Morphology-based QT Interval Measurement Using Frame-based Representation of the ECG Signal

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Abstract

We propose a new method for QT interval measurement which first detects the morphology of the T-wave and then finds the T-end according to the detected morphology. The proposed method has more emphasis on detection of the T-wave morphology which helps more accurate detection of the T-end and better lead selection for QT interval measurement. Six types of T-wave morphologies (normal, invert, biphase +-, biphase -+, only upward and only downward) have been considered and a rule-based algorithm employed to detect the T-wave morphology by examining the primitive components. Followed by the detection of the morphology, the T-end is determined as the point on the signal that has maximum distance to the line representing the last segment of the T-wave.

The proposed method has been tested against the QT database available on Physionet. The mean difference between the T-end in the reference annotation and the calculated one by our method is 0.9 ms and the standard deviation is 18.9 ms.

1. Introduction

Acute increases in the QT interval can be observed in multiple clinical situations. QT prolongation is associated with an increased risk of syncope and sudden death from torsades de pointes (Tdp) ventricular tachycardia. Tdp can degenerate into ventricular fibrillation, leading to sudden death [1]. QT interval of the patients in these cases should be monitored periodically for possible prolongation.

Current measurement techniques rely on manual or semi- manual methods by health care professionals either with calipers on a printed ECG strip, or utilizing a caliper function on a digital waveform display. However manual or semi-manual QT measurement is time consuming and automatic and continuous measurement of the QT interval in ECG monitors is highly valuable to complement the sporadic manual measurements.

Several methods have been proposed for automatic measurement of the QT interval [2][5]. Some of the main challenges for all methods include accurate detection of the T-wave morphology and determination of the end of the T-wave which has a slow transition toward iso-electric segment. On top of these challenges the algorithm should have low computational complexity in order to be implemented in patient monitors.

Accurate detection of the T-wave morphology is the key to have a valid T-wave end determination. Knowing the T-wave morphology helps the algorithm to look for the T-end in the right part of the T-wave. In addition, different T-wave morphologies may need a different algorithm for T-wave end determination. Martinez et al. [2] proposed a method for QT measurement by categorizing the T-wave morphology into six different types: normal, invert, biphase +-, biphase -+, only upward and only downward. In this work we use similar categories for T-wave morphology.

In general, algorithm development for detection and delineation of the ECG wave components involves a lot of thresholdings and search windows on the signal and its derivatives which resembles the story of "The Elephant in a Dark Room" by *Rumi*. Despite these difficulties this task is quite easy for human mind even for a minimally trained person. The proposed method in this paper is a preliminary attempt to address this problem by processing the signal in different level of abstraction [4] and frame-based representation of the signal followed by syntactic pattern recognition [3]. At the same time we keep in mind that the proposed method has to be simple to be able to implement it in patient monitors.

2. Method

To determine the T-wave end we first detect the QRS complex using our algorithm developed based on Pan-Tompkins method [6]. Different wave components are then analyzed in the interval from QRS offset of each beat to the QRS onset of the next one. To analyze the wave components we represent the signal in different levels of abstraction [4]. In the lowest level the signal is represented by the signal samples. In the next level the signal is represented by its characteristic points (maximum, minimum and deflection points). Finally in the highest level the signal is represented by its components (P, T and F waves). This method of implementation is more efficient than direct analysis of the ECG samples and it makes the maintenance of the algorithm easier. In what follows different steps toward T-wave end determination is explained.

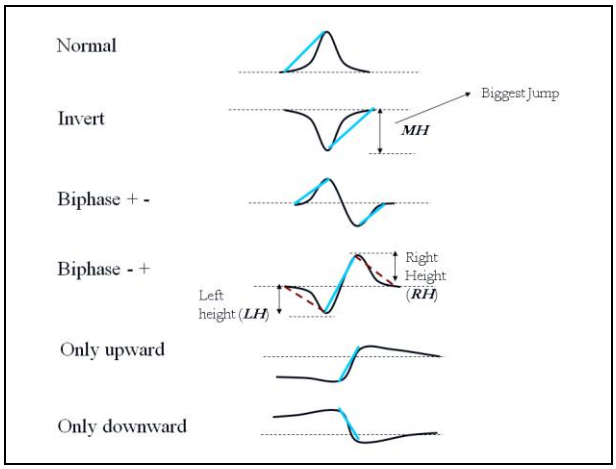

Figure 1. T-wave morphologies

a) Signal Preprocessing: Lowpass and highpass filters are used to decrease the high frequency noise and baseline wandering of the ECG signal prior to implementation of other steps. It is crucial to use filters with linear phases in order to prevent phase distortion from altering various wave properties of the cardiac cycle. The cutoff frequencies of the lowpass and highpass filters in the current implementation are 1Hz and 25Hz respectively. Both filters are second order Butterworth and they are applied in the forward and backward direction to create zero phase filters. The signal from QRS offset of each beat to the QRS onset of the next one is then fed to the next step (in the current implementation we use the signal from 100ms after the current R wave fiducial to 100ms before the next R wave fiducial).

b) Recognition of Peaks/Valleys: In this step we process the raw signal to extract minimum and maximum points of the signal. To prevent the algorithm from falling into local min/max points, the magnitude of a min/max point has to be smaller/bigger than all points in a certain window around it. The length of this window depends on the frequency range of the signal of interest. Since the frequency content of the T wave is generally less than 10 Hz, the length of the window can be up to 50 samples given the sampling frequency of 250Hz. In the current implementation the window length is 30 samples. This value is chosen heuristically based on the implementation of the method on Physionet QT database.

c) Representation by Primitive Patterns: The characteristic points obtained in the previous step are connected by straight lines to represent the signal with primitive patterns. This decreases the number of parameters and makes the processing easier. In this implementation we only use line segments to represent the signal but other primitive patterns like parabolic segment can be used for more accurate representation [3].

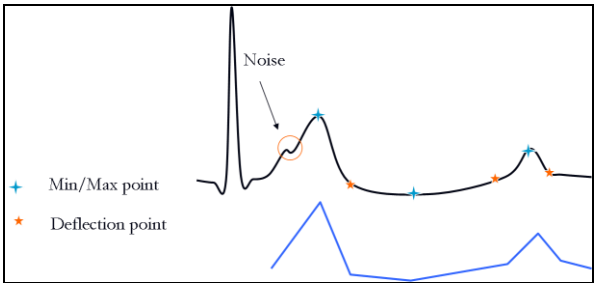

Figure 2. Representation of signal with primitive patterns

d) Rule based detection of T-Wave and T Morphology: The detection of T-wave location and morphology are tied together. It is crucial to detect the morphology prior to the T-end determination. The goal here is to analyze the primitive patterns in order to detect different waveform components. In this implementation we represent the signal with line segments connecting only the minimum and maximum points of the signal and do not use the deflection point for the purpose of pattern recognition. We first look for the segment that represents the biggest jump, which we call it the main segment (MS), in a search window. The beginning and end of the search window is 100ms and *min*(0.7RR,800ms) respectively after the R wave fiducial, where RR is the R to R interval in which we look for the T-wave. We consider this segment as part of the T-wave and then examine the neighboring segments to detect the T-wave morphology. We refer to the right and left segments of MS as right segment (RS) and left segment (LS) respectively. In some cases we also need to consider the neighboring segments of RS and LS where we use RRS and LLS to refer to the right segment of RS and left segment of LS. These terms are illustrated in Figure 1 along with different T-wave morphologies. We also use height and derivative of each segment in the decision process as well where we term them as the segment label without S followed by H for height and D for derivative (for example RH and RD represent the height and derivative of RS).

Thus far we have developed symbols to represent the signal. We are now ready to generate rules for detecting T-wave morphology based on the attributes of the segments. We use a set of logics and thresholds based on the height and derivative of the T-wave segments to detect T-wave morphology. The decision rules are illustrated below:

IF LH < 0.3 *MH or (LS not exist)
  IF RH < 0.2*MH or (RH < 0.5*MH and RSD < MD/4)
    Only Upward
  ELSEIF RH < 1.3*MH or (RRS is the last segment)
    Normal
  ELSE

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      IF RRH > 0.3 _ RH and (LS not exist) and (RRH in search win)
and RRRH < RRH/3
         Biphase +-
       ELSE
         Normal
ELSEIF (LS exists)
   IF LH < 0.7*MH
     IF RH < 0.2*MH or RD < MD/4
         Invert
     ELSEIF RH < 0.9*MH
         Biphase -+
     ELSEIF RH < 1.3*MH
         Normal
     ELSEIF RRH > 0.3*RH
         Biphase +-
     ELSE
         Normal
   ELSEIF LH < 1.3*MH
     IF RH > 0.3MH and RD > MD/4
         Biphase -+
      ELSE
         Invert
   ELSE
         Invert
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e) T-end Determination: Recognition of the T-wave morphology is the key step toward T-end determination. Given the morphology we look for the T-wave end in the last segment of the T-wave. We search the signal in the last segment of the T-wave to find the farthest point to the line segment. The distance of a point on the signal to the line is proportional to the vertical distance of that point to the line segment (the vertical distance is easier to calculate). Figure 3 illustrates this method on a Normal T-wave. Similar method has also been proposed in [5] for T-wave end determination.

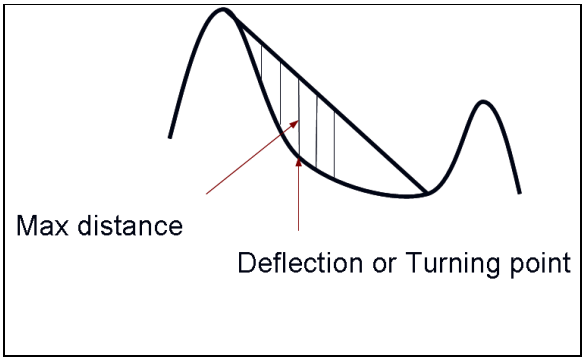

Figure 3. Method of finding the T-wave end

f) Multi-lead QT analysis: For clinical QT analysis it is recommended to measure QT on all leads and choose the longest one. QT dispersion across different leads is also a useful parameter that needs QT measurement on several leads. However because of the presence of noise in ECG monitors and also different presentation of the T-wave morphology in different leads, it is hard to measure the QT interval in all leads accurately. Therefore our goal here is to exploit multi-lead ECG to improve the accuracy of our QT analysis. This is a Data Fusion problem that can be done in different levels. Some previous work [5] has done this in the signal level by calculating the RMS of different leads, although it is not clear what happens to the morphology of the RMS signal using this method. In our study we fuse the data in the feature level where we combine the QT interval measurements according to their confidence level. We define the confidence level based on the T-wave morphology assuming high confidence level for the QT measurements of the leads containing Normal or Invert morphology and low confidence level for other morphologies. We choose this approach based on the performance of our method over the Physionet QT database. The logic of the lead combination follows:

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IF Lead 1 is Normal/Invert AND Lead 2 is Normal/Invert
   THEN  QT=(QT1+QT2)/2
IF Lead 1 is Normal/Invert AND Lead 2 is not Normal/Invert
   THEN QT=QT1
IF Lead 1 is not Normal/Invert and Lead 2 is Normal/Invert
   THEN QT=QT2
IF Lead 1 is not Normal/Invert AND Lead 2 is not Normal/Invert
   THEN   QT=(QT1+QT2)/2
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3. Results

The proposed method is applied to QT database [7]. The preliminary results show that the T-end determination error is -0.9±18.9 ms. The Percentage of records with mean < 15ms and std < 30.6 ms is %61 and the percentage of records with mean < 30 ms and std < 30.6ms is %78. This result is comparable to the results reported in [2].

4. Discussions

We propose a method for determination of the T-wave end with the emphasis on detecting the morphology of the T-wave. We use frame-based representation of the signal in order to decrease the number of parameters and hopefully move toward using more global patterns of the signal similar to human mind. The proposed method is designed to tolerate some level of noise in the signal that is normally present in patient monitors. It has also low computational complexity suitable for implementation in patient monitoring systems.

The current algorithm measures the QT interval for each beat while in real application averaging over a period of time could improve the results. Also for multi-lead analysis it would be useful to consider the noise level in each lead in addition to the T-wave morphology to improve the data fusion result.

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