Generalized Procrustes problem allows to estimate subject-specific functional connectivity in fMRI data

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Metodi e tecniche per lo studio delle differenze individuali

nelle neuroscienze e nella psicologia cognitiva

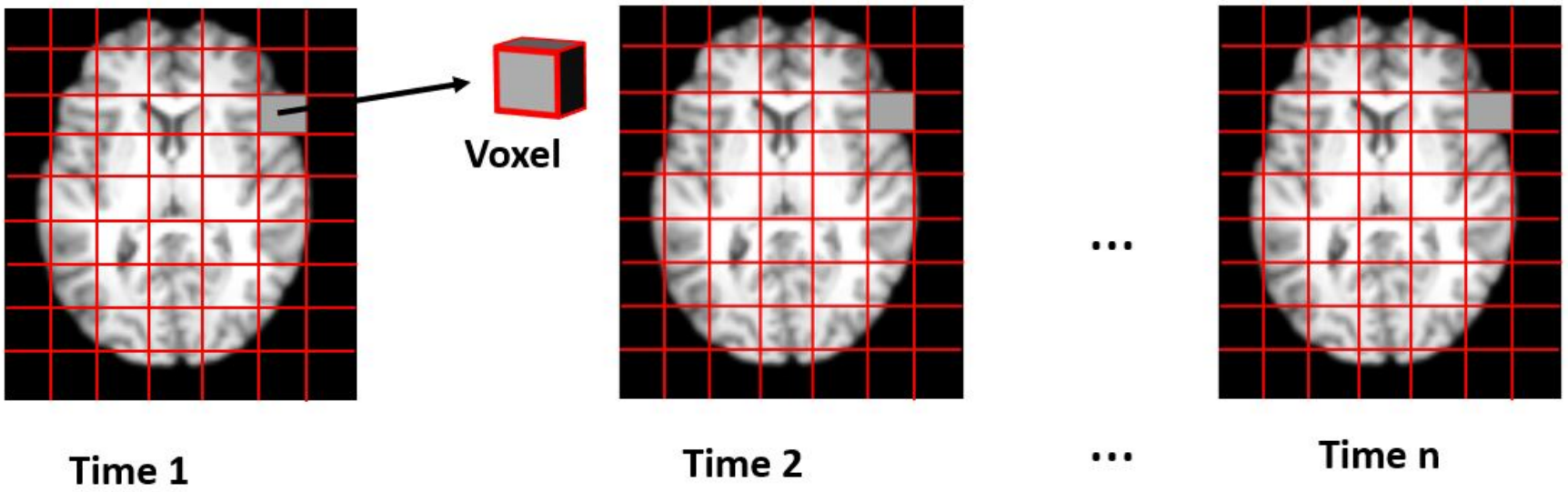
Multi-subjects fMRI studies permit to compare studies across subjects, to generalize and to validate the results.

The anatomical and functional structure of brains vary across subjects even in response to identical sensory inputs.

ALIGNMENT STEP

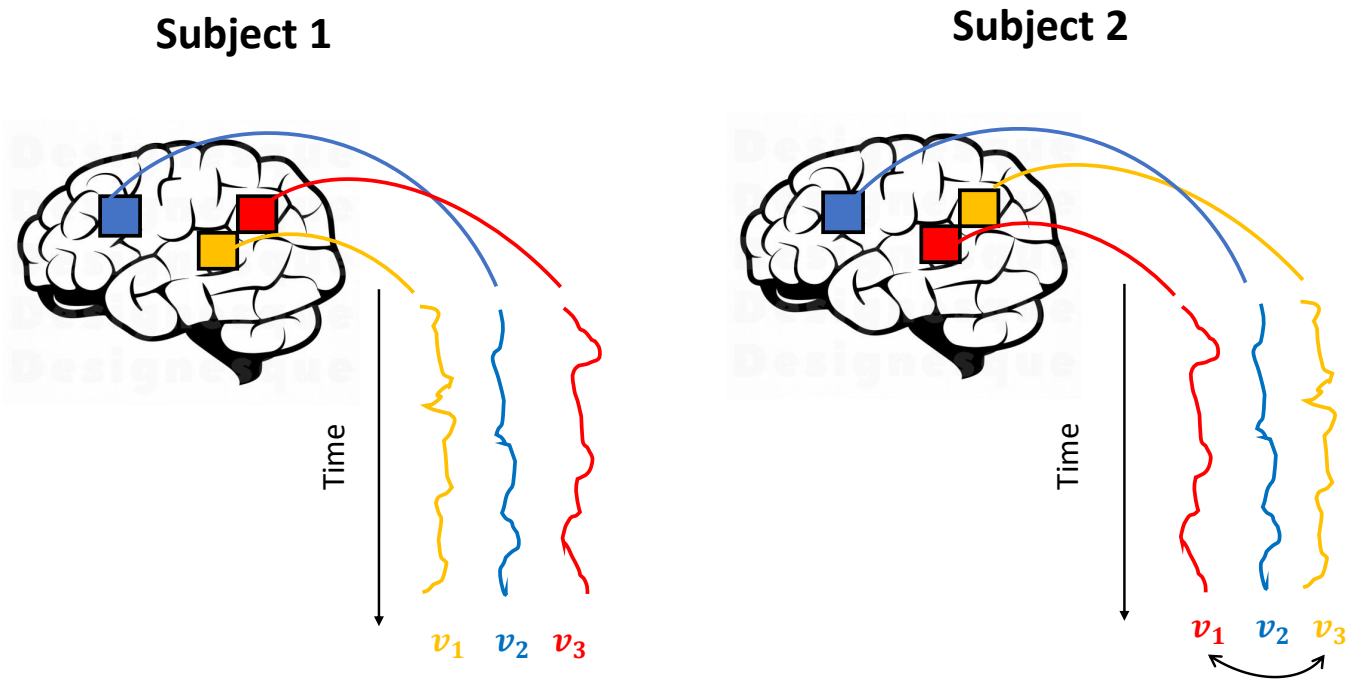
- **Anatomical Alignment**: Talairach normalization [1];
- **Functional Alignment**: Procrustes Method [2] - Hyperalignment [3].

[1] Talairach, J. J. and Tournoux, P. (1988)
[2] Gower, J.C. and Dijksterhuis, G.B. (2004)
[3] Haxby et al. (2011)



Each subject *i* is represented by a matrix $\mathbf{X}_i \in \mathbb{R}^{n \times v}$:

- the **rows** represent the **response stimuli activation** of voxels
  → the stimuli are time synchronized
- the **columns** represent the **time series of activation** for each *m* voxel
  → not assumed to be in correspondence across *N* subjects.



We can assume that the neural activities in different brains are **noisy rotations of a common space**.

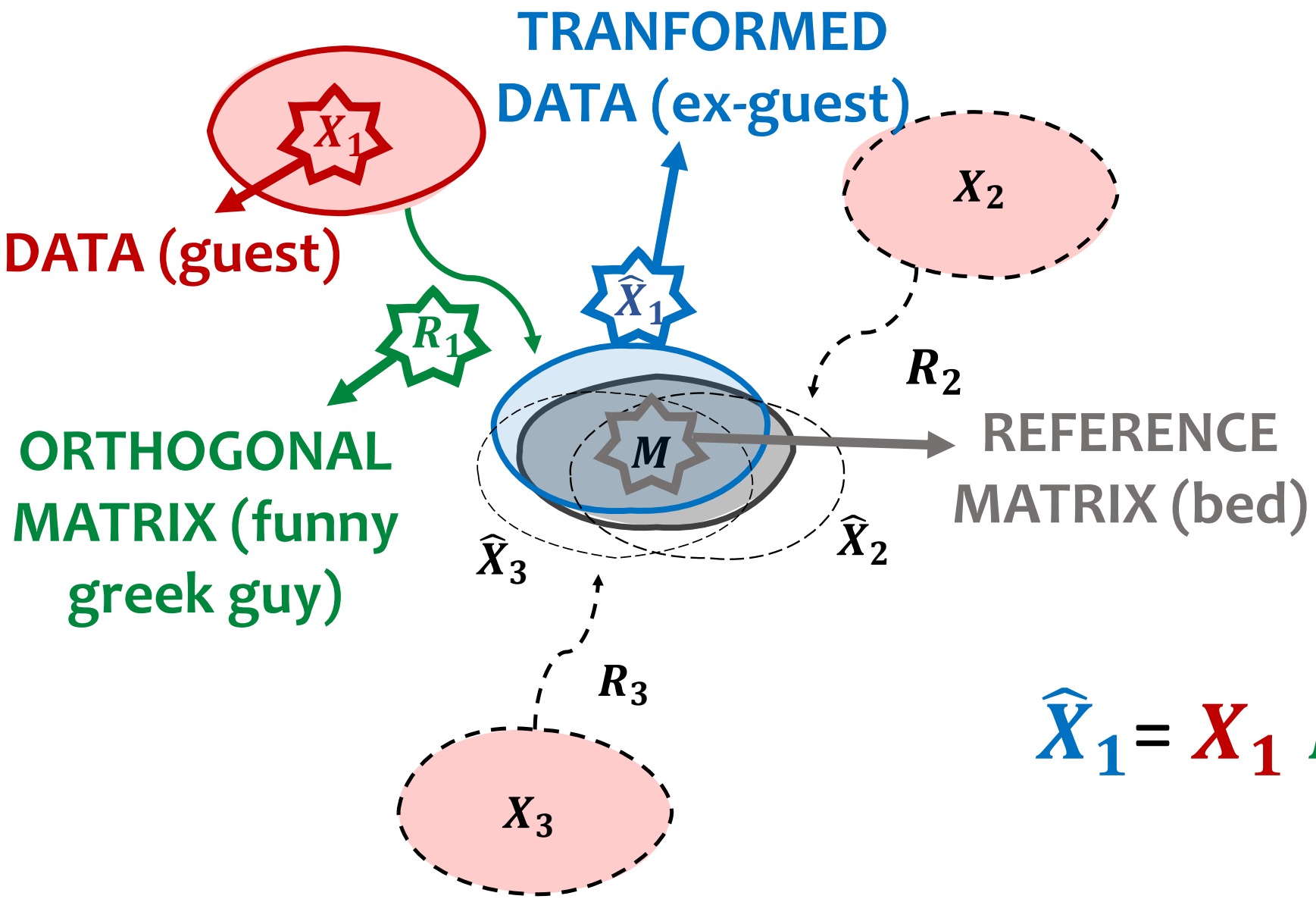
The **Procrustes** method uses **similarity transformation** to match matrices onto the **reference** one as close as possible.

$$\min_{\mathbf{R}_i} \sum_{i=1}^{N} \|\mathbf{X}_i - \mathbf{M}\mathbf{R}_i^{\top}\|_F^2 \quad \text{subject to} \quad \mathbf{R}_i^T \mathbf{R}_i = \mathbf{I}_v$$

IN A NUTSHELL

Find the **best orthogonal** matrix-transformation that **MINIMIZE THE DISTANCE** between $\mathbf{X}_i$'s (guest) and M (bed)

Procrustes Method



$$\hat{X}_1 = X_1 R_1$$

We rephrase the Procrustes method as **statistical model** called **ProMises model**:

$$\mathbf{X}_i = \mathbf{M}\mathbf{R}_i + \mathbf{E}_i \qquad \text{where} \qquad \vec{\mathbf{E}}_i \sim \mathcal{N}_{nv}(0, \Sigma)$$

- We think that also the **anatomical features** are important!

  ⟶ **Prior distribution** (Fisher Von Mises[4]) for $\mathbf{R}_i$

- The estimation process is computationally heavy; only ROIs can be aligned

  ⟶ **Semi-orthogonal transformation** on $\mathbf{X}_i$

The regularization leads to a unique solution for $\mathbf{R}_i$.

[4] Downs, T. D. (1972). Orientation statistics. Biometrika, 59 (3): 665-676

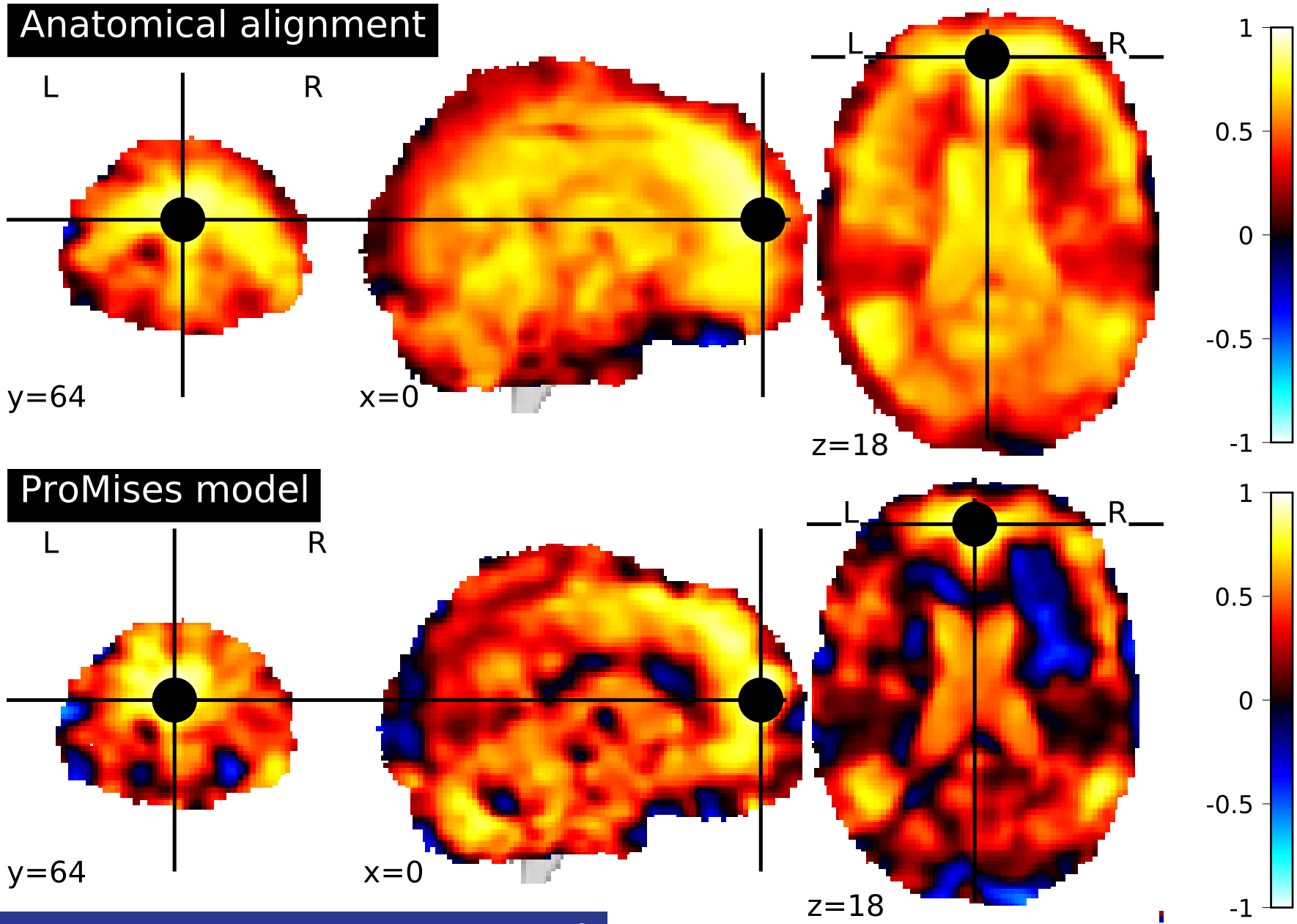
We align the brain images from Pernet et al. (2015)[5] of 18 subjects passively listening to vocal, i.e., speech, and non-vocal sounds.

After the $\mathbf{X}_i$ matrices' alignment:

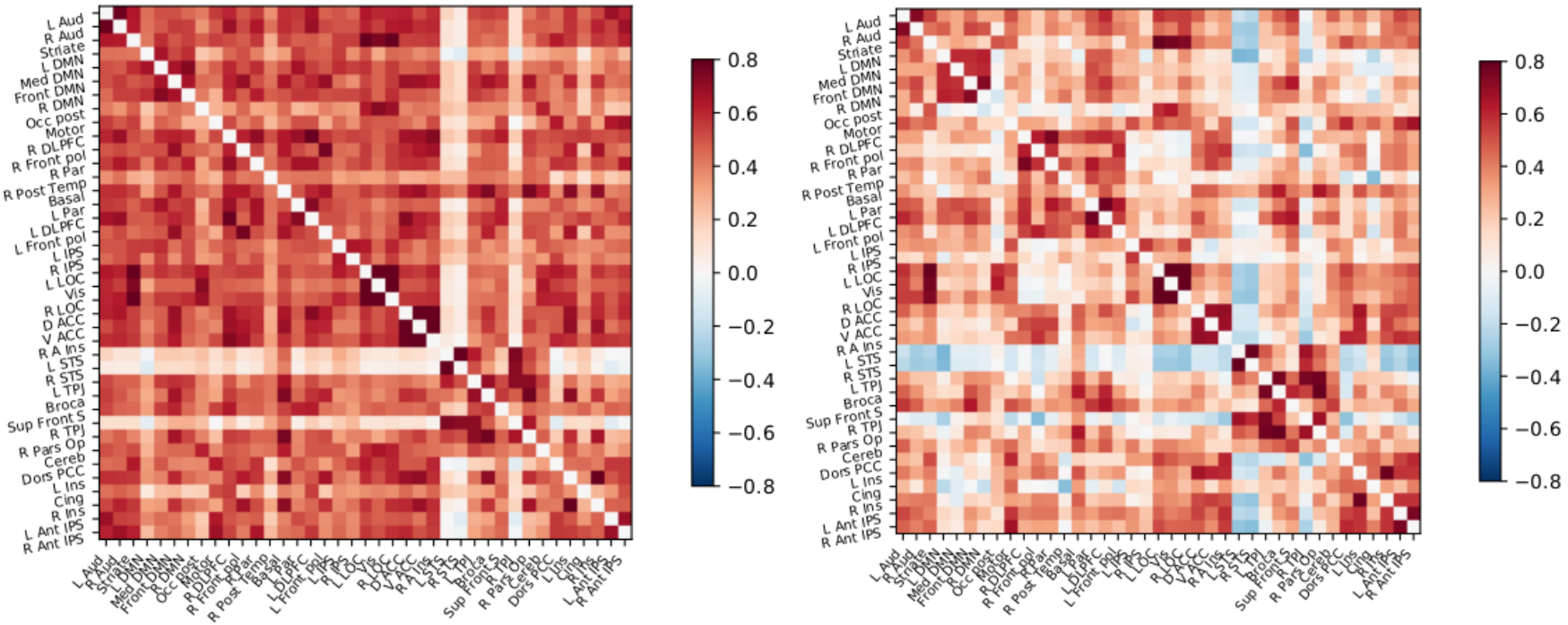
- **Seed-based correlation analysis**;
- **ROI correlation analysis**;
- **Statistical Parametric Mapping**.

[4] https://openneuro.org/datasets/ds000158/versions/1.0.0

Auditory Data - Seed-based correlation analysis

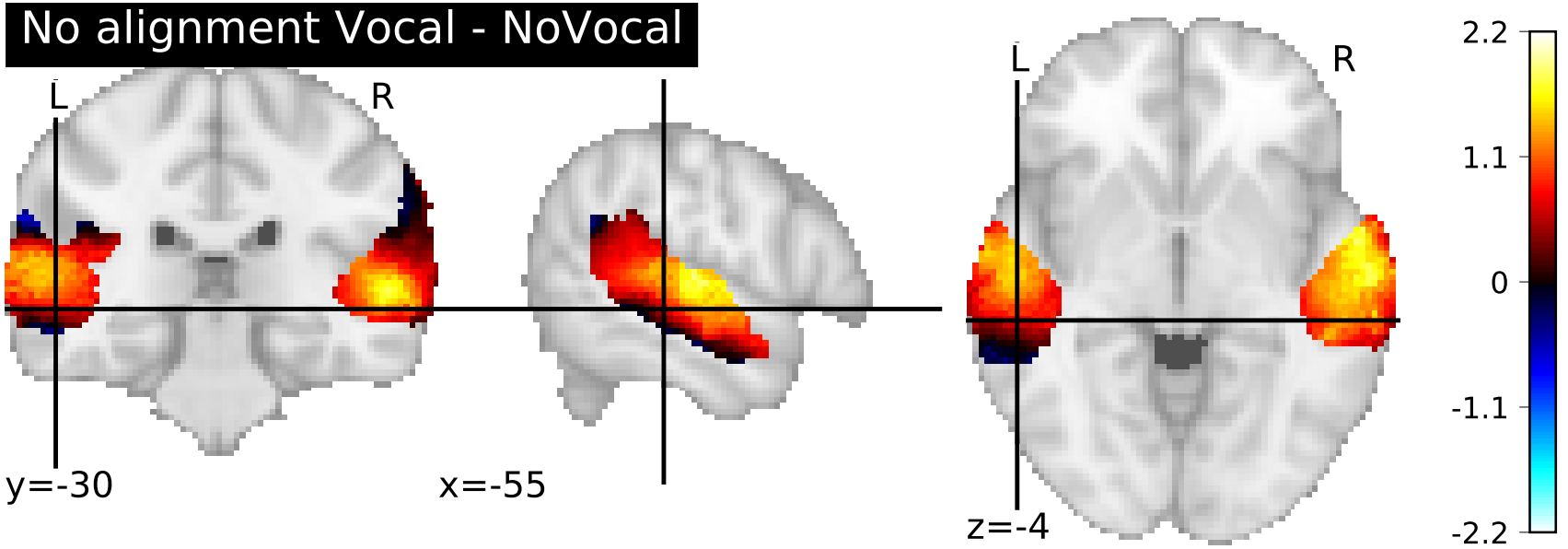


Auditory Data - ROI correlation analysis

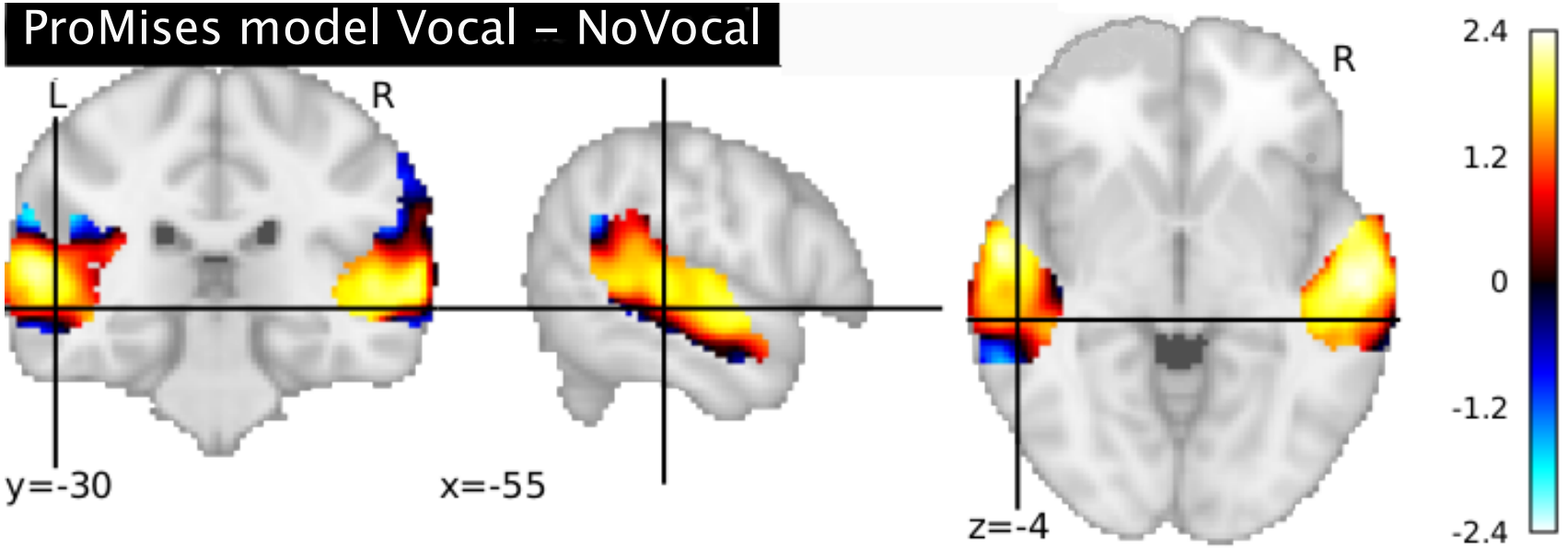


Auditory Data - Statistical Parametric Mapping

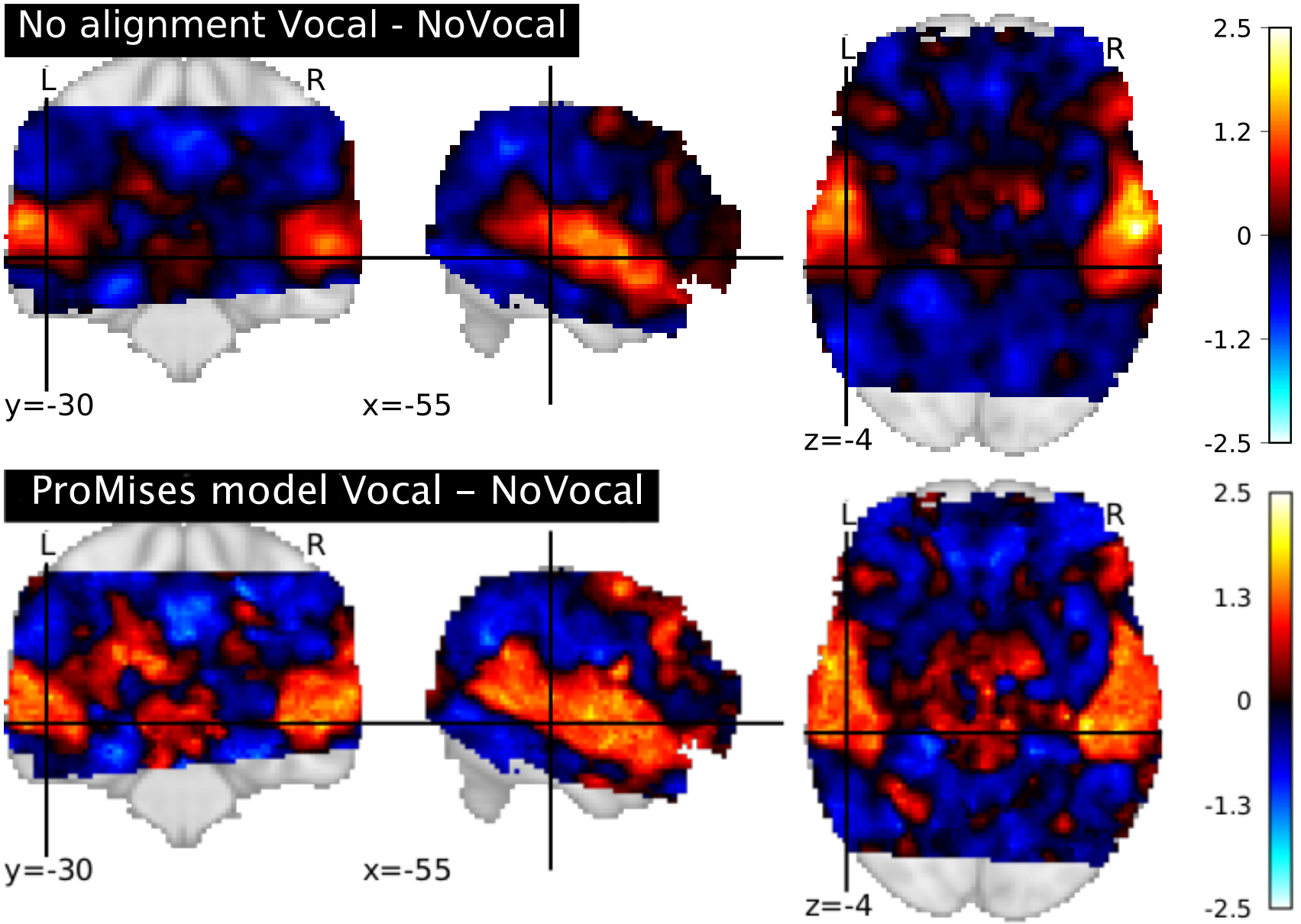
No alignment Vocal - NoVocal



ProMises model Vocal – NoVocal



Auditory Data - Statistical Parametric Mapping

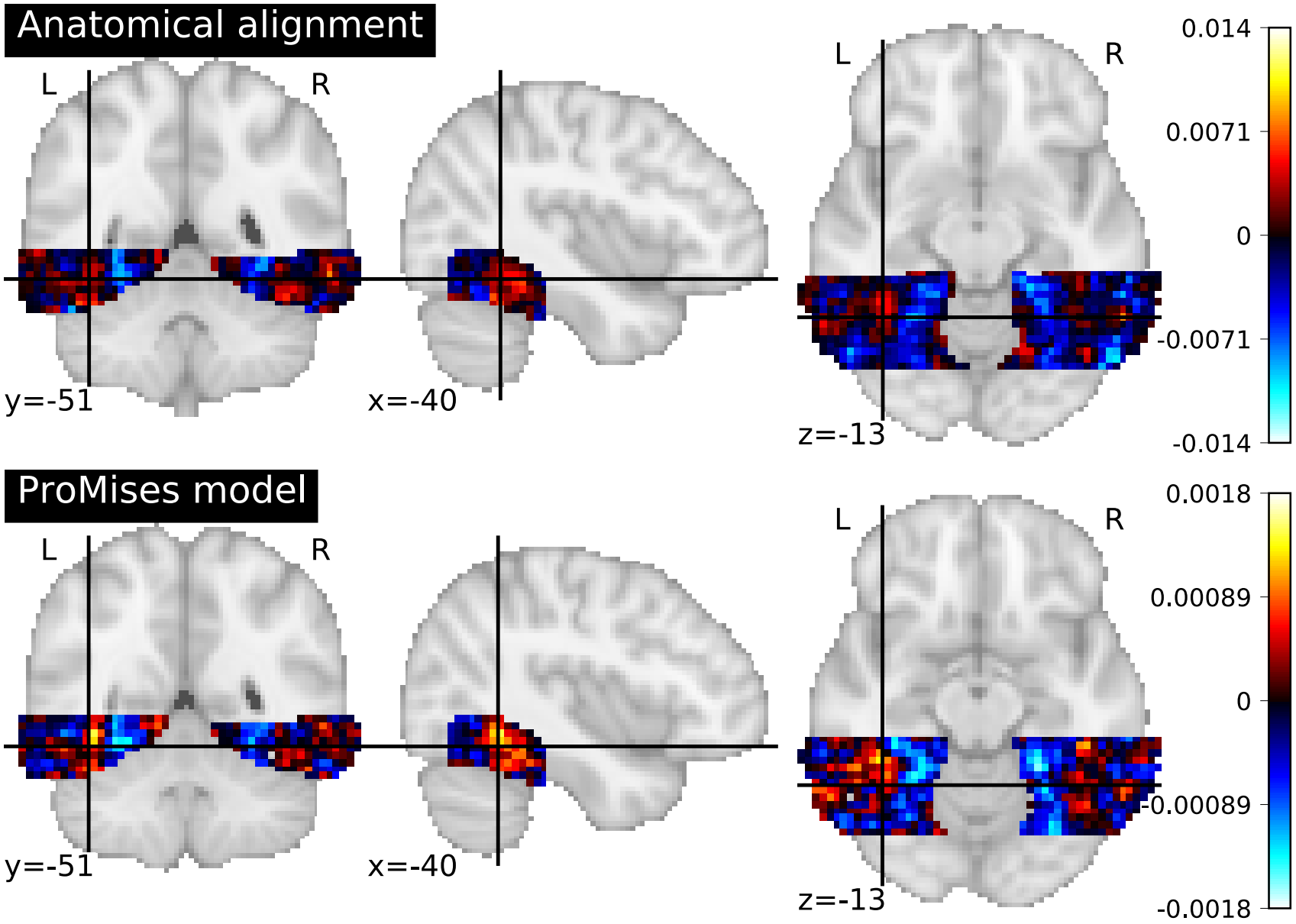


Faces and Objects Data

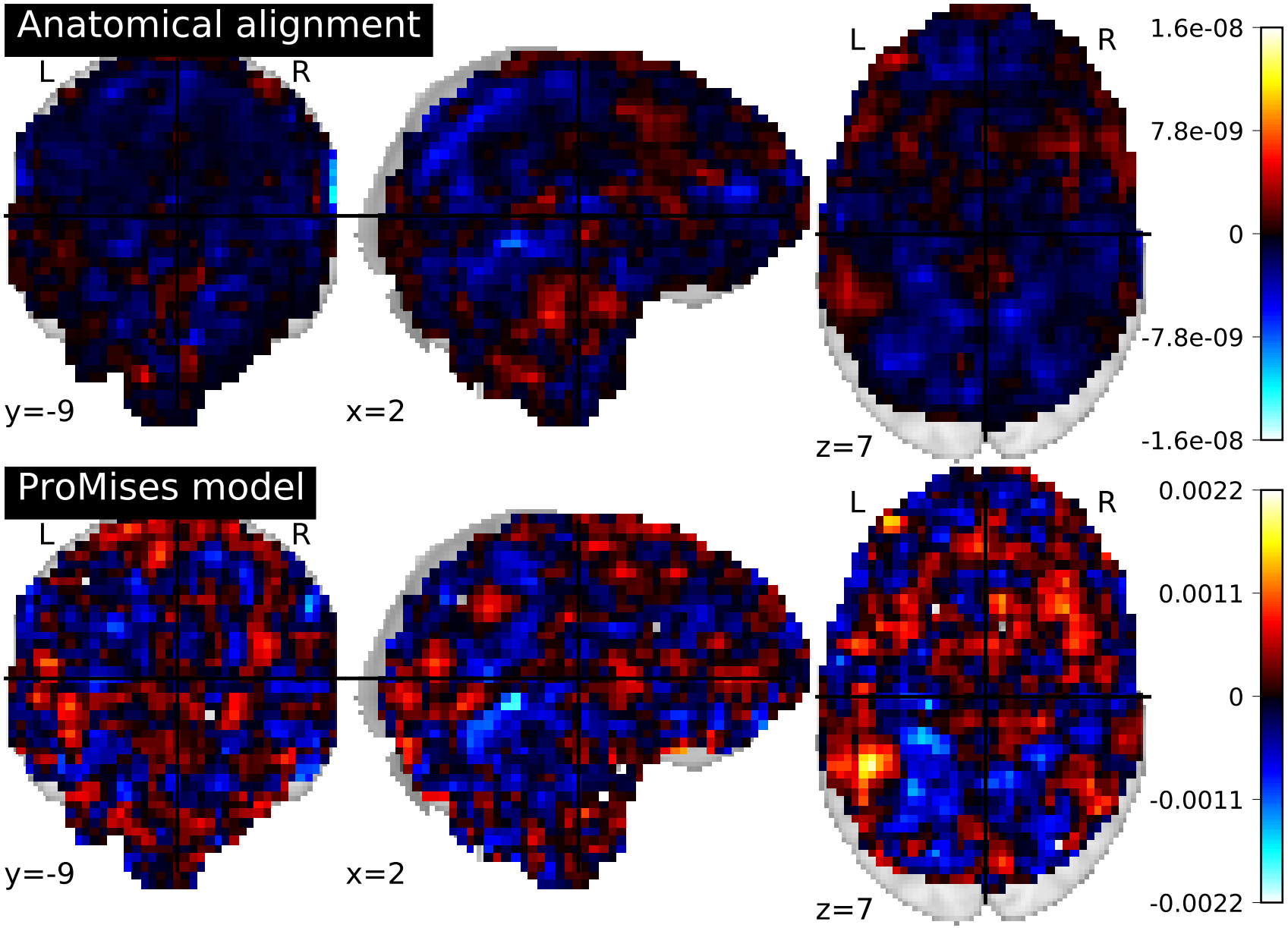
- We align the images of the **Ventral Temporal Cortex** and **whole brain** from Haxby et. al (2001)[6] of 10 subjects watching static, grey-scale images of faces and objects;
- The **Multi-class Linear Support Vector Machine** is used as classifier with leave one out subject cross-validation.

[6] https://openneuro.org/datasets/ds000105/versions/00001

Faces and Objects Data - Ventral Temporal Cortex



Faces and Objects Data - Whole Brain



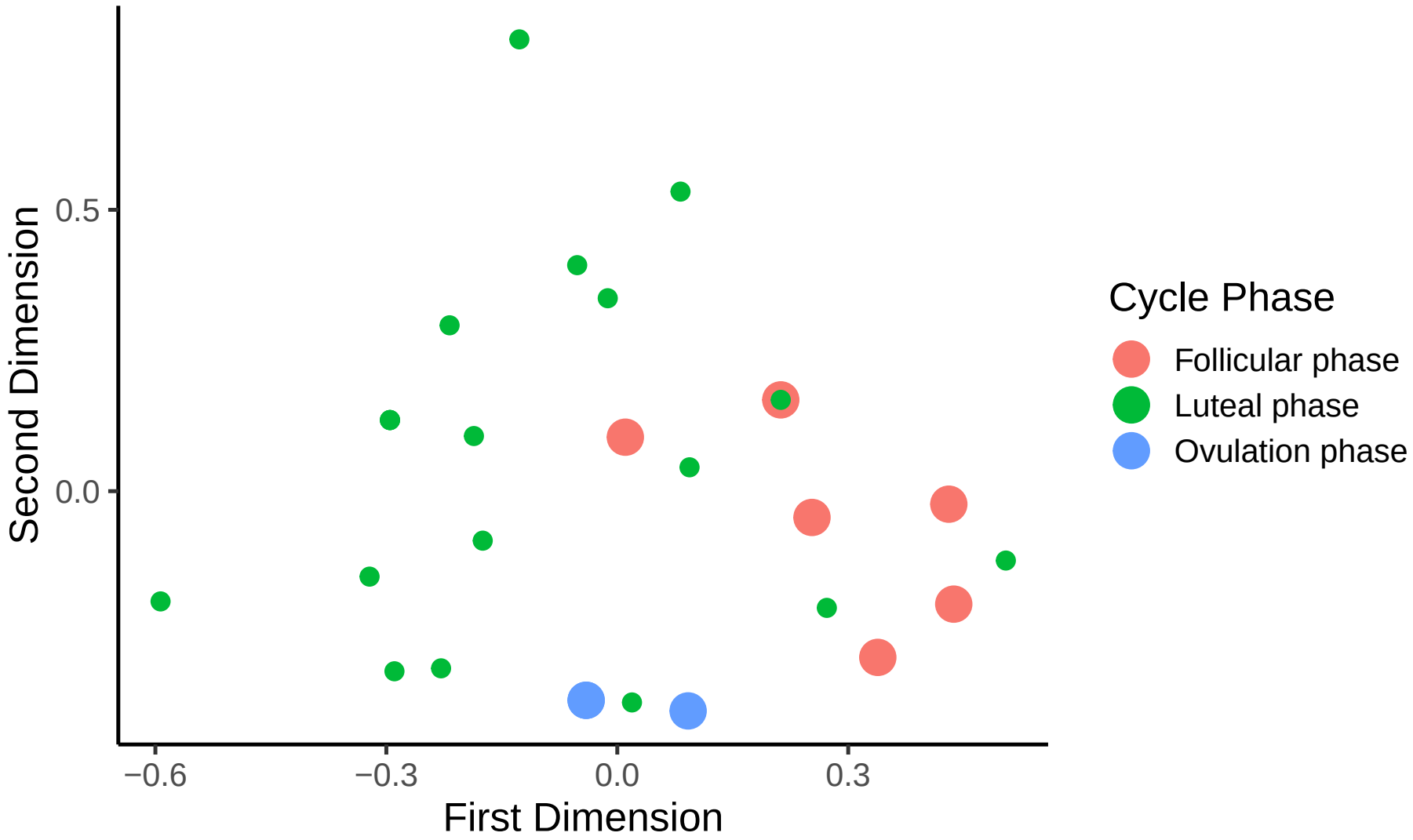
- **ProMises Model** gives us a set of orthogonal matrices, one for each subject.
- We can use these matrices to understand underlying clusters,
- associating also some available covariates.

We align the brain images from Smeets et al. (2013)[6] of 29 subjects watching food and no-food images.

After that, the **multidimensional scaling** is applied on the $\mathbf{R}_i$ pairwise distance matrix.

[6] https://openneuro.org/datasets/ds000157/versions/00001

Food Data - Multidimensional scaling



The **ProMises Model**:

- leads to a **unique** solution of the transformation → unique representation/interpretation of the final result;
- allows alignment of the **whole brain**;
- exploits the information of voxels' **spatial position**;
- yields more **reliable** measures of individual differences both:
  1. by reducing confounds from topographic idiosyncrasies;
  2. by capturing variation around shared functional and anatomical response across individuals;
- allows to find **groups** of individuals sharing patterns of neural brain activation.

You can find the `Python` module and the `R` package on my GitHub profile `https://github.com/angeella`.