

INTRODUCTION



➤ 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?

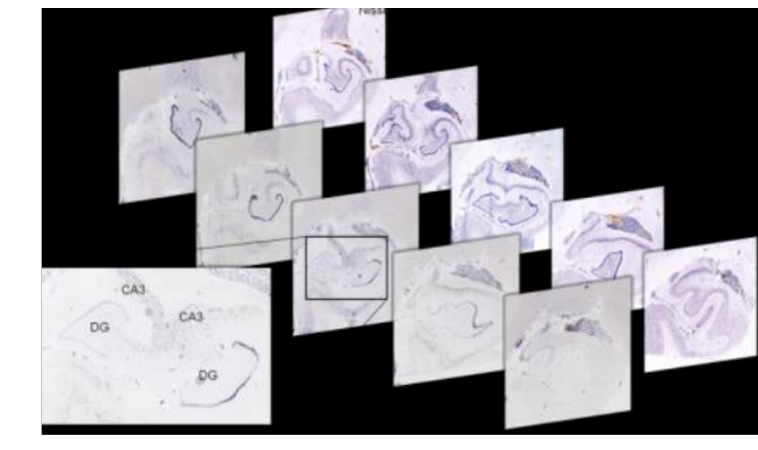
➤ Highlights

- 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.



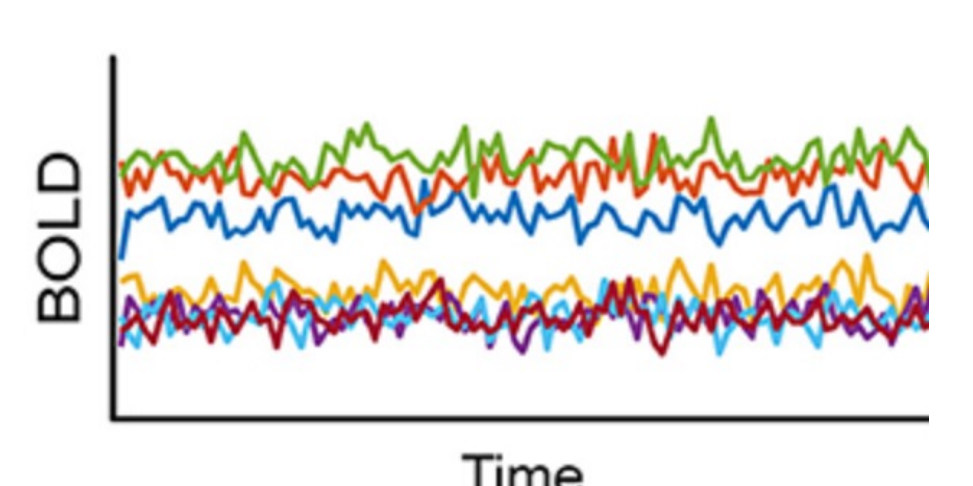
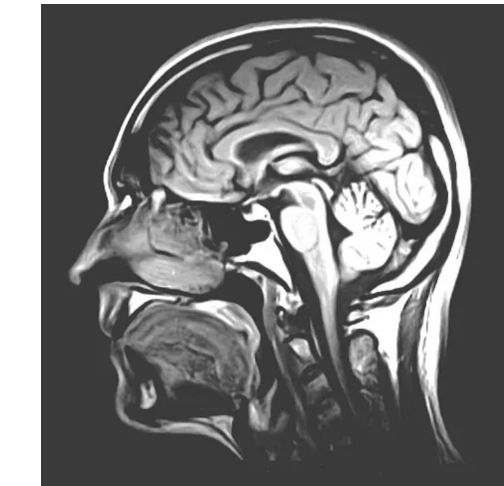
6 donors
 ■ M, 24yrs
 ■ M, 39 yrs
 ■ M, 57 yrs
 ■ M, 31 yrs
 ■ F, 49 yrs
 ■ M, 55 yrs

User provided

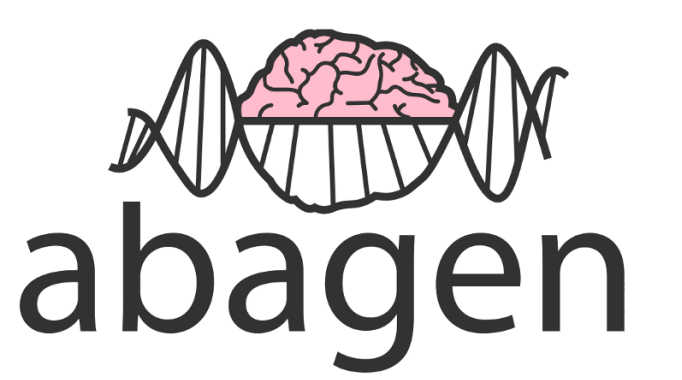
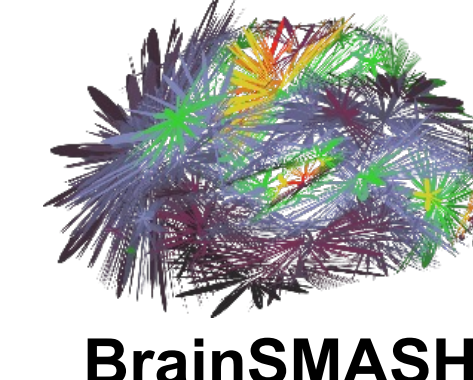
Brain atlas: Schaefer atlas.

MRI Markers: Measurements extracted for each parcel.

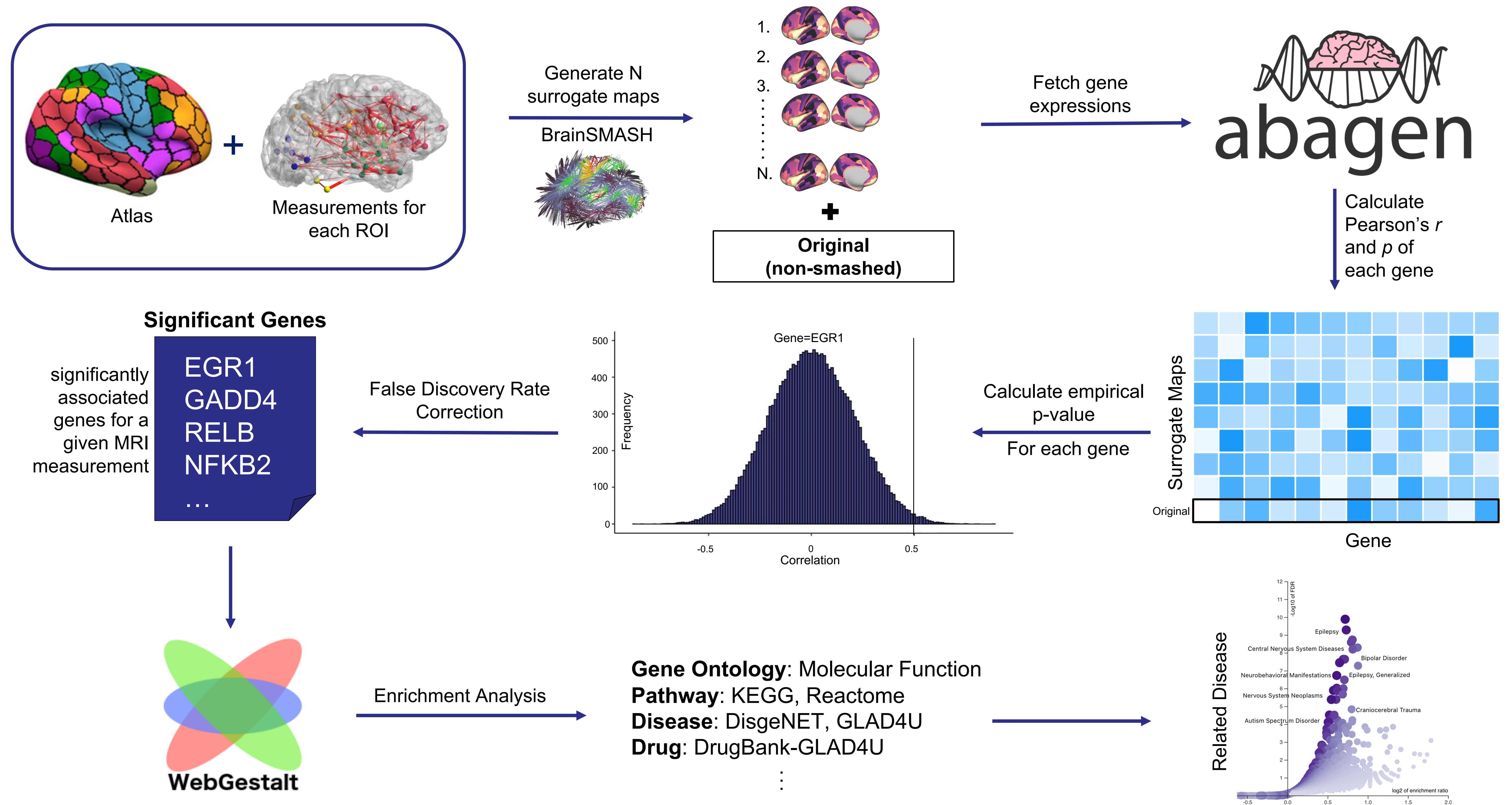
- Structural: Voxel-based morphometry
- Functional: Degree centrality



TOOLS



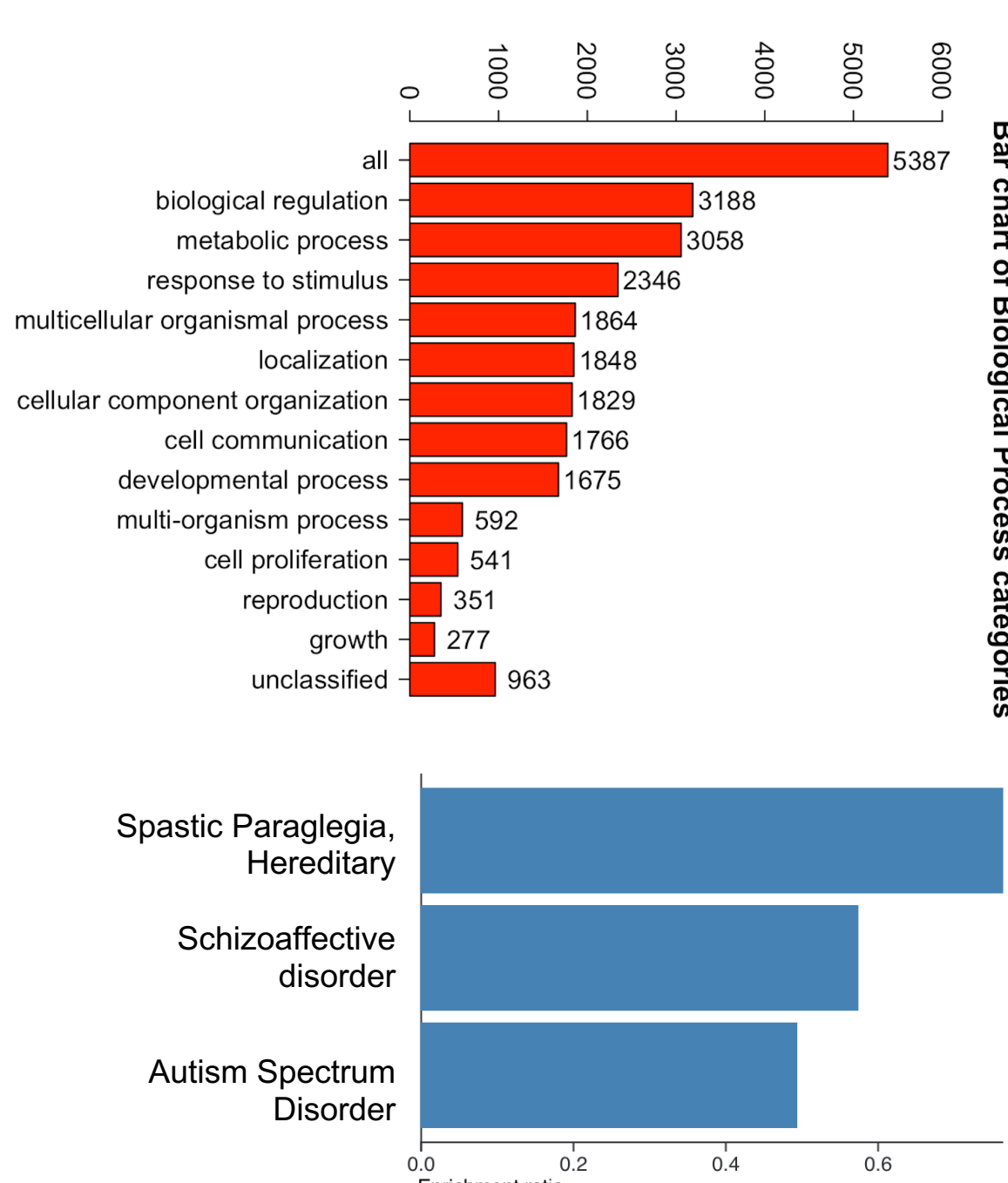
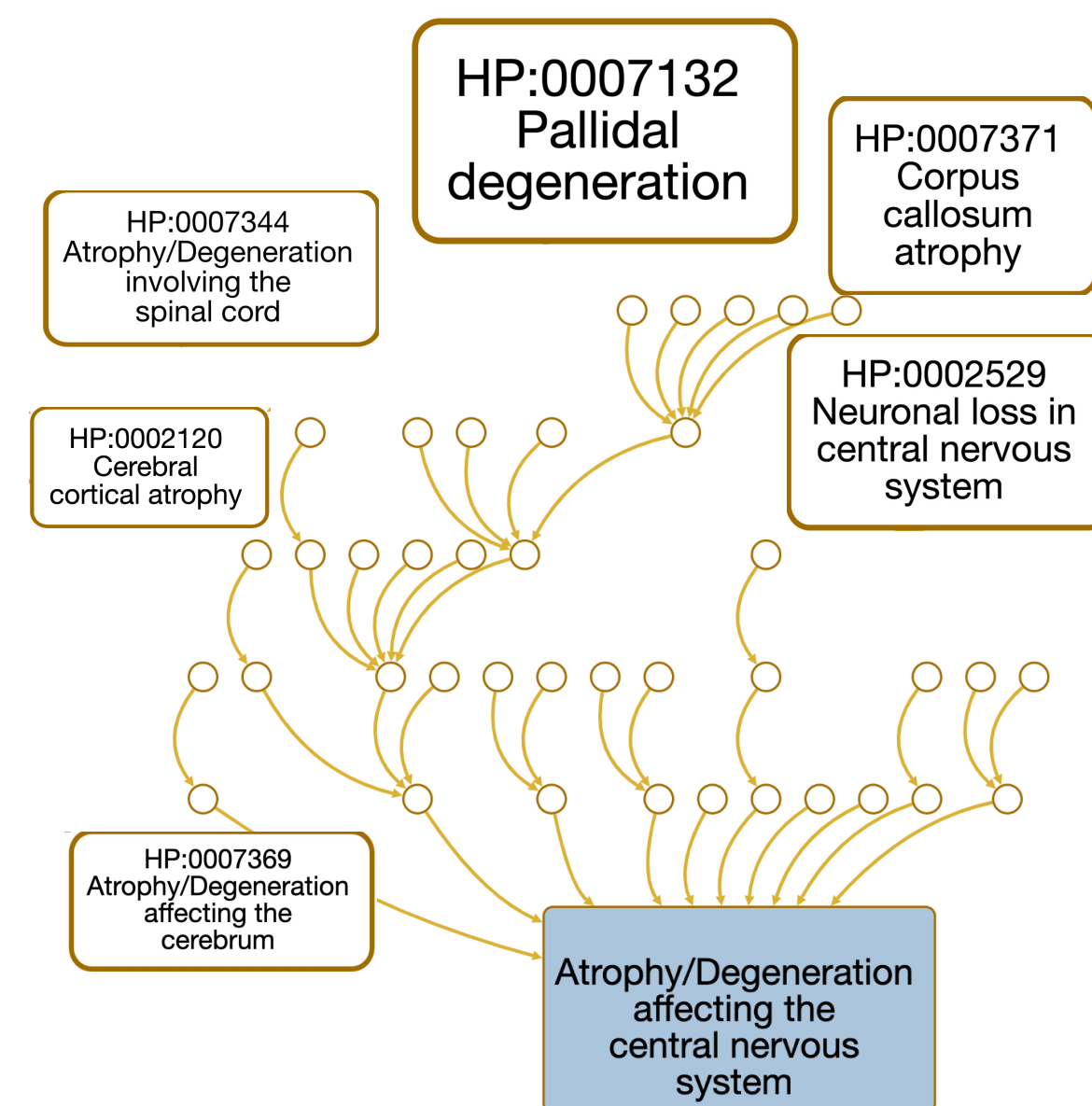
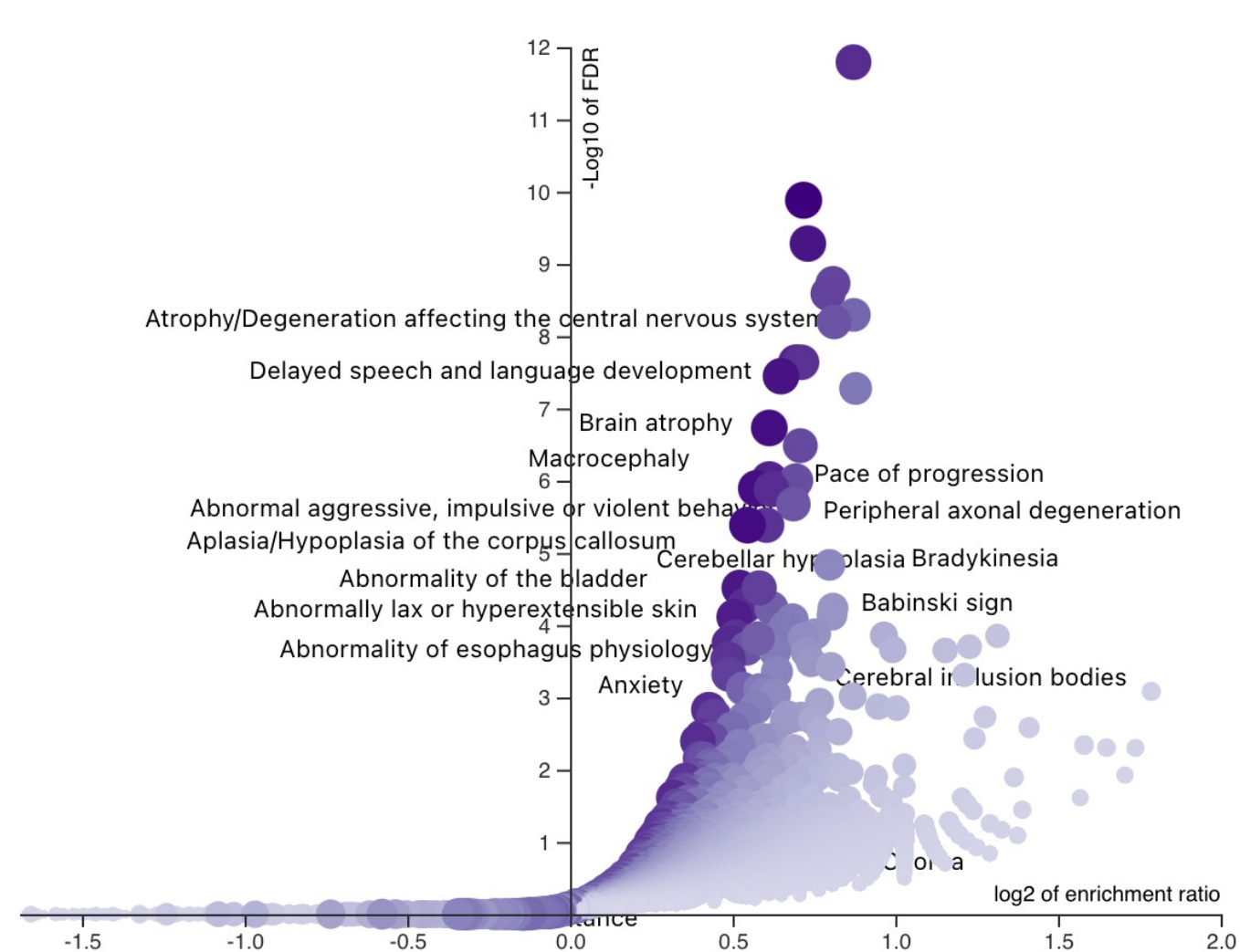
METHODS



RESULTS

- ❖ Schaefer2018 100 Parcels
- ❖ 1000 surrogate maps

Human Phenotype Ontology



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