Modeling and Analysis Methods I

Monday, Jun 18: 2:45 PM - 4:00 PM
Oral Sessions
Monday - Oral Session

Presentations

2533: All Resolution Inference: Increasing Spatial Specificity of fMRI with Valid Circular Inference

2:45 PM - 2:57 PM
Most neuroimaging studies identify brain activation as clusters of contiguous supra-threshold voxels corrected for multiple comparisons using random field theory (RFT). This approach suffers from a spatial specificity paradox (Woo et al., 2014): the larger the cluster detected, the less we know about the location of activation within that cluster. It is a consequence of cluster inference by which a detected cluster means: "there exists at least one truly active voxel in the cluster" and not "all voxels in the cluster are active". One solution to this problem is to change the cluster-forming threshold and run the RFT analysis again. However, since this is a circular inference, false positives are no longer controlled, and there is no information on which threshold is optimal. We propose a solution to the spatial specificity paradox and threshold selection termed 'All Resolution Inference' (ARI).

Presenter

Wouter Weeda, Leiden University

2354: Hierarchical Prediction Errors in MMN under Pharmacological Manipulations: Single-Trial EEG Analyses

2:57 PM - 3:09 PM
A central theme of contemporary neuroscience is the notion that the brain embodies a generative model of its sensory inputs to infer on the underlying environmental causes, and that it uses prediction errors (PEs) to continuously update this model [1]. Recently, it has been suggested that during learning in volatile environments, multiple, hierarchically related, precision-weighted PEs are computed [2,3], and that these might be signaled by different neuromodulators, such as dopamine (DA) and acetylcholine (ACh) [4, 5]. Here, we present the first investigation of hierarchical PEs during the auditory mismatch negativity (MMN), an electrophysiological response to violations of the regularity of sensory inputs, which depends on NMDA-receptor mediated plasticity, is sensitive to manipulations of ACh [6,7] and has repeatedly been shown to be reduced in schizophrenia. In two pharmacological EEG studies, we investigate hierarchical belief updating with PEs during the auditory mismatch negativity (MMN) using computational analyses of single-trial EEG data. In study 2, we introduce a new variant of the roving MMN paradigm (Fig. 1) which induces volatility in the underlying probability structure.

Presenter

Lilian Weber, Translational Neuromodeling Unit (TNU), University of Zürich & ETH Zurich

2442: A Principled Approach to Statistical Connectomics and Mega-Analysis

3:09 PM - 3:21 PM

Fundamental to scientific progress is reproducibility and replicability. Many studies fail to replicate across disciplines [1], including numerous examples in neuroimaging [2]. Failures to replicate can have many causes, including questionable research practices [3], measurement error [4], variability in sample demographics, data acquisition details, analysis methods, and statistical errors [5]. We developed a set of statistical and computational principles to guide the design of pipelines that eliminate as many sources of variability as possible. Previously, we've demonstrated these principles with a diffusion connectomics pipeline, NeuroData's MRI to Graphs pipeline, ndmg-d, and here we extend this principle to functional connectomics and introduce the ndmg-f pipeline. Running ndmg on data from 17 functional studies and 11 diffusion studies (a total of 3,571 individuals and 5,993 scans) demonstrates that certain coarse-scale connectome properties are consistently preserved across all studies in both structure and function, regardless of scanner manufacturer, acquisition protocols, and demographics. Nevertheless, other more fine-scale connectome properties remain highly variable, even after harmonizing data processing and controlling for these additional sources of variability.

Presenter

Eric Bridgeford, Johns Hopkins University

2571: Progress in multivariate analysis in brain imaging with Nilearn

3:21 PM - 3:33 PM

The application of statistical learning techniques to human neuroimaging data is increasingly popular in the study of brain diseases and cognition. Emerging data-processing needs are addressed by Nilearn (http://nilearn.github.io), a statistical learning package for neuroimaging written in Python. Nilearn is developed to easily apply statistical learning techniques on a vast amount of human functional brain data [1]. This facilitates communication between statistical learning scientists and imaging neuroscientists. Nilearn leverages the main Python machine learning package, Scikit-Learn [2], making it possible to apply almost any machine learning technique to neuroimaging data. It is a complete package with visualization utilities. Nilearn can handle both task functional MRI and resting state fMRI for predictive modelling, classification, decoding, or connectivity analysis. This submission is focused on the current development in Nilearn including decoding, estimation of functional biomarkers from Rest-fMRI, automatic Neurovault data download for meta-analyses, and surface visualizations.

Presenter

Kamalaker Dadi, INRIA

2331: Bootstrapping FOD: Accuracy advantages and other benefits of estimating shape uncertainty

3:33 PM - 3:45 PM

Inherently noisy diffusion-MRI results in considerable uncertainty in fibre orientation estimation is propagated in tractography. Probabilistic tractography tries to account for this uncertainty either by sampling from the underlying fibre orientation distribution (FOD)[sup]1,2[/sup]or applying Bayesian model to estimate the local uncertainty of the FOD[sup]3,4[/sup]. Bootstrapping – a non-parametric statistical approach for estimating uncertainty of a given statistic by resampling from repeated measures - has been proposed to estimate the local uncertainty in derived fibre

orientations[sup]5[/sup]. Residual bootstrapping[sup]6–8[/sup] provides a plausible alternative to signal repetitions, by resampling only from residuals of the modelled signal. We investigate how true/conventional and model-based residual bootstrapping methods perform in challenging fibre configurations by evaluating the accuracy of the average peak direction, and propose more information can be extracted from the variation in the entire shape of the FOD, as opposed to just the local maxima.

Presenter

Marina Rakic, King's College London

2535: Matrix-normal models for fMRI analysis

3:45 PM - 3:57 PM

Early approaches to fMRI data analysis used the univariate general linear model (GLM), but the fundamentally spatial nature of fMRI limited their success, driving development of multivariate methods organized under the umbrella of Multi-Voxel Pattern Analysis (MVPA; Norman et al., 2006). Unlike univariate methods, MVPA has not been organized in a unified theoretical framework. Rather, methods are developed independently on a per-problem basis, e.g. dimension reduction (SRM: Chen et al., 2015; HTFA: Manning et al., 2017), correlation estimation (RSA: Kriegeskorte et al. 2008; BRSA: Cai et al., 2016; ISFC: Simony et al., 2016), multivariate regression (Allefeld and Haynes, 2014). Alongside the success of these methods came new challenges for interpretation and hypothesis testing (Allefeld et al., 2015; Cai et al., 2016; Schreiber and Krekelberg, 2013). Furthermore, the lack of unified theoretical perspective has led to a lack of consistency even in addressing identical problems. We propose matrix-variate normal (MN) models as a unifying framework for fMRI analysis. MN models combine explicit spatiotemporal modeling with the interpretability of probabilistic generative models. They include as special cases many existing methods: PCA, generalized CCA, the GLM, MANOVA, as well as the fMRI-specific methods noted above including SRM and (H)TFA, ISFC, and (B)RSA. The shared structure enables the creation of a modeling toolkit that admits flexible prototyping of spatiotemporal analysis methods, which we use to develop a number of new method variants that yield advantages relative to the original formulations.

Presenter

Michael Shvartsman, Princeton University