

Electrical Engineering

Elixir Elec. Engg. 90 (2016) 37300-37305

Elixir
ISSN: 2229-712X

A Real Time Approach of Cardiac Profiling Scheme for ECG Beat Classification using Shared Counters

Chinmay Chandrakar and Monisha Sharma

Department of Electronics & Telecommunication, Shri Shankaracharya College of Engineering and technology, Bhilai, India

ARTICLE INFO

Article history:

Received: 5 April 2015;

Received in revised form:

24 December 2015;

Accepted: 29 December 2015;

Keywords

QRS complex classification,
Repeated binary strings,
Hashing,
Shared counters,
Adaptive profile.

ABSTRACT

The QRS complex is the most striking waveform within the electrocardiogram (ECG). QRS provides the fundamentals for almost all automated ECG analysis algorithms. We proposed a novel method for classification of ECG beats using shared counters. We first developed a real-time QRS detection technique using two-phase hashing to extract precise QRS points. Then we implement a novel ECG beat classifier to profile each patient's normal cardiac behavior. Our technique relies more on the data stream corresponding to ECG beats than any particular feature. We use the concept of shared counters to minimize the memory requirement. The algorithm automatically adjusts parameters periodically to adapt to ECG changes as QRS morphology and heart rate. Having such profile is essential for various diagnosis (e.g., arrhythmia) purposes. One application of such profiling scheme is to automatically raise an early warning flag for the abnormal cardiac behavior of any individual.

© 2016 Elixir All rights reserved.

Introduction

Background

The electrocardiogram (ECG) is an indirect measure of the electrical activity of the heart. In fact, QRS waveform detection is necessary to determine the heart rate, and several related arrhythmias such as Tachycardia, Bradycardia and Heart Rate variation. It is also necessary for further processing of the ECG signal in order to detect abnormal beats [1]. Particularly, the detection and classification of QRS complexes between normal and abnormal waveforms are very important clinical criteria for diagnosing of patients. Producing an algorithm for the detection of QRS waveforms is a difficult problem due to the time-varying morphology of the signal subject to physiological conditions and with a presence of noise. Signatures of new QRS are obviously unknown. One common property of all QRS is that they appear frequently within a short time. In other words, the signature of the QRS is frequently repeated in a certain time interval. Therefore, during an outbreak, similar patterns of signature are received across the entire ECG signal.

After the beat detection, effective beat classification is required for correct analysis of different types of arrhythmia as well as normal and abnormal ECG waveform. So far, several techniques such as maximum likelihood, (artificial) neural networks [27], and support vector machines [25, 26] have been introduced for the ECG beat classification. Automated arrhythmia-diagnosis systems that can provide high-classification accuracy rates for inter and intra-patient variation cases are still an active area of research.

Implementation Challenges

It is crucial for ECG QRS detection systems to result in high sensitivity, even if this results in a large number of false detections. Such systems can be used to reduce considerably the amount of data that need to be reviewed then cardiologists can easily discard false detections. Additionally, false positive and false negative detection errors are inevitably generated in any imperfect detection system. A false positive indicates a normal

QRS that is incorrectly identified. In other words, it means labeling a normal QRS as abnormal, while it is actually not. A false negative means missing the detection of a normal QRS by incorrectly labeling abnormal QRS one.

Basic Concept and Paper Organization

An efficient software based QRS detection and classification system is presented in this paper. The basic idea used for QRS detection was the technique of Network Intrusion Detection Systems (NIDS) used in networking application for finding the frequently repeated strings in a packet stream for further investigation [2]. Our technique relies more on the data stream corresponding to ECG beats than any particular feature. ECG signal is converted in the form of string and the part of QRS waveform string can be treated as a worm. The strategy search algorithm for finding frequently repeated strings (signature) within a given time frame of the stream has been used to detect the R-peak and QRS waveform. We use a phase hashing in which shared counters are used to determine whether a string has been repeated more than a certain number of times. Second, we introduce a novel technique for profiling a patient's normal ECG. As our system was proposed on binary data stream, any variation in the morphology on QRS waveform (amplitude and time) all comes under consideration as compared to conventional system which worked on fixed parameters to derive certain ECG patterns specific to a patient. Our technique clearly identifies a normal region for a person and can, thus, identify abnormal beats that fall outside this normal region.

The rest of this paper is organized as follows. In Section II we take a glance at prior work related to QRS detection and classification systems. We describe the functions of our QRS detection and classification system in Section III. We summarize our simulation results in Section IV. Finally, concluding remarks are in Section V.

Database used

We used data from the MIT-BIH arrhythmia database to test the performance of our methodology [3]. All ECG data used

here are sampled at 360 Hz, and the resolution of each sample is 8 bits/sample, therefore the bit rate of these data is 2880 bps. All of the tests were conducted both on normal and abnormal ECG for the robustness of the proposed method.

Prior Work

Particularly, the detection and classification of QRS complexes between normal and abnormal waveforms are very important clinical criteria for diagnosing of patients. Over the last decades there have been a number of techniques proposed to detect these waveforms. For instance early attempts of Senhadji et al who compared the ability of wavelet transform based on three different wavelets (Daubechies, Spline, and Morlet) to recognize and describe isolated cardiac beats [4]. Sahambi et al used a first-order derivative of the Gaussian function as a wavelet for the characterization of the ECG waveforms, where they used modulus maxima-based wavelet analysis to detect and measure various parts of signal, especially the location of the onset and offset of the QRS complex and P and T waves [5]. The other algorithms have been developed based on spectral [6, 7] or wavelet features [8, 9], amplitude relative to background activity [10, 11] and spatial context [12, 13] to characterize the ECG signal.[14-19] Jiapu Pan and Willis J. Tompkins of the University of Wisconsin were perhaps the first to develop a real-time QRS detection algorithm on a Z-80 microprocessor [14]. Ning et al. proposed the location of the true peak can be determined according to the fact that the true peak has the largest magnitude within its 200 ms time window [20]. Jain et al. Proposed, the ECG Feature Extractor provided by LabVIEW Biomedical toolkit detects QRS waves [21]. Yazdani et al. proposed that for QRS detection with peaks at R-waves and valleys before and after, Q- and S- points. QRS-onset and QRS-Offset are calculated [22]. Nallathambi et al. proposed, the preprocessed ECG signal is converted into a train of pulses using the IF sampler [23]. After the beat detection, effective beat classification is required for correct analysis of different types of arrhythmia. Methods such as pattern recognition, maximum likelihood, (artificial) neural network, and support vector machines have been widely used for classifying ECG beats [25, 26]. Machine-learning techniques learn from the samples of training data and map new data instances based on the information extracted from the annotated training data samples [27]. De Chazal et al. classified the beats by analyzing the RR intervals and ECG morphology features along with heart beat segmentation information [28]. Christov et al. provided a thorough comparison of time-frequency ECG features for beat classification [29]. Pathological cardiac events identified using the method introduced in [30] is also a patient-adaptive classifier. This method analyzes the deviation of the RR interval from the mean value and the deviation of QRS patterns from the sustained rhythm. Haseena et al. [31] use a hybrid of fuzzy clustering and artificial neural networks to discriminate between different classes of beats.

QRS Detection And Classification System System Design Approach

Our technique relies more on the data stream corresponding to ECG waveform than any particular feature. The basic idea is to break the input ECG signal into binary string. For this, analog to digital conversion was performed. The final output was the binary data stream corresponding to ECG waveform. These data stream was now used for further processing. Next step was to select a string of L bytes. The boundaries of these strings are chosen so that when a long string is repeated, the boundaries within that string are repeated at the same parameter locations. To achieve this, the boundaries are decided based on R-peaks.

Between these two consecutive boundaries the minimum value of binary data bits Q and S points starting from middle R-peak to the left and right are determine for frequent occurrence within a fixed time duration. Hereafter the data bits between Q point and S point will be called as signature which is W bytes. L is not fixed as it depends on the boundaries, which in turn depends on R-R interval. Similarly W is not fixed because it depends on Q point and S point locations. To achieve real-time QRS detection and classification, we use the concept of shared counters. In order to avoid counting approach using numerous memory arrays number of times, a string was hashed to a certain value. Instead, we use shared-counters in which smaller memory units are simulated to function in parallel. In our design, a two-level hashing is used in two phases. The string is used to first generate a Phase 1 hash. This hash value is used as the signature of the string henceforth for simplification. The signature is used in a second phase hash to produce 'm' independent hash values indexed into 'm' arrays. Assuming the width of each memory array to be 'n', each 'm' hash memory would have 2^n locations in depth. Each array location that is indexed is incremented. Effectively, 'm' shared counters per signature during monitoring are used. If, say 'k' out of 'm' counters exceeds the threshold THR value, the signature is suspect as a QRS waveform. Then cardiac profile is plotted against the time duration of the suspected QRS waveform (In form of number of samples) and the number of count the suspected QRS waveform has repeated. Our technique is a local beat classifier that can be designed on top of a global classifier for performance enhancement.

Architecture

Phase 1:

In Phase 1, we assumed the width of sliding window to be one R-R interval as shown in "Fig.1,". It means, every consecutive two R-R interval blocks in the packet stream is processed. Therefore size of the string between two boundaries (in bytes) in the first phase is the data stream between two consecutive R-R intervals. On each clock cycle, one R-R interval string is shifted and a new byte for the packet stream of two consecutive R-R intervals was taken to form a next packet stream i.e. boundaries (in bytes). Now from this packet stream we search for the second consecutive eight ones (binary) which is actually R-peak. With reference to this R-peak we go on finding Q point and S point to the left and right side respectively. Between these two consecutive boundaries the minimum value of binary data bits starting from middle R-peak to the left and right are determine for frequent occurrence within a fixed time duration. This minimum value is taken as Q and S point. Now the binary stream found between this detected Q and S point, we declare that portion of the stream as a boundary of detected signature and can act as a hash value in phase 1. This hash value is obtained by compacting L bytes using an eight bit comparator. We use the binary stream between Q point and S point as a signature of W bytes as the final result of phase 1. The next signature boundary is considered to be part of the next L byte. In other words, the resulting string in phase 1 results from L-bytes hashing to W -bits. "Fig. 1," shows the function blocks of phase 1.

**Table I. Performance of our QRS detector on mit-bih
Arrhythmia dataset 103 (10 sec. Long)**

Sr. No.	R-peak Time	MIT BIH Sample Index	R-peak Index Calculated	R-R interval	QRS Duration (No of Samples)	Sum of Q-S Array
1	0	21	0	0.736111	20	3584
2	0.736111	265	265	0.863889	18	3446
3	1.6	575	576	0.836111	19	3567
4	2.436111	876	877	0.844444	18	3411
5	3.280556	1180	1181	0.836111	18	3688
6	4.11667	1482	1482	0.897212	18	3516
7	5.013887	1795	1802	0.897111	20	3942
8	5.911111	2127	2128	0.897333	18	3379
9	6.788889	2444	2444	0.836111	20	3664
10	7.625	2744	2745	0.830556	19	3599
11	8.455556	3044	3044	0.841667	20	3767
12	9.297222	3347	3347	0.833333	20	3963
13	10.13056	3647	3647	0.883315	22	4161

Table II. Performance of our qrs classification on mit-Bih arrhythmia database (15 min. Long each)

Sr. No.	Data Sets					
	232		100		200	
	No. of Samples between Q & S points	Counts of sample	No. of Samples between Q & S points	Counts of sample	No. of Samples between Q & S points	Counts of sample
1	8	4	4	1	4	2
2	9	1	5	1	7	2
3	10	5	6	1	8	1
4	11	13	7	1	9	8
5	12	11	8	6	10	11
6	13	15	9	3	11	13
7	14	8	10	4	12	11
8	15	22	11	3	13	14
9	16	10	12	2	14	10
10	17	8	13	2	15	25
11	18	16	14	46	16	12
12	19	29	15	303	17	6
13	20	33	16	309	18	10
14	21	44	17	200	19	25
15	22	245	18	97	20	16
16	23	341	19	65	21	23
17	24	43	20	56	22	75
18	25	11	21	25	23	190
19	26	2	22	6	24	270
20	27	1	23	5	25	277
21	28	7	25	1	26	138
22	29	79	29	1	27	41
23	30	1			28	28
24					29	205
25					30	1

Phase 2 :

In Phase 2, we use the phase 1 hash value (final signature of phase 1) to produce m independent hash values as shown in "Fig. 2.". We use these hash values as memory indices in phase 2. Similar to phase 1, the hash functions were designed. The index (hash value) i is used to index into array i . The hit location is incremented hence the 2^n locations also function as counters. If out of the ' m ' counters, for a given string, ' k ' counters exceed the threshold, an alert flag is raised that the string may be a QRS waveform. "Fig.2," shows the conceptual diagram of phase 2. The counters chosen by hash units (black locations in "Fig. 2,") will be incremented. After calculating final result for phase 1, which is binary stream between Q point and S point as a signature of W bytes, the ' m ' independent hash value for phase 2 has been determined. The number of samples between Q point and S point of first R-peak has been calculated. This total number of sample will act as an independent hash value i.e. m . This process is repeated for all the determined R-peak. Due to the time-varying morphology of the signal subject to physiological conditions there is a variation in QRS waveform (duration and amplitude), hence the number of samples as shown in Table I. This different number of sample will act as an independent hash value in phase 2 i.e. ' m '. Once the hash value has been found for phase 2, then for the respective hash value of the entire signature, the binary addition was performed for the entire sample found between Q point and S point. This addition was used to index into array i . The resultant value acts as a memory address ' n ' for the array i . Therefore when hit location is incremented, the array locations also function as a counter.

If any counter exceeds the threshold, the string is reported as a suspicious worm i.e. QRS waveform. In other words, all the processing, e.g. counting of number of samples in a signature, addition of binary value of all the sample within the signature and threshold computation are done within each time frame.

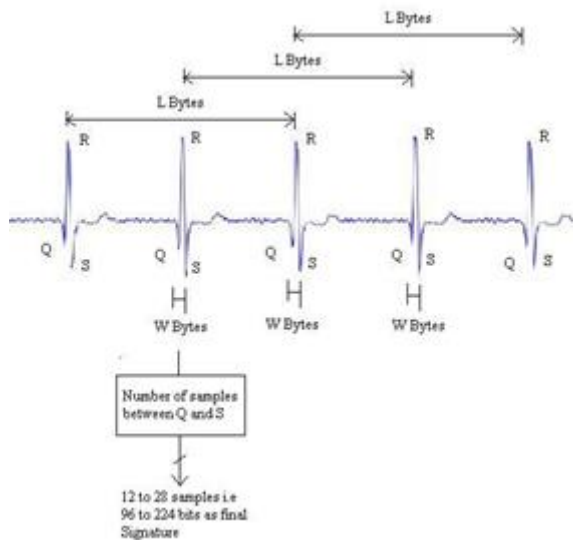


Figure1. Functional blocks of Phase 1.

We clear counters and entries from the hash tables periodically. Our parametric settings of the system are summarized as follows:

- $L \approx 288-432$: L is a variable as it depends on boundaries. Size of the string between two boundaries (in bytes) in the first phase depends on two consecutive R – R interval.

- $W \approx 12 - 28$: W size of the signature (in bytes) in the first phase. W is variable as it depends on the location of Q point and S point.
- $l=8$: size of the number (in bits) for boundary check of the signature in the first phase of hashing.

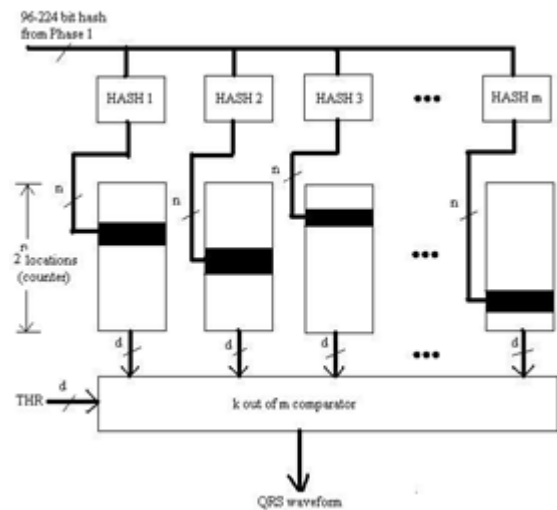


Figure 2. Functional blocks of Phase 2.

- $m \approx 12-21$: number of hash units in the second phase of hashing.
- $n \geq 12$: address bus size of memory arrays in the second phase. The binary addition of the entire sample found between Q point and S point.
- k : number of hash units that need to exceed threshold to raise an alert flag. The term policy ' k ' out of ' m ' is referred to when ' k , out of ' m ' counters exceeds the threshold value.
- THR : threshold value for counters was chosen to be a factor of average content of counters for the best performance.

The main idea in ECG profiling is based on the underlying concept of pattern matching. We treat ECG signals as data packets and in ECG packets there is no global pattern (with fixed waveform dimensions) for a normal ECG waveform, making the problem more complicated. Therefore, we need a patient-adaptive profiling scheme, similar to repetition-based pattern detection schemes, to derive a normal ECG pattern for an individual. Based on the contents of the counters as shown in Table II, a bell-shaped profiling curve would be provided, where anomalies would lie on the tail(s) of the curve [24]. Abnormal ECG beats of the ECG profiling curve will be seen where humps exist on the tail of the bell-shaped curve. Essentially, different ECG features or a combination of features, can collectively classify the beats into normal versus abnormal beats, where the abnormality type (class) depends on the ECG features used for profiling.

Experimental Results

Performance Evaluation of Beat Classification

We have applied our patient-adaptive profiling scheme on the entire 15-min timeframe of each record in the open-source MIT-BIH arrhythmia database [3]. In this proposed technique, we have used one hash function (Number of samples between Q and S points) in the first and second phases. In general,

abnormal ECG beats are reflected as distortions and humps on the tail of the bell-shaped curve. Highly distorted bell curve indicates the presence of too many irregular beats. "Fig. 3," shows the distribution of the counter contents for datasets 103, 100, 200 and 232, respectively, when considering a 15-min (first fifteen minutes) timeframe of

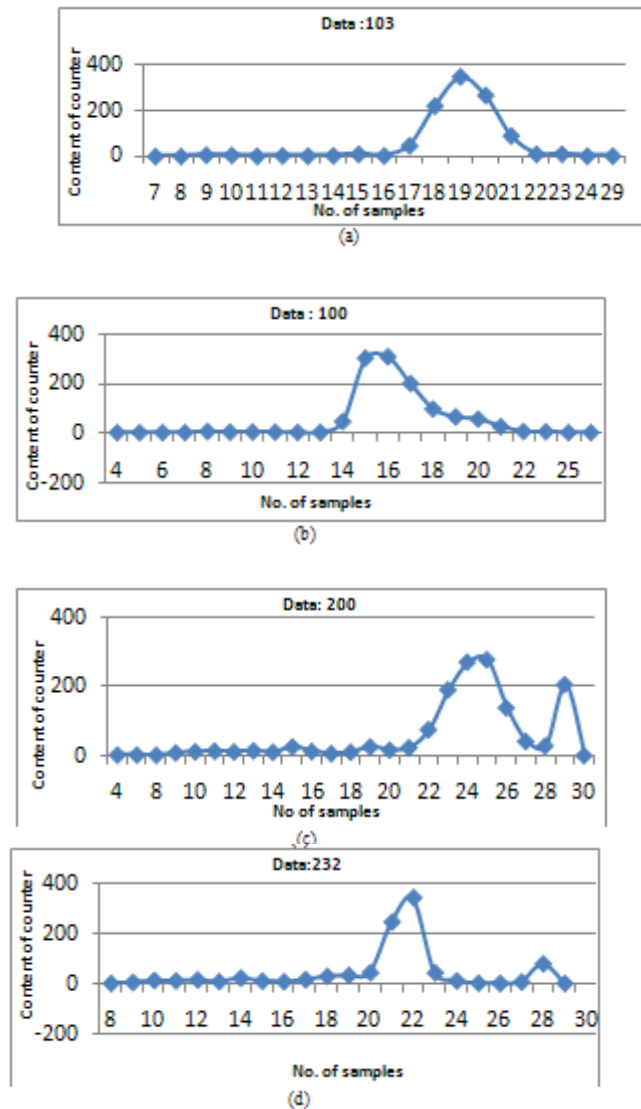


Figure3. Distribution of counter contents for MIT-BIH arrhythmia database readings.

profiling analysis. As can be seen, a bell-shaped curve represents the normal distribution of the content of the counters. The curve clearly depicts a normal region of the ECG beats. Any nonzero counter content that falls outside the normal region would indicate the existence of abnormal beats as shown in "Fig. 3,". Datasets 103 do not contain any abnormal beats, as the curves reflect this fact. Datasets 100 contain very few abnormal beats, which is reflected on the curves as very few counter contents outside the normal region. Datasets 200 and 232 contain too many abnormal beats, as a normal region can be hardly defined on the curves. All these results match the MIT-BIH arrhythmia database annotations for beat classification. To numerically verify our results, we computed the percentage of area under the curve for the abnormal region and compared it with the

percentage of abnormal beats within the same analysis timeframe of the MIT-BIH database shown in Table III.

The Equation 1 gives the area under the curve for abnormal regions.

$$A = \sum_{x=a}^b y(x) \quad (1)$$

where a and b are the points (often on the tail of the curve) that fall out of the normal (bell-shaped) region, and $y(x)$ refers to the content of counter with index x . Table IV compares the performance of our scheme with the MIT-BIH arrhythmia database beat annotations (normal versus abnormal). The y-axis corresponds to the number of memory with index x . For example, point (16,309) in "Fig. 3," (b) corresponds to the hash value of 16 as the ECG features (Number of samples between Q and S points) of particular beat. The memory location required is 309. Our approach demonstrate which beats are irregular in terms of time sequencing and it graphically represents the presence of abnormal beats on the distorted tail of the curve.

Significance of proposed method

1. The significance of our proposed method lies within the efficiency of the binary data processing and the accuracy required in the ECG profiling technique. Since we consider the ECG signal record as a stream of binary data only one feature is sufficient for classification.
2. Another significance is that this type of binary data stream processing could be effectively applied to other biometrics signal. The reason is that our type of processing is relatively feature-independent, and rather looks into the biometric signal as one single string of binary data.
3. Our architecture requires simple logic, e.g., comparator, counters; it could be easily implemented on customized hardware for clinical applications.
4. Our approach demonstrates which beats are irregular in terms of time sequencing and it graphically represents the presence of abnormal beats on the distorted tail of the curve.

Conclusion

We proposed a technique for profiling of ECG waveform for any individual irrespective of the patient's physical condition by first detecting the beat accurately. Our beat detection scheme was the technique of Network Intrusion Detection Systems (NIDS). We then classified the detected features of the beats by means of repetition-based packet-processing techniques. Most approaches rely on extracting several features, adding to the complexity and overall latency of the beat classification procedure. Our technique relies more on the data stream corresponding to ECG beats than any particular feature therefore any variation in the morphology on QRS waveform (amplitude and time) all comes under consideration as compared to conventional classification system. The outcome of our work is a profiling curve specific to any individual, representing a graphical view of the existence of abnormal beats. This is a novel technique that can be used for early warning monitoring systems. More specifically, our method has resulted in high accuracy in the range of other well known approaches.

References

- [1] Lilly, L. S., Pathophysiology of heart disease, 3rd edition. Lippincott Williams & Wilkins, Philadelphia, pp. 57–90, 2003.
- [2] SNORT Network Intrusion Detection System, www.snort.org.
- [3] MIT-BIH (<http://www.physionet.org>)

- [4] Senhadji, L., Carrault, G., et al., "Comparing wavelet transforms for recognizing cardiac patterns," *IEEE Eng. Med. Biol.* vol. 14, no.2, pp. 167–173, 1995.
- [5] Sahambi, J. S., Tandon, S. M., and Bhatt, R. K. P., "Using wavelet transforms for ECG characterization: an on-line digital signal processing system," *IEEE Eng. Med. Biol.*, vol. 16, no. 1, pp. 77–83, 1997.
- [6] Hamilton, P. S., and Tompkins, W. J., "Quantitative investigation of QRS detection rules using the MIT-BIH arrhythmia database," *IEEE Trans. Biomed. Eng.*, vol. 33, no. 12, pp. 1157–1165, 1986.
- [7] Thakor, N. V., Webster, J. G., and Tompkins, W. J., "Estimation of QRS complex power spectra for design of a QRS filter," *IEEE Trans. Biomed. Eng.*, vol. 31, no. 11, pp. 702–706, 1986.
- [8] Li, C., Zheng, C., and Tai, C., "Detection of ECG characteristic points using wavelet transforms," *IEEE Trans. Biomed. Eng.*, vol. 42, no.1, pp 21–28, 1995.
- [9] Castro, Kogan, D., and Geva, A. B., "ECG feature extraction using optimal mother wavelet," *IEEE EMBE Int. Conf.*, pp. 346–350, April, 2000.
- [10] Romero, I., Serrano, L., and Ayesta, "ECG frequency domain features extraction: A new characteristic for arrhythmias classification," *Conf. IEEE Eng. Med. Biol. Soc.*, vol. 2, 2001.
- [11] Kadambe, S., Murray, R., and Boudreaux-Bartels, G. F., "Wavelet transform based QRS complex detector," *IEEE Trans. Biomed. Eng.* vol. 46, no.7, pp. 838–848, 1999.
- [12] Romero, L., Addison, P. S., and Grubb, N., "R-wave detection using continuous wavelet modulus maxima," *IEEE Proc. Comp.Cardiol.*, vol. 30, pp. 565–568, 2003.
- [13] Tkacz, E. J., and Komorowski, D., "An improved statistical approach to the QRS detection problem using matched filter facilities," *Biomed. Technik/Biomed. Eng.*, vol. 37, no.1, pp 99–109, 1992.
- [14] J. Pan and W. J. Tompkins, "A real-time QRS detection algorithm," *IEEE Trans. Biomed. Eng.*, vol. BME-32, no. 3, pp. 230–236, Mar. 1985.
- [15] I. A. Dotsinsky and T. V. Stoyanov, "Ventricular beat detection in single channel electrocardiograms," *BioMedical Engineering Online*, vol. 3, pp. 3, 2004.
- [16] F. Zhang, J. Tan, and Y. Lian, "An effective QRS detection algorithm for wearable ECG in body area network," in *Proc. IEEE Biomed. Circuits Syst. Conf.*, 2007, pp. 195–199.
- [17] I. Iliev, V. Krasteva, and S. Tabakov, "Real-time detection of pathological cardiac events in the electrocardiogram," *Physiol. Meas.*, vol. 28, no. 3, pp. 259–276, 2007.
- [18] H.-Y. Zhou and K.-M. Hou, "Embedded real-time QRS detection algorithm for pervasive cardiac care system," in *Proc. 9th IEEE Int. Conf. Signal Process.*, pp. 2150–2153, 2008.
- [19] M. Cvikl and A. Zemva, "FPGA-oriented HW/SW implementation of ECG beat detection and classification algorithm," *Digital Signal Process.*, vol. 20, no. 1, pp. 238–248, Jan. 2010.
- [20] Ning X., Selesnick I. W. "ECG Enhancement and QRS Detection Based on Sparse Derivatives". *Biomedical Signal Processing and Control* vol. 8, pp. 713–723, 2013.
- [21] Jain, S., Kumar P. Subashini M.M. "LABVIEW based expert system for Detection of heart abnormalities". *International Conference on Advances in Electrical Engineering (ICAEE)*, pp. 1-5, 2014.
- [22] Yazdani S., Vesin J-M. "Adaptive Mathematical Morphology for QRS Fiducial Points Detection in the ECG". *Computing in Cardiology*, vol.38, pp. 725–728, 2014.
- [23] Nallathambi G., Principe J. C. "Integrate and Fire Pulse Train Automaton for QRS detection". *IEEE Transactions on Biomedical Engineering*, vol. 61, no. 2, pp. - 317-326, 2014.
- [24] M. Faezipour, M. Nourani, and R. Panigrahy, "A real-time worm outbreak detection system using shared counters," in *Proc. 15th Annu. IEEE Symp. High Perform. Interconnects*, Aug. 2007, pp. 65–72.
- [25] M. H. Song, J. Lee, S. P. Cho, K. J. Lee, and S. K. Yoo, "Support vector machine based arrhythmia classification using reduced features," *Int. J. Control, Autom., Syst.*, vol. 3, no. 4, pp. 571–579, Dec. 2005.
- [26] R. Besrou, Z. Lachiri, and N. Ellouze, "ECG beat classifier using support vector machine," in *Proc. 3rd IEEE Int. Conf. Inf. Commun. Technol.: From Theory Appl.*, Apr. 2008, pp. 1–5.
- [27] Y. H. Hu, S. Palreddy, and W. J. Tompkins, "A patient adaptive ECG beat classifier using a mixture of experts approach," *IEEE Trans. Biomed. Eng.*, vol. 44, no. 9, pp. 891–900, Sep. 1997.
- [28] P. de Chazal, M. O'Dwyer, and R. B. Reilly, "Automatic classification of heartbeats using ECG morphology and heartbeat interval features," *IEEE Trans. Biomed. Eng.*, vol. 51, no. 7, pp. 1196–1206, Jul. 2004.
- [29] I. Christov, G. Gómez-Herrero, V. Krasteva, I. Jekova, A. Gotchev, and K. Egiastian, "Comparative study of morphological and time-frequency ECG descriptors for heartbeat classification," *Med. Eng. Phys.*, vol. 28, no. 9, pp. 876–887, Nov. 2006.
- [30] I. Iliev, V. Krasteva, and S. Tabakov, "Real-time detection of pathological cardiac events in the electrocardiogram," *Physiol. Meas.*, vol. 28, no. 3, pp. 259–276, 2007.
- [31] H. H. Haseena, A. T. Mathew, and J. K. Paul, "Fuzzy clustered probabilistic and multi layered feed forward neural networks for electrocardiogram arrhythmia classification," *J. Med. Syst.*, pp. 1–10, Aug. 2009.