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Elodie Germani, Elisa Fromont, Camille Maumet

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Exploring variability patterns in the task-fMRI analytical space

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Authors:

ELODIE GERMANI¹, Fromont Elisa², Camille Maumet³

Institutions:

¹Univ Rennes, Inria, CNRS, Inserm, Rennes, Bretagne, ²Univ Rennes, IUF, Inria, CNRS, IRISA, Rennes, Bretagne, ³Inria, Univ Rennes, CNRS, Inserm, Rennes, France

First Author:

ELODIE GERMANI

Univ Rennes, Inria, CNRS, Inserm
Rennes, Bretagne

Co-Author(s):

Fromont Elisa

Univ Rennes, IUF, Inria, CNRS, IRISA
Rennes, Bretagne

Camille Maumet

Inria, Univ Rennes, CNRS, Inserm
Rennes, France

Introduction:

Neuroimaging workflows are highly flexible with many possible choices at each step of an analysis (Carp, 2012). In a recent study (Botvinik-Nezer et al., 2020), 70 research teams were asked to analyze the same task-fMRI dataset with their favorite pipeline to answer the same set of pre-defined research questions. In the end, each team used a different pipeline and results varied in terms of final activation maps and conclusion to binary hypotheses. This phenomenon effectively puts into question the validity of published results and calls for dedicated methodologies to handle this new level of variability (Dafflon et al., 2020).

But the pipeline-space is especially large and challenging to investigate due the pipeline's sensitivity to particular properties of the data under study. A better understanding of the relationships between results coming from different pipelines is essential in order to reuse existing and develop new methods to tackle this variability, for instance using style transfer (Isola et al., 2018) across pipelines.

To explore this pipeline-space, we propose the use of dimensionality reduction and clustering methods to visualize and assess distances between statistic maps generated by different pipelines in task-fMRI.

Methods:

We used data of the motor task from the Human Connectome Project (HCP) release S1200 analyzed with pipelines in SPM and FSL with different options: smoothing kernel (5 or 8mm), motion regressors included in

the design (0, 6 or 24) and the use of derivatives for the HRF. A total of 24 pipelines were applied to each subject of and each base contrasts (hand/foot/lip and right/left). We analyzed the data of 400 subjects and performed a group-level analysis on 50 randomly sampled subjects as well as on the 400 subjects to assess the mean effect in the group.

To explore the relationships across pipelines, we performed different types of clustering. First, we reduced the dimension of statistic maps using a PCA and clustered data using a K-mean algorithm. We also computed the correlation matrices between maps of different pipelines and clustered these using Ward clustering.

Results:

Fig. 1A shows the first two components of a PCA applied to the maps of contrast "right hand" with different pipelines, clustered using K-means. Maps are mainly clustered depending on the analysis software used (SPM vs FSL) but also on other parameters such as the use of HRF derivatives for SPM clusters. In both cases, a small cluster is identified, separated from the large FSL cluster, with the main characteristic of these pipelines being the use of the derivatives of the HRF and the absence of motion parameters.

Visually, the mean statistic maps for each cluster (Fig. 1B) show different patterns. Maps of clusters composed of SPM pipelines with no HRF derivatives and FSL pipelines except the two outliers mentioned above, seem closer than those of clusters containing SPM pipelines with HRF derivatives and the two FSL outliers.

Fig. 2 shows the clustered correlation matrices of the statistic maps for the contrasts "right hand", "right foot", "left hand" and "left foot". Depending on the contrast and on the group of subjects, statistic maps are clustered differently. However, for 7 clusterings out of 8, the two FSL pipelines mentioned earlier are still in a specific cluster, distant from the other FSL pipelines.

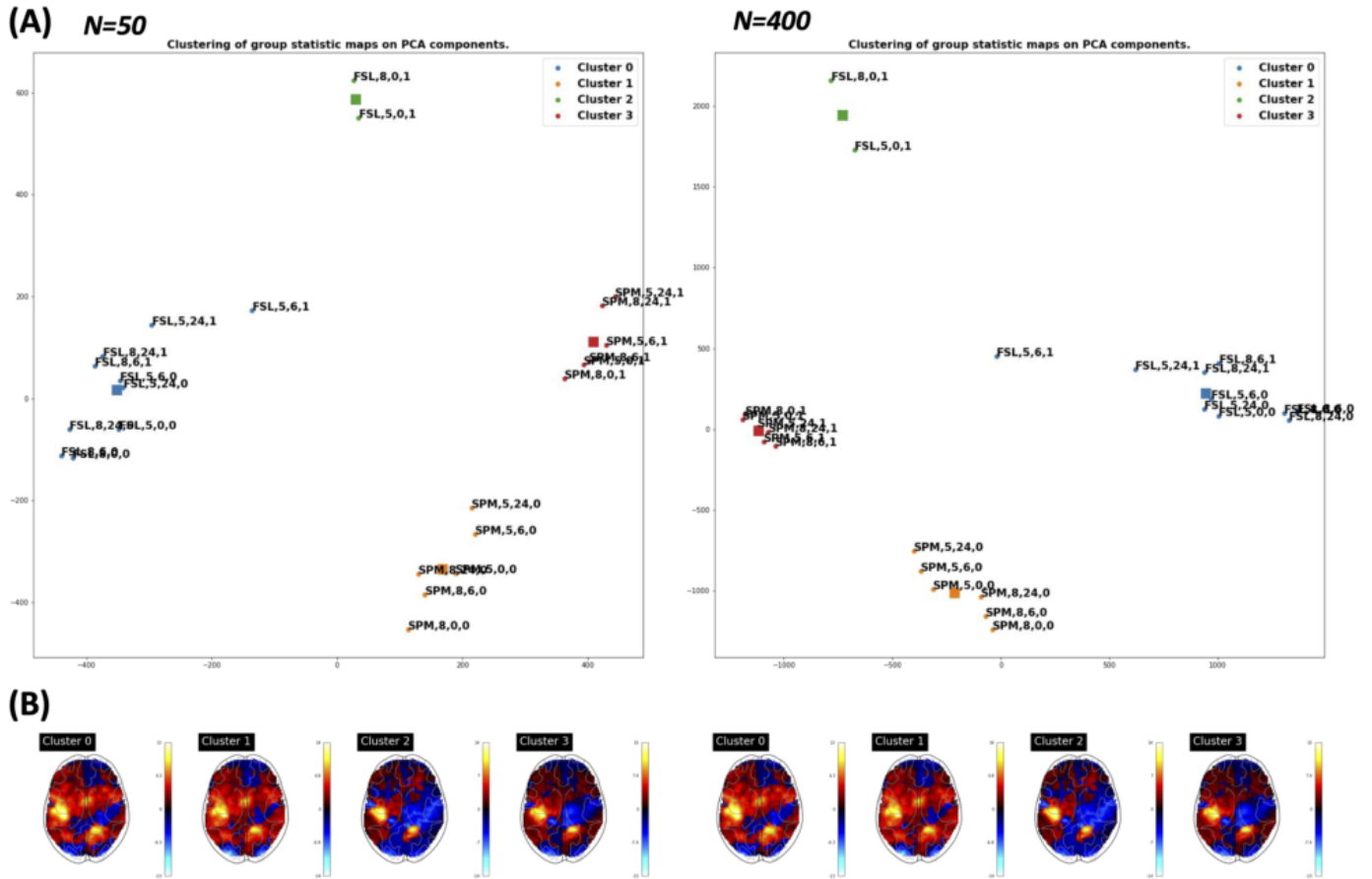


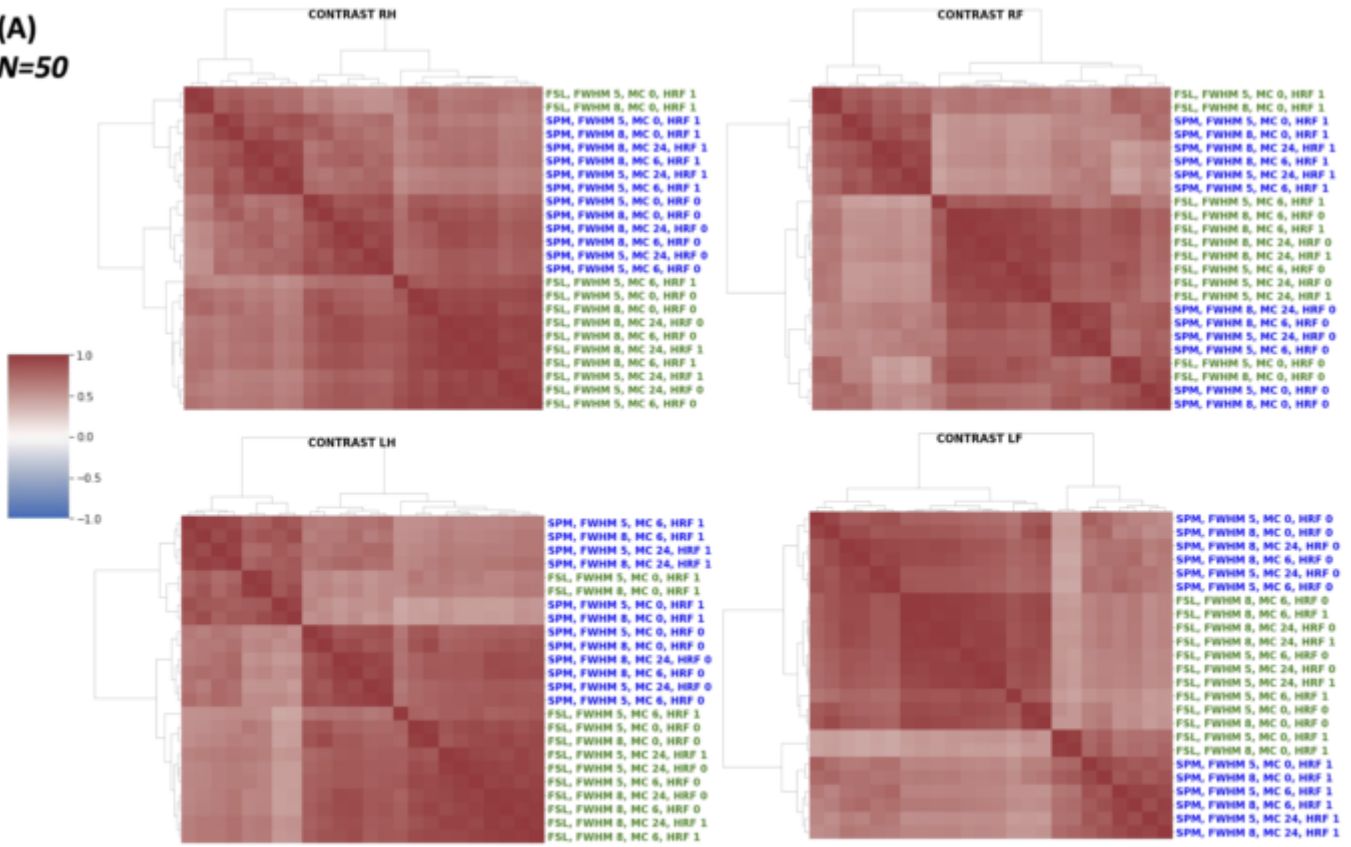
Figure 1. Variability of group statistic maps (n=50) of contrast right hand.

(A) K-mean clustering on PCA components of the statistic maps. For each point, annotations are of the form “Software (FSL or SPM), Smoothing kernel (5 or 8), Number of motion parameters (0, 6 or 24), Presence (1) or absence (0) of HRF derivatives”.

(B) Mean statistic maps for each cluster represented in (A).

For (A) and (B), left part of the figure corresponds to group statistic maps obtained with a group of N=50 subjects and right part to a group of N=400 subjects. Clusters look similar (same pipelines in the same clusters) between the two analyses but the mean statistic maps associated with each cluster look more distant.

(A)
N=50



(B)
N=400

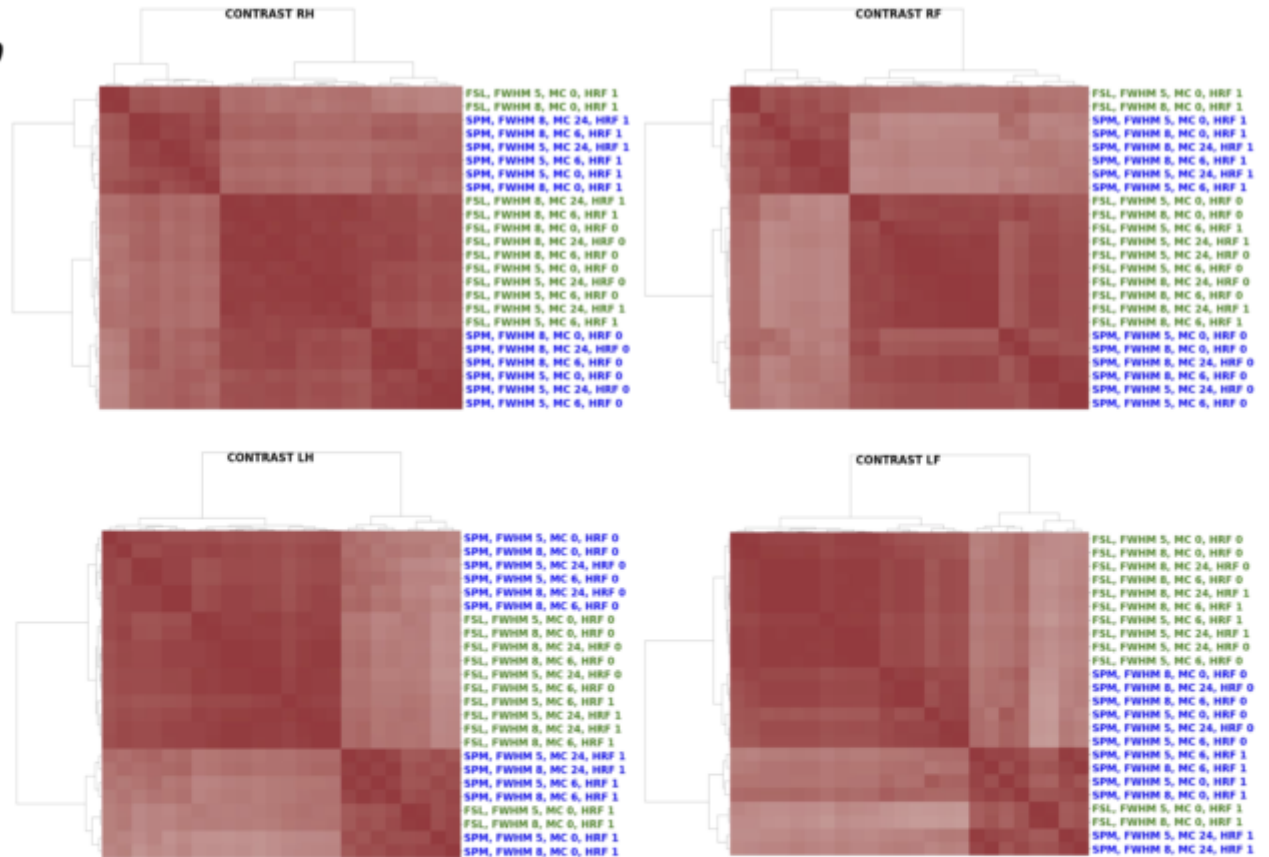


Figure 2. Hierarchical clustering of group-level statistic maps for different contrasts.

Correlation matrices of statistic maps of each contrast obtained with different pipelines are clustered using Ward clustering. Ticks correspond to the specific parameters of each pipelines: "DATASET_SOFT_FSL_FWHM_8_MC_PARAM_6_HRF_0" corresponds to a pipeline implemented in FSL software package, a smoothing kernel of 8 mm, use of 6 motion regressors and no use of HRF derivatives. For a better visualization, FSL pipelines are colored in green and SPM ones in blue. Contrast RF = "right foot", RH = "right hand", LH = "left hand", LF = "left foot".

(A) Corresponds to clustering of group maps with N=50 subjects, (B) with N=400 subjects.

Clustering patterns are different between contrasts, but also between groups highlighting the difficulty of analyzing the pipeline space.

Conclusions:

With this work, we aim at studying the effect of pipeline choice on statistic maps, visualize clusters of pipelines and evaluate distance between different clusters. Our findings show that pipelines have different behaviors depending on contrasts, probably due to particular properties of the data. Some pipelines give closer results than others, especially those sharing specific parameters. Further work will be needed in order to determine specific patterns of the clusters, understand why some pipelines behave differently and how to use these patterns to tackle analytical variability with, for instance, style transfer techniques.

Modeling and Analysis Methods:

Activation (eg. BOLD task-fMRI)

Neuroinformatics and Data Sharing:

Workflows ¹

Informatics Other

Novel Imaging Acquisition Methods:

BOLD fMRI ²

Keywords:

Data analysis

FUNCTIONAL MRI

Machine Learning

Workflows

Other - Clustering

¹²Indicates the priority used for review

Abstract Information

My abstract is being submitted as a Software Demonstration.

No

Please indicate below if your study was a "resting state" or "task-activation" study.

Task-activation

Healthy subjects only or patients (note that patient studies may also involve healthy subjects):

Healthy subjects

Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.

Not applicable

Was any animal research approved by the relevant IACUC or other animal research panel? NOTE: Any animal studies without IACUC approval will be automatically rejected.

Not applicable

Please indicate which methods were used in your research:

Functional MRI

Which processing packages did you use for your study?

SPM

FSL

Provide references using author date format

Botvinik-Nezer et al. 2020. « Variability in the analysis of a single neuroimaging dataset by many teams ». Nature 582 (7810): 84-88. <https://doi.org/10.1038/s41586-020-2314-9>.

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