Neuroanatomy and Its impact on Structural and Functional Imaging (In Memory of Karl Zilles)

Hiromasa Takemura Co Organizer
National Institute for Physiological Sciences
Department of System Neuroscience
Okazaki, Aichi
Japan

Nicola Palomero-Gallagher Organizer
Research Centre Julich
Julich, NRW
Germany

Sunday, Jun 19: 1:00 PM - 5:00 PM
1105
Educational Course - Half Day (4 hours)
SEC Armadillo
Room: Clyde Auditorium

Since its inception, OHBM has had an Educational Course during its annual meeting that educated researchers across the board - from students to PIs - on the importance of neuroanatomy to understand the organization of human brains as well as to interpret non-invasive neuroimaging data. In contrast to the proposal made in the last year, we included experts in comparative studies as speakers (Amiez and Vanduffel), since comparative neuroimaging has become a popular field in the OHBM as a result of the pressing need to extend knowledge obtained from invasive studies performed in animal models into humans. The educational course is not limited to classical neuroanatomy and conventional neuroimaging methods, but includes speakers introducing how to combine neuroimaging and neuroanatomy data with gene expression and cellular analyses to understand cortical function and plasticity (Gomez and Sampaio Baptista). Finally, since there are an increasing number of datasets available to the community, there is a need to learn about software tools to combine structure and functional data. Therefore, we also invited a software developer (Benson) to make a tutorial talk on open-source software tools to the community. The desired learning outcome for the audience would be to learn (1) key concepts of neuroanatomy to understand the human brain, (2) how to critically evaluate comparative neuroimaging studies, (3) how to combine molecular and cellular approaches with neuroimaging and (4) software tools to integrate structural and functional data.

Objective

Understand key concepts of neuroanatomy, such as macroanatomical landmarks, white matter tracts and laminar organization.
Understand the importance of comparative studies and integration of neuroimaging with molecular/cellular analyses, to discern brain organization and biological mechanisms.
Operate publicly available software tools to perform analyses on structural and functional datasets.

Target Audience

The prime target audience is researchers with an interest in understanding the relationship between brain structure and function. This includes researchers with limited anatomical knowledge, but prior experience with

neuroimaging.

Presentations

Why do we need anatomical knowledge for a correct and comprehensive interpretation of neuroimaging data?

This talk aims to provide an overview of the course and discuss how knowledge on neuroanatomy is essential to accurately interpret neuroimaging data. Neuroanatomy is a wide concept including both macroscopic and microscopic structural properties. I will discuss the following three topics regarding anatomical structure of human brains and introduce modern findings obtained by combining neuroanatomy and neuroimaging. First, I will provide a brief introduction of sulci and gyri in the human brain and discuss examples of studies demonstrating the relationship between functionally-defined regions and sulcal patterns. Then I will introduce recent debates on how sulcal folding can impact the analysis of neuroimaging datasets (including both functional and diffusion MRI), and discuss considerations for proper analysis pipelines. Second, I will elaborate on the importance of characterizing white matter fiber tracts to understand human brain functions with some examples of how high-resolution neuroanatomy data helped to interpret non-invasive diffusion MRI data acquired at millimeter scale. Third, I will provide an overview on anatomical knowledge, methods and functional significance of the laminar structure of cortical and subcortical areas, and discuss recent studies combining neuroimaging and neuroanatomy approaches to understand the properties of cortical and subcortical layers.

Presenter

Hiromasa Takemura, National Institute for Physiological Sciences
Department of System Neuroscience
Okazaki, Aichi
Japan

Sulcal organization predicts the evolution of the anatomo-functional organization of the primate frontal cortex

Although the relative expansion of the frontal cortex in primate evolution is generally accepted, the nature of its scaling and inter-species anatomo-functional comparisons of the frontal areas remain controversial. Indeed, a large literature has emphasized the link between the extent of gyrification, the rapid expansion of the cerebral cortex, and the complexity of the computational processing performed in a given brain. Although important, these discussions of cortical gyrification have not considered another major dimension of sulcal pattern organization, i.e. its variability. I present here results showing how the medial and the lateral frontal cortical sulcal organization has evolved through the primate order. Based on a within- and an across-species comparison of sulcal morphological variability based on neuroimaging anatomical scans, I provide evidence that both regions are comparable anatomically from Old World monkeys to Hominoidea. I also present functional data in relation to the sulcal organization of these regions in both macaque and human, showing that these regions are also highly functionally preserved. Altogether, these results demonstrate an evolutionarily conserved organizational principle from Old World monkeys to Hominoidea species, providing a new framework to compare sulcal morphology, cytoarchitectonic areal distribution, connectivity, and function across the primate order, leading to clear predictions about how other primate brains might be anatomo-functionally organized.

Presenter

Celine Amiez, Inserm U1208 Stem Cell and Brain Research Institute Bron, N/A
France

Probabilistic retinotopic maps in the macaque

The visuotopic organization of human and nonhuman primate cortex remains highly contested, despite > 60 years of research. Different mapping techniques yielded diverse parcellation models, with the exception of areas V1 and V2. Hence, the location and/or exact borders of dozens of visual areas are still uncertain. We performed phase-encoded retinotopic fMRI mapping using colored and dynamic naturalistic stimuli in more than 13 macaques (at 1.25 or 0.6 mm isotropic resolution). This large data set allowed us to accurately estimate eccentricity, polar angle, and population receptive field sizes in individual subjects. The combined information from all hemispheres was used to establish probabilistic and group-average maps of striate and extrastriate visual areas in both flattened and 3D volume representations. The maps are presented in a new space (MEBRAINS) based on high resolution T1w and T2w data to which other template atlases and parcellation schemes were registered. The probabilistic retinotopic information will be highly valuable to i) determine targets for invasive studies of monkeys without the need to perform functional scans, ii) anchor other types of information such as receptor density maps, connectivity data, genetic information, and electrophysiology results, and iii) last but not least to objectivate cross-species comparisons.

Presenter

Wim Vanduffel, KU Leuven Leuven, Flemish Brabant
Belgium

Relating macroscale functional representations in the human brain to tissue microstructures

While the field of neuroscience advances in uncovering the functional organization of the human brain, equally important is an understanding of the anatomical structures that underlie functional variation across the cortex. In this session, we will review ways in which researchers can enrich their understanding of functional organization of cortex through fine-scale structural metrics such as 1) the Allen Brain Atlas of gene expression, 2) quantitative magnetic resonance imaging (qMRI), and 3) mass spectroscopy. Through three vignettes, we will examine pipelines that researchers can use to probe gene expression across functionally-defined regions of cortex, measure tissue properties across cortex with recent advances in qMRI, and examine how mass spectroscopy of formalin-fixed tissue can be used to measure proteomics of any given brain region. In the first, we will discuss how genetic transcription datasets can be related to functional representations in visual cortex. In the second, we will discuss how slight changes to one’s scan parameters can yield quantitative maps of human brain tissue in adulthood and across development. In the third, we will examine recent efforts to relate functional differences across the cerebellum to differences in its underlying structure through the use of proteomics. This session will provide a strong review of neuroanatomy ranging in the large-scale from the major folds that define different regions of cortex and cerebellum, to the fine-scale from the genes and proteins that comprise a given brain region. Attendees will ideally have gleaned enough information about these resources to potentially embark on their own transcriptional, qMRI, or proteomics-based analysis of brain data in their brain regions of interest.

Presenter

Jesse Gomez, Princeton Princeton, NJ
United States

Neuroimaging and cellular correlates of white matter plasticity

White matter plasticity is a recently described mechanism by which experience shapes brain structure and function during adulthood. This phenomenon was first described in adult humans in response to complex motor skill learning using diffusion tensor imaging (DTI). DTI and other MRI modalities are sensitive to a range of tissue properties but lack specificity. Still, MRI allows for whole brain acquisitions, non-invasively and longitudinally, making it an unmatchable tool to probe white matter plasticity in response to interventions in healthy and in clinical populations. Combining multimodal magnetic resonance imaging (MRI) with established cellular techniques and transgenic rodent models can contribute to elucidate the underlying cellular mechanisms of white matter plasticity of the adult human brain. This educational course will address the cellular basis of white matter plasticity and provide examples of studies that have tried to link MRI metrics to specific cellular plasticity mechanisms.

Presenter

Dr. Cassandra Sampaio-Baptista, Dphil, University of Glasgow/University of Oxford Glasgow
United Kingdom

Uniting Structure and Function in Human MRI Research: a Software Tutorial

The field of neuroscience has changed substantially in recent years, and many of these changes have been driven by software. Even as the cost of computation and storage has declined precipitously, the availability of neuroscientific software has grown, and the resolution of neuroscientific measurements has increased. In many cases, the amount of neuroanatomical data collected by neuroscience groups has expanded beyond the ability of individual humans to process, label, and organize it. This session will discuss the evolution of software tools that have both enabled and solved these problems and will demonstrate their use and power via interactive live-coding in shared Jupyter notebooks. It will introduce tools such as fMRIprep, FreeSurfer, and BIDS, which greatly reduce the complexity of preparing, working with, and sharing neuroanatomical data, as well as libraries such as neuropythy, which can easily express models of functional measurements in terms of cortical anatomy. Finally, the session will conclude by discussing machine learning tools and recent developments connecting neuroanatomy and neural function using AI. Attendees will obtain an understanding of how existing software tools enable functional and anatomical measurements to be co-registered together in neuroscience datasets and to complement each other in future work.

Presenter

Noah Benson, eScience Institute, University of Washington Seattle, WA
United States