A Multilead Wavelet-based ECG Delineator based on the RMS Signal

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Abstract

In this work a multilead (ML) algorithm for ECG delineation was validated against the CSE and the PTB databases (DB). This algorithm is based on a previously validated single-lead (SL) algorithm, which is also used as reference in this work. For both DB a set of manual reference annotations made by experts is available. The algorithm performance was assessed by the measurement of QRS onset (QRS_{on}) and T wave offset (T_{off}) in both DB. The differences (mean±sd in ms) between automatic and experts annotations for CSEDB was for QRS_{on} 6.7 ± 7.2 and for T_{off} 0.1 ± 10.2. For the PTBDB, results were for QRS_{on} -5.7 ± 6.9 and for T_{off} 11.3 ± 24.4. Also standard deviation of QT interval in 10 consecutive beats was calculated as a measurement of stability in the PTBDB, resulting in 6.7 ± 14.3. In conclusion this ML approach is more recommendable than SL in applications where measurement stability is mandatory and when absolute value of QT is required as a lead-independent measure.

1. Introduction

Delineation of the ECG characteristic waves (e.g. determining their onsets and ends) supplies fundamental features for cardiac diagnosis and monitoring (e.g. the QT interval, as an indicator of propensity to arrhythmia). Long ECG recordings and subsequent automatic analysis make mandatory the development of well validated automatic delineators. Several delineation methods working on a single-lead (SL) can be found in the literature [1]. Comparison with annotations made by expert cardiologists is usually performed for validation purposes. However, the determination of some characteristic points, as the end of the T wave (T_{off}) is a difficult task, even for expert cardiologists. When applied to a multilead (ML) signal, SL delineators provide a set of characteristic points for each available lead. However, since the intervals determined by the ECG characteristic points are manifestations of physiologic intervals of the cardiac cycle, it is reasonable to have a unique delineation which takes into account all the information available in the different leads (ML delineation). We developed and evaluated a ML approach founded on the previously validated SL ECG delineator based on the wavelet transform (WT) [1]. Moreover, we hypothesize that ML delineation should supply more robust and stable annotations.

2. Methods

2.1. Algorithm description

Our approach to ML delineation starts in creating a new signal from the combination of a set of ECG leads ($x_i[n]$) in an RMS sense.

$$x[n] = \sqrt{\frac{1}{M}\sum_{i=1}^{M} x_i^2[n]} \qquad (1)$$

Being M the size of the set. This set could be either the standard 12 ECG leads (12L) or the Frank orthogonal leads (3L), with the requirement that baseline wandering (BW) must be previously removed in every individual lead $x_i[n]$. This can be achieved by fitting an estimate of the BW with cubic splines, and subtract it from the original signal (Ch. 7.1.3 in [2]). The proposed ML algorithm is founded on a previously validated SL delineator based on the wavelet transform (WT), which is defined for a signal $x[n]$ as

$$W_a x(b) = \frac{1}{\sqrt{a}} \int_{-\infty}^{+\infty} x(t)\psi\left(\frac{t-b}{a}\right) dt, a > 0 \qquad (2)$$

We use a typical discrete dyadic scheme where the scale factor is $a = 2^k$ for $k \in Z^+$, with the same sampling rate at each scale (Algorithme à trous). As a result of this transformation, the original signal can be analyzed at different scales (frequency bands) and (time) translations. The SL algorithm uses this feature of wavelets transform to analyze each ECG wave or complex at the most appropriate scale/s. So $x[n]$ is then delineated with an SL algorithm with some specific modifications to take into account new morphologies present in $x[n]$. Those new morphologies

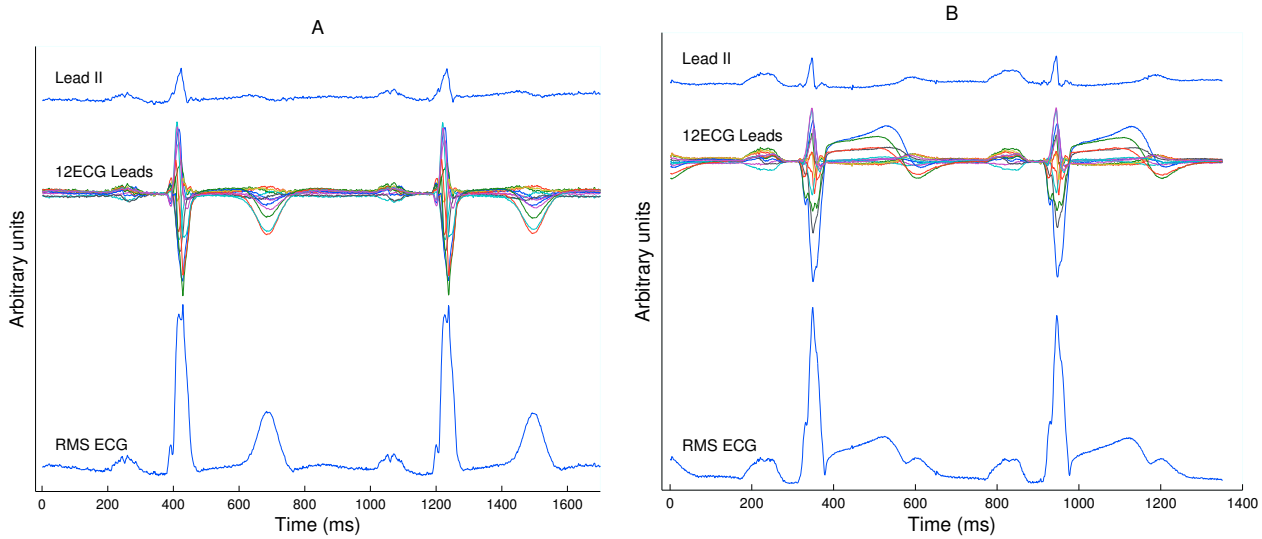

Figure 1. Both panels show the derivation of RMS signal from the 12 standard ECG leads. Lead II is shown in both panels as an example of poor projection of the T wave to this lead. As can be seen in the RMS ECG signal, new morphologies come up from the QRS complex and T wave morphology heterogeneity found throughout the set of leads.

come up as a result of calculating the RMS of different wave morphologies in a set of leads (Fig. 1), or in an undesirable case when the BW removal process is deficient causing distortion in $x[n]$ (Fig. 2).

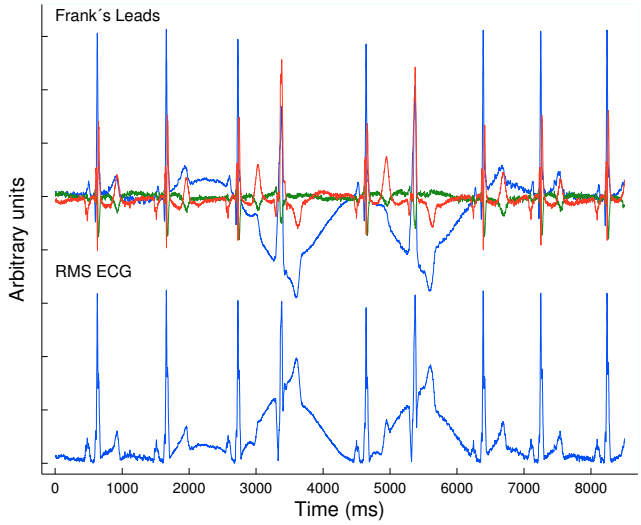

Figure 2. Example of how poor baseline wander removal affects RMS ECG signal.

As $x[n]$ is entirely positive, most of the morphologies found are monophasic, or notched monophasic. Thus, the delineation rules used in this algorithm are somewhat reduced from the SL approach due to the reduced set of morphologies present. Basically we extend the concept from [1] looking for the sample of maximum moduli (n_U) before the QRS complex apex (n_{QRS}) at $W_{2^2}x[n]$. Then the QRS onset (QRS_{on}) is considered to be at the first value of $|W_{2^2}x[n]|$ below the threshold $\xi_{QRS_{on}}$, or at the first local minimum, whichever event occurs first. The value of $\xi_{QRS_{on}}$ is relative to $|W_{2^2}x[n_U]|$ previously detected. An adaptation to the RMS signal in terms of QRS_{on} detection is the ability to jump notches at the upward slope of the QRS complex, refining the value of n_U to the previous maximum moduli before n_U. The notch detection is implemented by looking for a local maximum within a search window and above a threshold relative to $|W_{2^2}x[n_U]|$. The same approach used for QRS_{on} can be adapted to T wave offset (T_{off}) detection, but at $W_{2^4}x[n]$ signal, considering that notches occur at the downward slope in this case, being n_D the sample of minimum moduli at $W_{2^4}x[n]$. Finally, T_{off} is determined either by the sample below the threshold $\xi_{T_{end}}$ relative to $|W_{2^4}x[n_D]|$, or the first local maximum, the first of the two events to occur. The notch detection was performed in a similar manner as described for QRS_{on}. If there is a local maximum of the same sign, and above the threshold $\xi_{Toff_{notch}}$ relative to $|W_{2^4}x[n_D]|$ then n_D is updated to the sample where this local maximum occurred, and this way the notch is *jumped*.

2.2. Algorithm validation

The Common Standards for Electrocardiography [3] (CSEDB) and PTB databases [4] (PTBDB) were used to evaluate the algorithm's performance as compared with SL delineation. Records in both databases include the 12 standard as well as Frank orthogonal leads. The main features of both databases are summarized in Table 1.

In both CSEDB and PTBDB, we evaluated the differences between automatic annotations and those of the "me-

Table 1. Main features of the validation DBs.

DB	Records	Leads	f_S (Hz)	V. res. (μV)	Length (s)
CSE	125	12+3	500	1	10
PTB	549	12+3	1000	0.5	32–120

dian cardiologist" ($mean \pm sd$). Despite that the CSEDB has a total of 125 recordings, only 31 QRS_{on} and 25 T_{off} annotations are available. In PTBDB, since no reference annotations were available at the moment of abstract submission, we computed the QT interval standard deviation in 10 consecutive beats (after excluding ectopic beats) as a measure of the QT interval stability (s_{QT10}). Those beats where the RR beat-to-beat difference is greater than 100 ms in absolute value are assumed as ectopic beats. We used as gold standard for PTBDB a set of reference measurements published by Christov et al [5]. They were the median of measurements made by 5 experts who annotated QRS_{on} and T_{off} in 548 recordings of the PTBDB. The annotations were made in lead II (SL approach), according to the rules suggested in Physionet Challenge 2006 [6]. This set of measurements is fully accessible on Internet to be downloaded.

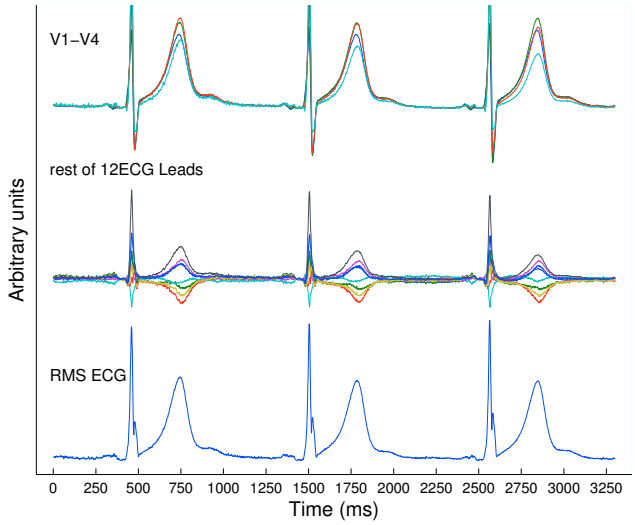

Figure 3. Smooth T wave prolongation observed particularly in V1-V4 leads, present in many recordings of PTBDB.

3. Results

3.1. CSEDB results

For the ML algorithm using 12 standard ECG leads differences between expert's annotations were (mean $\pm$ sd in ms) for QRS_{on} 6.7 ± 7.2 and for T_{off} -3.84 ± 17.3. For Frank's leads 6.3 ± 7.5 and 0.3 ± 15.8 respectively (table 2). For the SL delineator in lead II (typically used for SL QT measurements) differences were for QRS_{on} 11.2 ± 13.8 and for T_{off} 4.5 ± 47.5.

3.2. PTBDB results

For the ML algorithm using 12 standard ECG leads differences were (mean $\pm$ sd in ms) for QRS_{on} -5.7 ± 6.9 and for T_{off} 12.8 ± 26.4. For Frank's leads -5.3 ± 9.1 and 12.6 ± 28.9 respectively (table 2). For the SL delineator in lead II were for QRS_{on} -10.3 ± 34 and for T_{off} -5.6 ± 55.7. The results regarding QT measurement stability were 6.7 ± 14.3 for 12 standard leads and 8 ± 16.6 for Frank leads. While for the SL delineator on lead II we obtained 20.1 ± 20.3. Those values are shown more in detail in table 2.

3.3. QT interval measurement challenge

This algorithm participated in the PhysioNet/Computers in Cardiology Challenge 2006 [6] in category 2, obtaining a score of 27.18.

4. Discussion and conclusions

Results in CSEDB show that ML algorithm is more accurate and as stable as SL applied to any available individual lead (table 2). This happens mainly because CSEDB was annotated using a ML criteria, and because the SL approach exhibits high dependence on the cardiac activity projection. Taking into account that electrical projection can be disturbed, between many causes, by respiration, inhomogeneities of the thorax and even lead placement (see Ch. 18 in [7]) the global effect is the addition of spurious measurement variability, making lead selection a very important issue.

For the PTBDB Christov et al. used an SL reference annotation approach (lead II) according to the Physionet Challenge 2006 [6], but also reported that in more than 15% of the recordings T wave was not recognized in lead II by expert annotators due to poor projection (Fig. 1), adopting for those situations an ad-hoc ML annotation approach looking for the lead with the best projection of T wave [5]. For QRS_{on}, the ML delineator performed little better or as good as the better SL within 12L and Frank's leads (12L vs V5 and 3L vs Vx in table 2). The same occurred with T_{off}, as can be seen by comparing 12L vs V3 and 3L vs Vy. It is possible that a ML reference annotation approach would improve the results of the ML approach, in detriment of the SL results. Looking at the bias, it can be observed that ML automatic annotations tend to anticipate QRS_{on} (negative bias) and to post-detect T_{off} (positive bias) with respect to the reference annotations, as it can be expected. Also in PTBDB, the s_{QT10} parameter is in the same order as the most stable leads for SL delineation (12L vs V2-V4).

Table 2. Differences between expert annotations and automatic delineations in CSE and PTB DB. Results of QT measurement stability in 10 consecutive beats (s_{QT10}) are shown in the rightmost column. All values are expressed as (# of annotated recordings) mean±sd in ms.

		CSE		PTB		
	Lead/s	QRS_{on}	T_{off}	QRS_{on}	T_{off}	s_{QT10}
Singlelead	I	(31) 9.9±12.1	(25) 3.5±47.5	(536) 1.4±11.0	(536) 7.3±33.5	(464) 18.8±22.3
	II	(31) 11.2±13.8	(25) 4.5±47.5	(536) -1.6±11.7	(536) 6.6±34.8	(454) 20.1±20.3
	III	(31) 9.0±15.2	(25) 3.8±48.8	(536) -3.2±14.6	(536) 2.8±33.7	(458) 19.0±19.6
	aVr	(31) 11.1±12.5	(25) -4.0±24.3	(536) 1.7±14.3	(536) 4.8±33.8	(473) 21.7±23.1
	aVl	(31) 12.4±15.5	(25) 2.6±40.8	(536) -2.4±13.8	(536) 2.4±34.8	(470) 18.7±21.1
	aVf	(31) 7.6±17.7	(25) 3.4±55.6	(536) -1.9±13.8	(536) 2.6±34.3	(455) 18.8±20.2
	V1	(31) 8.6±15.3	(25) -25.3±24.9	(536) -4.6±14.0	(536) -6.1±38.7	(476) 13.3±18.3
	V2	(31) 11.7±10.6	(25) -2.2±43.5	(536) -3.4±13.1	(536) -4.5±30.6	(459) 6.9±13.1
	V3	(31) 11.7±9.2	(25) -12.2±23.7	(536) -2.1±12.6	(536) 0.6±26.5	(458) 6.8±12.3
	V4	(31) 12.6±10.4	(25) -5.6±20.6	(536) 0.0±11.7	(536) 3.9±30.1	(459) 8.6±14.1
	V5	(31) 13.2±10.9	(25) 1.4±36.5	(535) 1.9±10.2	(535) 1.6±31.9	(474) 13.4±17.7
	V6	(31) 11.9±10.2	(25) -3.4±34.6	(535) 0.2±11.0	(535) 1.0±32.4	(478) 15.3±18.8
	Vx	(31) 10.9±10.3	(25) -9.3±21.2	(536) 1.3±11.4	(536) 2.6±34.2	(482) 12.9±18.4
	Vy	(31) 12.5±15.0	(25) 3.1±43.8	(536) -2.6±13.2	(536) 1.4±30.2	(461) 16.5±18.9
	Vz	(31) 10.9±12.6	(25) -14.5±28.0	(535) -4.0±11.6	(535) -1.1±31.8	(483) 10.8±14.8
ML	3L	(31) 6.3±7.5	(25) 0.3±15.8	(536) -5.3±9.1	(536) 12.6±28.9	(488) 8±16.6
	12L	(31) 6.7±7.2	(25) -3.84±17.3	(536) -5.7±6.9	(536) 12.8±26.4	(490) 6.7±14.3

As a final observation, many recordings in PTBDB exhibit an smooth prolongation of the T wave, particularly notorious in the precordial leads V1-V4 (Fig. 3). In such cases, despite of the feasibility of measuring this smooth ending with ML algorithm, a more conservative criterion was followed (also according with expert's annotations) because of the present controversy about U wave as a separate wave or a prolongation of the T wave (Ch. 31 of [8] and [9]).

As a limitation, this algorithm presents high dependence on baseline wander removal. In those leads where problems like low SNR or a rapidly changing BW cause an erroneous estimation of the PQ segment baseline, distorted ECG waves arise when the RMS signal is computed (Fig. 2). This limitation will be improved in future works with more sophisticated methods of baseline removal.

In conclusion this ML strategy is more recommendable than SL delineation in applications where measurement stability is mandatory, as, for example, to quantify physiological QT variability, and when absolute value of QT is required as a lead-independent measure.

References

[1] Martínez J, Almeida R, Olmos S, Rocha A, Laguna P. A wavelet-based ecg delineator: Evaluation on standard databases. IEEE Transactions on Biomedical Engineering 2004;51:570–581.

[2] Sörnmo L, Laguna P. Bioelectrical Signal Processing in Cardiac and Neurological Applications. Elsevier, 2005. ISBN 0-12-437552-9.

[3] Willems JL, Arnaud P, van Bemmel J, et al. A reference data base for multilead electrocardiographic computer measurement programs. J Amer Coll Cardiol 1987;10:1313–1321.

[4] Bousseljot R, Kreiseler D, Schnabel A. Nutzung der ekg-signaldatenbank cardiodat der ptb über das internet. Biomedizinische Technik 1995;40:S317–S318.

[5] Christov I, Dotsinsky I, Simova I, et al. Dataset of manually measured qt intervals in the electrocardiogram. BioMedical Engineering OnLine 2006;5.

[6] Moody GB, Koch H, Steinhoff U. The physionet / computers in cardiology challenge 2006: Qt interval measurement. In Computers in Cardiology 2006, volume 33. IEEE Computer Society Press, 2006; .

[7] Malmivuo J, Plonsey R. Bioelectromagnetism. Oxford University Press, 1995. ISBN 0-19-505823-2.

[8] Malik M, Camm AJ. Dynamic Electrocardiography. Blackwell Futura, 2004. ISBN 1-405-11960-8.

[9] Kors JA, Ritsema van Eck HJ, van Herpen G. The u wave explained as an intrinsic part of repolarization. In Computers in Cardiology 2005. IEEE Computer Society Press, 2005; 101–104.

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