

# Brain parcellations and functional territories

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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

## From post-mortem to in vivo parcellations

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 based on a wealth of different features, ranging from local properties of brain tissue to long-range connectivity patterns, in addition to structural and functional markers. Given the high diversity of these various approaches, assessing the convergence and divergence among these ensuing maps can be a challenge.

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## Structural connectivity parcellation

Exploring brain connectivity is fundamental to understanding the functional architecture of the cortex. Tractography-based parcellation is a method based on diffusion imaging tractography, which segregates the human brain in vivo into distinctive areas showing sharp differences in their connections with the rest of the brain. Measures of anatomical connectivity combined with statistical classification or dimension reduction analyses allow dividing the brain into several areas. Tractography-based parcellation may provide a new promising anatomical subdivision of the living human brain based on its anatomical connectivity, which may benefit the understanding of clinical-neuroanatomical dissociations and functional neuroimaging results. Articles discussed [http://www.bcblab.com/BCB/Publications\\_files/Cereb.%20Cortex-2016-Thiebaut%20de%20Schottencercor\\_bh215.pdf](http://www.bcblab.com/BCB/Publications_files/Cereb.%20Cortex-2016-Thiebaut%20de%20Schottencercor_bh215.pdf) <https://onlinelibrary.wiley.com/doi/10.1002/hbm.21338> <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3910152/> Software employed <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/> <https://www.ibm.com/analytics/spss-statistics-software> <http://stnava.github.io/ANTs/> Data available at <http://www.bcblab.com/BCB/Opendata.html>

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## 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. Reading Croxson et al., 2018  
<https://www.ncbi.nlm.nih.gov/pubmed/29045561> Software [www.fmrib.ox.ac.uk/fsl](http://www.fmrib.ox.ac.uk/fsl) <http://brainvisa.info>  
<http://brainvis.wustl.edu/> [picssl.upenn.edu/software/ants](http://picssl.upenn.edu/software/ants) [www.humanconnectome.org](http://www.humanconnectome.org)

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## Machine learning versus statistics in brain parcellation

Biomedical data analysis in the 21st 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 neuroscience D Bzdok, BTT Yeo Neuroimage 155, 549-564 Software employed <https://github.com/nilearn/nilearn> Data available at <https://www.ukbiobank.ac.uk/>

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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 functional connectivity and how it can inform us about brain organization. We will then discuss several approaches (e.g., boundary mapping and spatial independent component analysis) 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 (i.e. function, architectonics, connectivity and topography). Finally, 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. 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/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

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## 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](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

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