Functional Magnetic Resonance Imaging via Independent Component Analysis for Human Brain

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Abstract: Functional Magnetic Resonance Imaging (fMRI) is a powerful noninvasive tool for localizing and analyzing brain activity. This study focuses on one very important aspect of the functional properties of human brain, specifically the estimation of the level of parallelism when performing complex cognitive tasks. Using fMRI as the main modality, the human brain activity is investigated through a purely data driven signal processing and dimensionality analysis approach. Specifically, the fMRI signal is treated as a multidimensional data space and its intrinsic ‘complexity’ is studied via dataset fractal analysis and blind source separation (BSS) methods. One simulated and two real fMRI datasets are used in combination with Independent Component Analysis (ICA) and fractal analysis for estimating the intrinsic (true) dimensionality, in order to provide data driven experimental evidence on the number of independent brain processes that run in parallel when visual or visuo motor tasks are performed.

Keywords: fMRI, ICA, fractal dimension, functional brain networks (FBN), human brain.

I. INTRODUCTION

Human brain is the most advanced and efficient signal processing machine known today. It corresponds to only 2% of total body weight in adults (about 1.5 kg), yet it consumes 20% of blood oxygen and 25% of glucose, with only 20W at power peak. It consists of roughly 100 billion neurons with 1,000,000 synapse interconnections each, packed in 11301260 cm$^3$ of volume, making it the most complex organ in the human body [42, 14, 30]. Analyzing its structure and functionality, especially during the actual process of some cognitive task or in relation to some mental impairment, has been a scientific challenge for centuries. However, only recent technological breakthroughs have enabled the study of the inner workings of living brains. Even today, simulating the structure and only basic neuron functionality of a full scale human brain in a digital computer is still an infeasible task.

Functional Magnetic Resonance Imaging (fMRI) [33, 30, 45] is a powerful noninvasive tool for localizing and analyzing brain activity. Most commonly it is based on blood oxygenation level dependent (BOLD) contrast, which translates to detecting localized changes in the hemodynamic flow of oxygenated blood in activated brain areas. This is achieved by exploiting the different magnetic properties of oxygen saturated versus oxygen desiderated hemoglobin.

In the human brain, tasks involving action, perception, cognition, etc., are performed via the simultaneous activation of a number of functional brain networks (FBN), which are engaged in proper interactions in order to effectively execute the task. Such networks are usually related to low level brain functions and they are defined as a number of segregated specialized small brain regions, potentially distributed over the entire brain. In order to properly detect these activations and identify the set regions that constitutes a FBN related to a specific task, the 3D space occupied by the brain is partitioned into a grid of ‘cubes’ or voxels. Each voxel constitutes the elementary spatial unit that acts as a signal generator, recorded and registered as a low resolution 1D time series. Actual fMRI voxel signals from brain scans can be considered as a mixture of various components or sources with different temporal and spatial characteristics. These sources can be classified as of interest and as artifacts [7].

In order to understand the true functionality and full potential of the human brain, data intensive approaches are required for analyzing the actual brain signal (e.g. fMRI, EEG) during specific cognitive tasks. Current research involves multidisciplinary endeavors, from Biochemistry and Neurophysiology to Simulation and VLSI design, with projects like the Human Brain Project (HBP) by EU [18] and Brain Research through Advancing Innovative Neuro technologies (BRAIN) by USA [47]. There is also very active research and development effort in the industry, where projects like the recently announced ‘True North’ chip by IBM implement a million scale neural network grid in special purpose VLSI and extremely high power efficiency [37,44]. However, all these efforts are currently focused on the structural properties of the human brain, i.e., the neural networks topology and connectivity, while the functional and higher level cognitive properties are still very difficult to model. In practice, this means that the hardware necessary to build and fully simulate (at the neuron cell level) an actual artificial ‘brain’ equivalent to a small animal’s now becomes available, but the problem of turning this construction to a machine with actual cognitive and abstract functionality still remains (for the most part) unsolved, with only application specific modules being developed successfully (e.g. artificial retina implants, with some visual processing capabilities [15]).
II. PROBLEM DEFINITIONS

Required to ‘run’ all the active cognitive tasks that are registered in the entire 3D brain volume while performing a typical fMRI experimental protocol that includes visual only or visuo motor tasks.

Using fMRI as the main modality, the human brain activity is investigated through a purely data driven signal processing and dimensionality analysis approach. Specifically, the fMRI signal is treated as a multidimensional data space and its intrinsic complexity is studied via dataset fractal analysis and blind source separation methods. Section 2.1 provides an overview of the fMRI experiments and the nature of sensory data; section 2.2 defines a proper mathematical formulation for the data unmixing task and its importance in understanding the true sources of brain activity; section 3.1 provides hints to proper data dimensionality reduction in fMRI; sections 4.1 And 4.2 describe the simulated and real fMRI datasets used in this study; section 5 includes the experiments and results, using all the methods and datasets described earlier; sections 5 conclude the results and their practical meaning.

2.1 The nature of fMRI data

In experimental fMRI procedures, there are two common activation schemes: the block paradigms and the even treated paradigms [5]. In the block paradigm, the subject is presented with a specific stimulus for a specific time frame, e.g., a set of images of different placement, colors, patterns or categories, and the subject has to press a switch to signal positive or negative feedback as a response. In the even treated paradigm, the subject is exposed to a series of randomized short time inputs, e.g., a noise or a pain stimulus, with or without the need for specific response from the subject. In both cases, the external input is considered as a primary ‘source’ and is temporally correlated with the brain activity. Areas of high activation and correlation to the stimulation/response pattern are considered as highly relevant to the specific functional task (visual/motor centers, pain receptors, etc). The same procedure can be followed when there is no specific external paradigm, constituting the steady state functional analysis of brain activity. In this setup, there is no correlation to previously known activation pattern and hence the analysis is essentially a search for functionally independent sources in the recorded fMRI signal.

The acquired fMRI signal is registered in both spatial (3D) and temporal (1D) domain, resulting in a composite 4D signal. Each spatial axis is registered as a grid of spatial resolution 35 mm , resulting in a 3D grid of voxels. Typically, a complete volume of voxel data, e.g. 60x60x30 to 64x64x48, is recorded every 12 seconds for a sequence of 100150 time points [33, 30, and 45]. This produces a total of roughly 108K197K voxels for every time frame or, equivalently, 116 to 306 data points organized as a two dimensional matrix, where each row corresponds to a complete brain ‘snapshot’. In practice, the number of actual brain voxels is smaller, since non brain areas of the grid are masked out before any further processing; however, the data volume still remains within the same order of magnitude. Additionally, typical fMRI experimental protocols involve several subjects, in order to exclude any

Subject specific characteristics that may affect the statistical properties of the fMRI data under consideration. Clearly, this creates a high volume data analysis process that makes it a very complex and computationally demanding task.

In terms of signal processing, the hemodynamic response function (HRF) [33,30,45] of the activated neurons, i.e., the changes in oxygen rich blood flow in the time domain, acts as a low pass filter in the temporal domain, which in turn modifies the true activation signal that it is registered as fMRI data. In other words, the HRF of the activated neurons, i.e., the changes in oxygen rich blood flow in the time domain, modifies the true activation time series signal that it is registered for each brain voxel as fMRI data. Moreover, the HRF is known to be spatially varying, which means that there are slightly different hemodynamic responses for different areas of the brain, as well as different HRFs between different subjects. This means that traditional regression approaches like General Linear Model (GLM) approximations [33,45,30] that require a predefined ‘design matrix’ are clearly suboptimal, since it is typically constructed as permutations, transformations, time shifts and derivatives of one (assumed) ‘universal’ HRF. There are also additional features that makes this approximation even more difficult in practice, such as the fact that the voxels’ activations are assumed to be statistically independent (while locally they are not, due to the physical properties of the veins and hemodynamic), as well the various artifacts that are introduced to the signal by external factors (scanner drift, electronic noise, head movements, respiration, cardiac pulsation, etc) [33, 30, 45].

2.2 Understanding brain activity

In fMRI analysis, the sources of interest include task related, transiently task related and function related sources, meaning that in a task specific fMRI experiment most of the task related activity is expected to be spatially isolated and temporally synchronized with the corresponding input/stimulation patterns. Therefore, these sources are expected to appear as super Gaussian in nature due to the spatial and temporal localization of such task related brain functionality.

Special matrix factorization algorithms are required to reformulate the fMRI data as a multiplication of two other matrices, where one is for the time courses of the estimated signal ‘sources’ and one for the corresponding spatial maps of related brain activity. Formally put, if Y 2 R n is the full fMRI data matrix with t rows as time points and n brain voxels ‘unwrapped’ into a linear vector, then the fMRI data matrix can be factorized as Y = TS, T 2 R t,p, S 2 R p,n, where the p spatial maps are collected as rows in S and each column of T contains the activation pattern along time for the corresponding spatial map.

III. INDEPENDENT COMPONENT ANALYSIS (ICA)

In blind source separation (BSS), ICA has been successfully applied to fMRI data for many years [25, 8, 27, 13].
Since the fMRI consists of a mixture of unknown components, corresponding to different brain sources of activity, the unmixing procedure is essentially a BSS problem. However, due to the relatively low temporal and spatial resolution of fMRI data, the no stationary properties of the signal due to brain and machine state variations, as well as the unknown number and exact statistical properties of the sources, the BSS of fMRI data is not a trivial task.

ICA is based on identifying non Gaussian properties between the sources and separating them from the mixture, essentially reconstructing the original signal as a linear combination of identified components, i.e., similarly to the previously discussed formulation $Y = TS$, $T \in \mathbb{R}^p$, $S \in \mathbb{R}^n$. In this case, $S$ is the matrix of independent components (spatial maps of brain activity) and $T$ is the mixture matrix (corresponding time courses). In fMRI, the ICA can be performed in the spatial or temporal dimension of the (vectorized) voxel data, producing either spatial or temporal components in matrix $S$. Several studies have been conducted in whether spatial or temporal ICA works better for BSS in fMRI data [8]; however spatial maps, i.e., retrieving $S$ as spatial components, seem to be more accurate and useful in most clinical applications of fMRI. The two most common approaches for ICA are the Info max [6] and fast ICA [26,24,25] algorithms.

Although ICA has been widely studied and employed in fMRI, recent works have identified the relevant advantages of analyzing brain activity under the

VI. Experiments and Results

Two separate sets of experiments were conducted in this study, one for BSS unmixing via ICA and one for dataset fractal dimension estimation. Both sets included all three fMRI datasets, namely one of simulated fMRI data and two of real fMRI data experiments (see sections 4.1).

4.1 ICA analysis

The ICA experiments that were conducted with the simulated fMRI data included two distinct realizations of the dataset, generated by the same procedure and the same specifications as described in section 4.1. Since the data generation includes several noise components, the two realizations were used as an additional verification check to validate those slightly different mixtures of (artificial) fMRI data do not produce significant differences in the ICA error versus components plots and estimated dataset fractal dimension.

Fig. 1 presents the time courses of the ICA factorization (matrix $T$), with the blue curves representing each of the eight ideal (true) sources and the red curves representing the corresponding ICA recovered sources. Figure 2 illustrates the corresponding activation maps (matrix $S$) recovered by ICA, spatially reshaped into proper 2D brain ‘slices’, where the reconstruction errors are visible as artifacts (‘ghost’ artifacts).

Fig. 1. Ideal (blue) and ICA recovered (red) time courses of the eight sources in the simulated fMRI dataset.

Parameter $r$ is the correlation coefficient between the original (ideal) and the recovered time course, $p$ is the corresponding $p$-value and rmse is the matching error. The first component (upper left corner) corresponds to the predefined external stimuli.

Figure 2 presents the plot of reconstruction error (RMSE) versus the number of ICA components used. Specifically, after the ICA unmixing model is complete, the ICA components are used one by one in rank1 reconstructions of the original data and the corresponding errors are used for sorting the components in ascending order (smallest RMSE first). Subsequently, a set of components starts from the first one (top of the list) and increased by adding the next one in each step, while estimating and registering the corresponding reconstruction error. The plot illustrates the total reconstruction error decreasing almost linearly as the number of used components increases, as expected. It should be noted that for ‘perfect’ ICA factorizations, as in the case of simulated fMRI data, the number of components recovered by ICA is exactly the same as the number of signal sources (true) used in the mixture that created these data (see section 4.1).
The number of true signal sources in the original mixture, and the final reconstruction error is practically zero. Fig. 3 ICA recovered activation maps of the eight sources in the simulated fMRI dataset, spatially reshaped into proper 2D brain ‘slices’. The lower left box corresponds to the activation areas for the predefined external stimuli. The lower right box illustrates the complete reconstructed fMRI mixture at time point $t = 150$.

Using the GIFT toolbox for Matlab [13], Figure 5 illustrates the ICA recovered time course (red plot) and the corresponding 2D ‘flattened’ activation map that represents the actual response of the human brain in a visuo motor task very similar to the experimental protocol employed in the ‘ds101’ dataset. Here, the ICA successfully recovered one particular component very similar to the external stimuli, which ideally is a square shaped pulse modulated by the HRF (see section 2.1), instead of the noisy sinusoid curve.
Figure 5 illustrates 10 of the 50 ICA recovered time courses of components in a sample run with the ‘ds101’ dataset. Although the ICA converged successfully with the minimum attainable reconstruction error, the unmixing model failed to detect one single component that closely matches the ideal time course of the stimuli. However, it is evident that one component (third from top left) matches component no.7 and two components (upper/lower left) match component no.8 of the simulated fMRI data as illustrated in Figure 1 in terms of overall shape and noise characteristics.

![Figure 5](image)

Fig. 5

Fig. 6. Sample result from the GIFT toolbox for Matlab [13], illustrating the ICA recovered time course (red plot) and the corresponding 2D ‘flattened’ activation map of the actual response of the human brain in a visuo motor task very similar to the experimental protocol employed in the ‘ds101’ dataset. Fig. 6. ‘ds101’ (no smoothed), 10 of the 50 ICA recovered time courses of components in a sample run.

![Figure 6](image)

(Rightmost) point in blue represents the maximum size, lowest RMSE in each case. Hence, the general slope of the red curves, as well as the dotted blue line connecting the end points, illustrate the robustness of the ICA unmixing process in each of the real fMRI dataset.

V. CONCLUSIONS

Tasks that are registered in the entire 3D brain volume while performing a typical fMRI experimental protocol that includes visuo motor tasks. It is very interesting to see that the real fMRI dataset ‘ds101’, which corresponds to a visuo motor task, produces much higher estimated FD values than the corresponding FD values for the ‘ds105’, which is a much simpler visual recognition only task. This means that, as expected, in the second task there is a much lower number of distinct activated brain areas, hence much fewer independent cognitive tasks involved, when no motor response is required by the experimental protocol. This does not mean that the total volume of brain activation is smaller but rather than fewer functionality components (‘sources’) are present in parallel when visual recognition is concerned, rather than when a proper motor response is required by the subject. ICA reconstruction plots show that when the human brain is concerned, this number is not defined as a strict threshold but rather in a continuous range; when a specific activation level is defined, a corresponding number of ‘brain cores’ can be evaluated. However, in real fMRI data, this range seems to be nonlinear and such a number can be retrieved at the point beyond which adding more components has only marginal impact to the modeled brain signal (see Figures 6).
In short, it seems that normal brain functionality, such as in typical visual or visuo motor tasks, involves only a limited number of independent processes that run in parallel. Some of them are related to this specific task, while others correspond to basic low level functionality, e.g. respiration. Although it is difficult to correctly identify and explain all these components in strictly data driven approaches (especially in BSS methods like ICA), the investigation of the number of major components, in combination with nonparametric dimensionality recovery methods such as dataset fractal analysis, can provide very useful hints for developing brain like technologies and algorithms.

Current research endeavors like the Human Brain Project (HBP) by EU [18] and Brain Research through Advancing Innovative Neuro technologies (BRAIN) by USA [47], as well as new innovative VLSI technologies like ‘True North’ project by IBM [37,44], require reliable evaluations of brain activity not only in the structural but also in the functional level. A typical voxel size of 3x3x3.55 mm³ corresponds to roughly 2.54 million neurons of several thousands of synapse interconnections each, or $\frac{1}{40000}$ to $\frac{1}{25000}$ of the total brain volume, while the currently state of the art ‘True North’ chip provides 1 million artificial neurons with only 256 synapses each. Hence, the level of true parallelism in human brain is a design aspect of paramount importance in future projects.

This study presents a purely data driven approach to the estimation of the level of parallelism in human brain. Using fMRI as the main modality, the human brain activity was investigated through ICA for BSS.

Analysis of the non smoothed variants of the real fMRI datasets (i.e., no information loss) proved that even when performing complex visuo motor tasks, the number of independent brain processes are in the order of 50 to 60, while it becomes much lower when visual recognition tasks (no motor response) is concerned. This means that, in theory, an artificial equivalent of a brain like cognitive structure may not require a massively parallel architecture at the level of single neurons, but rather a properly designed set of limited processes that run in parallel on a much lower scale. Hence, although current state of the art VLSI technologies still includes very limited features and processing power when compared to the real human brain, the assertion of employing actual parallelism level of much lower order can provide useful hints to future projects.

REFERENCES