Whole Brain Mapping of the Hemodynamic Response Function

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Functional Magnetic Resonance Imaging (fMRI) indirectly investigates neuronal activity from the associated vascular response. The observation of the Blood Oxygenation Level Dependent (BOLD) signal, which depends on local changes in deoxyhemoglobin concentration in the brain, allows to draw information on the underlying neuronal activity. Conventional approaches model BOLD response as the convolution of the HRF (hemodynamic response function, i.e. the response to an impulsive stimulation) and the known experimental conditions. Hence, accurate knowledge of the HRF is a fundamental issue in fMRI, preventing from false positive/negative results and both power and effectiveness loss [1].

Phenomenological models for the HRF spanned from a single canonical shape to the use of a basis set of more or less complex functions [1] and, to date, the investigation of the performance of these models is an ongoing challenge. Indeed, interpretation of BOLD response as neuronal activity changes is difficult for the complexity of the neurovascular coupling itself. Activity-related neural signal is task and region dependent and not constant over time [2]. The hemodynamic response reflects the integral across time of the neuronal/glial activity and saturates over time [3]. Moreover, statistical model of the HRF could be source of potential confounds leading to miss-modeling and incorrect inference [1].

Purpose of this study was to explore the shape of the HRF across tasks and brain regions in a large cohort of subjects, by means of the investigation of the distributions of parameters characterizing its magnitude, latency and duration.

Subjects (24 females and 24 males) included in this study were part of the Human Connectome Project (HCP) [4]. The stimulations, administered in blocked design, elicited several classes of neural processing, including visual, motion and somatosensory, emotional, language, relational, social and cognition. Stimulations and preprocessing are fully described elsewhere [5]. Functional analysis were performed on a voxel basis by modelling the signal as the convolution of the unknown HRF with task paradigm. We used two basis set for HRF: a combination of gamma function and its time and dispersion derivatives, and a combination of sine functions. The estimated HRF was then characterized by its parameters (FWHM and time-to-peak). In Figure1 and 2 the HRF time to peak and FWHM mapping of a representative subject were shown for two different neuronal processing (motion and cognitive), for gamma functions (a) and sine functions (b) combinations, in regions of statistically significant ($p<0.05$ FEW corrected) activation. Our results showed that HRF shape varies across activated regions and, although to a lesser extent, depending on set basis functions.

Changes across activates areas could be related to a different geometry of local vascular structures while differences across set basis functions could be expression of differences in model flexibility, estimate potential errors and different degree of freedom and power of collinear regressors, which depends on the number and type of set basis functions.

In agreement with [1], our results suggest that the choice of the HRF is fundamental to avoid model misspecification and to increase fMRI sensitivity. Moreover, characterizing HRF could be useful in the investigation of neurovascular coupling and its variation with aging and disease, since hemodynamic response is highly correlated to synaptic activity [2].

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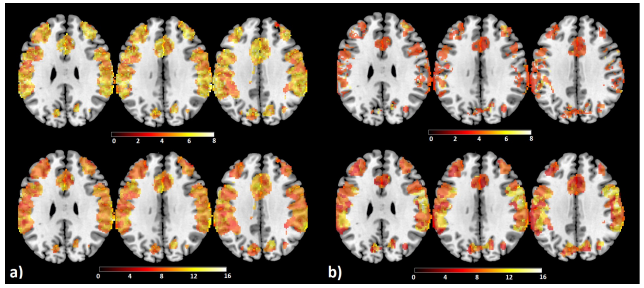

Figure1: Mapping of the HRF FWHM (up) and time-to-peak (bottom) of a representative subjects for the motion processing for (a) gamma functions and (b) sine functions combinations, in regions of statistically significant ($p<0.05$ FEW corrected) activation.

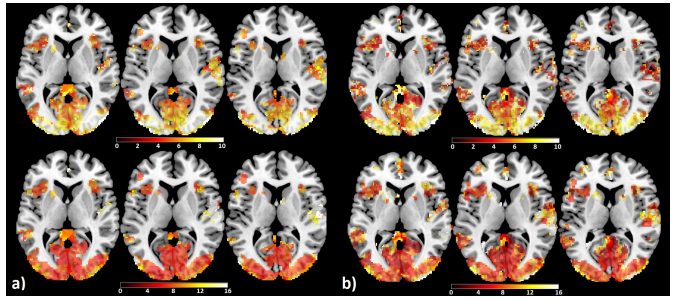

Figure2: Mapping of the HRF FWHM (up) and time-to-peak (bottom) of a representative subjects for the cognitive processing for (a) gamma functions and (b) sine functions combinations, in regions of statistically significant ($p<0.05$ FEW corrected) activation.