Brain Parcellations and Functional Territories

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Educational Course - Half Day

Over the past century and an half, human brain mapping consisted in pinning small functionally responsive areas within the brain. However the real extent of these areas and their eventual overlap remains unknown.
The challenge now facing neuroscience is to define boundaries for functionally responsive areas at the group and the individual level. Many approaches parcellating the brain in areas with different features became recently available including post-mortem and in vivo architectonics, tractography-based connectivity, functional coactivation, and resting state functional connectivity. However, what these methods really measure and what conclusion can be drawn, are not yet fully clear to the scientific community. This course addresses this need and is intended for a large audience of research scientist (e.g. from beginner to advanced level).

Objective

Having completed this course, participants will be able to
- Understand the rationale and the difference between the different methods for brain parcellation.
- Understand the advantage and the limitation between the different methods for brain parcellation.
- Give examples of approaches to parcellate the brain
- Choose the appropriate method to fulfill a research project objective.

Target Audience

The prime target audience is researcher with an interest with the relation between new brain subdivision results and functional specialization of the brain. This includes researchers with limited knowledge in neuroimaging. Background will be provided for those without experience in methods for brain parcellation but some parts of the talks will also address advanced methodological issues that would be of interest to people with more experience.

Presentations

Brain Variability Parcellation

A large amount of variability exists across human brains; revealed initially on a small scale by postmortem studies and, more recently, on a larger scale with the advent of neuroimaging. Here we compared structural variability between human and macaque monkey brains using grey and white matter magnetic resonance imaging measures. The monkey brain was overall structurally as variable as the human brain, but variability had a distinct distribution pattern, with some key areas showing high variability. We also report the first evidence of a relationship between anatomical variability and evolutionary expansion in the primate brain. This suggests a relationship between variability and stability, where areas of low variability may have evolved less recently and have more stability, while areas of high variability may have evolved more recently and be less similar across individuals. We showed specific differences between the species in key areas, including the amount of hemispheric asymmetry in variability, which was left-lateralized in the human brain across several phylogenetically recent regions. This suggests that cerebral variability may be another useful measure for comparison between species and may add another dimension to our understanding of evolutionary mechanisms. Article discussed Croxson et al., 2018 https://www.ncbi.nlm.nih.gov/pubmed/29045561 Software www.fmrib.ox.ac.uk/fsl http://brainvisa. Info http://brainvis.wustl.edu/ www.humanconnectome.org Human Data www.humanconnectome.org

Presenter

Stephanie Forkel, GIN Bordeaux, France, France

Structural Connectivity Parcellation

Brain regions have distinctive long-range anatomical connections that in part determine their degree of functional specialisation. These structural connections can be measured in vivo with diffusion MRI tractography, and then used to parcellate the brain white matter and grey matter into areas of unique connectivity profiles. This talk covers the main variations on this approach, including statistical methods, validation, gotchas, and a number of different applications. Article discussed https://www.ncbi.nlm.nih.gov/pubmed/28514668 https://www.ncbi.nlm.nih.gov/pubmed/29749930 https://www.ncbi.nlm.nih.gov/pubmed/27461122 Software www.fmrib.ox.ac.uk/fsl www.humanconnectome.org Data www.humanconnectome.org www.ukbiobank.ac.uk

Presenter

Saad Jbabdi, FMRIB, Oxford, United Kingdom

Machine Learning Versus Statistics in Brain Parcellation

Biomedical data analysis in the 20iest century has been often dominated by certifying robust effects in circumscribed variables. The advent of multi-modal population datasets with deep phenotyping has ushered neuroscience in the age of high-dimensional data. Clustering and matrix decomposition consequently take center stage as quantitative tools to harness the information richness and enable data-guided conclusions about the brain and clinical treatment interventions. Here, we will contemplate the epistemological consequences of these rapidly changing data-analysis practices in theory and in practice. Articles discussed Towards algorithmic analytics for large-scale datasets. D Bzdok, TE Nichols, SM Smith Nature Machine Intelligence 1 (7), 296. Exploration, inference, and prediction in neuroscience and biomedicine. D Bzdok, JPA Ioannidis. Trends in neurosciences. Inference in the age of big data: Future perspectives on neuroscienceD Bzdok, BTT Yeo Neuroimage 155, 549-564 Software employed https://github.com/nilearn/nilearn Data available at https://www.ukbiobank.ac.uk/

Presenter

Danilo Bzdock, Department of Biomedical Engineering - McGill Montreal, Canada

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Functional Connectivity-based Parcellation

Resting-state functional connectivity has shown great promise as a tool for parcellating the human brain into functional areas and networks. Until recently, most parcellations have relied on data averaged across many individuals. However, such group-level parcellations might obscure biologically meaningful individual-specific features. In this educational course, we will first introduce resting-state fMRI. We will then discuss several approaches (e.g., boundary mapping and clustering) for estimating network-level and areal-level brain parcellations at the group-level, as well as in individuals. We will also outline a systematic approach for assessing the quality of brain parcellations based on FACT (function, architectonics, connectivity and topography). After that, we will provide a comparison of various group-level and individual-specific parcellations with a particular focus on the behavioral relevance of individual-specific parcellation features not visible in group-level parcellations. Finally, we will briefly discuss individual-specific gradients and compare gradients with parcellations for behavioral prediction. Article discussed https://www.physiology.org/doi/full/10.1152/jn.00338.2011 (Yeo et al. 2011) https://www.sciencedirect.com/science/article/pii/S0896627311007926 (Power et al. 2011) https://academic.oup.com/cercor/article/26/1/288/2367115 (Gordon et al. 2016) https://academic.oup.com/cercor/article/28/9/3095/3978804 (Schaefer et al. 2017) https://www.cell.com/neuron/fulltext/S0896-6273(17)30613-X (Gordon et al. 2017) https://academic.oup.com/cercor/advance-article/doi/10.1093/cercor/bhy123/5033556 (Kong et al. 2018) Software employed https://github.com/ThomasYeoLab/CBIG https://fsl.fmrib.ox.ac.uk/fsl/fslwiki https://surfer.nmr.mgh.harvard.edu/ Data available at https://db.humanconnectome.org https://openfmri.org/

Presenter

Ruby Kong, National University of Singapore, Singapore

Microstructural Cortical Parcellation and Connectivity

Parcellating the human brain into functionally meaningful regions has been a long-standing interest in brain research. While a diversity of such atlases exists, the level of information about the brain contributing to the final parcellation largely differs between atlases. For a functional meaningful parcellation, the neuronal architecture as the functionally relevant building blocks is of high relevance. The talk will introduce the principles of microstructural analysis and atlasing in the human brain. Linking this to connectivity information could happen on different levels, i.e. on the microstructural level directly or across levels via the atlas and joint implementation with respective macroanatomical connectivity information (e.g. from MRI) in a unifying software framework. Examples for both approaches will be given, including an ongoing effort of multilevel multimodal data integration for unified analyses from the Human Brain Project (HBP), the EBRAINS platform. Articles discussed Caspers et al. 2013. Microstructural grey matter parcellation and its relevance for connectome analyses. NeuroImage 80: 18-26. Amunts et al. 2020. Julich-Brain: A 3D probabilistic atlas of the human brain's architecture. Science 369 (6506): 988-992. Goulas et al. 2018. Cortical gradients and laminar projections in mammals. Trends Neurosci 41 (11): 775-788. Software employed: EBRAINS: https://ebrains.eu Julich-Brain: https://jubrain.fz-juelich.de/apps/cytoviewer2/cytoviewer-main.php

Presenter

Svenia Casper, Institut für Anatomie I Heinrich-Heine-Universität Düsseldorf Dusseldorf, Germany

Parcellating the White Matter with Functional Neuroimaging

The functional role of white matter connections has remained an open question for the past 250 years. Based on 1333 stroke lesions, here we reveal the human Disconnectome and demonstrate its relationship to the functional segregation of the human brain. Results indicate that functional territories are not only defined by white matter connections, but also by the highly stereotyped spatial distribution of brain disconnections. While the former can grant us the possibility to map functional neuroimaging on the white matter of the whole brain, the latter compels a revision of the taxonomy of brain functions. We will also introduce our freely available Atlas of White Matter Function that enable improved clinical-neuroanatomical predictions for brain lesion studies and provide a platform for explorations in the domain of cognition. Articles discussed Thiebaut de Schotten et al. Nature Comm. 2020 https://academic.oup.com/gigascience/article/7/3/giy004/4838040 Foulon et al. Gigascience 2018 https://www.nature.com/articles/s41467-020-18920-9 Software employed http://www.bcblab.com/BCB/Software.html https://github.com/chrisfoulon/BCBlib/blob/devel/bcblib/scripts/generate_synth_lesions.py, https://github.com/chrisfoulon/BCBlib/blob/devel/bcblib/scripts/pick_up_matched_synth_lesions.py https://github.com/chrisfoulon/BCBlib/blob/devel/bcblib/scripts/effectsize_T2R.py Data available at The two sets of component maps and the atlas of white matter function (original and replication) are available at https://identifiers.org/neurovault.collection:7735. The atlas of white matter function is also available at A–C terms: https://identifiers.org/neurovault.collection:7756 D–H terms: https://identifiers.org/neurovault.collection:7757 I–N terms: https://identifiers.org/neurovault.collection:7758 O–R terms: https://identifiers.org/neurovault.collection:7759 S–U terms: https://identifiers.org/neurovault.collection:7760 V–Z terms: https://identifiers.org/neurovault.collection:7761 The raw dataset analysed in the current study is available at https://www.humanconnectome.org (7 T diffusion data) and http://www.neurosynth.org (metanalytic functional MRI maps). In addition, processed data are available at http://www.bcblab.com/BCB/Opendata.html and https://osf.io/5zqwg/

Presenter

Michel Thiebaut de Schotten, BCBlab Bordeaux, United Kingdom