Spatial consistency of FMRI Resting State Networks across sessions and across subjects

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Introduction

Resting State Networks (RSNs) represent correlations in the brain in the "resting" condition. Previous work [2,3] has showed that the main frequency power is localized around 0.02Hz, thus contributing to low frequency physiological "noise". It has also been shown how to find RSNs using a model-free approach such as ICA [3]. Characterizing the spatial nature of RSNs is important for their interpretation. We studied a group of subjects at rest in order to study the spatial consistency of FMRI RSNs both in a within-subject and in an across subject analyses. The group analysis of RSNs was carried out using probabilistic ICA at the single-session level, followed by cross-correlation of the resulting spatial maps in order to identify patterns consistent across subjects/sessions. We show that 4 distinct RSNs are consistent across sessions and across subjects.

Methods

Within-subject analysis-reproducibility across session. We studied 3 subjects at rest, each in 4 different sessions (3T Varian, EPI, TR=3s, TE=40ms, Number of volumes=200). In order to study the reproducibility of RSNs across sessions, we used probabilistic ICA (PICA [1]) on each data set separately. Then for each subject and for each pair of sessions, we found the correlation between each PICA spatial component found from one session with each component found from the other. To find which PICA map was always present in all the sessions, we applied the RSN-selection algorithm (below). 4 RSNs survived as being consistent across sessions for each subject.

Cross-subject analysis. We studied 7 subjects, 6 at a spatial resolution of 4x4x7mm, TR=3s, TE=40ms, in resting state; 1 at higher spatial resolution (2x2x4mm) but same temporal resolution. First we transformed the PICA maps into standard space and smoothed them slightly (to increase spatial correlations in the case of small local spatial localisation differences in different subjects) using a Gaussian kernel (5 mm FWHM). Next we measured the correlation coefficient between each PICA spatial map of one subject with each PICA map of the next subject. We did this for all pairs of subjects. Next we use the RSN-selection algorithm to automatically identify the PICA maps "most correlated" between all subjects.

RSN-selection algorithm

1. Threshold the correlation coefficient with a pre-set threshold to discard all non-correlating pairs (we use r>0.15, *P<0.00015*).
2. Identify all sets of N PICA spatial maps where each subject's PICA spatial map correlates with every other subject's PICA spatial map.
3. Choose "best" sets of RSNs according to the cost-function of sum of each pairs' cc

We know then which PICA map has a strong spatial pattern common in all the subjects. Once we have the maps we can proceed to do a group analysis. The PICA maps in standard space are averaged together and on the resulting mean PICA map we apply mixture-modelling [1] for inference. Note that the PICA maps are demeaned and variance-normalized to 1. The group analysis is therefore analogous to a fixed-effect analysis on the PICA maps.

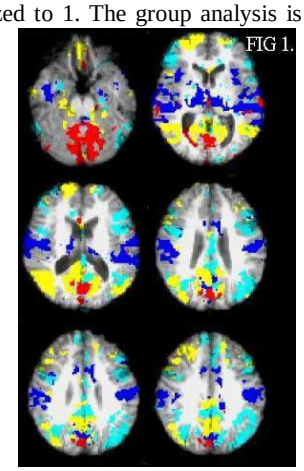
FIG 1.

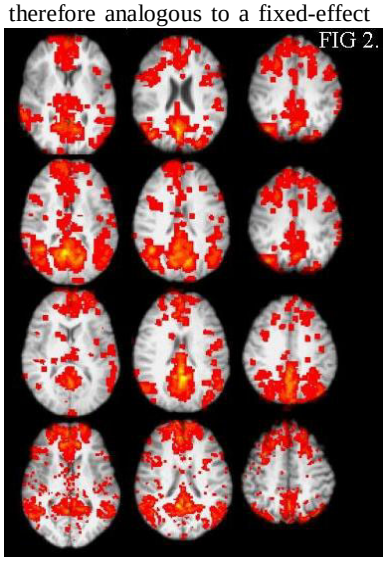
FIG 2.

Results

For the within subject analysis, the RSN-selection algorithm found 4 PICA components, and the highest correlation coefficients were found for the pattern showed in fig2.

In the cross-subject analysis, the RSN-selection algorithm found 5 PICA components, 4 representing RSNs and one clearly representing an artefactual component (falling within the frontal EPI susceptibility artefact). The artefact component was discarded and the group analysis carried out on 4 maps. On the results of the fixed-effect analysis, we run the (alternative hypothesis) mixture-modelling to threshold the results showed in fig1 and fig. 2 (at P>0.5 for "activation" vs null). The mixture-model used is the same as for the complete PICA algorithm (MELODIC, www.fmrib.ox.ac.uk/fsl).

Here we classify the RSNs in terms of brain anatomy and functionality. The maps were therefore summed spatially (associating different colours to different RSNs, fig.1). Where there was spatial overlap, we considered the voxel as belonging to the RSN which had the highest fixed effects Z value. Fig.2 shows one of the original RSNs (the yellow component from fig.1) for 4 subjects. Each row is one subject.

The RSNs can be classified approximately thus:

1. Red: Visual Area (V1, medial occipital cortex).
2. Yellow: Visual Area. Lateral Occipital Lobe, precuneus, medial parietal cortex and posterior cingulate cortex. Same areas as the physiological baseline areas proposed by [4].
3. Dark Blue: Primary and Secondary Sensory Cortex. Anterior Insula Cortex. Pain Area.
4. Light Blue: Attention, Working Memory and Spatial Association Area. Posterior parietal and prefrontal cortex. Activation in the posterior region of the thalamus deputed for Motor Activity.

Conclusion

The results show that RSNs, as found with PICA, are spatially reproducible across sessions and even across subjects. The mechanisms causing these reproducible patterns are still unknown and further experimentation and interpretation is necessary.

References

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