HIBALL Winter School



Report of Contributions

Type: not specified

EBRAINS Data & Knowledge - how to share own data and explore the shared data from others - Part I

Friday 10 February 2023 13:00 (1h 30m)

The EBRAINS Data & Knowledge service facilitates Findability, Accessibility, Interoperability and Reusability of neuroscience research products (experimental research data, computational models, or software tools). In the first part of this session you will learn how to prepare your research products for sharing them with other researchers through EBRAINS. For this we will discuss good practices for data organizations, metadata annotations, and data descriptors.

In the second part of this session you will learn how you can explore the research products shared through the EBRAINS Knowledge Graph (KG). For this we will provide a demo for data queries using the KG Search UI, the KG Query Builder and Core Python SDK, as well as fairgraph.

Requirements:

EBRAINS account (please register in advance)basic Python knowledge (for some parts of the lecture).

Please contact us if you do not come with your own laptop.

Primary author: Dr ZEHL, Lyuba (Institute for Neuroscience and Medicine, INM-1, Forschungszentrum Jülich)

Presenter: Dr ZEHL, Lyuba (Institute for Neuroscience and Medicine, INM-1, Forschungszentrum Jülich)

Type: not specified

EBRAINS Data & Knowledge - how to share own data and explore the shared data from others - Part II

Friday 10 February 2023 14:45 (1h 30m)

The EBRAINS Data & Knowledge service facilitates Findability, Accessibility, Interoperability and Reusability of neuroscience research products (experimental research data, computational models, or software tools). In the first part of this session you will learn how to prepare your research products for sharing them with other researchers through EBRAINS. For this we will discuss good practices for data organizations, metadata annotations, and data descriptors.

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BigBrain as a tool to understand c...

Contribution ID: 3

Type: not specified

BigBrain as a tool to understand cortical types - Part I

Thursday 9 February 2023 14:00 (1 hour)

What you always wanted to know about the different types of cortex, but didn't dare to ask.... after your possible initial surprise when hearing that such a thing as "cortical types" exists! Why differentiate between neocortex and allocortex? Do the terms neocortex and isocortex mean the same thing? What kind of differences in lamination can we expect within the neocortex or the allocortex? And perhaps the most difficult question of all. How do these differences help us to identify cortical borders?

At the end of this session you will understand why, despite the technical challenges associated with this process, the analysis of the 1µm resolution version of BigBrain is required to capture the more subtle aspects of cytoarchitectonic organization in the cerebral cortex.

Presenter: Prof. PALOMERO-GALLAGHER, Nicola (Institute for Neuroscience and Medicine, INM-1, Forschungszentrum Jülich)

BigBrain as a tool to understand c...

Contribution ID: 4

Type: not specified

BigBrain as a tool to understand cortical types - Part

Thursday 9 February 2023 15:15 (1 hour)

What you always wanted to know about the different types of cortex, but didn't dare to ask.... after your possible initial surprise when hearing that such a thing as "cortical types" exists! Why differentiate between neocortex and allocortex? Do the terms neocortex and isocortex mean the same thing? What kind of differences in lamination can we expect within the neocortex or the allocortex? And perhaps the most difficult question of all. How do these differences help us to identify cortical borders?

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Presenter: Prof. PALOMERO-GALLAGHER, Nicola (Institute for Neuroscience and Medicine, INM-1, Forschungszentrum Jülich)

Type: not specified

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.

Contact: vincent.bazinet@mail.mcgill.ca 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:

neuromaps abagen

Optional readings:

neuromaps abagen spatial nulls

Presenters: Prof. MIŠIĆ, Bratislav (Network Neuroscience Lab, McGill University); BAZINET, Vincent (McGill University)

Type: not specified

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

Friday 10 February 2023 17:50 (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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Type: not specified

siibra -programming with multiscale brain atlases in Python - Part I

Thursday 9 February 2023 16:35 (1 hour)

siibra is a software tool suite implementing an openly accessible brain atlas framework which connects multimodal datasets from different resources to anatomical structures in reference spaces at different spatial scales. The tool suite is designed to address both interactive exploration through an interactive 3D web viewer (siibra-explorer) as well as integration into data analysis and simulation workflows with a comprehensive Python library (siibra-python). In this session, we first introduce the multidimensional concept of the atlas framework and explore some key features such as the BigBrain interactively. We then turn to concrete programming tutorials in Python. These include fetching brain region maps, accessing the BigBrain dataset, and extracting multimodal regional features such as cortical thicknesses, cell and neurotransmitter densities, gene expressions and connectivity data. We will finish with some concrete data analysis examples.

Requirements: For the practical examples you need a laptop with a current browser. All examples will be run in prepared Jupyter notebooks, which we will make available for download. Please contact us if you do not come with your own laptop.

Presenter: Prof. DICKSCHEID, Timo (Institute for Neuroscience and Medicine, INM-1, Forschungszentrum Jülich)

Type: not specified

siibra -programming with multiscale brain atlases in Python - Part II

Thursday 9 February 2023 17:50 (1 hour)

siibra is a software tool suite implementing an openly accessible brain atlas framework which connects multimodal datasets from different resources to anatomical structures in reference spaces at different spatial scales. The tool suite is designed to address both interactive exploration through an interactive 3D web viewer (siibra-explorer) as well as integration into data analysis and simulation workflows with a comprehensive Python library (siibra-python). In this session, we first introduce the multidimensional concept of the atlas framework and explore some key features such as the BigBrain interactively. We then turn to concrete programming tutorials in Python. These include fetching brain region maps, accessing the BigBrain dataset, and extracting multimodal regional features such as cortical thicknesses, cell and neurotransmitter densities, gene expressions and connectivity data. We will finish with some concrete data analysis examples.

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Welcome

Contribution ID: 9

Type: not specified

Welcome

Thursday 9 February 2023 13:50 (10 minutes)