ORAL SESSION: Modeling and Analysis - Multivariate multimodal analysis

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Oral Sessions

Presentations

Principal axes of gene-regulated spatial organization of the human brain

The human brain is characterized by a strong relationship between functional specialization and space. This relationship can be observed as a modular representation, where brain tissue self-segregates into structures and sub-structures with shared behavioral functions, as well as a gradient representation, where gradation in function appears to be organized systematically across specific continuous axes. These principles of spatial-functional organization are ostensibly mirrored by, and perhaps regulated by, similar modular and graduated patterns of gene expression. Furthermore, both phenomena appear to be hierarchically organized, such that they can be observed globally across the whole brain, and locally within subregions. These relationships may be crucial for describing the complexity of neural organization, however, few studies have directly analyzed the relationship between gene expression and physical (i.e. Euclidian) space. It is also unclear at what point during development these gradients manifest. We employ statistical cross-decomposition to identify patterns of gene expression that vary systematically along the three cardinal spatial axes of the brain: rostral-caudal (y), dorsal-ventral (z) and medial-lateral.

Presenter

Jacob Vogel, McGill University Montreal, QC Canada

Molecular genetics of the biological age of the brain in the UK Biobank

Twin and adoption studies suggest that psychiatric and neurological disorders are highly heritable. This observation has largely been confirmed by contemporary genome-wide complex trait analyses in unrelated individuals (Lee et al., 2013). Nevertheless, the biological mechanisms through which genetic variation increases the risk for respective diseases remain largely unknown. Recent evidence suggests that the biological age of the brain may play a prominent role in disease etiology (Cole et al., 2017). In the present study, we investigated the molecular genetics of brain age gap, i.e. the difference between the biological age and chronological age of the brain, and examined its genetic overlap with cognitive, affective and neurobehavioral health phenotypes.

Presenter

<u>Philippe Jawinski</u>, Humboldt-Universität zu Berlin Berlin, Berlin Germany

Advanced vs. resilient brain aging in a harmonized cohort of 29,841 MRIs; the iSTAGING consortium

Brain aging is highly heterogeneous and is driven by multiple underlying neuropathologic processes. The current study aims to elucidate neuroanatomical patterns of brain aging, by leveraging the iSTAGING consortium of 13 studies with a total of 29,841 brain MRI scans, along with multivariate methods for defining advanced and resilient brain agers. Statistical harmonization methods were used to pool and integrate data from these studies, allowing us to achieve sufficiently large sample size and to sample the diversity of structural imaging measures across ethnicities, scanners, and acquisition protocols.

Presenter

<u>Ioanna Skampardoni</u>, National Technical University of Athens ATHENS, Attiki Greece

Unfairness in RSFC-based behavioral prediction across African American and White American samples

While machine learning will likely play a major role in precision medicine, there are growing concerns that machine learning algorithms might exhibit unfairness against under-represented and other sub-populations (Chouldechova2018; Martin2019; Obermeyer2019). Given significant interests and efforts in predicting behavioral phenotypes with resting-state functional connectivity (RSFC; Finn2015), here, we examined potential differences in RSFC-based behavioral prediction performance between African American (AA) and matched White American (WA) samples.

Presenter

Jingwei Li, ECE, CSC, CIRC, N.1 & MNP, National University of Singapore, Singapore Singapore

Assessing the utilities of resting-state functional gradients as a novel imaging biomarker

Central to the development of clinical applications in functional neuroimaging is the discovery of reliable biomarkers [1]. Although improving, progress towards this goal have been slowed by the challenges of high-dimensional fMRI data, which hinder the identification of core latent data structures from raw functional signals. To address this, recent studies [2, 3] applied dimensionality reduction techniques to resting-state fMRI (R-fMRI) and unveiled multiple neurocognitively meaningful gradients from both human and primate brains. Despite clear advantages for use as summary statistics, the process by which gradients are computed entail several methodological parameters - the choice of which may significantly affect the resultant findings. Moreover, gradients are yet to be evaluated for biomarker properties, which makes its clinical utility elusive. Here, we assessed the reliability and reproducibility of functional gradients across different combinations of key parameters to evaluate their potential as biomarkers.

Presenter

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Signal routing via cortical hierarchies

Numerous studies suggest that the brain is organized along a continuous gradient or hierarchy that spreads from unimodal primary and sensory areas to transmodal areas [1,2,3]. What is the effect of this hierarchy in the communication processes required for complex human behavior? Here we explore the profile followed by the shortest paths on a functional gradient space. In this space the brain areas are classified on hierarchical levels in a continuous way from unimodal (sensory processing areas) on one end to transmodal on the other end (association areas) [2]. This approach allows us to ask how the functional and structural configuration of the brain transform the way messages are transmitted across its different areas.

Presenter

Bertha Vázquez-Rodríguez, McGill University Brain Imaging Center Montreal, Quebec Canada