Comparative Study of Signal Decomposition Methods for Enhancement of the Accuracy of T-wave End Localisation

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Abstract

The goal of this study was to compare several ECG signal decomposition methods in order to enhance the accuracy of T wave end localisation. PTB Diagnostic ECG Database comprising 549 recordings was used. The idea was to combine the 8 independent leads (I, II, V1,..., V6) of the standard 12-leads ECG into a single lead.

The signal decomposition methods were applied to reconstruct the combined T wave in such a way as to obtain maximal accuracy of the automatic T-end localisation. Four signal decomposition methods were used: Dominant T-wave (DTW), Principal Component analysis (PCA), and two Spatial Vectors (SV1 & SV2) synthesized from the orthogonal x, y, and z vectors.

The T-ends were localized using the same previously published software program. The results were compared to a published 'gold standard' dataset of manually determined T ends. Mean and standard deviation of the difference between the automatic and manual T-end locations were calculated in [ms]:

The best results (i.e. smallest standard deviation) were obtained by PCA followed by DTW. Compared to manual measurement, all signal decomposition methods except SVI moved the mean Tend location slightly to the right.

1. Introduction

Delineation of T-end alone and as a part of the measurement of the QT interval is a classical problem in quantitative ECG, approached in many different ways, especially after the automation of the process.

The accurate assessment of the QT interval duration is very important for clinical practice. A long list of cardiovascular and non-cardiovascular drugs are causing QT interval prolongation and triggering to a potentially lethal polymorphic ventricular tachycardia known as torsades de pointes (TdP).

The so-called "acquired long QT syndrome" (LQTS) is mainly observed during treatment with antiarrhythmic agents (in up to 10%) and much more rarely during treatment with non-cardiovascular medications. The congenital long QT syndrome is an inherited disorder with prolonged and heterogeneous ventricular repolarisation and increased risk of ventricular arrhythmias. A corrected QT interval (QTc) > 500 ms identifies patients with the highest risk of malignant ventricular arrhythmias [1].

The short QT syndrome (SQTS) is a relatively new clinical entity (first described in 2000 [2]) which is characterized by abnormally short repolarisation (QTc < 300 - 320 ms) and increased incidence of atrial fibrillation and sudden cardiac death.

Before approval every new chemical entity requires accurate estimation of its potential to prolong the QT interval (the so-called "thorough QTc studies").

The QT dispersion defined as the difference between the longest and the shortest QT intervals or as the standard deviation of the QT duration in the 12-lead ECG [3,4,5], continues to be the subject of some clinical interest although the currently prevailing opinion is that it does not reflect the dispersion of ventricular repolarization as initially thought [6].

PhysioNet/Computers in Cardiology Challenge, 2006 [7] sought an answer to a question of a high clinical interest: 'Can the QT interval be measured by fully automated methods with accuracy acceptable for clinical evaluations?' Evidence that this is feasible was given by several of the top-scored participants [8-13] with results of <20 ms difference between the 'gold standard' of manually and automatically measured QT [7].

There are various approaches to obtain a single value for end of the T wave in multilead ECG. Electrophysiologically if all T end in all leads is correctly located the latest one, where the electrical activity of the heart has the longest temporal projection should be selected. However, due to noise or other factors errors could occur. Laguna et al. $[\underline{14}]$ reduce the risk by checking for other T end locations in the time segment of 12 ms before the latest T end. If no more than two other leads have their marks in that interval, the latest T end is rejected as a possible noisy detection.

In recent years, there has been a tendency to localize the T wave end in a single lead obtained by signal decomposition methods from all available leads. Agostinelli et al. [15] reported that by using the 'Dominant T wave' decomposition [16-18], the intermethod variability of T end localization was reduced significantly compared to the inter-method variability of the same method applied to a single lead.

The goal of this study was to compare several ECG signal decomposition methods in order to enhance the accuracy of the T wave end localization.

2. Materials

2.1. PTB diagnostic ECG database

The data which we used comprised 549 recordings of the PTB Diagnostic ECG Database, which was contributed to PhysioNet in September 2004 by its creators Bousseljot *et al.* [19] and Kreiseler [20].

Each of the 549 recordings contains 15 simultaneously acquired signals: the conventional 12 leads and the 3 Frank (x, y, z) leads. All ECGs have been digitized at 1000 samples per second, with 16 bit resolution over a range of ± 16.384 mV. The recordings were acquired in 294 subjects (1 to 5 recordings per subject) with a broad range for age and diagnosis. About 20% of the subjects were healthy controls. The recordings were typically about two minutes in length, with a small number of shorter recordings (not less than 30 seconds).

Each ECG recording was accompanied by a detailed clinical summary, including age, gender, diagnosis, and where applicable, data on medical history, medication and interventions, coronary artery pathology, ventriculography, echocardiography, and hemodynamics. Diagnostic classes such as coronary artery diseases, heart failure, hypertensive heart disease, rhythm disturbances, etc., were also described.

No ECG-like tracings were observed in the recordings of patient 285/s0544_re, and it was excluded from the study, as it has been done by the manually created reference database [21].

2.2. Dataset of manually located Q-onsets & T-ends

A dataset of manually measured Q-onsets and T-wave ends which is available in the Internet was created by Christov *et al.* [22] for a selected heart beat for all of the 458 recordings in the PTB Diagnostic ECG database. More than 6000 manual markings done by 5 experts (4 cardiologists and 1 biomedical engineer) were collected and analysed. Thus, a reference library was established through a comprehensive, interactive review process in three rounds in accordance with the recommendations of the CSE Working Party [23]. The available in WEB 'gold standard' of the median locations [21] can be used for the development of automated methods for the detection of Q-onsets, T-wave ends and for QT interval measurement.

3. Methods

3.1. Signal decomposition

In order to combine the 8 independent leads (I, II, V1,..., V6) of the standard 12-lead ECG into a single lead, four signal decomposition methods were applied to reconstruct the combined T-wave in such a way as to obtain maximal accuracy of the automatic T-end localisation. The decomposition methods included:

Dominant T-wave (DTW)

The DTW was introduces by van Oosterom [16-18] as a means to characterize the general signal shape of the T wave by a waveform that describes the slope of the transmembrane potentials. DTW can be obtained as a weighted average of the T waves of all leads [15]:

$$DTW = \frac{1}{L} \sum_{l=1}^{L} w_l * T_l ,$$

where T_1 is the T wave in lead 1 (l=1,2,...,L) and w_1 is the weight of lead 1 obtained by integrating T_1 from T-onset to T-end.

Principal Component Analysis (PCA)

PCA is a statistical procedure that uses orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. It is defined in such a way that the first principal component has the largest variance (that is, accounts for as much of the variability in the data as possible), and each succeeding component in turn has the highest variance under the constraint that it is orthogonal to (i.e., uncorrelated with) the preceding components.

In this study we used only the first vector of the PCA.

Spatial Vector 1 (SV1)

The magnitude of SP1 was synthesized from the orthogonal x, y, and z vectors as follows:

$$SV1 = \frac{1}{3}\sqrt{x^2 + y^2 + z^2}$$

Spatial Vector 2 (SV2)

The SV2 transform is also synthesized from the orthogonal x, y, and z vectors:

$$SV2 = 0.5(x + y + z + 0.25(|x - y| + |x - z| + |y - z|))$$

It has been successfully used by us for wave delineation for more than 15 years [24].

Unlike the PTB database, in the majority of the available databases the Frank leads (x,y,z) are not available. Therefore we decided to synthesize the x, y, and z leads using Dower's coefficients [25]

All T wave decompositions are shown in Figure 1.

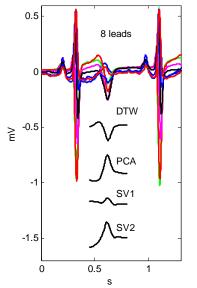


Figure 1. The 8 independent lead I,II,V1,...V6 and the four signal decompositions: Dominant T wave (DTW), Principal Component Analysis (PCA) and 2 Spatial Vectors (SV1 and SV2).

3.2. T-end location

The T-end localization was based on a previously published method of Daskalov and Christov [26, 10].

3.2.1. Delineation of the time interval for T-wave end search

An 'isoelectric' (flat or of low slope) segment is searched in the interval from the biggest peak of the complex (QRS_P , Figure 2) to 120 ms forwards on the time axis. The segment is found if all successive differences in 20 ms interval between adjacent samples are less than a preset value Crit and the difference between the end-samples of the 20 ms interval is less than 4*Crit. The value of the Crit is dependent to the QRS magnitude: Crit = 0.02(maxQRS - minQRS).

The rightmost sample of this segment is the QRS-offset point (J, Figure 2).

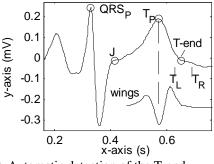


Figure 2. Automatic detection of the T-end.

Two adjacent segments of common mid point forming 'wings' are defined, each segment being of 40 ms length:

 $W_1 = D_{i-40ms} - D_i$ $W_2 = D_i - D_{i+40ms}$ where **D** are the corresponding signal samples.

The 'wings' function $(W=W_I*W_2)$ in the interval from J to J+QTc-100 ms is shown in Figure 2 (lower trace). QTc is calculated by the well known equation of Bazett. The minimum of 'wings' corresponds to the T-wave peak T_p , no matter if the T-wave has a positive or negative direction.

The steepest slope is searched as a maximum of the Win the interval from T_p to $T_p+QTc/5$. The right sample of the search interval T_R (Figure 2) is sought as a minimum of the W in the interval from the point of the steepest slope to $T_p+QTc/5$. The left sample of the search interval T_L (Figure 2) is obtained as a point where the amplitude of the T-wave is $0.8(T_p-T_R)$.

3.2.2. T-wave end location

Our method for automatic location of the T-end (Figure 2) is based on the minimum value of the angle between two segments having a common mid point and equal lengths of 10 ms. The minimum of the angle is searched in the defined time interval for the T-end.

4. **Results**

The results of the T-end automatic locations of the four decompositions are shown in Figure 3. Lead II was chosen to show (with 'o' and dashed line) the mean manual location of the 5 experts. The differences between the manual markings and the four decompositions in the Figure are: -6 ms for DTW, +10 ms for PCA, -18 ms for SV1 and +12 ms for SV2.

Mean and standard deviation (SD) [ms] of the difference between the automatic and the 'gold standard' dataset of manually determined T-ends for each signal decomposition were as follows:

DTW=8.72±14.19;	PCA=10.30±12.69;
SV1= -8.14±14.53;	SV2=8.59±17.93.

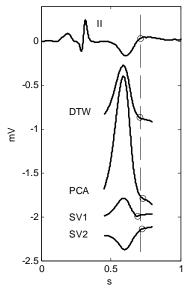


Figure 3. Results of the T-end automatic locations of the four decompositions: DTW, PCA, SV1, SV2

5. Discussions and conclusion

The best results (i.e. smallest SD) were obtained by PCA followed by DTW. Compared to the manual measurement, all signal decomposition methods except SV1 moved the mean Tend location slightly to the right.

Christov and Simova [27] reported mean and SD of 1.28 ± 16.75 for single lead T-end locations using the same T-end detection algorithm and the same 'gold standard' dataset of manually determined T-ends.

The current study illustrate that the signal decompositions methods (PCA, DTW and SV1) give better results for T-end localisation compared to the single lead one.

References

- Priori SG, et al. Risk stratification in the long QT syndrome. New England J of Med 2003;348:1866-74.
- [2] Gussak I, et al. Idiopathic short QT interval: a new clinical syndrome? Cardiology 2000;94:99-102.
- [3] Bortolan G, Bressan M, Golferini F. QT dispersion in the elderly. The ILSA study. Aging Clin Exp Res 2004;16:342-8.
- [4] Campbell RWF. QT dispersion may reflect vulnerability to ventricular fibrillation. Br Med J 1996;312:878–9.
- [5] Shah BR, et al. Computerized QT dispersion measurement and cardiovascular mortality in male veterans. Am J of Cardiol 2004;93:483-6.
- [6] Malik M, Batchvarov VN. Measurement, interpretation and clinical potential of QT dispersion. J Amer Coll of Cardiol 2000;36:1749-66.
- [8] Moody GB, Koch H, Steinhoff U. The PhysioNet / Computers in Cardiology Challenge 2006: QT Interval Measurement. Comput in Cardiology 2006;33:313-6.

- [9] Chesnokov YC, Nerukh D, Glen RC. Individually adaptable automatic QT detector. Comput Card 2006;33: 337-40.
- [10] Christov I, Simova I. Fully automated method for QT interval measurement in ECG. Comput Card 2006;33:321-24.
- [11] Hayn D, Kollmann A, Schreier G. Automated QT interval measurement from multilead ECG signals. Comput Cardiol 2006; 33: 381-4.
- [12] Martínez JP, Almeida R, Olmos S, Rocha AP, Laguna P. Stability of QT measurements in the PTB database depending on the selected lead. Comput Cardiol 2006;33:341-4.
- [13] Xue JQ. QT interval measurement: What can we really expect? Comput Cardiol 2006;33:385-8.
- [14] Laguna P, Jané R, Caminal P. Automatic detection of wave boundaries in multilead ECG signals: validation with the CSE database. Comput Biomed Res 1994;27:45-60.
- [15] Agostinelli A, Giuliani C, Burattini L, Use of the dominant T wave to enhance the reliability of T-wave offset identification. J of Electrocard 2014;47:98–105
- [16] van Oosterom A. Genesis of the T wave as based on equivalent surface source model. J Electrocardiol 2001;34(Suppl):217–27
- [17] van Oosterom A. Singular value decomposition of the wave: its link with a biophysical model of repolarization. Int J Bioelectromagnetism 2002;4:59–60.
- [18] van Oosterom A. The dominant T wave. J Electrocardiol 2004;37:193–7.
- [19] Bousseljot R, Kreiseler D, Schnabel A. Nutzung der EKG-Signaldatenbank Cardiodat der PTB über das Internet. Biomed Technik 1995;40:s317-18.
- [20] Kreiseler D, Bousseljot R. Automatisierte EKG-Auswertung mit Hilfe der EKG-Signaldatenbank Cardiodat der PTB Biomed Technik. 1995;40:s319-20.

[21] <u>http://www.biomedical-engineering-</u> online.com/content/supplementary/1475-925x-5-31-s1.doc

- [22] Christov I, et al. Dataset of manually measured QT intervals in the electrocardiogram Biomed Eng Online 2006;5(31):1-8.
- [23] The CSE Working Party. Recommendations for measurement standards in quantitative electrocardiography Eur Heart J 1985;6:815-25.
- [24] Daskalov IK, Dotsinsky IA, Christov II. Developments in ECG acquisition preprocessing parameter measurement and recording. IEEE Eng in Med & Biol. 1998;17:50-8.
- [25] Dower GE. A lead synthesizer for the Frank system to simulate the standard 12-lead electrocardiogram. J Electrocardiol 1968;1:101-16.
- [26] Daskalov IK, Christov II. Automatic detection of the electrocardiogram T-wave end, Med & Biol Eng & Comput 1999;37:348-53.
- [27] Christov I, Simova I. Q-onset and T-end delineation: Assessment of the performance of an automated method with the use of a reference database. Physiol Meas 2007; 28:213-21.

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