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Study of cerebral connectivity patterns with neuroimaging techniques.

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Abstract

In this work we investigated the reproducibility of the resting state functional connectivity patterns across 35 healthy subjects when measured by functional magnetic resonance imaging (fMRI). We observed that the presence of motion artifacts can dramatically improve reproducibility of data, although it does not affect the average results.

Key words:

connectivity, fMRI, neuroimaging.

Introduction

Functional Magnetic Resonance Imaging (fMRI) has been largely employed to study brain function at rest over the past decades. The Blood Oxygen Level Dependent (BOLD) signal measured by fMRI reflects spontaneous cerebral hemodynamic fluctuations over time.¹ By comparing the temporal fluctuations of different brain regions one can find cerebral connectivity patterns, which reflects the functional connectivity of the brain at rest.

Based on this approach, several studies have previously characterized functional connectivity networks in the human brain. Most of the studies, however, use averages of a group to identify such networks. In addition, pre-processing steps vary in previous studies, and it is unclear whether some critical pre-processing fMRI steps affect the networks reported in the literature.

In this work, we aimed to investigate: i) how similar the connectivity networks for a single subject is when compared to the average, and; ii) how two important pre-processing steps affect the connectivity patterns reported in the literature. In particular, we investigated how slice-timing correction (STC) and motion artifacts affect the results in BOLD-fMRI functional connectivity.

For that, we collected BOLD-fMRI data from 35 healthy adults (23 ± 5 years old). For each subject, 6-minute baseline runs were performed from 2 to 5 times. At each baseline run subjects were instructed to rest, close their eyes and not to focus on any specific thought (resting state).

For pre-processing, data were smoothed and band-pass filtered (0.009–0.08 Hz) with standard SPM routines gathered in UF²C. We also performed STC and removal of motion artifacts (DRMA) approaches. The processed image was then parcellated into 238 cortical regions,² in which voxels inside the same region-of-interest (ROI) were averaged for ROI-based processing analysis.

For each ROI time series, we calculated the Pearson correlation coefficient (ρ) with all the other ROIs. The calculated ρ 's were organized in a correlation matrix. Then, some ROIs were chosen (based on the literature) as seeds to find the most common functional connectivity maps, such as the default mode network (DMN)^{3,4}, visual network^{3,5}, sensory-motor network^{3,5}, auditory network^{3,5} and higher order cognitive networks^{3,4}.

Results and Discussion

Similar to what has been previously reported in the literature, we successfully found the main connectivity patterns when we considered the average data across all subjects. The networks can be seen with or without the presence of motion artifacts. However, these networks could not be identified for each individual separately when we considered the average of the multiple runs for the same subject. The DMN, for example, was observed only in approximately 50% of all subjects in the cohort. The low reproducibility of the functional connectivity networks appears to be correlated with the presence of motion artifacts. When DRMA were performed in the data, the DMN was seen in 75% of subjects. Similarly, the run-by-run reproducibility was higher after motion artifact removal.

We observed no difference in the appearance of the functional networks related to the STC pre-processing step.

Conclusions

In this study we observed that motion artifacts can influence functional connectivity networks in a single subject. Results reported for an average group, however, does not appear to be affected by motion artifacts. In addition, the use of STC has almost no effects in the connectivity maps.

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