



## Neuroimaging-Genetics bridge for better understanding of human brain organization

Magnetic Resonance Imaging (MRI) has promising potential for clinical translation due to its non-invasive nature and high spatial resolution. MRI offers structural and functional measurement modalities which capture the fundamental principles of human brain organization and variability in neurological disorders. Combining information from the MRI-derived phenomics and DNA-derived transcriptomics can provide a holistic view of human brain organization and deeper insights into disease pathologies.

Here, we aimed to develop a Python package called *nimgen* to bridge MRI organization and gene expression data. The package allows extracting gene expression levels for parcellations commonly used in the neuroimaging community leveraging the 62,000 probes from the Allen Human Brain Atlas (AHBA) [1] using the *abagen* package [2]. Then each gene's expression levels can be correlated to an MRI marker of interest. False discovery rate control is applied resulting in a statistically significantly correlated subset of genes. With the assistance of gene enrichment analysis tools (i.e. *WebGestalt*, [3]), the significant genes are examined to obtain higher-order biological processes. However, since increasing the number of parcels can inflate statistical significance, *nimgen* provides a permutation-testing approach based on *BrainSMASH* [4]. An efficient, reproducible, and rapid pipeline with several MRI markers may be constructed due to the *nimgen* package's modular design and functionality. Besides, this user-friendly package allows researchers to rapidly analyze NIfTI files with only a basic computational background and minimal effort. We hope that marker-specific candidate gene sets found by the *nimgen* package will help to better understand genetic makeup of the human brain and develop strategies for the diagnosis and treatment of diseases. Our codes are publicly available at <https://github.com/juaml/nimgen>. With the flexibility this software provides, we aim to create a comprehensive mapping of biological processes based on transcriptome and MRI measurements, leveraging state-of-the-art neuroimaging data repositories such as the Human Connectome Project (HCP) [5] S1200 release.

**Keywords:** Gene Expression, Bioinformatics, Neuroimaging

### References:

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**Session Classification:** Poster Session