A Low complexity Architecture for Online on-chip Detection and Identification of f-QRS feature for Remote Personalized Health Care Applications

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Abstract— This paper introduces a novel low complexity highly accurate on- chip architecture for the detection of fragmented QRS (f-QRS) feature including notches and local extrema in the QRS complexes and subsequently identifies its various morphologies (Notched S, rsR', RsR' without elevation etc.) under the real-time environment targeting remote personalized health care. The proposed architecture uses the outcome of recently proposed Hybrid feature extraction algorithm (HFEA) [1] Level 3 detailed coefficients and detects and identifies the fragmentation feature from the QRS complex based on the criteria of the positions, and the magnitudes of the extrema (maxima and minima) and notches from the wavelet coefficients with no extra cost in terms of arithmetic complexity. To verify the proposed architecture 100 patients were randomly selected from the MIT-BIH PhysioNet PTB database and their ECG was examined by two experienced cardiologists individually and the results were compared with those obtained from the architecture output wherein we have achieved 95 % diagnostic matching.

Keywords- fragmented QRS (f-QRS), Electrocardiography, morphology, wavelet transform, Remote Health Care

I. INTRODUCTION

Cardio Vascular Disease is one of the prime causes of human mortality responsible for around 30% deaths as per the WHO statistics. With the advent of Cyber Physical System (CPS), Internet of Things (IoT) based system and with the advancement of information and communication technology along with the huge growth in the VLSI industry is gradually making the remote CVD monitoring a reality. In this context recently we proposed a low-complexity Hybrid Feature Extraction Algorithm (HFEA) [1] which would detect the conventional ECG features including, QRS duration, R peak, P and T wave etc. on-chip to facilitate the remote personalized continuous health monitoring. However, as per the recent medical studies [4, 5], bio-markers based on these conventional features, fail to detect fatal CVD diseases including myocardial infarction, cardiac sarcoidosis, non-ischemic cardiomyopathy etc. myocardial infarction, cardiac sarcoidosis, non-ischemic cardiomyopathy etc. in a non-invasive way, which on the contrary, can be detected by recently proposed f-QRS complex. To expedite and enhance the CVD diagnosis, we recently proposed an automated f-QRS Detection and Morphology Identification (FDMI) methodology in [3, 6].

In this paper, our aim is to take this idea further to the system level from the concept and propose a low-complexity but medically reliable architecture which can be integrated with the state-of-the art ECG feature extraction algorithm [1, 2] on-chip like HEFA without increasing any extra arithmetic complexity of the circuit.

The paper is organized as follows. Section II provides the necessary theoretical background and the proposed architecture for both f-QRS detection and f-QRS morphology identification, Section III presents the experimental results and validates the proposed architecture against the algorithm and doctor's diagnosis and finally Section IV concludes the discussion.

II. PROPOSED ARCHITECTURE

A. Theoretical Background

We proposed an automated algorithm in [3] to implement a raw ECG signal preprocessing module followed by fragmentation detection and morphology identification. The flow of the FDMI algorithm [3] is shown in Fig.1.

In Figure.1 HFEA extract the crucial points of the ECG signal and provides the QRS complex, which is then interpolated to enhance the detection of all the discontinuities for a better accuracy. FDMI module takes the interpolated QRS complex signal as input to detect the fragmentation and identify the morphologies as output to the corresponding QRS complex.

Fundamentally there exists six morphologies (Notched-S, Fragmented-QRS, Notched-R with Q, Notched-R without Q etc.) of the fragmented QRS complex and several other RSR' variations [3, 6]. Morphology identification step begins after getting the information regarding the number of notches, maxima(s) and minima(s), and their point of occurrence. Based on the conditions [3] we get morphology as the output for that corresponding QRS complex.
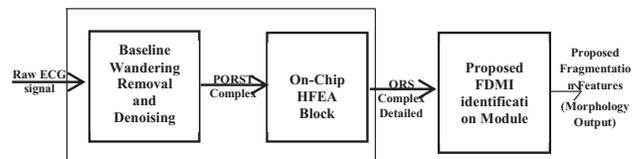

Figure 1. Algorithm for f-QRS detection and morphology identification

1. Baseline wandering removal and Denoising:

DWT (Discrete Wavelet Transform), SWT (Stationary Wavelet Transform) [8], UWT (Undecimated wavelet Transform) [9] and TIWT (Translation Invariant Wavelet transform) are main four approaches for baseline wandering removal and denoising [10-11] the ECG signal, all these approaches are based on wavelet transform and use different wavelet filters. All these techniques were employed and from the observation of all these approaches on 40 subjects it was found that approach 3 and 4 gives better performance in retracing the original signal by removing the artifacts. In this work we have taken approach 4 as the denoising technique.

2. Hybrid Feature extraction Algorithm and interpolation:

Hybrid Feature Extraction Algorithm (HFEA): HFEA [1] takes PQRST complex as input and gives QRS complex as output, it is the combination of MMA applied on the Discrete Wavelet Transform *(DWT)* decomposition levels and the time-domain morphological analysis of the ECG signal.

The analysis is performed at five decomposition levels of DWT, each level having a highpass and lowpass filter. The Detail wavelet coefficients (WT) (cD lx) and Approximate WT coefficients (cA lx) are obtained at the output of highpass filter and lowpass filter respectively. We extract QRS complex and P/T waves by using the third and fifth decomposition level of DWT respectively.

The main advantage of using this DWT with Haar as basis function compared to other WT based approaches for feature extraction is it allows for a major reduction in computational complexity in terms of required mathematical operations.

B. Proposed Architecture

The overview of proposed FDMI architecture is shown in Fig. 2 and the detailed internal block diagram of the same is shown in Fig.4.

1. Proposed Fragmentation Detection Architecture

Fragmentation detection module is used to detect all the kind of discontinuities which may be present in the QRS complex. It provides the information regarding the number of notches, maxima(s) and minima(s) and their positions as the output. The proposed architecture for the fragmentation detection module is shown in Fig.4.

We have tried to reduce the complexity of the proposed fragmentation detection architecture by bypassing the process of interpolation and detailed DWT coefficient calculation, since the DWT block is present in the HFEA module proposed earlier [1] and the level 3 detailed coefficients are already computed, thus the fragmentation detection block would only use these coefficients and not recomputed, thereby removing the need of any extra arithmetic computations.
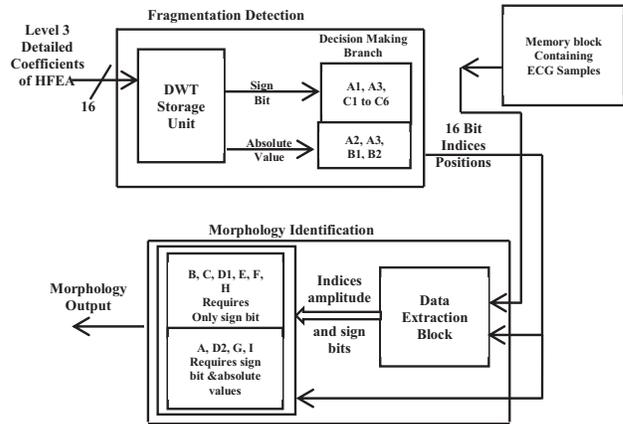

Figure 2. Proposed Fragmentation Detection and Morphology Identification Block

The behavior of the DWT coefficients is altered based on the discontinuities occurring in the QRS complex [3]. The DWT coefficients are 16 bits long. They are transferred serially to the *DWT storage unit (Fig.4)* using a 16 bit data-bus, i.e. one DWT coefficient per clock cycle. The DWT storage unit consists of four registers, each having a word length of 16 bits. For the first four clock cycles, only the data storage is carried out and no further processing is initiated.

At the end of fourth clock cycle, when all the four register of the DWT storage unit are filled, the device passes on the data from these four registers in parallel to the various *decision branches (Fig.4)*. These branches checks for the presence of a maxima (or peak), or a minima (or nadir) or a notch in the QRS complex data points corresponding to the detailed DWT coefficients under processing. The *decision branches* (Fig.4) use the rules [3] for detection of discontinuities to make all the decisions. This procedure is followed till the analysis of all the detailed coefficients is over.

The patterns for the detection of notches are categorized as A1, A2, A3, A4, B1 and B2, whereas the patterns C1 to C6 are classified as extrema's, as shown in Fig.3 The *decision branches* (Fig.4) are connected only with the sign bit line and not to entire data lines of the DWT storage unit (except for the branches A2, A3, B1 and B2, which require magnitude of the DWT coefficient as well) *thereby it results in reducing the hardware complexity*. For example to detect the pattern A1 and A3 we require only the sign bit of the data bus where as to detect the pattern A2 and A4 we require both the sign bit and the 16 bit absolute value of the DWT coefficient. These connections are shown in Fig.4. The connection in this fashion, of only the sign bit line instead of the entire data line, helps in reducing the area consumed for routing. The module begins its evaluation from left to right side of the bar plot of DWT coefficients and if it recognizes any of the patterns matching to those rules for identification of discontinuities [3], the corresponding discontinuity is noted. To keep the count of the DWT coefficients which are being transferred to
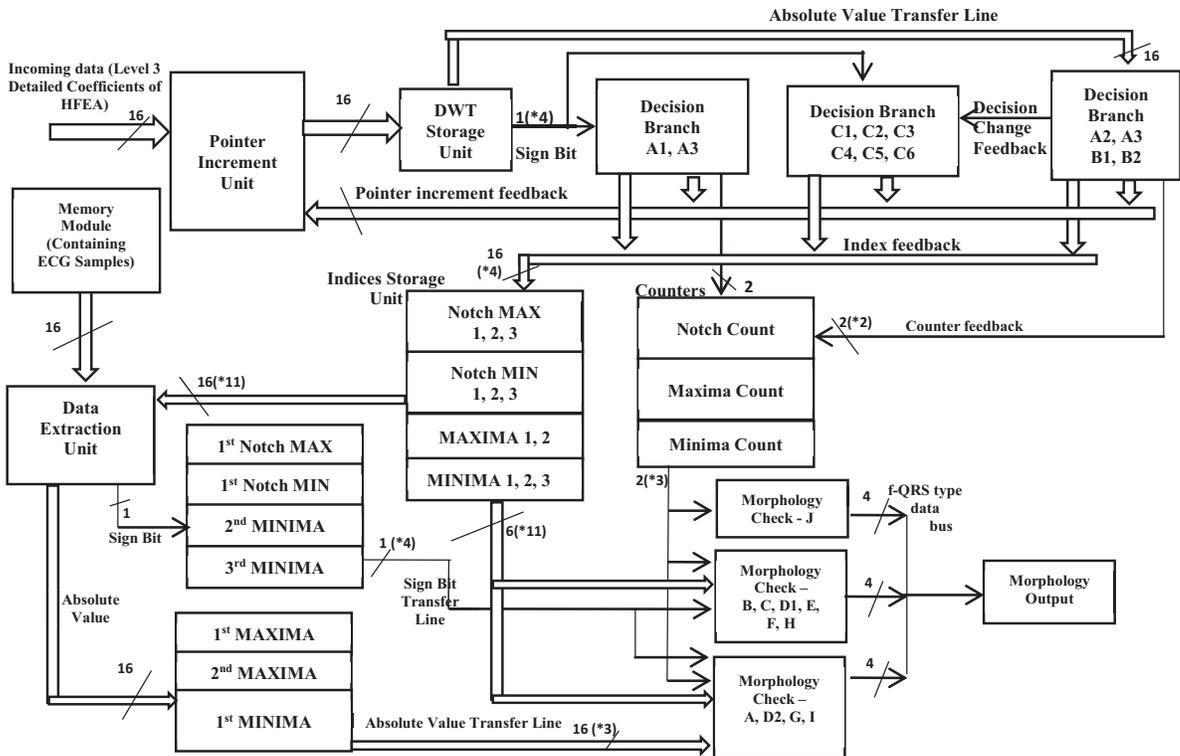
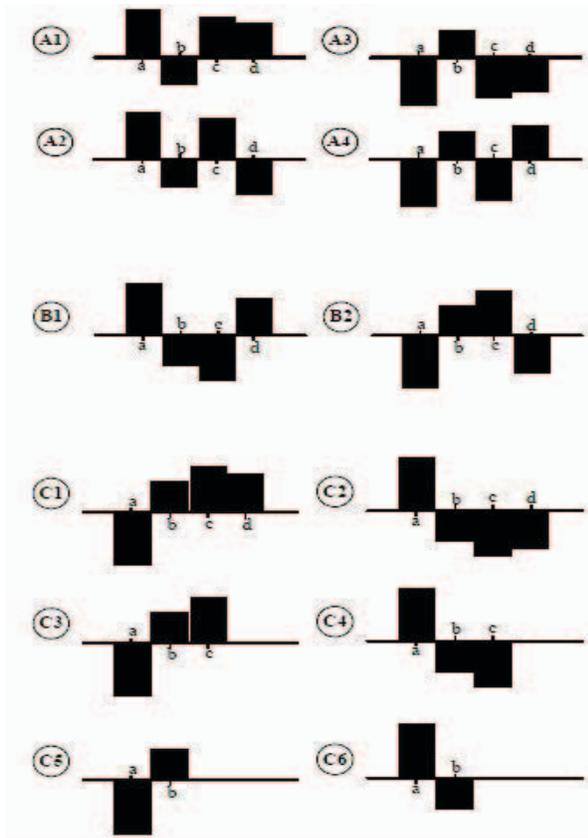Figure 4. Detailed internal view of overall proposed FDMI Architecture

Figure.3 Rules for the identification of discontinues

the DWT storage unit, an algorithm pointer (*Pointer increment unit* block in Fig.4) 'k' is used. For each condition [3] there exists a corresponding condition on the increment of the pointer 'k'. The pointer 'k' points to the position of the data to be transferred to the DWT storage unit with respect to the DWT coefficients currently under analysis. The fragmentation detection module accomplishes the pointer increment by bypassing the DWT coefficients as per the desired increment condition. For example, if the condition which is satisfied by a particular set of four detailed DWT coefficients corresponds to a pointer increment of 3, then the module will bypass the incoming DWT coefficients for the next three clock cycles. Meanwhile, the previously stored data in the DWT storage unit will be shifted to free one register, by discarding the least recent data. This free register will then store the incoming DWT coefficient after three clock cycles. The output of the fragmentation detection module is stored in *Indices Storage Unit* and *counter Blocks* (Fig.4) comprises of the number of notches, maxima(s) and minima(s) along with the indices where the maxima, the minima and the notch (i.e., the notch-maxima and the notch-minima) will lie in the QRS complex. Meticulous study of the FDMI algorithm has enabled us to accomplish the processing of the morphology identification module (explained later) with the usage of only the first three notch maxima, the first three notch-minima, the first two local-maxima and the first three local-minima out of the entire set of the QRS complex data points. The device thus

has only eleven registers, each of word length 16 bit, dedicated for the storage of these indices.

2. Proposed Morphology Identification Architecture

The various morphologies of fragmented QRS are demonstrated in literature [3]. Fig.4 shows the internal dataflow for the morphology identification architecture, where it can be noted that as discussed in section III A the *indices storage unit and the counter registers (Notch Count, Maximum Count, and Minimum Count)* blocks (Fig.4) are already used, this avoids us in having the need of extra hardware by reusing them in morphology identification block.

The data extraction block has two inputs. One of its inputs is from memory which gives the 16 bit QRS complex data and it is received at each clock cycle. This incoming data is stored in a register of word length 16 bit and is overwritten at each clock cycle. The second input to the data extraction block consists of the indices of notches, maxima(s) and minima(s) which is received from the output of the fragmentation detection module. Data extraction module analyzes the incoming QRS complex data corresponding to the indices received at its second input. This analysis produces the value of the sign bits of the first notch-maxima, first notch-minima and the second and third-minima and the amplitude (absolute value) of the first minima and the first and second maxima as the output of the data extraction block.

By examining all the morphologies [3] we deduced that to identify the morphologies B, C, D1, E, F, H we require only the sign bit of the corresponding QRS complex data (the first notch-maxima, first notch-minima, the second and third minima) and to identify the morphologies A, D2, G, I we require both the absolute value and the sign bit of the corresponding QRS complex data (absolute values of the first minima and the first and second maxima). Using this fact, we have optimized the architecture by taking only four registers, each of word length 1 bit, to store the sign of the first notch maxima, first notch minima, the second and third minima and three registers, each of word length 16 bits, to store the absolute value of the first minima and the first maxima and second maxima. This description is shown Fig.4. To identify the 'J' morphology, we only need to know the number of notches and extrema in the QRS complex. Hence, only register values of the *count registers* (Fig.4) is the input to the *'J' morphology detection unit* (Fig.4)

The morphology identification process starts after all the relevant information about the notches, maxima(s) and minima(s), i.e. their number, position on the horizontal axis and relative position on the vertical axis, is obtained from the fragmentation detection module and the data extraction block. Based on the criteria [3] of the number of notches and extrema and their relative position at vertical and horizontal axis, we get the output of the morphology identification module.

III. RESULTS AND DISCUSSIONS

A. Implementation

The results obtained from the Fragmentation detection and morphology identification algorithm [3] (coded in MATLAB) and the proposed architecture (coded in VERILOG, simulated in ModelSim and synthesized in RTL compiler using 130 nm technology at 1 MHz with V_{dd}=1.3 v) compares favorably with 100% matching between the algorithm [3, 6] and the proposed architecture's outcome. The morphologies detected by the proposed architecture for the corresponding QRS complex was tested independently by two experienced cardiologists (acknowledged at the end of this paper). The design occupies 0.19 mm^2 and consumes 32μW power at 1MHZ.

B. Low Complexity Justification

We have achieved the low complexity f-QRS architecture as follows

1. By eliminating the interpolator and DWT generation block in the proposed architecture wherein these were the sub blocks in the algorithm [3, 6].
2. Some of the *decision branches* (Fig.4) are fed with the sign bit from the *DWT storage unit* (Fig.4) instead of feeding the entire data line.
3. *Indices storage unit and the counter registers (Notch Count, Maximum Count, and Minimum Count)* blocks (Fig.4) of fragmentation detection are being reused in the *morphology identification process*.

In this way we have achieved low complexity by removing some of the extra arithmetic complex blocks which drastically reduce both power and area consumption.

TABLE I. FDMI Performance Results

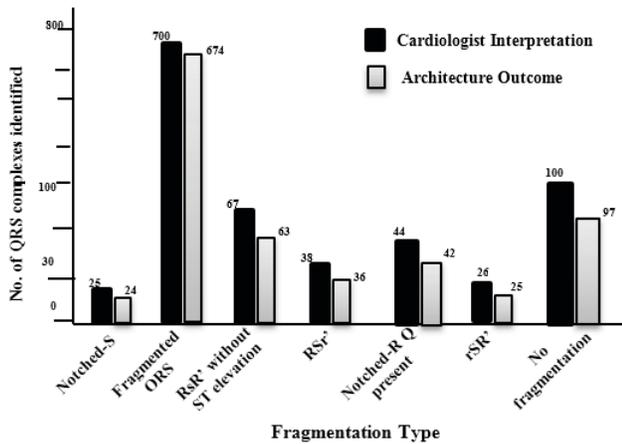| Fragmentation Type	QRS complex interpretation by Cardiologist	QRS COMPLEX OUTCOME FROM ARCHITECTURE	Matching Accuracy (%)
Notched-S	25	24	96
Fragmented-QRS	700	674	96
RsR' without ST elevation	67	63	94
RSr'	38	36	95
Notched-R Q present	44	42	95
rSR'	26	25	96
No fragmentation	100	97	97

Figure 5. Correlation between cardiologist Interpretation and Architecture outcome

C. *Architecture Validation and Accuracy Justification*

For testing the proposed architecture and obtaining the result we have randomly selected 100 patients from each patient we have taken 10 ECGs to get 1000 'QRS' complexes (classified into various fragmented features like Notched-S, Fragmented QRS etc.) from the MIT-BIH PhysioNet PTB database [7], the diagnostic results and the matching accuracy obtained from the cardiologist to that of the proposed architecture are shown in Table. I. We observed that the type of FDMI for a given 'QRS' complex' is same as in the algorithm developed in MATLAB in comparison with the architecture developed using Verilog, while the architectural outcome (verilog results) was 95% accurate when compared to the interpretation obtained from cardiologists.

The results are shown in Fig. 5 which demonstrates the number of 'QRS' complex identified with the given type of fragmentation by the proposed architecture to that of the cardiologist. The proposed architecture has been tested for 1000 such 'QRS' complexes for validation and the corresponding results are shown in Table I.

IV . CONCLUSION

In this paper we introduced on-chip architecture for fragmented QRS detection and identification of its various morphologies targeting remote personalized health care applications. Cardiologist interpretation has taken into consideration and compared with the architecture results which match 95% of accuracy. The proposed architecture low complexity has also been discussed in details which makes it suitable for low power applications like remote healthcare. Chip fabrication and the system design form part of our feature work.

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