Wavelet Transform Based Detection of the First-Degree Atrioventricular Block

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Abstract

Introduction: First-degree atrioventricular block (AVB I) is a pathology defined on ECG by a PR interval greater than 200 msec. This paper aims to automatically detect AVB I by measuring the length of the PR interval.

Method: Our method consists of the following steps: a) Records with atrial fibrillation or atrial flutter were excluded. b) QRS complexes were detected. c) QRS onset and T offset was detected for each ECG cycle. The median distance between QRS onset and the end of the previous T-wave is calculated (marked as X). d) QRSs were aligned and clustered according to morphological similarity. QRSs of the most frequent morphology were averaged. e) QRS onset and offset were detected for the averaged QRS. The signal between QRS onset and offset was replaced by a line intersected by the QRS onset and offset points. This signal was transformed by a wavelet transform. f) The P wave was detected in the transformed signal. The P onset was detected in the section from QRS onset minus X to the P wave position. g) AVB I was detected when the PR interval was longer than 200 msec.

Results: The algorithm was set up and validated on private data and tested on publicly available databases. The algorithm achieves sensitivity 0.81, 0.81, 0.82, 0.84 and specificity 0.91, 0.90, 0.86, 0.93 for CPSC, CPSC-Extra, PTB-XL and Georgia database, respectively.

1. Introduction

This paper describes a fully automated algorithm for detecting the first-degree atrioventricular block (AVB I). AVB I is a pathology manifesting with prolongation of the duration of impulse transfer from the atria to the ventricles through the AV node. On ECG, this pathology can be recognized by the PR interval longer than 200 msec.

The AVB I is associated with an increased risk of heart failure, atrial fibrillation, and mortality. There is also an increased probability that a higher degree of AV block will develop. [1]

The PR interval is measured from the beginning of the P wave to the beginning of the QRS. The physiological transfer of the impulse through the AV node is shown in Figure 1, A (PR 156 msec). The P wave can also be hidden inside the T wave, but in some cases, it remains detectable, as shown in Figure 1, B (PR 172 msec). A typical AVB I is shown in Figure 1, C (PR 403 msec).

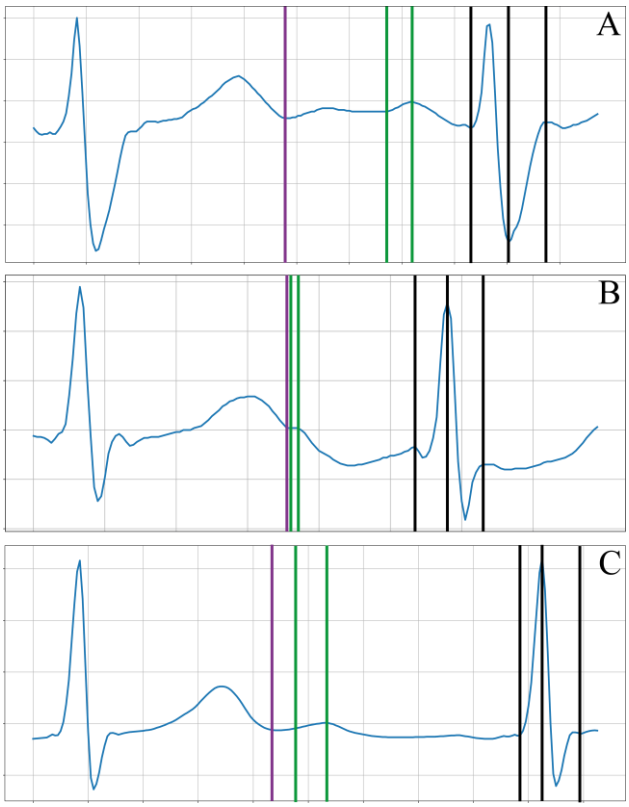

Figure 1. Example of points detected by our algorithm: T wave offset – magenta line; P wave onset and peak – green lines; QRS onset, peak and offset – black lines. The distance between two lines in the grid is 100 ms.

2. Data

In this study, we used five independent datasets. The designed algorithm was set up and validated on private data (MDT, s. r. o., Brno, Czech Republic). This dataset contains 1508 single-lead Holter ECG recordings. ECG recordings were sampled at 200 Hz.

The algorithm was tested on publicly available databases: China Physiological Signal Challenge 2018 database (CPSC) [2], Southeast University in China database – data unused in Physiological Signal Challenge 2018 (CPSC-Extra), PTB-XL database [3, 4, 5], and Georgia 12-lead ECG Challenge databases (G12EC) [6].

Table 1. A number of recordings in used databases and a number of AVB I in each database.

Database	Total number of recordings	Number of AVB I recordings
CPSC	6,877	722
CPSC-Extra	3,453	106
PTB-XL	21,837	1,137*
G12EC	10,344	769
MDT	1,508	758

*Signals from the "prolonged PR interval" group were also included among AVB I in the PTB-XL database. There is probably no difference between these groups.

3. Methods

The block diagram of the designed algorithm is shown in Figure 2. Each step of the algorithm is described in a separate subchapter.

3.1. Preprocessing

Records with atrial fibrillation or atrial flutter were excluded from the evaluation because there is no P wave.

For remaining signals, baseline wandering was suppressed by subtracting the median value in a 1,300 msec floating window.

3.2. QRS detection

The QRS complex detector is based on the analysis of signal amplitude envelopes calculated using the Hilbert transform. Potential positions of QRS complexes are obtained by thresholding these envelopes. The validation of each QRS position is done by analyzing the statistical parameters of the signal close to the potential QRS position.

If multiple leads are available, then the above procedure is performed for each lead separately. Subsequently, a zero signal is generated for each lead, where a 100 msec Hann window is inserted in the place of the positions of the QRS complexes. Subsequently, these signals from the individual leads are summed. The resulting positions are located at positions of local maxima greater than half the global maximum.

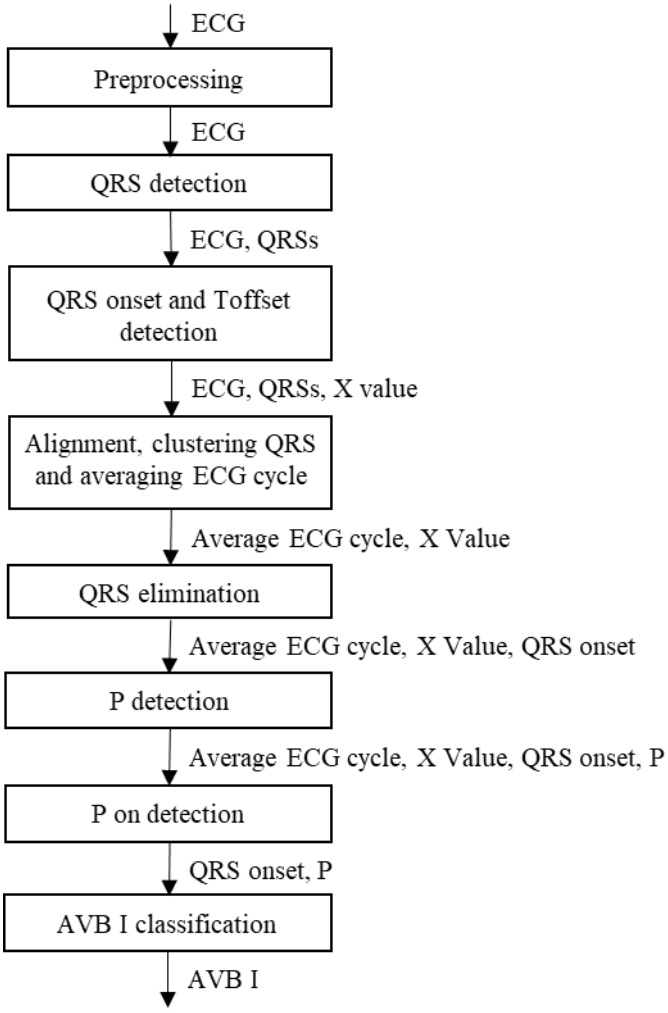

Figure 2. Block diagram of the designed algorithm.

3.3. Determination of the distance between T wave offset and QRS onset

QRS onset and T wave offset were detected for each ECG cycle. QRS onset was detected in the transformed ECG. A wavelet transform with a bior1.5 waveform and a scale of 0.03 × sampling frequency (fs) was used. First, zero-crossings were found in the transformed signal. The initial position of the beginning of the QRS was determined at the zero-crossing as close as possible to the QRS complex that met at least one of the following conditions: a) the maximum absolute value of the transformed signal between the current and previous zero crossings is less than 0.1 × standard deviation (STD) of the transformed signal, b) the distance of the current zero-crossing from the center of the QRS is greater than median

RR interval divided by 11, c) the ratio of the maximum absolute value between the current and previous zero-crossing and the distance between the previous and current zero-crossing is less than 0.12 × STD of the transformed signal.

The final position of the QRS onset was determined as close as possible after the selected zero-crossing, where the transformed signal exceeds 0.07 of its STD.

The T wave was detected in the signal section from 20 msec after the end of the previous QRS to 200 msec before the next QRS. A wavelet transform with a bior1.5 waveform, and a scale of 0.082 × fs was used. The zero crossings of the transformed signal are detected again. Each zero crossing is assigned a score indicating the probability it is a T-wave. This score is calculated as the product of the maximum deviation of the transformed signal 30 msec before the potential T-wave and 30 msec after the potential T-wave. The more negative this score is, the greater the probability that it is a T-wave. The resulting position T is finally selected at the location closest to the previous QRS, where the zero-crossing score is at least 90 % of the maximum calculated score.

The T-wave position offset is determined at the first point after the T-wave peak, where a sign of the first difference of ECG changes.

Finally, we calculate the median value of the distance between the QRS onset and the preceding end of the T wave. This value is called the X value.

3.4. Alignment and clustering QRS and averaging ECG cycle

The cross-correlation between the individual QRS complexes is calculated. We use sections starting 100 msec before the center of the QRS and ending 100 msec after the center of the QRS for the computation. The QRS complexes are divided into clusters according to morphology. The PQRST segments containing the QRS of the most frequent morphology are finally averaged. Further processing is done in this averaged PQRST segment.

3.5. QRS elimination

Before detecting the P-wave, it is first necessary to remove the QRS, which affects the signal transformed by the wavelet transform in a wide area around the QRS. Correct detection of the beginning and end of QRS is crucial to remove the QRS.

The QRS onset was detected in the same manner as for each QRS (see section 3.2).

The end of QRS was also detected in the ECG transformed by wavelet transform with bior1.5 and scale 0.03 × fs. First, zero crossings were found in the transformed signal. The preliminary position of the QRS offset was determined at the zero-crossing point that met at least one of conditions a) or b) and at least one of conditions c), d) or e): a) the maximum absolute value of the transformed signal between the previous and currently analyzed zero-crossing is less than 0.3 × STD of the transformed signal, b) the zero crossing distance from the QRS peak is greater than 150 msec, c) the maximum absolute value of the transformed signal between the currently analyzed and the next zero-crossing is less than the maximum absolute value of the transformed signal between the currently analyzed and the previous zero-crossing, d) the maximum absolute value after the analyzed zero-crossing is less than 1.1 × STD of the transformed signal, e) the distance of the next zero-crossing from the QRS peak is more than 150 msec. If no zero-crossing met the above conditions, the last zero-crossing was marked as the preliminary QRS offset position.

The final position of the QRS offset was determined as close as possible before to the selected zero-crossing at the point where the transformed signal was greater than 0.3 × STD of the transformed signal.

The QRS complex is removed by inserting a line between the QRS onset and QRS offset points.

3.6. P wave detection

The P wave is searched in the ECG transformed by the wavelet transform using the bior1.5 wavelet and a scale of 0.082 × fs. The P wave is searched for in the averaged ECG cycle from QRS onset minus X value (see chapter 3.2) to QRS onset minus 50 msec. First, zero-crossings were found in this section in the transformed signal. We calculated the median absolute value for each zero-crossing in the centered 80 msec window. The resulting position of the P wave was determined at zero-crossing, where the median absolute value was maximal.

3.7. P onset detection

Before searching for the beginning of the P wave, the ECG signal is smoothed by a median filter with a window size of 10 msec (minimum three signal samples). The beginning of the P wave is determined at the point as close as possible before the P peak, where the sign of the first difference of ECG changes or the absolute value of the first difference did not increase for 25 msec. At the same time, the beginning of P cannot be found before the end of the previous T wave.

3.8. AVB I classification

The AVB I was detected when the PR interval was longer than 200 msec. This threshold is based on the medical definition.

4. Results

Table 1. Sensitivity and specificity of AVB I detection.

Database	Sensitivity	Specificity
CPSC	0.81	0.91
CPSC-Extra	0.81	0.90
PTB-XL	0.82	0.86
G12EC	0.84	0.93
MDT	0.86	0.65

5. Discussion

The sensitivity and specificity of our algorithm are shown in Table 1. The sensitivity is consistent across all databases. In the MDT database, the detection specificity is significantly lower than in other databases, although the algorithm was prepared using this database. Lower specificity may be caused by the fact that the wearable device records the data in usual daily activities, resulting in a higher amount of noise. The P-wave detection in the noisy data is complicated due to its usually low amplitude.

6. Conclusion

In this work, the AVB I detector was designed and validated. Detection is based on PR interval measurement. First, an area is found in which the P-wave is then searched. This area is located between the detected positions of the end of the T wave and the beginning of the QRS. The P wave is then detected using a wavelet transform. Due to the low amplitude of the P wave, the detection is difficult in signals with a low signal-to-noise ratio. Noise suppression is realized by averaging QRS complexes.

The detector achieves consistent sensitivity across all databases but lower specificity in the dataset recorded during usual daily activities.

The shortcomings of the designed algorithm are as follows. The detector finds the P wave even in signals where the P wave is not visible (for example, a junctional rhythm). Only one P wave is always found in signals where there are multiple P waves between two consecutive QRSs. These shortcomings should be eliminated in further work.

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