Comparison of accuracy and reproducibility of MR Fingerprinting with conventional T1 and T2 mapping

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Target Audience: Scientists interested in quantitative brain imaging and its possible clinical applications.

Purpose:

Recently, a new method for simultaneous mapping of various different tissue specific MR parameters - called MR Fingerprinting (MRF) - has been proposed by Ma et al. [1]. Traditional methods for mapping typically use multiple weighted images by varying a specific sequence parameter. In contrast, MRF varies multiple parameters, e.g., TR, TE, flip angle, in a pseudo-random but defined fashion. Simulations of the Bloch-equation provides a comprehensive dictionary for different tissue properties (e.g. T1, T2, off-resonance) for the specific measured sequence. The signal evolution observed during the actual scan can be matched with the signal evolutions of the dictionary. As soon as a match is found, the tissue properties can be assigned to a given voxel. Thus, MRF is an intrinsically multi-parametric quantitative technique, in contrary to commonly used MR modalities. However, few studies are published to determine the validity of the values provided by MRF. The aim of our study was to evaluate the accuracy and reproducibility of MRF in a longitudinal volunteer study and to compare MRF with accurate clinically available T1 and T2 mapping sequences [2].

Methods:

To test the reproducibility and accuracy of MRF, brain scans in five volunteers (1-5) were repeated five times (A-E; each week) on a clinical 1.5T whole-body MR scanner (MAGNETOM Aera, Siemens Healthcare, Erlangen, Germany) using a 20 channel head coil. Three axial MRF slices were acquired in each session with an inter-slice gap of 30 mm, on the level of the brain stem, the lateral ventricles and the supraventricular white matter. The slices were automatically positioned using Auto-Align [3]. MRF was acquired with two methods: a prototype FISP-based and a TrueFISP-based variable-density spiral sequence, both with a resolution of 1.2x1.2x5 mm³ (256x256 matrix). Highly undersampled images were acquired within 30 and 40s, respectively. As a reference for T1 and T2 mapping, a 3D MP2RAGE and a 2D multi echo spin-echo sequence were used. MP2RAGE images were acquired with 1 mm³ isotropic resolution, TR/TI1/TI2 = 5/0.7/2.7s, total scan time of 8 minutes For the T2-maps, 15 slices with TR 2.5s, eight TEs ranging from 20 to 160 ms, and a resolution of 1x1x5 mm³ (256x192 matrix) were acquired in 4.5min. The 15 slices were set up to match the positions of the three MRF slices. Standard processing of T1 and T2 maps was performed by dedicated software (MapIt, Siemens Healthcare, Erlangen).All conventional T1- and T2-maps were resampled to the corresponding MRF slices within each subject using MINC tools[4]. Five homogeneous and representative Regions of Interest (ROIs), in both grey and white matter, were defined once per volunteer by an experienced neuroradiologist. The maps of each volunteer were aligned between the different time points using a rigid transformation so that all maps were aligned with the ROIs. The coefficients of variation (CV) were computed over the whole time series A-E in dependency of all three methods, volunteers, ROIs, and T1s and T2s to test for reproducibility. To evaluate the accuracy, the T1- and T2-values were averaged over all volunteers and all time points A-E and compared between the MRF and conventional methods for each ROI.

Results:

Figure 1 illustrates the CVs of the T1- and T2-values calculated over the time series A-E for each volunteer and each ROI. Figure 2 shows the T1- and T2-values of the different methods for all five ROIs, averaged over the time series A-E and the volunteers. In figure 3, representative T1- and T2-maps are shown. The mean CVs of the T1-values were 3.2% (TrueFISP), 3.5% (FISP), and 5.0% (conventional), and those of the T2-values were 7.2% (TrueFISP), 6.9% (FISP), and 6.8% (conventional).

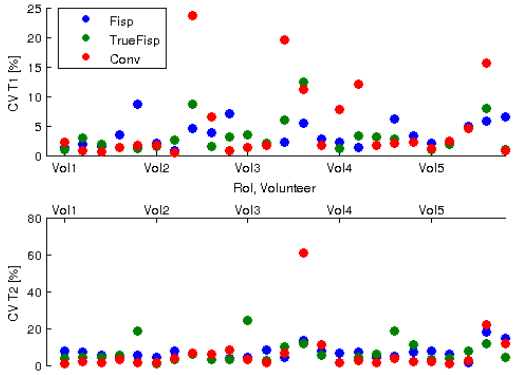

Figure 1: The Coefficients of Variation (CV) of the conventional and MRF methods, calculated over the time series A-E, for all ROIs and volunteers.

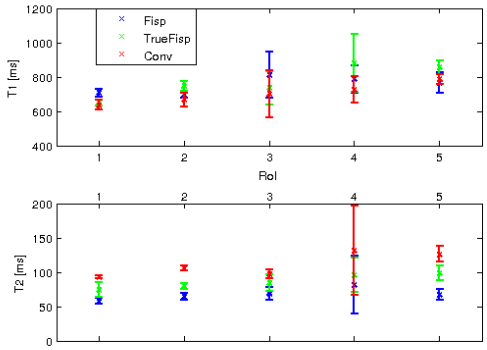

Figure 2: The T1- and T2-values of the conventional and MRF methods for all ROIs.

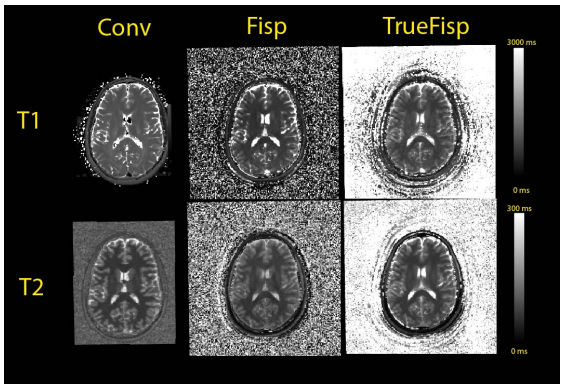

Figure 3: Representative T1- and T2- maps of the conventional and the two MRF methods.

Discussion and Conclusions:

The CVs of the conventional methods showed a similar variability over time for different ROIs and volunteers as the MRF methods, apart from a few larger deviations caused by spatial misregistration. Yet, especially the conventional T1 sequences were acquired with much longer scan times than MRF, which provides a significant SNR advantage for the conventional methods. Thus, when measuring with similarly long scan times or more sophisticated parallel imaging reconstruction methods, better results with narrower dictionary steps may be expected from the MRF methods than shown here. Differences in the absolute T1- and T2- values were found, however with no true gold standard available in the *in-vivo* brain, the interpretation is difficult. In comparison to literature values, MRF, especially the FISP method, estimated shorter T2 values [5]. Phantom studies are necessary to decisively quantify the accuracy of MRF. One currently limiting factor for clinical use of MRF is the long reconstruction time, which was about 7 minutes per MRF slice in our study. Our results provide evidence that MRF has the potential to replace conventional T1- and T2-mapping. Moreover, improved implementations of MRF may yield even more information from a single MRF scan, such as diffusion or perfusion parameters. Together with the calculated spin density, MRF provides a solid basis for quantitative assessment of different pathologies and tissues.

References:

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