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INTRINSIC ACTIVITY

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MEETING ABSTRACT

A2.6

A pseudo-population-based approach for the analysis of pharmacological and naturalistic fMRI experiments

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Background: The classical schemes for functional magnetic resonance imaging (fMRI) experiments comprise block, event-related and mixed designs. These are evaluated using a general linear model (GLM) for fitting the time courses of the different conditions to the data and by comparing the resulting activation maps. However, such restrictive designs hardly mirror everyday situations and the stimuli timing as well as the shape of the physiological responses need to be known in advance. Two less restrictive schemes for which these preconditions do not apply are naturalistic paradigms (such as watching a movie or listening to a conversation) and pharmacological fMRI (phMRI). Inter-subject correlations (ISCs) offer a way to analyze such experiments [1] but provide neither information on the underlying physiological signals nor ways for comparing the different magnitudes of activation. Here, a new analytical model is presented that combines the complementary advantages of the GLM and ISC approaches.

Methods: It is known from the analysis of event-related electroencephalographic data, that the shape of a physiological response can be estimated by averaging over the available epochs / measurements of the study population. Thus, voxel-wise models of the fMRI signal for each subject are calculated as the amplitude-normalized average over all other subjects. By using a simple leave-one-out approach to create pseudo-populations (LOOPP), circularity in the estimation is avoided while model variance is minimized. Activation maps are then calculated as voxel-wise ordinary least-squares fits. The LOOPP method is applied to previously published phMRI data with known response time course [2]. The final results are derived using parametric and non-parametric inferences and compared to the original analysis.

Results: The newly developed LOOPP approach reliably identifies the same activated regions as the previous model-based analysis without requiring any prior information on the shape and timing of the expected response. The derived population model provides the different time courses of the separate regions. Both, parametric as well as non-parametric, inferences result in similar activation patterns.

Discussion: The method introduced here offers a novel and easy approach to analyze fMRI experiments when the underlying model is unknown, which is the standard situation in phMRI and naturalistic scanning. It combines the complementary advantages of the established GLM and ISC approaches and eliminates their respective weaknesses. Different inference strategies yielded comparable results but further investigations are necessary to exactly determine the power and false-positive rate of the LOOPP approach.

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