Analysis of Normal and Pathological Fetal Magnetocardiograms Using Clustering Algorithms

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ABSTRACT: In the present paper we propose a novel technique for the analysis of the fetal MagnetoCardioGram (f-MCG) in normal and pathological pregnancies. The f-MCG is a measure of the magnetic component of the electromagnetic fields emitted from the fetal heart, reflecting the underlying dynamics. The extremely weak magnetic fields emitted from the fetal heart can be recorded with the use of specific totally non-invasive Superconductive Quantum Interference Devices (SQUID). From a total of 10 considered cases, 5 were complicated and presented arrhythmia and 5 were normal. Recordings were performed at the late stage of pregnancy. The analysis of the collected signals is based on the reconstruction of the phase space form the one-dimension signals to higher-dimension phase space. An especially developed clustering algorithm is applied on the reconstructed data in order to investigate the distribution of the dynamics in the higher-dimension reconstructed phase space.

KEYWORDS: Cluster Analysis, Clustering Algorithms, Biomagnetometry, Fetal Magnetocardiogram

INTRODUCTION

Among the classical techniques for fetal heart dynamics monitoring are the CardioTocoGram (CTG), the fetal ElectroCardioGram (f-ECG) and the Doppler UltraSound (US). Although all the above mentioned techniques provide useful information to the medical doctors and are very widely used in the clinical routine, they all are characterized by disadvantages [1]. The CTG method provides only the momentary heart rate and moreover, with limited accuracy. The f-ECG is limited due to the low signal to noise ratio and the observed interference by the strong-amplitude maternal ECG. Furthermore, the f-ECG is hardly detectable at the early stages of pregnancy and in the interval from the 27th to the 35th week of pregnancy due to the fact that vernix caseosa insulates the fetal skin [2], [3]. The US technique is able to detect efficiently the Fetal Heart Rate (FHR) but with lower accuracy than the f-ECG since it can't provide information on the waveform of the electric potentials generated form fetal heart function or the electric fields emitted form the fetal heart.

A method that sufficiently overcomes the above mentioned limitations is the fetal magnetocardiography (f-MCG) which is based on a high sophisticated technique for the detection and recording of the magnetic fields that are emitted from the fetal heart. The f-MCG is the recording of the magnetic component of the time-varying electromagnetic fields that are generated from the ionic micro-currents at the fetal heart; these ionic movements are originated at the cellular level. It is believed that, under the proper analysis and interpretation of the f-MCG signals, we can obtain useful information for the underlying fetal heart dynamics that can be used for assessing fetal rhythm [4]. It was shown that the f-MCG can be recorded with no maternal interference, thus the method provides improved reliability of the fetal QRS detection. Moreover, it was shown that the f-MCG features higher signal to noise ratio than the f-ECG and it is not affected by the electrically insulating properties of the vernix caseosa [5], [6], [7], [8], [9]. Also, it was proved that the fetal heart magnetic fields are practically unaffected by the poor electrical conductivity of the surrounding tissues and the maternal heart and they fall rapidly with distance. Soon it was clear that the f-MCG can provide information supplementary and additional to the other techniques and therefore can be used in the clinical routine for the monitoring of fetal heart dynamics even at the early stages of pregnancy. Since then, a number of studies appeared for the detection of arrhythmia [10], [11], QT syndrome [12] and heart blocks [13]. The f-MCG signals are recorded with the use of specific Superconductive Quantum Interference Devices (SQUIDs). SQUIDs are very sensitive superconductive magnetometers with the ability to detect and measure very weak magnetic fields, of the order of fT (= 10^{-15}T) and they can be used ideally for the recording of the f-MCG, since they do not emit any radiation and they are totally non invasive. On the other hand, SQUIDs are extremely sensitive and they provide high spatial and temporal resolution and therefore they can account as a promising monitoring technique of the development of the fetus and the pregnancy.

Along with the existing methods for the analysis of the f-MCG, in the present work we propose a new method. The proposed method refers to the application of clustering algorithms on the reconstructed multi-dimensional phase space of the fetal heart dynamics. To derive the multi-dimensional phase space from the one-dimensional f-MCG signals a well-known technique from the field of the theory of non-linear dynamics and chaos is used. This technique is the embedding method for the reconstruction of multi-dimensional dynamics of a system from a one-dimensional observable. According to the embedding theorem [14] the reconstructed multi-dimensional phase space from a one-dimensional observable of a system is topologically equivalent to the original phase space of the system under consideration. This embedding method has been widely used the last two decades for the detection of chaotic dynamics and the estimation of the fractal dimension of the existing attractors using the method the computation of the correlation integrals [15], [16]. After this preprocessing and the reconstruction of the phase space, an especially developed clustering algorithm is used in order to detect and estimate the number and the characteristics of clusters that would probably be observed in the dynamics of the f-MCG.

Clustering is a widely used technique whose goal is to partition a set of patterns into disjoint and homogeneous clusters. Clustering is fundamental in knowledge acquisition and it has been utilized in many areas including data mining, engineering, taxonomy, compression and vector quantization, statistical data analysis and business applications.

Clustering algorithms have been widely studied in various fields including Machine Learning, Neural Networks and Statistics. They can be classified as either partitional clustering or hierarchical clustering algorithms. k-means [17],[18] along with its variants (e.g [19],[20],[21],[22]), hill-climbing [23] and the density-based DBSCAN [24] are of the most popular partitional clustering algorithms. Complete-link and single-link algorithms [25], [26] are the most popular hierarchical clustering algorithms.

There is a fundamental step in cluster analysis, independent of the particular clustering technique; namely to determine how many clusters are present in the results of a clustering study. This fundamental step is among the as yet unsolved problems of cluster analysis. The very popular iterative techniques, as the k-means algorithm, require the user to specify the number of clusters present in the data prior to the creation of the clusters by the iterative technique.

In this paper, we use the x-means algorithm [27], an iterative clustering technique that tackles the above problem. The x-means algorithm is based on the k-windows clustering algorithm [22], that uses a windowing technique in order to reduce the number of patterns that need to be examined for similarity in each iteration. The key idea of x-means algorithm is to use a sufficiently large number of initial windows that are properly merged during the algorithm. The merge operation is guided by certain parameters that are set by the user. The windows that remain after the execution of the x-means algorithm correspond to clusters of data. The windowing technique of k-windows algorithm allows a large number of initial groups (windows) to be examined, without any significant overhead in time complexity.

MATERIAL AND METHODS

The material considered for analysis in the present work is consisted of f-MCG signals. To obtain these signals the pregnant women were referred to the Laboratory of Medical Physics of the University of Thrace by their special gynecologists of the University Hospital Clinic of Gynecology and Obstetrics. All participated subjects were informed for the methodology and the purpose of the study. The experimental protocol was reviewed and approved by the University Hospital Ethics Committee. All f-MCG recordings were performed at the presence of an expert genealogist. A single-channel SQUID was used to record the f-MCG activity emitted from the fetus. In each case, the position of the fetal heart was localized using ultra-sonography. This allowed the SQUID sensor to be positioned to the minimum source-detector distance. All fetuses were in cephalic presentation. During the recording procedure the pregnant women patients were lying on a wooden bed with eyes closed in order to avoid artifacts from eye flickering. Each f-MCG recording consisted of 32 seconds and was digitized and stored in the computer with a sampling frequency of 256 Hz. A representative 4 seconds epoch (consisting of 1024 samples) of normal f-MCG activity is shown in Fig. 1 (f-MCG measured in pT = 10^{-12} T). For purpose of comparison, in Fig. 2 it is shown a representative abnormal f-MCG.

For the application of the clustering algorithm the f-MCG data were embedded in higher dimension dynamics with the use of the embedding theorem [14]. According to that theorem the dynamics of the system under consideration can be reconstructed in the phase space with no loss of information from an one-dimensional observable of the system.

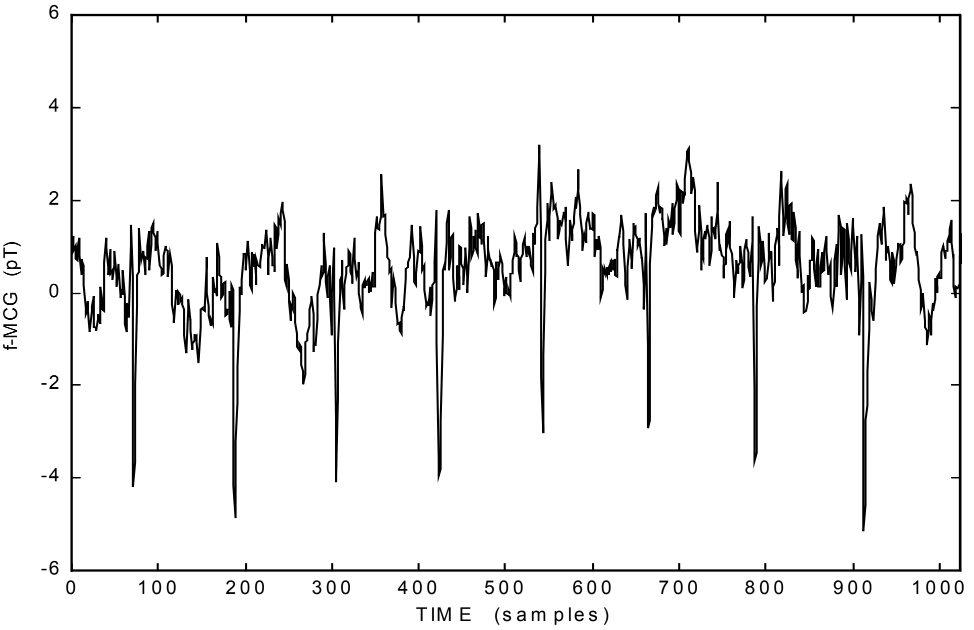

Figure 1. Representative 4 seconds epoch of a normal f-MCG.

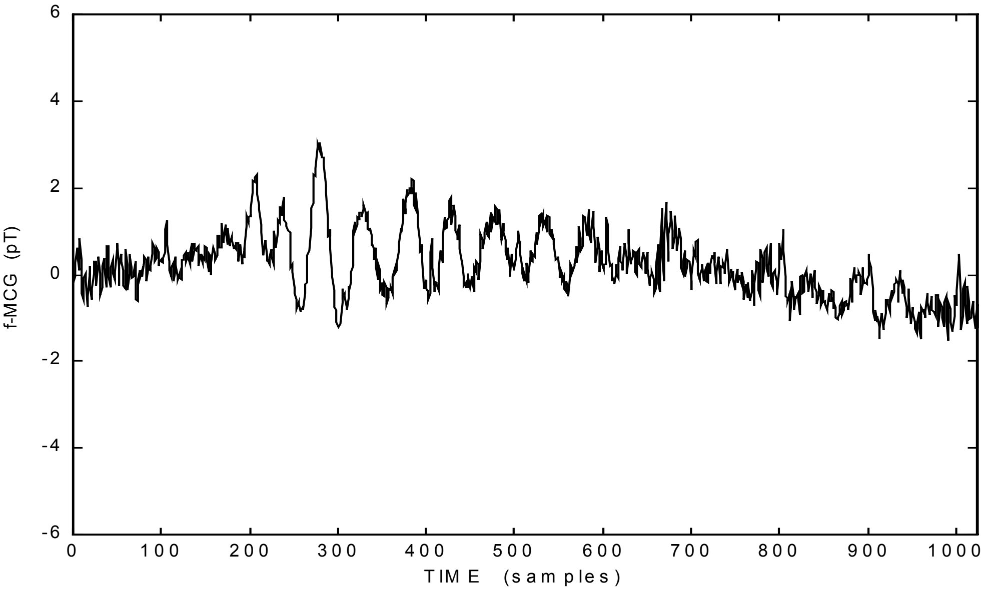

Figure 2. Representative 4 seconds epoch of an abnormal f-MCG.

By considering that,

$$B_i = B(t_i), \tag{1}$$

construct the one-dimension f-MCG timeseries with N samples (t=1, 2, …, N), the reconstruction of the dynamics in a higher-dimensional phase space with dimensionality m is obtain by the construction of d-dimensional points (vectors) that are generated by the formula:

$$V_i = (B_i, B_{i+\tau}, B_{i+2\tau}, ..., B_{i+(d-1)\tau}), \tag{2}$$

where τ is a suitable time parameter called reconstruction time or delay time.
Having reconstructed the f-MCG dynamics in a d-dimensional phase space the clustering algorithms can be applied.

THE x-MEANS CLUSTERING ALGORITHM

We apply the x-means clustering algorithm [27] in order to extract clusters that would probably be observed in the dynamics of the f-MCG. The reason behind this is that the x-means algorithm can automatically determine the number of clusters that are present in the input data.
The x-means clustering algorithm is based on the k-windows clustering algorithm [22]. The key idea behind the k-windows algorithm is to use a window in order to determine a cluster. The window is defined as an orthogonal range in the d-dimensional Euclidean space, where d is the number of numerical attributes. Therefore each window is an d-range and has a fixed size. Every pattern that lies within a window is considered as belonging to the corresponding cluster. Iteratively, each window is moved in the Euclidean space by centering itself on the mean of the patterns included. This takes place until any further movement does not result in any increase in the number of patterns that lie within it (see solid line squares in Fig. 3, where a pictorially representation of the way the algorithm works is given). After this step, we can determine the means of clusters as the means of corresponding windows. However, since only a limited number of patterns is considered in each movement, the quality of a partition may not be optimum. The quality of a partition is calculated in a second phase. At first, windows are enlarged, in order to contain as many patterns from the corresponding cluster as possible (dotted line squares in Fig. 3). The quality of a partition is determined by the number of patterns contained in any window, with respect to all patterns.

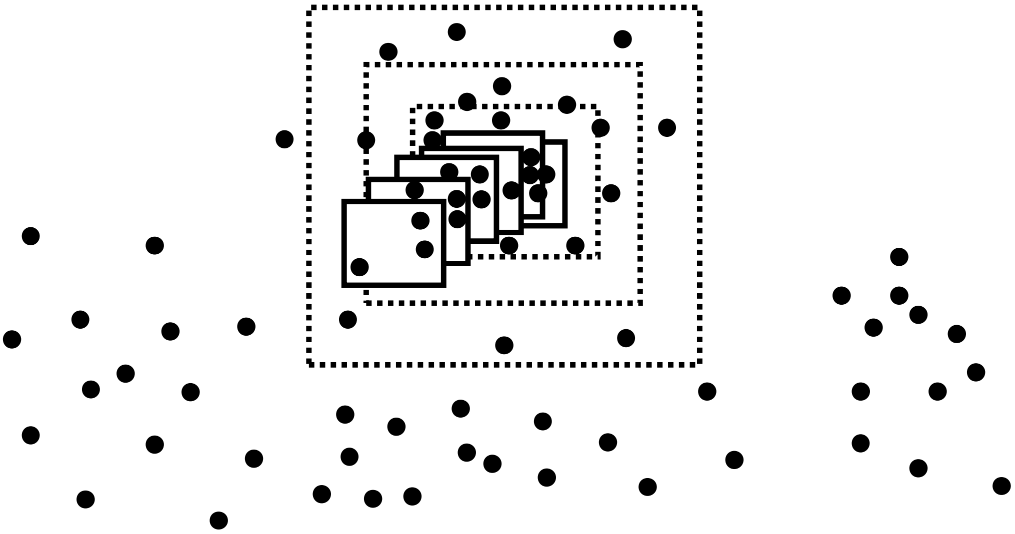

Figure 3. Movements and enlargements of a window.

The k-windows algorithm works as follows: at first, k means are selected (possibly in a random way). Initial d-ranges (windows) have as centers these initial means and they all have the same area. Then, the patterns that lie within each d-range are found, using the Orthogonal Range Search technique of Computational Geometry [28]. Then, the mean of patterns, that lie within each range, is calculated. Each such mean defines a new d-range, that is considered a movement of the previous d-range. The last two steps are executed repeatedly, until there is no d-range that includes a significant increment of patterns after a movement.
In a second phase, the quality of the partition is calculated. The d-ranges are enlarged in order to include as many patterns as possible from the cluster. This can be achieved by forcing d-ranges to preserve their mean during enlargement. Finally, if the relative frequency of patterns assigned to a d-range in the whole set of patterns is small, then the whole process is repeated.
The key idea of the x-means algorithm is to apply the k-windows algorithm using a sufficiently large number of initial windows. The windowing technique of the k-windows algorithm allows a large number of initial windows to be

examined, without any significant overhead in time complexity. Then, any two overlapping windows are merged, before the step of enlarging the windows is performed. The merge operation is guided by certain parameters that are set by the user. The windows left, after the quality of the partition criterion is met, will constitute the final set of clusters.
The x-means clustering algorithm described above was used on the reconstructed d-dimensional phase space data of the f-MCG recordings of normal and arrhythmic pregnancies [29]. During the numerical experiments, all the parameters of the algorithm were kept constant for purpose of comparison. In addition, all the parameters of the algorithm, especially the merge parameters, were set for a medium accuracy so that neither a lot nor a few clusters to be discovered.

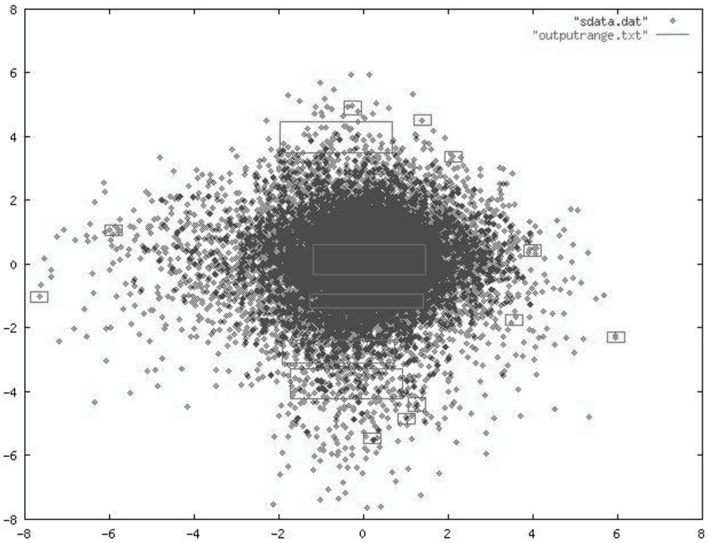

Figure 4. Pictorial representation of the 2-dimensional f-MCG reconstructed phase and the detected clusters.

RESULTS AND DISCUSSION

In all cases the algorithm applied it was shown that it is capable to track the existence of clusters in the reconstructed phase space. Preliminary, but representative results of the application of the method are presented in Table 1 for a 2-dimensional phase space reconstruction. In the first column of Table 1 it is shown the number of the detected cluster; in the second and the third cell of each row they are shown the 2–dimensional coordinates of the cluster box; in the fourth cell of each row it is shown the coordinates of the centre of the cluster; finally in the fifth cell of each row it is shown the number of points that are included in the cluster box.
A pictorial representation of the reconstructed points in the 2-dimensional phase space and the application of the x-means clustering algorithm is shown in Fig. 4. The obtained results clearly indicated that the reconstructed f-MCG dynamics are not uniformly distributed in the phase space. This observation has to be related to the type of the f-MCG (normal or pathological), since the f-MCG recordings are reflecting the underlying fetal heart dynamics. Such a suggestion needs more exhaustive analysis that will be presented in a future work. Closing the paper we would like to state that we plan to apply the methodology presented above to other real world signals, as well as to well-known nonlinear systems and compare our findings to the ones that are obtained using chaotic analysis methods.

Table 1. Results of the application of the x-means cluster algorithm on a 2-d f-MCG phase space.

Cluster #	First Coordinates	Second Coordinates	Centre Coordinates	Concentration
1	(-1.464 , -0.394)	(-3.438 , -2.983)	(-0.929 , -3.211)	84
2	(1.652 , -0.582)	(1.330 , 1.786)	(-1.116 , 1.558)	342
3	(-0.539 , 0.531)	(-1.426 , -1.075)	(-0.004 , -1.251)	578
4	(-0.402 , 0.667)	(0.691 , 1.146)	(0.132 , 0.918)	1085
5	(-0.431 , 0.639)	(0.276, 0.732)	(0.104 , 0.503)	1388

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