3D-Relaxometry - Quantitative T1 and T2 Brain Mapping at 3T

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Introduction: Quantitative T1 and T2 analysis of the whole brain is of particular interest for the understanding, diagnosis and follow-up of neurological diseases as well as for general research purposes, e.g. measuring in-vivo water content, myelin quantification, and segmentation of different brain structures. Generally speaking, both methods are very time consuming since the transverse magnetization theoretically needs to fully relax to its equilibrium state before subsequent excitation. The problem is that most methods for T1 as well as T2 mapping either provide low spatial information, or require excessive scan times to assure a reasonable signal to noise for further analysis. Another challenge arises from elevated RF-deposition at higher field strengths, limiting the use of composite refocusing pulses and the number of spin echoes for accurate T2 measurements, as well as adequate repetition times (TR) for an acceptable total scan time. Several methods have been proposed in recent years to either speed up the acquisition process (Look Locker, EPI readout) or provide high spatial resolution with simultaneous T1 and T2 estimation (steady state [1], variable nutation angle [2], fully rewound gradient echo techniques (balanced FFE, True FISP) [3]). The disadvantages of the latter ones are more complex relaxation models with increased demand for SNR improvement because of the higher number of fit variables.
Quantitative multi-slice, multi-component T2-Mapping furthermore has the limitation of magnetization transfer artifacts and long scan times to eliminate excessive T1-weighting. Additionally, the requirements for multiple component T2 analysis demand a very high intrinsic SNR and minimal contamination of the decay curve from stimulated echoes or residual out of slice magnetization. We show here that some of these limitations can be eluded by using 3D-acquisition techniques in combining speed, reasonable SNR and limited cross-talk between adjacent slices.

Methods: All imaging was performed on a Philips Intera 3T whole body scanner with an eight-element phase-array head coil. 6 normal controls were scanned for validation of the sequences. Two sequences were used for quantitative relaxation time analysis:

a) T1-Mapping: 3D Inversion Recovery (IR) prepared ultra-fast gradient echo (TFE) with low flip angle excitation (12°), radial 3D-k-space encoding, and an elliptical k-space shutter (75%) to further reduce scan time. Acquisition matrix 256x256, TFE factor 111, TR=6 ms, TE=3 ms, IR-delays: 100, 150, 300, 500, 800, 1200, 2500 ms, an adiabatic hyperbolic secant pulse was used for inversion, shot interval= 5000ms, SENSE=2.0, 30 slices at 4mm, total scan time: 10 min

b) Multi-component T2-Mapping: 3D 32-echo CPMG (12 slices) with slice selective optimized refocusing pulses, driven equilibrium, acquisition matrix 256x128, partial k-space sampling (70%), TR=1600 ms, TE=10 ms, total scan time: 16 min

Image Analysis: T1-analysis was performed on IR-magnitude data and included a likelihood estimate for the goodness of the inversion pulse (F-factor). A first iteration over each entire slice evaluated the F-factor on a per pixel basis. The mean F-factor for every individual slice was then calculated and the T1 fit repeated with the F-factor kept fixed at the determined value. Also corrections for initial relaxation effects were considered [4]. No additional filtering of the data was performed. For the multi-component T2-analysis, we used a regularized NNLS algorithm as described in [5]. In this study we only present the geometric mean GMT2 (amplitude weighted mean on a logarithmic scale, boundaries 12 ms < T2 < 200 ms) as well as the amplitude-to-noise ratio ANR which is defined as the extrapolated amplitude from the NNLS-fit at TE=0 ms divided by the standard deviation of the NNLS-fit residual.

Results: Table 1 summarizes the ROI-analysis of both the T1-maps and GMT2 estimates, respectively. T1- and GMT2-values are in good agreement with published data [6, 7]. The total scan time of 25min for both relaxation time measurements make them well suited for clinical purposes. Although individual T1-variation of certain brain structures can be relatively high (e.g. <sdev>/ROI of cingulate gyrus, insular cortex in table 1), the reproducibility of mean T1-values between different subjects is excellent. The 3D-CPMG sequence furthermore allows for multi-component T2 analysis and verification of compartmental brain tissue changes (e.g. demyelination, white matter disintegration, prolonged T2 components in lesions and normal appearing white matter). The strong variation in ANR across different brain structures needs further exploration and might be attributed to local susceptibility changes, B1-inhomogeneity, and interference from flow in blood vessels and ventricles.

Brain structure	T1 / ms (±sdev)	<Sdev> / ROI /ms	GMT2 / ms	ANR
genu	721 ± 2	37	57.3 ± 4.3	395 ± 133
splenium	730 ± 7	38	58.3 ± 4.2	771 ± 183
post. intern. caps.	800 ± 21	49	55.4 ± 1.8	801 ± 55
min. forceps	776 ± 7	43	67.9 ± 1.2	173 ± 82
maj. forceps	795 ± 34	41	70.2 ± 6.0	341 ± 193
frontal WM	806 ± 9	48	69.1 ± 1.3	124 ± 34
parietal WM	798 ± 15	43	69.4 ± 1.1	162 ± 42
occipital WM	804 ± 4	46	72.3 ± 2.1	189 ± 51
pons	998 ± 17	122	-	-
optic nerve	778 ± 150	141	-	-
(vitreous humor)	3350 ± 25	125	-	-
cingulate gyrus	1351 ± 230	245	81.6 ± 1.5	128 ± 53
head caud. nucleus	1401 ± 41	105	67.4 ± 2.7	655 ± 195
putamen	1280 ± 18	83	65.8 ± 1.2	901 ± 203
thalamus	1181 ± 15	117	64.3 ± 4.5	767 ± 109
insular cortex	1188 ± 60	321	80.8 ± 3.0	251 ± 102
globus pallidus	951 ± 9	52	-	-
CSF	3300 ± 90	155	-	-

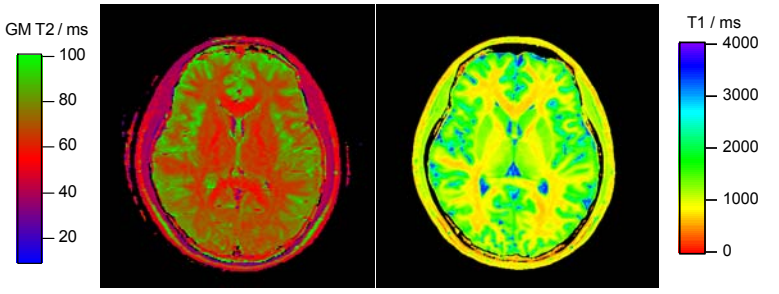

Figure 1: Examples of geometric mean T2-map (left) created from multi-component T2-amplitude distributions between 12 and 200ms (longer components are therefore suppressed) and the corresponding T1-map (right) from one control subject.

Table 1: T1 and GMT2 values based on ROI analysis of various brain structures from 6 healthy control subjects. <sdev>/ROI depicts local variations of T1 across the ROI. ANR represents a measure of fit precision and model accuracy.

Conclusion: We demonstrated and evaluated the feasibility of two novel 3D imaging techniques for the purpose of quantitative T1 as well as multi-component T2-relaxation measurements under clinical relevant time constrains (<25min) at high magnetic field strength (3T). RF power deposition for the 3D-CPMG sequence can be minimized by using optimized slab selective refocusing pulses and adjusting the TR time.

References: [1] Deoni et al., MRM 49: 515-526 (2003); [2] Deoni et al., MRM 51: 194-199 (2004); [3] Schmitt et al., MRM 51: 661-667 (2004); [4] Deichmann, MRM 54: 20-27 (2005); [5] Whittall et al., MRM 37: 34-43 (1997), [6] Wansapura et al., JMRI 9: 531-538 (1999), [7] Hanzhang et al., JMRI 22: 13-22 (2005)