

# Assessing functional hyperalignment of fMRI data through different sample sizes and cognitive tasks



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## INTRODUCTION

Functional hyperalignment (Haxby, 2011) turned out to be an effective multivariate method to functionally align different participants' brain responses that consistently outperforms the more common anatomical alignments. However, it has been applied only on tasks that involved a strong activations of the human ventro temporal cortex.

Here, we explore the robustness of such method under two conditions:

1. We consider time-series referring to **working memory** (WM) and **motor tasks** (MT), involving brain areas different from the ventro-temporal cortex;
2. The relationship between the number of participants considered to build the *commonsense* and the quality of such alignment measured in terms of classification accuracy between conditions;

## METHODS

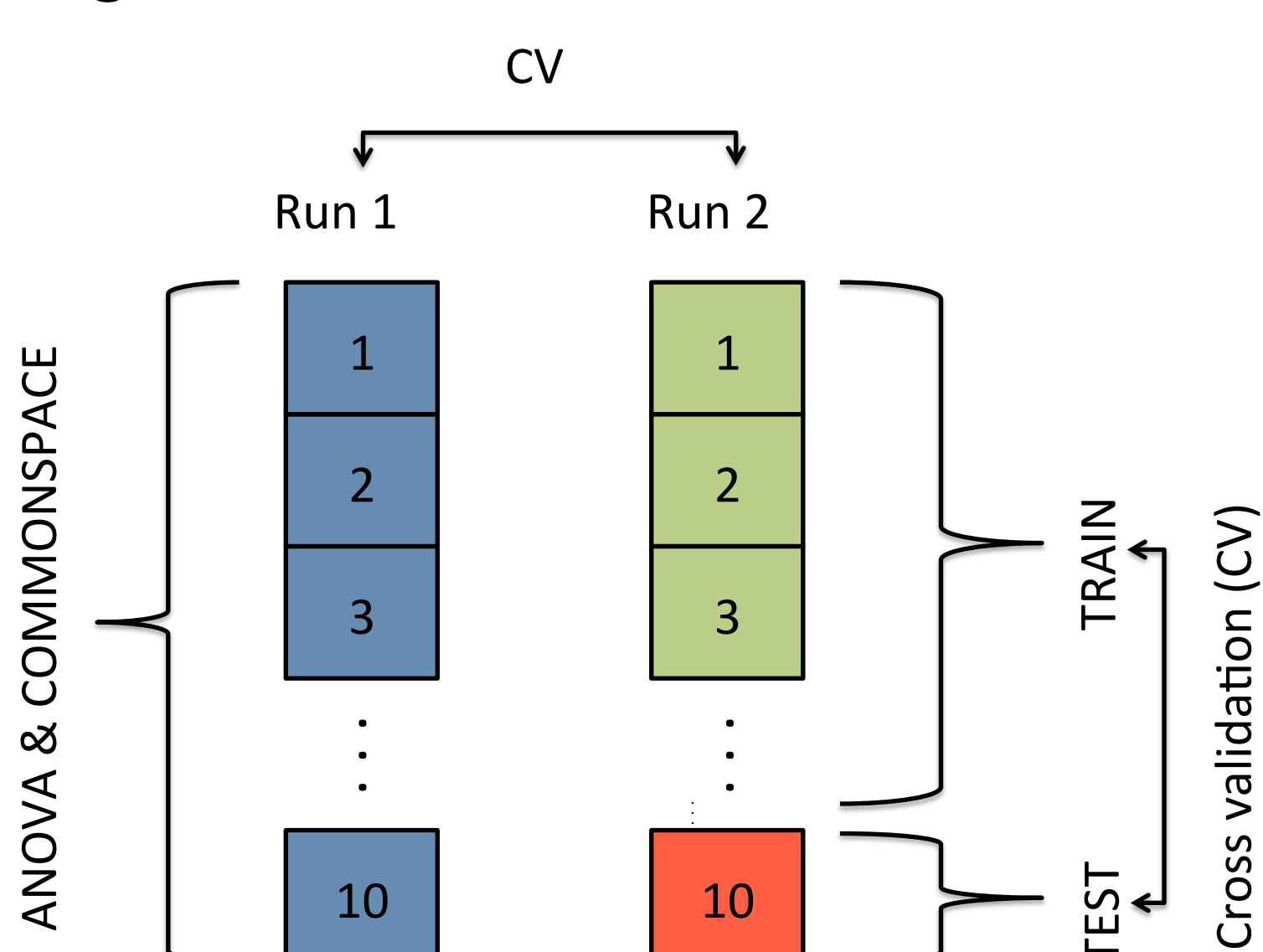
### Dataset

We considered 65 participants of the open dataset "Human Connectome Project (HCP)"[3]. We focused on 2 experiments made up of 2 runs. In one, participants underwent a category representation / working memory (WM) task and in the other a motor task (MT).

### fMRI data preprocessing

The dataset were provided in a standard (MNI) space. First, we performed motion correction with respect to a reference volume on both runs. We then removed linear trends and smoothed using a isotropic gaussian kernel (FWHM = 4mm). Brain regions mask were manually created on the Harvard-Oxford Atlas using spatial information of previous works.

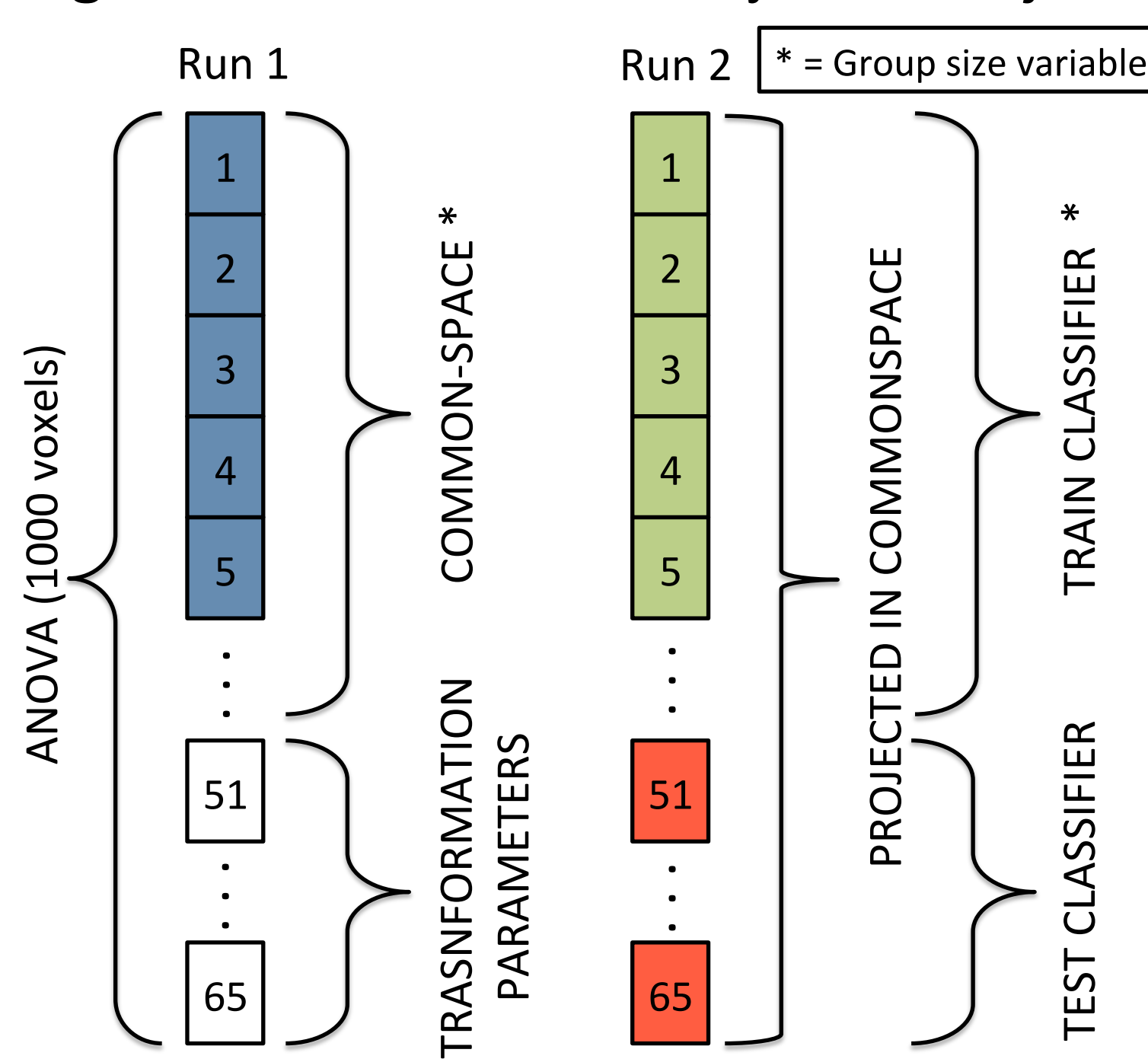
**Fig.1** Methods for WM and Motor task



### WM and Motor task analysis

- Voxel selection (run1):**
- ANOVA top 1000 voxels
- Commonspace (run1):**
- 10 participants
- Classification (run2):**
- Linear Support Vector Machine
  - Leave-one-out partitions by cross-validations

**Fig.2** Methods for scalability over subjects

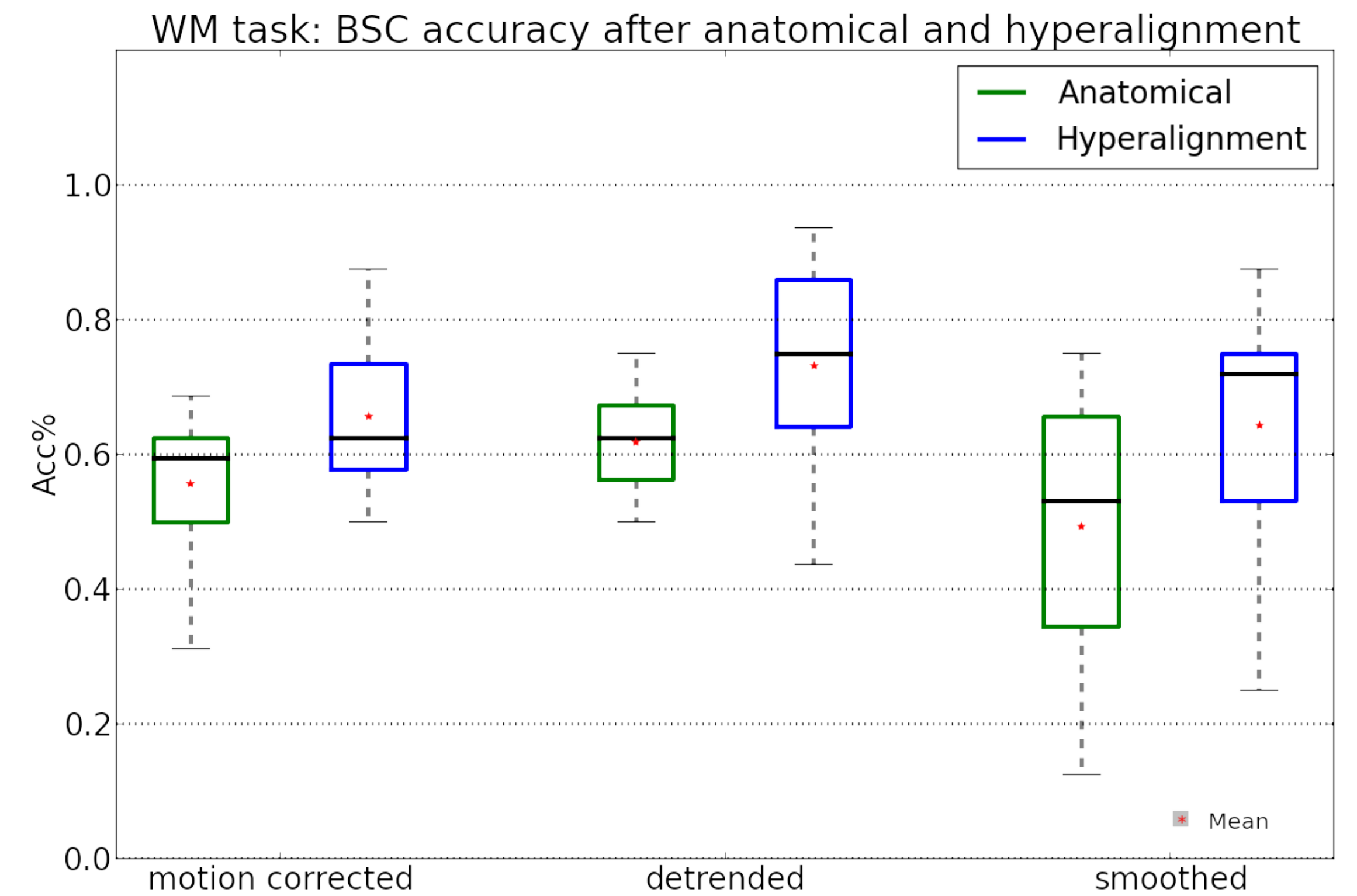


### Effect of group size for building the commonsense

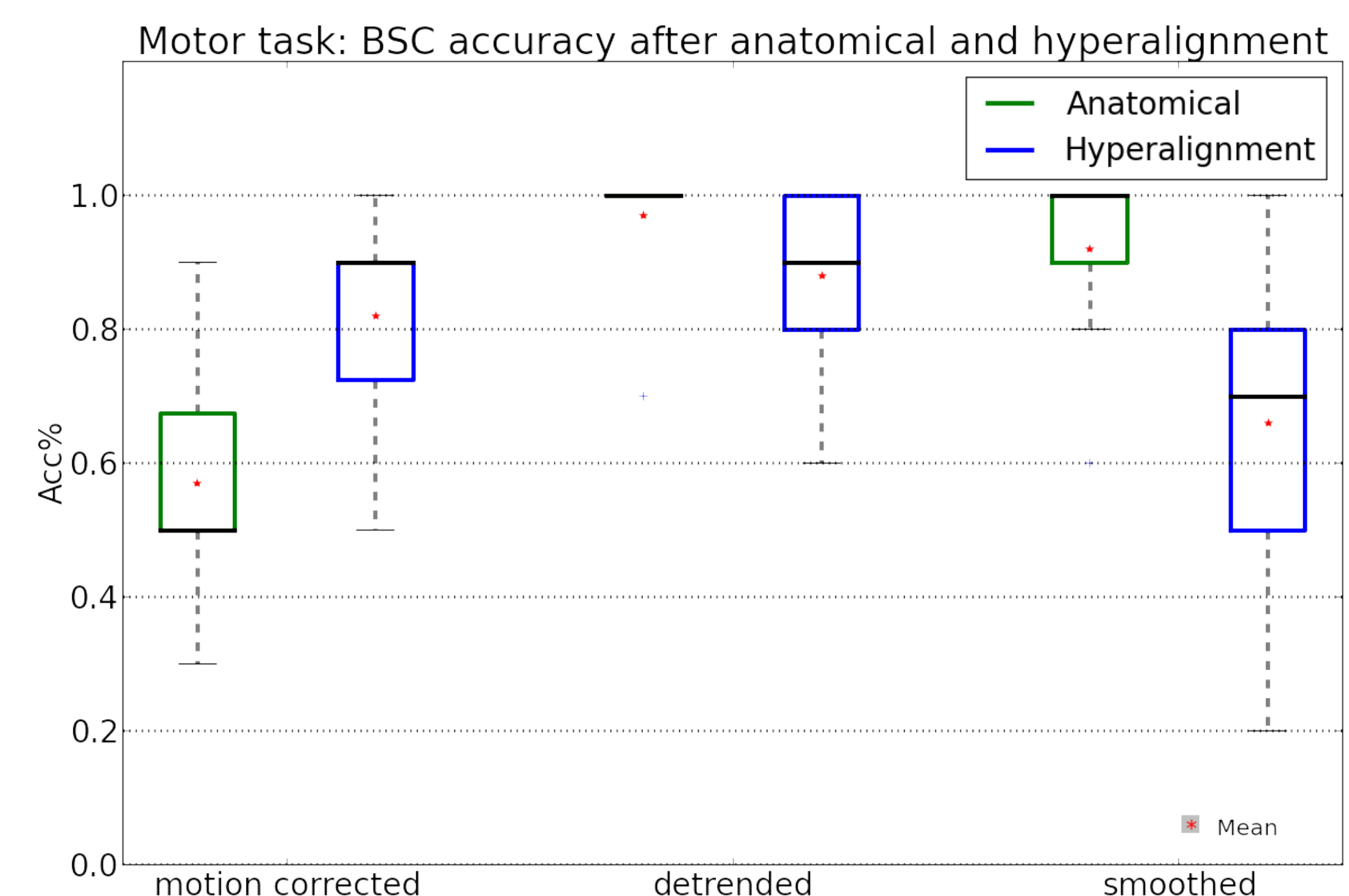
Replicated as WM and Motor but train and test set independent

- Commonspace (run1):**
- Train had different sizes (10...50 step=5)
- Classification train (run2):**
- Size of 10, 20 or 30
- Classification test (run2)**
- 15 participants
- resampling

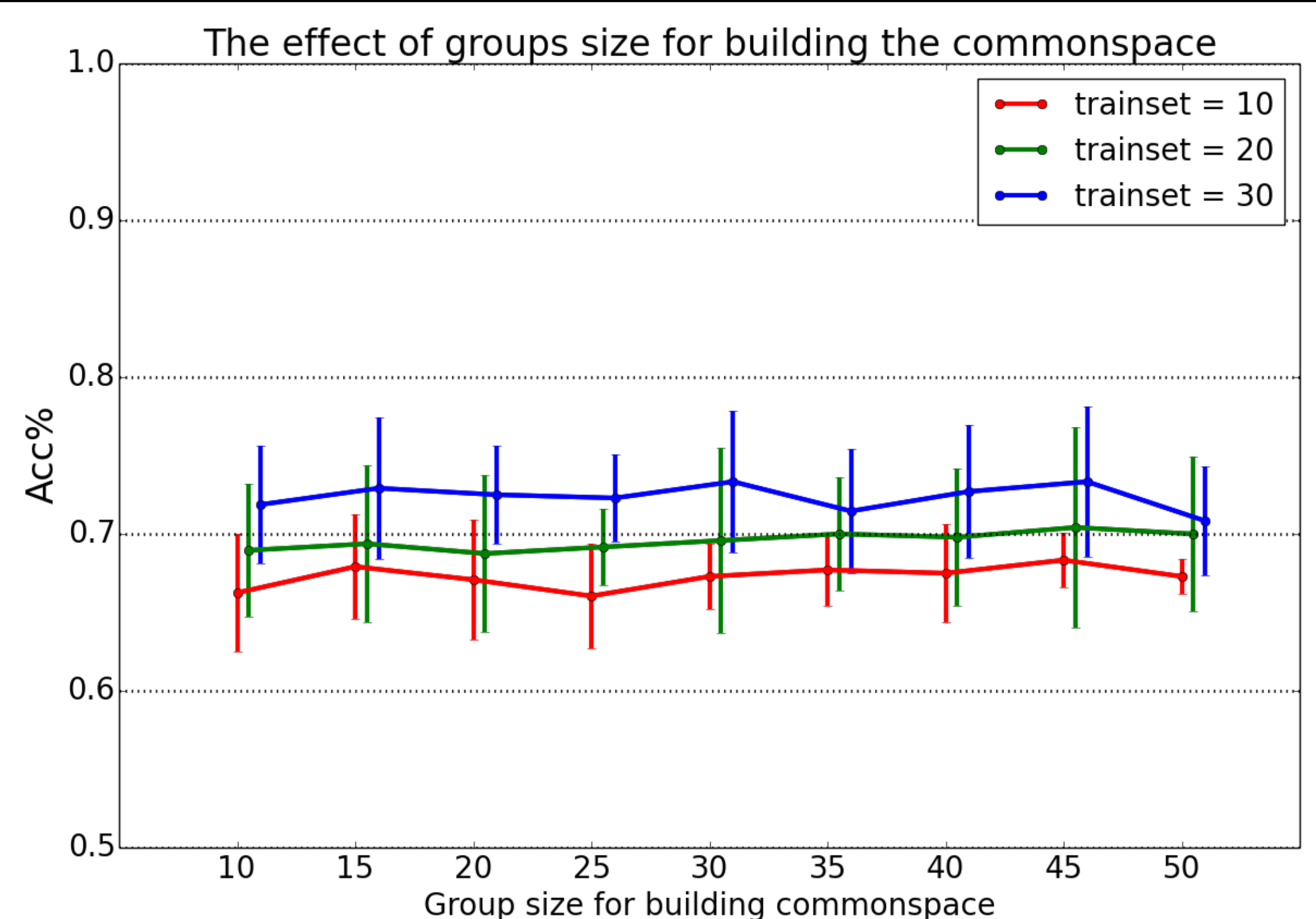
## RESULTS



**Figure 3.** Working-memory task. Classification accuracy over four categories (Place, Face, Body, Tools) under two alignments (Anatomical and Hyperalignment) and three different preprocessing steps (motion correction, detrending, smoothing). Hyperalignment perform better than plane Anatomical alignment for most preprocessing steps. Furthermore, while removing trends significantly increase the sensibility of our classifier, the smoothing negatively affect the quality of our data.



**Figure 4.** Motor task. Classification accuracy over 5 movements (Left hand, right hand, left foot, right foot, tongue). Here, anatomical alignment seems to perform better (detrending around 97% accuracy) than hyperalignment. It might be an effect of the different feature selection methods required by the theoretical implications of both alignments.



**Figure 5.** Scalability. In the y axis is shown the classification accuracy for training set of variable size. Labels on the x axis refer to the number of participants used for building the commonsense.

## CONCLUSIONS

- Hyperalignment can be applied on tasks and areas of the brain others respect to category representation task that mainly involved activations on the ventro-temporal cortex.
- No effect can be measured by adding more participants on the process of building the commonsense, while increasing the training set improve classifier performance.

## REFERENCES

- [1] Haxby, J. V., Guntupalli, J. S., Connolly, A. C., Halchenko, Y. O., Conroy, B. R., Gobbini, M. I., Hanke, M. & Ramadge, P. J. (2011). **A Common High Dimensional Model of the Representational space of the Human Ventro Temporal Cortex**, *Neuron*, 72, 404-416.
- [2] Hanke, M., Halchenko, Y., Sederberg, P. B., Hanson, S. J., Haxby, & Pollmann, S. (2009), **PyMvPA: A python toolbox for multivariate pattern analysis of fMRI data**,
- [3] <http://www.humanconnectomeproject.org>