



Contribution ID: 34

Type: Talk

Multimodal registration of high-resolution histology and ultra-high field MRI using BigBrain2 pipeline in the rat brain

Wednesday 29 October 2025 11:30 (15 minutes)

Introduction: Accurate co-registration of high-resolution histology data to multimodal MRI provides complementary benefits for validation of imaging biomarkers from healthy brain and its alterations. While BigBrain [1] and Julich-Brain atlas [2] provide multi-level probability maps for cell distribution and morphology, BigMac [3] extends these efforts to co-registration of multi-contrast microscopy to 7-T MRI. In this work, we report the development of a customized pipeline of BigBrain2 [4], applied to a rat model of traumatic brain injury (TBI), for co-registration of high-resolution, multiple contrast microscopy cut from coronal or horizontal sectional planes to the anatomical and diffusion MRI at various resolutions.

Methods: Our semi-automated pipeline for histology-MRI co-registration and volumetric reconstruction includes (a) automated, section-to-section alignment at cellular resolution; (b) affine registration to ex vivo structural and diffusion-weighted MRI maps; (c) iterated 2D and 3D linear and nonlinear transformations between stacked histology and reference MRI to account for translation, rotation, scaling, and shearing; and (d) optical balancing of the reconstructed histology volumes.

We tested this pipeline on the left hemisphere of four rats –one each of naïve, sham-operated, mild TBI (mTBI), and moderate TBI (moTBI) animals - from a larger dataset introduced in Table 1. Details of surgical procedures, lateral fluid percussion, and tissue processing are presented in [5]. We used the 11.7-T ex vivo MRI with T1-w and T2-w sequences (70-100 μm isotropic) and orientationally averaged diffusion image (150- μm isotropic) as the reference volume. We processed the Nissl- and myelin-stained sections to assess the cyto- and myeloarchitectonics. The stained sections were scanned at 136.9 nm/pixel in-plane, quality controlled, and downsampled to 10.95 μm . Histology photomicrographs and MRI images were masked, and the MRI volumes were re-oriented along the stacking axis of the corresponding histological object.

Results: Our customized pipeline was successful in volumetric reconstruction of Nissl- and myelin-stained histology at 10.95 μm in-plane resolution from anatomical and diffusion reference 11.7-T MRI volumes in both coronal and horizontal cutting planes. We ran experiments with section-to-section co-registration at anatomical extremes to evaluate the orientation of misaligned and broken histological pieces. Optical intensity balancing was also able to resolve staining imbalances.

Conclusions: The developed pipeline has the potential for facilitating multimodal data integration in pre-clinical and clinical studies. The ongoing work includes extracting anatomical landmarks from MRI and histological blocks for quantitative evaluation of linear and nonlinear transformations and section-to-section registrations.

[1] Amunts K et al. BigBrain: an ultrahigh-resolution 3D human brain model. *Science*. 2013 Jun 21;340(6139):1472-5.

[2] Amunts K et al. Julich-Brain: A 3D probabilistic atlas of the human brain's cytoarchitecture. *Science*. 2020 Aug 21;369(6506):988-92.

[3] Howard AF et al. An open resource combining multi-contrast MRI and microscopy in the macaque brain. *Nature communications*. 2023 Jul 19;14(1):4320.

[4] Lepage C et al. 3D reconstruction of BigBrain2: Progress report on semi-automated repairs of histological sections. 8th BigBrain Workshop 2024.

[5] Molina IS et al. In vivo diffusion tensor imaging in acute and subacute phases of mild traumatic brain injury in rats. *Eneuro*. 2020 May 1;7(3).

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Session Classification: Session 3: Applications & Clinical Translation