ORAL SESSION: Neuroinformatics and Data Sharing

David Kennedy Chair
University of Massachusetts Medical School
Worcester, MA
United States

Heather Whittaker, BSc MSc Chair
McGill University
Montreal, Quebec
Canada

Oral Sessions

Presentations

Original to digital: microstructural and functional brain atlases in common MRI space

The subdivision of the brain's cortical surface into distinct areas is a topic of ongoing investigation throughout the history of neuroscientific research. The field gains additional modalities upon which such subdivisions are based with emerging technological advances. In recent years, several new MR-based atlases have been presented that combine multiple modalities to determine areal boundaries (e.g. Glasser et al. 2016), while simultaneously cytoarchitectural data of the 1925 Von Economo atlas has proven its continued relevance in modern-day neuroimaging (Scholtens et al. 2018). Building on these developments, we here present digital versions of six brain atlases in common MRI space for incorporation into the FreeSurfer neuroimaging pipeline. These brain atlases represent a range of modalities: Campbell and Smith based their atlas on cyto- and myeloarchitecture (Campbell 1905, Smith 1907). Brodmann used cytoarchitecture for his atlas (Brodmann 1909). Flechsig studied the temporal profile of myelogenesis (Flechsig 1920). The cortical type atlas of Von Economo includes 6 main types of cortex (Von Economo et al. 1925). Finally, Kleist constructed a functional brain atlas by mapping symptomatic information of World War I soldiers with the spatial location of brain lesions (Kleist 1934). The digital version of these atlases offers the opportunity to compare and combine (in vivo) imaging-based atlases with these microstructural and lesion-based functional atlases, thereby bridging modern-day neuroimaging and microscale biological properties.

Presenter

Rory Pijnenburg, VU Amsterdam
Center for Neurogenomics and Cognitive Research
Amsterdam, Noord Holland
Netherlands

Methodological variability and vibration effects in transcriptomic processing pipelines

As use of the Allen Human Brain Atlas data has become more widespread in human neuroimaging research, numerous strategies and methods for processing the data have emerged (Hawrylycz et al., 2012). While researchers have begun to explore the extent of these strategies and make recommendations on best practices (Arnatkevičiūtė et al., 2019), the impact of processing choices on results previously reported in the literature is unknown. Previous studies in the field of functional neuroimaging have highlighted how processing variability can dramatically change both the quantitative and qualitative outcomes of research analyses (Carp et al., 2012), raising concerns about the reproducibility of published findings. Here, we conduct a similar assessment to investigate how researcher choices in processing the Allen Human Brain Atlas data may impact analyses relating neuroimaging and transcriptomic data.

Presenter

Ross Markello, McGill University Montreal, Quebec
Canada

Prospective Data Harmonization for Multi-site Diffusion MRI Data Analysis

Harmonization of multi-site diffusion MRI (dMRI) datasets can dramatically increase the statistical power of neuroimaging studies and enable comparative studies pertaining to several brain disorders1–3. Previous studies have demonstrated how minor variations in data preprocessing affects diffusion MRI derived measures4. To minimize the effects of preprocessing as well as subsequent data modeling, we propose to harmonize (i.e., remove scanner specific effects) the dMRI data as early as possible, at the raw signal. Two primary approaches have been proposed from our group to harmonize multi-site dMRI data: (i) Retrospective harmonization5; this is a very effective method that can be utilized in many neuroimaging studies. It has been tested in multiple datasets including a large schizophrenia database consisting of 1092 subjects derived from 13 sites5,6. In addition, this approach was selected as the best performing method in the Multi-shell Diffusion MRI Harmonization challenge3. (ii) Prospective harmonization, which requires traveling subjects scanned at each site to create a within-subject overlap cohort. Although the approach in (i) can also be used in this design, more advanced non-linear strategies can be used for harmonization or image quality enhancement across scanners7. In this work, we present our novel deep learning harmonization technique in category (ii) for learning an efficient mapping of dMRI signal from the same set of subjects across sites using CycleGAN with segmentation loss (CycleGANS).

Presenter

Suheyla Cetin-Karayumak, Brigham and Women's Hospital and Harvard Medical School
Psychiatry
Boston, MA
United States

A Bayesian normative model to estimate multi-scanner effects in structural

neuroimaging data

Group comparisons are the predominant approach in clinical neuroimaging studies. However, since this approach is based on comparing group means, it assumes the existence of an average patient. Hence, this approach has been criticised for not covering the heterogeneity in patient groups[1]. Bayesian normative modelling can capture interindividual differences by comparing each individual's score to the average variation in a reference group[2]. Accommodating both for aleatoric and epistemic noise, the Bayesian approach also allows for the predictive confidence of a z-score of deviation of each patient from the norm[3]. However, the normative modelling approach requires large sample sizes to capture sufficient normal variation, which are often obtained by pooling data datasets from multiple MRI scanning sites. Those combined datasets are confounded by non-biological effects like field strength of the scanner, thereby, impeding the application of normative models for structural neuroimaging data across sites[4]. Thus, making the potential of normative models applicable to neuroimaging requires a method to deal with multi-scanner effects. We propose a method to estimate scanner effects by a normative modelling approach in order to make this method available within a neuroimaging framework.

Presenter

Johanna Bayer, The University of Melbourne Melbourne, Victoria
Australia

Improving discovery of the genetic architecture of the cerebral cortex

Understanding the genetic architecture of the cerebral cortex has been a strongly pursued endeavour, which has become more attainable with the availability of imaging genetics data from several large-scale projects. Genome-wide association studies (GWAS) of cortical phenotypes incorporate atlases that are not informed by genetic information, which could impede discovery of meaningful genetic variants and functional pathways. Here we apply genetically-informed atlases ("Chen" atlases), which have been shown to significantly increase GWAS discovery [1], to uncover genetic variants contributing to cortical thickness and surface area in individuals included in the UK Biobank (UKB). We also investigated whether findings from a late adulthood cohort converge or diverge from a developmental cohort from the Adolescent Brain Cognitive Development (ABCD) Study.

Presenter

Carolina Makowski, University of California San Diego La Jolla, CA
United States

Validating cellular dimensions of cortical organization through neuroimaging-transcriptomics

The Allen Human Brain Atlas (AHBA) was released close to a decade ago, and remains the most spatially-comprehensive transcriptomic atlas of the human brain. The AHBA has revealed striking regional differences in bulk tissue gene expression across the cortical sheet, which have since been related to spatial patterns of age- and disease-related cortical changes from neuroimaging. The variable cellular composition of different cortical regions

may provide a logic to link regional differences in bulk gene expression with regional differences in macroscale anatomical variation. Here, we leveraged openly available human neuroimaging and transcriptomic data to i) quantitatively describe the topographies of cell-type specific gene expression and their relationships to neuroimaging and histological features of cortical structure, and ii) validate these results using additional in situ hybridization and transcriptomic datasets.

Presenter

Jakob Seidlitz, National Institutes of Health Kensington, MD
United States