

ORAL SESSION: Advances in Multi-modal Acquisitions

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Oral Sessions

Presentations

Quantitative, multimodal cell and fiber mapping in full primate brain sections

Detailed multi-modal architecture information is the basis for understanding function, dysfunction, and potential treatment of the brain. Mouse models have led the establishment of new molecular markers and have engendered a rise in understanding cell-specific function. Information based on such markers in the human brain is highly fragmented, and major parts are missing. While cell types often exhibit homology across species, the size and organizational complexity of the human brain make direct inference of function from mouse data problematic. There are multiple efforts to generate complete and consistent maps for various species, but none addresses (quantitative) protein expression in combination with direct imaging of fiber distribution patterns. We aim to bridge this gap by using our newly developed method to integrate multi-channel, cell-type specific immunohistochemistry with polarized light imaging (3D-PLI), to map protein expression, as well as fiber architecture in 3D-space, in the same, full, primate brain sections.

Presenter

Roxana Kooijmans, PhD, Netherlands Institute for Neuroscience
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Dynamically Acquired 1H MRS for Detection of 13C Labeled Cerebral Glucose Metabolism In-vivo

NMR spectroscopy has been used to probe metabolic pathways in vivo following infusion of specific ^{13}C -enriched substrates. In the current study, we investigate the ability of the short TE SPECIAL sequence and the MEGA-PRESS J-editing sequence, without a ^{13}C radiofrequency channel, to detect ^{13}C labeled glucose metabolism in the brain, and we demonstrate for the first time its application in human participants.

Presenter

Masoumeh Dehghani, McGill university Montreal, Quebec
Canada

Simultaneous mapping of T_2^* and major neurotransmitters using MRSI at 3T

Gamma-aminobutyric acid (GABA) and glutamate (Glu) are the brain's primary inhibitory (I) and excitatory (E) neurotransmitters. They are both strongly implicated in functional changes in neural circuitry and to be associated with learning and plasticity 1. The E-I balance/imbalance has been examined non-invasively by using proton (^1H) magnetic resonance spectroscopy (MRS) to measure the glutamatergic-GABAergic system 2. MRS imaging (MRSI) methods are superior to single-voxel by recording multiple spectra from different regions simultaneously 3. In this study, we propose using a MEGA semi-LASER sequence with non-water suppressed metabolite-cycling as 2D MRSI data acquisition method at 3T for high-resolution GABA, Glutamate and T_2^* detection throughout a whole axial slice. Simultaneous measurement T_2^* with neurotransmitter maps will provide useful information on functional hemodynamic changes due physiological interventions.

Presenter

Fatimah Almomen, Purdue University West Lafayette, IN
United States

Fast, quantitative myelin maps: Macromolecular pool fraction (MPF) using an optimized protocol

The macromolecular pool fraction (MPF) has been shown to correlate with myelin (Khodanovich 2017). Whole brain MPF maps can be generated efficiently from TI, BI and B0 maps and the collection of two additional volumes: a reference with no MT pulse (MT₀) and an MT-weighted volume (MT₁) acquired at an optimal frequency offset, Δ (Yarnykh 2012). Further time efficiency was proposed by using the TI and BI maps to create a synthetic MT₁, synMT (Yarnykh 2016). In the original work, TI maps were generated using a variable-flip-angle method from two images that were acquired with the same sequence (spoiled-gradient echo, SPGR) and resolution as MT₀. Restrictions on TR for MT-prepared scans makes matching scans across MT and TI mapping acquisitions not optimal. Recently, we showed that synMT can be created using a TI mapping method relying on fastSPGR (FSPGR) scans if a calibration procedure is used to account for systematic differences across sequences (Chavez 2019). The calibration was found to be subject-independent and thus the scaling factor, f , was determined a priori and applied on subsequent synMT. However, discrepancies in bandwidth across sequences led to inaccuracies in synMPF in regions of large susceptibility gradients ($\Delta\chi$). In this work, we optimize TI and BI mapping acquisitions to reduce scan time for synMT generation and we match sequences to reduce inconsistencies in regions of large $\Delta\chi$.

Presenter

Kimberly Desmond, PhD, CAMH
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Canada

Short Echo-Time fMRI using Magnetization Transfer Contrast

Magnetization Transfer (MT) [Wolff1989] is an MRI technique generating contrast in the presence of molecules with bound protons. While brain tissue is known to show an MT contrast (MTC), blood does not display such behavior [Balaban1991]. Hence, an MT-weighted signal may be sensitive to cerebral blood volume (CBV) changes, with a maximum at echo-time $TE=0$. By contrast, most fMRI studies rely on Blood-Oxygenated Level Dependent (BOLD) experiments, whose optimal sensitivity is obtained at $TE \sim T_2^*$ (30ms at 3T). Changes in CBV during brain activation can be expected to occur mainly in the arterioles and capillaries [Kim2006], and may therefore be expected to have a better spatial localization than BOLD, which is dominated by the downstream vasculature. Previous investigations into enhancing BOLD with MT have used off-resonance MT combined with long TR [Zhou2005] or inversion recovery [Song1997] which preclude efficient fMRI studies. Here, it is shown that an acquisition using on-resonance MT preparation can be sensitive to the hemodynamics induced by brain activations at short TE, which maximizes the sensitivity to CBV and reduces BOLD contamination, without increasing acquisition time.

Presenter

Jenni Schulz, Donders Institute, Radboud University Nijmegen, -
Netherlands

Time-of-Flight-MRA-Derived-Probabilistic-Map of Each Major Cerebral Artery

The human brain is perfused by three main arteries: the middle cerebral arteries (MCA), anterior cerebral artery (ACA) and posterior cerebral arteries (PCA), each with distinct [1] and variable perfusion territories [2]. Attempts to parcellate the brain into functionally important regions have largely ignored these arteries; yet functional imaging methods are dependent on cerebral hemodynamics. Recent advancement in non-contrast enhanced Time-of-Flight (TOF) magnetic resonance angiography (MRA) allow non-invasive imaging of cerebral arteries and previous work from our lab has shown that this can be segmented into a whole-brain vascular tree [3], thus allowing for the isolation and study cerebral arteries with other MRI modalities. Here, we build on this by classifying tissue according to the cerebral artery's perfusion territory it resides in.

Presenter

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