

Brain parcellations and functional territories

Sarah Genon Co Organizer
Jülich Research Centre
Jülich, Germany
Germany

Michel Thiebaut de Schotten Organizer
CNRS UMR 5293 - IMN - DISCONNECTOME
Bordeaux, Aquitaine
France

Sunday, Jun 19: 8:00 AM - 4:30 PM

1114

Educational Course - Full Day (8 hours)

SEC Meeting Academy

Room: M1

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 parcellation and functional territories introduction

A defining aspect of brain organization is its spatial heterogeneity, which gives rise to multiple topographies at different scales. Brain parcellation — defining distinct partitions in the brain, be they areas or networks that comprise multiple discontinuous but closely interacting regions — is thus fundamental for understanding brain organization and function. The past decade has seen an explosion of in vivo MRI-based approaches to identify and parcellate the brain on the basis of a wealth of different features, ranging from local properties of brain tissue to long-range connectivity patterns, in addition to structural and functional markers. In this talk, I will introduce brain parcellation and provide an overview of the main approaches. I will then focus more particularly on connectivity-based parcellation (CBP) applied to different connectivity features. This will lead us to discuss convergence and divergence across features and the related open challenges.

Articles discussed:

Eickhoff, S. B., Yeo, B. T. T., & Genon, S. (2018). Imaging-based parcellations of the human brain. *Nat Rev Neurosci*, 19(11), 672-686. doi:10.1038/s41583-018-0071-7

Genon, S., Bernhardt, B. C., La Joie, R., Amunts, K., & Eickhoff, S. B. (in press). The many dimensions of human hippocampal organization and (dys) function. *Trends in Neurosciences*.

Plachti, A., Eickhoff, S. B., Hoffstaedter, F., Patil, K. R., Laird, A. R., Fox, P. T., . . . Genon, S. (2019). Multimodal Parcellations and Extensive Behavioral Profiling Tackling the Hippocampus Gradient. *Cereb Cortex*, 29(11), 4595-4612. doi:10.1093/cercor/bhy336

Software employed:

CBBtools: <https://github.com/inm7/cbptools>

Data:

<https://www.humanconnectome.org/study/hcp-young-adult/data-releases>

Presenter

Sarah Genon, Jülich Research Centre Jülich, Germany
Germany

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

Svenja Caspers, Institute for Anatomy I, Medical Faculty & University Hospital Düsseldorf Düsseldorf, Nordrhein-Westfalen
Germany

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, UK

United Kingdom

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, CNRS Bordeaux, France

France

Functional connectivity 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](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, Singapore
Singapore

Multi-modal Parcellation

Multi-modal parcellations have inherent advantages in that the various modalities often provide complementary information, and agreement between modalities increases our confidence in areal borders, particularly in data that have been processed to achieve precise alignment across individuals without loss of spatial resolution. We will discuss the integration of sharp transitions (gradients) across the cortical surface in architectural information (in vivo myelin maps and cortical thickness maps), functional information (task fMRI activation maps), connectivity information (resting state functional connectivity), and topographic information (visuotopic resting state functional connectivity) to generate a multi-modal cortical parcellation at the group level. We will then discuss an approach for capturing the variability in the individual subject parcel arrangements that cannot be removed by areal topology preserving spatial registrations (e.g. two areas swapping positions as opposed to simple spatial shifts in areas) by using a machine learning classifier to learn the multi-modal areal fingerprint of each parcel so that one can define the areas in individual subjects automatically.

Articles discussed

<https://www.nature.com/articles/nature18933> (Glasser et al 2016 Nature)

<https://www.nature.com/articles/nn.4361> (Glasser et al 2016 Nature Neuroscience)

<https://www.sciencedirect.com/science/article/pii/S0896627318305427> (Van Essen and Glasser 2018 Neuron)

Software employed

<https://www.humanconnectome.org/software/connectome-workbench> (Connectome Workbench)

<https://github.com/Washington-University/HCPpipelines> (The HCP Pipelines)

https://github.com/ecr05/MSM_HOCR (Multi-modal Surface Matching)

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki> (FSL)

<https://surfer.nmr.mgh.harvard.edu/> (FreeSurfer)

Data available at

<https://balsa.wustl.edu/study/show/RVVG> (The Balsa Neuroimaging Results Database)

<https://db.humanconnectome.org> (Connectome DB)

Presenter

Matthew Glasser, Washington University Medical School St. Louis, MO
United States

Brain parcellation and large-scale functional connectivity gradients

Ye Tian: Brain parcellation and large-scale functional connectivity gradients

Topographic variation in brain structure, function and connectivity can be parsed into discrete regions or represented with smooth gradients. In this educational course, I will introduce principled approaches to reconcile these two complementary representations of brain topography and demonstrate how doing so can reveal new insight into the organization of the human cerebral cortex and subcortical nuclei. In particular, I will introduce the concept of gradientography, which is an fMRI analogue of diffusion MRI tractography that yields striking visualizations of brain gradients and enables identification of gradient magnitude peaks. I will present a new model selection process to determine which regional peaks are sufficiently large to warrant boundary delineation. In the second part of my talk, I will showcase the Melbourne Subcortex Atlas that I have delineated by applying this approach to 3 and 7 Tesla functional MRI data acquired in more than 1000 individuals. The new atlas can be incorporated in existing cortex-only MRI parcellation atlases to enable holistic connectome mapping. Time permitting, I will also discuss how gradient mapping and boundary delineation can be used to reveal the functional connectivity architecture of the human brain in health and individuals with psychiatric illness.

Article discussed

Tian et al 2020. Nat. Neuro. <https://www.nature.com/articles/s41593-020-00711-6>

Tian et al 2019. BioPsy CNNI. <https://doi.org/10.1016/j.bpsc.2018.12.003>

Tian et al 2018. NeuroImage. <https://doi.org/10.1016/j.neuroimage.2018.08.055>

Gordon et al 2016. Cerebral Cortex. <https://doi.org/10.1093/cercor/bhu239>

Margulies et al 2016. PNAS. <https://doi.org/10.1073/pnas.1608282113>

Glasser et al 2016. Nature. <https://www.nature.com/articles/nature18933>

Software

<https://github.com/yetianmed/subcortex>

<http://trackvis.org/>

Data

www.humanconnectome.org

Presenter

Ye Tian, The University of Melbourne Melbourne, Victoria
Australia

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, CNRS UMR 5293 - IMN - DISCONNECTOME Bordeaux, Aquitaine
France

Parcellating the white matter with neuropsychological symptoms

Stroke significantly impacts quality of life. However, the long-term cognitive evolution in stroke is poorly predictable at the individual level. There is an urgent need for a better prediction of long-term symptoms based on acute clinical neuroimaging data. Previous works have demonstrated a relationship between the location of white matter disconnections and clinical symptoms. However, rendering the entire space of possible lesion-deficit associations optimally surveyable will allow for a systematic association between brain disconnections and cognitive-behavioural measures at the individual level. Here we exploit nonlinear dimensionality reduction to report the characteristics of disconnection patterns of more than 1000 stroke lesions in a two-dimensional summary morphospace. Acute disconnectomes drawn from an independent distribution were projected into the morphospace to predict neuropsychological scores 1 year after stroke. Linking the latent disconnectome morphospace to neuropsychological outcomes yields a comprehensive atlas of disconnectome-deficit relations across 86 neuropsychological scores. Out-of-sample prediction derived from this atlas achieved average accuracy

over 80%. Our novel predictive framework is available as an interactive web application, the disconnectome symptoms discoverer (DSD), to provide the foundations for a new approach to modelling cognition in stroke.

Article discussed

Talozzi et al., 2021 DOI: 10.13140/RG.2.2.17963.36641

Software

<http://www.bcblab.com/BCB/Software.html>

<https://www.djangoproject.com>

<https://www.digitalocean.com>

Data available at:

<http://disconnectomestudio.bcblab.com>

Presenter

Lia Talozzi, BCBlab France, Aquitaine

France

A Framework for Brain Atlases: An Overview and Discussion on Selecting an Atlas for a Study

Brain atlases are essential tools for studying brain function and organization. The abundance of available atlases used across the neuroscience literature, however, creates an implicit challenge that may alter the hypotheses and predictions we make about neurological function and pathophysiology. In this educational course presentation, we will first take an overview of many common brain atlases used in the literature. We will discuss how atlases are typically created and the wide variety of features contained within the atlases. We will then look at a specific case-study on how parcellation scale, shape, and anatomical coverage may impact our prediction of the brain's function from its underlying structure (i.e., the structure-function relationship within the brain). We show that the power to test a specific hypothesis about epilepsy pathophysiology may change because of atlas choice and atlas features. Finally, we propose a generalized framework for selecting a brain atlas for a study with respect to the previous discussion and findings. We hope this presentation provides guidance to other investigators utilizing the various atlases published over the last century in their own work.

Background reading on brain atlases:

<https://pubmed.ncbi.nlm.nih.gov/22248580/>

<https://pubmed.ncbi.nlm.nih.gov/19787067/>

<https://pubmed.ncbi.nlm.nih.gov/22647262/>

<https://pubmed.ncbi.nlm.nih.gov/28154532/>

<https://pubmed.ncbi.nlm.nih.gov/25914639/>

<https://pubmed.ncbi.nlm.nih.gov/30002509/>

Presenter

Andy Revell, University of Pennsylvania Philadelphia, PA

United States