

The hMRI toolbox for quantitative imaging and in vivo histology using MRI (hMRI)

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Introduction:

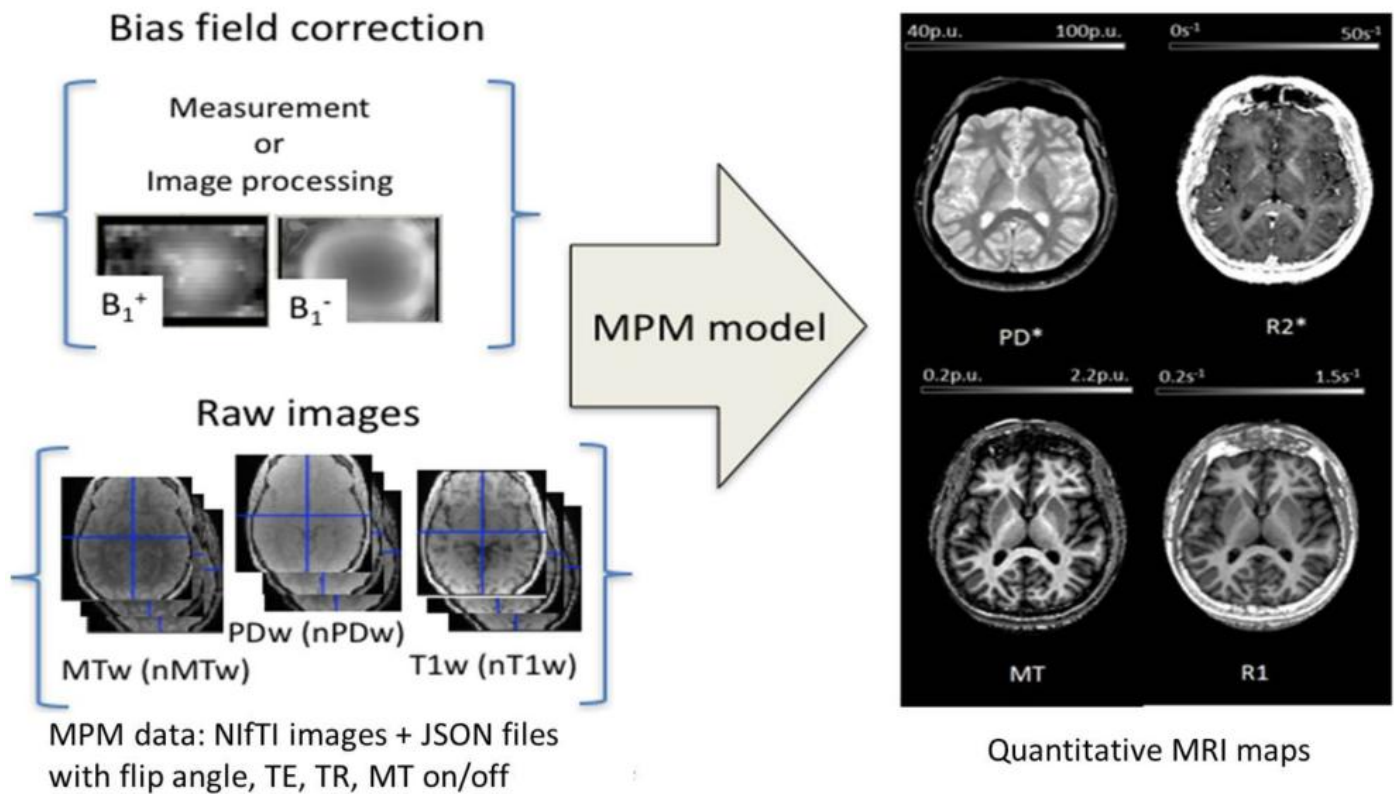
Quantitative MRI (qMRI) finds increasing application in neuroscience and clinical research due to its greater specificity and its sensitivity to microstructural properties of brain tissue - myelin, iron and water concentration. Multi-parameter mapping (MPM) is a comprehensive qMRI protocol, including an acquisition, modeling, and processing framework that ultimately provides high-resolution maps of the magnetization transfer saturation (MT), proton density (PD), longitudinal ($R1=1/T1$) and apparent transverse ($R2^*=1/T2^*$) relaxation rate. Here, we present the hMRI toolbox for neuroscience research, an easy-to-use open-source tool for creating and processing these qMRI data.

Methods:

The hMRI toolbox is organized in five parts:

1. The "Configure toolbox" module provides a set of standard default processing parameters. It allows the user to define site- or protocol-specific default parameters to be used across the following data processing modules.
2. "DICOM import" is a tool to convert DICOM data into NIfTI files, storing the whole DICOM header as JSON-encoded metadata. By enabling the storage of data acquisition and processing parameters alongside the brain imaging data sets, the hMRI toolbox follows the BIDS recommendations [1].
3. "Auto-reorient" is a simple tool for rigid-body reorientation of all images to the MNI space prior to data processing, in order to ensure the stability of spatial processing steps (mainly segmentation [2]).
4. "Map creation" computes quantitative estimates of $R2^*$, $R1$, PD, and MT from unprocessed multi-echo T1 -, PD-, and MT-weighted FLASH acquisitions stored as NIfTI volumes (Fig. 1) [3,4]. This module corrects the qMRI estimates for spatial receive and transmit field inhomogeneities based on additional reference data [5,6] or using image processing methods [3,7].
5. "Process hMRI maps" provides dedicated tools and tissue probability maps [8] for the spatial processing of the qMRI data based on the SPM processing framework. In particular, spatial registration of the qMRI parameters in standardised space is implemented using the voxel-based quantification approach [9], taking a weighted sum of the qMRI estimates over the spatial extent of the smoothing kernel in native space, and incorporating the Jacobian determinant of the deformation into the weighting (Fig. 2). The weighting is carried out in a tissue-specific manner, producing sets of qMRI maps separately for each tissue class, while reducing partial volume effects on parameter estimates [9].

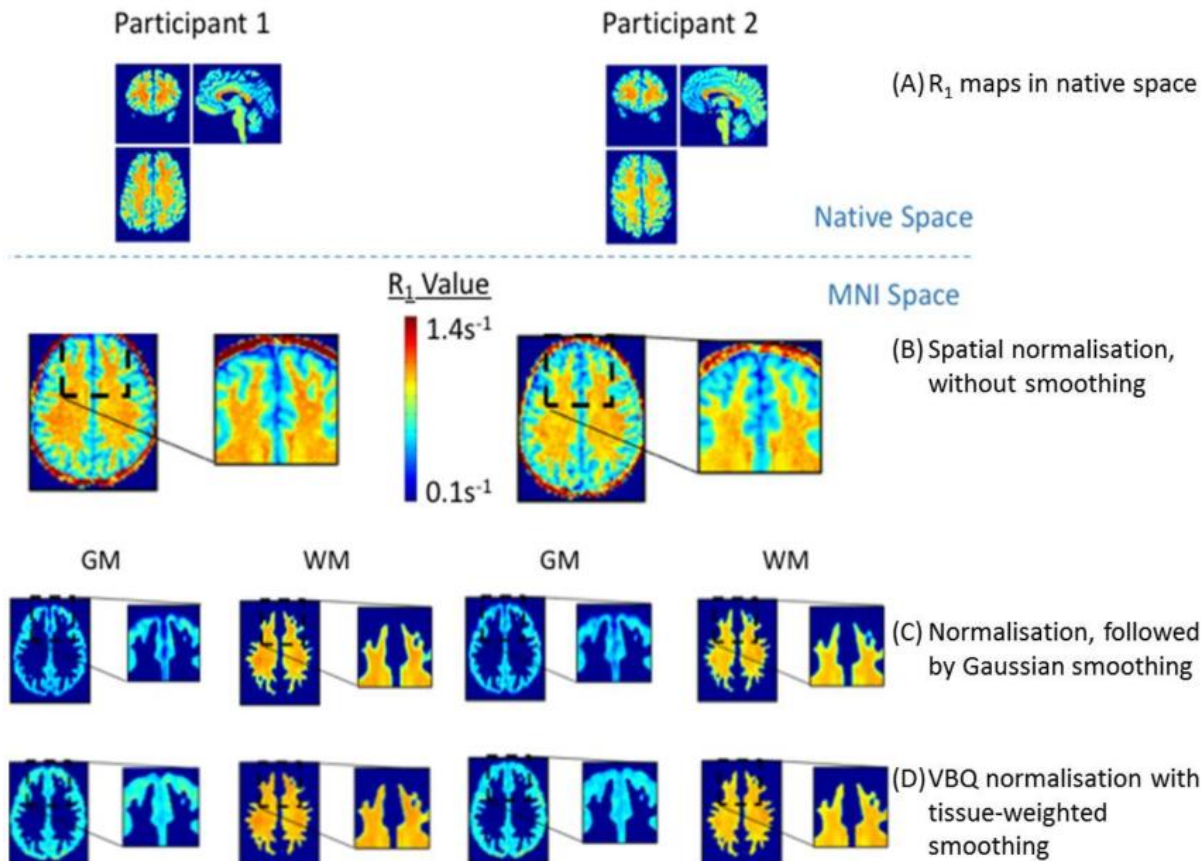
Map creation



The MPM protocol includes different multi-echo FLASH scans with predominant T1-, PD-, and MT-weighting (MTw, PDw, T1w) by appropriate choice of the repetition time and the flip angle. Optional RF transmit and receive field measurements can be added to the protocol. The map creation module produces maps of effective proton density (PD^*), effective transverse relaxation rate ($R2^*$), magnetization transfer saturation (MT), and longitudinal relaxation rate (R1).

Fig. 1. Map creation.

Map spatial processing



Spatial registration of qMRI data. Highly parameterised non-linear deformations (e.g. Dartsel) allow spatial registration of the qMRI data in standardised space, from (A) to (B). With standard routines, residual inter-individual differences, e.g. arrow in zoomed region in (B), are addressed by spatial smoothing. However, spatial smoothing leads to bias of the qMRI data, shown in the zoomed region of (C) as a rapid decay in R_1 values at tissue boundaries. The voxel-based quantification approach of the hMRI toolbox greatly reduces this smoothing-induced bias (D). Data shown here were acquired at 3T with 800 μm resolution. In all cases the final voxel size of the R_1 maps in MNI space was 1mm isotropic resolution. A Gaussian smoothing kernel of 4mm FWHM was used in (C) and with tissue-weighting in (D).

·Fig. 2. Map spatial processing.

Results:

The hMRI toolbox provides a time-efficient, robust, and simple framework for use of qMRI data in clinical and neuroscience research. Quantitative MPM maps computed with the hMRI toolbox have been used for e.g. (a) the combined study of myelin and iron concentration in brain tissue [10], (b) the study of brain atrophy using improved delineation of tissue boundaries [11], and (c) assessment of layer-specific microstructure [12] acquiring high-resolution data (800 μm in 25 min @3T and 400 μm in 70 min @7T [13]). Segmentation of subcortical areas benefits from the multiple, bias-free contrasts of the qMRI data computed by the hMRI toolbox, leading to improved sensitivity in subcortical regions [14]. The MPM framework is currently used in a multi-site clinical trial (NISC trial [15]), including different vendors. This has been possible because the MPM acquisition relies mostly on multi-echo FLASH that is available on all modern scanner platforms. The hMRI toolbox allows advanced biophysical modelling of MRI data, such as g-ratio mapping [16], for improved inference of brain tissue differences at the microscopic level.

Conclusions:

This toolbox is embedded in the SPM framework, profiting from the high accuracy spatial registration to common space and the variety of available statistical analyses. It is available from <http://www.hmri.info>. It also offers flexibility for calculation of novel MRI biomarkers of tissue microstructure.

Imaging Methods:

Anatomical MRI ¹
Multi-Modal Imaging

Imaging Methods Other ²

Informatics:

Workflows

Neuroanatomy:

Neuroanatomy Other

Keywords:

MRI
MRI PHYSICS
Spatial Normalization
STRUCTURAL MRI
White Matter
Other - quantitative MRI

^{1|2}Indicates the priority used for review

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Yes

Please indicate which methods were used in your research:

Structural MRI

For human MRI, what field strength scanner do you use?

3.0T
7T

Which processing packages did you use for your study?

SPM
Other, Please list - hMRI toolbox

Provide references using author date format

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