I. INTRODUCTION

The functional Magnetic Resonance imaging (fMRI) is currently the most prominent method used for functional brain imaging, and it is a big step forward in the process of answering the main question asked to all the functional imaging methods: What are the brain regions involved in mediating a specific brain function? And thought the fMRI’s obvious qualities have allowed for its fast acceptance and development, its limitations are far from letting this question to become a “closed problem”.

The fMRI experiments usually look for the change in blood oxygenation and blood volume resulting from altered neural activity. This signal, called blood-oxygenation-level-dependent (BOLD), results from the endogenous paramagnetic contrast property of the deoxygenated hemoglobin. Hence, increased blood flow reduces the local concentration of deoxygenated hemoglobin causing an increase in the MR signal on a T2*-weighted image [1]. It is commonly accepted, and has been empirically proved, that there is a strong correlation between neural activity and the vascular response that leads to the consequent increase of this BOLD signal citation. This relation, known as the hemodynamic response function (HRF), is at the core of fMRI data analysis. Inferences about which brain regions are involved in the particular stimulated cognitive and sensorimotor functions are based on how well the BOLD signal correlates with this stimulation, mediated by the HRF.

Contrary to the impression one might get in a brief review of the literature, there are not many ways to analyze fMRI time-series with a diversity of statistical and conceptual approaches. In fact, with very few exceptions, every analysis is a variant of the general linear model (GLM), that expresses the observed response variable in terms of a linear combination of explanatory variables [2]. Based on this model, data analysis is usually processed in a number of steps involving image processing and statistical evaluation that, in the end, produce a functional brain map. Often methods used involve several modules for image preprocessing, spacial transformation, statistical tests and the final inferences procedures. This work focuses on the last two steps and how our Bayesian method compares with the most commonly used method, Statistical Parametric Mapping (SPM) [3] when applied to single voxel time-course data. This last method makes use of univariate statistical tests (T of F tests) at each brain voxel and subsequent statistical inferences about the observed responses using a user defined p-value threshold, for the 1D data case. This classical approach maybe a simple one with reasonable results, but it has several disadvantages that can be tackled. On this work we propose a Bayesian approach for the binary (activated or not) analysis of simulated 1D block-designed data and present the Monte Carlo results from the comparison between the presented method and the standard SPM procedure.

II. PROBLEM FORMULATION

Let us consider the voxels (volume element) displayed in Fig. 1. After the application of a given experimental paradigm (comprised of one or more stimulus p) to the subject, each brain voxel may ($\exists_k : \beta_k = 1$) or may not ($\forall_k : \beta_k = 0$) be activated by one or more applied stimulus.

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Fig. 1. Activated and non activated regions in fMRI

In this work we consider only a single voxel at a time with the following observation model (see Fig. 2 for...
$y(n) = h(n) * \sum_{k=1}^{N} \beta_k p_k(n) + \eta(n)$  

(1)

the only unknown here are the binary variables to model the activation of the voxel by the k\textsuperscript{th} stimulus.

In this work we describe a Bayesian Statistical Parametric Mapping algorithm (SPM) based on the maximum a posteriori (MAP) criterion to estimate the vector $\beta = \{\beta_1, \beta_2, ..., \beta_N\}$, associated with each voxel, called SPM-MAP\textsuperscript{1}. We use the observation model displayed in Fig. 2 and described by the equation (1) and model the noise corrupting process in fMRI with the standard additive white Gaussian noise, although other models may also be used, e.g., Rice [4] and Rayleigh. The proposed SPM-MAP method makes use of a two priors in the pretended binary solutions. To achieve this, very low variance, Gaussian functions were used to force the obtained solution to 1 (activated) or (2) not activated. As obvious by its title, the proposed method uses the maximum a posteriori (MAP) to estimate the optimum solution. Monte Carlo tests with synthetic 1D block-designed data are used to evaluate the performance of the algorithm and compare it with the SPM based on the general linear model (GLM), here called SPM-GLM [3], which is one of the most commonly used methods to detect activated voxels in the functional MRI scope.

III. MONTE CARLO TEST RESULTS AND FINAL COMMENTS

To compare The proposed method with the standard SPM-GLM method the probability of error $P_e$ in each voxel, for each noise energy, $\sigma$ and number of epochs (periods), $n$, in a block design paradigm approach, is estimated as follows

$P_e(\sigma, n) = \frac{1}{R} \sum_{i=1}^{R} b_i \oplus \tilde{b}_i$  

(2)

\textsuperscript{1}Statistical parametric mapping is generally used to identify functionally specialized brain responses[3]

where $\oplus$ is the exclusive OR operator and $R = 250$ is the number of repetitions used in the Monte Carlo tests used in this work. In the SPM-GLM method a 95% significance level is used.

The graph displayed in Fig.3 displays the difference of the probability of error, $P_e$, between both methods, i.e: $\Delta P_e = P_e(\text{SPM-MAP}) - P_e(\text{SPM-GLM})$. Although the performance of both algorithms decrease, as expected, with the amount of noise and with the decreasing on the number of epochs, the $\Delta P_e$ obtained is negative for almost all pairs $(N, \sigma)$ tested, which means that the SPM-MAP outperforms the SPM-GLM methods for almost every configuration tested: noise and epochs, $(\sigma_k, N_l)$.

IV. REFERENCES


