

RECOVERING THE PRECISE HEART RATE FROM SPARSELY SAMPLED ELECTROCARDIOGRAMS

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Abstract

This work deals with a potential possibilities of improvement to the precision of time dependencies (e. g. heart rate) derived from a standard digital Holter record. The sampling frequency of a typical 24-hour ECG record is usually a compromise between signal quality and memory requirements. But even with a sampling interval of about 8 ms, is still possible to maintain the accuracy of 1...2 ms in R-wave delimitation and in consequence – precise heart rate measurement. The proposed method uses quadratic approximation of the ECG signal in 32-ms surroundings of R-wave peak and delivers satisfying results without significant increase of computing time.

1. Introduction

Since early 60-ties the 24-hour (Holter) ECG recordings turn out to be useful in clinical practise. The main advantages are real-live conditions of heart load and abilities of ECG analyses over a long period (i.e. circadian rhythms or heart rate variability). Unfortunately, the reliability of the ambulatory recorders is usually worse than the standard 12-lead ECG machines. A significant progress was made using digital sampling techniques and digital solid state memories for mass and lossless storage of ECG signal. But even using a large - and expensive - memory of 100MB, the maximum sampling rate does not exceed 400 Hz (3 channels, 8 bits per channel). Currently the average digital recorder uses the sampling frequency in the order of 120 Hz (120, 125 or 128 Hz), some most sophisticated systems of scientific use achieve the sampling frequency of 256 Hz [1].

Maintaining the good precision of the time parameters does not necessarily mean increase of memory requirements and system costs. Some advantages of the ECG signal could be taken to partly recover the accurate position of the R-wave peak, and - in consequence - to improve the precision of RR-intervals measurement. The main goal of our work was to investigate how far sampling at 120 Hz deteriorates the ECG signal, and to which extend the lost information may be recovered by approximation techniques. The standard CSE – Multilead

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database [2] was used to assure the unlimited choice of ECG-leads, and compatibility with the assumed reference R-wave peak, that means the moment of maximum length of three-dimensional cardiac vector. The standard signals were subsampled, and the approximation was performed on both original and subsampled signals in the same time window. The derived pairs of R-wave maximum's positions were statistically processed, that led to final conclusion. The completion of theoretical work is a simple algorithm performing the computation of the R-wave peak's position.

2. Materials And Methods

The source of test signals, the *Common Standard of Quantitative Electrocardiography* (CSE) – Multilead database [2], was chosen for several reasons:

- the signal set provides the simultaneous record of 15 leads: I, II, III, aVL, aVR, aVF, V1...V6, X, Y, Z
- the signal is originally sampled at 500 Hz, and available in raw version,
- all frequent morphology types of QRS-complexes are represented in database,
- CSE records contain the specification of QRS-onset and QRS-end points, so there is no necessity of any additional processing.

The original multilead signals (sampling frequency: 500Hz) from ECG-leads V2 and V5 (the closest to Holter leads: CS2 and CM5 equivalently) of a representative beat for all of 123 records made up the control set C1. Two records containing paced beats were rejected. The original multilead signals (sampling frequency: 500Hz) from ECG-leads X, Y and Z of a representative beat for all of 123 records made up the reference set R1. The vectocardiography leads (Frank) provide the easiest way of computing the absolute value of cardiac electrical field:

$$H = \sqrt{X^2 + Y^2 + Z^2} \quad (1)$$

that is necessary to precise the moment of maximal length of cardiac vector (R-wave peak).

In order to reduce the signal quality to the level typical of the standard Holter records, both signal sets C1 and R1 were subsampled by 4:1 (corresponding sampling frequency: 125Hz). That means every four samples of original signal were replaced by their mean value rounded to the nearest integer. The loss of information was than the same, as with use of digital Holter recording system with solid state memory. The subsampled versions of ECG-leads V2 and V5 of a representative beat for all of 123 records made up the test set T1, and the subsampled versions of ECG-leads X, Y and Z of a representative beat for all of 123 records made up the reference set R2 (Fig. 1).

Before having apply the approximation technique the choice of approximating function is worth to be justified. The process of the heart muscle excitation and contraction is very complicated, especially in case of some disturbances. The electrical representation of the heart activity on the body's surface is additionally distorted by irregularity of electrical properties of chest tissues, electrodes contact and others. But even when the initial and terminal parts of QRS complexes are strongly influenced by several intra- and extracardiac processes, the middle part, representing the avalanche depolarisation of most myocardium fibres, contains

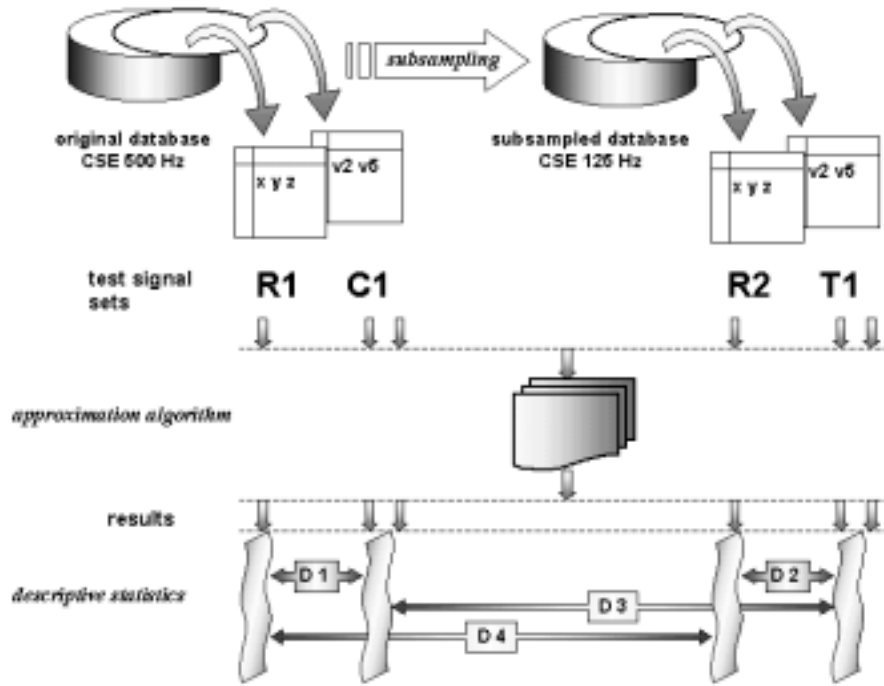


Fig. 1. Data flow and experiment organisation

high energy and is not susceptible to influences. This process is well described and modelled as a two-phase phenomenon: firstly, the electric field increases as the depolarisation front becomes wider (the majority cells are not jet depolarised), secondly, the electric field decreases as the percentage of depolarised cells exceeds certain limit [3].

For those reasons we propose the approximation of the R-wave with quadratic function:

$$y(x) = ax^2 + bx + c \quad (2)$$

The main advantage of this approach is the simplicity of algorithm and thus low cost of processing (that is especially important in case of Holter records containing typically ca. 100000 beats). On the other hand, it is difficult to find a justified reason applying a higher-order polynomial.

In general case, the computation of a best-fitted parabola may not seem straightforward, since the minimisation of the squared errors needs a solution of an overdetermined equation system (3) [4]:

$$Y = AX \quad (3)$$

where:

$$Y_{[N,1]} = \begin{bmatrix} y_1 \\ \dots \\ y_N \end{bmatrix} \quad (4)$$

$y_1 \dots y_n$ - are samples in approximation window

$$A_{[N,3]} = \begin{bmatrix} 1 & 1 & 1 \\ \dots & \dots & \dots \\ N^2 & N & 1 \end{bmatrix} \quad (5)$$

N – number of samples in approximation window

$$X_{[3,1]} = \begin{bmatrix} a \\ b \\ c \end{bmatrix} \quad \text{where } y(x) = ax^2 + bx + c \quad (6)$$

In the particular case, the length of approximation window is constant (N is constant), and determining the position of the parabola extreme is the only interest, so the pseudoinverted matrix A (5) can be entered as a table of constants.

The proposed approximation needs to be verified with use of statistic methods. That was done by descriptive statistics analysis (mean value M and standard deviation S) of difference δ between the maximum's positions of corresponding R-wave peaks in two data sets. The R-wave peak's position was computed as a time abscise of best fitted parabola extreme and was expressed in milliseconds, floating-point values. Regardless of sampling frequency, the length of approximation window was chosen of 32 ms.

In case of signals sampled at 500Hz the parabola was fitted to 17 consecutive points, while in case of subsampled signals (125Hz), the parabola was fitted only to 5 points. The window's length was chosen with respect to assure the minimum samples to fit the parabola to and, on the other hand, to not exceed the QRS complex length.

Assuming no data loss, that is evident false, means expecting zero values for both M and S . To assert the values of M and S as estimators of informative equivalence of data sets, first the difference $D1$ between the original reference $R1$ and original control set $C1$ was tested. That difference, having explanation in physiology, is expected not to increase when comparing subsampled reference $R2$ and subsampled test set $T1$ ($D2$). When those signals differs more, that is because of data loss, in that way the statistical results becomes estimators of loss of accuracy.

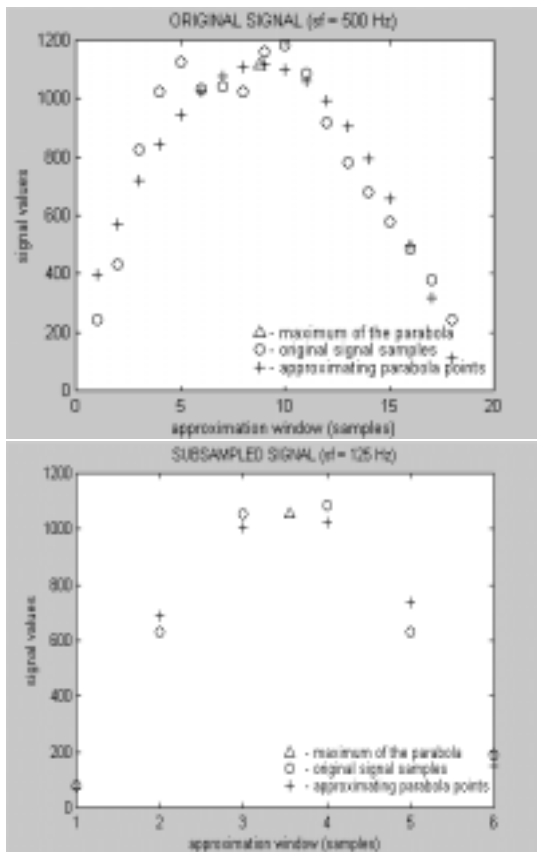


Fig. 2. The parabola fitting to the original and subsampled version of the signal (CSE-3/V2). The maximum's positions differ slightly.

Comparing test set T1 with control set C1 (*D3*) gives additional information based on the close-to-Holter ECG leads, while comparing references R1 with R2 (*D4*) gives information based on absolute maximum's difference.

3. Results

The difference *D1* between the original reference R1 and original control set C1 and difference *D2* between subsampled reference R2 and subsampled test set T1 are presented in table 1.

ECG lead	<i>D1</i> (C1 & R1)		<i>D2</i> (T1 & R2)	
	M	S	M	S
V2	1.65	10.90	1.80	11.65
V5	-0.62	9.29	-1.12	9.41

The projection of a QRS loop in its initial part influences more the V2 lead, and in its terminal part – the V5 lead. Thus, for physiological reasons, the maximum of R-wave in lead V2 is slightly ahead of the global maximum (in average 1.65 ms), while those in lead V5 is slightly delayed (in average 0.62 ms). Significant values of standard deviation (of order of 10 ms for *D1_S*) are caused by the different QRS morphologies, all frequent morphology types are represented in CSE database. The analysis of subsampled signals provides very similar results. The mean values do not differ significantly, while the standard deviations are greater only of about 1 ms.

The first conclusion is quite surprising – using the sampling frequency 125Hz instead of 500Hz causes only a slight loss in precision when the quadratic approximation was used.

The results of differences *D3* and *D4* are presented in table 2.

ECG lead	<i>D3</i> (T1 & C1)		<i>D4</i> (R1 & R2)	
	M	S	M	S
V2	1.36	2.11		
V5	2.01	1.58		
H			1.51	1.92

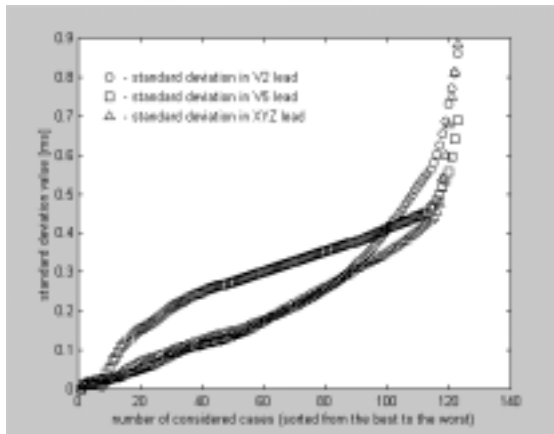


Fig. 3. Scatter plot of standard deviation of the R-wave peak position in original (500 Hz) and subsampled (125 Hz) signals in leads v2, v5 and XYZ

Comparing the results of difference between Holter-specific ECG leads and the difference derived from absolute length of cardiac vector one can hardly find a value exceeding 2 [ms]. Even assuming the worst case of error superposition, the accuracy of R-wave peak positioning is still better than 4 ms, that is beyond of reach of standard Holter recorders sampling at 125 Hz without any R-wave approximation.

4. Discussion

Presented work and its conclusion justify the hope that the exact position of the R-wave peak is not irreparably lost, and may be partially recovered even from sparsely sampled signals. The assumed regularity of the ECG signal in the surroundings of the R-wave peak makes the quadratic approximation applicable.

There are several serious interests for the other Holter processing algorithms to have precisely delimited R-wave peak. Some of them are worth to point out:

- delivers a stable fiducial point for QRS classification,
- is a reliable reference for baseline and ST-segment measurements,
- the precise RR interval measurements makes possible the analyses of heart rate variability (HRV) [5].

After some modification of general equations, the approximating algorithm is not necessarily complicated. In the application environment the pseudoinverted matrix A is constant and the whole processing of a single beat needs 8 multiplication, 9 additions and one division on floating point data (Fig. 4.). It delivers satisfying results without significant increase of computing time.

```
double approx(double PVals[5])
// five points approximation PVals=A*PCoeff
// A=  1   1   1
//    4   2   1
//    9   3   1
//   16   4   1
//   25   5   1
{
  double PCoeff[2]={0};
  double PinvA[2][5]={{0.1429, -0.0714, -0.1429, -0.0714, 0.1429},
                      // the first row is symmetrical
                      {-1.0571, 0.3286, 0.8571, 0.5286, -0.6571}};
  // the third row is not relevant
  PCoeff[0]=(PVals[0]-PVals[2]+PVals[4])*PinvA[0][0]
            +(PVals[1]+PVals[3])*PinvA[0][1]; // thanks to symmetry
  for (i=0; i<5; i++)
    PCoeff[1]+=PVals[i]*PinvA[1][i];
  return -PCoeff[1]/(2*PCoeff[0]);
}
```

Fig. 4. Simple C++ subroutine providing accurate position of best fitted parabola's extreme

References

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