

Poster # 1981 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.
- The BrainSync transform [1] solves this issue by synchronizing each subjects to a 'reference' chosen as the most representative subject (based on minimizing pairwise distances of all subjects from the reference) – see Fig. 1.
- The limitation of this approach is that the study is biased towards 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 as a common template for the group.

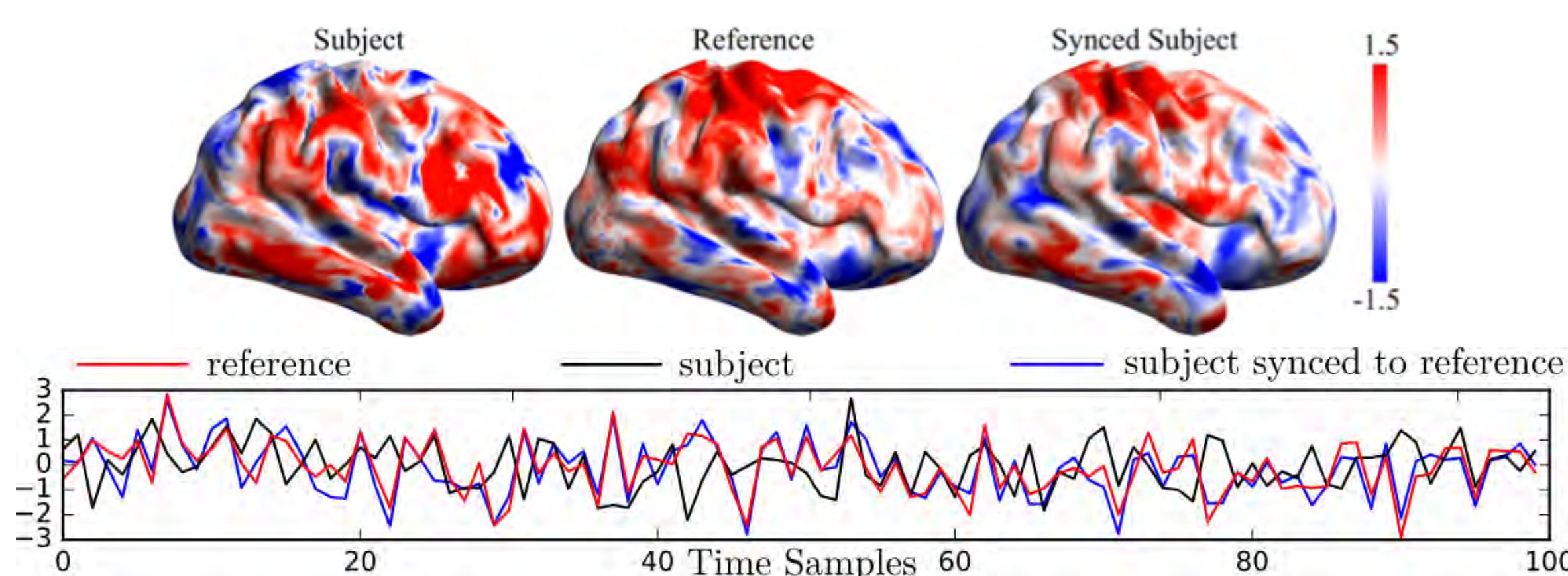


Fig 1 (upper) A single frame of synced data is shown: (left) subject, (middle) reference and (right) subject synchronized to reference; (lower) Representative time-series for two subjects for a single cortical location before and after synchronization from a subject to the reference [1].

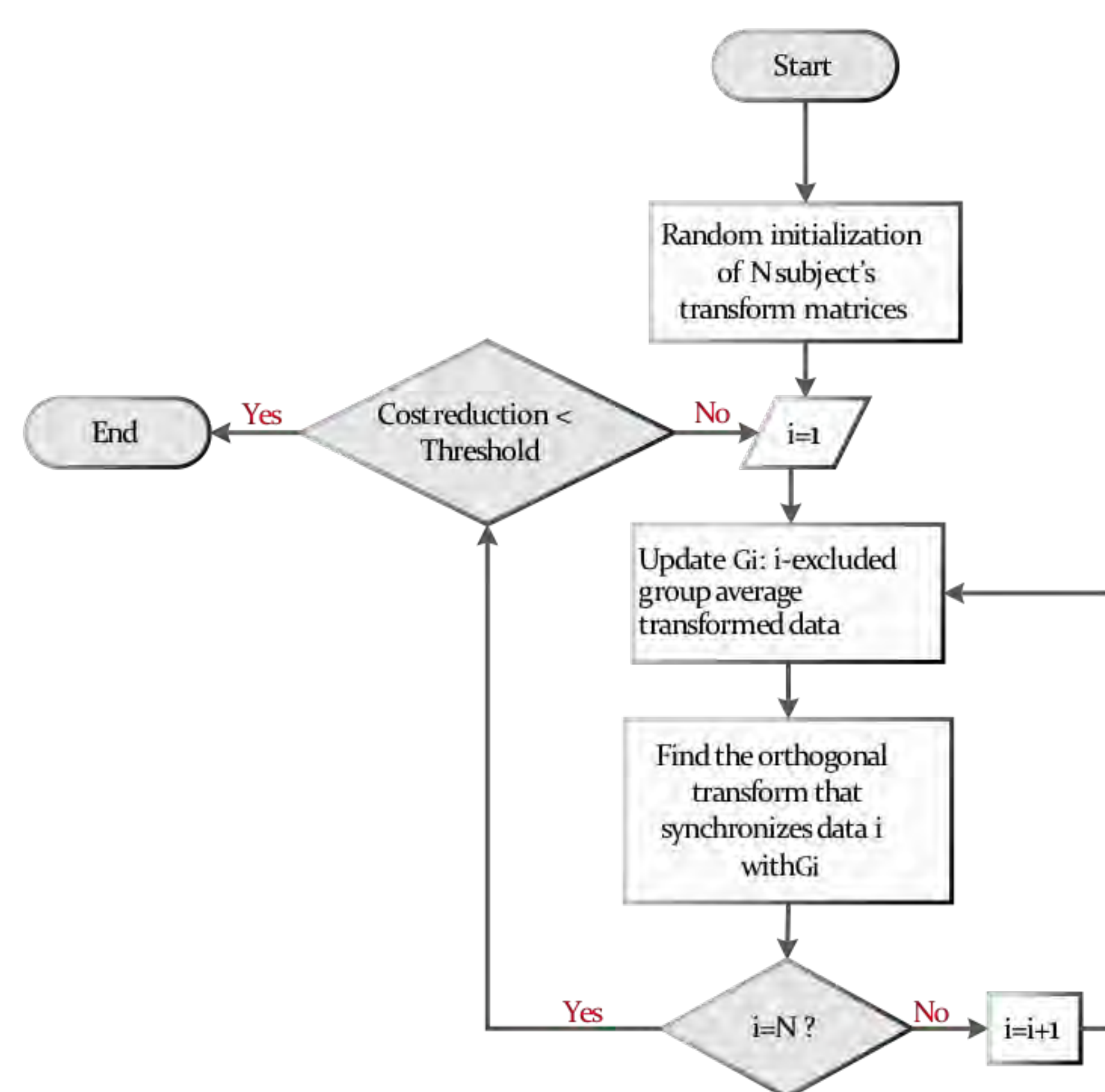
Materials and Methods

- We use minimally processed rfMRI data from 40 subjects from the Human Connectome Project [2].
- We remove the mean and normalize the time series to unit length for each subject producing data X_i for subject i of dimension N voxels/vertices by T time samples.
- Our goal is to find a set of orthogonal transforms, O_i (one per subject), that when applied to the rfMRI data jointly minimize the distance to the average of the transformed data across all subjects.
- This is done by minimizing a cost function based on the Frobenius norm of the pairwise differences between each of the synchronized subject datasets and their average:

$$\arg \min_{O_i (i=1,2,\dots,M)} M \sum_{i=1}^M \|X_i O_i - G\|^2 = \sum_{j=1}^M \sum_{i < j} \|X_i O_i - X_j O_j\|^2$$

$$\text{where } G = 1/M \sum_i X_i O_i, \quad M: \text{Number of subjects}$$

- To find the set of orthogonal transforms we used the iterative algorithm [3,4,5]:



Results

- 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 [1] Fig.2 .
- It can be seen from Fig. 3 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 a little off-center indicating a larger distance to some of the subjects in this group.
- We also computed the vertex-wise average correlation between each subject and each of the two templates, Fig. 4.
- The average correlation over the entire cortex is 0.36 for the single subject template but increases to 0.63 for the JSGA template.

Fig 2. MDS embedding of the 40 subjects and JSGA template based on the rfMRI data. The best representative individual template and the JSGA template are marked

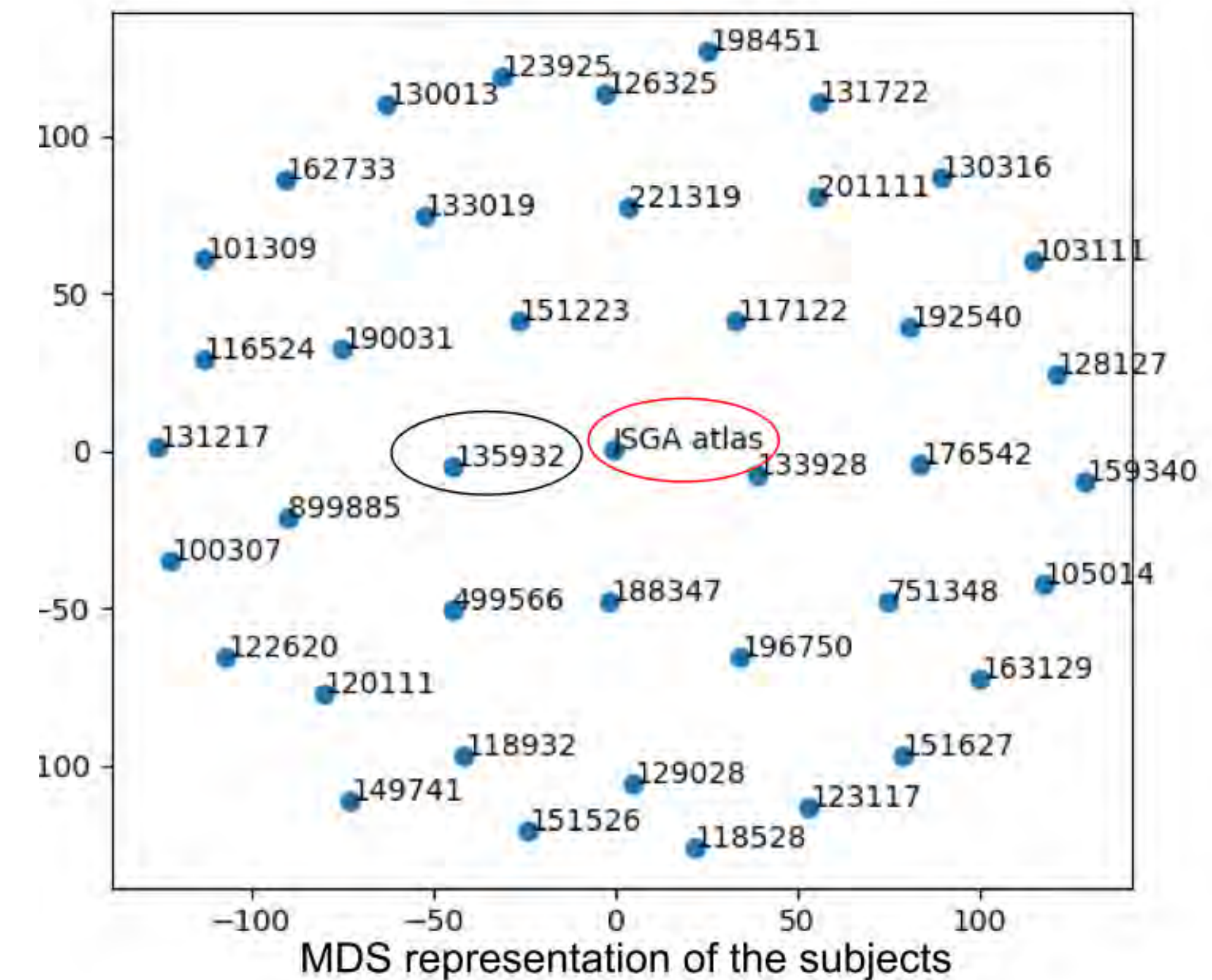


Fig 3. Convergence: using i-excluded (rather than true) mean in algorithm leads to significantly faster convergence. Can be that the shown the associated cost functions are equivalent.

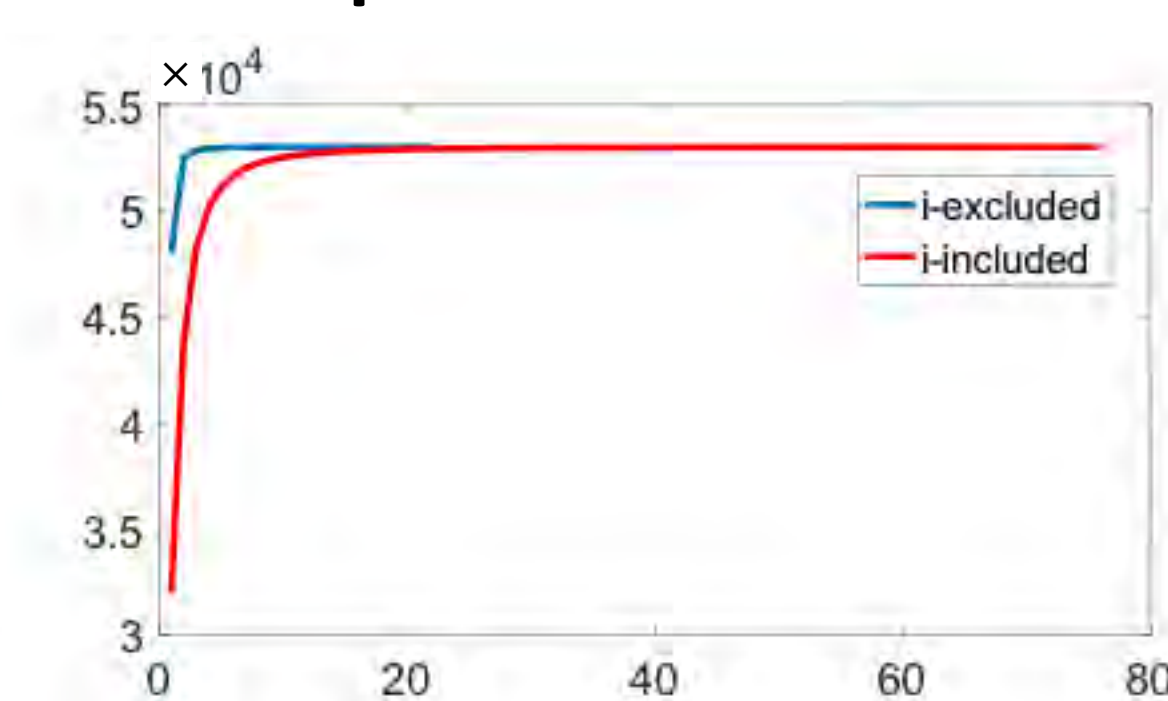
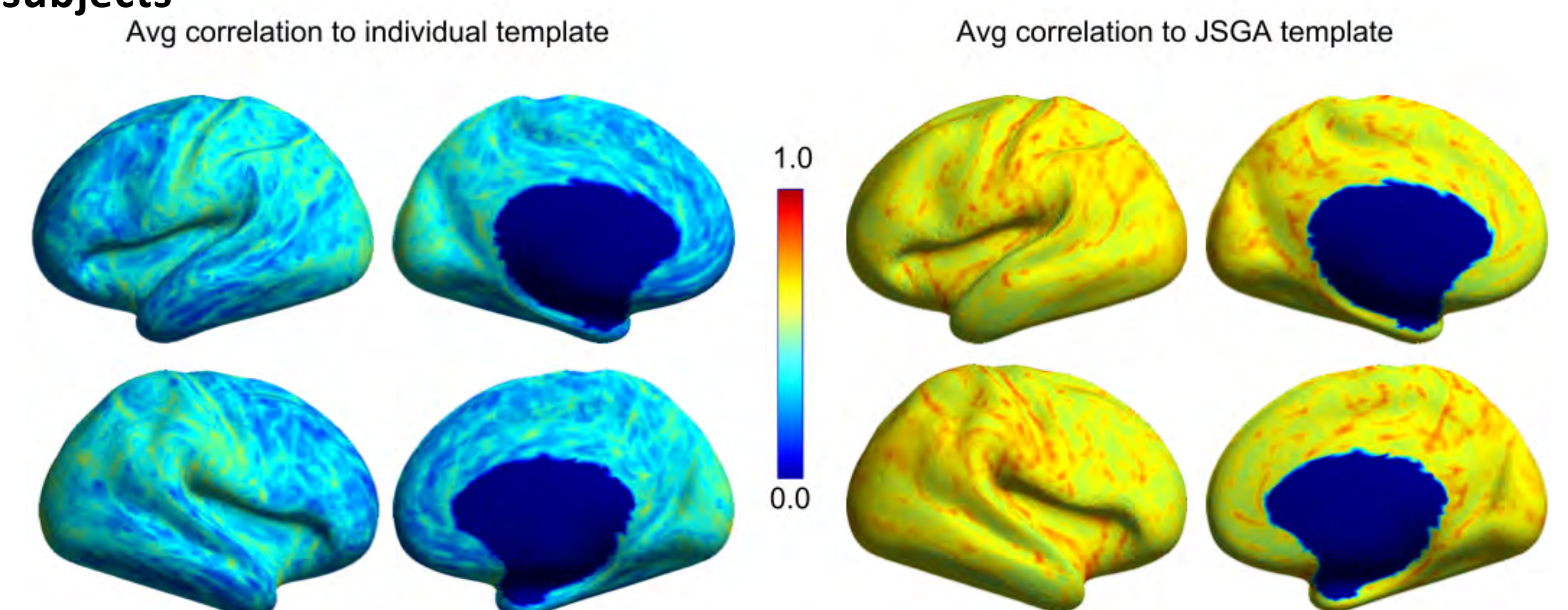


Fig 4. Averaged correlation between the two templates and all the 40 subjects



Discussion and Conclusion

- Using a group average rather than individual subject as template results in closer match of the template to each subject after rotation (Fig. 4) and, equivalently, reduced distance from the template to each subject (Fig. 2).
- Using this template as the basis for comparison of rfMRI will also avoid bias towards any individual in computing the 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.
- We note similarity to hyperalignment [3,5] in which orthogonal transforms are performed with respect to the spatial rather than temporal dimension. A similar group template approach for hyperalignment is described in [5].

References

- Joshi A. A et al. (2018), 'Are you thinking what I'm thinking? Synchronization of resting fMRI time-series across subjects', Neuroimage, vol. 172, pp. 740-752.
- Glasser, M. F et al.(2013). 'The minimal preprocessing pipelines for the Human Connectome Project'. Neuroimage, vol. 80, pp.105-124.
- Chen, P.-H. C et al. (2015). 'A reduced-dimension fMRI shared response model'. Advances in Neural Information Processing Systems, pp. 460-468.
- Ten Berge, J. M. F. (1977). 'Orthogonal procrustes rotation for two or more matrices'. Psychometrika, vol. 42, no. 2, pp. 267-276
- Xu, H et al. (2012). 'Regularized hyperalignment of multi-set fMRI data'. IEEE Statistical Signal Processing Workshop, pp. 229-232.

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