

# ANALYSIS OF EPILEPTIC MAGNETOENCEPHALOGRAM DYNAMICS THROUGH CLUSTERING ALGORITHMS

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**Abstract:** In the present work we propose a novel method for the analysis of the MagnetoEncephaloGram (MEG) of epileptic patients. The proposed method was based on the reconstruction of the phase space from the one-dimension signals to higher-dimension phase space. An especially developed clustering algorithm was applied on the reconstructed data in order to investigate the distribution of epileptic MEG dynamics in higher order reconstructed phase spaces.

## 1. INTRODUCTION

MEG signals are generated from the ionic micro-currents of the brain, originated at the cellular level [1], [2], [3]. The MEG analysis can provide information of vital importance for the monitoring of brain dynamics in both normal and pathological conditions of the Central Nervous System [2], [4], [5], [6], [7]. The MEG signals are recorded with the use of specific Superconductive Quantum Interference Devices (SQUIDS) [8], [9]. 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 MEG, 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 diagnostic technique for the investigation of neurological diseases and the exploration on normal brain function [10], [11], [12], complementary to the EEG method and other brain functioning techniques [13], [14].

Along with the existing methods for the analysis of the epileptic MEG, 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 MEG signals a well-known technique from the field of the theory of non-linear dynamics and chaos was used. This technique is the embedding method for the reconstruction of multi-dimensional dynamics of a system from an one-dimensional observable. According to the embedding theorem [15] the reconstructed multi-

dimensional phase space from an 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 [16], [17]. After this preprocessing and the reconstruction of the phase space the x-means clustering algorithm was used in order to detect and estimate the number and the characteristics of clusters that would probably be observed in the dynamics of the epileptic MEG.

An especially developed clustering algorithm was applied on the reconstructed data in order to investigate the distribution of epileptic MEG dynamics in higher order reconstructed phase spaces. 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 partitionial clustering or hierarchical clustering algorithms. K-means [18],[19] along with its variants (e.g. [20],[21],[22],[23]), hill-climbing [24] and the density-based DBSCAN [24] are of the most popular partitionial 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 [28], an iterative clustering technique that tackles the above problem. The xmeans algorithm is based on the k-windows clustering algorithm [23], 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 xmeans algorithm define the 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.

## 2. MATERIAL AND METHODS

The material considered in this work is consisted of MEG signal of epileptic patients. Patients that had independently diagnosed by special neurologists to suffer from idiopathic epilepsy were referred to the Laboratory of Medical Physics of the University of Thrace. All patients have had normal serum biochemical studies as well as normal CT or MRI scans. A single-channel SQUID was used to record the MEG activity of these patients. During the recording procedure the patients were lying on a wooden bed with eyes closed in order to avoid artifacts from eye flickering. For each patient MEG recordings were performed from both the temporal lobes (left and right), as well as from the occipital and the frontal lobes. For each lobe measurements were recorded from 32 points arranged in a 4x8 equally spaced grid. All these recording have had 32 sec duration and were digitized and stored in the computer with a sampling frequency of 256 Hz. A representative 4 seconds epoch (consisting of 1024 samples) of the MEG activity of an epileptic patients suffering from temporal lobe epilepsy is shown in Fig. 1 (MEG measured in pT =  $10^{-12}$  T).

Considering that ,

$$B_i = B(t_i) \quad (1)$$

construct the one-dimension MEG timeseries with N samples ( $i=1,2,\dots,N$ ), 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:

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

where  $\hat{o}$  is a suitable time parameter called reconstruction time or delay time.

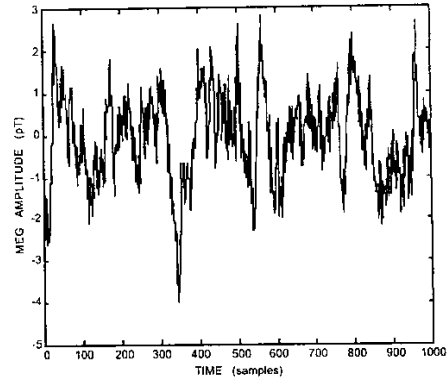
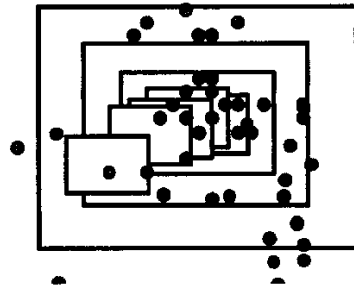


Figure 1. An 1000 samples epoch of the epileptic MEG.

After the reconstruction of the MEG dynamics in a d-dimensional phase space the clustering algorithms can be applied. 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 a 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. 2). The quality of a partition is determined by the number of patterns contained in any window, with respect to all patterns.



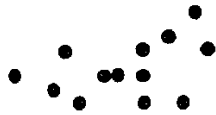


Figure 2. Movements and enlargements of a window.

More specifically, 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 [29]. 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 xmeans clustering algorithm described above was used on the reconstructed ddimensional phase space data of the MEG recordings of normal and arrhythmic pregnancies. 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.

### 3. RESULTS

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 center 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. 3.

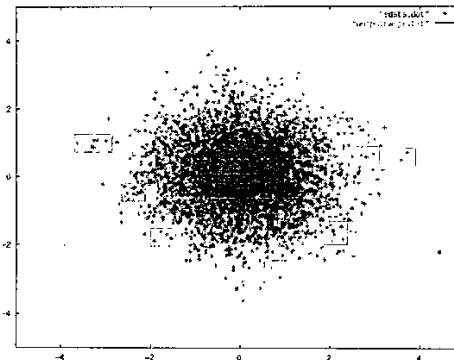


Figure 3 Clustering in 2-d phase space

The obtained results clearly indicated that the reconstructed MEG dynamics are not uniformly distributed in the phase space. This observation has to be related to the type of the MEG signal (normal or epileptic) since the MEG recordings are reflecting the underlying brain 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 above-presented methodology 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	Center Coordinates	Concentration
1	0.127135 0.678465	-4.188870 -3.638230	0.402800 -3.913550	2
2	0.598335 1.149670	2.434680 2.985320	0.874003 2.710000	1
3	-2.638950 -2.08762	-0.774187 -0.223547	-2.363285 -0.498867	6
4	2.402530 2.953870	-1.649850 -1.099210	2.678200 -1.374530	4
5	-1.737950 1.875250	-0.887095 0.043487	0.068650 -0.421804	953

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