Wave Sequence Based Identification of Sinus Rhythm Beats on a Microcontroller

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Abstract

Holter recorders are currently changing their typical arrhythmia detection focus towards additional ECG evaluation objectives like ST-T-segment or heart rate variability analysis. Such estimations are only applicable when they are related to normal sinus rhythm excitations. However, up to now most approaches do not actively inquire this question but label every beat normal which is not sufficiently pathologic to be identified as abnormal beat.

In this work we propose a real time applicable algorithm to identify sinus rhythm beats depending on their characteristic wave sequence regularity.

Identification results are evaluated against the AAMI standard conform beat reference annotations in the MIT-BIH Arrhythmia database (Se=93.52%; +P=90.24%), European ST-T-Database (Se=95.09%; +P=99.86%) and the MIT-BIH Normal Sinus Rhythm database (Se=98.56%; +P=99.65%).

Additionally we prove the algorithms to be running on an ARM Cortex-M3 microprocessor by detailed execution time and memory usage evaluation.

The presented real time applicable algorithm allows an active beat by beat identification of sinus rhythm excitations to continue with comprehensive evaluations which rely on physiological conduction properties.

1. Introduction

In the last years Holter recorders improved significantly in terms of battery lifetime, signal quality and computational capabilities. With these new resources the classic focus on ventricular arrhythmia detection slowly augments towards other long term applications like: atrial fibrillation detection for stroke risk stratification, ST-T-segment evaluation to detect myocardial ischemia, heart rate variability (HRV) observation to draw conclusions on the autonomous nervous system or calculation of heart rate turbulence (HRT) to predict myocardial infarcts. However, these methods prerequisite an accurate identification of physiological excited sinus rhythm beats to work properly.

Current ECG analysis approaches, which are usually searching for arrhythmias tend to label each beat as normal which could not be identified as abnormal. An inspection if the beat fulfils the requirements of a physiological excitation is usually not done. Within this study we present an algorithm to actively identify sinus rhythm beats on a mobile long term ECG monitoring device.

2. Material and methods

2.1. Evaluation on databases

To evaluate the algorithms capability to identify physiological excited beat deflections in the ECG signal, three standard physionet databases are used: the MIT-BIH Arrhythmia Database (MITDB) [1], the European-ST-T-Database (EDB) [2] and the Normal Sinus Rhythm database (NSRDB) [3]. All Databases provide reference annotations for each dataset, with detailed beat type labels according to the AAMI standards [4]. In total more than 2.5 million beats have been evaluated.

Evaluation results are stated as sensitivity (Se) and positive predictive value (+P) depending on the number of true positive (TP), false negative (FN) and false positive (FP) beat identifications, as specified in (1) and (2).

$$Se = TP/(TP + FN) \tag{1}$$

$$+P = TP/(TP + FP) \tag{2}$$

For QRS detection results these values are well known. For the beat identification evaluation a beat is counted as TP if the proposed algorithm identifies it as sinus rhythm beat (SR) and the corresponding reference annotation is labeling it as normally excited beat type as well. According to the AAMI beat type scheme [4] these annotations are namely: normal (N), left bundle (L), right bundle (R) and unspecified bundle branch blocks (B). For any other reference they are considered as FP. Beats which are identified as non-sinus rhythm but do have a N, L, R or B reference type are labeled as FN.

2.2. Hardware performance evaluation

The described algorithms are implemented on an AMR Cortex-M3 microcontroller based wearable ECG monitoring system. The device records a 3 channel ECG, each with a resolution of 12 Bit and a sampling frequency of 250 Hz. The signal is filtered with a 0.5-40 Hz band pass and then fed into the signal processing chain on the microprocessor. [5]

The processor provides 256 kB of internal read only memory (ROM), 52 kB of random access memory (RAM) and is running with a reduced core frequency of 4 MHz due to power constrains on the mobile system.

To prove the algorithms to be running in real time on the low power optimized microprocessor, execution times are simulated and compared against the available system resources. Since the beat evaluation algorithm will only be activated when a beat was detected, execution time estimates will be given as total mean to describe the overall burden of the system, as maximum value to evaluate the influence of peak events and as mean value when a specific signal processing block is executed.

3. Signal processing

Signal evaluation is done using several algorithmic blocks, which are coordinated by timestamp variables to ensure previous steps to be completed before entering a subsequent one. Figure 1 shows an overview of how the signal processing blocks are arranged and how they are diversified to avoid processing delays.

In the first block each incoming sample is processed with a quadratic spline wavelet transformation (WT) down to the 4th decomposition level. The second block uses a wavelet modulus maximum pair (MMP) to detect QRS-Complexes [6]. When a QRS was detected the delineation of the iso level is done. Therefore the first position within a window of 40-100 ms before the R trigger, where the 3rd and the 4th WT scale $X(3,n)$ and $X(4,n)$ fulfill (3) against a preliminary determined threshold θ_{iso} is considered as iso level fiducial point.

$$|X(3,n)| < \theta_{iso} \land (|X(3,n)| + |X(4,n)|) < 2 \cdot \theta_{iso} \quad (3)$$

For P and T wave delineation a similar MMP approach as described by Martinez et al. [7] and Rincon [8] is used. However, for a more persistent execution on the microprocessor several modification have been done: bitshift operations are used to substitute multiplications; repeated iterations through the same search window are avoided by saving relevant extrema for the next evaluation step. This reduces execution duration down to almost 50%. Also a second evaluation on the 5th scale if no fitting modulus maximum pair can be found is not implemented. This would not only increase the computational costs for the wave delineation, but also for the WT block, which is executed for every sample.

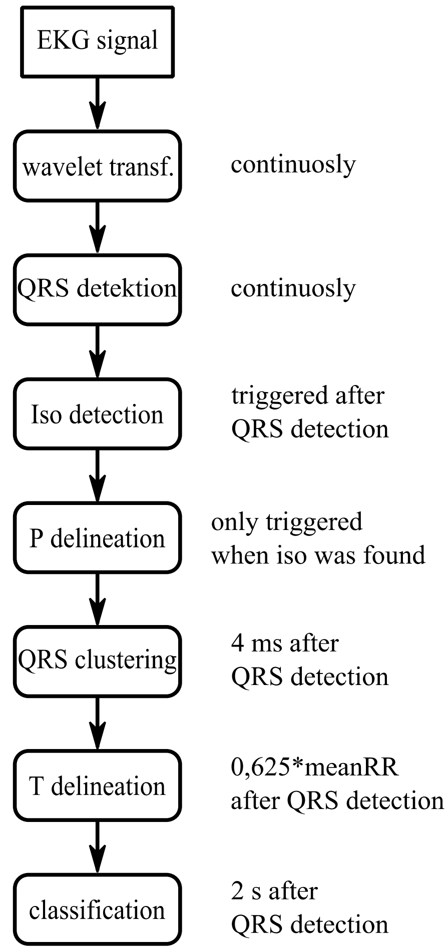

Figure 1. Signal processing blocks and their trigger delay

To inspect the QRS morphology a previously presented dynamic QRS morphology clustering step is used, which will serve as an additional feature to increase robustness against signal disturbances. Within this clustering step each beat receives a cluster identification number (ID) which relates its morphology to previously inspected beats of the current dataset. [9]

Finally the beat identification step is done based on the extracted P-wave, iso-level and T-wave fiducial points and the morphologic cluster ID the beat received. The beat to be analyzed is evaluated within the context of its neighboring beats. Therefore the three preceding beats and one succeeding beat are compared against the current beat in terms of their wave sequence similarities. Within a sinus rhythm all sequence features should resemble within minimal variations.

Using table 1 a beat alikeness index (BAI) is calculated for each of the available surrounding reference beats. Depending on that value the similarity between the current beat and the reference beats is classified as

Table 1. SR criterions and their value for the BAI.

Criterion	BAI-Value
Same cluster ID	+1
Iso-R distance ± 8 ms	+1
P-R distance ± 8 ms	+1
R-T distance ± 8 ms	+1

high (BAI≥3), medium (BAI≥2) or low (BAI<2).

The current beat is labeled as SR if at least two high similarity beats exist, or all surrounding beats are at least at medium similarity level.

However, since supraventricular beats may still fulfill these requirements also the inter beat regularity is evaluated. Therefore three rules proposed by Tsipouras et al. [10] are used to decide if the current inter beat interval RR_i is shortened, in which case the beat was not labeled as SR.

4. Results

4.1. Identification performance

Table 2 shows QRS detection and the sinus rhythm identification rates evaluated on MITDB, EDB and NSRDB. All datasets were evaluated without any exclusion and according to the AAMI protocol which ignores the first five minutes of each record to allow the algorithms to initialize and adapt to the signal.

Table 2. QRS detection and SR identification results on MITDB, EDB and NSRDB.

Database	MITDB	EDB	NSRDB
Number of beats	91 285	759 878	1 722 008
QRS detection			
Se in [%]	99.75	99.10	99.88
+P in [%]	99.92	99.54	99.46
SR identification			
Se in [%]	93.52	95.09	98.56
+P in [%]	90.24	99.86	99.65

4.2. Execution times and memory usage

In table 3 the execution times and specific memory usage are listed for each signal processing block. The final row shows the total estimated values. It is important to notice that the mean block duration actually do not just simply sum up for this row. Despite the WT block and the QRS-Detection block, which are continuously executed, the other algorithms are usually not processed at the same time. The mean value of the total execution time estimation is therefore slightly higher than the sum value

Table 3. Resource usage on the microprocessor (4 MHz / 256 kB ROM / 52 kB RAM)

Signal processing block	Execution times [ms] Mean	Max	Mean burden	Memory [byte] ROM	RAM
WT	0.24	0.24	0.24	916	2 544
QRS detect.	0.28	0.88	0.28	13 072	3 136
Iso detection	0.002	0.70	0.37	1 452	20
P delineation	0.006	2.23	1.47	2 332	16
T delineation	0.01	6.20	3.73		
clustering	0.02	7.60	5.20	5 460	740
classification	0.01	2.09	1.37	2 732	416
total	0.65	19.94	-	25 964	6 872

of all block mean values, because the total down time, where no signal processing block runs is lower.

The total maximum value, however, does sum up to describe the worst case scenario, assuming all the algorithms would be executed consecutively with their longest duration value.

Memory estimations are given for ROM and RAM. ROM memory includes code space and constant variables, RAM values consist of static and dynamic allocated variables. Since P and T delineation are sharing the same code, using different thresholds and timing variables, only one memory estimation is given for both signal processing blocks.

5. Discussion

The overall performance of the presented method shows very promising results.

However, the identification results on the MITDB are low compared to the other two databases. This shows some weaknesses of the proposed solution.

With each non SR beat within the 4 reference beats, the probability to fit the SR requirements for the current beat is reduced. The highest possible identification performance is therefore not only depending on the classification step, but is directly influenced by the QRS detection quality as well. Nevertheless, this relation is not only applying to false positive QRS detections but also to correctly detected abnormal beats. In the MITDB, where a lot of abnormal beats are present, this often leads to several FN identifications, especially if motion artefacts and muscle noise is corrupting the evaluated wavelet scales. Under these conditions it is more difficult to find high similarity BAI values and with at least one low similarity reference beat, the current beat under inspection will also not fulfill the SR requirements. The lower Se value for the MITDB is therefore reasonable.

However, the even worse +P value is caused by another effect. Dataset 102, 104, 107 and 217 of the MITDB are mainly consisting of fusion beats (F). These beats are mostly regular in terms of rhythm, wave sequence and beat morphology and are thus labeled as SR by the algorithm. These 4 records alone contribute more than 6000 FP detections, which corresponds with approximately 8% of the total number of found SR beats in the MITDB.

Considering the effect of these two observed problems under real application conditions, the outcome of the evaluations will not interfere with their intended results. If a patient, for example, suffers several arrhythmic events an estimation on HRV or a ST-T-segment evaluation may not be expedient in that particular situation. However, if the patient's ECG is continuously showing an unusual beat morphology, but with a repeating wave sequence within a regular rhythm, there is no mistake in considering this beat type to be the normal and sinus exited deflection of the heart's potential differences.

Only for an application which aims on precisely identifying SR beats between differing beat types, like the HRT, the proposed solution may have difficulties in case of other additional disturbances.

The hardware focused part of this study, however, shows the applicability under computational restrains. With a RAM memory usage of about 7 kB and a request for approximately 26 kB of nonvolatile memory the proposed algorithm is also portable to other platforms than the herein used Cortex-M3 microprocessor.

Within the presented study the overall mean values show, that the implemented algorithms are usually able to resolve all calculation in less than one millisecond. This leaves a down time of more than 3 ms to set the system to low power sleep mode, which has a significant impact on the device life time. Of cause this measure is only a rough estimation which will vary with the heart rate. As can be seen in the mean burden column, these processing steps are usually taking more than one millisecond. However, except for the morphology clustering they are typically resolved before the next sample is ready for processing (4 ms for a sampling rate of 250 Hz).

In the worst case scenario, where all signal processing blocks are executed with their maximum duration in a row, the computations are still manageable within 20 ms (5 samples). Even at a very high beat frequency of 150 beats per minute the interval between two consecutive beats has a duration of 400 ms, which allows these calculations to be done 20 times.

According to these results an input data buffer of at least 5 samples will ensure proper data evaluation without any difficulties.

6. Conclusion

Usually ECG analysis algorithms focus on the identification of diagnostically relevant pathologies. If a beat cannot be identified as such an abnormality it will typically be labeled as N. This may either happen due to the fact, that the algorithm noes not know this pathology, or just by misclassification. In any case the correct label for such a beat would simply be *not sufficiently abnormal*. However, for applications which analyze the changes of the hearts physiological conduction properties non SR beats may change their outcome significantly.

The results of this study show that the proposed approach is quite promising to actively confirm SR, especially considering the fact that it can be integrated in devices with high resource constrains. Additionally to applications where a SR is necessary to obtain meaningful results, it may also be used to shut down other more energy draining processes if sinus rhythm is present to increase the battery lifetime of mobile devices.

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