International Journal of Bioelectromagnetism *http://www.ijbem.org*
Vol. 10, No. 1 pp. 22 - 24, 2008

Synopsis of brain activations from high temporal resolution data.

Florence Gombert, Sylvain Baillet *

Cognitive Neuroscience & Brain Imaging Lab., Pierre & Marie Curie University, La Pitié-Salpêtrière Hospital, CNRS UPR 640-LENA, MEG-EEG Center, Paris, France

Correspondence: Florence Gombert, CNRS-UPR 640 LENA, Hopital de la Pitié-Salpêtrière, 47, boul. de l'hôpital, 75651 Paris Cedex 13 – France. E-mail ; florence.gombert@chups.jussieu.fr, phone : + 33 1 42 16 14 03, fax : + 33 1 45 86 25 37

Abstract. Sequences of functional brain images obtained from image reconstruction techniques applied to Magneto- and Electro-encephalography (M/EEG) data convey a large amount of information in space and time; typically 1,000 images per second. Conventional analysis approaches to this data mining issue require considerable input from human experts. Hence, there is an emerging need for fast and automatic extraction of pertinent spatiotemporal activation patterns, which should also facilitate subsequent group analysis. We therefore introduce an automatic sequencing procedure of series of brain activation maps. The method detects the evolution of patterns of interest called *activation cells*. These cells are tracked across time with consistent labeling following a small set of predefined evolutionary scenarios. Resulting graphical synopsis are exemplified on epileptic spike analysis and indicate satisfactory consistency with human expertise.

Keywords: Magnetoencephalography, Data Analysis, Computer-aided decision, Epilepsy, Spike classification.

1. Introduction

Image reconstruction techniques applied to scalp Electro and Magnetoencephalography (E/MEG) data produce brain activation maps with excellent time resolution at the infra millisecond scale. This results in series of image activation sequences of typically 1,000 images per second of recording. This information rate makes the analysis cumbersome to experimentalists. The choice of salient features of interest for subsequent analysis and inferences may even end-up being very subjective. The E/MEG expert usually describes the instantaneous activation maps obtained in terms of number of activation sources. For each source, the location, amplitude and occasionally spatial extension of the cortical areas involved are reported and considered for subsequent inference and classification across subjects and/or conditions. Though E/MEG benefits from unique time resolution, the very description of the evolution of brain activations with time is usually discarded from further consideration and exploration. This paper introduces a systematic approach to the automatic analysis of these brain image sequences. We exemplify the concepts and methodology in the context of epileptic spike classification.

2. Material and Methods

The primary objective of our approach consists in reaching significant dimension reduction in the description of the original data (i.e. spatiotemporal sequences of cortical currents). Space and time must therefore be compactly encoded in 2D graphs that need to be easily understood by an operator with minimum training. Beyond human readability, specifications also enforce that data decomposition will be subjected to quantitative analysis for e.g. data classification such epileptic spike sorting. Therefore, instantaneous activation maps that support a dense distribution of currents need to be efficiently resampled through segmentation into elementary spatiotemporal blocks that will be evolving in space and time according to a set of admissible scenario. These specifications translate into a sequential process that unfolds as the following:

1. Cortical current map at each time instant $t+1$ is spatially segmented into elementary activation cells;
2. For each activation cell at time t, its descent at time $t+1$ is identified from the activations cells according to a predefined set of evolutionary scenarios;
3. Cells are tracked from t to $t+1$ with consistent labeling.

The entire process is iterated over all available time instants. Once completed, the resulting spatiotemporal decomposition into activation cells and their associated genealogy are conveniently synthesized in a graphical synopsis. Each activation cell is displayed as a horizontal bar which length encodes its lifespan. Its color encodes the instantaneous location of its spatial centroid (Fig.1).

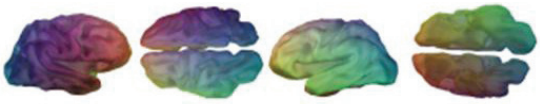

Fig. 1. *Reference cortex: color encoding all possible positions of activation cell centroids.*

3. Results and Discussion

This sequencing approach is evaluated on two types of averaged interictal epileptic spikes detected in a patient with a 151-channel CTF/VSM Medtech MEG system. Two types of spikes were considered in this study: H-spike originated from the right hippocampal region (Fig. 2), and two distinct T-spike samples (T1 & T2, Fig. 3 & 4) were initiated from the right lateral temporo-occipital junction. t=0 defines the time of maximum scalp signal amplitudes.

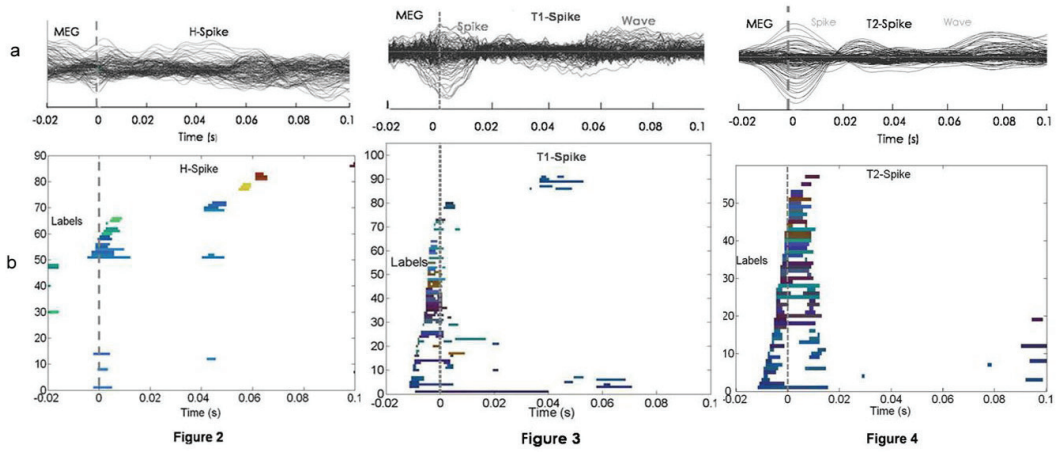

Figure 2 3 4. *(a) Butterfly plot of times series acquired on the 151 MEG channels during epileptic spikes and (b) their associated graphical synopsis. The x-axis represents time and y-axis labels. Each bar represents an activation cell, its length encodes its lifespan and its color the location of its centroid on the reference cortex (fig.1). Fig. 2 corresponds on hippocampal spike and fig. 3 and 4 on temporo-occipital spikes*.

T1 and T2 cell genealogy graphs show a striking similarity, thereby confirming the consistency of the cell decomposition with the outcome of human expert identification. About 10ms before spike maximum, the spike lifespan is decomposed into a waterfall of brief activation cells that reveals a limited network of neighboring temporo-occipital cortical regions involved in the spike generation. The graphical synopsis later shows the resurgence of activity in these brain areas during the subsequent slow wave of the spike-wave complex with significantly slower dynamics. As expected, the contrast in terms of location and dynamics of activations with the sequencing of the H-spike is quite striking.

4. Conclusions

We propose a new tool for the facilitated exploration, decomposition and quantitative analysis of functional brain mapping data at high-temporal resolution. Resulting graphs offer a direct and synthetic

visualization of cortical activation pattern and conserve a high density of spatio-temporal information. Results indicate satisfactory consistency with human expertise

This tool also offers interesting perspectives on new measures for quantitative group analysis of brain functional images at high temporal resolution.

References

Baillet S. & al. Electromagnetic BrainMapping. IEEE Sig. Proc. Mag., 25:355-368, 2001.

Grewal S., Gotman J., An automatic warning system for epileptic seizures recorded on intracerebral EEGs, Clinical Neurophysiology , 116:2460-2472, 2005.

Ossadtchi A. & al. Automated interictal spike detection and source localization in magnetoencephalography using independent components analysis and spatiotemporal clustering. Clin. Neurophys., 115:508-522, 2004.

Van't Ent D., Manshandena I., Ossenblokb P., et al.,Spike cluster analysis in neocortical localization related yields clinically significant equivalent source localization in magnetoencephalogram (MEG), Clinical Neurophysiology, 114:1948-1962, 2003.

Wahlberg P., Lantz G. Methods for robust clustering of epileptic EEG Spikes. IEEE Trans. Biomed. Eng., 47(7), July 2000.

* This research is supported by the French Ministry of Research: ACI Nouvelles Interfaces des Mathématiques.