Identification of Fetal QRS Complexes in Low Density Non-Invasive Biopotential Recordings

Alessia Dessì, Danilo Pani, Luigi Raffo

DIEE - Dept. Electrical and Electronic Engineering, University of Cagliari, Italy

Abstract

Non-invasive fetal Electrocardiogram (ECG) is currently a missing diagnostic tool. Despite the technology advancements and the improvements of the signal processing techniques, the possibility of extracting this signal from recordings of biopotentials gathered on the maternal abdomen is still unexploited in the clinical practice.

The 2013 Physionet/Computing in Cardiology Challenge proposes to address this specific problem, making available a dateset of annotated abdominal signals, with a reduced number of channels, taken with different instruments and protocols. In this paper a novel algorithm based on template matching for maternal QRS subtraction and fetal ECG detection is presented and evaluated on the available dataset. The algorithm achieves a score of 639.465 and 23.821 on dataset B and of 684.158 and 47.990 on dataset C.

1. Introduction

Fetal Electrocardiogram (ECG) by non-invasive biopotential measurements is a long-standing research topic [1]. The difficulty in defining a standard set-up for the recordings, in terms of number and position of the electrodes and instrumental setting, and the lack of good signal repositories, hampers the development of algorithms able to solve the problem [2]. The usefulness of the fetal ECG is manifold. From a diagnostic viewpoint, it would help the diagnosis of some arrhythmias in early pregnancy, when only ultrasound-based techniques can be applied, directly providing the information of the electrical activity of the fetal heart. From a monitoring perspective, fetal ECG could allow a harmless long-term monitoring of the fetal heart rate for fetal well-being assessment at home [3] or intrapartum (as the AN24 device by Monica Healthcare Ltd.). In both cases, a set-up with a reduced number of electrodes, which would be poor for a diagnostic tool, is more practical.

Since the non-invasive fetal ECG recording relies on electrodes applied on the maternal abdomen, it is not possible to look at a particular projection of the fetal ECG at any gestational age, even knowing the exact position of the baby, because of the propagation of the signals inside the maternal body [4]. The choice of both the number of signals to acquire and the displacement of the electrodes, dependent on the kind of analysis required afterwards, strongly influences the signal processing technique which can be used for the fetal ECG extraction. The 2013 Physionet/Computing in Cardiology Challenge proposes low-density recordings (only 4 channels), acquired with different instruments and unknown setup. The low density hampers the adoption of traditional Independent Component Analysis (ICA) methods [5], whereas the absence of a reference signal for the mother prevents the direct exploitation of adaptive filtering techniques [6]. In this case, the maternal ECG subtraction is the most immediate way to solve the problem.

In this paper, a method for the reduction of the maternal P-T waves, subtraction of the maternal QRS complex, and extraction of the fetal ECG R peaks is presented and evaluated. It is based on recurrent use of automatic template creation and matching procedures. Templates of parts of the filtered signals possibly representing QRS complexes are automatically extracted from the signal by incremental synchronized averaging performed in order to smooth over the noise components. The reference points for the templates extraction are identified by a QRS enhancement technique based on a feature signal created exploiting a wavelet denoising stage. Periodicity correction stages help in removing unwanted noise peaks, recovering parts of the signals where no QRSs have been identified. The identification of the fetal R peaks is based upon a QRS detector and a template matching followed by periodicity correction, refining the output according to the fetal QRS morphology.

2. Methods

The proposed algorithm allows the identification of the fetal QRS complexes in 4-channel non-invasive abdominal recordings at 1000 Hz. It includes two main stages, the first one allowing the detection and the subtraction of the maternal QRS complexes, the second one for the identi-

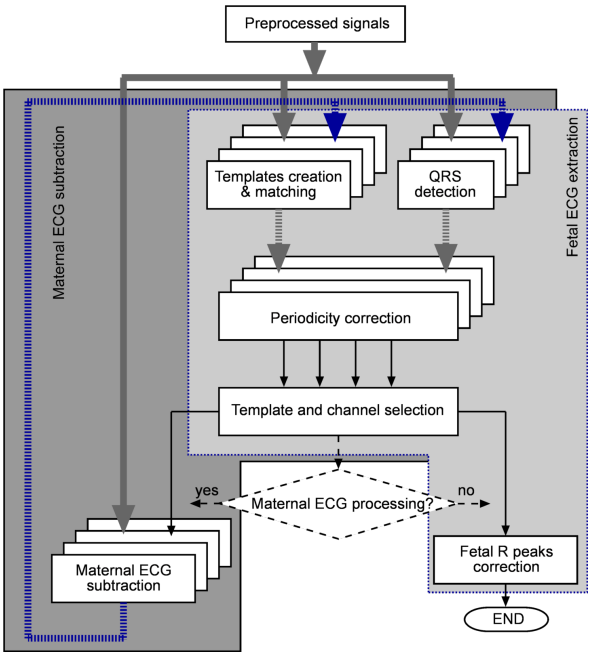

Figure 1. Block diagram of the proposed algorithm.

fication of the fetal QRS complexes. Their structures are quite similar and will be described in the hereafter. Before the two main stages, signals are preprocessed by:

- identification of the saturated values in every channel,
- replacement of them by cubic spline interpolation,
- low-pass zero-phase digital filtering at 46 Hz to reduce noise interference,
- high-pass zero-phase digital filtering at 8 Hz to emphasize the QRS, attenuating P and T waves.

2.1. The maternal ECG subtraction stage

The block diagram of the maternal ECG subtraction stage is shown in Fig. 1. It includes five processing steps, which are: QRS detection, template matching, periodicity correction, channel identification and MECG subtraction.

2.1.1. Maternal QRS detector

This step works on downsampled signals (250 Hz) and is based on a simple QRS detector algorithm [7]. Since the QRS detector exploits a linear combination of the first and the second derivatives of the signal, it could better identify the fetal R peaks if these are really high with respect to the maternal one. To solve this problem, the detector is independently applied to all the signal channels, assuming that at least one of them allows the clear identification of the maternal QRS complexes.

2.1.2. Template matching

This algorithm step aims at extracting the average QRS waveform exploiting a correlation based approach. Due to the different projections, shaping the QRS morphology, templates for subtractions must be identified for each channel. In order to have a template adapted to slightly different changes (mainly in the width due to heart rate changes), the signal is divided into frames by 20 seconds, analyzed separately. Every frame is scanned in order to find the positions of the QRS complexes, identified by means of a feature signal obtained after a wavelet denoising (WD) of the preprocessed signal at 250 Hz. The WD uses the *bior6.8* mother wavelet, with 3 decomposition levels, clearing the approximation signal and hard thresholding the details exploiting a minimax scaling for the median absolute deviation of the signal, computed at each scale. The resulting signal undergoes a peak detection based on a modified version of the previously introduced QRS detection algorithm. For every peak identified in the WD processed signal, a 200ms window on the preprocessed signal at 1000 Hz is extracted and cross-correlated with the templates present at the moment. If the correlation is below a threshold of 0.8, the extracted window creates a new template, otherwise it undergoes a weighted synchronized averaging with the best-matching template. At the end of the analyzed frame, the similar templates are merged and the two most frequent ones used for a global cross-correlation (only one if the other seldom matches). The points where the cross-correlation exceeds 0.85 are marked, defining a temporal series.

2.1.3. Periodicity correction

In this step, the output of the template matching is compared with the output of the QRS detector, identifying a time series where the element are differently tagged: 0 stands for the QRSs not matching with any of the two identified templates and 1 or 2 stands for the QRSs matching with template 1 or 2 (if both, by default only the number 1 is assigned). The time series is analyzed to verify whether only one non-zero tag is present, a predominant non-zero tag is present (in this case the other one is set to zero), alternation between the non-zero tags is present (in this case they are separately analyzed and compared), or none of the above. The median value of the lag between different instants of this time series, computed on the longest non-zero sequence of tags and called ***RRm***, is used as a starting value to forecast, point by point, the occurrence of the next QRS, iteratively adapting RRm as $RRm = RRm(1-\gamma)+\gamma\hat{RR}$, with $\gamma = 0.25$ and $\hat{RR}$ the RR associated to the next valid point in the sequence. Information about the tags assigned to the identified QRSs is used to improve the choice of the supposed QRS points when more than one are present. The algorithm tries to add a point after RRm samples if

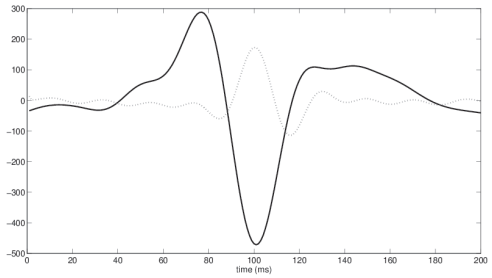

Figure 2. An example of maternal (solid) and fetal (dashed) average template.

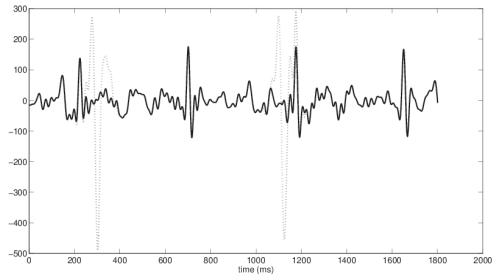

Figure 3. An example of maternal subtraction: the signal before (dashed) and after (solid) maternal QRS subtraction.

missing beats are identified. This behavior increases the number of false positives in the outputs of this stage when such a correction is repeatedly applied. Added QRSs are marked differently from the confirmed QRSs, which in turn are marked differently whether they were confirmed after cancelling other points classified as false positives in the nearby or not.

2.1.4. Maternal source identification

The number of QRSs identified by the QRS detector and corrected by the periodicity corrector for each channel is used to create two classes with a similar number of QRSs, assuming that usually the fetal heart rate is higher than the maternal one. If two classes are found, one for the maternal complexes and one for the fetal ones, that with the smallest number of peaks is chosen. Among all the channels with a similar number of peaks, it is chosen that with a minimum score obtained taking into account the number of QRS complexes removed and added by the periodicity corrector. Once the maternal QRSs have been identified, their positions are used to choose the maternal template for each channel, avoiding the risk of subtracting the fetal template whenever identified by the template extraction. An example of maternal and fetal average template is shown in Fig. 2.

2.1.5. Maternal QRS complexes subtraction

The maternal R peaks positions are used to subtract the maternal average QRS complexes on each channel. Among the extracted templates, the one with the highest correlation with the maternal signal around the R peak position is used. Before subtraction, the chosen average template is multiplied by a Tukey window to avoid the generation of artificial peaks on the borders of the subtraction window. The subtraction of the best-correlating template allows to optimize the suppression of the maternal QRS complexes in signals where the maternal frequency and consequently the QRS complexes duration changes over time. At the same time it ensures the integrity of the fetal R peak morphology, as shown in Fig. 3

2.2. The fetal QRS identification stage

The second main stage includes the same QRS detector and template matching steps of the first one, with adapted thresholds, aiming to the identification of the residual peaks belonging to the fetus. The periodicity correction step is also applied, with slight modifications, to all the channels to choose the one in which the fetal QRSs are well identifiable. Compared to the maternal case, the tolerance on the heart rate variability is higher to follow the typical fetal rate variations. At this time only one class should be obtained after the periodicity correction so, taking into account the number of QRS complexes added and removed by such a step, the series with the minimum score is chosen. As it could be possible that the algorithm identifies maternal residues, the average RR interval of maternal annotation series is compared with that of the chosen sequence. If they are really close (i.e. the mother and the fetus have almost the same heart rate), the position of the QRS complexes is also considered, to choose the channel with different annotations compared to the maternal one.

2.2.1. Fetal QRS complexes correction

To center the identified fetal QRSs on their R peaks, the average QRS fetal template obtained in the template matching stage is taken into account. Once the morphology of the fetal QRS peaks have been identified, they are used to correct the position of the R peaks, improving the accuracy. If the fetal QRS balance is positive, the maximum is searched around the R fetal annotation, otherwise the minimum is searched.

3. Results and discussion

To evaluate the performance of the proposed algorithm a collection of one-minute abdominal recordings at 1000

Hz from the Physionet database was used. Each recording consists of four non-invasive abdominal signals obtained using a variety of instruments with differing frequency response, resolution, and configuration. Reference annotations marking the locations of the fetal QRS complexes are derived by crowd-sourcing using a mixture of experts, volunteers, and algorithms, using the direct fetal ECG when possible. The results have been evaluated on the open test set B, which includes non-invasive signals only (reference annotations withheld) and on the hidden test set C, which includes unpublished records reserved for evaluation of open-source challenge entries, according to two index scoring. The first one is obtained as the mean square error between the fetal heart rate time series estimated from both the test and reference annotation according to the WFDB TACH function (http://www.physionet.org/physiotools/wag/tach-1.htm). The second one is obtained comparing the RR series using the MXM function (http://www.physionet.org/physiotools/wag/mxm-1.htm) which calculates the scores by picking the closest RR pair between both time series and measuring the mean square error distance.

The algorithm achieves a score of $639.465bpm^2$ and $23.821ms$ on dataset B and of $684.158bpm^2$ and $47.990ms$ on dataset C. The score related to the fetal heart rate is quite high, suggesting that the algorithm produces more false negatives than false positives, underestimating the fetal heart rate whenever the maternal ECG is erroneously assumed to be representative of the fetal one.

The subtraction of the best correlated QRS maternal complex allows to preserve the fetal morphology when the fetal beat overlaps the maternal one. At the same time, the preprocessing is often unsatisfactory in removing high frequency P and T waves, considerably compromising the algorithm performance. In fact the presence of these residues in some signals makes the algorithm completely ineffective in fetal QRS identification, strongly worsening the scores on the entire database. Furthermore, the algorithm tends to identify in any case the fetal R peaks, even where they cannot be detected, producing a large number of false positives if no fetal R peaks are present, and of false negatives when it tracks the residual maternal ECG rather than the fetal ECG.

4. Conclusions

The proposed algorithm allows the identification of fetal QRS complexes in abdominal recordings of four signals at 1000 Hz. It is based on the subtraction of the maternal average QRS complex autonomously created by a template creation and matching stage. The occurrences of the maternal QRS complexes to be subtracted are identified by a QRS detector and corrected in order to enforce a pseudo-periodicity, using the information of the occurrences individuated by the template matching stage. On the obtained denoised signals, the fetal QRS are individuated in the same way, adjusting the thresholds and the rules for the identification of the signal with the best detection.

The achieved results can be improved. In the next future we are planning to include the P and T waves in the average and subtraction of the maternal complexes and to enhance the stage for maternal source identification after the periodicity correction. The fetal periodicity correction will be also improved in order to avoid the enforcement of the periodicity on long segments of the signal.

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Address for correspondence:

Alessia Dessì
DIEE - University of Cagliari
Via Marengo 3, 09123 Cagliari, Italy
pani@diee.unica.it