A WAVELET-BASED T WAVE END DETECTION: PROTOTYPE WAVELETS COMPARISON

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ABSTRACT

In this paper, we present a simple T wave end detection algorithm based on a continuous wavelet transform. We used this algorithm to test, which prototype wavelets are optimal for the T wave end detection. Several prototype wavelets were tested on four different T wave morphologies in a chosen wavelet transform scale range. The result of this study is, that efficient prototype wavelets are *bior1.1*, *bior1.3*, *bior1.5* and *gaus1*. Another conclusion is, that biorthogonal wavelets are less sensitive to a scale selection, so an algorithm based on a biorthogonal wavelet is more robust, than an algorithm based on a Gaussian derivative wavelet.

1. INTRODUCTION

The accurate detection of individual electrocardiogram (ECG) significant points is very important to a cardiac disease diagnosis. Manually annotate long ECG recordings is very time consuming, so methods for an automatic ECG delineation are needed. A lot of modern approaches are based on a dyadic (DWT), or a continuous wavelet transform (CWT).

The most problematic part of ECG delineation is an accurate detection of the T wave end position. In this paper, we used the T wave end detection algorithm based on a CWT approach to test, which prototype wavelets are most efficient for the T wave end detection.

2. MATERIALS AND METHODS

2.1. USED WAVELET TRANSFORM APPROACH

The proposed algorithm is based on a CWT approach. The wavelet transform (WT) at different scales describes the time characteristic of a signal in different frequency bands. While the DWT is restricted to scales, that are powers of two (used in [1], [2]), the CWT can be evaluated in any real positive scale (used in [3]).

Authors in [1], [2] also used a multi-scale WT approach, based on finding similarities across several DWT scales. In this study and also in [3], we used a single-scale CWT approach. This approach is very fast and simple and provides results comparable with a DWT multi-scale approach.

The CWT of a time-continuous signal $x(t)$ is defined by the integral

$$CWT\left(b,a\right)=\frac{1}{\sqrt{a}}\int_{-\infty}^{\infty}x(t)\psi^{*}\left(\frac{t-b}{a}\right)dt\,, \tag{1}$$

where $\psi(t)$ is the wavelet function (prototype wavelet), a is the scale parameter and b is the translation parameter.

In [3], we used for the wavelet-based ECG delineation the biorthogonal wavelet *bior1.5*, while the authors in [4] used the derivative of a Gaussian smoothing function *gaus1*, as the prototype wavelet, Figure 1. In this study, we tested several prototype wavelets from Biorthogonal, Gaussian, Daubechies and Symlets wavelet families.

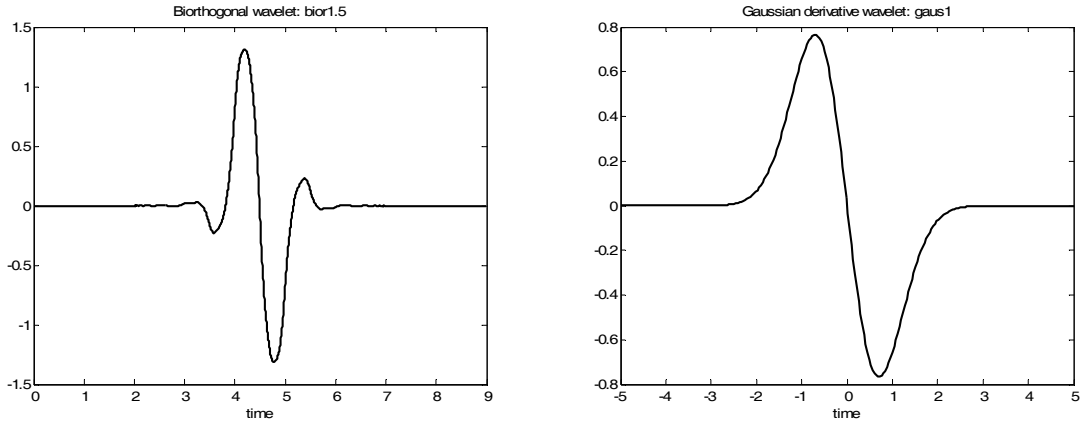

Figure 1: Prototype wavelets *bior1.5* (left) and *gaus1* (right).

2.2. DETECTION OF T WAVE AND T WAVE END

The T wave has several possible morphologies: positive (+), negative (-), biphasic (+/- and -/+), only upwards or only downwards. The proposed algorithm is capable of detect any of mentioned morphologies.

Regarding tested prototype wavelets, zero-crossings of the CWT correspond to the local maxima of the signal modulus and the local maxima of the CWT modulus correspond to maximum slopes in the signal (Figure 2).

In the first step, the algorithm searches in a selected scale and area for the pair of modulus maxima exceeding the threshold ξ_T. The T wave is found as a zero-crossing between the pair maximum-minimum, or minimum-maximum (Figure 2). In the next step, the delineator is testing, whether the modulus maximum between two adjacent zero-crossings is larger than the threshold ξ_T. If it is larger, than the algorithm is testing the modulus maximum between another two adjacent zero-crossings. Once the modulus maximum is smaller than the threshold ξ_T, the T wave end is found between the previously tested pair of zero-crossings. The T wave end is determined as the last sample larger (in absolute value) than the threshold ξ_T (Figure 2). The threshold ξ_T is defined by the equation

$$\xi_T = 0.66\ RMS(W_k, x[n])\,, \tag{2}$$

where *RMS* stands for Root Mean Square, W_k is the k-th scale of the CWT and $x[n]$ is the selected T wave area.

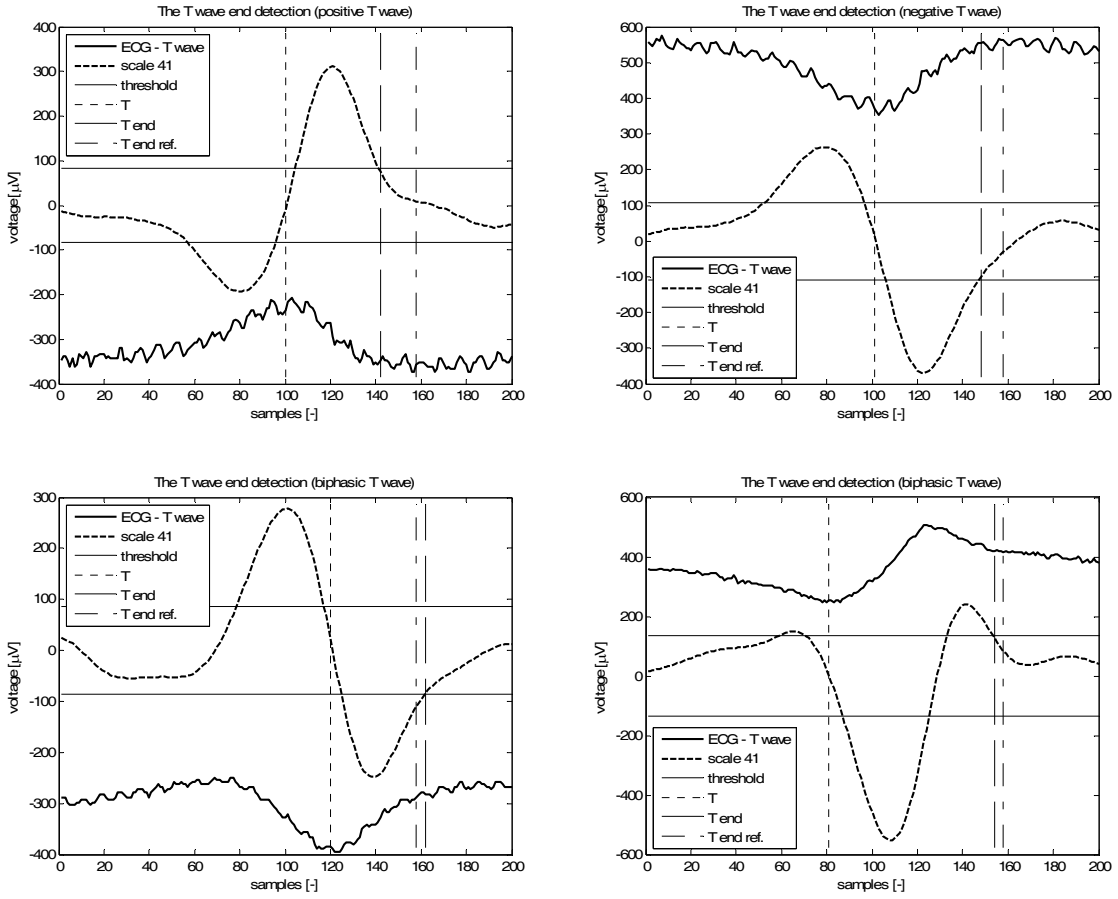

Figure 2: T wave end detection approach (positive, negative and biphasic T wave).

3. RESULTS

We tested the designed T wave end detector on four different T wave morphologies: positive (+), negative(-) and two biphasic (+/- and -/+). The detector was tested in a scale range between scales 16 (2^4) and 64 (2^6), with the step 2 (25 tested scales) for several different prototype wavelets. The difference between referential and detected T wave end position was calculated for each combination of a scale, T wave and prototype wavelet. These differences are shown in Figure 3.

T wave/wavelet	*bior1.1*	*bior1.3*	*bior1.5*	*gaus1*
positive (+)	-27.3 ms	-31.5 ms	-32.0 ms	-15.0 ms
negative (-)	-15.5 ms	-19.4 ms	-20.1 ms	-7.0 ms
biphasic (+/-)	16.0 ms	9.8 ms	8.0 ms	29.8 ms
biphasic (-/+)	-5.9 ms	-6.8 ms	-6.9 ms	7.0 ms
global pos. diff.	**-5.9 ms**	**-6.8 ms**	**-6.9 ms**	**7.0 ms**

Table 1: Mean differences between referential global position and positions detected by the algorithm, calculated from 25 values (one for each scale). Last row values are differences between global referential position and global positions detected by the algorithm.

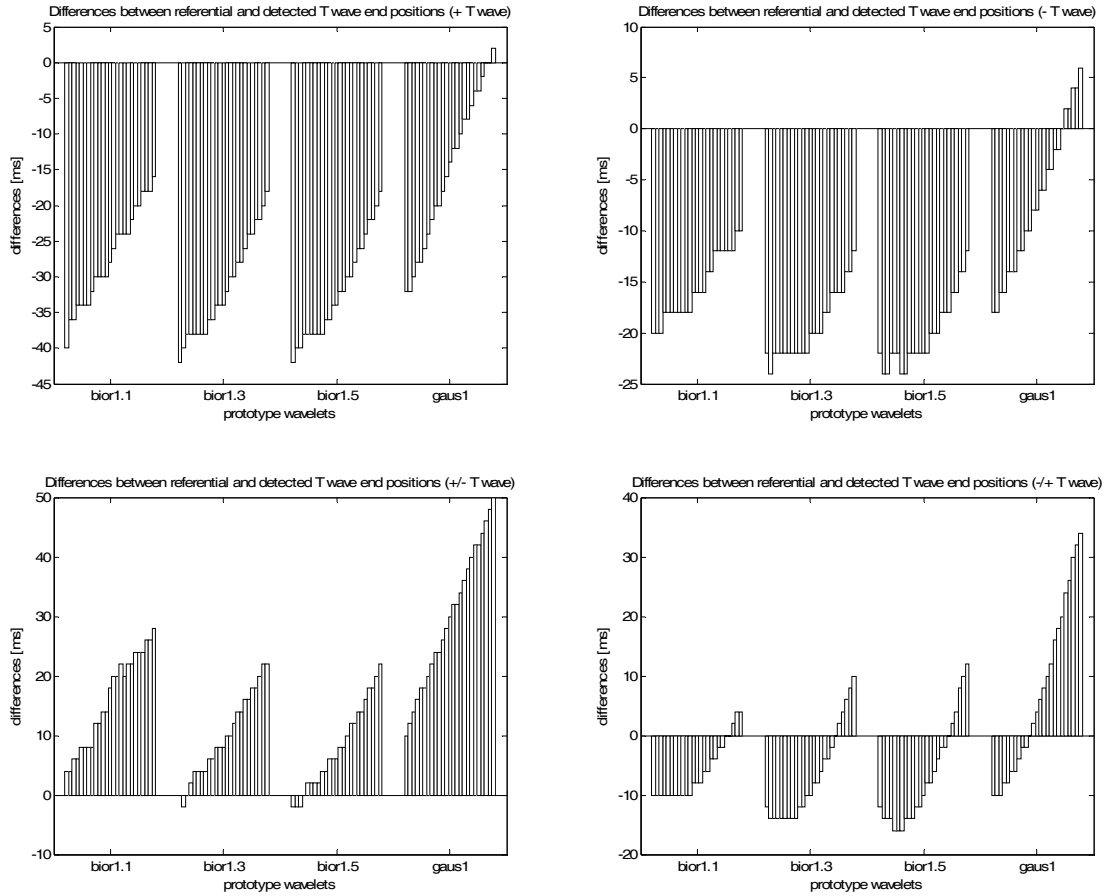

Figure 3: Differences between referential and detected T wave end positions.

We calculated mean differences for each combination of a prototype wavelet and T wave, from differences across the scale range, Table 1. Global position differences in a last row of Table 1 were obtain from Table 1 values by selecting the third highest value in each column. Global position is a common position for all four tested T wave morphologies.

We also calculated standard deviations for each combination of a prototype wavelet and T wave, from differences across the scale range, Table 2. Mean standard deviations in a last row of Table 2 were calculated as a mean of each column values.

T wave/wavelet	*bior1.1*	*bior1.3*	*bior1.5*	*gaus1*
positive (+)	6.7 ms	6.8 ms	6.9 ms	10.6 ms
negative (-)	3.2 ms	3.2 ms	3.4 ms	7.2 ms
biphasic (+/-)	7.7 ms	7.0 ms	7.1 ms	11.7 ms
biphasic (-/+)	4.7 ms	7.7 ms	8.5 ms	14.1 ms
mean stan. dev.	**5.6 ms**	**6.2 ms**	**6.5 ms**	**10.9 ms**

Table 2: Standard deviations of differences between the referential global position and positions detected by the algorithm, calculated from 25 values (one for each scale). Last row values are mean standard deviations calculated as a mean of each column values.

4. DISCUSSION

Global positions difference values (Table 1), calculated for each tested prototype wavelet, are between 5 and 7 *ms* (in absolute value) for prototype wavelets *bior1.1*, *bior1.3*, *bior1.5* and *gaus1*. These values are comparable and algorithms based on these prototype wavelets are very accurate in the T wave end detection.

The mean standard deviation value calculated for the prototype wavelet *gaus1* is almost twice higher, than mean standard deviation values calculated for biorthogonal wavelets. The conclusion is, that biorthogonal wavelets are less sensitive to a scale selection, than the wavelet *gaus1*. The difference between the referential position and a position detected by the algorithm will change much more in the case of the wavelet *gaus1*, than biorthogonal wavelets, if we change the used scale (shown in Figure 3).

5. CONCLUSION

In this paper, we used several prototype wavelets to test, which prototype wavelet is optimal for the T wave end detection in ECG signals. Among of all tested prototype wavelets, only four wavelets are applicable, wavelets *bior1.1*, *bior1.3*, *bior1.5* and *gaus1*. All other tested prototype wavelets had a much higher mean standard deviation value, than mentioned four wavelets. We also proved in this study, that wavelets from biorthogonal wavelet family are less sensitive to the scale selection, than Gaussian derivative wavelet *gaus1*. The conclusion is, that the algorithm based on a biorthogonal wavelet is more robust, than the algorithm based on a Gaussian derivative wavelet.

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