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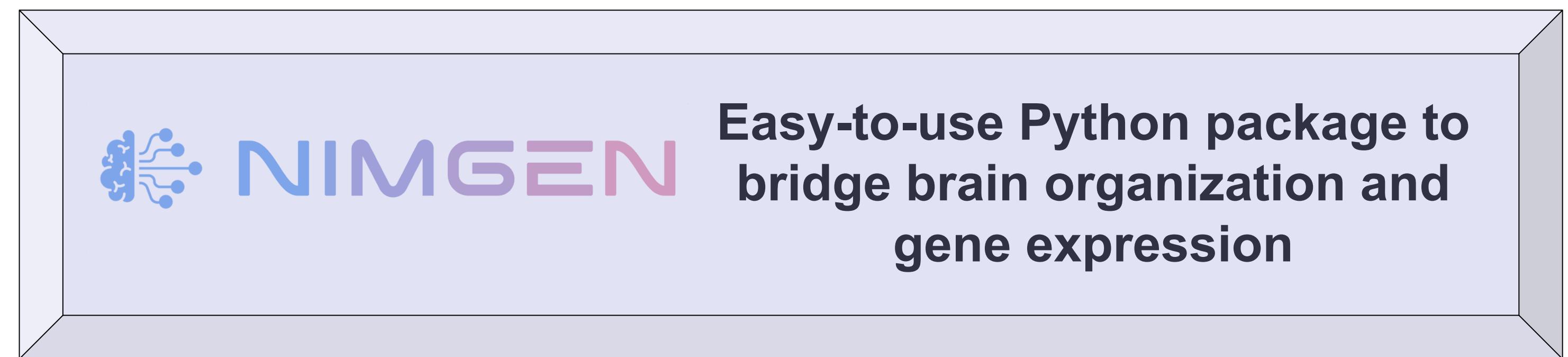
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INTRODUCTION



Easy-to-use Python package to bridge brain organization and gene expression

Motivation

- How genes shape the human brain?
- What biological processes are behind brain structure and function?
- Can we help early diagnosis of neurodegenerative and mental disorders and aid drug discovery?

Highlights

- Fully automated: Brain measures → Biological processes
 - Gene expression analysis using abagen [1].
 - Gene set enrichment analyses using WebGestalt [2].
 - Permutation testing using BrainSMASH [3].
- User-friendly and flexible toolbox based on robust statistics.

DATA

Genetic

Gene expression data from the Allen Human Brain Atlas (AHBA) [4] providing microarray probes from six postmortem brains.



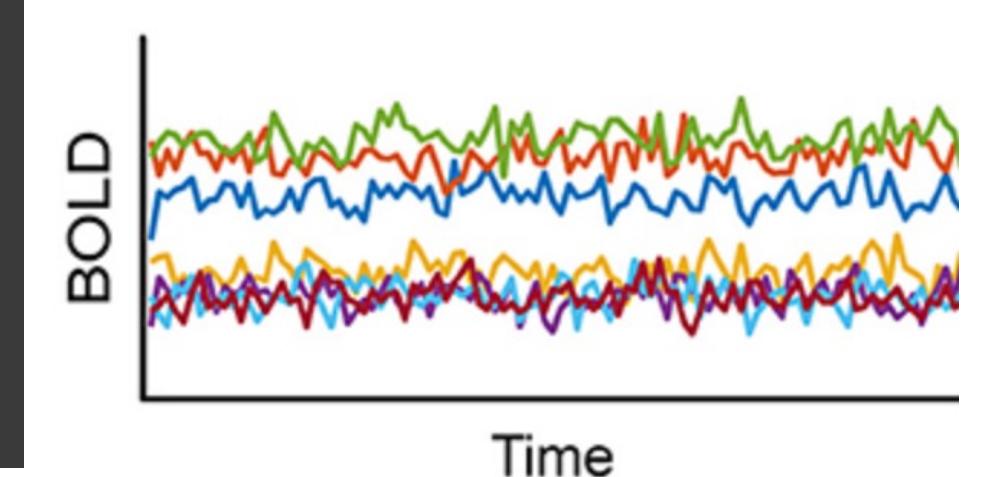
6 donors
■ M, 24 yrs
■ M, 39 yrs
■ M, 57 yrs
■ M, 31 yrs
■ F, 49 yrs
■ M, 55 yrs

User provided

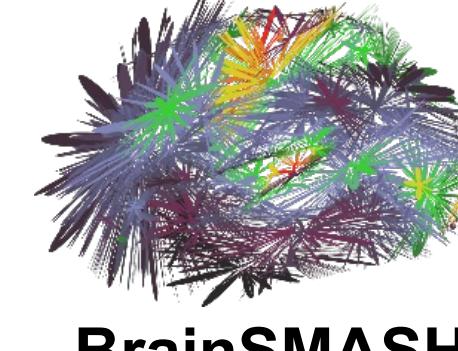
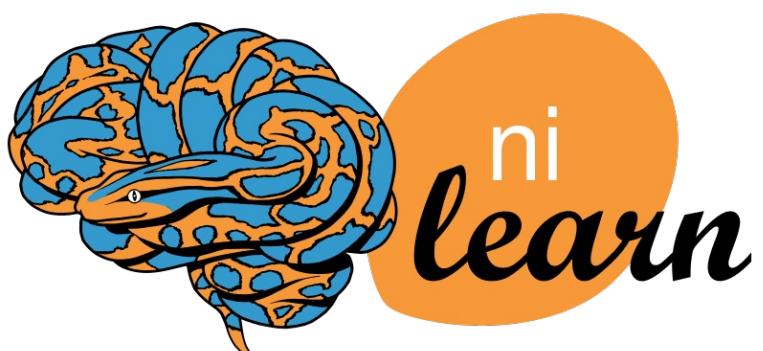
Brain atlas: Schaefer atlas.

MRI Markers: Measurements extracted for each parcel.

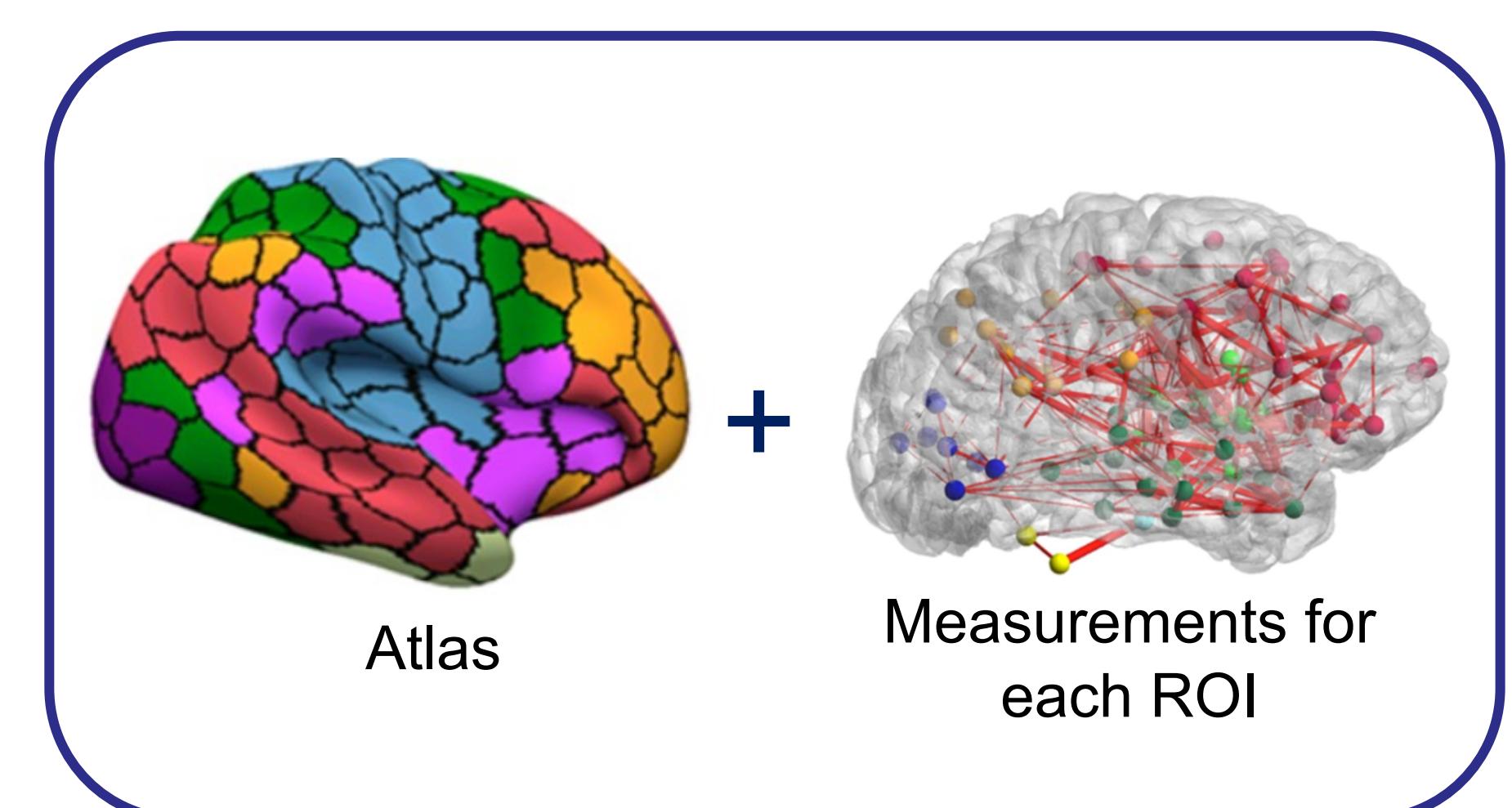
- Structural: Voxel-based morphometry
- Functional: Degree centrality



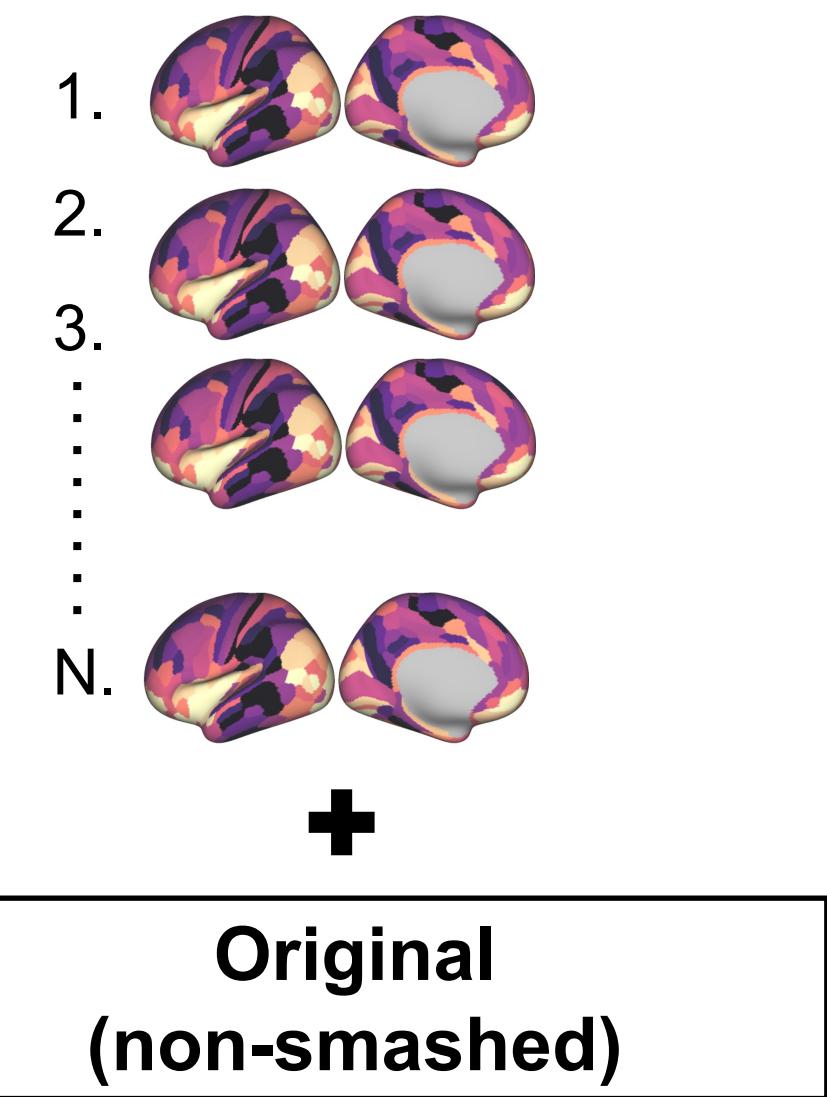
TOOLS



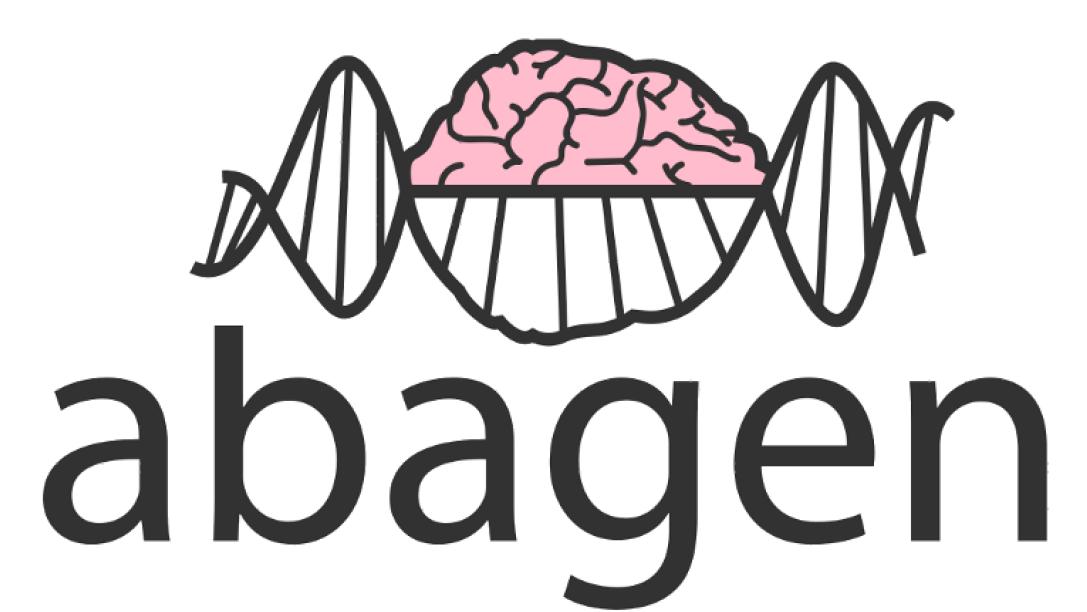
METHODS



Generate N
surrogate maps
BrainSMASH



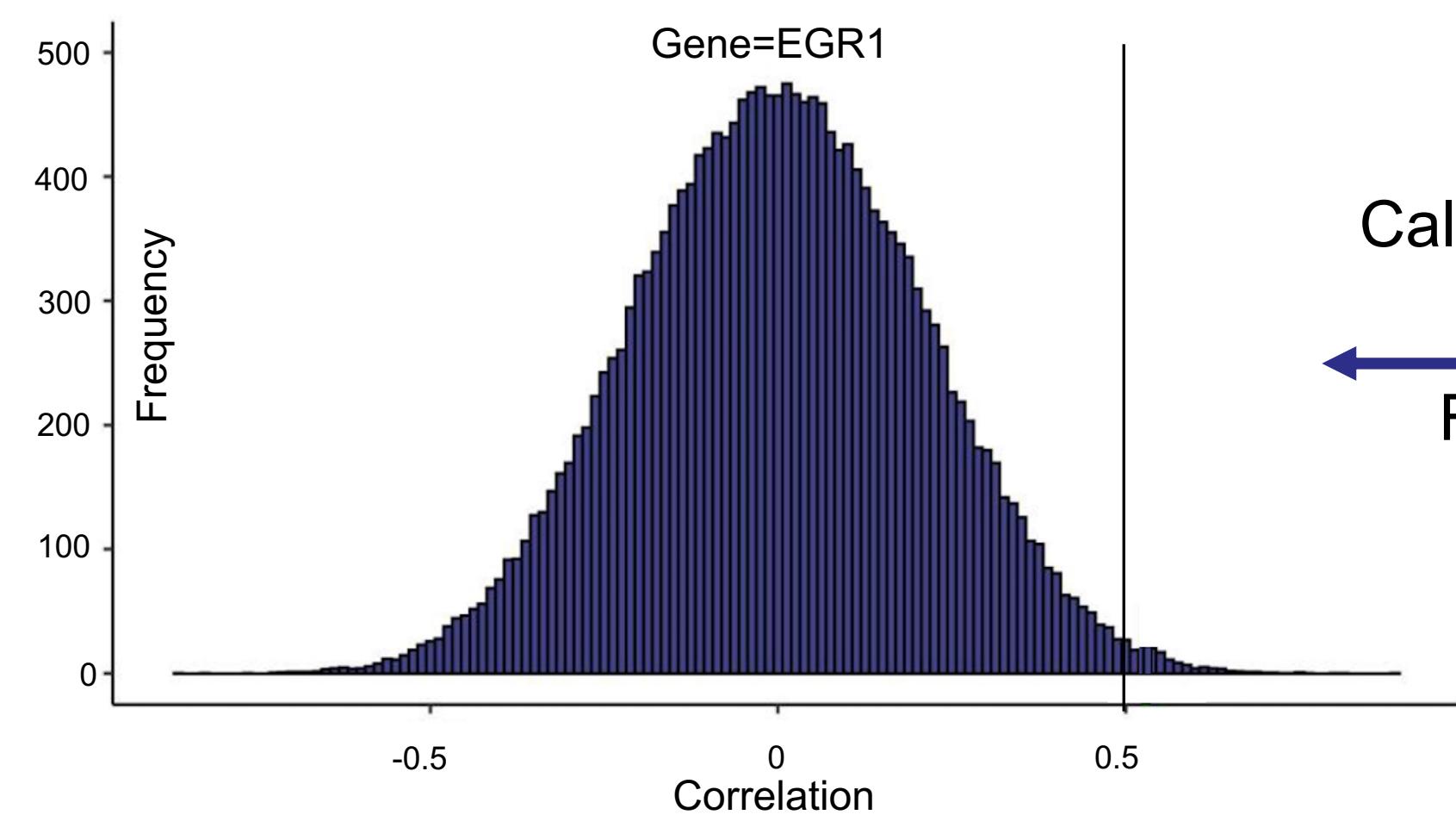
Fetch gene
expressions



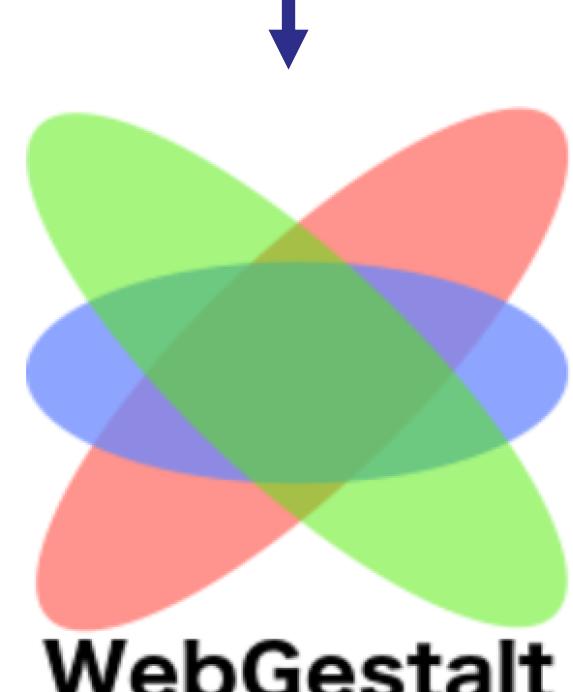
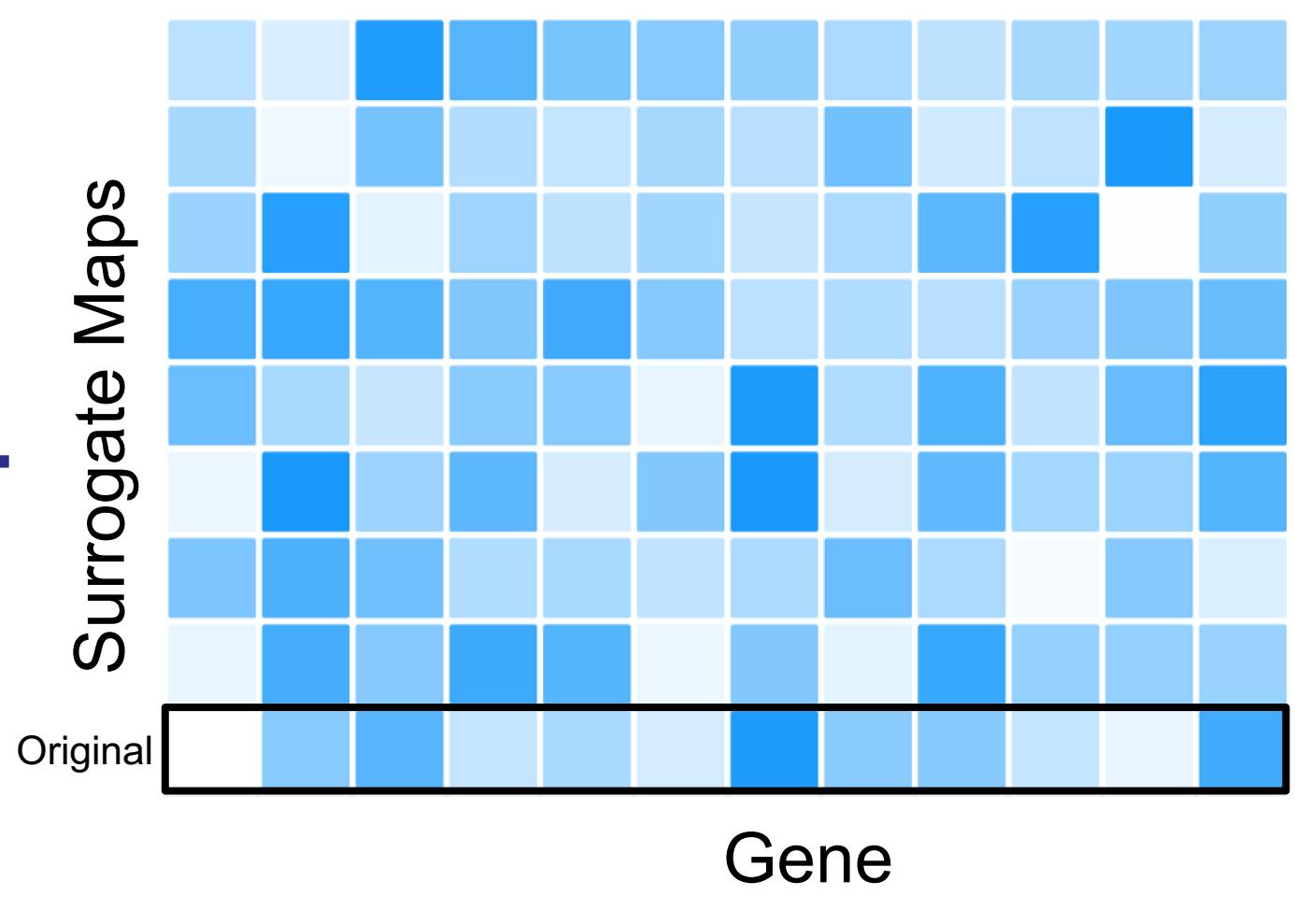
Calculate
Pearson's r
and p of
each gene

Significant Genes
significantly associated genes for a given MRI measurement
EGR1
GADD4
RELB
NFKB2
...

False Discovery Rate Correction



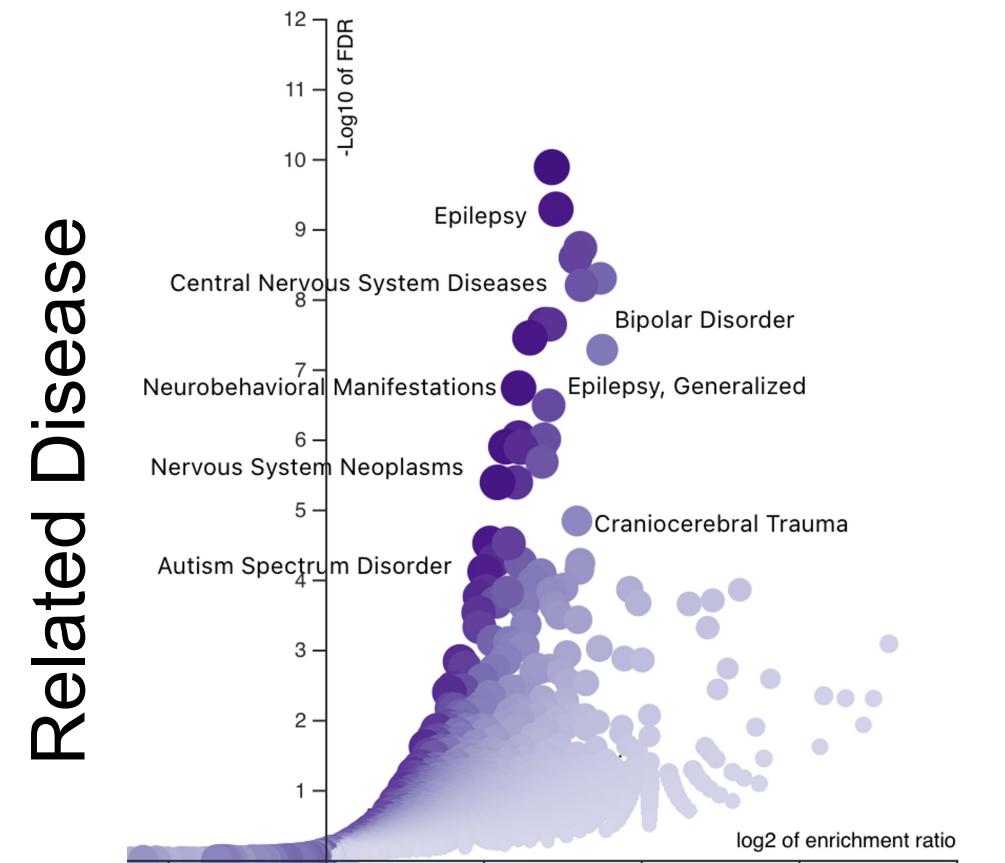
Calculate empirical
p-value
For each gene



Enrichment Analysis

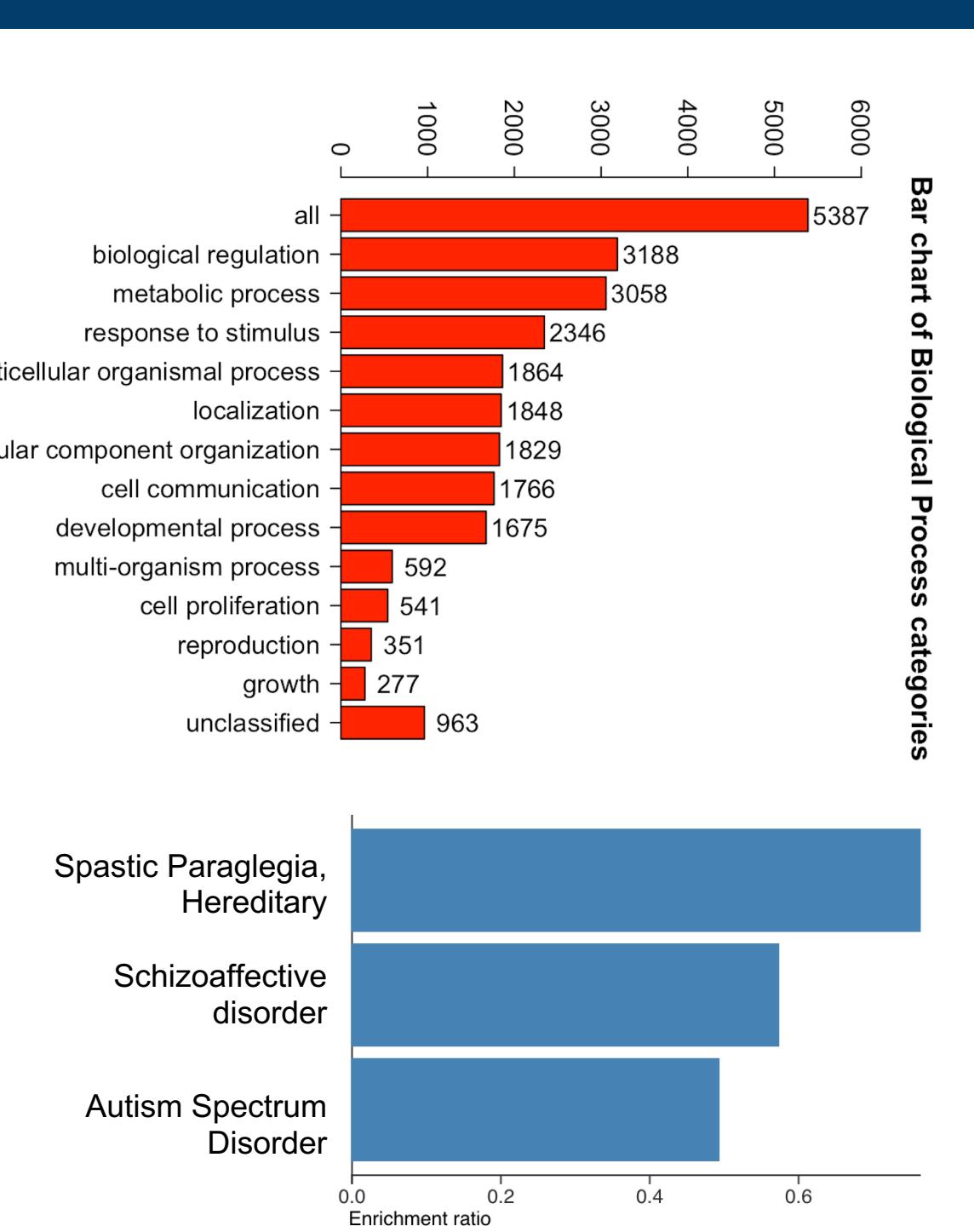
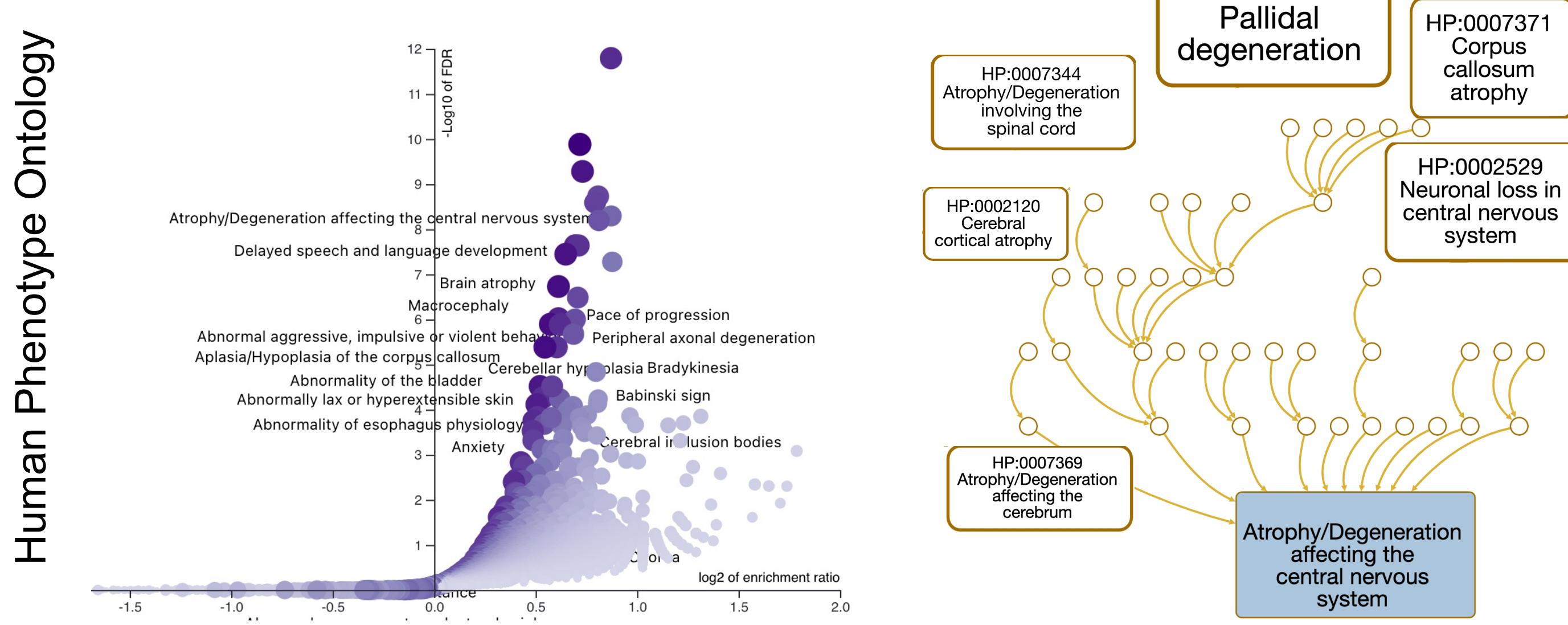
Gene Ontology: Molecular Function
Pathway: KEGG, Reactome
Disease: DisgeNET, GLAD4U
Drug: DrugBank-GLAD4U

⋮



RESULTS

- ❖ Schaefer2018 100 Parcels
- ❖ 1000 surrogate maps



DISCUSSION

Open-source software framework for elucidating neuroimaging genetics mappings

Demonstrate usefulness using several MRI-derived markers

Marker-specific candidate gene sets to better understand genetic makeup of the human brain

Develop strategies for diagnosis and treatment

References:

- [1] R. D. Markello, A. Arnatkevičiūtė, J.-B. Poline, B. D. Fulcher, A. Fornito, and B. Misić, "Standardizing workflows in imaging transcriptomics with the abagen toolbox," *ELife*, vol. 10, p. e72129, 2021.
- [2] Y. Liao, J. Wang, E. J. Jaehnig, Z. Shi, and B. Zhang, "WebGestalt 2019: gene set analysis toolkit with revamped UIs and APIs," *Nucleic Acids Res.*, vol. 47, no. W1, pp. W199–W205, 2019.
- [3] J. B. Burt, M. Helmer, M. Shinn, A. Anticevic, and J. D. Murray, "Generative modeling of brain maps with spatial autocorrelation," *NeuroImage*, vol. 220, p. 117038, Oct. 2020, doi: 10.1016/j.neuroimage.2020.117038.
- [4] E. H. Shen, C. C. Overly, and A. R. Jones, "The Allen Human Brain Atlas: comprehensive gene expression mapping of the human brain," *Trends Neurosci.*, vol. 35, no. 12, pp. 711–714, 2012.