# 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<sub>S</sub> 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)  $^{1} \rightarrow$  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.

<sup>1</sup>Resenblatt, 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 <sup>2</sup>;
- Gene expression cluster analysis <sup>3</sup>;
- Cluster EEG data analysis <sup>4</sup>.

<sup>2</sup>Woo, C. et al. (2014).
<sup>3</sup>Berge, K. et al. (2017).
<sup>4</sup>Maris, 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.

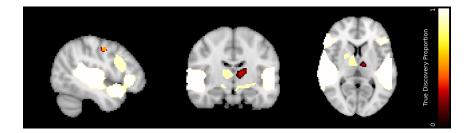
Group analysis on 140 subjects of the Vocal > Non-vocal **contrast** by the one sample t-test flipping the sign of 140 voxel-wise contrasts maps.

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)
```

Cluster S	Threshold t	Size	% active $ar{\pi}(S)$		P-Values P <sub>FWER</sub>
			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%	о%	_

## map\_TDP: Create true discovery proportion map in nifti format.



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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!

O https://github.com/angeella/useR\_2021

# 🖸 @aangeella

