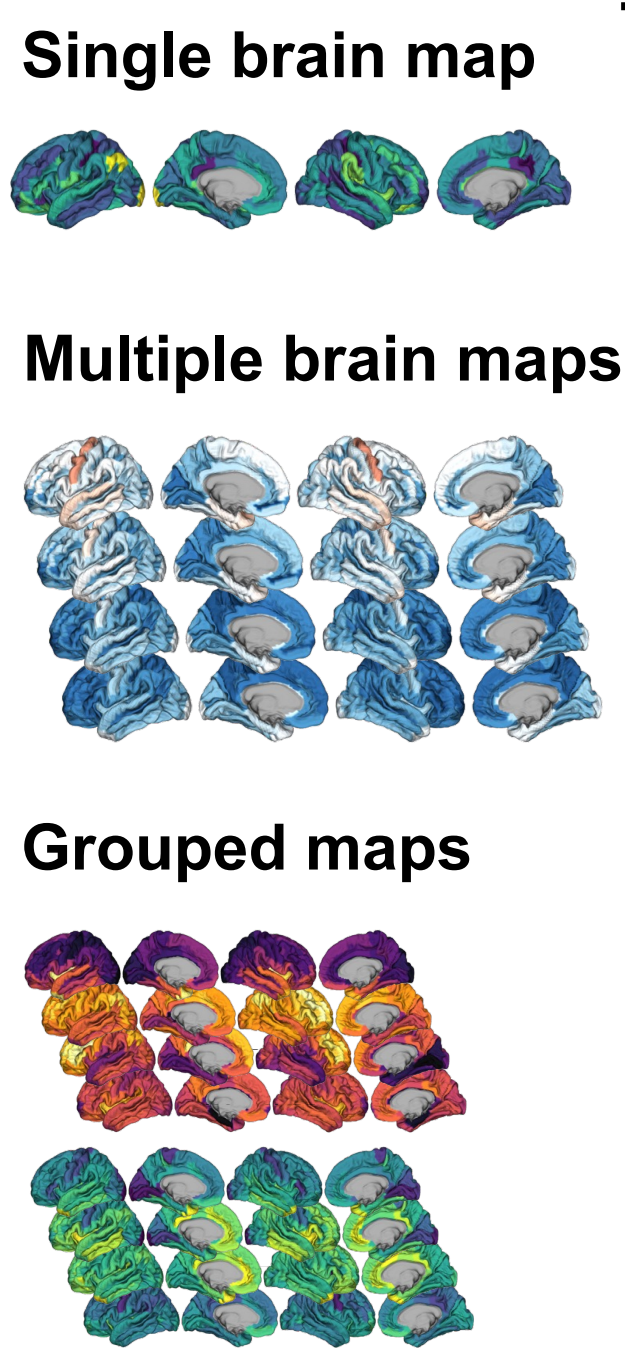


## Introduction

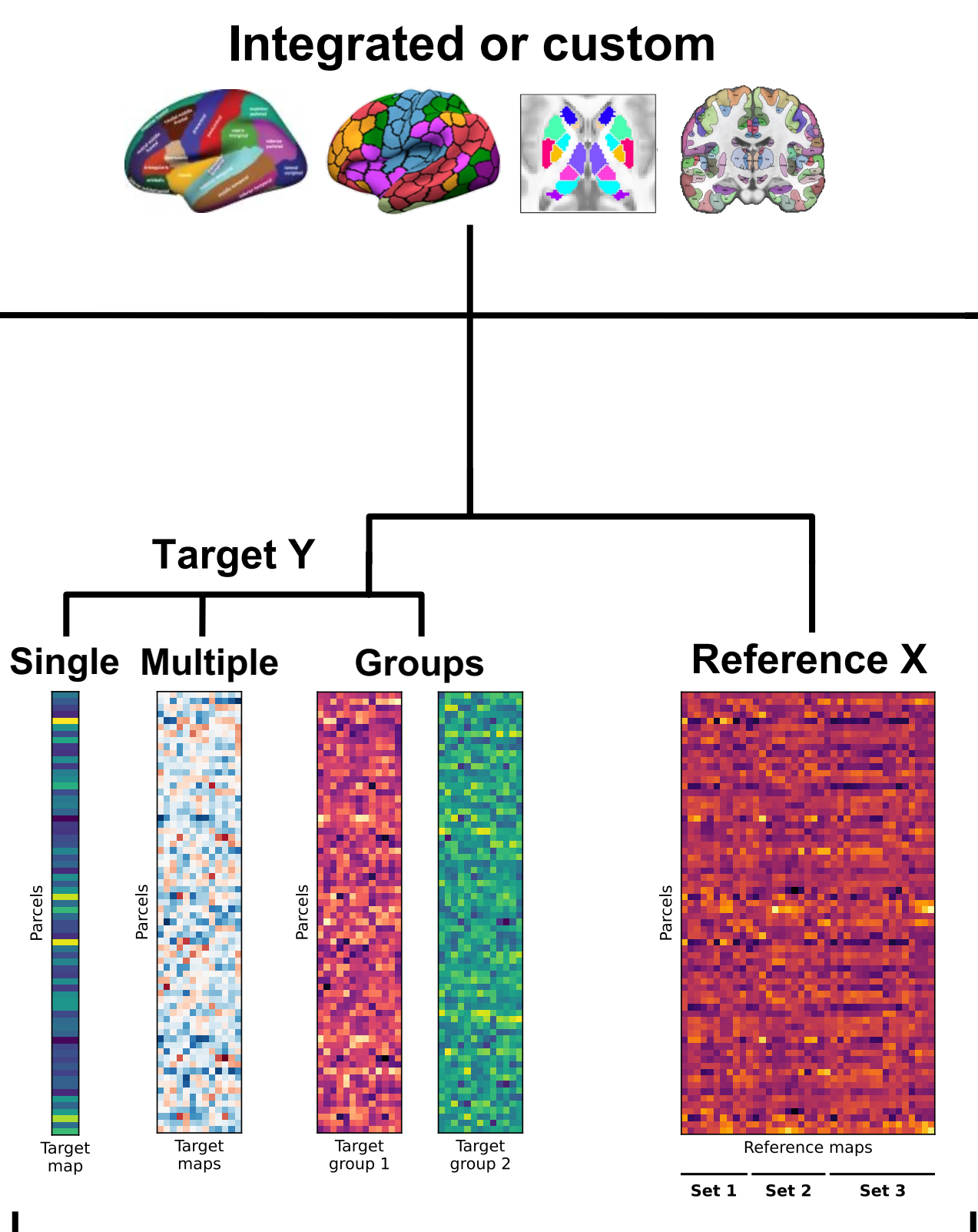
- Most neuroimaging research focuses on **brain-regional effect estimates** as outcomes of interest.
- Spatial patterns across the whole brain, cortex, or subcortex** may convey important information missed by regionally constrained analysis approaches.
- These patterns are found in any given brain map, from **individual neurodevelopment** over time [1] to effect size maps reflecting **case-control differences** on the **individual** [2] or **group level** [3].
- By testing a **target brain map** for its **colocalization** with **reference atlases** of known biological or functional entities (e.g., neurotransmitters, gene expression, or meta-analytic maps of cognitive functions), one can derive **interpretable inferences from in-vivo human neuroimaging data** [1–5].
- NiSpace** is a **user-friendly API-focused toolbox** integrated in the **Python** neuroimaging ecosystem that allows for **fast, flexible, and easily scalable colocalization analysis**.
- NiSpace** aims to provide **high-level tools and workflows** for both novice and experienced users, starting with preprocessed **volumetric and surface** neuroimaging data, over **data cleaning and harmonization**, as well as **several statistics** and different **permutation procedures**, to results **visualization**.
- NiSpace** applies and advances methods provided or introduced by other **related toolboxes**, e.g.: JuSpace [2], neuromaps [4], ENIGMA toolbox [5], BrainSpace [6], BrainSMASH [7], MENGA [8], Virtual Histology [9], or GCEA [10].
- NiSpace** integrates **prior approaches into a unified framework**, allowing for combinations of, e.g., subject- and group-level analyses, uni- and multivariate methods, or autocorrelation-preserving group, map, and set permutations.
- The **Python API** is under development; a **GUI** will be available in the future.

## Approach

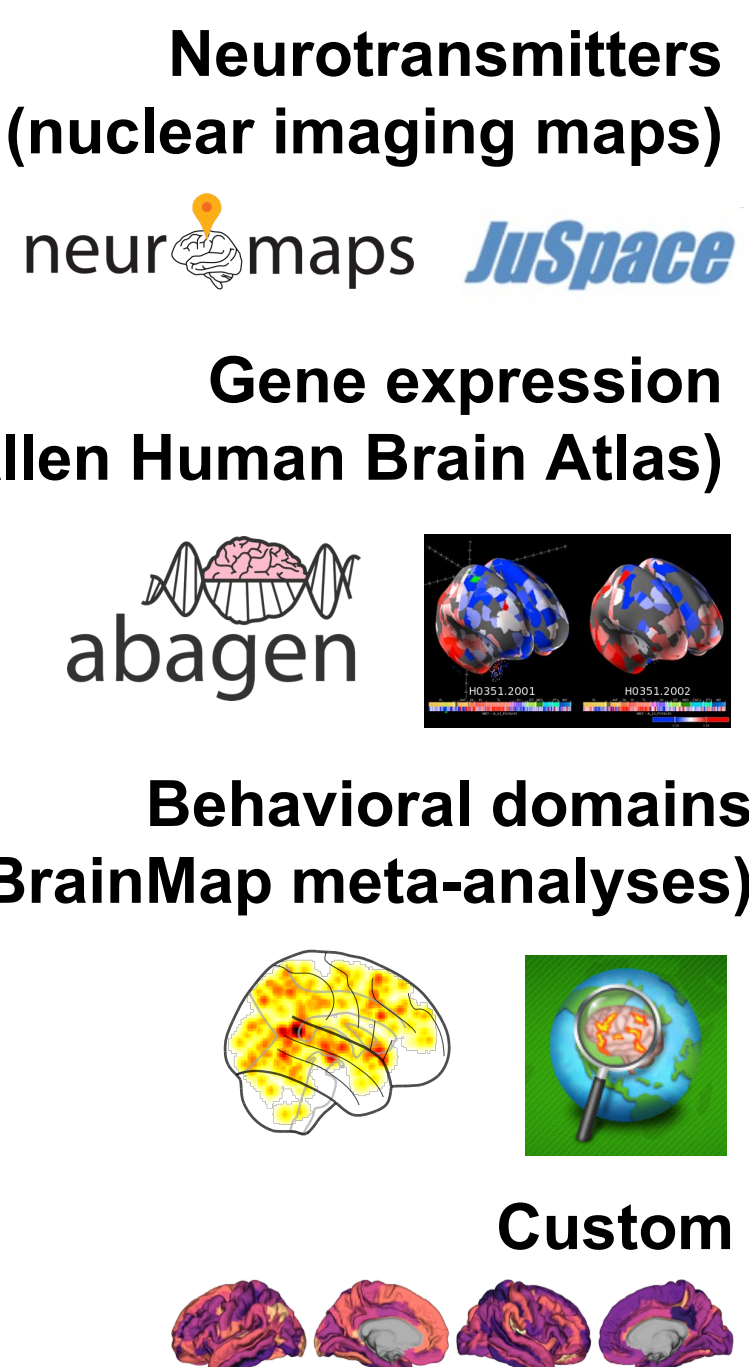
### Target ("Y")



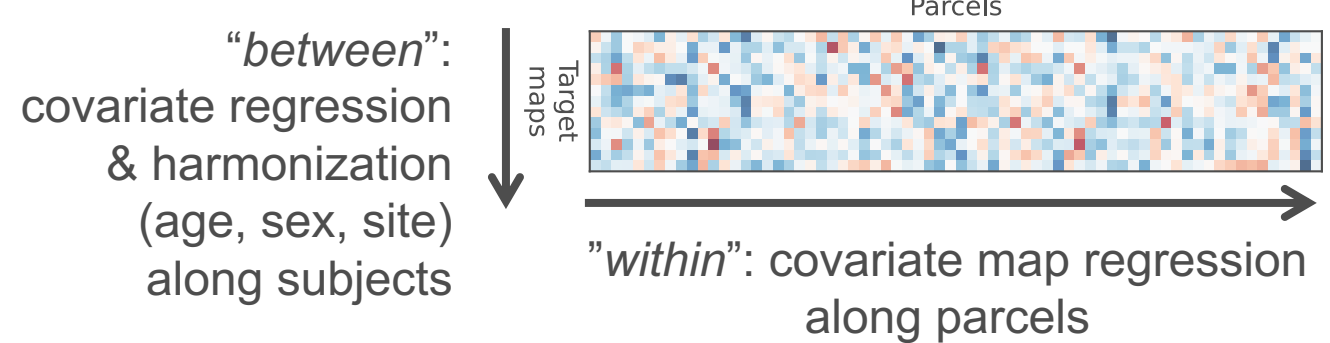
### Parcellation



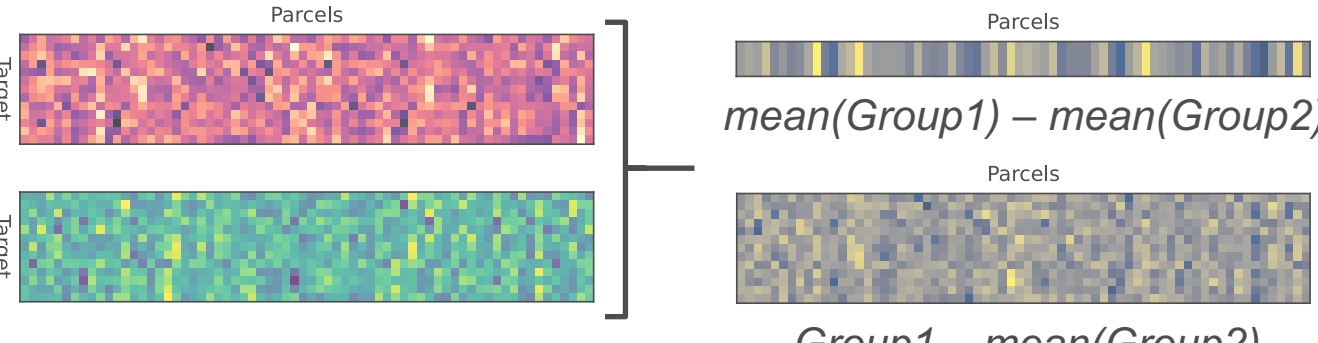
### Reference ("X")



### Optional: Data cleaning

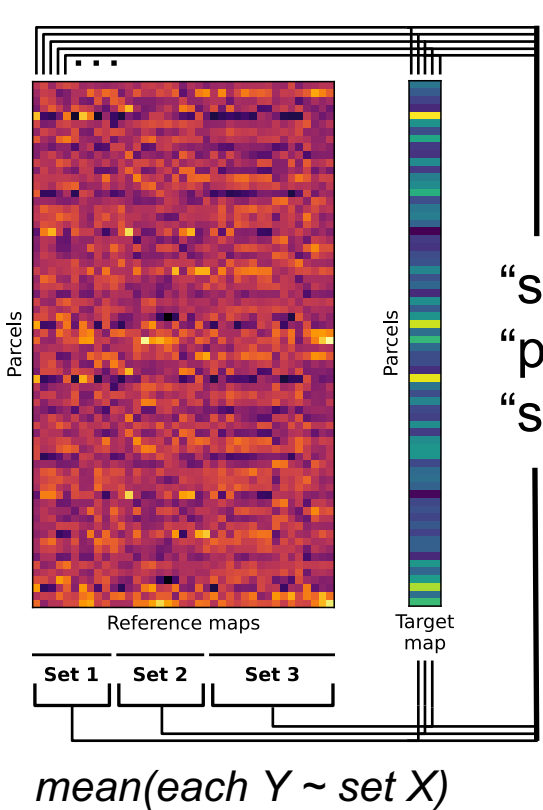


### Optional: Parcel-wise group comparison

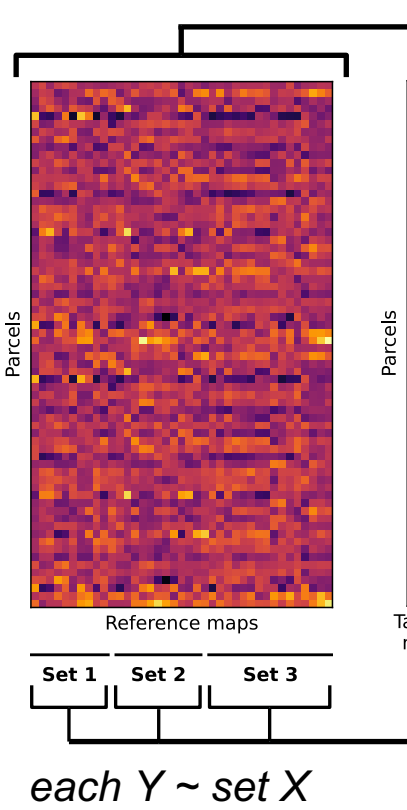


## Colocalization

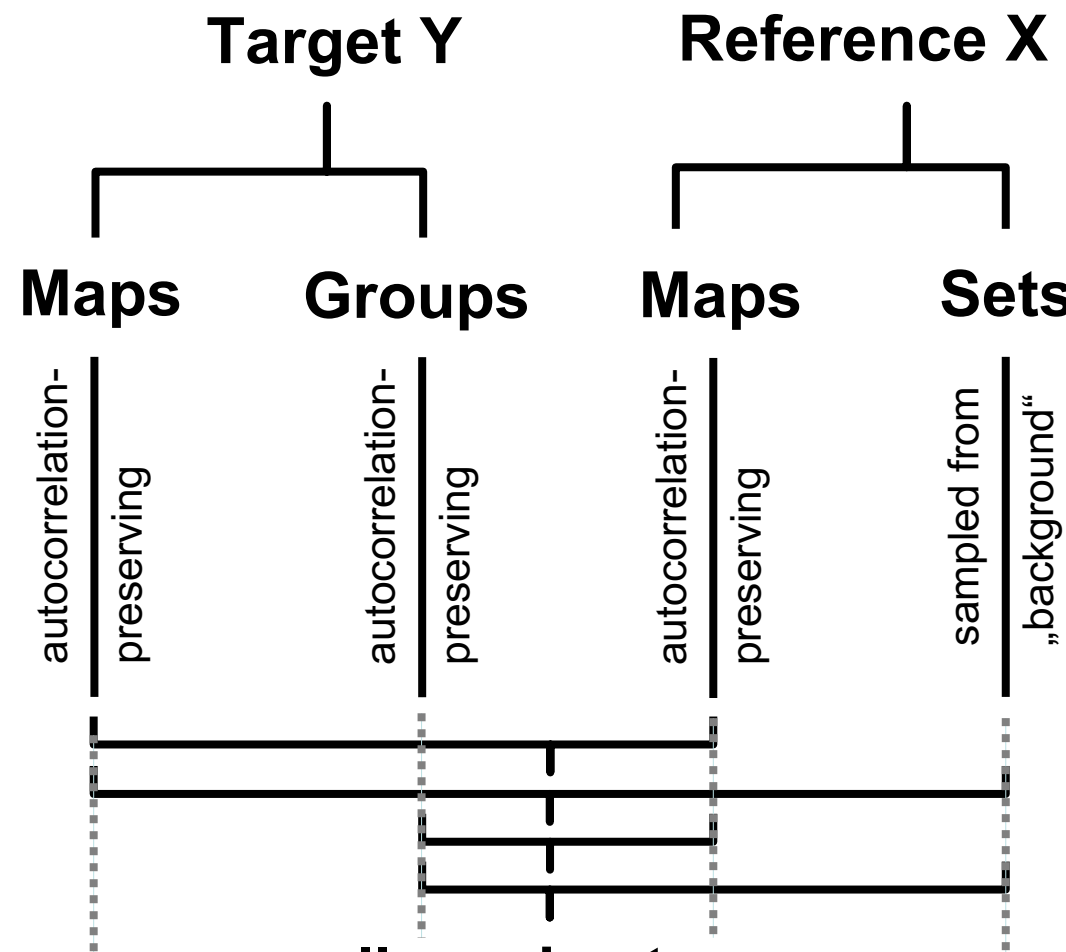
### Univariate



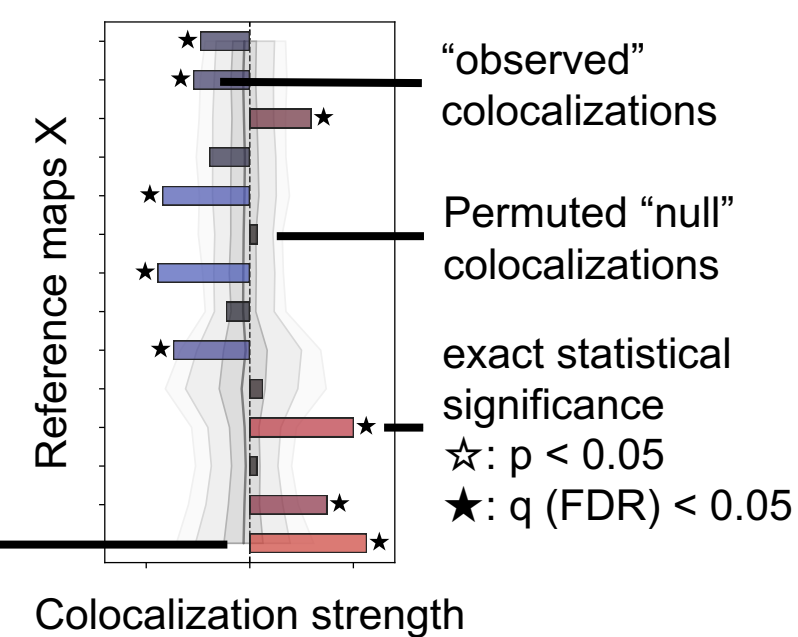
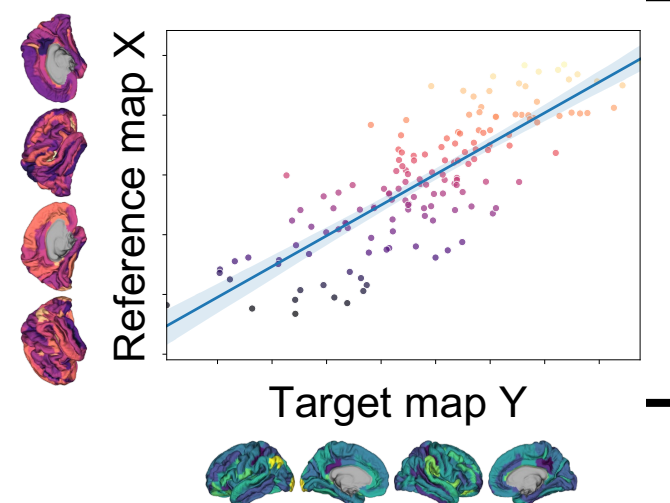
### Multivariate



## Permutation



## Visualization



## Post-hoc analyses

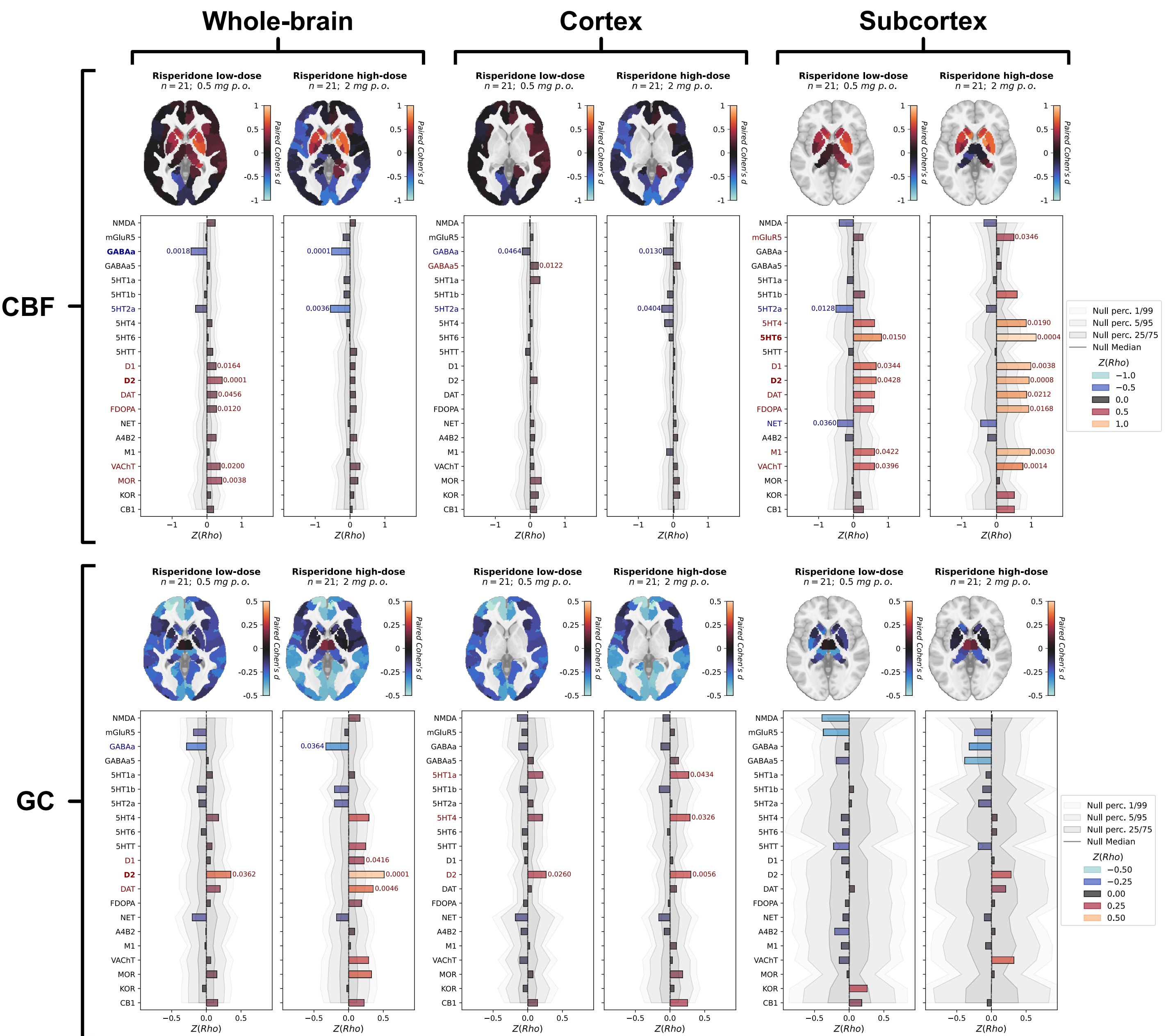
Further group comparisons  
Subject-level correlations with behavioral & clinical data  
Prediction/ machine learning applications

## Case studies

### Drug challenge – Session permutation

Colocalization between placebo-controlled drug effects on MRI (cerebral blood flow, CBF, and global correlation, GC) and independent neurotransmitter reference maps.

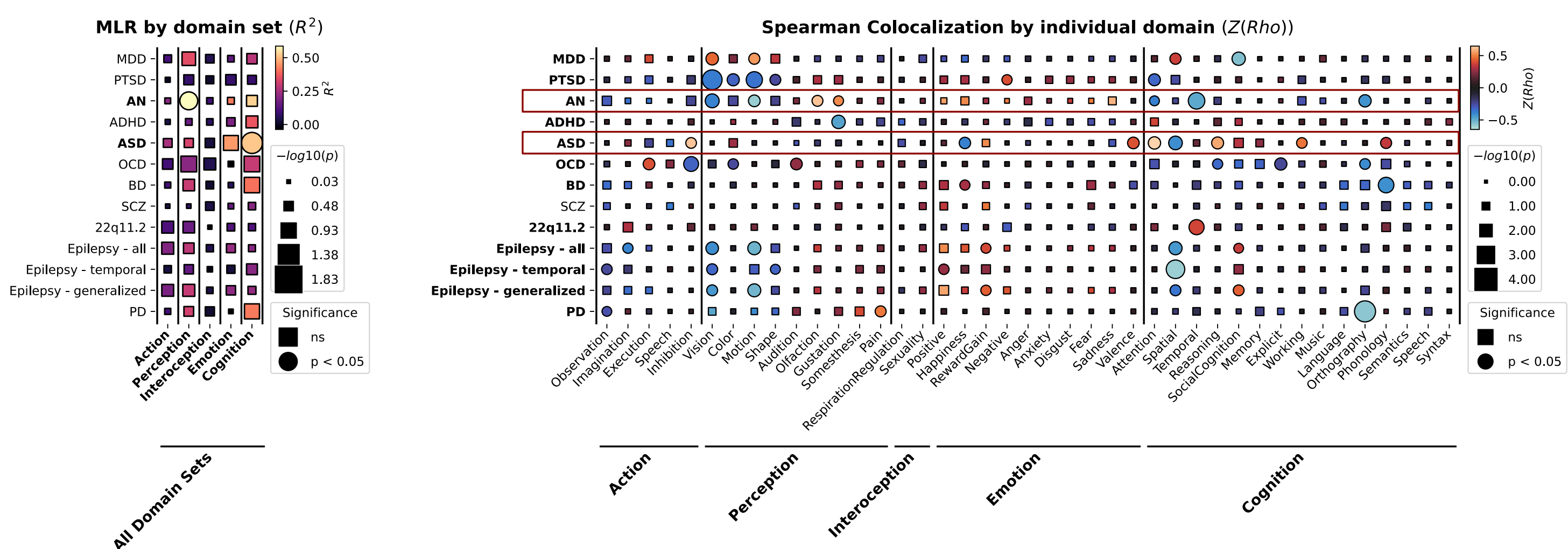
**Target:** CBF/GC maps [11] | **Reference:** group-average nuclear imaging maps (included in **NiSpace**) | **Parcellation:** Schaefer-200/ Melbourne-S2 | **Processing:** gray matter (GM) regression across parcels | **Comparison:** group level: parcel-wise paired Cohen's *d* | **Colocalization:** Spearman's Rho | **Permutation:** drug vs. placebo labels, shuffled within each subject, retaining constant 50/50 drug/placebo splits.



### ENIGMA cortical thickness effect sizes – Map permutation

Colocalization between ENIGMA effect sizes maps and BrainMap behavioral domains in a multilevel analysis: MLR by domain class, followed by individual analyses for each specific domain. AN (anorexia nervosa): perception; ASD: cognition.

**Target:** ENIGMA effect size maps [mostly 5] | **Reference:** meta-analytic maps calculated from BrainMap coordinates [15] (included in **NiSpace**) | **Parcellation:** Desikan-Kiliany | **Colocalization:** Multivariate regression (MLR); Spearman's Rho | **Permutation:** Spatial autocorrelation-preserving reference null maps ("Moran" method [4,6]).



### Autism spectrum disorder (ASD) – Gene ("X")-set enrichment analysis

Colocalization between ASD-related resting-state brain activity/connectivity alterations and brain cell type markers: Consistent colocalization with astrocyte markers.

**Target:** ABIDE-I fALFF maps [12]; Group level DC t-contrast maps from four ASD cohorts [13] | **Reference:** Cell type marker genes [14] (included in **NiSpace**) | **Parcellation:** Schaefer-200+Melbourne-S2 | **Processing:** GM regression across parcels; age/sex regression & ComBat harmonization across subjects | **Comparison:** group level: parcel-wise Hedges' *g* (left); individual level: parcel-wise Z-scores (center) | **Colocalization:** Spearman's Rho (set-wise signed average) | **Permutation:** gene sets retaining original set sizes, sampled from the full (*n* ~ 7000) mRNA dataset.

