

pARI PACKAGE: VALID DOUBLE-DIPPING VIA PERMUTATION-BASED ALL RESOLUTIONS INFERENCE

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fMRI measures brain activation as changes in blood flow (BOLD) under a sequence of stimuli.

Cluster-wise method:

- Analyze set of contiguous voxels (S);
- H_S rejected means that S contains at least one active voxel
→ We don't know which ones and how many!!
- **Spatial specificity paradox;**
- **Double-dipping.**

Solution: All-resolutions inference (ARI) ¹ → Inference on the number of truly active voxels.

- **pARI** is the Permutation-based version of **ARI**. The permutation structure permits to account for the correlation structure between tests unlike **ARI**;
- Both methods are based on the **closed testing procedure** for controlling the familywise error rate.

¹Resenblatt, J. et al. (2018).

Every time that we want to infer inside a **data-driven (and not) cluster** (features set), we can use **ARI/pARI**:

- **Cluster fMRI data analysis** ²;
- **Gene expression cluster analysis** ³;
- **Cluster EEG data analysis** ⁴.

²Woo, C. et al. (2014).

³Berge, K. et al. (2017).

⁴Maris, E. et al. (2007).

```
devtools::install_github(angeella/pARI)  
library(pARI)
```

■ fMRI framework:

```
pARIBrain(copes, thr, mask, alpha, ...)
```

where **copes** is a list of **contrast** parameter estimates involving brain activation differences for each subject in NIfTI format.

■ General framework:

```
pARI(data, ix, alpha, test.type, ...)
```

where **ix** is the **features set** of interest. It can be a vector of indices or a vector with length equals the number of features where different values indicate the different sets.

We analyzed the **Auditory data** collected by Pernet et al. (2015), i.e, people listening vocal and non-vocal sounds.

Group analysis on 140 subjects of the Vocal > Non-vocal **contrast** by the one sample t-test flipping the sign of 140 voxel-wise contrasts maps.

First, let download the data from the fMRIData package:

```
devtools::install_github(angeella/fMRIData)
library(fMRIData)
data(Auditory_clusterTH3_2)
data(Auditory_copes)
data(Auditory_mask)
```

```
pARIBrain(copes = Auditory_copes,  
          cluster = Auditory_clusterTH3_2,  
          mask = Auditory_mask,  
          alpha = 0.05)
```

Cluster	Threshold	Size	% active		P-Values
S	t	$ S $	$\bar{\pi}(S)$		p_{FWER}
			pARI	ARI	
Right STG/PT HG/IFG/T	3.2	11683	92.36%	84.98%	< 0.0001
Right STG/PT HG/IFG/T	4	8875	99.54%	98.5%	—
Right IFG	4	422	91.47%	83.18%	—
Right T	4	292	85.96%	64.04%	—
Right T	4	15	13.33%	0%	—

map_TDP: Create **true discovery proportion map** in nifti format.




Thanks to the amazing group that worked on the paper
Permutation-based true discovery proportions for fMRI cluster analysis! (in arXiv)

- Livio Finos University of Padua;
- Jelle Goeman Leiden University Medical Centre;
- Jesse Hemerik Wageningen University;
- Wouter Weeda Leiden University;

and thanks for your attention!

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