurs in close proximity of each other and such patterns have to be handled carefully for accurate results. We have attempted to encompass all such cases by iteratively refining the criteria mentioned in table I. Since, this work is first of its kind so we are unable to compare the performance of the proposed methodology with the existing ones'.

IV. CONCLUSIONS

In this paper, we propose a novel approach to capture all the discontinuities in QRS complex of ECG signal to detect the presence of fragmentation. The algorithm has been verified on PTBDB with the help of cardiologists. This approach introduced in this paper is not limited to ECG but can be used for other biomedical signals for detection of their key aspects and features.

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