A Real-Time Algorithm for Tracking of Foetal ECG Sources Obtained by Block-on-Line BSS Techniques

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Abstract

The foetal ECG (FECG) can be digitally extracted in real-time from non-invasive recordings using Blind Source Separation (BSS) techniques. BSS suffers the permutation ambiguity, scrambling the estimated sources over time and then hampering the FECG visual and automated analysis.

In this paper a block-on-line tracking algorithm, including an unsupervised morphological stage able of creating an average FECG beat, is presented. It allows the automatic identification of the FECG sources block-wise even in presence of permutations. The algorithm has been successfully tested on both real and synthetic signals, showing a percentage of correct foetal ECG peaks identification up to 93.44%. Its porting on the OMAP L137 embedded processor, with the OL-JADE FECG extraction algorithm, allowed the assessment of its real-time capabilities.

1. Introduction

The analysis of the foetal electrocardiogram (FECG) is a technique not yet exploited in antenatal cardiology that could allow the direct diagnosis of some foetal arrhythmias. Among the different algorithms for the extraction of this hidden signal from non-invasive recordings, Blind Source Separation (BSS) marks the best scores in terms of separation quality. On-line BSS techniques allow to deal with time-varying mixing processes due to both maternal and foetal movements better than batch solutions but suffer the permutation ambiguity in time of the estimated sources (FECG, maternal ECG (MECG) and noise) [1, 2].

In this paper, a real-time tracking algorithm for the automatic identification of the FECG sources for both an easier visualization and successive automated analyses is presented and evaluated. The tracking features allow to deal with permutations and are enhanced by an unsupervised morphological stage also able of creating the average FECG beat to ease the characteristic waves delineation usually hidden in the noise. The proposed algorithm can work with any on-line FECG extraction technique and can aid other processing stages, as the creation of a Body Surface Map of the FECG on the maternal abdomen [3, 4].

The automatic FECG channel classification without any clinician intervention is seldom addressed in literature. In [5] a Fast Fourier Transform (FFT) technique is used to identify which of the Independent Component Analysis (ICA) output waveforms include the foetal beats. The system proposed in [6] computes for each channel its probability of being maternal or foetal using a modified Pan Tompkins QRS detection algorithm and the autocorrelation function to find the heart rate in the estimated FECG and MECG. Conversely, many systems integrate a stage to enhance signal morphology highlighting the characteristic waves. For instance, the BSS system described in [7] computes the average FECG beat by maximizing the correlation between consecutive pulses. Also the ICA system described in [8] exploits an average waveform to measure the characteristic ECG intervals using the autocorrelation to align approximately 50 consecutive foetal complexes. To the best of our knowledge, the on-line application of these techniques has not been reported in literature.

2. Methods

The proposed tracking algorithm can be used with any FECG extraction technique. Nevertheless, in this work the OL-JADE one [2] has been used because of the particularly critic slow permutations (compared to other approaches [9]). Even though scalable, the original algorithm works with 8 input channels, with a sliding window with length $L = 1024$ samples and an overlap of $L-T$ samples, where T is set to be 256 at a sampling rate of 250 Hz. The proposed tracking algorithm has been sized accordingly.

The block diagram of the proposed algorithm is shown in Fig. 1. It includes 2 main stages, the tracking and the morphological ones. The former is further divided in 3 steps, namely: feature signals creation, noise channel identification, ECG clustering.

2.1. The tracking stage

At first, the tracking algorithm creates Feature Signals (FS) for all the estimated Source Signals (SS_i with $i =$

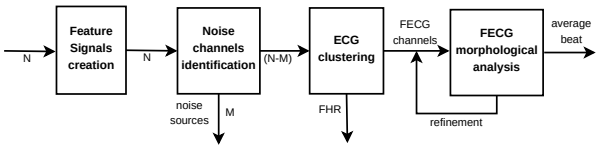

Figure 1. Block diagram of the proposed algorithm

$1, 2, ..., N$ where N is the number of input signals). SS_i are created as follows (n spans from 1 to 256):

- rectified first order derivative of the SS_i:

$$x_i[n] = \frac{1}{2}(|SS_i[n] - SS_i[n-1]|) \quad (1)$$

- rectified second order derivative of the SS_i:

$$w_i[n] = \frac{1}{4}(|S_i[n] - 2SS_i[n-2] + SS_i[n-4]|) \quad (2)$$

- a 7-tap matched filter to emphasize the presence of QRS waves, applied on the rectified first derivative:

$$\begin{aligned} y_i[n] = &\frac{1}{44}(2x_i[n+3] + 4x_i[n+2] + 8x_i[n+1] + \\ &+ 16x_i[n] + 8x_i[n-1] + \\ &+ 4x_i[n-2] + 2x_i[n-3]); \end{aligned} \quad (3)$$

- $y_i[n]$ is used to compute $z_i[n]$ through a multiplication operation between two adjacent samples, using an approach described in MOBD QRS detection algorithms [10], for magnification of high peaks:

$$z_i[n] = y_i[n] * y_i[n-1] \quad (4)$$

- a linear combination of z_i and w_i, inspired to the Balda QRS detector [11], emphasizes the highest signal peaks:

$$f_i[n] = z_i[n] + 0.5w_i[n] \quad (5)$$

- the f_i signals are then smoothed exploiting an 8 tap moving average filter in order to merge bicuspid peaks in FECG and MECG FS related to the same QRS event.

At this point, the noise channel identification step finds the M noise sources among the N channels. The FS are soft thresholded to remove the baseline information in the ECG signals (the threshold th_{tp} is equal to 45% of the average between the maximum in the analysed block and the maximum in the previous one). Then the first derivative operator of equation (1) is applied to FS_i and the transitions from positive to negative and vice versa are counted (turning point count). As shown in Fig. 2 on real mixtures by courtesy of Prof. L. De Lathauwer, slope inversions in noise are significantly more than those in ECG FSs so it can be identified adopting a threshold on the turn count.

At this point the ECG clustering step occurs, with the aim of identifying two clusters among the $N - M$ remaining FS which represent MECG and FECG sources.

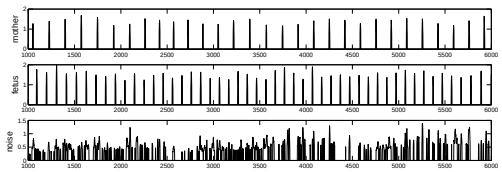

Figure 2. An example of foetal, maternal and noise processed signals on which the turning points are evaluated

We chose as metric for clustering a distance defined as $d = 1 - |\rho|$, where ρ is the Pearson's correlation coefficient. Every FS is standardized subtracting the mean value and dividing by the standard deviation, block wise. Then they are soft thresholded to remove the lowest 20%. The actual clustering stage can be described as follows:

1. creation of the $(N - M) \times (N - M)$ proximity matrix **D**, which is filled according to the defined distance;
2. research of the most similar pair of clusters *(r,c)* by searching for the minimum value of **D**:

$$d(r, c) = min\, \mathbf{D}(i, j), \quad with\ i \neq j \quad (6)$$

3. comparison of the minimum distance with a fixed threshold th_d (0.2, which corresponds to a $|\rho|$ of 0.8, an empirical value which allows the discrimination between maternal and foetal sources). If $d(r, c) < th_d$ the clustering proceeds, otherwise it is stopped;
4. merge of the clusters r and c and update of the proximity matrix according to the single linkage method. All the information about the position of channels composing a cluster is preserved;
5. if the number of clusters is greater than 2 (which is the ideal situation where MECG and FECG are identified) the analysis goes to the step 2 to complete the clustering, otherwise the clustering is finished.

If the number of clusters is greater than 2, the algorithm tries to merge them according to their R-peaks positions. If unsuccessful, a tracking error occurs and the FECG and MECG cannot be properly identified, otherwise the 2 clusters are classified as MECG or FECG according to the heart rate. Chosen one signal per cluster, any sample exceeding the 50% of the maximum in a block is marked as belonging to a QRS complex. Then a refractory period of 30 samples is used to clear multiple occurrences belonging the same complex. Since $FHR > MHR$, if the number of QRS complexes in the two clusters is different, the highest one indicates the FECG, otherwise the RR intervals are computed and the minimum used to identify the FECG.

2.2. The morphological stage

The tracking stage sends to the morphological one the FECG channels number and their R-peaks positions. This

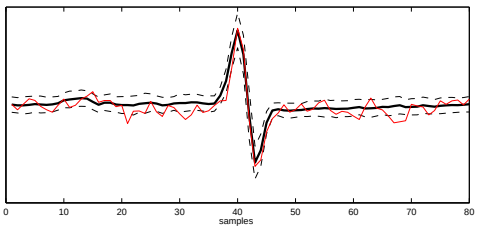

Figure 3. Average FECG beat obtained from a one minute signal. Dashed lines represent the standard deviation. A single beat from the ensemble average is also shown.

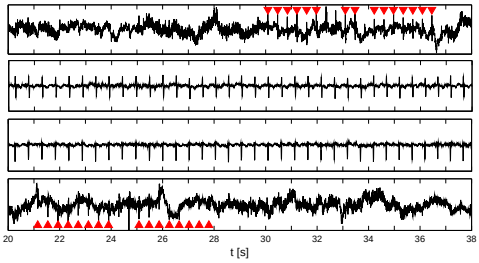

Figure 4. An example of tracking on real extracted ECG sources, acquired on a 20-week pregnant woman.

stage allows to identify possible foetal signals permutations and to enhance the signal to remove noise by synchronized averaging based on a cross-correlation analysis between the foetal source and a proper template. In the proposed approach, rather than using a synthetic template, for up to 2 FECG channels a template of 80 samples per channel (320 ms @250 Hz) centred on the R peak of the first identified beat is extracted.

At first, the morphology of every new beat is evaluated according to its QRS balance (polarity). Then a cross-correlation, based on the Pearson's index, between every template and a window around the R peak is applied. In this way, if the algorithm identifies in one of the foetal channels some consecutive QRS complexes whose morphology belongs to the other foetal channel, it reports a permutation between the two channels. Every time a QRS complex is found, it is also evaluated for updating a template by synchronized averaging. Because of the limited memory resource, an incremental averaging is preferred, without any precision loss. The necessary updating conditions are:

- the correlation index has to exceed a specific empirical threshold, which is 0.8 at the steady state (it slowly grows from a first value of 0.6);
- the QRS complex polarity has to be coherent with that of the related template.

Since the correlation index is obtained for every sample around the R peak, its value allows the individuation of the exact R-peak position which reflects the better alignment between the template and the beat. If the template is not updated within 25 consecutive beats found by the tracking stage, the algorithm selects a new template to be representative of the channel morphology. Also, since the FECG channels permutation can cause a polarity inversion, the algorithm takes into account this possible inversion when aligning the QRS complexes before updating the mean beat. In this way, a real-time updated template represents the average beat until then: Fig. 3 shows the average FECG beat after the analysis of a one minute signal, compared to a single real beat.

3. Results

To evaluate the performance of the proposed tracking algorithm, we performed tests on both real and synthetic mixtures processed by the OL-JADE algorithm [2]. The real signals used here were acquired non-invasively by an ADI PowerLab16/30 and a *g.tec* GT201 16 channels Bioamp from two voluntary subjects respectively at the 36^{th} and the 20^{th} week of pregnancy. An example of online tracking of the FECG traces produced by OL-JADE is shown in Fig. 4, where the identified foetal R-peaks are marked. It is possible to see how the quality of the extracted MECG is higher than that of the FECG, which in turn has reverberations on the permutation aspects.

For the synthetic signals generation, the OSET tool [12], which enables the creation of two rotating dipoles with selectable parameters (including position) for both mother and foetus, was used. It allows to add to the clean sources also some parameterized time variant noise, weighting 3 different contributions of baseline wandering (BW), electrodes movements (EM) and muscle artefacts (MA). Since on real signals it is difficult to recover all the 3 foetal components, we decided to constrain the foetal dipole to a planar rotation. With this choice, for every single kind of noise and for the composite one (CN, with the same weight for the individual noises) we created segments of 30 seconds with a different SNR, with or without expressly introduced foetal movements (position and 3D rotation of the foetal dipole abruptly changed at second 15), passed to OL-JADE to estimate the independent sources on which the tracking algorithm is applied.

The tracking results are shown in Tab. 3 in terms of percentage of True Positive (TP) revealed peaks, obtained considering the number of the FECG peaks correctly identified by the tracking algorithm, with respect to the total amount identifiable by visual inspection. All the permutations in the FECG sources have been detected and their number is also indicated in the same table.

In order to assess the capability of the algorithm of properly operating in real-time along with the main FECG extraction algorithm, it has been coded in C and optimized

Table 1. Tracking algorithm performance.

	FECG source 1		FECG source 2	
	% TP	# perm	%TP	# perm
real signal (36^{th})	66.7	5	64.9	3
real signal (20^{th})	69.7	4	-	-
CN, SNR=5	79.2	1	51.9	1
CN, SNR=10	78.4	3	65.8	1
CN, SNR=15	83.3	0	78.8	2
CN, SNR=20	90.3	0	89.8	0
CN, SNR=20‡	62.7	1	52.5	1
CN, SNR=20†	93.4	0	93.4	1
MA, SNR=15	89.6	0	83.9	2
EM, SNR=15	86.9	0	52.2	2
BW, SNR=15	90.2	0	70.2	2

‡: with abrupt translation of the foetal dipole
†: with abrupt rototranslation of the foetal dipole

to run on the C6747 floating point DSP core of the OMAP L137 embedded processor by Texas Instruments. When the processor is clocked at 300MHz and the sampling rate is 250Hz, the proposed tracking algorithm requires only 3.7ms (1.6ms for the morphological stage), which is a short time compared to the worst-case 158ms required by the main separation algorithm.

4. Discussions and conclusions

As can be seen in Tab. 3, the results are affected by the noise level, which influences the separation quality. The performance does not grow monotonically with the SNR because of the stochastic nature of the process used to create the noise in OSET. Since the FECG sources identification works block-wise, some errors lead to the misdetection of more than one consecutive FECG beat (as clearly visible in Fig. 4) but such isolated errors can be easily filtered out.

The poor signal quality influences the noise sources identification step, which has been identified as the weakest step of the algorithm because of the high variability of the turning point count. Wrong noise sources identification produces wrong ECG clustering, preventing the identification of the FECG sources. From this viewpoint, the tuning of th_{tp} can be beneficial and, thanks to the real-time capabilities of the proposed solution, this can be performed at run time. It should be noted that the th_{tp} tuning is mainly required when changing acquisition setup (e.g., we changed its value from 0.45 to 0.15 for all the synthetic signals). Even though the algorithm can be improved, its performance is compatible with the needs of an embedded system implementation and for this reason it has been integrated with OL-JADE on a prototypical embedded platform based on the dual core OMAP L137 processor for advanced studies in the field of FECG extraction.

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References

[1] Spence G, Clarke I, Smith M. Blind signal separation and its application to long-term bio-medical monitoring. In Medical Applications of Signal Processing. November 2005; 93–98.

[2] Muceli S, Pani D, Raffo L. Real-time fetal ECG extraction with JADE on a floating point DSP. Electronics Letters August 2007;43(18):963–965.

[3] Pani D, Argiolas S, Raffo L. Real-time back-projection of fetal ECG sources in OL-JADE for the optimization of blind electrodes positioning. In 37th Int. Conf. on Computing in Cardiology. 2010; 289–292.

[4] Taylor MJ, Smith MJ, Thomas M, Green A, Cheng F, Oseku-Afful S, Wee LY, Fisk NM, Gardiner HM. Non-invasive fetal electrocardiography in singleton and multiple pregnancies. BJOG International Journal of Obstetrics Gynaecology 2003;110(7):668–678.

[5] Kolluri et al. Extrapolating ICA knowledge from one epoch to another for improved fetal ECG separation. U.S. Patent No. US 7,831,300, Nov 2010.

[6] Marossero et al. Maternal-fetal monitoring system. U.S. Patent Application No. US2005/0267377, Dec 2005.

[7] De Lathauwer L, Moor BD, Vandewalle J. Fetal Electrocardiogram Extraction by Blind Source Subspace Separation. IEEE Trans on Biomedical Engineering May 2000; 47(5):567–572.

[8] Mensah-Brown NA, Lutter WJ, Comani S, Strasburger JF, Wakai RT. Independent component analysis of normal and abnormal rhythm in twin pregnancies. Physiological Measurement 2011;32:51–64.

[9] Pani D, Argiolas S, Raffo L. Impact of the approximated on-line centering and whitening in OL-JADE on the quality of the estimated fetal ecg. In 37th Int. Conf. on Computing in Cardiology. 2010; 549–552.

[10] Suppappola S, Sun Y. Nonlinear transforms of ECG signals for digital QRS detection: a quantitative analysis. IEEE Trans on Biomed Eng April 1994;41(4):397–400.

[11] Balda RA, Diller G, Deardorff E, Doue J, Hsieh P. The HP ECG analysis program. North Holland, 1977; 197–205.

[12] OSET - The Open-Source Electrophysiological Toolbox. URL `http://www.oset.ir`.

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