fetal heart rate variability,
time event series,
sampled signal,
duplicated sample

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RECONSTRUCTION OF FHR SERIES RECORDED VIA ULTRASOUND – METHOD VALIDATION USING ABDOMINAL FETAL ELECTROCARDIOGRAPHY

Analysis of variability of the fetal heart rate (FHR) is very important for fetal wellbeing assessment. The beat-to-beat variability is described quantitatively by the indices originated from invasive fetal electrocardiography which provides the FHR signal in a form of time event series. Nowadays, monitoring instrumentation is based on Doppler ultrasound technology. The fetal monitors provide the output signal in a form of evenly spaced measurements. The goal of this work is to present a new method for the FHR signal processing, which enables extraction of time series of consecutive heartbeat intervals from the evenly repeated values. The proposed correction algorithm enables recognition and removal of the duplicated measurements. Reliable evaluation of the algorithm requires the reference event series, thus the FHR signals were obtained from abdominal fetal electrocardiograms to be used in this research study.

1. INTRODUCTION

Cardiotocography is an essential part of the present-day perinatal medicine, which allows monitoring of the fetus and evaluation of its state during pregnancy and labor. This method relies on recording of the fetal heart rate signal (FHR) in relation to the uterine contractions and fetal movement activity. At the beginning of 70s, the ultrasound Doppler technique was introduced for obtaining the FHR signal [6][9]. The representation of FHR data accessible on the fetal monitor output depends on the Doppler signal processing method implemented. The main commonly used technique is autocorrelation function which, among many advantages, has one primary drawback - it does not provide any information on heartbeat occurrence in time, but in natural way it delivers the evenly spaced FHR measurements [8]. From the physiology of the fetus, the FHR can reach up to 240 bpm (beats per minute), which corresponds to beat-to-beat interval T = 250 ms. Thus, not to lose any interval the consecutive values of FHR are determined and provided on the monitor output at least every 250 milliseconds. This sampling rate is used in bedside monitors as an established standard.

Considering the time-domain analysis of FHR, the most important diagnostic information is connected with indices which quantitatively describe the so called short-term and long-term variability of the fetal heart rate [1]. Those indices were defined over one-minute intervals on a basis of direct invasive fetal electrocardiography [7]. As it has been proved the accuracy of the short-term variability indices is very low when they are calculated using the evenly spaced FHR measurements obtained by ultrasound

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Doppler [5]. To improve this accuracy it is necessary to convert the evenly spaced measurements into a form of time series of events – consecutive T intervals.

The FHR values from a normocardia range (110 ÷ 150 bpm) correspond to 545 ÷ 400 ms, therefore the measurement repetition of 250 ms causes that one singular beat-to-beat interval can be represented by more than one measurement. These additional values are called duplicated measurements. In this work, we have proposed a method which removes duplicated values in order to ensure an accurate extraction of the time series of events from the evenly spaced measurements. Normally, when using the Doppler method, we have no possibility to access the reference signal. In such case, efficiency of the algorithm can be estimated only through comparing the signal duration calculated by multiplying the number of measurements by repetition period with the sum of resulting intervals [4]. Therefore, in this study we used the FHR signals acquired by the fetal electrocardiography that enables their representation both as reference event series and corresponding evenly spaced measurements (obtained by sampling of the event series with 250 ms period). Having reference signal, it was possible to carry out reliable statistical analysis of the results obtained and estimate the efficiency of the algorithm.

2. METHODOLOGY

The research material comprises the real electrocardiography records indirectly acquired from the maternal abdomen using the Komporel system developed in our Institute, which ensured the FHR measurement resolution of 1 ms [3]. Only the recordings without signal loss with duration of at least 20 minutes, which corresponds to typical monitoring session, were classified for further analysis. In such way, 10 records were obtained, whose number of intervals varied from 2400 to 3000 (2680 in average). Each FHR signal recorded by the system is provided both in a form of event series corresponding to consecutive cardiac cycles and as evenly spaced samples (every 250 ms). Figure 1 presents an exemplary segment of FHR record where duplicated samples to be removed are marked by a dotted line.

The algorithm is aimed at as accurate as possible determination of the number of true beat intervals represented by the signal samples. Figure 2 shows a segment of the FHR signal with duplicated samples. It contains four consecutive samples (2 to 5) of the same value: 425 ms (case A) and 380 ms (case B). The dotted line follows the expected signal in form of event series. In case A, it can be noticed that the sequence of four samples with 450 ms value is represented by two consecutive intervals of the same duration. It is only one correct interpretation of such combination of number and value of the samples considered. It is caused by the fact that neither singular interval of 425 ms nor three intervals of total duration of 1275 ms can be represented by 4 samples spaced at 250 ms regardless the sampling phase.

Example with one interval is obvious, since four samples comprise much longer time period than the interval value does. Example with three intervals is illustrated by case A", where even for the most

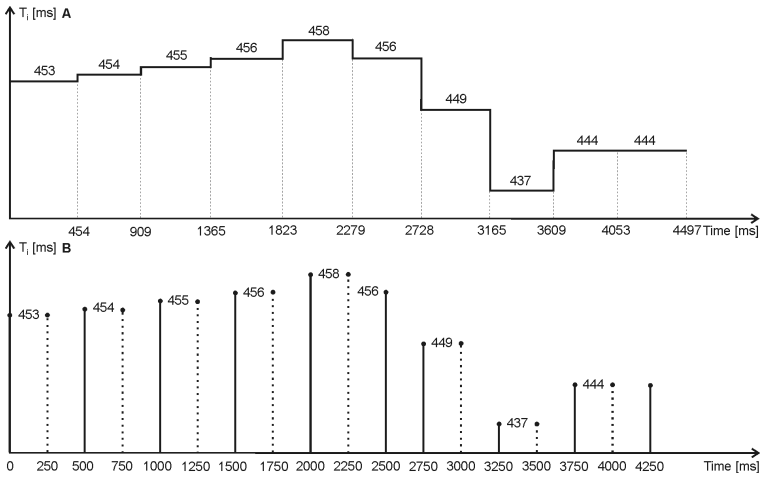

Fig. 1. Segment of the FHR signal in a form of time event series (A) and the corresponding evenly spaced samples (250 ms) (B).

preferred sampling phase (the considered intervals start just after the sample no. 1) the sample no. 6 takes incorrect value. Hence, four samples (425 ms each) represent two intervals in fact, whereas two samples recognized as being duplicated have to be removed during extraction of time event series. Unfortunately, not every sequence of samples can be as easily interpreted as in the above example. Four samples of 380 ms value may, depending on the established phase, represent both two (B') and three (B") intervals.

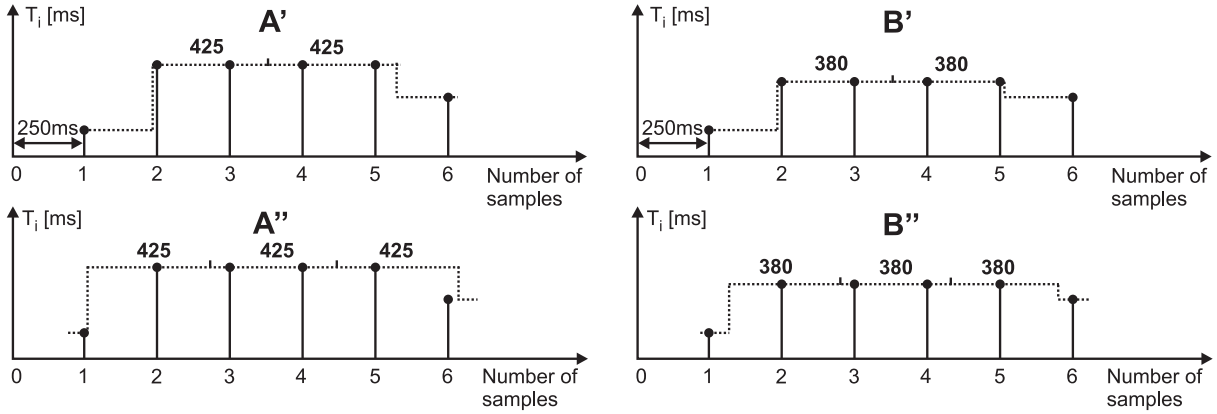

Fig. 2. Segments of the FHR signal in a form of sample series spaced at 250 ms including duplicated samples. Sequences of four equal samples of value 425 ms (A) or 380 ms (B) are presented together with two hypothetical interpretations for each of them (represented by the dotted lines).

The simplest ad-hoc method to remove duplicated samples is to replace every series of samples of the same value with only one sample, considering the remaining samples as duplicated. Further part of this paper shows the results obtained with the simple algorithm, in order to compare them with the new proposed algorithm for identification and removal of duplicated samples. The idea of proposed algorithm is presented in Figure 3, together with results obtained for signal segment from Figure 2B. The value of particular variables assigned for the given input data are put in shaded rectangles. The table Ts includes the consecutive signal samples expressed in milliseconds.

In the first step of this algorithm, two consecutive samples of the same value are searched. Until this occurs, every consecutive sample is stored in the array Te, which will store the resulting event series after the algorithm completes. Once two identical samples are found, the initial $Size\_series$ is set at value of 2, and then incremented with every consecutive sample of the same value. When the analyzed samples have different values, the number of valid intervals is estimated basing on the sample series of current size. In the analysed example the series consists of 4 samples of 380-ms value. The values of Min and Max are determined, and they define the range containing the number of intervals being searched.

Since the number of intervals has to be an integer the Min and Max values as being real numbers must be rounded up and down respectively. If $Round\_up(Min)$ and $Round\_down(Max)$ are equal they define a unique and correct number of intervals. Otherwise, the integer value is chosen whose rounding error ($delta\_Min$ or $delta\_Max$) is larger, because probability of a given value occurrence in relation to the sampling phase is higher for the value of larger round-off error (Figure 2B).

Analyzing the four samples of value 380 ms, the number of correct intervals can be 2 or 3 ($Min = 1.97$ and $Max = 3.29$). Corresponding rounding errors are equal to $delta\_Min = 0.03$ and $delta\_Max = 0.29$ respectively. So, the algorithm takes the correct $Number = 3$ as much more probable. Considering event series shown by dotted line it can be seen, that slight change of the sampling phase does not affect the number of samples and thus 3 intervals will be still represented by 4 samples. Alternative $Number = 2$ refers to very special case, when even a slight shift of the sampling phase of 2 intervals of duration 380 ms leads to 3 samples obtained. For the phase in a range from 0 to 249 ms, the $Number = 2$ refers to only 4.4 % of cases where 2 intervals are represented by 4 samples. In turn, the $Number = 3$ means 43.6 % of cases where 3 intervals are represented by 4 samples.

When considering four samples of 425 ms value (from Figure 2A) we obtained $Min = 1.76$ and

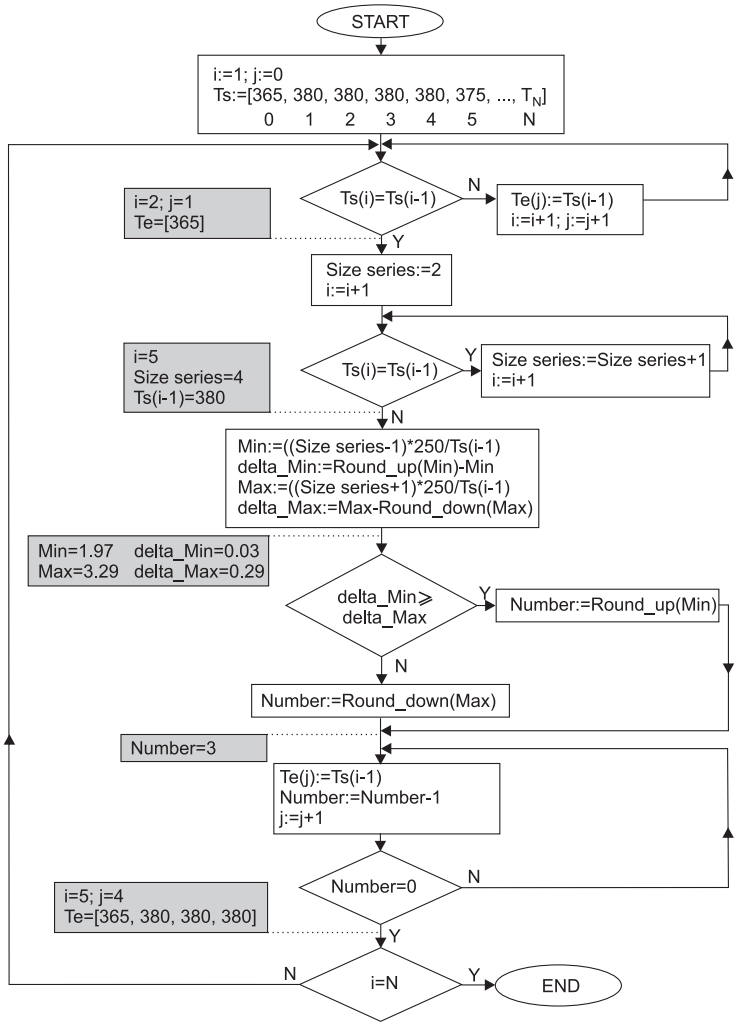

Fig. 3. Algorithm for identification and correction of the duplicated samples.

$Max = 2.94$ which define, without any doubt, the number of correct intervals equal to two. In the last stage of the algorithm the correct intervals are stored in the array of the event series Te and then it is checked if the whole record was analyzed.

3. RESULTS

Descriptive statistics of ten signals together with the results of the proposed correction algorithm are presented in Table 1. The signals include 26800 intervals in total. For the signals represented as samples, most of the intervals are represented by more than one measurement (the duplicated samples occur), which results in 45277 of samples. The number of duplicated samples depends on the value of sampled intervals, and for our data its percentage in relation to the true number of intervals was equal to 68.9% on average. The lowest number of duplicated samples – 52.4% was noted in record 7, whereas the highest one – 86.7% in record 3. Considering the analysis of FHR variability on beat-to-beat level, such amount of redundant and false information is unacceptable. The simplest approach for removing of the duplicated samples is to replace every sequence of samples of the same value with one sample. The other samples in this sequence are considered as duplicated and thus rejected. However, this simple algorithm does not provide satisfying results, since for the material collected, as much as 24% of correct intervals were removed. Depending on the signal, it led to signal loss from 11.7% for record 10 to 31.7% for record 6.

The number of intervals obtained using our new algorithm – 26856, is very close to the reference

Table 1. Results of FHR signal correction provided by both simple and the new proposed algorithm.

Record No.	Intervals	Samples	Intervals (simple algorithm)	Intervals (new algorithm)	Sequences	Sequences with one solution	Erroneous corrections	Erroneously rejected	Erroneously accepted
1	3000	4608	2188	3026	1447	1191	54	14	40
2	2700	4617	1869	2699	1506	1450	9	5	4
3	2400	4481	1988	2404	1787	1777	4	0	4
4	2700	4681	1988	2696	1602	1556	4	4	0
5	2700	4669	2113	2704	1672	1646	4	0	4
6	2800	4642	1913	2804	1460	1392	12	4	8
7	2400	3659	1762	2408	1139	861	22	7	15
8	2800	4607	2206	2807	1599	1507	25	9	16
9	2800	4681	2135	2806	1590	1522	10	2	8
10	2500	4632	2208	2502	1855	1841	2	0	2
Total	26800	45277	20370	26856	15657	14743	146	45	101

number – 26800. It should be noted however that the estimation of algorithm efficiency when based on criterion of resulting number of intervals is not reliable due to two types of possible error that can occur. For every sequence of the analyzed samples of the same value the algorithm can either leave or remove one interval too much. Therefore, in this study the reference FHR signal was provided, which enabled more detailed error analysis. In Table 1, both types of errors are listed and their total number for each signal is provided. When analyzing the results for all signals, we concluded that the algorithm made 146 erroneous corrections in all 15657 analyzed sequences of samples, which constitutes 0.93% of all corrections. It should be noted, that for substantial number of the sequences being analyzed the algorithm provided only unique correct number of intervals, that did not required the probability criterion to be applied additionally. Number of such cases was as much as 14743 that leads to 94.2% of all sequences analyzed.

Considering particular signals, it can be seen that the highest number of erroneous corrections was obtained for record 1 (3.73%). What is interesting, in this signal the percentage of sequences giving the unique solution was not the lowest one and equal to 82.3%, whereas for the record 7 only 75.6%. Such analysis, when error value is related to the number of sequences, generally well estimates the algorithm efficiency, however taking into account the FHR analysis, it seems that more reliable is to relate the result to the number of reference intervals in the signal. Using such approach, only 146 erroneous corrections occurred for total number of 26800 intervals which means 0.54%. For the mentioned above record 1, with the highest number of erroneous corrections, the error was equal to 1.8%. Obtained results confirmed high efficiency of the proposed algorithm for removing the duplicated samples.

The probability of incorrect interpretation of sequences in relation to their length and sample values was analysed in details. For this purpose the equations for determining the number of real intervals (Min, Max) were solved for different combinations of input data: the sequence length ($Size\_series$, between 2 and 10 samples) and the value of samples in sequence (Ti, from 250 ms to 1000 ms with 1 ms step). For each combination of $Size\_series$ and a given sample value Ti two values $Round\_up(Min)$ and $Round\_down(Max)$ were calculated. If these values are equal then the probability of correct interpretation of the sequence is 100%. In other cases the probability of correct interpretation was calculated on a basis of $delta\_Min$ and $delta\_Max$ values, according to the formula (1).

$$p = \frac{\max(delta\_Min, delta\_Max)}{delta\_Min + delta\_Max} \cdot 100\% \tag{1}$$

On Figure 4 the probability of correct interpretation is presented as a function of interval values for sequences of different length. Only the most frequent sequence lengths (from 2 to 6 samples) were depicted. The gaps in the traces are related to the situations when a given combination of $Size\_series$ and sample value Ti cannot exist, e.g. four samples of value 720 ms.

Distribution of the analyzed sample sequences in relation to their length together with the number of erroneous correction made by the algorithm is presented in Table 2. The vast majority of errors

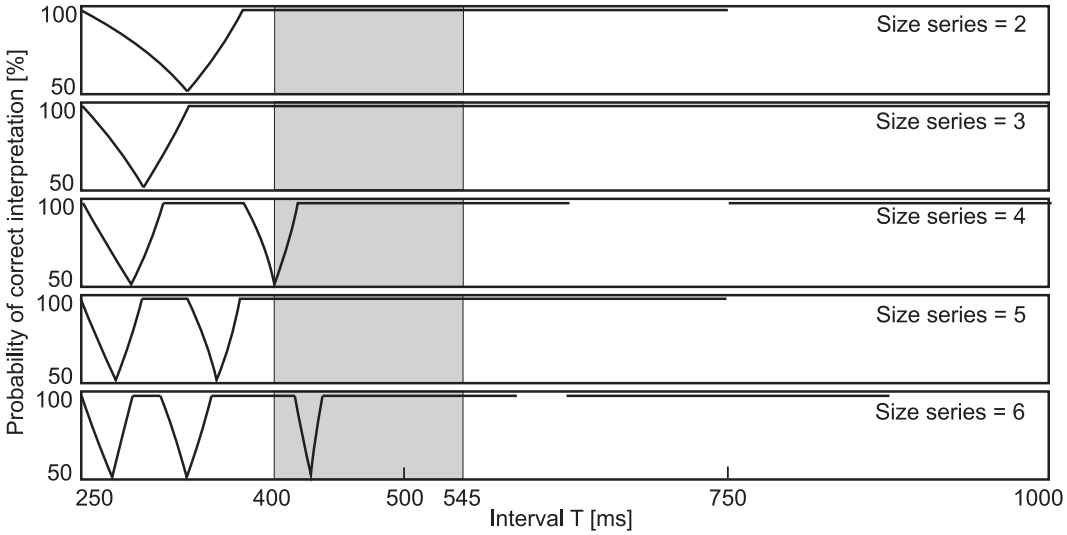

Fig. 4. The probability of correct interpretation of a sequence in relation to its length ($Size\_series$) and interval value (T). The normocardia range was additionally marked with grey.

Table 2. The distribution of sample sequences in particular recordings with regard to their length (from 2 to 10 samples) together with the global results.

Records	Length of sequence								
	2	3	4	5	6	7	8	9	>= 10
1	892/12#	344/0	94/35	66/6	31/0	9/1	4/0	6/0	1/0
2	993/0	200/0	131/7	101/0	29/2	25/0	13/0	9/0	5/0
3	1452/0	88/0	182/4	20/0	37/0	4/0	3/0	0/0	1/0
4	1178/1	151/0	142/2	68/0	19/0	18/0	8/0	8/1	10/0
5	1234/0	181/0	145/2	76/0	13/2	14/0	2/0	5/0	2/0
6	897/0	253/0	115/12	122/0	14/0	35/0	10/0	5/0	9/0
7	740/7	233/0	73/14	50/0	25/0	8/1	6/0	3/0	1/0
8	1159/1	242/0	107/21	57/1	11/0	11/1	10/0	1/1	1/0
9	1131/0	213/0	115/6	78/0	16/3	21/1	9/0	6/0	1/0
10	1499/0	215/0	92/0	33/0	10/2	5/0	1/0	0/0	0/0
Σ	11175/21	2120/0	1196/103	671/7	205/9	150/4	66/0	43/2	31/0
Σ[%]	71.4/14.4	13.5/0	7.6/70.5	4.3/4.8	1.3/6.2	1.0/2.7	0.4/0	0.3/1.4	0.2/0

the number of segments with a given length / the number of erroneous corrections

(up to 70.5%) was noted for the sequences of 4 samples of the same value. It is caused by the fact that, taking into account the most common range of FHR variability – normocardia which covers the values from 400 to 545 ms, the analysis of the sequences of 2 or 3 samples spaced at 250 ms always returns the unique result, and there is no need to use additional probability criterion. Otherwise, in case of 4 equal samples in sequence, in the range of 376 to 416 ms, the probability criterion decides on the result selected. For the interval value of 400 ms, the probability of selection of correct result ($Round\_up(Min)$ or $Round\_up(Max)$) reaches only 50% (as shown on Figure 4) , and causes a higher number of algorithm errors. For longer sequences the interval ranges, for which the probability criterion has to be applied, also occur. However, even if they fall into the normocardia range they are not as wide as for the 4-sample sequences (41 ms). What is more, 4-sample sequences occur in the FHR signals quite often – 7.6% of all cases, whereas all the longer ones stand for 7.2%. All these facts are responsible for the highest number of erroneous corrections made by the algorithm in the sequences of 4 samples.

4. CONCLUSIONS

The indices describing quantitatively both the beat-to-beat fetal heart rate variability and the long-term tendency of these fluctuations have been considered as the most significant for a prediction of the fetal wellbeing. These indices were defined in 70s on the basis of invasive fetal electrocardiography providing the signal in a form of time event series. Nowadays, the widely used monitoring instrumentation is based on the Doppler ultrasound technique and provides signal in a form of evenly spaced samples. In this work, the method for processing of FHR was proposed, which enables extraction of a series of consecutive intervals Ti from the sampled signal. The correction is aimed at recognition and removing of the FHR distortions typical for bedside monitors – duplicated samples. Efficiency of the algorithm for removing the duplicated samples was estimated basing on FHR signals obtained from fetal electrocardiography which provided reference event series.

When applying the simple algorithm, which replaces every sequence of samples of the same value with one sample, on average as much as 24% of valid intervals was removed. It makes this approach practically useless for reliable FHR analysis. In case of the algorithm proposed there are possible two erroneous corrections of every analyzed sequence: one valid interval is removed or one incorrect is left. Yet, the total number of such corrections in relation to the number of reference intervals was equal to 0.54%. Although in [2] the reported results show no error in extraction of the time event series, but such perfect results seem to be obtained thanks to the methodology used. The authors evaluated their algorithm on a basis of simulated FHR signals (in form of event series) which were afterwards sampled with 250 ms period. What is important the event series was always sampled synchronously with the beginning of the first interval T. In case of real FHR signals acquired using ultrasound Doppler technique the beginning of a given heart cycle can be shifted in relation to the signal sample by an unknown value between 0 and 249 ms. Without the assumption of synchronous sampling the algorithm [2] would also interpret some sequences erroneously.

The results obtained in this paper provide evidence for usability of the developed correction algorithms for fetal heart rate in the computerized fetal monitoring system as some kind of preprocessing stage carried out before the procedure for determination of indices describing the FHR variability.

ACKNOWLEDGEMENT

This work was financed in part by the Polish National Science Centre.

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