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AIDA

Workflows for automated analysis of mouse brain imaging data

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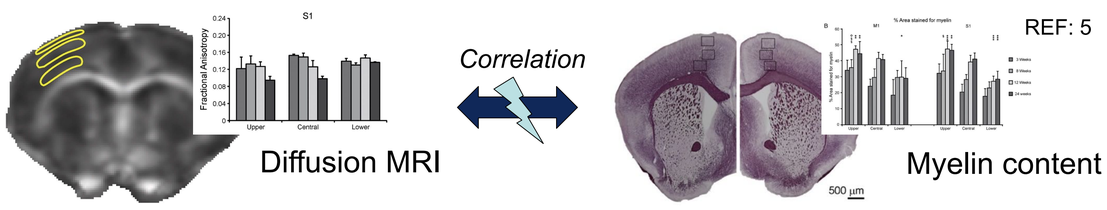
Objective

An efficient way to integrate imaging data sets with variable image resolution and image content is key for cross-modality correlations, e.g., structural to functional or in vivo biomarker to ex vivo histology[1-3]. We present our atlas-based approach in which all contributing images are accurately aligned through image registration algorithms with the Allen Mouse Brain Atlas (CCF v3)[4]. The atlas resource facilitates the analysis of macroscopic to microscopic features across subjects and integration of viral tracing and gene expression data.

Workflows for:
- T1/2-weighted MRI
- DWI/DTI
- (rs-)fMRI
- microscopy

Current approach

- Individual selection of ROIs somewhere on the image
- Manual delineation of the anatomical regions based on the visible brain structure



Novel approach

We have created automated workflows for the specific needs of cross-modality mouse brain experiments:

- *AIDAdb:* cloud-based relational database[6]
- *AIDAqc:* MRI quality control
- *AIDAmri:* automated processing of MRI data[7]
- *AIDAhisto:* whole slice cell counting[8]
- *AIDAconnect:* graph theory algorithms for fMRI/DTI data[9]

GitHub

Workflow MRI

Data aquisition

Possible input mouse brain MRI as input:
T2-weighted
MSME (T2 map)
Diffusion (DTI)
Resting-state fMRI

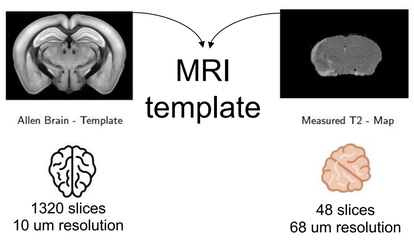
Preprocessing

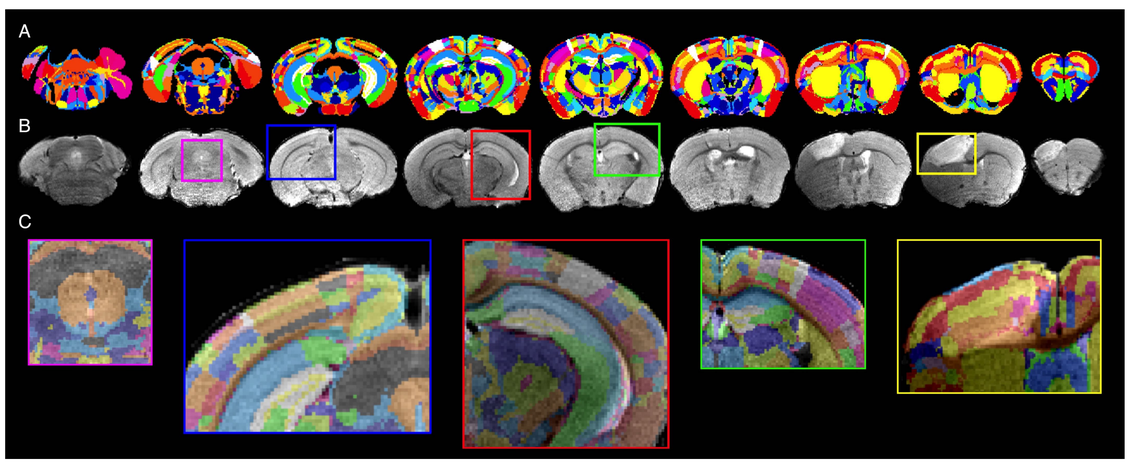
Re-orientation

Bias-field correction

Brain extraction

Registration





Workflow histology

Data aquisition

Possible input:
Immunostainings, confocal and conventional fluorescence microscopy, tif format

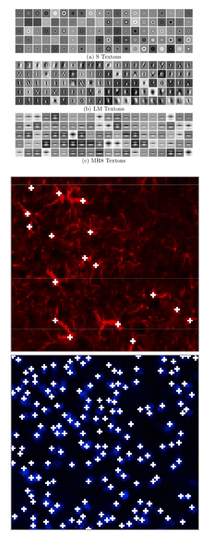
Registration

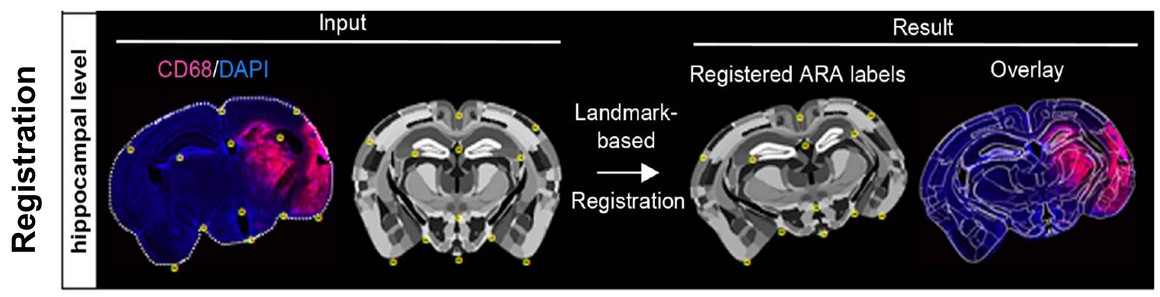
Landmark-based using Slicer3D or ImageJ (plugin landmark correspondence)

Counting

Classification of cellular structures with a set of filters

Use the segmented cell nuclei to correct the cell counting

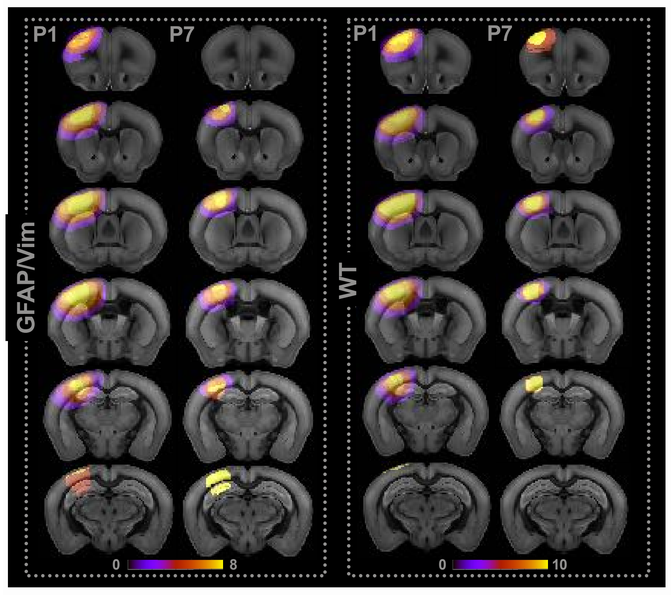




Applications

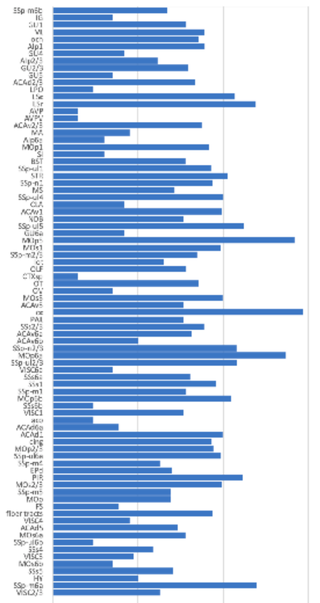
- Stroke lesion location and size determine functional deficits and recovery potential[10]
- Lesion mapping and region-wise analysis of cellular features facilitate the correlation between *in vivo* and *ex vivo* data, but also allow to monitor the individual development of the lesion and hence help to answer the question, which brain areas are most relevant for behavioral deficit and recovery of function

MRI incidence maps and detailed anatomical lesion mapping

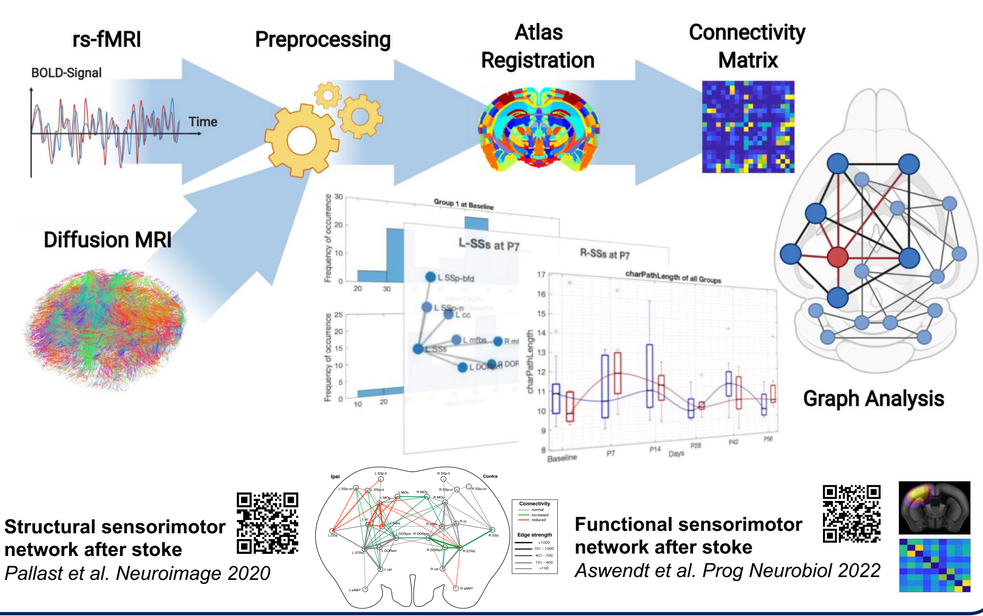


P1	P7	P1	P7	
100.0	100.0	100	100	Primary_motor_area
87.5	25.0	100	30	Secondary_motor_area
25.0	12.5	20	0	Retrosplenial_area
100.0	87.5	100	40	Primary_somatosensory_area,_barrel_field
100.0	87.5	100	80	Primary_somatosensory_area,_lower_limb
100.0	100.0	100	100	Primary_somatosensory_area,_upper_limb
100.0	87.5	100	100	Primary_somatosensory_area,_mouth
100.0	87.5	100	80	Primary_somatosensory_area,_nose
75.0	25.0	80	0	Primary_somatosensory_area,_trunk
100.0	62.5	80	100	Primary_somatosensory_area,_unassigned
25.0	0.0	0	0	Supplemental_somatosensory_area
50.0	25.0	100	30	Striatum_dorsal_region
50.0	25.0	60	0	Hippocampal_region
50.0	0.0	50	0	Posterior_parietal_association_areas
50.0	0.0	80	20	Anterior_cingulate_area
12.5	0.0	0	0	Auditory_areas
37.5	12.5	40	20	Visual_areas
0.0	0.0	10	0	Prelimbic_area
100.0	87.5	100	70	Corpus_callosum
75.0	50.0	100	50	Medial_forebrain_bundle_system

Atlas-based cell counting results



Functional/structural network changes after stroke



Structural sensorimotor network after stoke
Pallast et al. Neuroimage 2020

Functional sensorimotor network after stoke
Aswendt et al. Prog Neurobiol 2022

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FRIEBE-STIFTUNG

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