

# Average template for comparison of resting fMRI based on group synchronization of their time series

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## Introduction

Group studies involving in vivo resting fMRI (rfMRI) are challenging since spontaneous brain activity is generally not directly comparable across subjects. Previously, we developed the BrainSync transform<sup>1</sup> that allows synchronization of rfMRI signals at homologous locations across subjects using an orthogonal transform. The resulting transformed time series exhibits high inter-subject correlation at homologous locations. In that work, we used the most representative subject (the subject with the minimum average distance to all others) as a common template for the group study. The limitation of that approach is that synchronization is biased toward the selected reference subject. Here we describe a new method for generating a Joint Synchronized Group Average (JSGA) rfMRI template through iterative estimation of the group average.

## Methods

We use minimally processed rfMRI data from 40 subjects from the Human Connectome Project<sup>2</sup>. We remove the mean and normalize the time series to unit length for each subject. Our goal is to find a set of orthogonal transforms, one per subject, that when applied to the rfMRI data jointly minimize the distance to the average of the transformed data across all subjects. The result is a set of transforms, which map each subject to a common temporal space, and the JSGA template, which is the average across subjects of these synchronized spatial-temporal data sets.

To find the set of orthogonal transforms we used an iterative algorithm<sup>3</sup> to minimize a cost function based on the Frobenius norm of the pairwise differences between each of the synchronized subject datasets and their average. We randomly initialize the orthogonal transform for each subject. We update the transform for each subject in turn, minimizing the Frobenius norm relative to the average template, and then update the template. Each subproblem is quadratic over the group of orthogonal matrices, with the solution at each iteration found using a singular value decomposition. The algorithm converges to a unique solution under reasonable conditions.

In order to visualize how well the JSGA template fits to the sets of rfMRI data, we computed pairwise distances between all pairs of rfMRI data for the 40 subjects as well as the distance of each to the JSGA template. We then used these pairwise distances to perform a 2D multidimensional scaling (MDS) embedding and compared the position of the JSGA template to that of the previous single subject template in Fig. 1. We also computed the vertex-wise average correlation between each subject and each of the two templates, Fig. 2.

## Results

It can be seen from Fig. 1 that the JSGA template lies close to the center of the group in the MDS embedding, indicating that it is representative of the group. In comparison, the single subject template (#135932) lies off-center indicating a larger distance to some of the subjects in this group. Maps of the average correlation confirm this observation, Fig. 2. The average correlation over the entire cortex is 0.36 for the single subject

template but increases to 0.63 for the JGSA template. One factor for increased correlation in case of JGSA template could be denoising due to averaging.

### Conclusion

The results in Figs. 1 and 2 show that the group average template is more representative than the best single subject template. Using this template as the basis for comparison of rfMRI will also avoid bias towards any individual in computing the template. This in turn should facilitate fair comparisons across subjects. Further, the increased average correlation with the JGSA template should be useful for group analysis with possibly increased statistical power relative to the earlier single subject template. Since the orthogonal transform is well conditioned and invertible, the template can also be transformed back into the native space of any individual facilitating calculation of individual differences in space and time for each subject.

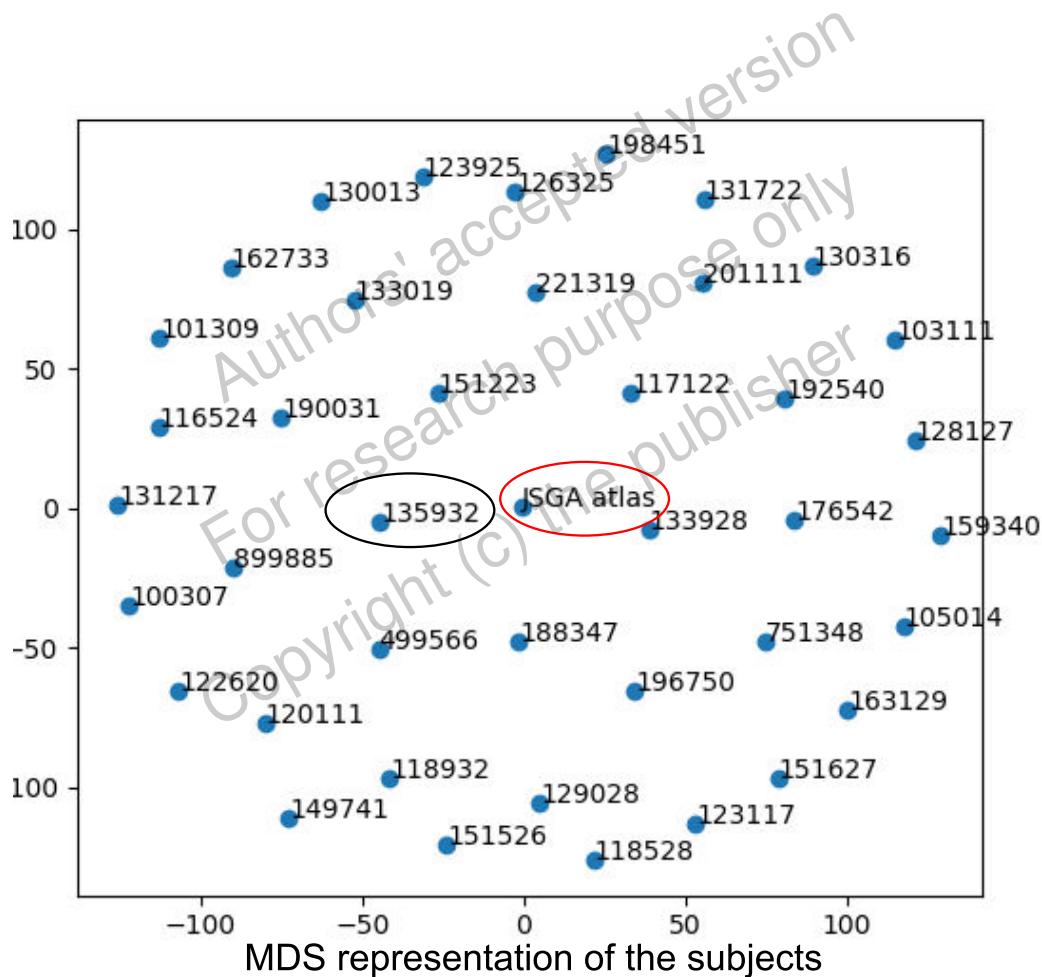


Figure 1: MDS embedding of the 40 subjects and JGSA template based on the rfMRI data. The best representative individual template and the JGSA template are marked

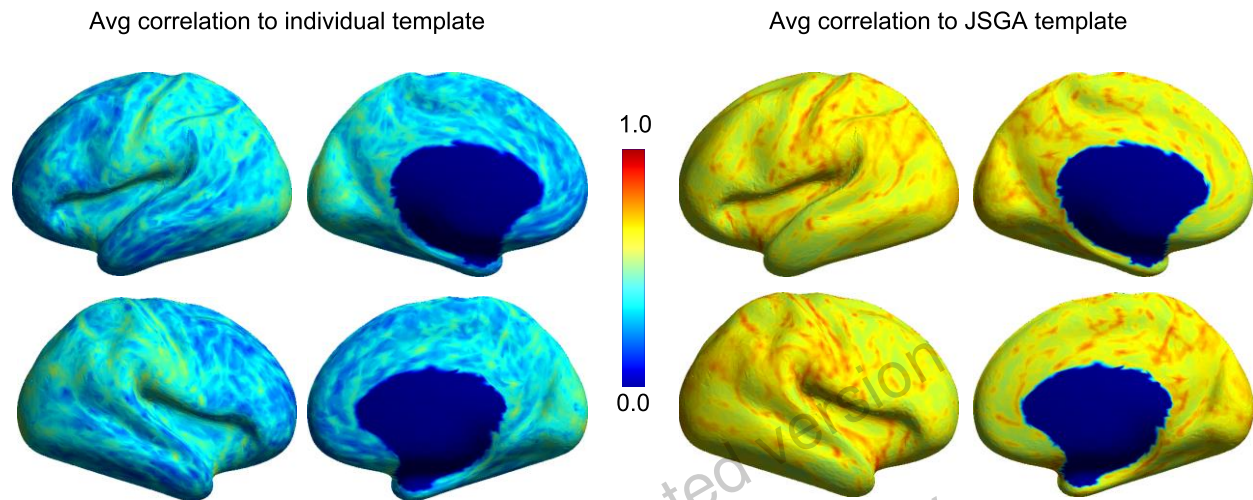


Figure 2: Averaged correlation between the two templates and all the 40 subjects

## References

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