Introducing Grammatical Evolution in Fetal Heart Rate Analysis and Classification

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Abstract—Electronic fetal monitoring is an essential tool for fetal surveillance during labor. It is mainly based on the monitoring and evaluation of the Fetal Heart Rate (FHR) signal, which has to be interpreted online. Evaluation and interpretation of FHR gives an indication of the fetal condition. A lot of research efforts have been done towards the development of automatic and reliable methods for processing and evaluating FHR. This research work introduces an integrated methodology for processing and classifying FHR based on the novel approach of grammatical evolution for feature construction and selection. The proposed methodology is presented, and it is applied to a data set. Experimental results are promising paving the way for further research in that direction.

Index Terms—Fetal heart rate, Genetic algorithms, Grammatical evolution, Hypoxia, Neural Networks, SMOTE

I. INTRODUCTION

Electronic Fetal Monitoring (EFM) consists of the continuous recording and monitoring of the instantaneous Fetal Heart Rate (FHR) (beats/min) and Uterine Activity (UA) that are called cardiotocogram (CTG). The typical printout of a CTG has the FHR at the upper part and the UA at the lower part for the same time axis (Fig. 1).

Obstetricians evaluate and interpret the CTG to infer about the fetal health condition so as to avoid neonatal compromise, namely metabolic acidosis [1]. The medical device, which is used to acquire, process, display and print out the FHR and UA signals, is the cardiotocograph.

Despite the fact that EFM was introduced into clinical practice more than four decades ago, there is still controversy regarding its effectiveness, especially among obstetricians. Another important issue is that statistical studies revealed an increase in operative vaginal deliveries when obstetricians are heavily depend on EFM to infer fetal condition [2]. Furthermore, studies on the FHR analysis and interpretation by obstetricians have shown significant inter-observer and intra-observer variation in tracing interpretation [3]. Even though specific guidelines have been published for FHR interpretation [4], [5], the different levels of experience of the various specialists, along with the subjectivity of the approach, have great influence on their final judgment. All these reports have created a mistrustful environment for FHR monitoring and interpreting methods.

There is a difficulty in distinguishing benign variant patterns from patterns associated with significant fetal acidemia. This may be caused because FHR monitoring was introduced into clinical practice before the physiological mechanism, which defines the FHR patterns was well understood.

On the other hand, there is an increasing need for automated methods for FHR processing and analysis that drives the development of computer based systems able to analyse, classify and interpret the FHR [7]-[30]. These approaches are based on classical signal processing methods, Neural Networks, Fuzzy logic and hybrid methods. Some of these efforts tried to develop a system not to just record the FHR, but to monitor the fetal health condition in a reliable, effective and reproducible manner. These research efforts have shown that it is still worth to further investigate methods to analyze the FHR not just by imitating the way a clinician does, but by employing techniques based on the signal processing and pattern recognition fields.



Fig. 1. A simple cardiotocogram (printout) consisting of the FHR at the upper part and UA at the lower part.

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In this research work we introduce a new integrated methodology for feature extraction and classification of the FHR. The proposed methodology uses the conventional well known method to identify the FHR features in the time domain, frequency domain and morphological features. Due to the imbalanced data set employed, which may induce a bias towards the class with the greatest number of instances, we introduce a stage of creating "synthetic" features for the undersampled class based on the original data belonging to that class, with the procedure of Synthetic Minority Oversampling Technique (SMOTE) [31]. Then, the grammatical evolution technique is applied to the balanced feature sets to produce new features and classify the FHR simultaneously with a hybrid approach for training the neural network classifier.

This paper is structured as follows; section II gives a brief introduction to the grammatical evolution method. Section III presents the overall proposed procedure and its main stages. Section IV presents the implementation and validation of the proposed methodology based on the grammatical evolution method and section V analyses and compares the experimental results in the FHR data set. Finally section VI concludes the paper and some ideas for future work are discussed.

II. GRAMMATICAL EVOLUTION

Grammatical evolution is a method that uses genetic programming and a Backus-Naur form (BNF) description to create programs in an arbitrary language. In grammatical evolution, chromosomes are a series of production rules of the appropriate BNF syntax. Each bit of the chromosome denotes a production rule from the BNF grammar. The algorithm starts from the first symbol of the grammar and gradually creates the program string by replacing nonterminal symbols with the right hand of the production rule [32], [33]. The selection of the appropriate rule is performed by using the scheme:

$$Rule=BmodRN$$
 (1)

where B is the specific chromosome element and RN is the number of rules for the specific non-terminal symbol. This selection process is repeated and it stops when the end of the chromosome has been reached. When newly constructed features have been created, a new training and test set are created from the original data set, according to the new features. The newly constructed feature is assigned a fitness value, which in this case is the test error of a supervised classifier. According to that fitness value, the newly constructed feature will be accepted or rejected in the successive generations.

The grammar of the proposed method uses mathematical functions and operators as non-terminal symbols and the original features $(x_1, x_2, ..., x_n)$ and the digits (0-9) as the terminal symbols. In the proposed method the sin, cos, exp and log functions are used but any other function can be utilized. More details about the proposed method can be found in [33].

An example of this grammar can be seen below:

S	::= <	expr>
<expr></expr>	::= <	expr> <op> <expr> <func> (<expr>)</expr></func></expr></op>
		$<$ digit> $ x_1 x_2 \dots x_n $
<op></op>	::=	+ - * /
<func></func>	::=	sin cos exp log
<digit></digit>	::=	0 1 2 9

Grammatical evolution is used to construct new artificial features reducing the number of the features. This allows the construction of a very small number of features (e.g. 2 or 3), which can achieve good classification performance. By constructing a small number of features, the well known problem of curse of dimensionality is alleviated.

III. OVERALL PROCEDURE

The overall proposed procedure is an integrated approach taking as input the FHR and classifying it, making a prediction about the pH value of the fetus. Fig. 2 depicts the overall procedure consisting of five stages, where the last one stage validates the proposed methodology [35].



Fig. 2. The overall procedure

A. Preprocessing stage

The FHR is a noisy signal due to the acquisition method employed and also due to extraneous interferences that cannot be isolated. Although the missing or "spiky" parts do not provoke serious difficulties to simple eye inspection and interpretation, they may lead to wrong results when digital processing is applied to FHR. Therefore, it is necessary to remove the "spiky" segments or segments where the signal is zeroed by employing a pre-processing stage. The pre-processing stage firstly detects a stable FHR segment, which is defined as a segment where the difference (in beats/min) between five adjacent samples is less than 10 beats/min [17]. Whenever a difference between adjacent beats higher than 25 beats/min is found, a linear interpolation is applied between the first of those two signals and the first signal of a new stable FHR segment.

B. Feature extraction stage

Feature extraction is the most important phase during the development of any classification system. As it is pointed out in [34], it is more an art than a science. Therefore sometimes it is worth testing a number of features to select an appropriate set. In this work the selection it is performed through the feature construction phase, which has the intrinsic ability to reject irrelevant features.

Since we are dealing with a time series signal, it is natural to extract features from both the complementary domains of time and frequency. In addition to this, from the medical point of view, there are a number of "morphological" features that are evaluated by the clinician in charge [35]. Thus the extracted features can be classified into 3 categories:

- Features extracted in time domain
- Features extracted in frequency domain
- Morphological features

1)Time domain features

Seven time parameters of FHR signal are calculated in the time domain and are used as features. The set of parameters and their definitions are given bellow.

- Mean value of FHR signal
- Standard deviation of FHR signal

• Delta=
$$\frac{\sum_{i=1}^{m} \left| \max\left(FHR(i)\right) - \min\left(FHR(i)\right) \right|}{m}$$

where max and min are computed within each minute of the signal and m is the number of minutes

•
$$STV = \frac{\sum_{i=1}^{24} \left| sFHR(i+1) - sFHR(i) \right|}{24}$$
, where

sFHR(i) is the value of the signal FHR(i) taken each 2.5 sec (i.e. once each 10 samples) (Short Term Variability)

•
$$II = \frac{STV}{std[sFHR(i)]}$$
 (Interval Index)

distribution

• *LTI* is defined as the interquartile range

 $\left[\frac{1}{4}, \frac{3}{4}\right]$ of

with

the

m(j)

$$m(j) = \sqrt{FHR^2(j) + FHR^2(j+1)}$$
 (Long Term
Irregularity)

Delta_total=max(FHR(i)) - min(FHR(i))

The above time domain parameters were successfully used in the anteparum case [20], [21], therefore it was reasonable to assume that they may also perform well in the intrapartum case

2) Frequency domain features

Contrary to what is in effect for adults, in the case of FHR, there is no standardized use of frequency bands. In this work we experimented following suggestions of [6], partitioning the frequency range into 4 bands and calculating the corresponding energies:

- the Very Low Frequency (VLF) 0-0.03 Hz
- the Low Frequency (LF) 0.03-0.15
- the Movement Frequency (MF) 0.15-0.5 Hz
- the High Frequency (*HF*) 0.5-1 Hz

As a fifth feature for this feature set we used the ratio:

• LF/(HF + MF)

3) "Morphological" features

Conventional interpretation of FHR is based upon certain morphological characteristics, according to the guidelines given in [4] and [5]. In this work we included the following set of morphological parameters:

- Baseline
- Number of accelerations
- Number of Small accelerations
- Number of Mild decelerations
- Number of Prolonged decelerations
- Number of Severe decelerations
- The percentage of the time occupied by decelerations

A detailed description of these features can be found in [35], [36].

C. SMOTE Stage

In this work, the data set consisted of 160 recordings. The recordings were collected in the context of the Research Project POSI/CPS/40153/2001, funded by Fundação para a Ciência e Tecnologia, Portugal. The data recordings had various lengths, ranging from 20 minutes to more than 1 hour. Regarding the recordings, 137 of them were acquired using an HP 1350 fetal monitor at a sampling frequency of 4 Hz, and 23 were acquired using a Toitu MT810B. In both cases, scalp electrodes were used for the acquisition, giving more accurate recordings [37]. The latter recordings were irregularly sampled and had to be transformed into "pseudo-regularly" sampled signals [38].

The data set consisted of 130 recordings belonging to fetuses with umbilical artery pH>7.2, which represent the "normal group" while the rest 30 having pH<7.1 consisted the "at risk" group of fetuses. As is obvious this segregation of data has an intrinsic imbalance and if no precautions are taken, the construction of the classifier may favor the class with the greatest number of instances, which in this case is the class with the normal subjects. In order to alleviate this problem we adopted the technique of Synthetic Minority Oversampling Technique (SMOTE), which creates "synthetic" instances for the undersampled class based on real data belonging to that class [31].

The algorithm for each instance of the minority class introduces a synthetic example along any/all of the lines joining that particular example with its k nearest neighbors that belong to the minority class. A representative example for the application of SMOTE on some artificial data is depicted in Fig. 3.



Fig 3. The minority class in marked with circles and the majority class with squares. The black circles indicate the original minority data while the grey circles indicate the produced ones. In the above example it is assumed that we want 200% oversampling and that the neighbourhood of each minority consists of 5 samples.

For this particular data set, we used 8 nearest neighbours and an oversampling percentage of 400%.

IV. FEATURE EXTRACTION AND CLASSIFICATION

After the SMOTE stage, there are available balanced feature sets ready for the grammatical evolution stage. The feature extraction and classification algorithm itself is divided into two phases: the construction and the evaluation phase.

A. Construction Phase

A new artificial set of features is derived from the original feature set using a combination of grammatical evolution and a neural network. The Feed Forward Multi Layer Perceptron with one hidden layer and one neuron is used. The network is trained using a Powell's BFGS variant algorithm [38]. The grammatical evolution is used to construct the features utilizing a non-linear mapping from the original ones. The training error of the neural network described above is used as the fitness function for the grammatical evolution procedure. In order to reduce the computation time, only a small number of steps in the training algorithm is performed. The grammatical evolution procedure is evolved for 200 generations and each generation has 500 genomes. The chromosome length for each genome is 100. The mutation rate is set to 5% and the crossover rate to 95%. The selection is performed using the tournamet selection algorithm and the tournament size is set to 10.

B. Evaluation Phase

The derived features are evaluated using neural networks with 5-10 hidden nodes. This neural network is trained using two phases. In the first phase the nodes are trained using a classical genetic algorithm and in the second phase the BFGS variant of Powell's is used in order to increase the efficiency of the network. The genetic algorithm, which is used to initialize the network weights, is evolved for 50 generations and has 100 genomes. Each genome is 100 length and the mutation and crossover operators are set to 5% and 95% respectively. Again, the tournament selection algorithm is applied and the tournament size is set to 10.

C. Validation

In order to validate the proposed method we employed the 10 fold stratified cross validation method [39]. We divided the 160 samples into 10 non overlapping sets each one containing 13 samples from the majority class and 3 samples from the minority class. Each time one set was excluded form the training phase and was used only for the estimation of the classification performance. The remaining 9 sets (consisting of 107 examples from the normal group and 27 of the at risk group) were used for training. We applied SMOTE to the 27 samples creating 4*27 synthetic examples, and those 108 examples plus the 27 original data comprised the set of the "at risk" cases that would be used for training.

V. EXPERIMENTAL RESULTS

The experimental results for the proposed method, tested for 1-3 constructed features are depicted in Fig 4.



Fig. 4. Performance for 1 to 3 different constructed features.

To test the efficiency of the proposed method, we compared the achieved results with the classification results when two well known conventional methods, the linear and the quadratic classifier [40], are applied to the same data set. The best results for the linear and the quadratic classifier are depicted in Fig. 5 and Fig. 6 respectively.



Fig. 5. Best performance of the linear classifier for different retained principal components.



Fig. 6. Best performance of the quadratic classifier for different retained principal components.

It is mentioned that we introduced a dimensionality reduction stage based on Principal Component Analysis in order to achieve better results for the conventional methods [41]. PCA is a very common method for the reduction of the dimensionality of the feature vector. It projects the original vectors onto a lower dimensional space whose axes are defined by the eigenvectors that correspond to the largest eigenvalues of the covariance matrix of the data.

Comparing the experimental results of the proposed method with the conventional classifiers, the superiority of the method is apparent despite the fact the performance of the conventional classifiers have increased with the introduction of the PAC method.

VI. CONCLUSIONS ANDFUTURE WORK

In this work we introduced grammatical evolution and we experimented with the use of constructed features combined with a neural network trained with a hybrid method, for the difficult problem of discriminating fetuses which are "at risk" from normal ones. For the alleviation of the problem concerning the imbalanced distribution of the examples we adopted the SMOTE procedure, which turned out to be a very effective technique. This is indicated by the fact that even the conventional classifiers perform better compared to our previous work [35], indicating the usefulness of the SMOTE technique as an intermediate stage in the whole process of building a classification system when dealing with imbalanced data sets. SMOTE technique may increase the performance of other successful proposed approaches to extract features and classify FHR [42]-[44].

The proposed method performs better compared to the scheme with the conventional classifiers and the PCA stage. However further investigation is needed since the results do improve the performance especially in the case of the "at risk" cases but do not overwhelm the conventional classifiers.

Another issue that we would also point out is that the pH value should be probably chosen lower for the "at risk" cases. A more justified threshold would be to choose

threshold value of pH at 7. In future work, we will try this cut off but in the current data set only 2 cases fulfill that criterion.

It must be mentioned that this is the first time that grammatical evolution method combined with a hybrid trained neural network is used for feature construction and classification of FHR. These results are promising but further investigation is required in order to achieve better results.

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