Robustness of the Segmented-Beat Modulation Method to Noise

Angela Agostinelli, Corrado Giuliani, Sandro Fioretti, Francesco Di Nardo, Laura Burattini0205

Department of Information Engineering, Università Politecnica delle Marche, Ancona, Italy

Abstract

Typically, ECG is corrupted by baseline wander (BW), electrode motion artifact (EM) and muscular artifact (MA). To eliminate them, ECG is usually pre-filtered by application of linear techniques which, however, do not remove in-band components which may limit the ECG clinical usefulness if further processing is not performed. The Segmented-Beat Modulation Method (SBMM) is a template-based filtering technique which segments each cardiac beat into QRS and TUP segments, respectively independent and proportional to heart-rate, and adaptively adjusts each reconstructed beat to its original length by modulating and demodulating the TUP segments. The aim of the present study was to evaluate SBMM robustness to noise by applying it to one synthetic and 18 clinical ECG tracings before and after corruption with BW, EM and MA. Results indicate that, in all cases, clean ECGs are estimated with errors <0.15 mV, typically greater in the QRS than in the TUP segments (0-123 µV µV vs 0-25 µV; $P<10^{-5}$). Moreover, MA little affected ECG estimation, while BW and EM caused higher errors especially in the QRS segment which however remained quite small. Thus, the SBMM resulted to be a filtering technique quite robust to noise.

1. Introduction

The electrocardiogram (ECG) is a simple, cheap noninvasive recording of the electrical activity of the heart worldwide used in clinics to assess its functionality [1]. Each heartbeat is represented by an ordered sequence of typical waves (namely P, QRS, T and eventually U waves) which represent the different phases of atrial and ventricular depolarization and repolarization. Each wave is characterized by a time duration, a range of amplitudes (voltages) and a typical morphology. Any deviation from the normal tracing is potentially pathological and therefore of clinical significance. However, ECG interpretation may be difficult in case of noise affecting, and thus distorting, the ECG. Typically, the ECG signal recorded by skin electrodes is corrupted by noise of different nature [1-4], mainly including baseline wander, electrode motion artefact and muscular artefacts. Baseline wander is usually a low-frequency and high bandwidth noise component that can be caused by respiration, body movements and perspiration [5]. Electrode motion artefact is a low frequency noise component that results from motion of the electrode [6]. Eventually, muscular artefacts, which is a high frequency noise component, is caused by the random contraction of muscles, as well as by sudden body-movements. The electrical activity of muscles during the contraction can generate surface potentials that could completely drown out the ECG [7]. To get rid of all the above mentioned kinds of noise, ECG is usually pre-filtered by application of linear techniques [8,9]. However, the noise frequency-components that fall within the ECG frequency band survive pre-filtering and change its morphological characteristics, making difficult the extraction of ECG clinically useful information [4,10]. In these cases the application of further signal processing techniques is required in order to get rid of the survived noise without distorting the signal of interest [5-7]. In the common situations in which the ECG morphology is corrupted by noise surviving pre-filtering but the R peaks (which are the highest amplitude waves in the ECG) are still detectable, template-based techniques have been proposed [11] to extract a clean version of the ECG from the noisy recording. Briefly, such techniques identify all the beats present in the ECG, overlap them after R-peak alignment, and eventually average them to reduce noise and get a clean template-beat. Eventually, such template-beat is concatenated to get a clean ECG tracing that estimates the ECG of interest. The major limit of most of such techniques is the missed ability to reproduce physiological heart-rate variability and morphological variability [12]. Recently, a new template-based filtered procedure, termed segmented-beat modulation method (SBMM), has been presented [13,14] to overcomes such limit by adaptively adjusting each reconstructed beat to the original beat length [14]. However, its robustness to noise has not been tested yet. Thus, the aim of the present study was to evaluate the SBMM robustness to noise.

2. Data and method

2.1. Data

Both synthetic and clinical data were used in this study. Synthetic data consisted of a 60 s ECG obtained by

N-fold repetition of a single clean 0.75 s beat from a healthy subject. Thus the synthetic ECG was characterized by a heart rate (HR) of 80 bpm and no HR variability (HRV) or morphological variability. Clinical data consisted of 18 ECG signals from healthy subjects with no significant arrhythmias, all belonging to the “MIT-BIH Normal Sinus Rhythm Database” [15] of Physionet (www.physionet.org). All clinical ECGs were 60 s long and, overall, they were characterized by a HR ranging from 63 bpm to 110 bmp, and a HRV, measured as the RR-interval standard deviation, ranging from 15 ms to 78 ms. All clinical tracings were pre-filtered (0.5-35 Hz bandpass filtering by a 3rd-order spline interpolation) to minimize the level of noise affecting them. Then, the three noise recordings containing baseline wander (BW), electrode motion artifact (EM) and muscolar artifacts (MA) available at the Physionet “MIT-BIH Noise Stress Test Database” [15,16] were added to each clean (synthetic or clinical) ECG after a 70% reduction of their amplitude in order to simulate low-amplitude noise surviving pre-filtering.

2.2. Segmented beat modulation method

The SBMM [13,14,17] provides a clean ECG signal from a noisy recording, under the hypothesis of knowing the R-peak positions. The algorithm is based on the practical observation that, in first approximation, the QRS complex duration is independent from HR, whereas the duration of all other ECG waves is proportional to it [18].

By considering the beginning of the cardiac cycle (CC) between the P-wave offset and Q-wave onset rather than at the beginning of the P wave, each beat can divided into two segments: the QRS and the TUP (Fig. 1), respectively identified $\pm\Delta t$ ms (for example Δt=40 ms) around the R peak, and within the time interval that begins Δt ms after the R peak and ends Δt ms before of the subsequent R peak. Thus, a CC is an ECG portion between Δt ms before the R peak and Δt ms before the subsequent R peak. Each CC is characterized by its own duration (CCd), which may vary due to HRV. However, the duration of all QRS segments is $2\cdot\Delta t$ in all CC, while the duration of the TUP segments is beat-dependent and equal to $\mathrm{CCd}-2\cdot\Delta t$. After having segmented all N beats, the median CCd (mCCd) is computed. Then, the median CC (mCC) is computed after having modulated (stretched or compressed) all CC to have their length to match mCCd. For the median operator properties, the noise level affecting mCC is drastically reduced. Since all QRS segments have the same duration, the modulation process involves the TUP segments only (Fig. 2). The mCC represents the basic template-beat which is concatenated N times to get the estimated ECG containing the same number of beats of the original one. Each mCC constituting this tracing is then segmented and each TUP segment is demodulated (compressed or stretched) to match the length of the relative TUP segment in the original noisy ECG tracing (Fig. 3). Consequently,

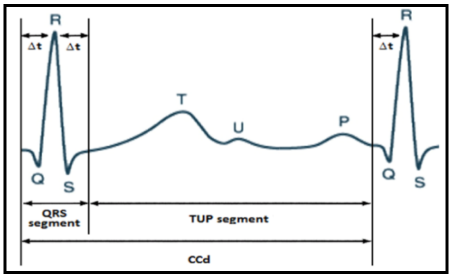

Figure 1. Segmentation of the CC into QRS and TUP segments (CCd: CC duration).

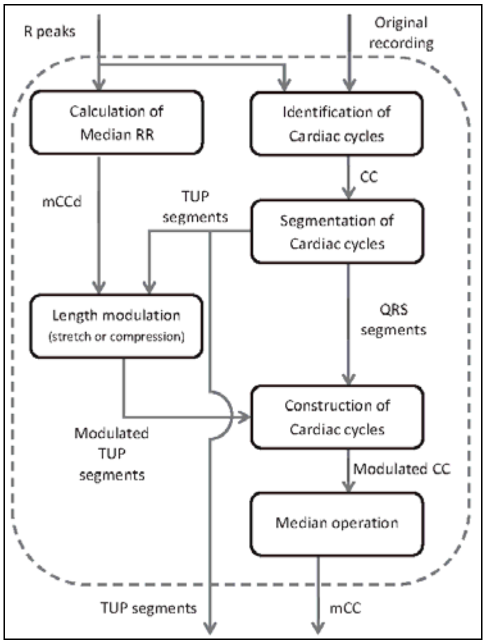

Figure 2. Block diagram relative to the mCC computation.

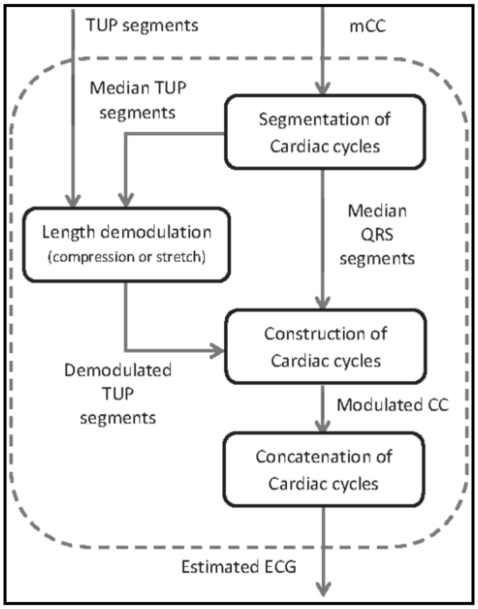

Figure 3. Block diagram relative to the clean ECG estimation.

estimated ECG and original ECG are equally long. Optimization processes, involving cross-correlation maximization and error minimization between each reconstructed beat and the corresponding one in the original signal, are performed in order to compensate for possible small inter-beat, HR-independent variations of the CC waveforms.

2.3. Statistical analysis

To evaluate the SBMM robustness to noise, two different errors (Eq. 1 and Eq. 2) were evaluated by comparing each clean estimated ECG with the corresponding noisy ECG:

$$\varepsilon_{QRS} = \mathrm{mdn}\left(\mathrm{mdn}\left(\left|eQRS(r,i) - QRS(r,i)\right|\right)\Big|_{i=1,2\ldots S_{QRS}}\right)\Big|_{r=1,2\ldots N} \qquad (2)$$

$$\varepsilon_{TUP} = \mathrm{mdn}\left(\mathrm{mdn}\left(\left|eTUP(r,i) - TUP(r,i)\right|\right)\Big|_{i=1,2\ldots S_{TUP}}\right)\Big|_{r=1,2\ldots N} \qquad (3).$$

Thus, ε_{QRS} and ε_{TUP}, in μV, indicate the median (over the N beats) QRS and TUP errors calculated as the median (over the samples S_{QRS} and S_{TUP}) of the absolute differences between the estimated (eQRS and eTUP) and the original (QRS and TUP) ECG segments. Normality of ε_{QRS} and ε_{TUP} distributions were evaluated using the Lilliefors' test. Not normal distributions were reported in terms of 50^{th} (median) [25^{th}–75^{th}] percentiles, and compared using the Wilcoxon Rank-Sum test for equal median. Statistical significance level was set at 0.05.

3. Results

When applied the clean synthetic ECG, the SBMM estimated the ECG with no errors ($\varepsilon_{QRS}=\varepsilon_{TUP}=0$ μV). Instead, when estimating the synthetic ECG from the noisy recordings, errors were $\varepsilon_{QRS}=78$ μV and $\varepsilon_{TUP}=4$ μV for BW; $\varepsilon_{QRS}=123$ μV and $\varepsilon_{TUP}=10$ μV for EM; and $\varepsilon_{QRS}=17$ μV and $\varepsilon_{TUP}=5$ μV for MA.

Figure 4 shows the effect of the SBMM on a clinical tracing. Quantitative results relative to all clinical ECGs are reported in Table 1. In all cases ECGs were estimated with errors <0.15 mV; ε_{QRS} (42-123 μV) were always greater than ε_{TUP} (13-25 μV; $P<10^{-5}$). MA little affected ECG estimation since errors were comparable to those obtained without adding noise ($\varepsilon_{QRS}=42$ μV and $\varepsilon_{TUP}=13$ μV for No noise vs $\varepsilon_{QRS}=46$ μV and $\varepsilon_{TUP}=14$ μV for MA). Instead, BW and EM caused comparable error increments ($\varepsilon_{QRS}=101$ μV and $\varepsilon_{TUP}=17$ μV for BW vs $\varepsilon_{QRS}=123$ μV and $\varepsilon_{TUP}=25$ μV for EM) significantly higher than those obtained with No noise ($P<10^{-3}$).

4. Discussion

This study evaluates the SBMM [13,14,17] robustness to noise. Similarly to other methods, the SBMM relies on the concatenation of a template-beat [11] to estimate a clean ECG. However, only this technique includes the segmentation of the CC into the QRS and TUP segments, respectively independent and proportional to preceding RR interval [18]. The modulation/demodulation procedure performed on the TUP segments initially to force all CC to become mCCd long before mCC computation, and then to have estimated beats to return to their original length, strongly improves accuracy of the estimated clean ECG [14,17], and makes the SBMM different from all other template-based techniques. The SBMM can be applied only if the R peaks relative to the noisy ECG signal are known. In most clinical cases, such

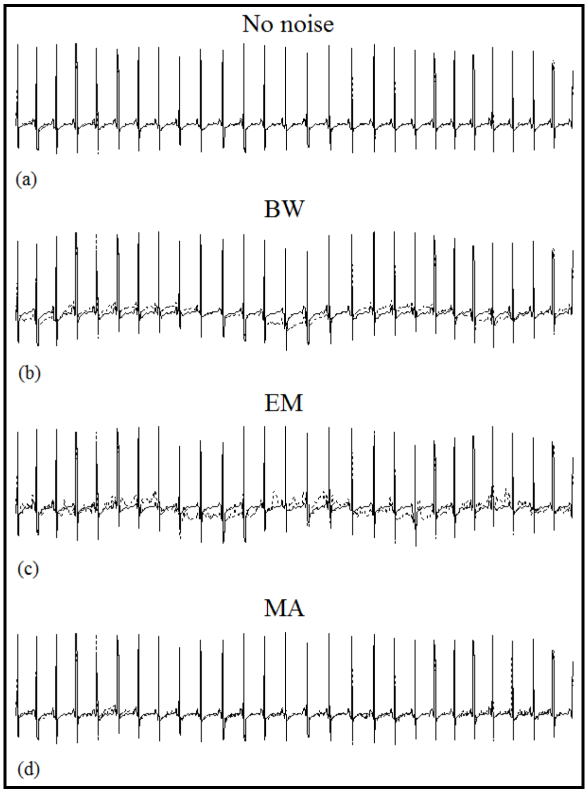

Figure 4. Example of a clinical ECG filtered by SBMM. An ECG (dotted line) is depicted before adding noise (panel a) and after adding BW (panel b), EM (panel c) and MA (respectively). The SBMM eliminates most of the noise and allow the extraction of a clean ECG (solid line) in each noisy condition.

Table 1. Errors values when estimating ECG tracing from clean and noisy recordings.

Noise	ε_{QRS} (μV)	ε_{TUP} (μV)	P_{Seg}
No noise	42 [27-49]	13 [11–19]	$<10^{-5}$
BW	101 [93–111]**	17 [15-28]	$<10^{-6}$
EM	123 [114-135]**	25 [21–33]*	$<10^{-6}$
MA	46 [38–60]	14 [12–20]	$<10^{-6}$

*, **: P-value$<10^{-3}$, $<10^{-6}$, when comparing errors of a segment (QRS or TUP) with a specific noise vs. no noise.

$P_{Segment}$: P-value when comparing errors relative to QRS vs. TUP segment for a specific noise.

condition is satisfied since ECG signals are supposedly pre-filtered and the amplitude of the R peaks is usually higher than the noise surviving pre-filtering so that they can be detected by specifically designed algorithms [19]. In less frequent cases in which the R peaks are not directly derivable from the original, possibly noisy original recording, the R peaks have to be indirectly obtained, for example using other ECG leads or from other signals before the SBMM can be applied.

In this study the SBMM was tested in synthetic as well as in clinical ECG tracings affected by the most common kinds of noises, which are BW, EM and MA in order to test its robustness to noise. The synthetic tracing was considered because, before being corrupted by noise, it represents the ideal condition of an ECG affected by no HRV and morphological variability. Consequently, the only confounding factor in its estimation by SBMM was identifiable in the added noise. Results indicate, the SBMM is able to estimate the synthetic ECG with no error (perfect reconstruction) if not corrupted by noise, and with errors ranging from few μV (in correspondence of the TUP segment) to tens of μV (in correspondence of the QRS segment) if corrupted by noise. EM was the noise that most affected ECG estimation, followed by BW and MA. Clinical data consisted of ECG tracings from healthy subjects, since these were real but as close as possible to ideal ECGs (characterized by limited HRV and morphology variability). Results indicate that, in all cases clean ECGs are estimated with significantly smaller ε_{TUP} than ε_{QRS}. Such results that the TUP segment is characterized by low frequency components than the QRS segment. In addition, very small values of ε_{TUP} are due to the SBMM ability to track physiological variability of TUP segment. Among the noises, MA little affected ECG estimation, while BW and EM caused higher errors especially in the QRS segment which however remained quite small (<0.15 mV). Thus, the SBMM resulted to be a filtering technique quite robust to the most common kinds of noise typically affecting ECG tracings.

5. Conclusions

The SBMM proved to be a useful tool for providing clean ECG estimations of tracings affected by the most common kinds of noise, which are BW, EM and MA.

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Address for correspondence.
Laura Burattini
Department of Information Engineering
Università Politecnica delle Marche
60131 Ancona, Italy
l.burattini@univpm.it.