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Open tools for multi-modal, multi-scale annotation of brain networks - Part I

Friday 10 February 2023 16:35 (1 hour)

Imaging technologies are increasingly used to generate high-resolution reference maps of brain structure and function. Modern scientific discovery relies on making comparisons between new maps (e.g. task activations, group structural differences) and these reference maps. Although recent data sharing initiatives have increased the accessibility of such brain maps, data are often shared in disparate coordinate systems (or “spaces”), precluding systematic and accurate comparisons among them. Here we introduce the neuromaps toolbox, an open-access software package for accessing, transforming, and analyzing structural and functional brain annotations. We implement two registration frameworks to generate high-quality transformations between four standard coordinate systems commonly used in neuroimaging research. The initial release of the toolbox features >40 curated reference maps and biological ontologies of the human brain, including maps of gene expression, neurotransmitter receptors, metabolism, neurophysiological oscillations, developmental and evolutionary expansion, functional hierarchy, individual functional variability, and cognitive specialization. Robust quantitative assessment of map-to-map similarity is enabled via a suite of spatial autocorrelation-preserving null models. Finally, we demonstrate two examples of how neuromaps can be used to contextualize brain maps with respect to canonical annotations. By discovering novel associations with previously-established features of brain structure and function, neuromaps generates biological insight about new brain maps. Altogether, neuromaps combines open-access data with transparent functionality for standardizing and comparing brain maps, providing a systematic workflow for comprehensive structural and functional annotation enrichment analysis of the human brain.

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 content for the tutorial: [link](#)

**** Requirements****

Practical examples will be shown in Python. If you want to follow along you will need your laptop. Please contact us if you do not come with your own laptop.

Please install the toolboxes that will be introduced:

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<ul> <li>neuromaps</li> <li>abagen</li> </ul>
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Optional readings:

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<ul> <li>neuromaps</li> <li>abagen</li> <li>spatial nulls</li> </ul>
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