Clinical benefits of resting-state networks identification using high-temporal resolution fMRI sequence

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TARGET AUDIENCE

MRI physicist and researcher in the field of functional connectivity could be interested in this study.

PURPOSE

Functional magnetic resonance imaging (fMRI) is a powerful tool for mapping brain functions. During the past decade, many studies have suggested that the brain shows a default state of activation during rest. BOLD (blood-oxygen level-dependent) signals often exhibit strong low-frequency correlations between distant brain areas that are related to functionally relevant networks. Echo planar imaging (EPI) is the primary imaging sequence used for resting-state fMRI requiring 2-3 seconds TR to acquire multi-slice whole brain coverage. Due to the low sampling rate, ten minutes are commonly used to investigate functional connectivity at rest. Recently, ultrafast fMRI sequences significantly increase the temporal resolution of whole brain fMRI but they decrease the spatial signal-to-noise ratio [1]. The aim of this study was to investigate the benefit of ultrafast acquisitions to be used to substantially shorten the total acquisition time.

METHODS

Functional MR images from fifteen healthy subjects were acquired with a 3T Philips Achieva Scanner over two 10-min scanning runs. The first one was a common EPI resting-state sequence (TR=2.4s, TE=30ms, flip angle of 90°, $3mm^3$ voxel, matrix of 64x64, 40 slices). The second one was an echo shifting approach, PRESTO [1], to increase volume coverage efficiency in fMRI by taking advantage of TE delays to apply additional RF pulses (TR=0.75s, TE=28.85ms, flip angle of 9°, 3.2x3.2x3.4 mm voxel, matrix of 64x64, 45 slices). Pre-processing consisted of 4 main steps: slice timing correction (only for standard EPI sequence) – motion correction – normalization to MNI space – spatial smoothing).

Group independent component analysis (Group ICA) framework was performed on both functional data [2]. The number of components was estimated by minimum description length approach in each dataset and the mean across datasets was selected. ICA algorithm was running 10 times with different initial conditions. Five resting-state networks (RSNs), which are amongst the most reported and studied networks, were automatically identified compared to some templates. These networks, called "RSNsTemp", were: the default mode (DMN), the visual (VIS), the sensory-motor (SMN), the auditory (AUD), and the frontoparietal (FPN) networks.

Then, both acquisitions of each subject were randomly divided into 4 subsets of durations T = {2, 4, 6, 8} minutes. Group ICA approach was performed on each subset. A similarity index was computed between each RSNs maps of subsets and "RSNsTemp" maps.

RESULTS

Figure 1 showed "RSNsTemp" maps from PRESTO sequence. Figure 2 showed Jaccard indexes between RSNs maps from each subset and "RSNsTemp" maps using both acquisitions. The Jaccard index measures the similarity between RSNs regions and is defined as the size of the intersection divided by the size of the union of two RSNs maps. PRESTO sequence had significant improvement for short datasets (2 and 4 minutes). No significant difference were found between 6 or 8 minutes datasets and the whole dataset for PRESTO sequence. Although a significant difference was found between 4 minutes datasets and the whole dataset, the RSNs maps' similarity was correct.

DISCUSSION

This study showed that ultrafast fMRI sequence can be useful to decrease the acquisition timing without loss of information. The comparison method of both acquisition was based on a similarity index. Additional approaches could be used for this step, such as bootstrap analysis of stable clusters [3]. Others fast acquisitions could be used to improve the spatial signal-to-noise ratio of fMRI sequences [4-5]. Finally, the reduced scan time could help the clinical acceptance of resting-state fMRI protocols.

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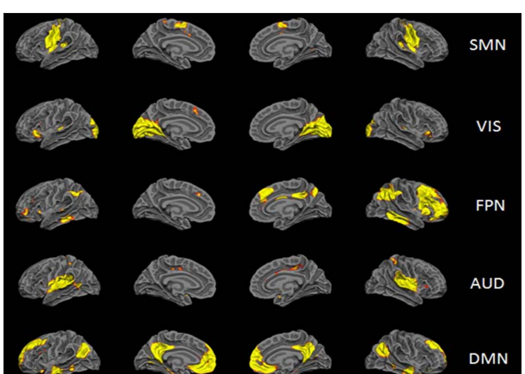

Figure 1: "RSNsTemp" from PRESTO sequence ; Group t-maps thresholded at p<0.05 (FDR) (yellow-red regions correspond to activation).

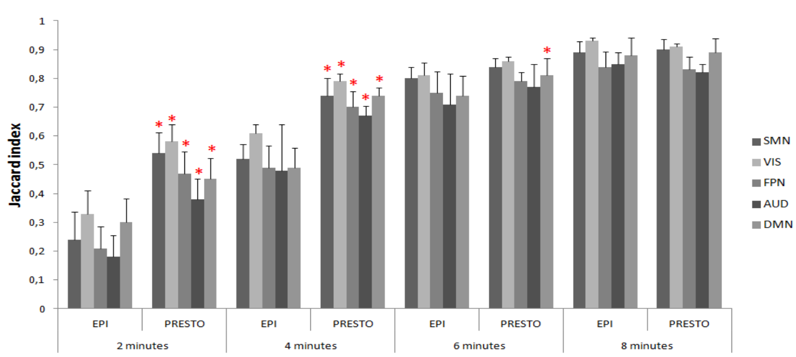

Figure 2: Jaccard index calculated between each RSN thresholded maps from each subset and those corresponding to the whole data. The red narrows indicate the sequence for which the Jaccard index was statistically improved (Mann-Whitney test; p < 0.05).