A fetal heart rate morphological analysis toolbox for MATLAB

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Original software publication

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ABSTRACT

The fetal heart rate (FHR) is a screening signal for preventing fetal hypoxia during labor. When experts analyze this signal, they have to position a baseline and then identify decelerations and accelerations. These steps can potentially be automated and made more objective by signal processing analysis. Various methods have been described in the literature but there are no open-source programs for performing these steps. The MATLAB toolbox presented here comprises a standard signal pre-processing function, 12 re-coded literature methods for fetal heart rate analysis, a signal viewer (enabling annotation by an expert) and an evaluation procedure with various criteria.

Software metadata

Current software version	V1.1c
Permanent link to executables of this version	https://github.com/utsb-fmm/FHR
Legal Software License	GPL v3.0
Computing platform / Operating System	MATLAB
Installation requirements & dependencies	Signal processing toolbox
If available Link to user manual — if formally published include a reference to the publication in the reference list	http://utsb.univ-catholille.fr/fhr-review
Support email for questions	samuel.boudet@univ-catholille.fr

Code metadata

Current Code version	V1.1c
Permanent link to code / repository used of this code version	https://github.com/ElsevierSoftwareX/SOFTX_2018_217
Legal Code License	GPL v3.0
Code Versioning system used	git
Software Code Language used	MATLAB
Compilation requirements, Operating environments & dependencies	Signal processing toolbox
If available Link to developer documentation / manual	http://utsb.univ-catholille.fr/fhr-review
Support email for questions	samuel.boudet@univ-catholille.fr

1. Motivation

The fetal heart rate (FHR) is a key parameter for monitoring fetal well-being during pregnancy, labor, and delivery. A good interpretation of FHR is important to reduce unnecessary cesarean section and operative delivery rate while reducing risk of fetal acidosis. Analysis of the FHR first consists in determining several elementary parameters: the baseline (i.e. the mean level of the most horizontal, least oscillatory FHR segments [1]), the variability (i.e. variations in amplitude during stable periods, in the absence of fetal movement or uterine contraction), acceleration episodes (i.e. an abrupt increase in the FHR of more than 15 beats per minute (bpm), and lasting more than 15 s), deceleration episodes (i.e. a temporary decrease in the FHR of more than 15

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bpm, and lasting more than 15 s), and sinusoidal patterns [1]. According to the *International Federation of Gynecology and Obstetrics (FIGO)* classification [1], an FHR recording is said to be normal if (i) the baseline ranges from 110 to 160 bpm, (ii) the variability ranges from 6 to 25 bpm, and (iii) there are accelerations but no deceleration (an acceleration is considered to be a reassuring feature of the FHR but a deceleration is not.)

The interpretation of FHR signals is subject to considerable inter-observer and intra-observer variability [2], as a result of sometimes imprecise assessment criteria and a lack of practical training. Automatic analysis could remove this variability and thus improve the prediction of the risk of hypoxia during the delivery. When attempting to analyze the FHR automatically, the main problem is computation of the baseline against which all the other parameters are determined. The baseline is defined by the FIGO as "the mean level of the most horizontal, least oscillatory FHR segments". However, it is not clear how these segments should be selected in clinical practice and, especially, using automatic analyses. In addition to the horizontality and the amount of oscillation, other criteria influence the choice of the segments: these include (i) the segment's duration (baseline segments are generally longer than the acceleration/deceleration (A/D) segments), (ii) differences in level (bpm) and duration between successive baseline segments (rapid, substantial changes in baseline level are rare), and (iii) synchronization with contraction (deceleration is usually the consequence of a contraction).

Several researchers have developed automatic analysis methods (AAMs) (some review on [3,4]). Unfortunately, there are almost no open-source programmed versions of any algorithms or standard tools for displaying FHR analysis and measuring each method effectiveness. The recently released MATLAB toolbox CTG-OAS [5] provides processes for automated cardiotocography-analysis, such as the computation of morphological, linear, non-linear, and time–frequency features. It also includes a predictive model of acidosis. However, it appears that CTG-OAS's baseline algorithm (i) has not been compared with those of other methods and (ii) has not been evaluated by expert physicians.

A key problem in FHR signal processing is the lack of a common, expert-annotated database. Each researcher has to perform his/her own evaluation and there are no common evaluation criteria. Here, we describe a MATLAB toolbox which gives some tools to tests, display and evaluates the various method of literature as well as future method. 11 methods of literature have been re-programmed in this way.

This work is related to three previous publications [4,6,7] . Sample data are also described in [8]. All the data and source code are distributed under a general public license (GPL version 3) and are available at [http://utsb.univ-catholille.fr/fhr-review].

2. Software description

2.1. Software architecture

The FHR Morphological Analysis toolbox works in MATLAB® versions R2017b and higher and requires the signal processing toolbox. Earlier versions of MATLAB® should also work but have not been tested. MATLAB® offers a large number of easy-to-use, built-in functions for mathematics in general, including signal processing. Hence, it is a very efficient software tool for developing new processes, and the majority of researchers working on FHR signal processing use it.

The toolbox has been designed as a modular software package. It includes a graphical user interface (GUI) (to be launched with `fhrmorpho`), which allows its use as a standalone tool. The user selects the FHR file to be opened and the AAM; the interface then displays the corresponding baseline and A/D. An expert can also use the interface to annotate and analyze the FHR recording by drawing a baseline and selecting the beginning and end of each A/D. Indices representing the level of disagreement between the AAM and the expert can then be displayed (see Section 2.2.5).

The toolbox includes a dataset of 156 FHR recordings (described in [8]). Sixty-six of these constitute a training dataset accompanied by an expert consensus analysis. The other 90 recordings constitute an evaluation dataset for which the consensus analysis is private. Researchers who develop new methods of FHR analysis are welcome to submit their AAM analysis (baseline and A/D) for evaluation. A leaderboard will be displayed at http://utsb.univ-catholille.fr/fhr-review.

The toolbox can also be called through a command line interface in MATLAB; it can therefore interact with other toolboxes or software.

2.2. Software functions

2.2.1. Opening an FHR file

Electronic fetal monitors (cardiotocographs) record the signal from a Doppler ultrasound probe or an ECG probe located on the fetus' scalp. This raw signal is used to determine the instantaneous fetal heart rate which is sent to a central computer via an RS232 protocol. We have developed a means of capturing and recording these signals [9]. All signals are sampled and stored at 4 Hz, with a precision of 0.25 bpm for the FHR and 0.5 mmHg for the tocograph signal (TOCO). Since there is no standard FHR file format, we design our own (which can be opened with the `fhropen` function): (i) A uint32 serves as the UNIX timestamp for the beginning of the recording. (ii) For each sample, (ii.a) a uint16 encodes the FHR from the first sensor (multiplied by 4), (ii.b) a uint16 encodes the FHR signal from the second sensor (in case of twins or when both Doppler and scalp ECG sensors are present) (x4), (ii.c) a uint8 encodes the tocograph signal (x2), and (ii.d) a uint8 for signal quality (0: no signal, 1: low-quality signal, 2: high-quality signal). The FHR signal is set to 0 when it is missing.

2.2.2. Pre-processing

Standard pre-processing can be performed using the `fhrpreprocess` function: aberrant samples (periods of less than 30 s and with a difference of more than 25 bpm with the next periods) are excluded. Next, a medical expert identified and excluded maternal heart rate segments and unreliable signals. Periods of missing data were completed by linear interpolation.

2.2.3. The automated method analysis

Eleven AAMs from the literature have been reprogrammed; a short description of the main idea behind each AAM is given in Table 1.

Each AAM provides a specific baseline algorithm, and some of them provide an algorithm for A/D detection (as described in the right-hand column of Table 1). We have also added a standard method for A/D detection (`simpleaddetection`) which can be applied to all baseline methods. This standard method simply consists in defining A/D as periods during which the FHR (i) is respectively above or below the baseline for at least 15 s and (ii) reaches a value of at least 15 bpm over the baseline at any moment during that period. This method is cited by Ayres [10] and Pardey [11], and was probably used by Wrobel [12] and Lu [13]. For the `aamcazares`, `aamjimenez`, `aammantel`, `aamtaylor` and `aamwmfb` functions, the user can then choose to perform the standard method or the developer's specific method.

Table 1
Description of the twelve morphological analysis methods in the toolbox.

Function name	First author, year(s) and reference(s)	Main idea for baseline computation	Acceleration/deceleration thresholding described?
aamayres	Ayres de Campos et al. (2000) [10]	Based on "frequent" FHR values in a 10-min moving window.	Yes (= standard thresholding)
aamcazares	Cazares et al. (2002) [14]	Based on morphological filters; an opening filter removes accelerations and a closing filter removes decelerations.	Only described for acceleration (presumably the same for deceleration)
aamhouze	Houzé et al. (1990) [15]	Based on a series of logic rules applied to various signal derivatives, followed by a smoothing step.	No (not described clearly enough to be reprogrammed)
aamjimenez	Jimenez et al.(2002) [16]	Unstable periods (with a derivative above a cut-off) are removed, and the baseline is calculated after smoothing the remaining signal.	Yes
aamlu	Lu and Wei (2012) [13]	A method using empirical mode decomposition; periods exhibiting significant differences between two successive local FHR minima are excluded from the baseline computation.	No (probably standard thresholding)
aammaeda	Maeda et al. (2012) [17]	The baseline is set to the FHR level that occurs most often within a 10 bpm-wide bin.	No (not described clearly enough to be reprogrammed)
aammantel	Mantel et al. (1990) [18,19]	The method uses the mode or another local maximum of the FHR histogram to obtain an initial baseline. The final baseline is obtained by progressively trimming the first baseline (based on Dawes et al.'s [19] method). This method was developed for antepartum recording.	Yes
aammongelli	Mongelli et al. (1997) [20]	This method computes a primary mode and a secondary mode; the two modes can be switched, depending on continuity and frequency criteria.	No
aampardey	Pardey et al. (2002) [11]	The method first uses the histogram's mode or another local maximum. The second baseline is obtained by linear filtering of the FHR and trimming as a function of the first baseline (based on Dawes et al.'s [19] method).	Yes (= standard thresholding)
aamtaylor	Taylor et al. (2000) [21]	A linear low-pass filtering method with progressive trimming.	Yes
aamwrobel	Wróbel et al. (2013) [12]	Based on myriad filters: an intermediate approach, between a linear average filter and use of the mode.	No (probably standard thresholding)
aamwmfb	Boudet et al (2019) [7].	Based on a weighted median filter baseline (WMFB). The weights are set to the prior probabilities that the FHR is in the baseline state. The unstable FHR periods have low probabilities. Successive baselines are computed with a progressive trimming process. Periods far from previous baselines have also low probabilities.	Yes

2.2.4. The viewer

By using the `fhrmorpho` function, the user can open an .fhr file and display it using the specific interface. This interface shows the FHR and TOCO signal on the usual grid, and enables the user to scroll through the recording. The viewer shows the raw FHR (in black) and the pre-processed, interpolated FHR (in gray). If an AAM is selected, the corresponding baselines and A/Ds are displayed. The file's expert analysis can also be displayed (if it exists) or can be created. Creating the expert analysis consists first in drawing a baseline by linear interpolation between designated points. A mouse left click adds a point, and a right click removes a point. Next, the acceleration (A) and deceleration (D) periods can be defined, along with three different types of excluded period: unreliable signal (U), overshoot (O), or a period not to be analyzed (N). These periods are selected by pressing the corresponding keys (A, D, U, O or N) on the keyboard.

It is possible to open two or more windows simultaneously (for each AAM), with synchronized scrolling.

2.2.5. Statistical evaluations

In [4], we described several indices of the discordance between an AAM's analysis and the expert analysis. These indices can be displayed on the main `fhrmorpho` interface for an individual recording (see Fig. 1) or via the `evaluateaam` function, which computes them for a whole set of recordings. The computed indices are summarized in Table 2. In [4], we suggested that the MADI was the best criterion for the overall evaluation of a given AAM; the MADI was designed to give appropriate weight to differences between two analyses, and provides more reproducible results for all FHR files. The MADI is a specifically developed index that corresponds to a fuzzy measurement of the proportion of time during which two baselines suggest that the FHR signal is in the same state (i.e. baseline state, acceleration state or deceleration state).

3. Illustrative example

Fig. 1 shows a screenshot of the main `fhrmorpho` function. Window (A) enables the user to select which methods to display and which file to analyze. Window (C) corresponds to the analysis using Lu et al.'s AAM [13], and window (D) corresponds the expert analysis. This signal show here contains a large number of accelerations (shaded in green). The weighted median filter baseline WMFB method recognizes most of them but adds some spurious decelerations (in pink), due to an incorrect baseline calculation. Window (B) displays the evaluation of the WMFB AAM. One can see that the PPV for deceleration is only 0.158, due to the number of decelerations added by the AAM.

4. Impact

This toolbox was used in studies [4,6] to compare the various literature AAMs by taking as reference an expert consensus. Using the data described in [8], all the experiments can therefore be

Table 2
Criteria used to measure the difference between an automated morphological analysis and an expert morphological analysis [4].

Baseline evaluation	Root mean square difference (RMSD) between baselines *(when A is the method's baseline and B is the expert's baseline, the RMSD is defined as* $\sqrt{\frac{\sum_{i=1}^{n}(A_i-B_i)^2}{n}}$ *)*
	Proportion of points displaying an absolute difference of more than 15 bpm (15 bpm difference rate)
Deceleration detection	Sensitivity (SEN, *the number of correctly detected A/D episodes as a percentage of the total number of episodes defined by expert)*
	Positive predictive value (PPV, the *number of correctly detected A/D episodes as a percentage of all the episodes detected by the AAM.)*
	F-measure *(the harmonic mean of SEN and PPV;* F − Measure $= \frac{2*PPV*SEN}{PPV+SEN}$ *)*
	RMSD between durations *(measures the disagreement between the durations of each deceleration)*
	Mean difference between durations *(measures whether an AAM tends to overestimate or underestimate the duration of a deceleration)*
Acceleration detection	Sensitivity
	Positive predictive value (PPV)
	F-measure
	RMSD between durations
	Mean difference between durations
Overall comparison	Synthetic inconsistency (SI) coefficient [3] *(takes account of the number, location, and area of both accelerations and decelerations, and corresponds to a percentage of the A/D surface difference.)*
	Morphological analysis discordance index (MADI, corresponds to a fuzzy measurement of the proportion of time during which two baselines suggest that the FHR signal is in the same state (i.e. baseline, A or D state). [4]
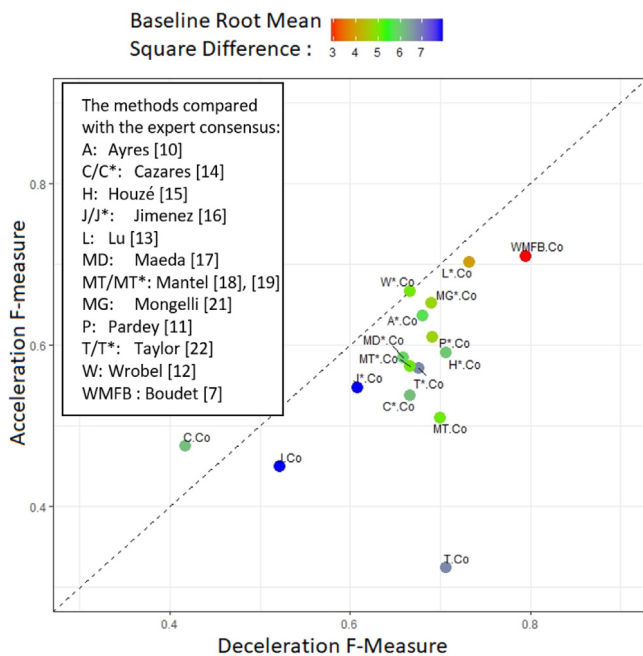
Fig. 2. Performance of each AAM taking as reference expert consensus with regard to three indices (the F-measure for deceleration, the F-measure for of acceleration, and the RMSD for the baseline) [4,7].

repeated. Fig. 2 shows each method's performance with regard to three criteria: the acceleration F-measure, the deceleration F-measure, and the baseline RMSD [4]. Each criterion evaluates a distinct feature of the FHR. The main conclusion of our original study [13] was that Lu et al.'s AAM is significantly better than the 10 other AAMs for reproducing the expert analyses with regard to almost all the criteria studied. More recently, our group developed a new WMFB method that performs significantly better than Lu et al.'s method [7]. However, the estimated baseline was still unsatisfactory for some recordings — suggesting that progress can and should be made before the WMFB method is used in clinical practice.

This toolbox will enable other researchers to (i) reproduce our experiments on the same dataset, (ii) visualize and better understand problematic patterns, and (iii) try to develop new AAMs and test them. The data used in [4,6] (described on [8]) are available at http://utsb.univ-catholille.fr/fhr-review. Researchers who wish to compare their results with others can submit their analysis of the evaluation dataset, and the leaderboard will be displayed on this website.

The toolbox might also be useful for researchers wishing to automatically analyze FHR signals and quantify pathologic features (the number and surface of A/D, the occurrence of tachycardia, etc.). This process might be very important for objectively measuring the effect of treatments during the labor (amnioinfusion, the administration of oxytocin, etc.).

Lastly, the final objective of AAMs for the FHR is to best predict the risk of fetal acidosis and thus provide decision support (caesarean section, operative delivery, etc.). This research requires a huge dataset of deliveries so that the basic outputs of the toolbox (e.g. the number of accelerations, the surface of decelerations, and the base level, etc.) can be used to build a risk score. A few trials have been performed recently [22] but AAMs do not yet significantly improve the decision-making process. We hope that the toolbox presented here will help researchers to build better models.

As a first step towards a risk score for acidosis, it might be useful to try to emulate the classifications used in the guidelines issued by FIGO [1], CNGOF [23], and NICE [24]. These classifications of the acidosis risk differ in some respects but all use the same definitions of baseline accelerations and decelerations. Consequently, the 12 morphological analysis methods could be applied to all three classification systems.

5. Conclusions

The FHR morphological analysis toolbox is an open-source program for researchers seeking to improve signal processing methods or physicians seeking to quantify the pathological FHR features. It offers tools of preparatory work on this subject: data, a pre-processing function, display functions, and evaluation functions.

The toolbox focuses solely on morphological analysis. In future research, we shall program indices for evaluating FHR variability
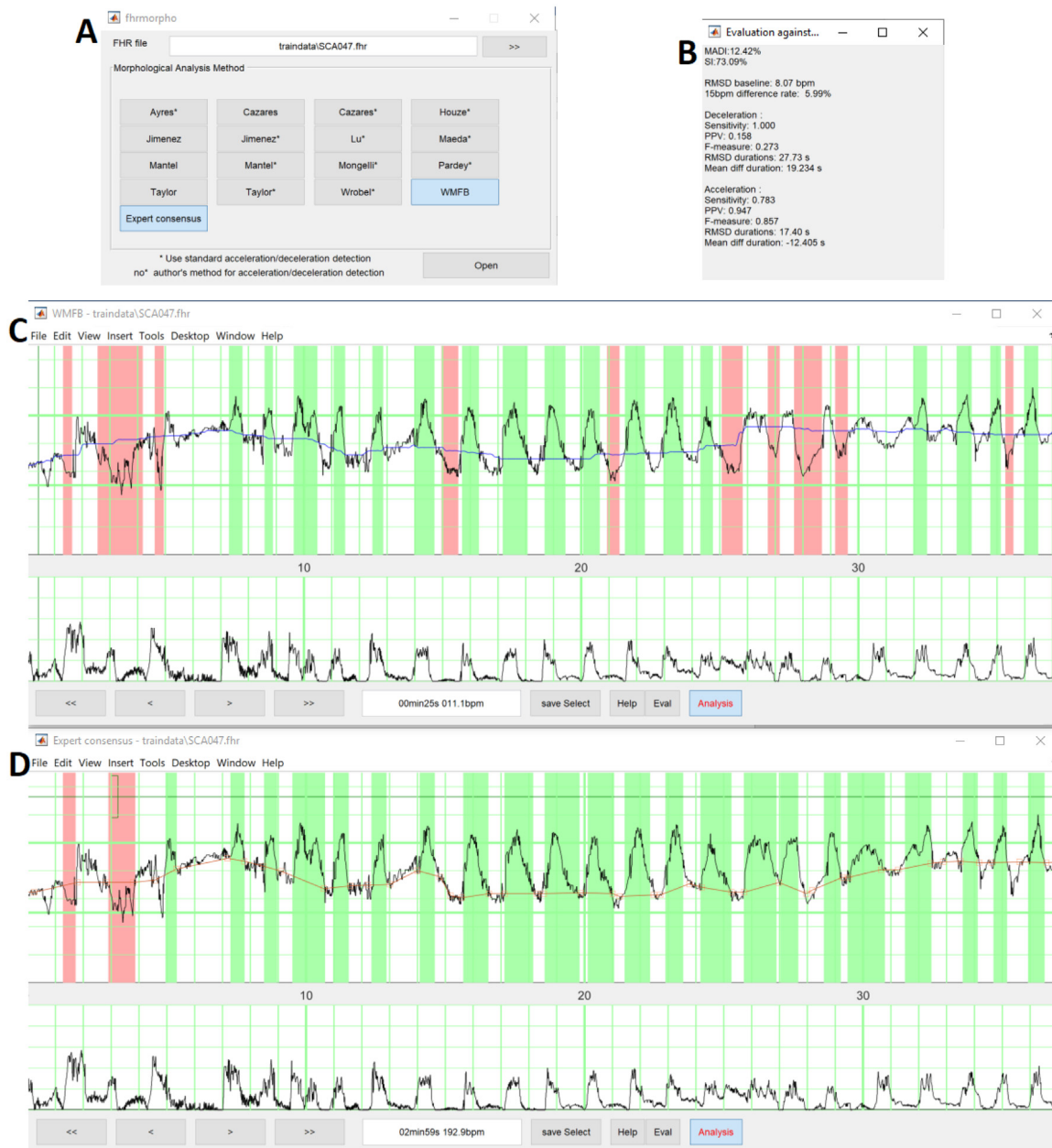
Fig. 1. Illustration of the main fhrmorpho interface: (A) the main window, (B) the disagreement evaluation for the WMFB method vs. the expert consensus, (C) the WMFB method's analysis, (D) the expert consensus analysis. . (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

and dynamics, which are other features used to predict fetal acidosis. The final objective is to develop a predictive model of fetal acidosis.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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