# Non-invasive Histology with Magnetic Resonance Imaging
The hMRI-toolbox

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Histology versus MRI
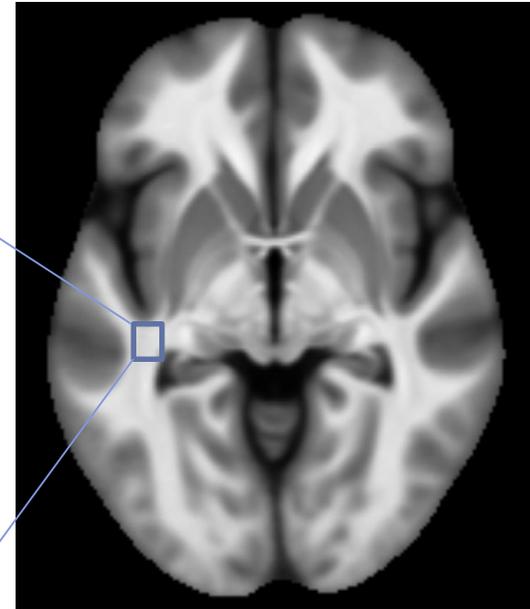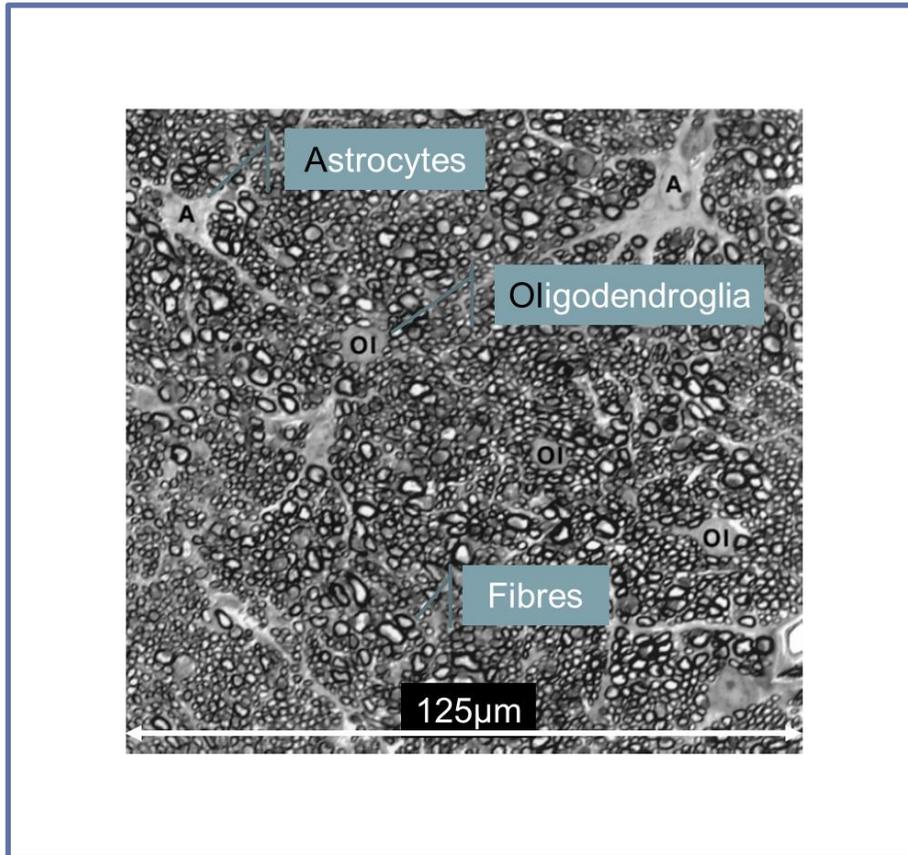
Average magnetization transfer map of 138 Individuals

- invasive vs. non-invasive
- high resolution vs. low resolution
- restricted vs. multiple contrast

The hMRI approach
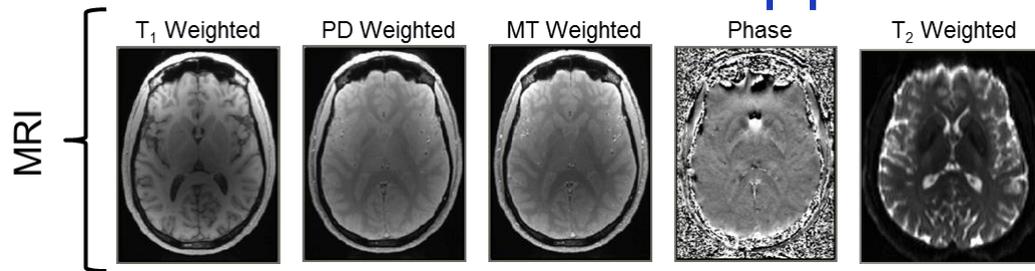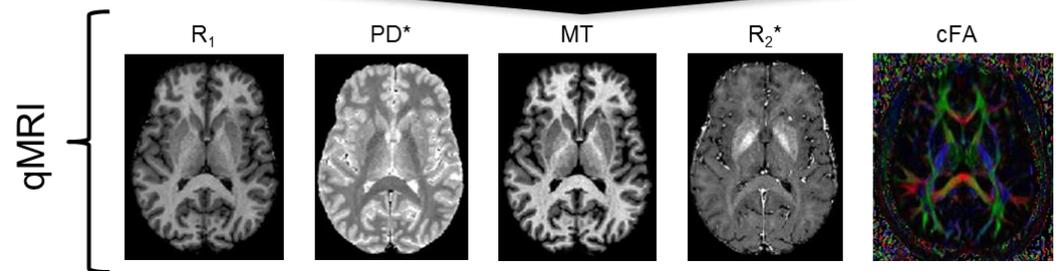
quantitative maps of specific parameters
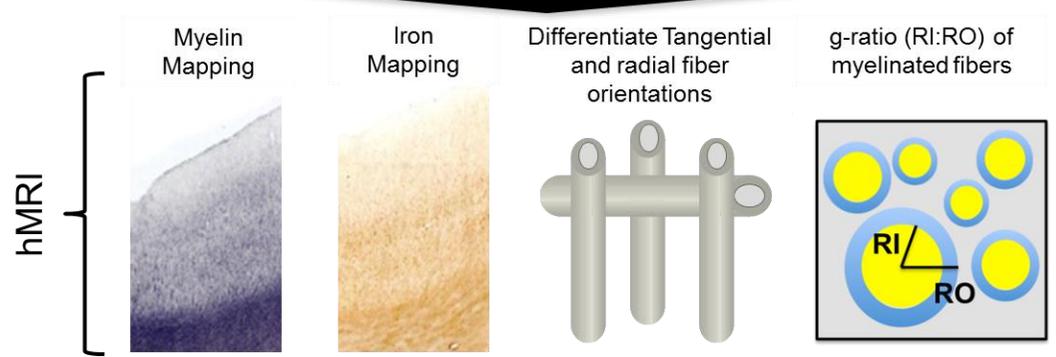
in-vivo biological mapping as ultimate target

Source: Weiskopf et al., Curr. Opin. Neurol., 2015

Multi-Parameter Mapping (MPM)

B1+ B1- T$_1$ Weighted PD Weighted MT Weighted

acquisition

R$_1$, PD

R$_2$*

MT$_{sat}$
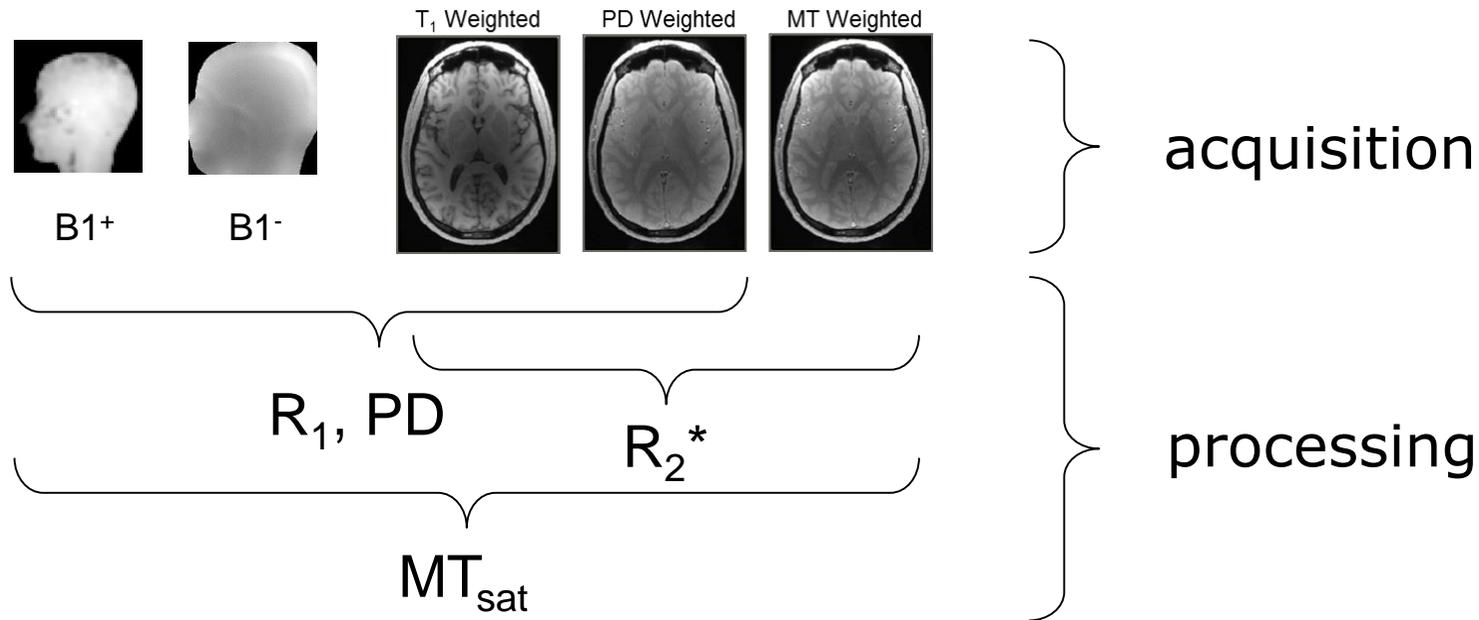
processing

- 3D RF spoiled gradient-echo sequences for T1, PD-, and MT-weighted multi-echo acquisitions
- RF field mapping, i.e. transmit and receive fields, to reduce instrumental bias

The hMRI-toolbox

Quantitative map: | R_1 (=1/T1) | Proton Density (PD) | Magnetization Transfer (MT) | R2* (=1/T2*)

Biological feature: myelin, water, iron | water content | macromolecules, myelin | iron
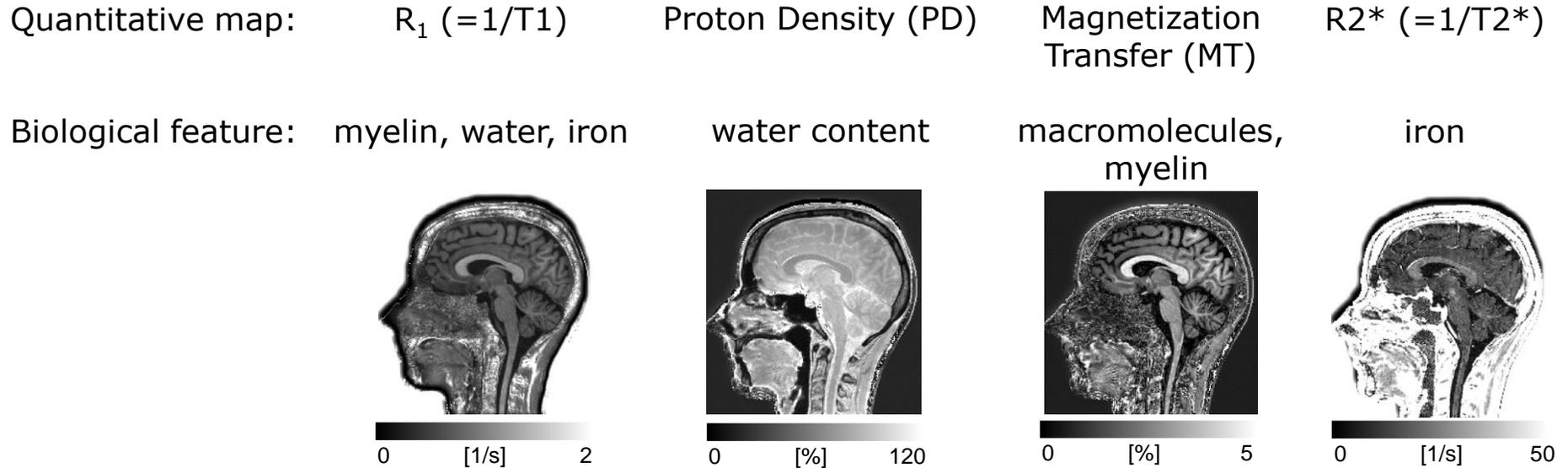
- SPM-toolbox (MATLAB based) for MPM data processing to get quantitative maps (depending on input)

hMRI-toolbox functionalities
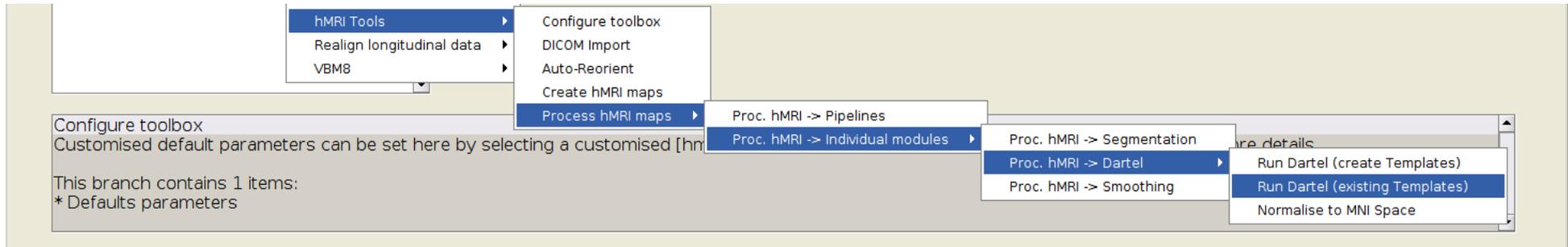
- including BIDS-like meta-data for traceability (from DICOM import to processed maps)

- process maps for longitudinal/cross-sectional analysis (DARTEL, tissue weighted smoothing, MNI normalisation)

Proposed hackathon project

Improve and extend data handling within the toolbox for *ex-vivo* data

- adapt GUI
- adapt processing scripts (e.g. not to use SPM segmentation, allow selection of echoes, use other physical models etc.)
- test processing

- branch to start off and work on: https://github.com/tleutritz-cbs/hMRI-toolbox/tree/mask_in_and_output
- sample data:
  https://owncloud.gwdg.de/index.php/s/hBLQeL97hb5Z5cW

Thank you!

The hMRI-toolbox Team:

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