AWARD NUMBER: W81XWH-13-1-0073

TITLE: 7T Magnetization Transfer and Chemical Exchange Saturation Transfer MRI of Cortical Gray Matter: Can We Detect Neurochemical and Macromolecular Abnormalities?

PRINCIPAL INVESTIGATOR: Seth A. Smith

CONTRACTING ORGANIZATION: Vanderbilt University

REPORT DATE: October 2014

TYPE OF REPORT: Annual

PREPARED FOR: U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for Public Release; Distribution Unlimited

The views, opinions and/or findings contained in this report are those of the author(s) and should not be construed as an official Department of the Army position, policy or decision unless so designated by other documentation.

R	REPORT DO		N PAGE		Form Approved OMB No. 0704-0188
Public reporting burden for this	s collection of information is es	timated to average 1 hour per resp	ponse, including the time for revie	ewing instructions, sea	arching existing data sources, gathering and maintaining the
this burden to Department of E 4302. Respondents should be valid OMB control number. PL	Defense, Washington Headqua e aware that notwithstanding a	rters Services, Directorate for Info ny other provision of law, no perso UR FORM TO THE ABOVE ADD	ormation Operations and Reports on shall be subject to any penalty	(0704-0188), 1215 Je for failing to comply w	collection of information, including suggestions for reducing ifferson Davis Highway, Suite 1204, Arlington, VA 22202- i/th a collection of information if it does not display a currently
1. REPORT DATE		2. REPORT TYPE		-	DATES COVERED
10/21/2014 4. TITLE AND SUBTIT	-1 E	Annual			30 Sep 2013 - 29 Sep 2014 A CONTRACT NUMBER
		nd Chemical Exc	hange Saturatio		a. CONTRACT NUMBER
					D. GRANT NUMBER - W81XWH-13-1-0073
		ay Matter: Can Abnormalities?		10- 0	S. ORART ROMBER - WORKWI-13-1-0073
				50	C. PROGRAM ELEMENT NUMBER
6. AUTHOR(S) Seth Smith				50	J. PROJECT NUMBER
				56	e. TASK NUMBER
				5f	. WORK UNIT NUMBER
E-Mail: seth.smith	@vanderbilt.edu				
7. PERFORMING ORG	GANIZATION NAME(S) AND ADDRESS(ES)		8.	PERFORMING ORGANIZATION REPORT NUMBER
The Vanderbilt	University				
Nashville, TN	37240-0001				
9. SPONSORING/MC	NITORING AGENCY	NAME(S) AND ADDRES	S(ES)	10). SPONSOR/MONITOR'S ACRONYM(S)
U.S. Army Medical	Research and Ma	ateriel Command			
Fort Detrick, Maryl				11	I. SPONSOR/MONITOR'S REPORT
,					NUMBER(S)
12. DISTRIBUTION / A	VAILABILITY STATE	MENT			
Approved for Publi	ic Release; Distrib	ution Unlimited			
	V NOTES				
13. SUPPLEMENTAR	T NOTES				
14. ABSTRACT					
We present the quantitative M	MRI set of MRI	scans at 7T in	healthy volunt	ceers and	loped and deployed a have developed an analysis
					dices reflective of
					titative MRI methods
		imized and vett			simulation. We are happy ifferences between the
					in conjunction with Dr.
					attery for correlation
					n and look forward to group
comparisions i					5 -
15. SUBJECT TERMS	-Not Provided				
	norrionada				
16. SECURITY CLASS	SIFICATION OF:		17. LIMITATION	18. NUMBER	19a. NAME OF RESPONSIBLE PERSON
			OF ABSTRACT	OF PAGES	USAMRMC
a. REPORT	b. ABSTRACT	c. THIS PAGE	UU		19b. TELEPHONE NUMBER (include area code)
U	U	U	00		
					Standard Form 298 (Rev. 8-98)

Prescribed by ANSI Std. Z39.18

Table of Contents

Page

1. Introduction	1
2. Keywords	1
3. Overall Project Summary	2-9
4. Key Research Accomplishments	9-10
5. Conclusion	10
6. Publications, Abstracts, and Presentations	10
7. Inventions, Patents and Licenses	10
8. Reportable Outcomes	10-11
9. Other Achievements	11
10. References	11-12
11. Appendices	12+

INTRODUCTION:

We recognize that many patients with Multiple Sclerosis (MS) suffer from cognitive impairment at some point in their disease course. However, characterization cognitive change in patients with MS has been difficult to pinpoint, and is hampered by poor quantitative markers. We have two hypotheses: 1) conventional imaging is insensitive to gray matter (GM) changes known to exist in patients with MS, and 2) ultra-high MRI field strengths (7T) would allow an opportunity to study the myelination and metabolic changes of the cortical GM in patients with MS and known cognitive impairment. The purpose of this proposal is to develop and implement a targeted quantitative magnetization transfer (qMT) and chemical exchange saturation transfer (CEST) MRI imaging paradigm at 7T to detect and quantify the level of myelin loss (qMT), protein/peptide changes (amide proton transfer CEST), neurotransmitter deficiencies (GluCEST) in the GM of patients with MS, and to relate these findings to neuropsychiatric evaluation outside the MRI scanner. The scope is to: 1) develop novel, highresolution, high field, quantitative MRI methods sensitive to myelination and neurochemicals for implementation in the cortical GM of human populations, 2) deploy these methods in patients with MS, 3) relate these findings to measures of cognitive impairment, and 4) develop a lower MRI field strength alternative for direct patient impact.

KEYWORDS:

- Magnetic Resonance Imaging (MRI)
- 7 Tesla (7T)
- Chemical Exchange Saturation Transfer (CEST)
- Magnetization Transfer (MT)
- Brain
- Cortical Gray Matter (cGM)
- Multiple Sclerosis (MS)
- Functional MRI (fMRI)
- Pool Size Ratio (PSR)
- Amide Proton Transfer (APT)
- Glutamate (Glu)
- Myoinositol (mI)
- Cognitive Impairment

OVERALL PROJECT SUMMARY

Task 1. IRB Preparation and Human Subjects Approvals. Completed

Task 2. Develop, optimize and implement advanced, quantitative Magnetization Transfer (MT) and Chemical Exchange Saturation Transfer (CEST) in phantoms and evaluate minimum achievable resolution and the associated reliability of derived indices

Simulation/Phantom Studies

The objective of this task was to develop a best-practice MT and CEST acquisition scheme to be deployed in Task 3 in healthy controls.

Summary of Results/Progress and Accomplishments

CEST -

APT-CEST – We have optimized through simulation and phantom studies a single-power, whole brain APT CEST acquisition for deployment in healthy volunteers and patients (Y2Q1). We began with the protocol presented by Jones et al (1) for whole brain coverage at 7T and increased the in-plane resolution, the coverage,

and modified the saturation scheme, readout, and fat-saturation (now a binomial excitation pulse) to minimize distortions in the phantoms while maintaining sufficient contrast to noise (CNR) for the APT CEST signatures in a reasonable scan time (9 minutes). The relevant scan parameters are as follows:

- Whole Brain (33 slices) 3D Gradient Echo (FFE) with multi-shot EPI (factor = 7) readout
- 1.5 x 1.5 x 5mm³ acquired resolution
- CEST RF Saturation $B1 = 2\mu T \times 25ms$ (each)
- 64 offset frequencies (Dw = -5 5ppm, $\Delta \omega$ step = 0.2ppm + 14 no Saturation Scans)
- Total Scan Time = 9:10

The simulations were performed using a 3 pool model of the CEST effect presented by Zaiss et al (2) and inputting estimates for T1, T2, pool sizes and exchange rates for the macromolecular, labile (amide protons) protons, and water as follows: Simulations were designed to identify optimal CEST preparation (RF irradiation power and bandwidth) parameters for APT contrast. All simulations were carried out utilizing the scripting environment in MATLAB 2012b (Mathworks, Natick, Massachusetts) on an Apple iMac (Cupertino, CA; 3.0 GHz, dual core CPU). Theoretical saturation was modeled according to the Bloch equations for three pools: bulk water (free), semisolid macromolecular (conventional MT), and mobile macromolecular (CEST) pools. This was achieved using the simple matrix solution to numerically solve the Bloch equations (3). This model assumes a T2-dependent Super-Lorentzian absorption lineshape for the macromolecules (4). Physical values of exchange rate, T1, and T2, were fixed according to (5.6). The bulk water was modeled as a Lorentizan with T1/T2 = 1538 ms/45ms. The semisolid macromolecular pool was modeled with T1/T2/exchange rate = 1600 ms/0.01 ms/20 Hz with offset = -2.34 ppm (7). The labile proton pool was modeled as a Lorentzian with T1/T2/exchange rate = 500ms/20ms/50Hz with offset = 3.5ppm and a concentration of 0.001 compared to bulk water (1.0) and macromolecular pool (0.1). Therefore our simulations included a single RF irradiation, a brief delay for spoiling, an on-resonance excitation, and a delay for readout. The B₁ amplitude (power) was varied over amplitudes from 1 μ T to 3 μ T while holding the duration constant at 25 ms. The B₁ amplitude was subsequently fixed to 1 μ T while the pulse duration was varied from 0 ms to 60 ms.

For phantom scans, we performed the above paradigm at various in-plane resolutions as low as 0.75mm², but determined through curve analysis that at these resolutions the CNR was insufficient to parse out the CEST effect from the background noise. From these simulations and phantom studies, the above pulse sequence paradigm was chosen to maximize CEST contrast derived from APT.

GluCEST – For glutamate, we performed the same simulations as above, but we modeled the off-resonance saturation as given in (8), and assumed an exchange rate for glutamate = 100 Hz, pool size = 0.001 compared to bulk water (1.0) and macromolecular concentration (0.01) and $\Delta \omega$ = 3.0ppm. For the GluCEST acquisition, due the concern of overlapping resonances (GABA, Glutamate, and other Amines) a high-spectral resolution acquisition needed to be obtained ($\Delta \omega$ = 0.2ppm spacing), thus scan time becomes prohibitive for extremely high resolution. However, it should be pointed out that the amine resonances that may reside in juxtacortical WM will be significantly less than the adjacent GM, so a slightly poorer resolution acquisition will not be problematic if a high spectral resolution scan is obtained. We therefore, decided to utilize a scan very similar to that which as been presented by Dr. Reddy (8,9) and thus we will implement a single slice GluCEST acquisition in vivo at a resolution of 1.9 x 1.9 x 5mm³.

- Single Slice (2D) Gradient Echo (FFE) with multi-shot TFE (40 shots) readout
- 1.9 x 1.9 x 5mm³ acquired resolution
- CEST RF Saturation $B1 = 4.25 \mu T \times 10 ms$ (each) x 100segments at 90% duty cycle
- 50 offset frequencies ($\Delta \omega = -5 5$ ppm, $\Delta \omega$ step = 0.2ppm)
- Total Scan Time = 11:36

qMT-

We have chosen to implement the selective inversion recovery (SIR) quantitative MT (qMT) to quantitatively extract the pool size ratio (PSR), which has been shown to be reflective of myelin. We have developed the SIR

approach at 7T as discussed in the Q1Y1 and Q2Y1 progress reports. This pulse sequence has been shown in previous reports, published (10) and provided in Appendix 3. However, in Q3Y1, we studied via simulation the impact of partial volume effects where we know there is a non-negligible MT effect in GM and certainly a strong effect in WM. Thus, in juxtacortical voxels where a blend of GM and WM may occur, poorer in-plane resolution results in an inability for the model to remain stable when deriving the PSR values (i.e. two different PSR values may fit equally well when there are two populations within a voxel). Therefore, we proposed a reduced number of slices but increased the in-plane resolution. From simulations, we feel that this provides the most robust acquisition method to be deployed in patients. Thus, from our phantom studies, we have determined that a 1 x 1 x 2mm³ acquisition with 5 slices sampled at 14 TIs (TI = 6ms, 10ms, 16ms, 26ms, 42ms, 68ms, 110ms, 178ms, 288ms, 468ms, 760ms, 1233ms, 2000ms, 8000ms) will be performed in patients with MS and healthy controls.

- Inversion prepared 3D Gradient Echo (FFE) with multi-shot TFE (2 shots) readout
- 1 x 1 x 2mm3 acquired resolution (5 slices)
- 14 Inversion Times (TI = 6ms, 10ms, 16ms, 26ms, 42ms, 68ms, 110ms, 178ms, 288ms, 468ms, 760ms, 1233ms, 2000ms, 8000ms) at a constant delay time (TD = 2500ms)
- Total Scan Time = 10:11

Conclusion of Task 2: Simulation and Phantom-optimized qMT and CEST acquisitions

Through simulation and phantom studies, we have devised a final protocol to be deployed in healthy volunteers and patients with MS. A summary of the protocol is given below, and a complete protocol is given in Appendix 1.

Final Summary of Protocol implemented in healthy controls (Task 3) and patients with MS (Task 5).

- Constant RF APT CEST 9:10
- Constant RF GluCEST 11:36
- SIR qMT 10:11
- Bloch-Siegert B1 mapping 1:42
- Dual-echo B0 mapping :04
- T1w MPRAGE Anatomical 2:12
- fMRI Resting State 8:34
- fMRI N-Back task 8:30
- fMRI Trailmaking task 4:14

The current scan time for all scans is approximately 1 hour.

Task 3 – Implement current best practice for MT and CEST in healthy volunteers and evaluate reliability

The objective of this task was to implement a best-practice MT and CEST acquisition scheme in healthy controls.

Summary of Results/Progress and Accomplishments

The above protocol has been implemented in 20 healthy volunteers at the close of year 1. We have additionally repeated this paradigm in 8 healthy volunteers. We have further scheduled the remainder of the healthy controls to be scanned in the coming month. There is one delay to report in that at the close of Year 1, our SOW stated that we would have recruited 50 healthy volunteers into the study. As pointed out in quarterly reports Q1Y1 and Q2Y1, we struggled initially making the phantoms to study the impact of resolution on the final protocol. This resulted in less than the expected 50 healthy controls. However, we have already scheduled these remainder healthy volunteers, and have a 40% return rate on for repeat visits to understand the reproducibility. We will complete the healthy volunteers and repeat visits in Q1Y1

In a follow-up to the Q3Y1 report, we have added three fMRI scans in collaboration with Dr. Paul Newhouse, our neurocognition expert. It is important that we note that this does not change the scope, but rather offers a unique opportunity to study the cognitive function in the MRI in healthy volunteers and patients for greater understanding of the relationship between the advanced, quantitative measures and outside-scanner neurocognitive battery. This is exceptionally unique as neither of these three fMRI scans have been studied in MS patients with known cognitive impairment and creates an exceptionally rich data set to mine for understanding neurocognitive decline in MS patients.

In 20 healthy volunteers (with 8 repeat acquisitions), we have obtained the entire proposed MRI protocol as given above. Preliminary results follow under Task 4.

Task 4 – Analyze the derived indices in healthy volunteers and evaluate reproducibility (1 month) The objective of this task was to 1) develop an analysis pipeline for constructing maps and deriving indices reflective of GM and juxtacortical WM from the quantitative MRI acquisitions prepared in Task 3, and 2) to ascertain these indices in preparation for analysis of reproducibility.

Summary of Results/Progress and Accomplishments

Develop an analysis pipeline for routine analysis of data generated.

As the first part of Task 4, we well understood the need to 1) correct patient motion in an individual scan (motion-correction), 2) co-register data across scans into the same space for robust analysis (co-registration), and 3) segmentation of WM and GM for histogram and descriptive statistics of each derived index.

WM/GM segmentation was performed in FAST using 3 classes as implemented in the FSL toolbox (FMRIB, Oxford, UK). The co-registration was performed using FNIRT (non-linear registration, FSL, FMRIB, Oxford,



Ing FNIRT (non-linear registration, FSL, FMRIB, Oxford, UK) to put the quantitative maps into the MPRAGE space such that the segmentation can be applied. To that end, Figure 1, shows two slices of an APT-CEST acquisition motion corrected and co-registered. The magenta color indicates the WM, and the green indicates the GM derived from the MPRAGE anatomical acquisition and overlaid on the APT map. It can clearly be seen that the agreement between the MPRAGE and the APT maps is high and the WM and GM clearly seen. The bottom panels show the process of joining the MPRAGE, the WM/GM Segmentation and the GluCEST-weighted acquisition for completeness.

Figure 1 – (Top) coregistration and segmentation results applied to APT maps, and (bottom) the target (MPRAGE), segmented map, and GluCEST-weighted acquisition.

APT CEST analysis and results

We have constructed the APT CEST maps in the following manner. First, the CEST spectrum for each voxel is normalized, corrected for B1 drift and fit to a single-lorentizian (11) and the minimum spectral intensity is shifted to an offset ($\Delta \omega$) = 0 for B0 correction. After this correction, the difference between the data and the fit create a Lorentzian residual. The residual between $\Delta \omega$ = 3.25 and 3.75 are integrated and termed the APT Lorentzian. An example of this is shown in Figure 2A left panel. To assess reproducibility we created a single

CEST spectrum for the whole brain and compared visit 1 to visit 2. Figure 2A right panel shows the results of two healthy repeated studies, where the green/blue curves are subject 1, and magenta/black curves are subject two over two times points. As it can be seen, the reproducibility is high over the whole brain. Individual structure assessments are ongoing. It can also be appreciated the spectral quality of the CEST spectrum using this analysis approach.



Figure 2: (A) APT maps for all slices derived in a healthy volunteer and concomitant test-retest CEST spectra in 2 healthy volunteers. The test-retest is over the whole brain, and the green/blue and magenta/black spectra pairs are from the same volunteers. (B) histogram analysis of segmented GM in 20 healthy volunteers and 1 MS patient with clinically noted cognitive impairment. Note that histograms at 2ppm and 3.5ppm show a downward shift of the MS patient relative to the healthy control indicating initial sensitivity to the pathology of cortical GM damage.

Once the data were segmented, we compared the GM averaged over all healthy volunteers (n = 20) and 1 MS patient with clinically diagnosed cognitive impairment histogram via analysis shown in Figure 2B. We performed the same calculation, but also examined resonances at 2ppm (hydroxyl and sensitive to myoinositol) and 3ppm (amine protons sensitive to GABA and Glutamate) and 3.5ppm transfer (amide proton sensitive to pH and protein concentration). It should be pointed out that the 1 MS patient examined here is actually part of Task 5, but it is important to show here as it points towards the sensitivity of the measurement. In this patient, there one is an obvious downward shift of the GM histograms at 2ppm and 3.5ppm giving the impression that we are detecting cortical and perhaps even some subcortical changes in protein concentration and myoinositol. In Figure 2B, the green is the MS patient, and the blue is the

average over healthy volunteers. We are exceptionally excited by this initial result and felt it important to share here as Task 5 will indeed prove the sensitivity of these advanced techniques to MS.

Glutamate CEST (GluCEST) analysis and results

GluCEST analysis proceeded as presented in (8,9). We performed GluCEST analysis in 20 healthy volunteers and 4 MS patients at the time of this report, though only one had been analyzed and is presented here. In short, GluCEST-weighted images were collected for a single slice with high spectral saturation fidelity (see Task 2) at a slice slightly superior to the corpus callosum. Sample GluCEST weighted images are shown as a function of offset frequency in Figure 3, top panel. From these maps, the GluCEST spectra were corrected for B0 and B1 in the fashion presented in (9), and a GluCEST asymmetry map at $\Delta \omega = 3.0$ ppm was generated. Figure 3, bottom panel shows two healthy volunteers and one patient with MS, clinically diagnosed with cognitive CEST-weighted ($\Delta \omega$ = -5 – 5ppm)



Figure 3: (top) example GluCEST-weighted images as a function of offset frequency (bottom) comparison of GluCEST maps for two healthy volunteers and one MS patient. Note the apparent differences between the MS patient and healthy volunteers (black and magenta arrows)

impairment. First, it can be seen that the GluCEST maps show excellent contrast between WM and GM, with the GM having higher GluCEST signal than the WM (expected). What is exciting to note (and in general, part of Task 5) is the visual differences between the patient and the two controls shown here. The MS patient shows elevated GluCEST signal (black arrow) on the left side, but apparently diminished GluCEST signal in the right cortical GM (magenta arrow) compared to healthy subject 1 (magenta arrow). This seems to indicate, at least at the early stages, that GluCEST is detecting cortical GM differences between healthy and MS patients.

As with the APT CEST, we examined the entire 20 healthy control cohort in comparison to the MS case and Figure 4A shows the average GluCEST spectra derived from GM and WM in healthy patients (blue and black, respectively) compared to the segmented GM in the MS case (red). It can be seen that the spectral quality is high and there is visual difference between the spectra for healthy and MS GM. Further, we analyzed the histogram of GluCEST signals for all GM

voxels in all healthy volunteers and compared that to the 1 MS patient clinically diagnosed with cognitive challenges (Figure 4B). As with the APT CEST, it can be seen that the MS patient shows a downward trend compared to the healthy volunteer indicating the possibility of being sensitive to cortical GM pathology, which



Figure 4: (A) Average GluCEST spectra for WM and GM in healthy (blue black) and MS patient (red) GM. (B) Histogram analysis shows that the MS has a downward shift of the GluCEST signal compared to the healthy volunteer (blue)

we will study in detail in Task 5. When we started this project, we decided against an "all-in-one" CEST acquisition scheme and rather have deployed two CEST acquisitions. One sensitive to APT (and apparently myoinositol) and one sensitive to glutamate. From Figure 4B, and in comparison to Figure 2B, the histograms from the APT-CEST analysis at $\Delta \omega = 3.0$ ppm (glutamate) show now difference between healthy controls and the 1 MS patient, however, when

utilizing the GluCEST acquisition, in the same patient, a difference can be appreciated. The rationale for this is

that the sensitivity to exchanging species is determined by the power of the RF CEST saturation. For the APT, the exchange rate is on the order of 20-100Hz, whereas for glutamate amines, the exchange rate is faster (50-200Hz). Thus, to be maximally sensitive to both, two separate pulse powers are necessary. We discovered this as part of Task 2 in the phantoms and are proud to note that it was the right choice going forward.

Quantitative Magnetization Transfer (qMT) analysis and results

High-resolution selective inversion recovery (SIR) qMT was performed in the same cohort as for CEST and analyzed according to (10) and given in Appendix 3. In short, an inversion recovery MRI sequence was performed using a modified inversion pulse that is relatively insensitive to B1 and B0 inhomogeneities. The inversion times were selected to sample the bi-exponential recovery known to exist when magnetization transfer is present. For every voxel, the SIR signal equation was fit to the recovery curve and the exchange rate (kmf), pool size ratio (PSR) and longitudinal relaxation time (R1f) was fit. Appendix 3 provides the manuscript that contains details of the pulse sequence, and fitting method.

Here we report the initial analyses and results from the newly deployed method. Figure 5, left panel shows the PSR, R1f, and kmf maps from a representative healthy volunteer and one patient with MS and concomitant cognitive impairment. From the PSR maps, it can be seen the high level of discrimination between WM (yellow/orange) and GM (blue) which agrees well with the R1f maps. Two things should be noted for the MS patient. First, the WM shows a globally decreased PSR which is indicative of demyelination across the entire slice, while the R1f and kmf maps do not show a similar pattern (discussed next). Secondly, when looking at the GM, it is not apparent that the patient and the control have different PSR values, yet MS patients are known



Figure 5: (left) qMT-derived maps for a healthy control (top) and MS patient (bottom). (right) segmentation results (top) and histogram analyses for the average healthy controls (red) and the MS patient (blue). Note the downward shift of the PSR for both WM and GM in this patient, while R1 and kmf are indistinguishable.

to have myelin loss in the GM. However, Figure 5, right panel, shows a histogram analysis of over the healthy volunteers (N = 20) and 1 MS patient. The top row shows the segmented WM and GM for an example healthy volunteer, and the bottom panels show the histograms for WM and GM for all of the qMT-derived indices. It can be seen again that for WM, the MS patient has a substantially downshifted PSR, normal R1f and kmf.

Importantly, however, in the GM, the patient also shows a small downshift of the PSR, while R1f and kmf are not markedly different (it should be noted that kmf showed some instabilities in this patient). This is important

to note in that one argument about MT imaging is that it is hypothesized that R1 drives the change in the MT effect moreso than does the macromolecular content. This figure shows that rather, in both WM and GM, the PSR is abnormal, but neither R1 nor kmf are indicating the sensitivity to WM and GM macromolecular pathology. Task 5 will explore this further when we examine a larger MS cohort.

fMRI analysis and results

In addition to the quantitative measures that have already been shown and at the advice of our mentor, Dr. Paul Newhouse, a neurocognition expert, we added 3 fMRI acquisitions to the MRI paradigm. Those three methods were an N-Back task, a Trail-making task, and a resting-state fMRI acquisition. The N-back and Trail-making tasks are important as they are also performed outside the MRI scanner, so we will be able to provide direct correlations between what is performed in the MRI and outside of the MRI. This further allows us to directly,



and non-invasively probe cognitive performance in a manner that is not only unique, but it has not been performed in the MS population at 7T. We are encouraged by

- the initial results and wish to present those here. We performed the fMRI in 20 healthy volunteers and 1 MS patient at the time of
- volunteers and T MS patient at the time of this report. Figure 6 shows a direct comparison of the N-back 3 (left panels) and the Trail-making (right panels) for a single healthy volunteer (top panels) and a patient with MS (bottom panels). As it can be seen, at the same significance threshold, there are activation differences between the healthy volunteer and the MS patient. These are especially noted for areas in the superior cortex where working memory is targeted. A greater confidence will be gained with a group analysis, but this will be reserved for Task 5.

Figure 6 (left) N-back 3 and (right) Trail-making fMRI activation patterns in a healthy (top panels) volunteer and one patient with MS (bottom panels). Note for the N-back, there is less activation in the MS patient, where as for the Trail-making task, there are greater areas of activation.

Discussion of Task 4

We are pleased with the quality of data that has been generated and are actively enrolling healthy volunteer sand patients with MS. We have scanned 20 healthy volunteers, and 4 MS patients to this point, and have had 8 healthy volunteers return for a 2nd visit. We are slightly behind the enrollment expectation, but this is in large part due to the ground work necessary to start the human studies. We are, however, encouraged that because of this extensive focus on sequence optimization, that the data quality remains superb in all subjects. We have scheduled the remainder of the healthy subjects, developed a robust pipeline for analysis, and have shown initial success in implementing these acquisitions in patients with MS. We expect no delays in finalizing enrollment and will continue with reproducibility analysis from which we can gauge the level of expected deviation from normal in patients with MS.

Task 5 – Implementation in Patients with MS and concomitant cognitive impairment The objective of this task is to deploy, and analyze the MRI acquisitions in patients with MS.

We have implemented the MRI paradigm in 4 patients with MS and expect no delays in enrollment for the remainder of the MS patients. The details of preliminary results are given in Task 4 with the goal of comparing both image quality, and quantitative differences. We have nothing else to report for Task 5 at the time of this annual report.

Task 6 – Cross-sectional analysis of derived indices between patients with MS and healthy volunteers and correlation with clinical measures of cognitive impairment derived from the Minimal Assessment of Cognitive Function in MS (MACFIMS)

The objective of this task is to compare quantitative MRI indices across cohorts, implement neuropsychiatric evaluations in both healthy and MS patient cohorts, and derive correlations with quantitative MR indices.

Neuropsychiatric Assessment Battery (Outside MRI Scanner)

In collaboration with Dr. Paul Newhouse, we have decided to additionally obtain neuropsychiatric evaluations in healthy volunteers in addition to patients with MS. This will provide us with a greater understanding of the variance across cohorts. Therefore, we have obtained neuropsychiatric data using the paradigm below in 20 healthy volunteers (8 repeats) and 4 MS patients.

Tasks - Outside the scanner and BEFORE coming to Vanderbilt

Questionnaire and survey already developed in REDCap to be completed at home and in a calm environment. These surveys will collect data related to baseline mood, anxiety, and cognitive profile.

Tasks - Outside the scanner at Vanderbilt (< 1 hour total)

- Short measure of day-of mood/anxiety
- N-back test (2-back or 3-back): measures working memory
- PASAT: measures working memory
- Trail making test (both A and B): measures planning/executive function
- "Black Box" (choice reaction time, critical flicker fusion; pre-scan and post-scan): measures processing speed/reaction time
- *Buschke selective reminding test (8 trials): measures include encoding and long-term memory
- Digit Symbol Substitution Test/DDST: measures visual memory
- Posner cueing task: measures attentional shift

KEY RESEARCH ACCOMPLISHMENTS:

- 1. Developed a Chemical Exchange Saturation Transfer (CEST) simulation pipeline to model the effects of glutamate, amide proton transfer, and myoinositol in the gray matter (GM) at 7T. These simulations reflect contributions from the metabolite of interest, the magnetization transfer (MT) effect, and the direct water saturation.
- 2. Developed a quantitative magnetization transfer (qMT) simulation pipeline to model the effects of macromolecular concentration of the white matter (WM) and GM in healthy tissue and tissue impacted by multiple sclerosis (MS). This pipeline incorporates modeling of the semisolid fraction while taking into account relaxation times (T1 and T2) changes that are known to occur in each cohort.
- 3. Phantoms have been created that attempt to model the in vivo scenario. That is, they have varied concentration of metabolite and concomitant concentration of semi-solid components (MT) at constant pH. These phantoms include: glutamate, myoinositol, glycogen, bovine serum albumin (BSA), and agarose. These phantoms can be leveraged for greater understanding of the in vivo results

- 4. Developed and optimized a set of novel MRI acquisition strategies to study the CEST effects of glutamate, myoinositol, amide protons, taking into account corrections for B1 and B0 inhomogeneities. These have been deployed in vivo.
- 5. Developed and optimized a high-resolution (1mm² in-plane resolution) qMT acquisition that is of sufficient resolution to assess cortical GM and juxtacortical WM in healthy and MS cohorts.
- 6. Developed a multi-modal motion-correction, coregistration and WM/GM/CSF segmentation strategy that not only maps the confidence of the measurements made in small structures, but also puts all acquisitions in the same space for descriptive statistics on each cohort.
- 7. Implemented a set of fMRI experiments to assess working memory and resting-state fluctuations in patients as compared to healthy controls. This will work in conjunction with item #8: neuropsychiatric evaluation
- 8. Created a detailed neuropsychiatric evaluation paradigm for assessing cognitive impairment that can be performed outside of the scanner environment and can be leveraged for correlation testing in the final year of this project.
- 9. In summary, we have developed, optimized, and deployed a multi-parametric, multi-modal MRI toolkit to assess neurochemical, macromolecular, functional, and structural changes in vivo at 7T. Additionally, we have developed a detailed neuropsychiatric evaluation paradigm to utilize for comparisons across cohorts, which can be further extended to any MRI study of cognitive impairment.

CONCLUSION:

We have concluded the first year of this project and have many significant contributions to report. First, we have for the first time, developed a battery of quantitative MRI methods that are of sufficient resolution and sensitivity to characterize cortical gray matter in healthy volunteers and patients with multiple sclerosis. To this end, we have a < 1 hour exam card that can be deployed on any 7T scanner that can investigate neurochemical composition, macromolecular/myelin deficiency, and functional impairment in a patient cohort. Additionally, we have generated data that suggests that there are differences between healthy volunteers and patients with MS, while expected, has yet to be shown because lower MRI field strengths have insufficient sensitivities to these macromolecules and neurochemicals, and insufficient resolution to study only gray matter. We have additionally partnered with a neurocognitive expert, and, with his help, developed a novel neuropsychiatric battery to assess cognition in MS. We understand that these techniques, while not novel, have not been implemented in patients with MS, and may provide evidence for greater scope in any patient with neurocognitive decline. We have studied 20 healthy volunteers and a handful of MS patients to this point and will expand the patient and control enrollment in year 2. We have finally, developed a pipeline for analysis that requires minimal human interaction and will deploy this for real-time analysis in year 2. It is important to note, however, that while these techniques are currently being explored for use at 7T, in year 2, we will develop a lower field, and thus, significantly more clinically relevant, set of exams that will provide a similar MRI toolkit. Lastly, the exam as developed here is not specific for MS and can be implemented in a wide range of patients and volunteers to explore the neurochemistry, functional processing, and macromolecular composition of cortical gray matter.

PUBLICATIONS, ABSTRACTS, AND PRESENTATIONS:

- 1. Lay Press: Nothing to report
- 2. Peer-Reviewed Scientific Journals: Nothing to report
- 3. Invited Articles: Nothing to report
- 4. **Abstracts**: 7 abstracts to the International Society for Magnetic Resonance in Medicine (ISMRM) annual conference have been prepared and will be submitted in Q1Y2 (November 12, 2014 deadline)

INVENTIONS, PATENTS AND LICENSES:

REPORTABLE OUTCOMES:

- 1. High-resolution, optimized 7T MRI acquisition strategies (so-called Exam Card in Philips language) to quantitatively evaluate the macromolecular, metabolic, functional, and structural characteristics that can (and currently is) be implemented in healthy controls and any patient cohort. A complete listing of the MRI acquisition paradigm (Exam Card) is given in Appendix 1.
- 2. Assessment of the reproducibility and stability of each measurement over time is currently ongoing.
- 3. A complete set of neuropsychiatric assessments, some of which are completely novel in patients with MS
- 4. Analysis pipeline for generation of quantitative MRI-derived indices. The pipeline includes motion correction, multi-modal image co-registration, and WM/GM/CSF segmentation along with generation of quantitative indices for further statistical comparisons.
- 5. A CEST simulation GUI for further studies of the CEST effect in vivo.
- 6. Collection of experiments, simulations, and phantom studies that have provided evidence for the minimal resolution attainable while maximizing sensitivity to change in patient populations.
- 7. Complete set of MRI and neuropsychiatric data in 20 healthy volunteers (with 8 additional repeat visits) and 4 patients with MS and clinically confirmed cognitive impairment. These data are summarized in the Overall Project Summary.

OTHER ACHIEVEMENTS:

- 1. Because of the nature of the experiments performed as a part of this grant, that is to implement the highest resolution quantitative MRI at 7T in WM and GM of healthy participants and MS patients, we have been able to extend these tools to the spinal cord, which has significant impact and scope for patients with other forms of neurological injury. One manuscript (*Dula AN, Pawate S, Dethrage LM, Conrad BN, Barry RL, Smith SA. CEST of the Cervical Spinal Cord at 7 Tesla. Submitted to NMR in Biomed on 30-Sept-2014*) has already been submitted on the results from this extension to other parts of the body.
- 2. The phantoms and simulations that were created are not MRI field strength dependent. Therefore, we have changed the simulations to study the impact of transitioning to a lower-field strength (i.e. 3T) for greater clinical implementation. We have begun to study the sensitivity for 3T utilization. This is critical, as it was noted in our initial application, that 7T MRI scanners are not directly clinically impactful. Thus, we have been able to create an MRI acquisition strategy at lower field strength which will be deployed in year 2. We are excited about the possibility of reaching a greater clinical community with the studies in year 2 at 3T.
- 3. From the preliminary results generated in the first year of this award, Dr. Pawate (co-investigator) is preparing a grant submission to the National Multiple Sclerosis Society in February 2015 to study cerebral changes in primary progressive MS (PPMS) patients.

REFERENCES: List all references pertinent to the report using a standard journal format (i.e. format used in *Science, Military Medicine, etc.*)

- 1. Jones CK, Polders D, Hua J, Zhu H, Hoogduin HJ, Zhou J, Luijten P, van Zijl PC. In vivo threedimensional whole-brain pulsed steady-state chemical exchange saturation transfer at 7 T. Magn Reson Med 2012;67(6):1579-1589.3291747
- 2. Zaiss M, Schmitt B, Bachert P. Quantitative separation of CEST effect from magnetization transfer and spillover effects by Lorentzian-line-fit analysis of z-spectra. J Magn Reson 2011;211(2):149-155
- 3. Woessner DE, Zhang S, Merritt ME, Sherry AD. Numerical solution of the Bloch equations provides insights into the optimum design of PARACEST agents for MRI. Magn Reson Med 2005;53(4):790-799
- 4. Morrison C, Stanisz G, Henkelman RM. Modeling magnetization transfer for biological-like systems using a semi-solid pool with a super-Lorentzian lineshape and dipolar reservoir. Journal of magnetic resonance Series B 1995;108(2):103-113
- 5. Michaeli S, Garwood M, Zhu XH, DelaBarre L, Andersen P, Adriany G, Merkle H, Ugurbil K, Chen W. Proton T2 relaxation study of water, N-acetylaspartate, and creatine in human brain using Hahn and Carr-Purcell spin echoes at 4T and 7T. Magn Reson Med 2002;47(4):629-633
- 6. Rooney WD, Johnson G, Li X, Cohen ER, Kim SG, Ugurbil K, Springer CS, Jr. Magnetic field and tissue dependencies of human brain longitudinal 1H2O relaxation in vivo. Magn Reson Med 2007;57(2):308-318
- Hua J, Jones CK, Blakeley J, Smith SA, van Zijl PC, Zhou J. Quantitative description of the asymmetry in magnetization transfer effects around the water resonance in the human brain. Magn Reson Med 2007;58(4):786-793.3707117
- 8. Cai K, Haris M, Singh A, Kogan F, Greenberg JH, Hariharan H, Detre JA, Reddy R. Magnetic resonance imaging of glutamate. Nature medicine 2012;18(2):302-306.3274604
- 9. Cai K, Singh A, Roalf DR, Nanga RP, Haris M, Hariharan H, Gur R, Reddy R. Mapping glutamate in subcortical brain structures using high-resolution GluCEST MRI. NMR in biomedicine 2013;26(10):1278-1284.3999922
- 10. Dortch RD, Moore J, Li K, Jankiewicz M, Gochberg DF, Hirtle JA, Gore JC, Smith SA. Quantitative magnetization transfer imaging of human brain at 7 T. NeuroImage 2013;64:640-649.3625658
- 11. Jones CK, Huang A, Xu J, Edden RA, Schar M, Hua J, Oskolkov N, Zaca D, Zhou J, McMahon MT, Pillai JJ, van Zijl PC. Nuclear Overhauser enhancement (NOE) imaging in the human brain at 7T. NeuroImage 2013;77:114-124.3848060

APPENDICES

Appendix 1

Diffice NDI Deate al Duran
Philips MRI Protocol Dump Created on
10/28/2014 10:40:51 AM
Comment
Created by ExamCard to XML with inputs: "E:\Export\20141021 CEST fMRI.ExamCard" on system (Vanderbilt University ::
192.163.71.10)
Software Stream
3.2.1.0
Expand All Collapse All
Hospital (2)
La lospia (2) La 2014/1021 CEST fMRI (13) 52:37.4
SCOUT SHC32 00:28.7
WIP MTX SENSE 32cb 01:28.9
T1 3D TFE iso1.25mm s2.5s SENSE Sagittal 02:12.2
CEST_interspersed_3uT 09:09.6
GEST Reddy, GluCEST 11:37.0
B1_Reddy_multiAngle 01:42.0
B0_Reddy_mulitecho 00:03.9
GaMT High Res 02:38.7
FINI RESTINGSTATE 08:34.0
FMRI TRAILMAKING 04:14.0
FMR_nback 08:30.0
T1_3D_TFE_quantGeo 00:55.7
T2star_multiEcho 01:02.7
B1860723-4F8F-476e-8075-D42C65706693} (0)

Hospital (2) 1201	41021 CEST fMRI	(13) 52:37.4 🖙 scou	T SHC32 00:28.7			
INFO PAG	GE	GEOMET	RY	CONTRAST		
Total scan duration	00:28.7	Multi-transmit	no	Scan type	Imaging	
Rel. signal level (%)	100	Nucleus	H1	Scan mode	M2D	
Act. TR/TE (ms)	7.8 / 4.9	Coil selection 1	RX-Intf-1	technique	FFE	
ACQ matrix M x P	256 x 128	Xmit Coil selection	MTX-Volume-	+ ZOOM	no	
ACQ voxel MPS (mm)	0.98 / 1.95 /		T/R	Contrast enhancement	T1	
	10.0	User def elem sel	no	Acquisition mode	cartesian	
REC voxel MPS (mm)	0.98 / 0.98 /	element selection	All	Fast Imaging mode	TFE	
Coord an annual to an (0/)	10.0	connection	conn-A	shot mode	multishot	
Scan percentage (%)	50	Coil selection 2	RX-Intf-2	TFE factor	64	
TFE shots TFE dur. shot / acg (ms)	2	element selection	All	startup echoes	default	
/ · · · · · /		Dual coil	yes	+TFE followup echoes	0	
TFE shot interval (ms)	1063.369	Multi coil	no	shot interval	shortest	
Min. TI delay	287.8819	CLEAR	no	profile order	linear	
Act. WFS (pix) / BW (Hz)	3.513 / 288.4	FOV FH (mm)	250	Echoes	1	
Min. WFS (pix) / Max.	1.297 / 781.3	AP (mm)	250	partial echo	no	
BW (Hz)	1.2777701.3	stack RL (mm)	50	shifted echo	no	
Min. TR/TE (ms)	7.8 / 2.8	Voxel size FH (mm)	0.9765625	TE	in-phase	
RF avg power computed		AP (mm)	1.953125	(ms)	4.93426	
(W)		Slice thickness (mm)	10	Flip angle (deg)	15	
SAR / head	< 100 %	Recon voxel size (mm)	0.9765625	TR	shortest	
Whole body / level	< 0.1 W/kg /	Fold-over suppression	no	Halfscan	no	
	normal	Reconstruction matrix	256	Water-fat shift	user defined	
B1 rms	1.32 uT	SENSE	no	(pixels)	3.5	
PNS / level // VUIIS :	35 % / normal	k-t BLAST	no	Shim	default	
dortch :		Stacks	3	mDIXON	no	
Sound Pressure Level	26.85212	current	A	Fat suppression	no	
(dB)		type	parallel	Water suppression	no	
МОТІО		slices	3	TFE prepulse	invert	
Cardiac synchronization	no	slice gap	user defined	slice selection	no	
Heart rate > 250 bpm	no	gap (mm)	10	shared	no	
Respiratory	no	slice orientation	sagittal	delay	user defined	
compensation		fold-over direction	AP	(ms)	800	
Navigator respiratory comp	no	fat shift direction	F	PSIR	no	
Flow compensation	no	Slice scan order	default	+inv pulse type	+default	
fMRI echo stabilisation	no	Stack scan order	ascend	МТС	no	
Motion smoothing	no	Move table per stack	no	T2prep	no	
NSA	1	Stack alignment	no	Research prepulse	no	
DYN/AN		Stack display order	no	Diffusion mode	no	
Angio / Contrast enh.	no	PlanAlign	no	Elastography mode	no	
Quantitative flow	no	REST slabs	0	SAR mode	high	
Manual start	no	Catheter tracking	no	B1 mode	default	
+Abuse dynamic loop	no	Interactive positioning	no	SAR Patient data	auto	
Dynamic study	no	Allow table movement	no	PNS mode	low	
Arterial Spin labeling	no	OFFC/A	NG	Gradient mode	default	
POST/PR		Stacks	3	SofTone mode	no	
		current	A			
Preparation phases Interactive F0	auto no	Stack Offc. AP	0			
SENSE ref. scan	no	(P=+mm)				
		RL (L=+mm)	0			
SmartPlan survey B0 field map	no no	FH (H=+mm)	0			
<u> </u>		Ang. AP (deg)	0			
B1 field map MIP/MPR	no no	RL (deg)	0			
		FH (deg)	0			
Images Autoviow imago	M, no, no, no					
Autoview image	M					
Calculated images	no, no, no, no Grey matter					
Reference tissue						
Preset window contrast	soft					
Reconstruction mode	real time					
Save raw data	no					
Hardcopy protocol	no					
	rectangular					
Ringing filtering Geometry correction	default					

INFO PACE GENMET# CONTRAST Total scan duration 01.29 Multi-transmit no Scan type Imaging Act. TRFIT (ms) 0.0 0.75 Outselection 1 RX-IntF1 technique FFE ACQ matrix M x P 96 x 75 Xmt Coll selection T/R technique FFE ACQ owald MPS (mm) 5.52 / 7.07 / 6.00 User def elem sel no Contrast chancement T/R ACQ wordd MPS (mm) 5.52 / 5.52 / 3.00 dement selection All Acquisition mode cartestan Scan percentage (%) 78 125 Coll selection 2 RX-Int7-2 30 non-selective no Packages 1 dement selection All Ecbres 1 partial echo no R1(P) 0.480 / 2033. FIP angle (deg) 1 TR shortest MIN PS (pip / Max. 0.480 / 2033. FIP angle (deg) 1 Shortest R2 (wh) 0.0808/94 RX (mm) 530 FR Shortest Shortest R3 (Poplachintains <	🗀 Hospital (2) 💷 201	41021 CEST fMRI	(13) 52:37.4 🖵 WIP N	ITX SENSE 32ch	01:28.9	
Rel signal level (%) 100 Nucleus H1 Scan minde 50 50 Act. TR/TE (ms) 8.0 / 0.75 Coll selection 1 RX-Int/T-1 Itechnique FFE ACQ workl MPS (mm) 5.52 / 7.07 / Kmit Coll selection 1 RX-Int/T-1 Icechnique FFE ACQ workl MPS (mm) 5.52 / 5.52 / Learnet selection 1 RII Contrast enhancement T1 REC workl MPS (mm) 5.52 / 5.52 / element selection 1 Acquisition mode Fast Imaging mode none Scan percentage (%) 78.125 Coll selection 2 RX-Int/-2 element selection 1 Acquisition mode Fast Imaging mode none Scan percentage (%) 78.125 Coll selection 2 RX-Int/-2 element selection 1 Acquisition mode Fast imaging mode none Mit woll 0.489 / 2071.3 Dual coll yes stack AP (mm) 5.00 File angle (deg) 1 TR Mit woll 0.05085949 Rt (mm) 5.00 File angle (deg) 1 TR Haffscan non More I wore Mare MS (need //	INFO PA	GE	GEOMETR	λ.	CONTRA	ST
Act. TRTE (ms) 8 0 / 0.75 Coll selection 1 RX-Int1-1 Itechnique FFE AGO matrix M x P 96 x 75 Xmit Coll selection MTX-Volume- T/R Ioop ardsr 2y_order AGO word IMFS (mm) 5.52 / 15.57 User def elem sele no Contrast enhancement 11 Acquisition mode Cartesian Act. WFS (pix) / Bax 0.489 / 2071.3 User def elem sele All Acquisition mode Cartesian Act. WFS (pix) / Bax 0.489 / 2071.3 element selection All Acquisition mode Cartesian Min WFS (pix) / Max 0.486 / 2083.3 CLEAR no Shifted cho no Min WFS (pix) / Max 0.486 / 2083.3 CLEAR no FE Shofted cho no White body / level 0.0508549 FOV FH (mm) 5.30 TR TR Rd Gal and Fault None body / level 0.0 W/kg / Normal Shofted cho no TR Hafscan no Sup respression 0.3 CLEAR No TR Hafscan no	Total scan duration	01:28.9	Multi-transmit	no	Scan type	Imaging
ACD matrix M x P 9 k x 75 Kmit Coli selection MTX-Volume- TR Ioop order y_order ACD voxel MPS (mm) 5.52 / 7.07 / 4.00 Liser def elem sel no Contrast enhancement TI REC voxel MPS (mm) 5.52 / 5.2 / 3.00 Sale percentage (%) 78.125 Coll selection 2 RX-intr-2 Past tanging mode none Scan percentage (%) 78.125 Coll selection 2 RX-intr-2 Past tanging mode none Packages 1 element selection All Acquisition mode Echoes 1 Act. WFS (pix) / Max. 0.486 / 2083.3 CLER no TE Salified echo no AK / head < 2 %	Rel. signal level (%)	100	Nucleus	H1		
ACO matrix M x P 9 & x 75 Kmit Coll selection MTX-Volume- TR Isogo order y_y, order y_y, order AGO voxel MPS (mm) 5.52 / 5.52 / 3.00 Liser def elem sel no Active Manuel	Act. TR/TE (ms)	8.0 / 0.75	Coil selection 1	RX-Intf-1	technique	FFE
ACQ voxel MPS (mm) 5.52 / 7.07 / 5.00 T/R + 200M - 200M REC voxel MPS (mm) 5.52 / 5.52 / 3.00 ielement selection All Acquisition mode cartesian Scan percentage (%) 78.125 Coll selection RX-infr-2 3D non-selective none Packages 1 element selection All Echoes 1 Act. WFS (bik) / BW 0.489 / 2013. Used element selection All partial echo no Whit Coll yes Multi coll yes partial echo no SR / head < 2 %	. ,				<u>. </u>	zv order
6.00 User def elem sel no Contrast enhancement T REC voreil MPS (rm) 5.5.2 / 3.00 cement selection All Acquisition mode cartestain Packages 1 connection conn A Fast Imaging mode none Act. WFS (pix) / BW 0.489 / 2011.3 Dual coll yes But coll yes Min. WFS (pix) / Max. 0.486 / 2083.3 CLEAR no shifted echo no SAR / head < 2.9%						
3.00 connection conn-A Fast Imaging mode none Packages 1 Coll selection 2 RX.Intf-Z 30 non-selection no Packages 1 Dual coll yes partial echo no Min. WFS (pix) / Max 0.486 / 2083.3 CLEAR no TE shifted echo no Min. WFS (pix) / Max 0.486 / 2083.3 CLEAR no TE shortest Min. WFS (pix) / Max 0.486 / 2083.3 FEV FH (mm) 530 FIP angle (deg) 1 SAR / head < 2 %			User def elem sel	no		
3.00 connection conn-A Fast Imaging mode none Packages 1 celement selection All Bonn-selective no Act, WFS (pix) / BW 0.489 / 2071.3 Dual coil yes partial echo no Mm. WFS (pix) / Max 0.486 / 2083.3 Dual coil yes shifted echo no Mm. WFS (pix) / Max 0.486 / 2083.3 CLEAR no TE shortest FM ay power computed 0.05085949 FU FH (mm) 530 TR shortest SAR / head < 2 %	REC voxel MPS (mm)		element selection	All	Acquisition mode	cartesian
Scan percentage (%) 78.125 Coil selection 2 RX-Intr-2 3D non-selective no Act. WFS (pk) / BW 0.489 / 2071.3 Dual coil yes partial echo no Min. WFS (pk) / Max 0.486 / 2083.3 Cuil selection 2 yes partial echo no Mill coil yes shifted echo no mo shifted echo no W1(z) No 0.05085949 RL (mm) 530 Flip angle (deg) 1 shortest FA vag power computed 0.05085949 Voxel size FH (mm) 530 Hafroan no R1 head < 2 %			connection	conn-A		none
Packages 1 element selection All Echoes 1 Act. WFS (pik) / BW 0.489 / 20713 Dual coll yes partial echo no Min. WFS (pik) / Max. 0.486 / 20833 Multi coll yes shifted echo no BW (Hz) 0.05085949 FUE Hrmm) 530 TE shortest SAR / head < 2 %	1 0 1 /	78.125	Coil selection 2	RX-Intf-2		no
Act. WFS (pik) / BW 0.489 / 2071.3 Dual coll yes partial echo no Min. WFS (pik) / Max. 0.486 / 2083.3 CLEAR no TE shortest Witi coll yes FIIp angle (deg) 1 shortest RF avg power computed 0.05085949 RL (mm) 530 FIIp angle (deg) 1 SAR / head < 2 %		1	element selection	All	ï	
(H2) (H2)0.486 / 2083.3Multi coli (LEARyesshifted echonoR avg power computed (W)0.0508549 (M)0.0508549 (R)RL (mm)530TRshortestSAR / head < 2 %Stack AP (mm)30HalfscannoWhole body / level0.0 W/kg / normalnormalStack AP (mm)30HalfscannoB1 rms0.18 uTAP (mm)3mDIXONnoNoSound Pressure Level27.92985Fold-over suppressionnoRecon voxel size (mm)5.20833Fat suppressionnoGardiac synchronizationnoReconstruction matrix96Statost AP (mm)MOTCOResearch prepulsenoCardiac synchronizationnoStacksnoStatost AP (mm)Statost AP (mm)Statost AP (mm)Statost AP (mm)Navigator respiratorynoStacksyesStatost AP (mm)Statost AP (mm)Statost AP (mm)NAGID / Contrast enh.noStack alignmentnoStack alignmentnoNAGID / Contrast enh.noStack alignavertnoStack alignavertNamat startnoStack dispay ordernoStack alignavertNoNare studynoStack dispay ordernoStack dispay ordernoNagin / Contrast enh.noStack dispay ordernoStack dispay ordernoNare studynoStack dispay ordernoStack dispay ordernoPresartion phasesfui		0.489 / 2071.3	Dual coil	yes	1	
Mm. Wr (bz) 0.486 / 208.3 CLEAR no TE shortest RF avg power computed (W) 0.05085949 RL (mm) 530 TR shortest SAR / head < 2 %			Multi coil	yes		
Far avg power computed (W) 0.05085949 FOV FH (mm) 530 FIip angle (deg) 1 R Ar J head < 2 %		0.486 / 2083.3	CLEAR	no		
N. MarginalPart (mm)530TRShortestSAR / head $< 2.\%$ stack AP (mm)300HalfscannoWhole body / level0.0 W/kg / normalNow size FH (mm)5.520833Water-fat shiftminimumB1 rms0.18 uTAP (mm)7.066667ShimdefaultPNS / level // VUIIS : toorth :18 % / normalRL (mm)5.520833FH (mm)noPNS / level // VUIIS : toorth :18 % / normalRecon voxel size (mm)5.520833FH (mm)noOut or suppressionnoRecon voxel size (mm)5.520833FH (mm)noOut or suppressionnoRecon voxel size (mm)S.520833FH (mm)noOut or suppressionnoRecon voxel size (mm)S.520833FH (mm)mDIXONReconstruction matrix96Elastography modenoReconstruction matrix96Elastography modenoCardiac synchronizationnoSENSEnoSAR modehigh HighB1 modedefaultNavigator respiratory compensationnoStacks2PNS modelowNavigator respiratory modenoStack alignmentnoSiteck alignmentnoNSA3Soft one modenoFI shift directionFOur or tigue dynamic loopnoStack alignmentnoFI shift directionFDynamic studynoStack alignmentnoSiteck alignmentnoPreparation phasesfull		0.05005040	FOV FH (mm)	530		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		0.05085949	RL (mm)	530		shortest
Order Order Voxel size FH (mm) 5.520833 Water-fat shift minimum B1 rms 0.18 uT AP (mm) 3 BNIXON no PNS / level // VUIIS : 18 % / normal AP (mm) 3 BNIXON no Sound Pressure Level (dB) 27.92985 FOId-over suppression no MTC no Gardiac synchronization no RE construction matrix 96 Eastography mode no Research prepulse no RS select: FOS no B1 mode no Navigator respiratory compensation no RC everontiguous slices yes SAR mode high NART yes fold-over suppression no SAR mode low Gradient mode default SMART yes fold-over direction RL Salces no SAR SofTone mode no Stack alignand no Stack alignand no Salce signaphy mode no Navigator respiratory no stack alignay order no Salces PNS Garadient mode </td <td>· /</td> <td>< 2 %</td> <td>stack AP (mm)</td> <td>300</td> <td>ï</td> <td></td>	· /	< 2 %	stack AP (mm)	300	ï	
normalRL (nm)7.066667ShimdefaultB1 rms0.18 uTAP (nm)3mDIXONnoPKS / level / VUIIS :18 % / normalRecon voxel size (nm)5.520833Fat suppressionnoGotth :27.92985Silce oversamplingdefaultResearch prepulsenoCarlae synchronizationnoRe seconstruction matrix96Diffusion modenoCarlae synchronizationnoSENSEnoSAR modehighNavigator respiratorynoStacks2PNS modelowCoronepensationnoStacks2PNS modelowFile d-over directionRsilce orientationSaff Patient dataautoNSA3Silce orientationFSaft AlignmentnoStack3Silce orientationfold-over directionRMarual startnoStack alignmentnoAbuse dynamic loopnoStack alignmentnoPOST/PROCREST slabs0Catheter trackingnoPreparation phasesfullIllow table movementnoInteractive F0noRest rakeg)0Preparation phasesno, no, no, noB1 field mapnoRL (=+mm)-3.434925FH (deg)0FH (deg)0FH (deg)0Reconstruction modeFH (deg)0Reconstruction modeFH (deg)0				5.520833	1	
B1 rms 0.18 uT AP (rmm) 3 mDXXON no PNS / level // VUIIS 18 % / normal Recon voxel size (rmm) 5.520833 Fat suppression no Sound Pressure Level 27.92985 Image shutter yes Water suppression no Cardiac synchronization no Rescon voxel size (rmm) 6.18 uT Research prepulse no Cardiac synchronization no Reservatory no Diffusion mode no Respiratory no SENSE no SAR mode high Navigator respiratory no SENSE no SAR mode high Navigator respiratory no Current A silces Gradient mode default SMART yes Stacks 2 PNS mode low Glo-over direction RL fat shift direction F SofTone mode no Stack alignment no Stack alignment no Stack alignment no Stack alignment no Stack alignment no REST siabs O Optimative flow no Stack alignment no REST siabs O Carterit Pina Nilgn no REST siabs O			 	7.066667	1	
PNS / level // VUIIS : 18 % / normal dortch : Recon voxel size (mm) 5.520833 Fat suppression in o Motion : 27.92985 Image shutter yes Water suppression in o MOTION Respiration : No Cardiae synchronization in on Heart rate > 250 bpm in o Silce oversampling default Respiratory : Research prepulse in o Diffusion mode : No Reson voxel size (mm) Silce oversampling default Respiratory : Research prepulse in o Navigator respiratory : no SENSE in o SAR mode Bit mode in o Navigator respiratory : no Stacks 2 PNS mode iow Bit mode in o SMART yes fat shift direction RL fold-over direction RL Fat suppression in o SofTone mode in o SMART yes fat shift direction RL fold-over direction RL SofTone mode in o SofTone mode in o Manual start in o Stack alignment in o Stack dignoren in o Stack dignoren in o Stack dignoren in o Rest slabs 0 Catheter tracking in o Interactive for in o Stack dignoren in o Rest slabs 0 Catheter tracking in o Interactive politioning in o Altow kinage in on	B1 rms		<u> </u>		ï	
dortch : Image shutter yes Not over suppression no Sound Pressure Level (dB) 27.92985 Fold-over suppression no MTC no Cardiac synchronization no RF select. FOS no Diffusion mode no Cardiac synchronization no RF select. FOS no Diffusion mode no Respiratory no RF select. FOS no SAR mode high Navigator respiratory no SENSE no SAR mode default Overcontiguous slices yes SAR mode default Navigator respiratory no current A slices Somponesation no current A slices SofTone mode no NSA 3 fold-over direction RL SofTone mode no Stacks 1 SofTone mode no SofTone mode no Stack alignment no Stack alignment no Stack alignment no Arbuse dynamic loop no Stack alignment no REST slabs O Catheter tracking no Stack display order no No Stack display order no Stack Sizes 2					1	
Sound Pressure Level (d8)27.92985Fold-over suppression noNot MTCMOTIONRespiratory compensationnoSilce oversampling Reconstruction matrixdefaultMTCnoRespiratory compensationnoReconstruction matrix96Elastography modenoNavigator respiratory componsationnoStacks2SAR Patient dataautoNavigator respiratory compnoStacks2PNS modelowFlow compensation NSA3Silce orientation fold-over direction100SAR Patient dataautoSMART Upsetyesfold-over directionRLFat shift directionFSat Patient datasoftManual start retration loop Dynamic study Dynamic study Dynamic study Dynamic studynoStack alignment nonosoftnoStack display order Dynamic study Distinker differencenoStack display order nonosoftRespiratory countitative fo nonoStack display order nonostack display order nonoStack display order 			 		1	
(dB) Image: Notion of the second se	Sound Pressure Level	27.92985			1	
MOTIONRF select. FOSnoDiffusion modenoCardiac synchronizationnoReconstruction matrix96Diffusion modenoRespiratorynoSENSEnoSatagraphy modenoRespiratorynok.1 BLASTnoSatagraphy modehighLift grantk.1 BLASTnoSatagraphy modehighNavigator respiratorynocurrentA slices2CompensationnocurrentA slicesGradient modedefaultNRI echo stabilisationnofold-over directionRLGradient modedefaultSMARTyesfold-over directionRLSoff one modenoManual startnoStack algnmentnoNoArterial Spin labelingnoStack display ordernoPost/PROCFreparation phasesfullInteractive positioningnoPiterative FOnoStack display ordernoStack display ordernoStack display ordernoAltow table movementnoStack display ordernoStack display ordernoStack display ordernoB1 field mapnoStack offic. APInteractive positioningInteractive FOnoStack offic. APRL (=+mm)B1 field mapnoStack offic. APRL (=+mm)Indegesno, no, no, no, noRL (L=+mm)4.208135Ango. AP (deg)0FH (deg)0Reference tissue <td>(dB)</td> <td></td> <td></td> <td></td> <td>1</td> <td></td>	(dB)				1	
Cardiac synchronizationnoReconstruction matrix96Housson modeHeart rate > 250 bpmnoSAR modehighRespiratory compensationnoSAR modehighNavigator respiratory componsationnoSAR modehighNavigator respiratory componsationnoSAR Patient dataautoFlow compensationnoCurrentA slicesPNS modelowGardient modedefaultCurrentA slicesGradient modedefaultSMARTyesfold-over directionRLSofTone modenoSMARTyesfold-over directionRLSofTone modenoAngio / Contrast enh.noStacks as packagesnoStack alignmentnoAngio / Contrast enh.noStack alignmentnoStack display ordernoPost /PROCPianAlignnoREST slabs0Catheter trackingnoPreparation phasesfullInteractive positioningnoREST slabs0Allow table movementnoStack display ordernoStack display ordernoBi field mapnoRL (L=+mm)-3.434925FH (H=+mm)4.208135Ang. AP (deg)0RE (deg)0FH (deg)0Reference tissueWhite matterFH (deg)0FH (deg)Preset window contrastsoftFH (deg)0FH (deg)Ardcopy protocolnoFH (deg)0FH (deg) <t< td=""><td>MOTIO</td><td>N</td><td></td><td></td><td>1</td><td></td></t<>	MOTIO	N			1	
Heart rate > 250 bpm no For the second determinants For the sec	Cardiac synchronization	no			ï	
Respiratory compensation no It BLAST no BI mode Ingr Navigator respiratory comp no K-I BLAST no BI mode default Navigator respiratory comp no Stacks 2 PNS mode low Flow compensation no No Stacks 2 PNS mode low SMAR TO yes Soffone mode no Soffone mode no SMART yes fold-over direction RL Soffone mode no May altart no Stacks as packages no no No Angio / Contrast enh. no Stack display order no No Stack display order no Quantitative flow no Stack display order no No PlanAlign no Preparation phases full Interactive positioning no Allow table movement no Stack Gisplay order no Stack Gisplay order no No No Stack Gisplay order no REST slabs 0 Catheter tracking no Stack Offic. AP 11.5916 FH (H=+mm) 4.208135 Ang. AP (deg) Nag. AP (deg) Reference tissue mode <t< td=""><td></td><td></td><td>1</td><td></td><td></td><td></td></t<>			1			
compensationINOB1 modedefaultNavigator respiratory compnoOvercontiguous silcesyesSAR Patient dataautoFlow compensationnoStacks2PNS modelowFlow compensationnoStacks2PNS modelowfMRI echo stabilisationnoSilce orientationcorronalGradient modedefaultSMARTyesfold-over directionRLfat shift directionFChunks1Outrats enh.noStacks as packagesnoMove table per stacknoAngio / Contrast enh.noStack alignmentnoStack alignmentnoAngual startnoStack display ordernoStack display ordernoArterial Spin labelingnoREST slabs0Catheter trackingnoPreparation phasesfullInteractive positioningnoAllow table movementnoStacks2currentAStacks2currentB0 field mapnoStack Offc. AP11.5916FH (H=+mm)-3.434925B1 field magesno, no, no, noAng. AP (deg)0FH (Heg)0Reference tissueWhite matterFH (Heg)0FH (Heg)0Preset window contrastsoftFH (deg)0FH (deg)0Reference tissueWhite matterFH (deg)0FH (deg)0Preset window contrastsoftFH (deg)0FH (deg) <td></td> <td></td> <td></td> <td></td> <td>1</td> <td><u> </u></td>					1	<u> </u>
Navigator respiratory comp no Stacks 2 PNX mode lots Flow compensation no stacks 2 PNX mode lots SMART yes fold-over direction RL Gradient mode default SMART yes fold-over direction RL SofTone mode no Angio / Contrast enh. no fold-over direction FL SofTone mode no Quantitative flow no Stacks as packages no stack alignment no Anual start no Stack display order no stack alignment no Preparation phases full Interactive positioning no Allow table movement no Stacks 1 stacks 2 current A B1 field map no Stack Offc. AP 11.5916 Preset window contrast soft RF. (Le+mm) -3.434925 FH (H=+mm) 4.208135 Ang. AP (deg) <t< td=""><td></td><td></td><td></td><td></td><td>ï</td><td></td></t<>					ï	
compNacks2PNS modelowFlow compensationnocurrentA slicesGradient modedefaultfMRI echo stabilisationnoNSA3100SofTone modenoSMARTyesfold-over directionRLfat shift directionFChunks1Angio / Contrast enh.noStacks as packagesnoMove table per stacknoSofTone modeNoAngio / Contrast enh.noStack as packagesnoMove table per stacknoStack alignmentnoAtabuse dynamic loopnoStack aligny ordernoStack display ordernoREST slabs0Post/PROCPerparation phasesfullInteractive positioningnoAllow table movementnoStacks2currentAMilow table movementnoB1 field mapnoStack offC. AP11.5916(P=+mm)Reference tissueWhite matterFH (H=+mm)4.208135Ang. AP (deg)0Reference tissueWhite matterFH (deg)0FH (deg)0FH (deg)0FH (deg)0FH (deg)0Retarction modeImmediateFH (deg)0FH (deg)Save raw datanoFH (deg)0FH (deg)0Ringing filteringdefaultFH (deg)0FH (deg)Save raw datanoFH (deg)0FH (deg)FH (deg)Save raw datanoFH (deg) <td< td=""><td>Navigator respiratory</td><td>no</td><td></td><td></td><td>1</td><td></td></td<>	Navigator respiratory	no			1	
Flow Compensation No fMRI echo stabilisation no NSA 3 SMART yes DYN/ANG Angio / Contrast enh. no Quantitative flow no Manual start no Abuse dynamic loop no Post/PROC Preparation phases full Interactive FO no B0 field map no STacks 2 Current A MIP/MPR no B1 field map no MIP/MPR no Reference tissue White matter Preset window contrast soft FH (H=+mm) Reference tissue White matter Preset window contrast soft FH (Heg) Radiation no Hardcopy protocol no Radiation mo						
Milki echo stabilisation No NSA 3 SMART yes DYN/ANG fold-over direction Angio / Contrast enh. no Quantitative flow no Manual start no +Abuse dynamic loop no Dynamic study no Preparation phases full Interactive FO no SENSE ref. scan yes Soff field map no B1 field map no Stack soft 2 current A Stack form. 1.5916 Preset window contrast soft FH (H=+mm) Reference tissue White matter Preset window contrast soft FH (Heg) Reference tissue White matter Preset window contrast soft FH (Heg) Radiated images no Reference tissue White matter Preset window contrast soft FH (deg) Reference tissue White matter Preset window contrast soft FH (deg) Radiateling no Hardcopy protocol no Hardcopy protocol no	Flow compensation	no	current		ï	
NSA3SMARTyesDYN/ANGfold-over directionAngio / Contrast enh.noQuantitative flownoManual startno+Abuse dynamic loopnoDynamic studynoArterial Spin labelingnoPOST/PROCStack display orderPreparation phasesfullInteractive F0noStacks ref. scanyesStacks ref. scanyesB1 field mapnoB1 field mapnoB1 field magesno, no, no, noReference tissueWhite matterPreset window contrastsoftReference tissueWhite matterPreset window contrastsoftRadtadatinoHardcopy protocolnoRadtadatinoReference tissueWhite matterPreset window contrastsoftRadtadatinoReference tissueMonte matterPreset window contrastsoftRadtadatinoReference tissueMonte matterPreset window contrastsoftRadtadatinoReference tissueMonte matterPreset window contrastsoftRadtadatinoRadtadatinoReference tissueMonte matterReference tissueMonte matterReference tissueMonte matterRadtadatinoRadtadatinoRadtadatinoReference tissue </td <td>fMRI echo stabilisation</td> <td>no</td> <td></td> <td></td> <td>SofTone mode</td> <td>no</td>	fMRI echo stabilisation	no			SofTone mode	no
SMR1yesDYN/ANGfat shift directionFAngio / Contrast enh.noChunks1Quantitative flownoStacks as packagesnoManual startnoStack alignmentno+Abuse dynamic loopnoStack alignmentnoPynamic studynoPlanAlignnoPreparation phasesfullInteractive positioningnoInteractive F0noStack display ordernoSSNSE ref. scanyesStacks2SmartPlan surveynoStack S2B0 field mapnoGFFC/ANGStack offc. AP11.5916Imagesno, no, no, noRE(L=+mm)Autoview imageno, no, no, noRL (L=+mm)Reference tissueWhite matterRI (deg)0Preset window contrastsoftFH (H=+m)4.208135Arg. AP (deg)0FH (deg)0Hardcopy protocolnoFH (deg)0	NSA	3	l			
DYVANCChunks1Angio / Contrast enh.noStacks as packagesnoQuantitative flownoMove table per stacknoManual startnoStack alignmentno+Abuse dynamic loopnoStack alignmentnoPortaities tudynoPlanAlignnoPostr/PROCCatheter trackingnoPreparation phasesfullInteractive positioningnoInteractive FOnoAllow table movementnoSmartPlan surveynoStacks2B0 field mapnoStacks2B1 field mapnoStack GfC. AP11.5916Imagesno, no, no, noRL (L=+mm)-3.434925Autoview imagenoRL (L=+mm)4.208135Agererent tissueWhite matterFH (H=+mm)4.208135Preset window contrastsoftFH (deg)0Reconstruction modeimmediateFH (deg)0Save raw datanoFH (deg)0Ringing filteringdefaultK	SMART	yes				
Angio / Contrast enh.noQuantitative flownoManual startno+ Abuse dynamic loopnoYabuse dynamic loopnoStacks as packagesnoAngio / Stack alignmentnoStack alignmentnoPostr/PROCPlanAlignPreparation phasesfullInteractive F0noStack fillInteractive positioningInteractive F0noStack stress2Catheter trackingnoSENSE ref. scanyesSoff field mapnoB1 field mapnoImagesno, no, no, noAutoview imagenoCalculated imagesno, no, no, no, no, Ang. AP (deg)Calculated imagessoftReference tissueWhite matterPreset window contrastsoftRevenstruction modeimmediateSave raw datanoRinging filteringdefault	DYN/AN	G				
Outanitative nownoManual startnoAttarial Spin labelingnoDynamic studynoPost/PROCPlanAlignPreparation phasesfullInteractive FOnoStack silgney ordernoPreparation phasesfullInteractive FOnoSENSE ref. scanyesSoffield mapnoB1 field mapnoB1 field mapnoMIP/MPRnoReference tissueWhite matterReference tissueWhite matterPreset window contrastsoftSave raw datanoRinging filteringdefault	Angio / Contrast enh.	no	l			
Manual startnoManual startno+ Abuse dynamic loopnoStack alignmentnoDynamic studynoArterial Spin labelingnoPOST/PROCPlanAlignPreparation phasesfullInteractive F0noInteractive F0noSmartPlan surveynoB0 field mapnoB1 field mapnoImagesno, no, no, noAutoview imagenoReference tissueWhite matterPreset window contrastsoftReconstruction modeimmediateSave raw datanoRinging filteringdefault	Quantitative flow	no				
+ Abuse dynamic loopnoStack alignmentnoDynamic studynoPianAlignnoArterial Spin labelingnoPianAlignnoPOST/PROCREST slabs0Preparation phasesfullInteractive positioningnoInteractive FOnoAllow table movementnoSENSE ref. scanyesOFFC/ANGSmartPlan surveynoStack offc. APB1 field mapnoStack offc. APImagesno, no, no, no,RE (L=+mm)Autoview imageno, no, no, no,AR. (Le=+mm)Calculated imagesno, no, no, no,Ang. AP (deg)0Reference tissueWhite matterFH (H=+mm)4.208135Preset window contrastsoftFH (deg)0Reconstruction modeimmediateFH (deg)0Rardcopy protocolnoFH (deg)0Ringing filteringdefaultFH (deg)0		no	· · · · · · · · · · · · · · · · · · ·			
Dynamic studynoStack display ordernoArterial Spin labelingnoPANAlignnoPOST/PROCPCST/PROCREST slabs0Preparation phasesfullInteractive positioningnoInteractive F0noAllow table movementnoSENSE ref. scanyesOFFC/ANGSmartPlan surveynoStacks2B1 field mapnoStack Offc. AP11.5916Imagesno, no, no, noRE (L=+mm)-3.434925Autoview imagenoFH (H=+mm)4.208135Calculated imagesno, no, no, no, Ang. AP (deg)0Reference tissueWhite matterFH (deg)0Preset window contrastsoftFH (deg)0Ardcopy protocolnoFH (deg)0Hardcopy protocolnoFH (deg)0						
Arterial Spin labelingnoPlanAlignnoPOST/PROCREST slabs0Preparation phasesfullInteractive positioningnoInteractive F0noInteractive positioningnoSENSE ref. scanyesAllow table movementnoSmartPlan surveynoStacks2B0 field mapnoStack Offc. AP11.5916Ingagesno, no, no, no,Reference tissueWhite matterReference tissueWhite matterAllow table0Recorstruction modeimmediateFH (deg)0Save raw datanoFH (deg)0Hardcopy protocolnoFH (deg)0			· · ·			
POST/PROCREST stabs0Preparation phasesfullCatheter trackingnoInteractive F0noInteractive positioningnoSENSE ref. scanyesAllow table movementnoSmartPlan surveynoStacks2B0 field mapnoStacks2B1 field mapnoStacks Offc. AP11.5916Imagesno, no, no, noRL (L=+mm)-3.434925Autoview imagenoRL (L=+mm)4.208135Calculated imagesno, no, no, noRL (deg)0Reconstruction modeImmediateFH (deg)0Save raw datanoFH (deg)0Ringing filteringdefaultFH (deg)1						
Preparation phasesfullCatheter trackingnoInteractive F0noInteractive positioningnoSENSE ref. scanyesAllow table movementnoSmartPlan surveynoOFFC/ANGB0 field mapnoStacks2B1 field mapnoStack OffC. AP11.5916Imagesno, no, no, no,RL (L=+mm)-3.434925Calculated imagesno, no, no, no,All (deg)0Reference tissueWhite matterFH (H=+mm)4.208135Preset window contrastsoftFH (deg)0Redronstruction modeimmediateFH (deg)0Save raw datanoFH (deg)0Ringing filteringdefaultFH (deg)0			l	-		
Interactive PO no Interactive positioning no SENSE ref. scan yes SmartPlan survey no B0 field map no B1 field map no MIP/MPR no Images no, no, no, no, Calculated images no, no, no, no, Calculated images no, no, no, no, Reference tissue White matter Preset window contrast soft Save raw data no Hardcopy protocol no			<u> </u>			
SENSE ref. scan yes Allow table movement no SmartPlan survey no OFFC/ANG B0 field map no Stacks 2 B1 field map no Stack Offc. AP 11.5916 Images no, no, no, no Reference tissue White matter Preset window contrast soft FH (H=+mm) 4.208135 Reconstruction mode immediate FH (deg) 0 Bardcopy protocol no FH (deg) 0	<u> </u>			no		
SmartPlan survey no OFFC/ANG B0 field map no Stacks 2 B1 field map no current A MIP/MPR no Stack Offc. AP (P=+mm) 11.5916 Autoview image no, no, no, no RL (L=+mm) -3.434925 Calculated images no, no, no, no RL (L=+mm) 4.208135 Calculated images no, no, no, no Ang. AP (deg) 0 Reconstruction mode immediate FH (deg) 0 Save raw data no FH (deg) 0			Allow table movement	no		
B0 field map no Stacks 2 B1 field map no current A B1 field map no Stack Offc. AP 11.5916 Images no,		-	OFFC/A	NG		
B1 field map no current A MIP/MPR no Stack Offc. AP 11.5916 Images no, no, no, no Reference tissue Nuite matter RL (L=+mm) -3.434925 Calculated images no, no, no, no RL (L=+mm) -3.434925 FH (H=+mm) Reference tissue White matter FH (H=+mm) 4.208135 Ang. AP (deg) 0 Reconstruction mode immediate FH (deg) 0 FH (deg) 0 Save raw data no Hardcopy protocol no FH (deg) 0			Stacks	2		
MIP/MPR no 11.5916 Images no, no, no, no, no (P=+mm) 11.5916 Images no RL (L=+mm) -3.434925 Autoview image no FH (H=+mm) -3.434925 Calculated images no, no, no, no Ang. AP (deg) 0 Reference tissue White matter FH (H=+mm) 4.208135 Reconstruction mode immediate FH (deg) 0 Save raw data no FH (deg) 0 Hardcopy protocol no FH (deg) 0			current	A		
Images no, no, no, no, no, (r'=+mm) -3.434925 Autoview image no RL (L=+mm) -3.434925 Calculated images no, no, no, no RE (L=+mm) 4.208135 Calculated images no, no, no, no Reference tissue White matter Preset window contrast soft RL (deg) 0 Reconstruction mode immediate FH (deg) 0 Save raw data no Hardcopy protocol no Hinging filtering default default				11.5916		
Autoview image no RE (l=+lmin) -3.434923 Calculated images no, no, no, no, FH (H=+mm) 4.208135 Calculated images White matter RE (deg) 0 Preset window contrast soft FH (deg) 0 Reconstruction mode immediate Save raw data no Hardcopy protocol no Ringing filtering default			, · · · ·		ļ	
Calculated images no,	*					
Reference tissue White matter Preset window contrast soft Reconstruction mode immediate Save raw data no Hardcopy protocol no Ringing filtering default			FH (H=+mm)	4.208135		
Preset window contrast soft Rt (deg) 0 Reconstruction mode immediate Save raw data no Hardcopy protocol no Ringing filtering default	<u>v</u>		Ang. AP (deg)	0		
Reconstruction mode immediate Save raw data no Hardcopy protocol no Ringing filtering default				0		
Reconstruction mode Immediate Save raw data no Hardcopy protocol no Ringing filtering default			FH (deg)	0	1	
Hardcopy protocol no Ringing filtering default					å	
Ringing filtering default						
Elliptical k-space shutter default						
	Elliptical k-space shutter	default				

10/28/14	3:39 PM
----------	---------

INFO PAG	GE	GEOMET	RY	CONTRA	ST
Total scan duration	02:12.2	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	3D
Act. TR/TE (ms)	2.8 / 1.32	Coil selection 1	RX-Intf-1	technique	FFE
ACQ matrix M x P	204 x 204	Xmit Coil selection	MTX-Volume-	+ ZOOM	no
ACQ voxel MPS (mm)	1.25 / 1.25 /		T/R	Contrast enhancement	T1
	1.25	User def elem sel	no	Acquisition mode	cartesian
REC voxel MPS (mm)	1.14 / 1.14 /	element selection	All	Fast Imaging mode	TFE
. ,	1.25	connection	conn-A	3D non-selective	no
Scan percentage (%)	100	Coil selection 2	RX-Intf-2	shot mode	multishot
TFE shots	30	element selection	All	TFE factor	256
TFE dur. shot / acq (ms)	1669.4 / 716.5	Dual coil	yes	3D free factor	no
Min. TI delay	381.0045	CLEAR	yes	startup echoes	default
Act. WFS (pix) / BW	0.579 / 1750.7	body tuned	yes	+TFE followup echoes	0
(Hz)		FOV FH (mm)	256	shot interval	user defined
Min. WFS (pix) / Max.	0.575 / 1763.2	AP (mm)	256	(ms)	4500
3W (Hz)		RL (mm)	172.5	profile order	linear
RF avg power computed	0.8993402	Voxel size FH (mm)	1.25	1	
W)	22.04	AP (mm)	1.254902	turbo direction	radial no
SAR / head	< 33 %	RL (mm)	1.25	CENTRA (spiral)	
Whole body / level	0.0 W/kg / normal	RE (IIIII) Recon voxel size (mm)	1.142857	Echoes	1
D1			no	partial echo	no
B1 rms	0.76 uT 57 % / normal	Fold-over suppression Slice oversampling	default	shifted echo	no
PNS / level // VUIIS : dortch :	5/%/normal			TE	shortest
Sound Pressure Level	37.43258	RF select. FOS	no	Flip angle (deg)	7
(dB)	37.43258	Reconstruction matrix	224	TR	shortest
MOTION		SENSE	yes	Halfscan	no
Cardiac synchronization	no	P reduction (AP)	2	Water-fat shift	minimum
	no	P os factor	1	Shim	auto
Heart rate > 250 bpm		S reduction (RL)	2	mDIXON	no
Respiratory compensation	no	k-t BLAST	no	Fat suppression	no
Navigator respiratory	no	Overcontiguous slices	no	Water suppression	no
comp	10	Stacks	1	TFE prepulse	invert
Flow compensation	no	slices	138	slice selection	no
fMRI echo stabilisation	no	slice orientation	sagittal	delay	user defined
Motion smoothing	no	fold-over direction	AP	(ms)	1300
NSA	1	fat shift direction	F	PSIR	no
		Chunks	1	+inv pulse type	+B1 opt (lov
DYN/AN		PlanAlign	no		BW)
Angio / Contrast enh.	no	REST slabs	0	MTC	no
Quantitative flow	no	Catheter tracking	no	T2prep	no
CENTRA	no	Interactive positioning	no	Research prepulse	no
Manual start	no	Allow table movement	no	Diffusion mode	no
+ Abuse dynamic loop	no	OFFC/AN	1	Elastography mode	no
Dynamic study	no	Stacks	1	SAR mode	high
Arterial Spin labeling	no	Stack Offc. AP	11.5916	B1 mode	default
POST/PRO		(P=+mm)	11.3710	SAR Patient data	auto
Preparation phases	auto	RL (L=+mm)	-3.434925	PNS mode	low
Interactive F0	no	FH (H=+mm)	4.208135	Gradient mode	full control
SENSE ref. scan	no	Ang. AP (deg)	0	max strength	33
SmartPlan survey	no	RL (deg)	0	(mT/m)	33
B0 field map	no	FH (deg)	0	max slew rate	166
B1 field map	no			(T/m/s)	
MIP/MPR	no			L. ,	
Images	M, no, no, no	Î			
Autoview image	M	İ			
Calculated images	no, no, no, no				
Reference tissue	Grey matter				
Preset window contrast	soft				
Reconstruction mode	immediate				
Save raw data	no				
		ł			
Hardcopy protocol	no				
Ringing filtering	rectangular				
Geometry correction Elliptical k-space shutter	default				
	default	1			

1	0/	2	8/	14	13	:3	9	PM
---	----	---	----	----	----	----	---	----

		(13) 52:37.4 🖵 CEST_	interspersed_3u	09:09.6		
INFO PAG)E	GEOMETR	2Y	CONTRAST		
Total scan duration	09:09.6	Multi-transmit	no	Scan type	Imaging	
Rel. signal level (%)	100	Nucleus	H1	Scan mode	3D	
Act. TR/TE (ms)	65 / 7.2	Coil selection 1	RX-Intf-1	technique	FFE	
Dyn. scan time	00:08.579	Xmit Coil selection	MTX-Volume-	+ ZOOM	no	
Time to k0	00:04.7		T/R	Contrast	T1	
ACQ matrix M x P	160 x 148	User def elem sel	no	enhancement		
ACQ voxel MPS (mm)	1.50 / 1.62 /	element selection	All	Acquisition	cartesian	
	10.0	connection	conn-A	mode		
REC voxel MPS (mm)	0.94 / 0.94 /	Coil selection 2	RX-Intf-2	Fast Imaging	EPI	
	5.00	element selection	All	mode		
Scan percentage (%)	92.77109	Dual coil	yes	3D non-	no	
Act. WFS (pix) / BW	8.715 / 116.3	CLEAR	yes	selective		
(Hz)		body tuned	no	shot mode	multishot	
BW in EPI freq. dir. (Hz)	1230.8	FOV AP (mm)	240	EPI factor	7	
Min. WFS (pix) / Max.	8.664 / 117.0	RL (mm)	240	epi	Y	
BW (Hz)		FH (mm)	165	direction	1	
Min. TR/TE (ms)	54 / 5.9	Voxel size AP (mm)	1.5	Echoes	1	
511 111	1.351341	RL (mm)	1.5	partial	no	
(W)			5	echo		
SAR / head	< 49 %	FH (mm)		shifted echo	no	
Whole body / level	< 0.1 W/kg /	Recon voxel size (mm)	0.9375	TE	ucor dofined	
	normal	Fold-over suppression	no		user defined	
B1 rms	0.93 uT	Slice oversampling	default	(ms)	7.2	
PNS / level // VUIIS :	50 % / normal	RF select. FOS	no	Flip angle (deg)	5	
dortch :	05.04065	Reconstruction matrix	256	TR	user defined	
Sound Pressure Level	25.24222	SENSE	yes	(ms)	65	
(dB)		P reduction (RL)	2	Halfscan	no	
MOTION		P os factor	1	Water-fat shift	minimum	
Cardiac synchronization	no	S reduction (FH)	2	Shim	volume	
Heart rate > 250 bpm	no	k-t BLAST	no	ShimAlign	no	
Respiratory	no	Overcontiguous slices	yes	mDIXON	no	
compensation		Stacks	1	Fat suppression	ProSet	
Navigator respiratory	no	slices	33	pulse type	1331	
comp		slice orientation	transverse	Water	no	
Flow compensation	no	fold-over direction	RL	suppression		
fMRI echo stabilisation	no	fat shift direction	L	MTC	+pulsed qMT/CEST	
NSA	1	Chunks	1	+Duration	25	
DYN/AN	G	PlanAlign	no	(ms)		
Angio / Contrast enh.	no	REST slabs	0	+B1 Mode	constant	
Quantitative flow	no			+Amp	3	
Manual start	no	Catheter tracking	no	+B1 Units	max amp. (uT)	
+Abuse dynamic loop	no	Interactive positioning	no	+Pulses/TR	1	
Dynamic study	individual	Allow table movement	no	+Offset	file	
dyn scans	64	OFFC/AN	G	Mode		
recon multiplier	1	Stacks	1	+Offset	G:/patch/rf_offsets.txt	
dyn scan times	shortest	Stack Offc. AP	-5.532147	File		
FOV time mode	default	(P=+mm)		+Offset	ppm	
dummy scans	0	RL (L=+mm)	-3.434925	Units		
immediate	no	FH (H=+mm)	35.45897	+RF Shape	gauss_cest_mt	
subtraction	110	Ang. AP (deg)	0	Research	no	
fast next scan	no	RL (deg)	-5.457352	prepulse		
synch. ext. device	no	FH (deg)	0	Diffusion mode	no	
MTC	no	Shim Size AP (mm)	180.7495	Elastography	no	
dyn stabilization	no	RL (mm)	134.1432	mode		
	no	FH (mm)	114.2866	SAR mode	high	
prospect. motion corr.	110	Offc. AP (P=+mm)		B1 mode	default	
Keyhole	no	RL (L=+mm)	-3.660397	SAR Patient	auto	
Arterial Spin labeling	no	FH (H=+mm)	33.86363	data		
POST/PR		Ang. AP (deg)	2.26406	PNS mode	low	
		RL (deg)	-6.580403	Gradient mode	default	
Preparation phases	sameprep	FH (deg)	4.637685	SofTone mode	no	
Interactive F0	no					
SENSE ref. scan	no					
SmartPlan survey	no					
B0 field map	no					
B1 field map	no					
MIP/MPR	no					
Images	M, no, no, no					
Autoview image	Μ					
Calculated images	no, no, no, no					
Reference tissue	Grey matter					
EPI 2D phase correction	no					
Preset window contrast	soft					
Reconstruction mode	real time					
reuse memory						
	no					
Save raw data	no					
Save raw data Hardcopy protocol	no					
Save raw data Hardcopy protocol Ringing filtering	no rectangular					
Save raw data Hardcopy protocol Ringing filtering Geometry correction	no					

		(13) 52:37.4 🖵 CEST_	Reddy_GluCEST	11:37.0		
INFO PAGE		GEOMETR	RA KA	CONTRAST		
Total scan duration	11:37.0	Multi-transmit	no	Scan type	Imaging	
Rel. signal level (%)	100	Nucleus	H1	Scan mode	2D	
Act. TR/TE (ms)	5.6 / 2.7	Coil selection 1	RX-Intf-1	technique	FFE	
Dyn. scan time	00:13.909	Xmit Coil selection	MTX-Volume-	+ ZOOM	no	
Time to k0	00:08.6		T/R	Contrast enhancement	T1	
ACQ matrix M x P	128 x 126	User def elem sel	no	Acquisition mode	cartesian	
ACQ voxel MPS (mm)	1.88 / 1.90 /	element selection	All	Fast Imaging mode	TFE	
	10.0	connection	conn-A	shot mode	multishot	
REC voxel MPS (mm)	0.94 / 0.94 /	Coil selection 2	RX-Intf-2	TFE factor	3	
	10.0	element selection	All	startup echoes	default	
Scan percentage (%)	98.4375	Dual coil	yes	+TFE followup echoes	0	
TFE shots	42	CLEAR	yes	shot interval	shortest	
TFE dur. shot / acq (ms)	134.0 / 16.8	body tuned	no	profile order	low_high	
TFE shot interval (ms)	331.1945	FOV AP (mm)	240	Echoes	1	
Act. WFS (pix) / BW	0.700 / 1446.8	RL (mm)	240	partial echo	no	
(Hz)		Voxel size AP (mm)	1.87	· · ·		
Min. WFS (pix) / Max.	0.649 / 1562.5	RL (mm)	1.87	shifted echo TE	no user defined	
BW (Hz)		Slice thickness (mm)	10			
Min. TR/TE (ms)	4.0 / 1.36	Recon voxel size (mm)	0.9375	(ms)	2.7	
RF avg power computed	2.058919	· · ·		Flip angle (deg)	10	
(W)		Fold-over suppression	no	TR	user defined	
SAR / head	< 75 %	Reconstruction matrix	256	(ms)	5.6	
Whole body / level	< 0.1 W/kg /	SENSE	no	Halfscan	no	
	normal	k-t BLAST	no	Water-fat shift	minimum	
B1 rms	1.15 uT	Slice orientation	transverse	Shim	volume	
PNS / level // VUIIS :	31 % / normal	Fold-over direction	RL	ShimAlign	no	
dortch :		Fat shift direction	Р	mDIXON	no	
Sound Pressure Level	17.13024	PlanAlign	no	Fat suppression	no	
(dB)		REST slabs	0	Water suppression	no	
MOTION	l l	Catheter tracking	no	TFE prepulse	no	
Cardiac synchronization	no	Interactive positioning	no	MTC		
Heart rate > 250 bpm	no	Allow table movement	no	INITC	+pulsed qMT/CEST	
Respiratory	no	OFFC/AN		+Duration (ms)	10	
compensation			-			
Navigator respiratory	no	Slice Offc. AP (P=+mm)	-4.247866	+B1 Mode	constant	
comp			2 424025	+Amp	4.25	
Flow compensation	no	RL (L=+mm)	-3.434925	+B1 Units	max amp. (uT	
fMRI echo stabilisation	no	FH (H=+mm)	35.88707	+Pulses/TR	10	
Motion smoothing	no	Ang. AP (deg)	0	+Duty Cycle	0.9	
NSA	1	RL (deg)	-5.457352	+Offset Mode	baseline+rang	
DYN/AN		FH (deg)	0	+Min Offset	-5	
		Shim Size AP (mm)	180.7495	+Max Offset	5	
Angio / Contrast enh.	no	RL (mm)	134.1432	+Offset Units	ppm	
Quantitative flow	no	FH (mm)	106.6376	+RF Shape	gauss_cest_m	
Manual start	no	Offc. AP (P=+mm)	-1.87074	+ Interpulse	no	
+Abuse dynamic loop	no	RL (L=+mm)	-3.660397	Spoiling		
Dynamic study	individual	FH (H=+mm)	33.86363	T2prep	no	
dyn scans	50	Ang. AP (deg)	2.26406	Research prepulse	no	
recon multiplier	1	RL (deg)	-6.580403	Diffusion mode	no	
dyn scan times	shortest		4.637685	Elastography mode	no	
FOV time mode	default	FH (deg)	4.037065	SAR mode	moderate	
dummy scans	0					
immediate	no			B1 mode	default	
subtraction	-			SAR Patient data	auto	
fast next scan	no			PNS mode	low	
synch. ext. device	no			Gradient mode	default	
MTC	no			SofTone mode	no	
dyn stabilization	no					
prospect. motion	no					
corr.						
Keyhole	no					
Arterial Spin labeling	no					
POST/PRO						
Preparation phases						
Interactive F0	sameprep no					
SENSE ref. scan						
	no					
SmartPlan survey	no					
B0 field map	no					
B1 field map	no					
MIP/MPR	no					
Images	M, no, no, no					
Autoview image	M					
Calculated images	no, no, no, no					
Reference tissue	Grey matter					
Preset window contrast	soft					
Reconstruction mode	real time					
reuse memory	no					
Save raw data	no					
Llordoony protocol	no					
Hardcopy protocol						
Ringing filtering Geometry correction	rectangular default					

INFO PA		(13) 52:37.4 🕞 B1_Re GEOMETE		CONTRA	ST
Total scan duration	01:42.0	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	MS
Act. TR (ms)	6000	Coil selection 1	RX-Intf-1	technique	SE
Act. TE (ms)	12	Xmit Coil selection	MTX-Volume-	+ ZOOM	no
Dyn. scan time	00:48.000	ATTIL COIL SELECTION	T/R	Modified SE	no
ACQ matrix M x P	128 x 120	User def elem sel	no	+Optim ref/crush	no
ACQ voxel MPS (mm)	1.88 / 2.00 /	element selection	All	· ·	cartesian
ACQ VOXELIVIPS (mm)	10.0	connection	conn-A	Acquisition mode	
REC voxel MPS (mm)	0.94 / 0.94 /	Coil selection 2	RX-Intf-2	Fast Imaging mode	TSE
REC VOXELIVIPS (IIIII)	10.0	l		shot mode	multishot
Scan percentage (%)	93.75	element selection	All	TSE factor	15
	1	Dual coil	yes	startup echoes	0
Packages		CLEAR	no	+followup echoes	0
Min. slice gap (mm)	10	FOV AP (mm)	240	profile order	low_high
WFS (pix) / BW (Hz)	1.986 / 510.1	RL (mm)	240	DRIVE	no
TSE es / shot (ms)	12.0 / 180	FH (mm)	10	ultrashort	no
TEeff / TEequiv (ms)	12 / 12	Voxel size AP (mm)	1.87	strong FID	no
Min. TR (ms)	589	RL (mm)	1.87	crushing	110
RF avg power computed	0.2697158	Slice thickness (mm)	10	Echoes	1
(W)			0.9375		no
SAR / head	< 10 %	Recon voxel size (mm)		partial echo	
Whole body / level	0.0 W/kg /	Small FOV imaging	no	TE	user defined
whole body / level	normal	Fold-over suppression	no	(ms)	12
B1 rms	0.41 uT	Reconstruction matrix	256	Flip angle (deg)	60
PNS / level // VUIIS :	30 % / normal	SENSE	no	Refocusing control	no
dortch :	JU 707 HUITIAL	k-t BLAST	no	TR	user defined
Sound Pressure Level	16.02466	Stacks	1	(ms)	6000
Sound Pressure Level (dB)	10.02400	type	parallel	Halfscan	no
· /		slices	1	Water-fat shift	user defined
+Ref Pulse Shape			user defined	<u></u>	2
+Ref Pulse Dur [msec]		slice gap		(pixels)	
+Ref MAX Dephase		gap (mm)	0	Shim	volume
+Ref MIN Dephase		slice orientation	transverse	ShimAlign	no
+Crusher b value		fold-over direction	RL	mDIXON	no
ΜΟΤΙΟ	N	fat shift direction	Р	Fat suppression	no
Cardiac synchronization	no	Minimum number of	1	Water suppression	no
Heart rate > 250 bpm	no	packages		Grad. rev. offres. supp.	no
Respiratory	no	Slice scan order	default	BB pulse	no
compensation	110	PlanAlign	no	MTC	
		REST slabs	0	(<u> </u>	no
Navigator respiratory comp	no	Catheter tracking	no	T2prep	no
	no			Research prepulse	no
Flow compensation		Interactive positioning	no	Zoom imaging	no
Temporal slice spacing	default	Allow table movement	no	Diffusion mode	no
Motion smoothing	no	OFFC/AN	IG	Elastography mode	no
NSA	1	Stacks	1	SAR mode	high
DYN/AN	G	Stack Offc. AP	-4.247866	B1 mode	user defined
Manual start	no	(P=+mm)		amplitude (uT)	9.5
+Abuse dynamic loop	flip angle	RL (L=+mm)	-3.434925	SAR Patient data	auto
···	diminish	FH (H=+mm)	35.88707	PNS mode	
Dynamic study	individual	Ang. AP (deg)	0		high
dyn scans	2	RL (deg)	-5.457352	Gradient mode	default
<u> </u>	1			SofTone mode	no
recon multiplier		FH (deg)	0		
dyn scan times	shortest	Shim Size AP (mm)	180.7495		
FOV time mode	default	RL (mm)	134.1432		
dummy scans	0	FH (mm)	106.6376		
immediate	no	Offc. AP (P=+mm)	-1.87074		
subtraction		RL (L=+mm)	-3.660397	1	
fast next scan	no	FH (H=+mm)	33.86363		
synch. ext. device	no	Ang. AP (deg)	2.26406		
dyn stabilization	no	RL (deg)	-6.580403		
prospect. motion	no				
corr.		FH (deg)	4.637685		
Keyhole	no	İ			
Arterial Spin labeling	no				
	1				
POST/PR		ļ			
Preparation phases	sameprep				
Interactive F0	no	Į			
		1			
SENSE ref. scan	no				
	no				
SmartPlan survey	no	-			
SmartPlan survey B0 field map	no no	-			
SmartPlan survey B0 field map B1 field map	no no no	-			
SmartPlan survey B0 field map B1 field map MIP/MPR	no no no no	-			
SmartPlan survey B0 field map B1 field map MIP/MPR Images	no no no M, no, no, no	-			
SmartPlan survey B0 field map B1 field map MIP/MPR Images	no no no no	-			
SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images	no no no M, no, no, no	-			
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images	no no no M, no, no, no M no, no, no, no				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue	no no no M, no, no, no M no, no, no, no Grey matter				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast	no no no M, no, no, no M no, no, no, no Grey matter soft				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode	no no no M, no, no, no M no, no, no, no Grey matter soft real time				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview Image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory	no no no M, no, no, no M no, no, no, no Grey matter soft real time no				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory Save raw data	no no no M, no, no, no M no, no, no, no Grey matter soft real time				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory Save raw data	no no no M, no, no, no M no, no, no, no Grey matter soft real time no				
SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode	no no no M, no, no, no M no, no, no, no Grey matter soft real time no no				

🗀 Hospital (2) 🔲 201	41021 CEST fMRI	(13) 52:37.4 🕒 B0_Re	ddy_mulitecho 0	0:03.9		
INFO PAG	GE	GEOMETR	Y	CONTRAST		
Total scan duration	00:03.9	Multi-transmit	no	Scan type	Imaging	
Rel. signal level (%)	100	Nucleus	H1	Scan mode	2D	
Act. TR/TE1/delta TE	53 / 3.4 / 3.9	Coil selection 1	RX-Intf-1	technique	FFE	
(ms)		Xmit Coil selection	MTX-Volume-	+ ZOOM	no	
ACQ matrix M x P	128 x 128		T/R	Contrast enhancement	no	
ACQ voxel MPS (mm)	1.88 / 1.88 /	User def elem sel	no	Acquisition mode	cartesian	
	10.0	element selection	All	Fast Imaging mode	none	
REC voxel MPS (mm)	0.94 / 0.94 /	connection	conn-A	Echoes	4	
Scan percentage (%)	100	Coil selection 2	RX-Intf-2	partial echo	no	
Act. WFS (pix) / BW	2.824 / 358.8	element selection	All	shifted echo	no	
(Hz)	2.0217 000.0	Dual coil	yes	TE first	shortest	
Min. WFS (pix) / Max.	0.649 / 1562.5	CLEAR	yes	echospacing	shortest	
BW (Hz)		body tuned	no	flyback	yes	
RF avg power computed	2.058916	FOV AP (mm)	240	Flip angle (deg)	65	
(W)		RL (mm)	240	TR	shortest	
SAR / head	< 75 %	Voxel size AP (mm)	1.87	Halfscan	no	
Whole body / level	< 0.1 W/kg /	RL (mm)	1.875	Water-fat shift	maximum	
D1 rmc	normal 1.15 uT	Slice thickness (mm)	10	Shim	volume	
B1 rms		Recon voxel size (mm)	0.9375	ShimAlign	no	
PNS / level // VUIIS : dortch :	46 % / normal	Fold-over suppression	no	mDIXON	no	
Sound Pressure Level	21.87152	Reconstruction matrix	256	Fat suppression	no	
(dB)	21.07132	SENSE	yes	Water suppression	no	
мотіо	N	P reduction (RL)	2	MTC	no	
Cardiac synchronization	no	P os factor	1	Research prepulse	no	
Heart rate > 250 bpm	no	k-t BLAST	no	Diffusion mode	no	
Respiratory	no	Slice orientation	transverse	Elastography mode	no	
compensation		Fold-over direction	RL	SAR mode	moderate	
Navigator respiratory	no	Fat shift direction	Р	B1 mode	default	
comp		PlanAlign	no	SAR Patient data	auto	
Flow compensation	yes	REST slabs	0	PNS mode	low	
fMRI echo stabilisation	no	Catheter tracking	no	Gradient mode	default	
NSA	1	Interactive positioning	no	SofTone mode	no	
DYN/AN		Allow table movement	no			
Angio / Contrast enh.	no	OFFC/AN				
Quantitative flow	no	Slice Offc. AP (P=+mm)	-4.247866			
Manual start	no	RL (L=+mm)	-3.434925			
+Abuse dynamic loop	no	FH (H=+mm)	35.88707			
Dynamic study	no	Ang. AP (deg)	0			
Arterial Spin labeling	no	RL (deg)	-5.457352			
POST/PR		FH (deg)	-5.457352			
Preparation phases	sameprep	Shim Size AP (mm)	180.7495			
Interactive F0	no	RL (mm)	134.1432			
SENSE ref. scan	no	FH (mm)	106.6376			
SmartPlan survey	no	Offc. AP (P=+mm)	-1.87074			
B0 field map	no	RL (L=+mm)	-3.660397			
B1 field map	no	FH (H=+mm)	33.86363			
MIP/MPR	no	Ang. AP (deg)	2.26406			
Images	M, R, I, no	RL (deg)	-6.580403			
Autoview image	М	FH (deg)	4.637685	l		
Calculated images	no, no, no, no		4.037003	l		
Reference tissue	Grey matter					
Preset window contrast	soft	l				
Reconstruction mode	real time	l				
Save raw data	yes	l				
Hardcopy protocol	no					
Ringing filtering	rectangular					
Geometry correction	default					

		(13) 52:37.4 🖵 qMT H		11	
		GEOMETRY		CONTRAST	
Total scan duration	02:38.7	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	3D
Act. TR/TE (ms)	4.2 / 2.2	Coil selection 1	RX-Intf-1	technique	FFE
Dyn. scan time	00:11.251	Xmit Coil selection	MTX-Volume- T/R	+ ZOOM	no
Time to k0	00:07.0	Lloor dof alam cal	no	Contrast enhancement	T1
ACQ matrix M x P	212 x 210	User def elem sel		Acquisition mode	cartesian
ACQ voxel MPS (mm)	1.00 / 1.01 /	element selection	All conn-A	Fast Imaging mode	TFE
DEC yourd MDC (mm)	2.00	connection Coil selection 2	RX-Intf-2	3D non-selective	no
REC voxel MPS (mm)	2.00			shot mode	multishot
Scan percentage (%)	99.08257	element selection Dual coil	All	TFE factor	54
TFE shots	12	CLEAR	yes	3D free factor	no
TFE dur. shot / acq (ms)	233.8 / 225.8	1	yes	startup echoes	user defined
TFE shot interval (ms)	3353.226	body tuned	no	(number)	0
Act. WFS (pix) / BW	1.142 / 887.5	FOV AP (mm)	212	+TFE followup echoes	0
(Hz)	1.1427 007.5	RL (mm)	212	shot interval	shortest
Min. WFS (pix) / Max.	1.133 / 894.1	FH (mm)	10	profile order	low_high
BW (Hz)		Voxel size AP (mm)	1	turbo direction	Y
	1.347757	RL (mm)	1	Echoes	1
(W)		FH (mm)	2	partial echo	no
SAR / head	< 49 %	Recon voxel size (mm)	1	shifted echo	no
Whole body / level	< 0.1 W/kg /	Fold-over suppression	no	TE	shortest
	normal	Slice oversampling	default	Flip angle (deg)	15
B1 rms	0.93 uT	RF select. FOS	no	TR	shortest
PNS / level // VUIIS :	50 % / normal	Reconstruction matrix	224	Halfscan	no
dortch :		SENSE	yes	Water-fat shift	minimum
Sound Pressure Level	29.07384	P reduction (RL)	2	7	PB-volume
(dB)		P os factor	1	Shim	
MOTIO	N	S reduction (FH)	1	ShimAlign	no
Cardiac synchronization	no	k-t BLAST	no	mDIXON	no
Heart rate > 250 bpm	no	Overcontiguous slices	no	Fat suppression	no
Respiratory	no			Water suppression	no
compensation	110	Stacks	1	TFE prepulse	no
Navigator respiratory	no	slices	5	MTC	+SIR
comp		slice orientation	transverse	+pulse dur (ms)	5.5
Flow compensation	no	fold-over direction	RL	+pulse shape	BRASORF
fMRI echo stabilisation	no	fat shift direction	P	+offset (Hz)	0
Motion smoothing	no	Chunks	1	+spoil amp	20
NSA	1	PlanAlign	no	(mT/m)	
		REST slabs	0	+spoil dur (ms)	2
DYN/AN		Catheter tracking	no	+TFE Saturation	yes
Angio / Contrast enh.	no	Interactive positioning	no	+td Mode	constant
Quantitative flow	no	Allow table movement	no	+td (ms)	2500
CENTRA	no	OFFC/AN		+ti (ms)	6, 10, 16, 26,
Manual start	no	Stacks	1		42, 68, 110,
+ Abuse dynamic loop	no	Stack Offc. AP		-	178, 288, 468
Dynamic study	individual	(P=+mm)	-4.247866		760, 1233,
dyn scans	14	<u> </u>	-3.434925	-	2000, 8000,
recon multiplier	1	RL (L=+mm)		-	2000, 10000,
dyn scan times	shortest	FH (H=+mm)	35.88707		1000, 10000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000,
FOV time mode	default	Ang. AP (deg)	0	4	1000, 1000,
dummy scans	0	RL (deg)	-5.457352	4	1000, 1000,
immediate	no	FH (deg)	0	4	1000, 1000,
subtraction		Shim Size AP (mm)	180.7495	4	1000, 1000,
fast next scan	no	RL (mm)	134.1432	1	1000, 1000,
synch. ext. device	no	FH (mm)	106.6376		1000, 1000,
MTC	no	Offc. AP (P=+mm)	-1.87074		1000, 1000, 1000, 1000,
dyn stabilization		RL (L=+mm)	-3.660397		1000, 1000,
prospect. motion	no	FH (H=+mm)	33.86363	T	1000, 1000,
prospect. motion	no	Ang. AP (deg)	2.26406	1	1000, 1000,
Keyhole	no	RL (deg)	-6.580403	1	1000, 1000,
,	no	FH (deg)	4.637685	1	1000, 10000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000,
Arterial Spin labeling				-	1000, 1000, 1000,
	н.				1000, 1000,
POST/PRO		t		1	1000, 1000,
Preparation phases	auto				
Preparation phases Interactive F0	auto no	-			1000, 1000,
Preparation phases Interactive F0 SENSE ref. scan	auto no no	- - -			1000, 1000, 1000, 1000,
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey	auto no	- - - -			1000, 1000, 1000, 1000, 1000, 1000,
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey	auto no no	- - - -			1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000,
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map	auto no no no	-		T2prep	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map	auto no no no no	-		T2prep	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR	auto no no no no no	- - - -		Research prepulse	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no
Preparation phases Interactive FO SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images	auto no no no no no no	- - - - -		Research prepulse Diffusion mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image	auto no no no no M, R, I, no M	- - - - -		Research prepulse Diffusion mode Elastography mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no no
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images	auto no no no no M, R, I, no M no, no, no, no			Research prepulse Diffusion mode Elastography mode SAR mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue	auto no no no no M, R, I, no M no, no, no, no Grey matter			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high default
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast	auto no no no no M, R, I, no M no, no, no, no Grey matter soft			Research prepulse Diffusion mode Elastography mode SAR mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode	auto no no no no M, R, I, no M no, no, no, no Grey matter soft real time			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high default
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory	auto no no no no M, R, I, no M no, no, no Grey matter soft real time no			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode SAR Patient data	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no high default auto
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map B1 field map Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory Save raw data	auto no no no no no M, R, I, no M no, no, no, no Grey matter soft real time no no			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode SAR Patient data PNS mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no no high default auto high
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory Save raw data Hardcopy protocol	auto no no no no M, R, I, no M M, R, I, no M no, no, no, no Grey matter soft real time no no no			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode SAR Patient data PNS mode Gradient mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high default auto high default
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map B1 field map Calculated images Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory Save raw data	auto no no no no no M, R, I, no M no, no, no, no Grey matter soft real time no no			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode SAR Patient data PNS mode Gradient mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high default auto high default
Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue Preset window contrast Reconstruction mode reuse memory Save raw data Hardcopy protocol	auto no no no no M, R, I, no M M, R, I, no M no, no, no, no Grey matter soft real time no no no			Research prepulse Diffusion mode Elastography mode SAR mode B1 mode SAR Patient data PNS mode Gradient mode	1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000 no no no high default auto high default

🗀 Hospital (2) 💷 2014		11		11	
INFO PAGE		GEOMETRY		CONTRAST	
Total scan duration	08:34.0	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	MS
Act. TR/TE (ms)	2000 / 25	Coil selection 1	RX-Intf-1	technique	FFE
Dyn. scan time	00:02.000	Xmit Coil selection	MTX-Volume-	+ ZOOM	no
Time to k0	00:15.0		T/R	Contrast enhancement	no
ACQ matrix M x P	96 x 95	User def elem sel	no	Acquisition mode	cartesian
ACQ voxel MPS (mm)	2.50 / 2.50 /	element selection	All	Fast Imaging mode	EPI
	2.50	connection	conn-A	shot mode	single-shot
REC voxel MPS (mm)	2.50 / 2.50 /	Coil selection 2	RX-Intf-2	Echoes	1
	2.50	element selection	All	partial echo	no
Scan percentage (%)	100	Dual coil	yes	shifted echo	no
Packages	1	CLEAR	yes	TE	user defined
Min. slice gap (mm)	0	body tuned	yes	(ms)	25
EPI factor	37	FOV RL (mm)	240	Flip angle (deg)	63
Act. WFS (pix) / BW	21.825 / 46.4	AP (mm)	240		
(Hz)		FH (mm)	115	TR	user defined
BW in EPI freq. dir. (Hz)	2878.9	· · · ·		(ms)	2000
Min. WFS (pix) / Max.	21.770 / 46.5	Voxel size RL (mm)	2.5	Halfscan	no
3W (Hz)	21.7707 40.5	AP (mm)	2.5	Water-fat shift	minimum
Min. TR/TE (ms)	1999 / 12	Slice thickness (mm)	2.5	Shim	auto
RF avg power computed		Recon voxel size (mm)	2.5	mDIXON	no
(W)	1.371004	Fold-over suppression	no	Fat suppression	no
SAR / head	< 50 %	Reconstruction matrix	96	Water suppression	no
Whole body / level	< 0.1 W/kg /	SENSE	yes	MTC	no
whole body / level	< 0.1 W/Kg /	P reduction (AP)	2.8	Research prepulse	no
B1 rms	0.93 uT	P os factor	1	7 <u> </u>	
		k-t BLAST	no	Diffusion mode	no
PNS / level // VUIIS : dortch :	59 % / normal			Elastography mode	no
Sound Pressure Level	20.01457	Stacks	1	SAR mode	low
Sound Pressure Level (dB)	28.01657	type	parallel	B1 mode	default
, ,		slices	46	SAR Patient data	auto
MOTION	1	slice gap	user defined	PNS mode	low
Cardiac synchronization	no	gap (mm)	0	Gradient mode	full control
Heart rate > 250 bpm	no	slice orientation	transverse	max strength	33
Respiratory	no	fold-over direction	AP	(mT/m)	
compensation		fat shift direction	P	max slew rate	130
Navigator respiratory	no	Minimum number of	1	(T/m/s)	
comp		packages	'	<u> </u>	
Flow compensation	no	Slice scan order	default	1	
Temporal slice spacing	equidistant	PlanAlign	no	+	
fMRI echo stabilisation	no	1 	0	-	
NSA	1	REST slabs		-	
DYN/AN	G	Catheter tracking	no	-	
Angio / Contrast enh.	no	Interactive positioning	no	4	
Quantitative flow	no	Allow table movement	no	4	
Manual start	yes	OFFC/AN	1	1	
+Abuse dynamic loop	no	Stacks	1	1	
		Stack Offc. AP	-5.532147		
Dynamic study	individual	(P=+mm)			
dyn scans	250	RL (L=+mm)	-3.434925		
recon multiplier	1	FH (H=+mm)	35.45897	1	
dyn scan times	shortest	Ang. AP (deg)	0	1	
FOV/			-5.457352	1	
FOV time mode	default	RL (deg)			
FOV time mode dummy scans	default 5			1	
		RL (deg) FH (deg)	0	1	
dummy scans immediate	5				
dummy scans immediate	5				
dummy scans immediate subtraction fast next scan	5 no no			1	
dummy scans immediate subtraction fast next scan synch. ext. device	5 no no yes			1	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn.	5 no yes 1			1	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn)	5 no yes 1 119			1	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization	5 no yes 1 119 no			1	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion	5 no yes 1 119			1	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr.	5 no yes 1 119 no no]	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole	5 no yes 1 119 no no no			1	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling	5 no yes 1 119 no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRO	5 no yes 1 119 no no no no DC]	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRO	5 no yes 1 119 no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRO	5 no yes 1 119 no no no no DC				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0	5 no yes 1 119 no no no DC full]	
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRO Preparation phases Interactive FO SENSE ref. scan	5 no yes 1 119 no no no DC full no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion pror. Arterial Spin labeling POST/PRC Preparation phases Interactive FO SENSE ref. scan SmartPlan survey	5 no yes 1 119 no no no no DC full no no no no no no no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map	5 no yes 1 119 no no no DC full no no no no no no no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion orr. Keyhole Arterial Spin labeling POST/PR Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map	5 no yes 1 119 no no no no full no no OC full no no no no no no no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRO Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR	5 no yes 1 119 no no no DC full no no no no no no no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images	5 no yes 1 119 no no no no no no no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive FO SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image	5 no yes 1 119 no no no full no no no no no no no no M, no, no, no M				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive FO SENSE ref. scan SmartPlan survey B0 field map B1 field map MIP/MPR Images Autoview image	5 no yes 1 119 no no no no no no no no no no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SEMSE ref. scan SEMSE ref. scan SEMSTPIAn survey B0 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images	5 no yes 1 119 no no no full no no no no no no no no M, no, no, no M				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PR Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue	5 no yes 1 119 no no no no full no no OC full no no no no M, no, no, no M no, no, no, no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRO Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map B1 field map B1 field map B1 field map Reference tissue Reference tissue EPI 2D phase correction	5 no no yes 1 119 no no no no o C full no no no no M, no, no, no M no, no, no, no Grey matter no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling Arterial Spin labeling POST/PRC Preparation phases Interactive FO SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map B1 field map Calculated images Reference tissue EPI 2D phase correction Preset window contrast	5 no yes 1 119 no no no full no no no no no no no no M, no, no, no M, no, no, no Grey matter no soft				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue EPI 2D phase correction Preset window contrast Reconstruction mode	5 no yes 1 119 no no no no DC full no no no no no no no M, no, no, no M no, no, no M ro, no, no M ro, no, no M ro, no, no M ro, no, no M ro, no, no Soft real time				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive FO SENSE ref. scan SmartPlan survey B0 field map B1 fi	5 no yes 1 119 no no no no full no no no no no no M, no, no, no M no, no, no, no M no, no, no, no Soft real time no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue EPI 2D phase correction Preset window contrast Reconstruction mode reuse memory Save raw data	5 no yes 1 119 no no no no DC full no no no no no no no M, no, no, no M no, no, no M ro, no, no M ro, no, no M ro, no, no M ro, no, no M ro, no, no Soft real time				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue EPI 2D phase correction Preset window contrast Reconstruction mode reuse memory Save raw data	5 no yes 1 119 no no no no full no no no no no no M, no, no, no M no, no, no, no M no, no, no, no Soft real time no				
dummy scans immediate subtraction fast next scan synch. ext. device start at dyn. interval (dyn) dyn stabilization prospect. motion corr. Keyhole Arterial Spin labeling POST/PRC Preparation phases Interactive F0 SENSE ref. scan SmartPlan survey B0 field map B1 field map B1 field map MIP/MPR Images Autoview image Calculated images Reference tissue EPI 2D phase correction Preset window contrast Reconstruction mode	5 no yes 1 119 no no no no full no no no no no M, no, no, no M, no, no, no Grey matter no soft real time no no no				

Hospital (2) | 20141021 CEST fMRI (13) 52:37.4 | Grmri_TRAILMAKING 04:14.0

Hospital (2) 201		(13) 52:37.4 🖿 FMRI_		1.14.0	
INFO PAG		GEOMETR		CONTRA	
Total scan duration	04:14.0	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	MS
Act. TR/TE (ms)	2000 / 25	Coil selection 1	RX-Intf-1	technique	FFE
Dyn. scan time	00:02.000	Xmit Coil selection	MTX-Volume- T/R	+ ZOOM	no
Time to k0	00:15.0			Contrast enhancement	no
ACQ matrix M x P	96 x 95	User def elem sel	no	Acquisition mode	cartesian
ACQ voxel MPS (mm)	2.50 / 2.50 /	element selection	All	Fast Imaging mode	EPI
DEC	2.50	connection	conn-A	shot mode	single-shot
REC voxel MPS (mm)	2.50 / 2.50 / 2.50	Coil selection 2	RX-Intf-2	Echoes	1
Scan percentage (%)	100	element selection	All	partial echo	no
Packages	1	Dual coil CLEAR	yes	shifted echo	no
Min. slice gap (mm)	0		yes	TE	user defined
EPI factor	37	body tuned	yes	(ms)	25
Act. WFS (pix) / BW	21.825 / 46.4	FOV RL (mm)	240	Flip angle (deg)	63
(Hz)	21.0237 40.4	AP (mm)	240	TR	user defined
BW in EPI freq. dir. (Hz)	2878.9	FH (mm)	115	(ms)	2000
Min. WFS (pix) / Max.	21.770 / 46.5	Voxel size RL (mm)	2.5	Halfscan	no
3W (Hz)		AP (mm)	2.5	Water-fat shift	minimum
Min. TR/TE (ms)	1999 / 12	Slice thickness (mm)	2.5	Shim	auto
RF avg power computed	1.371604	Recon voxel size (mm)	2.5	mDIXON	no
(W)		Fold-over suppression	no	Fat suppression	no
SAR / head	< 50 %	Reconstruction matrix	96	Water suppression	no
Whole body / level	< 0.1 W/kg /	SENSE	yes	MTC	no
-	normal	P reduction (AP)	2.8	Research prepulse	no
B1 rms	0.93 uT	P os factor	1	Diffusion mode	no
PNS / level // VUIIS :	59 % / normal	k-t BLAST	no	Elastography mode	no
lortch :		Stacks	1	SAR mode	low
Sound Pressure Level	28.01657	type	parallel	B1 mode	default
dB)		slices	46	SAR Patient data	auto
MOTION	N	slice gap	user defined	PNS mode	low
Cardiac synchronization	no	gap (mm)	0		
Heart rate > 250 bpm	no	slice orientation	transverse	Gradient mode	full control
Respiratory	no	fold-over direction	AP	max strength	33
compensation				(mT/m)	120
Navigator respiratory	no	fat shift direction	P	max slew rate (T/m/s)	130
comp		Minimum number of	1	(1/11/5)	
Flow compensation	no	packages	ا م ا م ا		
Temporal slice spacing	equidistant	Slice scan order	default		
fMRI echo stabilisation	no	PlanAlign	no		
NSA	1	REST slabs	0		
DYN/AN		Catheter tracking	no		
		Interactive positioning	no		
Angio / Contrast enh.	no	Allow table movement	no		
Quantitative flow	no	OFFC/AN	IG		
Manual start	yes	Stacks	1		
+Abuse dynamic loop	no	Stack Offc. AP	-5.532147		
Dynamic study	individual	(P=+mm)			
dyn scans	120	RL (L=+mm)	-3.434925		
recon multiplier	1	FH (H=+mm)	35.45897		
dyn scan times	shortest	Ang. AP (deg)	0		
FOV time mode	default	RL (deg)	-5.457352		
dummy scans	5	FH (deg)	0		
immediate	no		l ~	l	
subtraction					
fast next scan	no				
synch. ext. device	yes				
start at dyn.	1	1			
interval (dyn)	119				
dyn stabilization	no				
prospect. motion	no				
orr.					
Keyhole	no				
Arterial Spin labeling	no				
POST/PR					
Preparation phases	full				
Interactive F0	no				
	no				
SENSE ref. scan					
SmartPlan survey	no				
B0 field map	no				
B1 field map	no				
MIP/MPR	no				
Images	M, no, no, no				
Autoview image	M				
Calculated images	no, no, no, no				
Reference tissue	Grey matter				
EPI 2D phase correction					
Preset window contrast	soft				
	real time				
Reconstruction mode					
Reconstruction mode reuse memory	no				
Reconstruction mode reuse memory Save raw data	no no				
Reconstruction mode reuse memory Save raw data Hardcopy protocol	no no no	- - -			
Reconstruction mode	no no	· · ·			

Hospital (2) 20141021 CEST fMRI		GEOMETRY		CONTRA	ST
Total scan duration	08:30.0	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	MS
Act. TR/TE (ms)	2500 / 25	Coil selection 1	RX-Intf-1	technique	FFE
Dyn. scan time	00:02.500	Xmit Coil selection	MTX-Volume-	+ ZOOM	no
Time to k0	00:18.7	•	T/R	Contrast enhancement	no
ACQ matrix M x P	96 x 95	User def elem sel	no	Acquisition mode	cartesian
ACQ voxel MPS (mm)	2.50 / 2.50 /	element selection	All	Fast Imaging mode	EPI
	2.50	connection	conn-A	shot mode	single-shot
REC voxel MPS (mm)	2.50 / 2.50 /	Coil selection 2	RX-Intf-2	Echoes	1
	2.50	element selection	All	partial echo	no
Scan percentage (%)	100	Dual coil	yes	shifted echo	no
Packages	1	CLEAR	yes	TE	user defined
Min. slice gap (mm)	0	body tuned	yes	(ms)	25
EPI factor	37	FOV RL (mm)	240	Flip angle (deg)	63
Act. WFS (pix) / BW	21.825 / 46.4	AP (mm)	240	TR	user defined
(Hz)		FH (mm)	115	(ms)	2500
BW in EPI freq. dir. (Hz)	2878.9	Voxel size RL (mm)	2.5	Halfscan	no
Min. WFS (pix) / Max.	21.770 / 46.5	AP (mm)	2.5	Water-fat shift	minimum
BW (Hz)		Slice thickness (mm)	2.5	74	
Min. TR/TE (ms)	1999 / 12	Recon voxel size (mm)	2.5	Shim	auto
RF avg power computed	1.097284			mDIXON	no
(W)		Fold-over suppression	no	Fat suppression	no
SAR / head	< 40 %	Reconstruction matrix	96	Water suppression	no
Whole body / level	< 0.1 W/kg /	SENSE	yes	MTC	no
	normal	P reduction (AP)	2.8	Research prepulse	no
B1 rms	0.84 uT	P os factor	1	Diffusion mode	no
PNS / level // VUIIS :	59 % / normal	k-t BLAST	no	Elastography mode	no
dortch :		Stacks	1	SAR mode	low
Sound Pressure Level	27.13099	type	parallel	B1 mode	default
(dB)		slices	46	SAR Patient data	auto
MOTIO		slice gap	user defined	PNS mode	low
Cardiac synchronization	no	gap (mm)	0	Gradient mode	full control
Heart rate > 250 bpm	no	slice orientation	transverse	max strength	33
Respiratory	no	fold-over direction	AP	(mT/m)	
compensation		fat shift direction	Р	max slew rate	130
Navigator respiratory	no	Minimum number of	1	(T/m/s)	
comp		packages		· · · · ·	
Flow compensation	no	Slice scan order	default	1	
Temporal slice spacing	equidistant	PlanAlign	no	1	
fMRI echo stabilisation	no	REST slabs	0	1	
NSA	1	Catheter tracking	no	-	
DYN/AN	G	Interactive positioning	no	-	
Angio / Contrast enh.	no	Allow table movement	no	-	
Quantitative flow	no			-	
Manual start	yes	OFFC/AN		-	
+Abuse dynamic loop	no	Stacks	1	-	
Dynamic study	individual	Stack Offc. AP	-5.532147		
dyn scans	197	(P=+mm)	2 424025	-	
recon multiplier	1	RL (L=+mm)	-3.434925	+	
dyn scan times	shortest	FH (H=+mm)	35.45897	+	
FOV time mode	default	Ang. AP (deg)	0	4	
	derault 5	RL (deg)	-5.457352	4	
dummy scans		FH (deg)	0]	
immediate subtraction	no				
fast next scan	no	-			
	no				
synch. ext. device	yes				
start at dyn.	1	-			
interval (dyn)	119				
dyn stabilization	no				
prospect. motion	no				
corr.					
Keyhole	no				
Arterial Spin labeling	no				
POST/PR		Ļ			
Preparation phases	full	ļ			
Interactive F0	no				
SENSE ref. scan	no				
SmartPlan survey	no				
B0 field map	no				
B1 field map	no	Ī			
MIP/MPR	no	İ			
Images	M, no, no, no	-			
Autoview image	M, 110, 110, 110				
Calculated images	no, no, no, no				
-		l			
Reference tissue	Grey matter				
EPI 2D phase correction	no				
Preset window contrast	soft	ļ			
Reconstruction mode	real time				
reuse memory	no				
Save raw data	no	ļ			
Hardcopy protocol	no				
Ringing filtering Geometry correction	default default	ĺ			

🗀 Hospital (2) 💷 201	41021 CEST fMRI	(13) 52:37.4 🖵 T1_3[_TFE_quantGeo	00:55.7	
INFO PAGE		GEOMETR	۲Y	CONTRA	sт
Total scan duration	00:55.7	Multi-transmit	no	Scan type	Imaging
Rel. signal level (%)	100	Nucleus	H1	Scan mode	3D
Act. TR/TE (ms)	2.8 / 1.44	Coil selection 1	RX-Intf-1	technique	FFE
ACQ matrix M x P	192 x 190	Xmit Coil selection	MTX-Volume-	+ ZOOM	no
ACQ voxel MPS (mm)	1.25 / 1.26 /		T/R	Contrast enhancement	T1
	2.50	User def elem sel	no	Acquisition mode	cartesian
REC voxel MPS (mm)	0.94 / 0.94 /	element selection	All	Fast Imaging mode	TFE
0 1 (01)	2.50	connection	conn-A	3D non-selective	no
Scan percentage (%)	98.9899	Coil selection 2	RX-Intf-2	shot mode	multishot
TFE shots	13	element selection	All	TFE factor	256
TFE dur. shot / acq (ms)	-	Dual coil	yes	3D free factor	no
Min. TI delay	386.7124	CLEAR	yes	startup echoes	default
Act. WFS (pix) / BW (Hz)	0.778 / 1302.1	body tuned	yes	+TFE followup echoes	0
Min. WFS (pix) / Max.	0.774 / 1308.4	FOV RL (mm)	240	shot interval	user defined
BW (Hz)	0.7747 1300.4	AP (mm)	240	(ms)	4500
RF avg power computed	0.8993402	FH (mm)	165	profile order	linear
(W)	0.0770102	Voxel size RL (mm)	1.25	turbo direction	radial
SAR / head	< 33 %	AP (mm)	1.254902	CENTRA (spiral)	no
Whole body / level	0.0 W/kg /	FH (mm)	2.5	Echoes	1
	normal	Recon voxel size (mm)	0.94	partial echo	no
B1 rms	0.76 uT	Fold-over suppression	no	shifted echo	no
PNS / level // VUIIS :	59 % / normal	Slice oversampling	default	TE	shortest
dortch :		RF select. FOS	no	Flip angle (deg)	7
Sound Pressure Level	29.78219	Reconstruction matrix	256	TR	shortest
(dB)		SENSE	yes	Halfscan	no
MOTIO	N	P reduction (AP)	2	Water-fat shift	minimum
Cardiac synchronization	no	P os factor	1	Shim	auto
Heart rate > 250 bpm	no	S reduction (FH)	2	mDIXON	no
Respiratory	no	k-t BLAST	no	Fat suppression	no
compensation		Overcontiguous slices	no	Water suppression	no
Navigator respiratory	no	Stacks	1	TFE prepulse	invert
comp		slices	66	slice selection	no
Flow compensation	no	slice orientation	transverse	(user defined
fMRI echo stabilisation	no	fold-over direction	AP	delay (ms)	1300
Motion smoothing	no	fat shift direction	L	PSIR	
NSA	1	Chunks	1		no
DYN/AN		PlanAlign	no	+inv pulse type	+B1 opt (low BW)
Angio / Contrast enh.	no	REST slabs	0	мтс	no
Quantitative flow	no	Catheter tracking	no	T2prep	no
CENTRA	no	Interactive positioning	no	Research prepulse	no
Manual start	no	Allow table movement	no	Diffusion mode	no
+Abuse dynamic loop	no			Elastography mode	no
Dynamic study	no	OFFC/AN	1	<u> </u>	
Arterial Spin labeling	no	Stacks	1	SAR mode	high
POST/PR	oc	Stack Offc. AP (P=+mm)	-4.247866	B1 mode	default
Preparation phases	auto	(P = +mm) RL (L=+mm)	-3.434925	SAR Patient data	auto
Interactive F0	no	FH (H=+mm)	35.88707	PNS mode	low
SENSE ref. scan	no	Ang. AP (deg)	0	Gradient mode	full control
SmartPlan survey	no		-5.457352	max strength (mT/m)	33
B0 field map	no	RL (deg)	-5.457352	max slew rate	166
B1 field map	no	FH (deg)	v	(T/m/s)	1.00
MIP/MPR	no			<u>x · · · · · · · · · · · · · · · · · · ·</u>	
Images	M, no, no, no				
Autoview image	M				
Calculated images	no, no, no, no				
Reference tissue	Grey matter				
Preset window contrast	soft				
Reconstruction mode	immediate				
Save raw data	no				
Hardcopy protocol	no	,			
Ringing filtering	rectangular				
000	default				
Geometry correction					
Elliptical k-space shutter	default				

🗀 Hospital (2) 💷 201	41021 CEST fMRI	(13) 52:37.4 🖵 T2star	_multiEcho 01:02	2.7		
INFO PA	GE	GEOMETR	Y	CONTRAST		
Total scan duration 01:02.7		Multi-transmit	no	Scan type	Imaging	
Rel. signal level (%)	100	Nucleus	H1	Scan mode	3D	
Act. TR/TE1/delta TE	34 / 3.3 / 3.2	Coil selection 1	RX-Intf-1	technique	FFE	
(ms)		Xmit Coil selection	MTX-Volume-	loop order	zy_order	
ACQ matrix M x P	240 x 240		T/R	+ ZOOM	no	
ACQ voxel MPS (mm)	1.00 / 1.00 /	User def elem sel	no	Contrast enhancement	T1	
	5.00	element selection	All	Acquisition mode	cartesian	
REC voxel MPS (mm)	0.94 / 0.94 / 5.00	connection	conn-A	Fast Imaging mode	none	
C		Coil selection 2	RX-Intf-2	3D non-selective	no	
Scan percentage (%) Act. WFS (pix) / BW	100	element selection	All	Echoes	10	
(Hz)	1.418 / 714.8	Dual coil	yes	partial echo	no	
Min. WFS (pix) / Max.	1.125 / 900.9	CLEAR	yes	shifted echo	no	
BW (Hz)	1.1237 700.7	body tuned	yes	TE first	shortest	
RF avg power computed	0.1353424	FOV AP (mm)	240	echospacing	shortest	
(W)		RL (mm)	240	flyback	yes	
SAR / head	< 5 %	FH (mm)	60	Flip angle (deg)	8	
Whole body / level	0.0 W/kg /	Voxel size AP (mm)	1	TR	shortest	
	normal	RL (mm)	1	Halfscan	no	
B1 rms	0.29 uT	FH (mm)	5	Water-fat shift	user defined	
PNS / level // VUIIS :	60 % / normal	Recon voxel size (mm)	0.9375	(pixels)	1.4	
dortch :		Fold-over suppression	no	Shim	PB-volume	
Sound Pressure Level	29.7646	Slice oversampling	default	ShimAlign	no	
(dB)		RF select. FOS	no	mDIXON	no	
MOTIO	1	Reconstruction matrix	256	Fat suppression	no	
Cardiac synchronization	no	SENSE	yes	Water suppression	no	
Heart rate > 250 bpm	no	P reduction (RL)	2	MTC	no	
Respiratory	no	P os factor	1	Research prepulse	no	
compensation		S reduction (FH)	1	Diffusion mode	no	
Navigator respiratory comp	no	k-t BLAST	no	Elastography mode	no	
Flow compensation	yes	Overcontiguous slices	no	SAR mode	low	
fMRI echo stabilisation	no	Stacks	1	B1 mode	default	
NSA	1	slices	12	SAR Patient data	auto	
	1.5	slice orientation	transverse	PNS mode	low	
DYN/AN	-	fold-over direction	RL	Gradient mode		
Angio / Contrast enh.	inflow	fat shift direction	P	1	maximum	
Quantitative flow	no	Chunks	1	SofTone mode	no	
Tone pulse	no	PlanAlign	no			
Manual start	no	REST slabs	0			
+Abuse dynamic loop	no	Catheter tracking	no			
Dynamic study	no	Interactive positioning	no			
Arterial Spin labeling	no	Allow table movement	no			
POST/PR		OFFC/AN	1			
Preparation phases	auto	Stacks	1			
Interactive F0	no	Stack Offc. AP	-5.532147			
SENSE ref. scan	no	(P=+mm)	-3.332147			
SmartPlan survey	no	RL (L=+mm)	-3.434925	1		
B0 field map	no	FH (H=+mm)	35.45897	1		
B1 field map	no	Ang. AP (deg)	0			
MIP/MPR	no	RL (deg)	-5.457352	1		
Images	M, R, I, no	FH (deg)	0	1		
			-			
Autoview image	M		180.7495			
Calculated images	T2, no, no, no	Shim Size AP (mm)	180.7495 134.1432			
Calculated images T2* clipvalue (ms)	T2, no, no, no 100	Shim Size AP (mm) RL (mm)	134.1432	-		
Calculated images T2* clipvalue (ms) Reference tissue	T2, no, no, no 100 Grey matter	Shim Size AP (mm) RL (mm) FH (mm)	134.1432 114.2866	_ - -		
Calculated images T2* clipvalue (ms) Reference tissue Preset window contrast	T2, no, no, no 100 Grey matter soft	Shim Size AP (mm) RL (mm) FH (mm) Offc. AP (P=+mm)	134.1432 114.2866 -1.87074	- - -		
Calculated images T2* clipvalue (ms) Reference tissue Preset window contrast Reconstruction mode	T2, no, no, no 100 Grey matter soft immediate	Shim Size AP (mm) RL (mm) FH (mm) Offc. AP (P=+mm) RL (L=+mm)	134.1432 114.2866 -1.87074 -3.660397			
Calculated images T2* clipvalue (ms) Reference tissue Preset window contrast Reconstruction mode Save raw data	T2, no, no, no 100 Grey matter soft immediate no	Shim Size AP (mm) RL (mm) FH (mm) Offc. AP (P=+mm) RL (L=+mm) FH (H=+mm)	134.1432 114.2866 -1.87074 -3.660397 33.86363			
Calculated images T2* clipvalue (ms) Reference tissue Preset window contrast Reconstruction mode Save raw data Hardcopy protocol	T2, no, no, no 100 Grey matter soft immediate no no	Shim Size AP (mm) RL (mm) FH (mm) Offc. AP (P=+mm) RL (L=+mm) FH (H=+mm) Ang. AP (deg)	134.1432 114.2866 -1.87074 -3.660397 33.86363 2.26406	- - - - -		
Calculated images T2* clipvalue (ms) Reference tissue Preset window contrast Reconstruction mode Save raw data Hardcopy protocol Ringing filtering	T2, no, no, no 100 Grey matter soft immediate no no default	Shim Size AP (mm) RL (mm) FH (mm) Offc. AP (P=+mm) RL (L=+mm) FH (H=+mm) Ang. AP (deg)	134.1432 114.2866 -1.87074 -3.660397 33.86363 2.26406 -6.580403	- - - - -		
Calculated images T2* clipvalue (ms) Reference tissue Preset window contrast Reconstruction mode Save raw data Hardcopy protocol	T2, no, no, no 100 Grey matter soft immediate no default default	Shim Size AP (mm) RL (mm) FH (mm) Offc. AP (P=+mm) RL (L=+mm) FH (H=+mm) Ang. AP (deg)	134.1432 114.2866 -1.87074 -3.660397 33.86363 2.26406	-		

Appendix 2

Exam Card



Viewing Environment



Appendix 3

Contents lists available at SciVerse ScienceDirect

NeuroImage



journal homepage: www.elsevier.com/locate/ynimg

Quantitative magnetization transfer imaging of human brain at 7 T

Richard D. Dortch ^{a,b,*}, Jay Moore ^{a,b}, Ke Li ^{a,b}, Marcin Jankiewicz ^{a,b}, Daniel F. Gochberg ^{a,b,c}, Jane A. Hirtle ^b, John C. Gore ^{a,b,c,d,e}, Seth A. Smith ^{a,b,d}

^a Department of Radiology and Radiological Sciences, Vanderbilt University, Nashville, TN, USA

^b Vanderbilt University Institute of Imaging Science, Vanderbilt University, Nashville, TN, USA

^c Department of Physics and Astronomy, Vanderbilt University, Nashville, TN, USA

^d Department of Biomedical Engineering, Vanderbilt University, Nashville, TN, USA

^e Department of Molecular Physiology and Biophysics, Vanderbilt University, Nashville, TN, USA

article info

Article history: Accepted 18 August 2012 Available online 23 August 2012

Keywords: Magnetization transfer 7 T White matter Myelin Brain Multiple sclerosis

abstract

Quantitative magnetization transfer (qMT) imaging yields indices describing the interactions between free water protons and immobile macromolecular protons. These indices include the macromolecular to free pool size ratio (PSR), which has been shown to be correlated with myelin content in white matter. Because of the long scan times required for whole-brain imaging (\approx 20–30 min), gMT studies of the human brain have not found widespread application. Herein, we investigated whether the increased signal-to-noise ratio available at 7.0 T could be used to reduce qMT scan times. More specifically, we developed a selective inversion recovery (SIR) qMT imaging protocol with a i) novel transmit radiofrequency (B_1^L) and static field (B_0) insensitive inversion pulse, ii) turbo field-echo readout, and iii) reduced TR. In vivo qMT data were obtained in the brains of healthy volunteers at 7.0 T using the resulting protocol (scan time \approx 40 s/slice, resolution = 2 × 2 × 3 mm³). Reliability was also assessed in repeated acquisitions. The results of this study demonstrate that SIR qMT imaging can be reliably performed within the radiofrequency power restrictions present at 7.0 T, even in the presence of large β^+ and β inhomogeneities. Consistent with qMT studies at lower field strengths, the observed PSR values were higher in white matter (mean \pm SD = 17.6 \pm 1.3%) relative to gray matter (10.3 \pm 1.6%) at 7.0 T. In addition, regional variations in PSR were observed in white matter. Together, these results suggest that qMT measurements are feasible at 7.0 T and may eventually allow for the high-resolution assessment of changes in composition throughout the normal and diseased human brain in vivo

© 2012 Elsevier Inc. All rights reserved.

Introduction

In addition to the free water protons typically observed in magnetic resonance imaging (MRI), there are protons residing on immobile macromolecules in tissue (Wolff and Balaban, 1989). Typical imaging sequences do not directly detect this pool of protons because they exhibit very short transverse relaxation times (≈ 10 Js) and, therefore, lose coherence before their signal can be captured. This macromolecule proton pool can, however, be indirectly detected by exploiting its interactions with the free water pool via chemical exchange and/or dipolar mechanisms [referred to together as the magnetization transfer (MT) effect]. Previous phantom studies (Koenig, 1991; Kucharczyk et al., 1994) have shown that the bulk of the MT effect in white matter (WM) arises from myelin-associated lipids, which suggests that MT contrast may be

a more specific marker for myelin pathology than conventional imaging methods. As a result, there is considerable interest in exploiting MT contrast to assay changes in myelination associated with a number of diseases [e.g., multiple sclerosis (Catalaa et al., 2000; Filippi and Rocca, 2004; Gass et al., 1994; Kalkers et al., 2001) and neuropsychiatric diseases (Bruno et al., 2004; Kabani et al., 2002a, 2002b)].

MT contrast can be generated by applying an off-resonance radiofrequency (RF) prepulse to selectively saturate the spectrally broad macromolecular proton pool (Wolff and Balaban, 1989). This saturation then transfers to the free water proton pool via MT, resulting in a decrease in the observed free water signal. The magnitude of this effect can be characterized by a semi-quantitative metric known as the magnetization transfer ratio (Dousset et al., 1992): $MTR = 1 - S_{sat}/S_0$, where S_{sat} and S_0 are the observed signal intensities with and without the application of an MT saturation prepulse, respectively. Although the MTR has been shown to correlate with myelin content (Odrobina et al., 2005; Schmierer et al., 2004), it is also sensitive to the choice of experimental parameters such as RF power (Berry et al., 1999) as well as non-MT-specific NMR parameters such as tissue relaxation times (Henkelman et al., 1993). As a result, quantitative MT (gMT) approaches have been developed. These gMT approaches



Grant sponsors: NIH K01 EB009120 (SAS), NIH T32 EB001628 (JCG), NIH EB00461 (JCG), and Vanderbilt Bridge Funding (DFG).

^{*} Corresponding author at: Vanderbilt University Institute of Imaging Science, AA-1101 Medical Center North, 1161 21st Avenue South, Nashville, TN 37232-2310, USA. Fax: +1 615 322 0734.

E-mail address: richard.dortch@vanderbilt.edu (R.D. Dortch).

^{1053-8119/\$ -} see front matter © 2012 Elsevier Inc. All rights reserved. http://dx.doi.org/10.1016/j.neuroimage.2012.08.047

quantify distinct tissue characteristics (e.g., the size of the macromolecular pool, rate of MT exchange) rather than the combined effect of multiple tissue and/or acquisition parameters. As such, qMT measures are thought to yield more specific information on tissue composition than the MTR.

Pulsed saturation qMT imaging (Graham and Henkelman, 1997; Pike, 1996; Sled and Pike, 2000, 2001) has received considerable attention for application in humans in vivo because it allows for the rapid collection of qMT data within the hardware constraints of most clinical systems. This approach involves a steady-state, spoiled gradient-echo acquisition interleaved with an MT-preparation pulse. By collecting images over a range of MT pulse offset frequencies and/or powers and fitting the resulting data to a two-pool model of the MT effect, one can extract parameters such as the macromolecular to free pool size ratio (PSR) and the rate of MT exchange. Previous work has shown that the PSR is correlated with myelin content (Odrobina et al., 2005; Ou et al., 2009; Schmierer et al., 2007; Underhill et al., 2011). The relationship between the rate of MT exchange and underlying tissue composition is less clear; however, previous work has suggested that the rate of MT exchange may reflect changes within the myelin lipid structure (Smith et al., 2009).

Unfortunately, qMT imaging has not found widespread application in practice. This can be attributed in part to the long scan times (\approx 20–30 min for whole-brain imaging) required to collect images at multiple offset frequencies and/or powers. The number of total images required can be reduced by designing optimal sampling strategies (Cercignani and Alexander, 2006; Levesque et al., 2011) or by fixing certain model parameters in the fitting procedure (Underhill et al., 2009, 2011). Potentially more efficient strategies based upon steady-state free-precession (SSFP) sequences (Garcia et al., 2010; Gloor et al., 2008) may also be employed.

As an alternative, or perhaps in combination with these strategies, one could translate qMT imaging approaches to higher field strengths. The resulting increase in SNR could then be used to obtain more reliable estimates of MT parameters or traded to reduce scan times and/or increase resolution. To date, qMT studies in humans in vivo have been primarily limited to 1.5 and 3.0 T and we are aware of only one report (Mougin et al., 2010) of MT parameters in the human brain in vivo at 7.0 T. The translation of pulsed saturation approaches to 7.0 T faces two primary challenges: i) RF power limitations [e.g., specific absorption ratio (SAR) limitations] and ii) transmit RF (B_{+}^{+}) and static magnetic field (B_{0}) inhomogeneities. SSFP-based approaches may also be limited at high field by banding artifacts associated with B_{0} inhomogeneities. In contrast, selective inversion recovery (SIR) qMT

imaging (Edzes and Samulski, 1977; Gochberg et al., 1997), which is based upon measuring the biexponential recovery of the free water pool in the presence of MT after an on-resonance inversion pulse, has been suggested (Dortch et al., 2011) to be less sensitive to these issues. Note that this approach is similar to the stimulated echo approach proposed by Ropele et al. (2003); therefore, both approaches may be well suited for qMT imaging at 7.0 T.

In this study, we have investigated the feasibility of using the SIR approach for high field qMT imaging of the human brain. More specifically, we have translated our previously published 3.0-T SIR protocol (Dortch et al., 2011) to 7.0 T with two significant modifications. First, we incorporated a novel B₁⁺- and !1B₀-insensitive composite inversion pulse to ensure a more uniform inversion of the free water pool over the whole brain. Second, we transitioned from a turbo-spin echo readout (TSE) to a turbo field-echo readout (TFE)—similar to an MP-RAGE sequence (Mugler and Brookeman, 1990)—as the former is susceptible to B₁⁺-related artifacts (due to imperfect refocusing) and is SAR-limited at high field. The TFE readout has the added benefit of covering k-space more efficiently than the TSE readout, which, in combination with some additional protocol optimization, allowed us to transition from a single-slice approach at 3.0 T to a whole-brain approach at 7.0 T (\approx 40 s/slice at 2.0 × 2.0 × 3.0 mm³ resolution). Using

641

this protocol, in vivo qMT data were obtained in the brains of 13 healthy volunteers at 7.0 T. To assess the reproducibility of the technique, six of the healthy volunteers were scanned twice. Additional numerical simulations were performed to determine the effect of TFE readout on our qMT parameter maps.

Theory

Consider free water (f) and macromolecular (m) proton pools between which MT can occur. Define unique equilibrium magnetizations (M_{0f} and M_{0m}), spin–lattice relaxation rates (R_{1f} and R_{1m}), and spin–spin relaxation rates (R_{2f} and R_{2m}) for each pool as well as an MT rate from the macromolecular to the free pool (k_{mf})—the rate in the other direction can be determined from $k_{fm} = k_{mf}M_{0m}/M_{0f}$. Assume MT of transverse magnetization to be negligible because of the short T_2 of the macromolecular pool. In this case, the transverse components of the macromolecular pool can be ignored. The time evolution of the remaining x, y, and z components of the magnetization vector $M = [M_{xf} M_{yf} M_{zf} M_{zm}]^T$ during a constant amplitude RF pulse can be expressed in matrix form as (Portnoy and Stanisz, 2007)

where

!1ω is the frequency offset from resonance for the RF pulse, $ω_1$ is the frequency of precession about the RF pulse, and φ is the phase of the RF pulse in the transverse plane. The standard Bloch equations implicitly assume a Lorentzian lineshape, which is invalid for the macromolecular proton pool. As a result, the Bloch equations for the macromolecular pool have been replaced in Eq. (2) by a single longitudinal component whose saturation is governed by the rate $R_{RF} = \pi \omega_{1,m}$ m

 2g (ω), where g is the lineshape function of the macromolecular pool. When applying off-resonance irradiation, a super-Lorentzian lineshape is typically used to model biological macromolecular protons (Morrison et al., 1995). Because the super-Lorentzian exhibits an on-resonance singularity, Gaussian (Gochberg and Gore, 2007) or super-Lorentzian functions extrapolated from a 1 kHz offset (Gloor et al., 2008) are typically used to model the macromolecular pool lineshape pool during on-resonance irradiation.

The general solution to this system of equations can be expressed as

Mðt
$$\frac{1}{4} \exp \delta At M \delta O p = \exp \delta At - I = \frac{1}{B};$$
 $\delta 3 p$

where M(0) is the initial condition of the system and I is an identity matrix. The same expression can be used to describe the system during free precession (i.e., when $\omega_1 = 0$). In this case, the solution can be further simplified by noting that the z-component is decoupled from the x- and y-components, resulting in the following expression for the longitudinal magnetization vector $M_z = [M_{zf} M_{zm}]^T$

$$M_z \delta t h \frac{1}{4} \exp \delta A_z t h \delta 0 h h \ln e \exp \delta A_z t h M_0;$$

where $M_0 = [M_{0f} M_{0m}]^T$ and A_z is the lower-right quadrant of A with $R_{RF} = 0$. Expanding the matrix exponentials in this expression yields

#

where $\lambda^{+\prime-}$ are the negative eigenvalues of A_z and U is a matrix whose columns are the corresponding eigenvectors. From Eq. (5), it can be seen that M_{zf} recovers as a biexponential function governed by the fast and slow rate constants λ^+ and λ^- , respectively, during free precession. As described below, one can obtain estimates of qMT parameters (e.g., PSR and k_{mf}) by measuring this biexponential recovery.

Methods

Pulse sequence

The SIR qMT sequence (Fig. 1) used herein is similar to the inversion recovery sequence used to measure T_1 with two modifications. First, short inversion times (\approx 10 ms or less) are sampled in order to capture the fast-recovering λ^+ component of the biexponential recovery. Second, a T2-selective inversion pulse is applied. This is achieved via a low power inversion pulse whose duration is much longer than the T₂ of the macromolecular pool (T_{2m} \approx 10 Us) and much shorter than the T₂ of the free water pool (T_{2f} \approx 10–100 ms). Ideally, this pulse inverts M_{zf} with minimal saturation of M_{zm} . In other words, this pulse maximizes the difference between the pools and, in turn, the sensitivity of the signal to MT. This is followed by a variable duration inversion recovery period to sample the transient biexponential recovery of M_{zf} and a center-out TFE readout (SIR-TFE) to efficiently sample k-space. For inversion recovery acquisitions, a predelay time $t_{d}\approx~5/\lambda^{-}$ is commonly employed to ensure full recovery of M_{zf}. However, if one can assume that the longitudinal magnetization of both pools is approximately zero at the end of the readout, the effect of a shorter predelay period can be accounted for in the signal model, allowing one to reduce t_d (and scan times) without biasing the estimated parameters. This assumption has been previously shown to hold true for a TSE readout (Gochberg and Gore, 2007); however, this cannot be assumed for the TFE readout employed herein. As a result, we empirically designed a train of RF pulses [number of pulses = 32, α = 135°, pulse spacing = 20 ms, pulse train duration $(t_{sat}) = 620 \text{ ms}$ to saturate both pools following the TFE readout. To assess the effect of this pulse train on the longitudinal magnetization of both pools, numerical simulations were performed via Eq. (3) and the following parameters: $R_{1m}\!=\!R_{1f}\!=\!0.8~s^{-1}, T_{2m}\!=\!10$ Us (Gaussian



Fig. 1. SIR-TFE pulse sequence diagram. The sequence employs i) a composite inversion pulse (Fig. 2) designed to uniformly invert M_{zf} over a range of expected $11B_0$ and B_1^+ values with minimal macromolecular pool saturation, ii) a variable duration inversion recovery (SIR) period to sample the free pool recovery, iii) a TFE readout to efficiently cover k-space, iv) a pulse train to saturate (SAT) the free and macromolecular pools (allows $t_d \, b \, 5/\lambda^-$), and v) a predelay (PD) period to allow for partial M_z recovery. Legend: t_i = inversion time, t_d = predelay, τ = TFE pulse-to-pulse interval, ACQ = acquisition.

lineshape), T_{2f} =60 ms, k_{mf} =15 s⁻¹, and PSR=15%. The results from these simulations indicate that this pulse train saturates both pools $[M_{zf}(t_{sat})/M_{0f} \le 0.01$ and $M_{zm}(t_{sat})/M_{0m} \le 0.06]$ over the range of expected B⁺ values (B⁺ /B⁺ =0.3–1.0) in the human brain 1.actual 1.nominal

at 7.0 T [n.b., the manufacturer-provided power optimization tended to yield a mean $B_{1,actual}^+/B_{1,nominal}^+$ b1.0 (Moore et al., 2010)].

Plugging the initial condition of $M_z(t_d=0) = 0$ into Eq. (4), signal equations can be generated for the predelay period of the SIR-TFE sequence. The ending values for this period can then be used as the initial condition for the inversion recovery period, taking account for the effect of the inversion pulse

where S is a diagonal matrix with elements that account for the inversion of the free pool (S_f= – 1 denotes complete inversion) and the saturation of the macromolecular pool (S_m=1 denotes no saturation) and t^{+/-} is the time immediately before/after the pulse. This yields the final expression for the evolution of M_z during the SIR period of the sequence

$$M_z \delta t_i; t_d \flat \frac{1}{4} \delta \exp \delta A_z t_i \flat S \mathbb{I} - \exp \delta A_z t_d \flat] \flat \mathbb{I} - \exp \delta A_z t_i \flat] \flat M_d : \delta 7 \flat$$

In addition to these pulse sequence modifications, a novel 64-element composite inversion pulse was designed and employed herein to ensure a uniform inversion of M_{zf} over the range of B^+ and !1B₀ values previously measured in the human brain at 7.0 T (Moore et al., 2010). The optimization procedure (Moore et al., 2010) tended to produce high power pulses with suboptimal T₂-selectivity. As a result, we included an additional RF power constraint into the procedure, which was weighted against the uniform inversion constraint. The resulting amplitudes and phases of the subpulses are shown in Fig. 2. To evaluate the pulse's performance, S_f and S_m were estimated from Eq. (6) by propagating Eq. (3) through each of the 64 subpulses [neglecting T₁ relaxation and MT during the pulse and



Fig. 2. Composite inversion pulse amplitudes (a), phases (b), predicted free water inversion efficiency S_f (c), and predicted macromolecular saturation fractions S_m (d). S_f = – 1 denotes complete inversion; S_m = 1 denotes no saturation. The two zero-amplitude discontinuities in the RF pulse (a) are a consequence of the power constraint used in the minimization procedure. The RF phase (b) of the pulse at these discontinuities is arbitrary; therefore, the phase at these points was set based upon linear interpolation of the neighboring RF phases for display purposes.

assuming a Gaussian macromolecular pool lineshape with $T_{2m} = 10 \ \text{Us}$ (Gochberg and Gore, 2007)]. From this procedure, the pulse is predicted to yield a uniform inversion of M_{zf} over a wide range of B_1^+ and $!1B_0$ values without complete saturation of M_{zm} .

Numerical simulations

The TFE readout employed herein effectively blurs the image along the phase-encoding direction according to its readout point-spread function (PSF), which is a complex function of the sequence timings and the NMR parameters of the tissue (Constable and Gore, 1992). If the readout PSF is constant as a function of t_i , then its effect will be to simply blur the final MT parameter maps. If, however, the readout PSF changes as a function of t_i , each image will be blurred to a different degree, potentially biasing the final parameter maps.

To evaluate this effect, the SIR-TFE signal arising from a onedimensional (1D) test object was numerically simulated. As shown in Fig. 3, MT parameters were defined for test object regions representing white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF). For each region and t_i, the signal evolution during each RF pulse and precession period of the TFE readout was simulated from Eq. (3) with the imaging parameters in the Data acquisition section—using $M_{z}(t_{i})$ from Eq. (7) as the initial condition and replacing each time-varying excitation pulse with a constant amplitude pulse of equivalent flip angle or root-mean-squared power (Ramani et al., 2002) for the free water or macromolecular pool, respectively. Complete spoiling of transverse magnetization was assumed prior to each RF pulse. The resulting M_{zf} immediately after each RF pulse was taken to represent the signal as a function of echo number. The signal was then re-ordered to account for the k-space trajectory and SENSE acceleration used, and the resulting re-ordered signal was taken to represent a k-space filter. To apply the k-space filters to the 1D test object, each uniform object region was Fourier transformed into k-space, multiplied by its corresponding k-space filter, and inverse Fourier transformed back into image space. The resulting object regions were then summed to generate



Fig. 3. Numerical simulations of the SIR-TFE readout (a) and resulting qMT parameter fits for the 1D test object defined in (b–d). (a) The M_{zf} for each region (WM shown here) and t_i was simulated and reordered into the corresponding k-space filter. The resulting filters were applied to the 1D test object as described in the text. (b–d) From the simulated fit parameters (solid gray lines), it can be seen that the TFE readout blurs the parameter maps with little or no bias (except for k_{mf} in CSF regions, which do not exhibit an MT effect).

the final blurred 1D object at each t_i . Finally, to assess the effect of the TFE readout on qMT parameter maps, the magnitude of the blurred test object signal at each voxel was fit to the M_{zf} component of Eq. (7) as described in the Data analysis section.

Subjects

MRI was performed on thirteen healthy volunteers (22–37 years old, 10 male, 3 female). To test reproducibility, six of the healthy volunteers were asked to undergo a second MRI scan at least two weeks after the first session. The study was approved by our local institutional review board, and signed consent was obtained prior to all examinations.

Data acquisition

Imaging was performed using a 7.0-T, Philips Achieva MR scanner (Philips Healthcare, Best, The Netherlands). A quadrature volume coil was used for excitation and a 32-channel head coil (Nova Medical, Wilmington, MA, USA) was used for signal reception. For qMT imaging, SIR-TFE data were collected in each subject using the general pulse sequence shown in Fig. 1.

An initial experiment was performed in one healthy volunteer to determine the effect of the post-TFE saturation train and predelay time t_d on the qMT parameter maps. For this initial experiment, SIR-TFE data were acquired in a single 5-mm axial slice with and without the post-TFE saturation train (see Fig. 1, shaded area labeled SAT) over a range of t_d values (0.125–10 s). Additional imaging parameters included: t_i logarithmically spaced between 6 ms and 2 s (15 values) and t_i = 10 s, TFE echoes per shot = 53, TFE pulse-to-pulse interval (τ)/TE/ α = 2.8 ms/1.4 ms/15°, SENSE factor = 2, field-of-view = 212 × 212 mm², resolution = 2.0 × 2.0 mm², and number of signal acquisitions averaged (NSA) = 2.

Based upon the results of this experiment along with previous numerical simulations (Gochberg and Gore, 2007), a t_d of 2.5 s was chosen to balance the scan time and SNR constraints for whole-brain SIR-TFE imaging. Whole-brain qMT data were acquired in 12 volunteers (six scanned twice) via a three-dimensional (3D) SIR-TFE sequence using the previously listed parameters except: t_i logarithmically spaced between 6 ms and 2 s (13 values) and t_i = 8 s, SENSE factor = 4 (2 anterior-posterior, 2 superior-inferior), field-of-view = 212 × 212 × 90 mm³, resolution = 2.0 × 2.0 × 3.0 mm³, and NSA = 1. This resulted in an acquisition time \approx 19 min for 30 slices.

Recall that the signal model [Eq. (7)] has terms (S_f and S_m) that account for the effect of the inversion pulse on the free and macromolecular pool magnetizations. S_f was included as a free parameter in the fit as described in the Data analysis section, while S_m was numerically estimated as described in the Pulse sequence section. Because S_m is sensitive to B_1^+ (see Fig. 2d), this numerical estimation required an independent measurement of B_1^+ . As a result, B_1^+ was estimated in same volume as the SIR-TFE data using the actual flip angle imaging (AFI) method (Yarnykh, 2007) with $TR_1/TR_2 = 125/25$ ms and a 60° slab-selective excitation pulse (asymmetric sinc pulse with Gaussian apodization).

Data analysis

All data analyses were performed in MATLAB (Mathworks, Natick, MA). Prior to data fitting, each SIR-TFE and AFI volume was co-registered to the SIR-TFE volume acquired at $t_i = 110$ ms (middle value) using a 3D rigid body registration based upon normalized mutual information (Viola and Wells, 1997). Following co-registration, automatic brain extraction was performed (Smith, 2002) and qMT parameter maps were calculated in each volunteer. The SIR-TFE signal model described in Eq. (7) has seven independent parameters: R_{1m} , R_{1f} , S_m , S_f , M_{0f} , PSR = M_{0m}/M_{0f} , and k_{mf} ($k_{fm} = k_{mf}$ PSR). As is the

case with pulsed saturation methods, the signal dependence on R_{1m} for SIR data is weak (Li et al., 2010). Therefore, R_{1m} was set equal to R_{1f} for fitting purposes. The parameter S_m was numerically estimated for each voxel. This required an independent estimate of the actual flip angle in each voxel (α_{actual}), which was calculated from the AFI data using the following relationship (Yarnykh, 2007):

$$\alpha_{actual} \frac{1}{2} \cos^{-1} \frac{(rn-1)}{n-r};$$

 $\delta 8^{b}$

where n = TR₂/TR₁, r = S(TR₂)/S(TR₂), and S is the signal intensity. The resulting α_{actual} map was smoothed with a 10 × 10 × 9 mm³ moving-average filter to minimize the impact of imaging artifacts. Following this operation, the flip angle values were converted to B⁺_{1,actual} values for the composite inversion pulse (see Fig. 2a) and S_m was estimated using the procedure described in the Pulse sequence section (see Fig. 2d). The remaining five parameters (R_{1f}, S_f, M_{0f}, k_{mf}, and PSR) were estimated for each voxel by fitting SIR-TFE

data (14 t_i values) to the M_{zf} component of Eq. (7) in a least-squares sense using the procedure described in Dortch et al. (2011).

SIR-TFE data had a mean SNR per voxel of 180 ± 50 (range = 60–320) within the defined ROIs, where SNR is defined as M_{of} divided by the standard deviation (SD) of the residuals of the fit. Monte Carlo simulations, similar to those described by Li et al. (2010), were performed to predict the uncertainty of the fit parameters at these SNR levels. The t_i and t_d values listed above were used for these simulations. Additional simulation parameters included: R_{1m} = R_{1f} = 0.8 s⁻¹, k_{mf} = 15 s⁻¹, PSR = 15%, S_m = 0.7, and S_f = -0.95. Over an

SNR range of 60–320, the SDs of the fit PSR, $R_{1f},$ and k_{mf} values were 0.4–2.2%, 0.01–0.03 s $^ ^1,$ and 0.9–5.5 s $^ ^1,$ respectively. This suggests

that PSR and R_{1f} can be robustly determined from the in vivo brain data collected herein. Consistent with previous studies (Li et al., 2010), the uncertainty in k_{mf} is expected to be much larger, especially in lower SNR regions.

Following this fitting procedure, qMT parameter maps were smoothed with a locally-adaptive Gaussian filter (kernel size = $10 \times 10 \times 9$ mm³, full width at half maximum = 1/2 kernel size) to remove outliers that tended to occur at tissue boundaries. To perform this operation, each filtered map was subtracted from the raw parameter map, and outliers were defined as voxels whose value was three standard deviations above the mean difference across all voxels. For these outliers, the value in the raw parameter map was replaced with the value in the filtered map. This process was iterated until the number of outliers was less than the expected value (0.3% of the total number of voxels).

Statistics

Mean qMT parameters (PSR, R_{1f} , and k_{mf}) were calculated within the following regions-of-interest (ROI): head of the caudate, putamen, thalamus, genu and splenium of the corpus callosum, internal capsule, corona radiata, occipital WM, and frontal WM. Statistical comparisons were performed on the mean ROI values to evaluate each parameter's i) variation across ROIs (i.e., regional differences), ii) variation and reproducibility across time, and iii) variation across volunteers. To compare parameters across WM regions, a non-parametric Wilcoxon rank-sum test was performed, with a pb0.05 deeming a significant difference between ROI values. To evaluate the test-retest reproducibility of each parameter, a Bland-Altman (BA) analysis was performed. For the BA analysis, the mean difference and the limits of agreement (LOA = mean difference ± 1.96 * SD) were tabulated across scans for all ROIs. Additionally, a Wilcoxon signed-rank test was performed between the test and retest parameter values for each ROI, with a p > 0.05 indicating a non-significant difference between scans at each time point. To assess the test-retest variability of each parameter within each ROI, the coefficient of variation was calculated from: CV S= M

(2Þ 100, where

S is the SD of the test-retest difference across subjects. M is the mean value across all test-retest scans and subjects, and the 2 term accounts for the propagation of uncertainty from the difference operation. The across-cohort variability of each parameter within each ROI was also assessed via: $CV_{cohort} = S/M * 100$, where S is the SD across the cohort and M is mean value across the cohort. All values are reported as the mean \pm SD unless otherwise stated.

Results

The results of the numerical simulations designed to assess the effect of TFE readout on qMT parameter maps are shown in Fig. 3. In Fig. 3a, the evolution of M_{zf} during the TFE readout is shown for WM as a function of t_i . Note that this evolution is related to the k-space filter of the readout. It can be seen that the shape (width and rate of decay) of the k-space filter changes as a function of t_i , which manifests as a change in object blurring as a function of t_i . The effect of this on the qMT parameter maps is shown in Figs. 3b–d. It can be seen that the resulting qMT parameter maps are smoothed in the phase-encoding direction with little bias in the fit parameters. It should be noted, however, that PSR values were slightly underestimated in the WM region of the 1D test object. Additional simulations indicated that this bias increased as the size of the WM region decreased.

Fig. 4 displays PSR maps acquired with and without application of the post-TFE saturation train (see the SAT region in Fig. 1) as a function of t_d . For scans with the saturation train, the fit PSR values at



Fig. 4. (a) Maps of PSR as a function of t_d without (top) and with (bottom) a post-TFE saturation train and (b) corresponding mean (\pm SD) slice-wise PSR values. For scans with the saturation train, all PSR values were nearly identical to the values at full recovery (dashed line). Without the saturation train, PSR values were increasingly underestimated with decreasing t_d .



Fig. 5. Sample SIR-TFE images (a) and model fit (b) from a slice at the level of the lateral ventricles in a healthy control. (a) Images from six of the 14 inversion times are shown. Note the characteristic center brightening of the images due to B_1^+ inhomogeneities. (b) Corresponding SIR data from a voxel in the genu of the corpus callosum. Note the agreement between the SIR data (circles) and biexponential model [solid black line, Eq. (7)] and the deviation from a monoexponential model, which is apparent at the shortest inversion times shown in the zoomed inset.

shorter t_d values were nearly identical to those at full recovery ($t_d = 10$ s). Without this train, small deviations in PSR were observed at $t_d = 2.5$ s; and these were more pronounced at $t_d = 1.25$ s. Thus, the post-TFE saturation train allows for reduction of t_d (and scan times) with minimal parameter bias.

Representative 3D SIR-TFE data are shown in Fig. 5. Fig. 5a shows a single slice at the level of the lateral ventricles acquired at six of 14 t_i values. Note the characteristic center brightening due to B_1^+ inhomogeneities. Fig. 5b shows data from a single voxel in the genu of the corpus callosum and the corresponding model fit. Note the agreement between the SIR-TFE data and the biexponential model described by Eq. (7). Additionally, note the deviation from monoexponential recovery, which is especially evident at the shortest inversion times.

Based upon these fits, maps of qMT parameters were generated. Recall that these maps were filtered to reduce the impact of outliers. Fig. 6 displays representative qMT parameter maps without filtering, with the previously described locally-adaptive Gaussian filter, and with a global Gaussian filter. The locally-adaptive and global filters both removed outliers in the parameter maps (see arrow in the top row and the masks in the bottom row); however, the locally filtered maps were blurred to a much smaller degree. As a result, we employed the locally-adaptive approach herein. For all parameter maps, 14% of all voxels in the post-brain-extraction volume were smoothed using this approach. However, as seen in the bottom row of Fig. 6, a majority of these voxels were located along the brain surface or within the CSF.

Fig. 7 displays results from four representative slices in one healthy subject. The qMT parameters were uniform over most of the volume despite the presence of large $!1B_0$ and/or B_1^{\star} field inhomogeneities (as indicated by the heterogeneity in the S_m maps). There does, however, appear to be some bias in the qMT parameter values in midbrain slices (black arrow), which typically (Moore et al., 2010) exhibit the largest field inhomogeneities and the lowest SNR. Nevertheless, these data suggest that robust qMT parameter mapping can be achieved throughout most of the brain using the 3D SIR-TFE protocol described herein.

ROIs were defined in a number of WM and GM regions as shown in Fig. 8. The boxplots in the top row of Fig. 9 display the mean ROI qMT parameters over the 12 healthy volunteers. For PSR, the mean value across all WM ROIs ($17.6 \pm 1.3\%$) was higher than the values across all GM ROIs ($10.3 \pm 1.6\%$). Additionally, heterogeneity within WM PSR values was observed, but should be interpreted with caution due to the effect of multiple comparisons. Nevertheless, differences between the following regions were detected: i) the genu of the corpus callosum and occipital WM (p = 0.026), ii) the genu of the corpus callosum and the corona radiata (p = 0.026), iii) frontal and occipital

WM (p=0.041), and iv) frontal WM and the corona radiata (p= 0.041). Fit k_{mf} values were higher in GM (24.4±4.4 s⁻¹) than in WM (14.5±1.5 s⁻¹). Additionally, note the large, biased k_{mf} values in and



Fig. 6. Representative qMT parameter (PSR, k_{mfr} , R_{1f}) maps with and without filtering. Shown are (1st row) raw parameter maps, (2nd row) parameter maps filtered with the locally-adaptive Gaussian filter, (3rd row) parameter maps filtered with the global Gaussian filter (with an identical kernel), and (4th row) masks of the outliers detected using the locally-adaptive filter. The arrow identifies a region with biased PSR values that are corrected by filtering. Note that the color-scale in these maps was chosen to highlight the outliers and is different than in Figs. 4 and 8.



Fig. 7. Representative parameter maps from one subject (four of 30 slices are shown). The qMT parameters (PSR, k_{mh} , R_{1f}) and the inversion efficiency S_f were uniform over most of the volume despite the presence of large field inhomogeneities. There does, however, appear to be some bias in the qMT parameter values in midbrain slices (black arrows), which typically exhibit the largest B_0 and B_1^+ inhomogeneities. This results in a deviation of S_f from -1 in these regions.

around areas containing CSF, which is likely a consequence of the weak dependence of the signal on k_{mf} when PSR ≈ 0 (see the simulated data in Fig. 3c). For R_{1fr} differences between WM (0.73 \pm 0.03 s $^{-1}$) and GM (0.58 \pm 0.05 s $^{-1}$) values were also observed. The boxplots in Fig. 9 give an indication of the variability of each parameter across the healthy cohort. To quantify this, the coefficient of variation was tabulated for each ROI, and the mean value across all ROI is given in Table 1. From this, it can be seen that the mean CV_{cohort} was b 10% for all of the qMT parameters, which is not surprising given the small age range of the healthy cohort scanned herein.

BA plots of the observed difference in mean ROI qMT parameters between scans are shown in the bottom row of Fig. 9; and the results from this analysis are given numerically in Table 1. The mean

difference for all ROIs across scans was close to zero for PSR (0.0%), $k_{\rm mf}$ (1.2 s $^{-1}$), and $R_{\rm 1f}$ (0.01 s $^{-1}$), indicating a lack of bias and reasonable reproducibility. To further test this, a Wilcoxon signed-rank test was performed on the test–retest parameter values in each ROI. At the p = 0.05 level, no significant difference was observed between test and retest qMT parameters in any of the ROIs except for $k_{\rm mf}$ in the genu of the corpus callosum (p = 0.031). The test–retest coefficient of variation (CV_{retest}) was also tabulated for each metric to further assess each parameter's variability across time. As shown in Table 1, the relative CV_{retest} values were consistent with the corresponding CV_{cohort} values, with $k_{\rm mf}$ exhibiting the highest variability. In terms of absolute CV values, the test–retest variability was approximately 20% lower than the across cohort variability.



Fig. 8. Representative PSR maps from a single volunteer with corresponding ROIs (a = corona radiata; b = occipital WM; c = frontal WM; d = corpus callosum, genu; e = corpus callosum, splenium; f = internal capsule; g = head of caudate; h = thalamus; i = putamen). White and black dots represent WM and GM ROIs, respectively. In practice, ROIs were defined bilaterally and results were averaged across hemispheres. Here we show ROIs in one hemisphere for display purposes.



Fig. 9. (a–c) Boxplot of the mean ROI qMT parameters (hc = head of caudate; put = putamen; thal = thalamus; owm = occipital WM; scc = corpus callosum, splenium; ic = internal capsule; cr = corona radiata; gcc = corpus callosum, genu; fwm = frontal WM). On each box, the central mark is the median, the edges of the box are the 25th and 75th percentiles, and the whiskers extend to the most extreme data points. (d–f) Bland–Altman plots of the difference in parameters for WM (black) and GM (gray) ROIs across scans. The solid line is the mean difference, and the dashed lines are the limits of agreement (mean difference \pm 1.96 SD).

Discussion

This study demonstrates the feasibility of performing whole-brain gMT measurements in the human brain in vivo at high field. Pulsed saturation and SSFP-based approaches are difficult to implement at high field due to RF power limitations and/or magnetic field (B1+ and !1Bo) inhomogeneities. In this study, we employed the SIR qMT approach, which has been suggested to be less sensitive to these issues. The biggest obstacles to overcome were i) the effect of B_1^+ and !1B₀ inhomogeneities on the inversion pulse and the readout and ii) the long scan times associated with SIR imaging. The former of these was mitigated by developing a novel ${\tt B}^+$ and ${\tt !1B}$ insensitive inversion composite pulse (Fig. 2) and employing a low-flip angle TFE readout; the latter was mitigated by the efficiency of the TFE readout along with additional protocol optimization (e.g., reducing the number of t₁ values to 14, applying SENSE acceleration in two directions). Together this resulted in a robust (Fig. 9), whole-brain qMT imaging protocol with a scan time of less than 20 min.

Previous qMT imaging studies at lower field strengths (Dortch et al., 2011; Garcia et al., 2010; Gloor et al., 2008; Ropele et al., 2003; Sled and Pike, 2001; Sled et al., 2004; Yarnykh and Yuan, 2004) have reported PSR values in the range of 11–16% and 5–9% for WM and GM structures, respectively [PSR = F using the notation of Sled and Pike (2000, 2001) and M_{0b} using the notation of Henkelman et al. (1993)]. The PSR values presented herein (WM: 15–20%, GM: 9–

13%) were approximately 25% higher. PSR should be independent of field strength, so these differences may be related to the SIR-TFE sequence. As previously discussed, we modified the inversion pulse and readout of our 3.0-T SIR-FSE sequence to perform qMT imaging at 7.0 T. The effect of the TFE readout on the fit qMT parameters was assessed via numerical simulations and was found to result in little bias in PSR (Fig. 3). However, it should be noted that our previous report at 3.0 T employed a much longer TE (74 ms) than was employed herein (1.4 ms). Previous work (Bjarnason et al., 2005; Stanisz et al., 1999) has demonstrated that MT contrast is TE-dependent in WM due to the microanatomical compartition of water into myelin and nonmyelin water spaces. As a result, it is reasonable to assume that PSR may also exhibit a TE-dependence. In terms of the inversion pulse, we recognize that PSR is sensitive to the macromolecular pool lineshape and T_{2m} assumptions used in the numerical estimation of Sm. Similar to our previous studies (Dortch et al., 2011; Gochberg and Gore, 2007), we modeled the macromolecular pool using a Gaussian lineshape ($T_{2m} = 10$ Us) because the Super-Lorentzian exhibits an on-resonance singularity. Previous work using a 1-ms block inversion pulse at 3.0 T (Dortch et al., 2011) found that this was a reasonable approximation; however, this may not be true for the longer (5.5 ms), higher power composite inversion pulse employed herein. Additional work is needed to explore the field- and TE-dependence of PSR values obtained via the SIR technique. Nevertheless, the reported regional variation in PSR values was consistent with previous qMT imaging studies (Dortch et al., 2011;

Table 1

Test-retest reproducibility analysis of each qMT parameter (PSR, R_{1f}, and k_{mf}). Shown are the mean \pm SD parameter values across all ROIs for the test and retest scans, the resulting mean paired-difference between time-points, the limits-of-agreement (LOA), and the mean \pm SD test-retest coefficient of variation (CV_{retest}) across all ROIs. For comparison, the corresponding across-cohort coefficient of variation (CV_{cohort}) is also given.

Parameter	Test scan (mean \pm SD)	Retest scan (mean \pm SD)	Difference	LOA	CV _{retest} (%)	CV _{cohort} (%)
PSR (%)	15.2 ± 3.9	15.2 ± 3.7	0.0	(- 2.2, 2.1)	4.9±1.5	5.6±1.9
$k_{mf} (s^{-1})$	16.8 ± 4.7	18.0 ± 5.5	1.2	(- 3.9, 6.3)	8.2±2.4	9.4 ± 3.6
$R_{1f} (s^{-1})$	0.68 ± 0.08	0.68 ± 0.08	0.01	(- 0.03, 0.04)	1.9 ± 1.4	3.2±1.3

Garcia et al., 2010; Sled et al., 2004; Underhill et al., 2009); and additional SIR-TFE studies in bovine serum albumin phantoms at 7.0 T (data not shown) found a linear relationship between macromolecular content and PSR. Thus, we postulate that the regional differences in PSR values reported herein are driven primarily by regional differences in myelin content, although the absolute values may be systematically larger than reported by other techniques.

Previous pulsed saturation and SSFP-based studies (Garcia et al., 2010; Gloor et al., 2008; Ropele et al., 2003; Sled and Pike, 2001; Sled et al., 2004; Yarnykh and Yuan, 2004) report k_{mf} values [k_{mf} = k_{f} / F using the notation of Sled and Pike (2000, 2001); $k_{mf} = R$ when $M_{of} = 1$ using the notation of Henkelman et al. (1993)] in the range of 20-40 s⁻¹ across the brain. A previous SIR study (Dortch et al., 2011) at 3.0 T reports k_{mf} values that are approximately 2-fold slower $(10-15 \text{ s}^{-1})$ with values that are slower in WM than GM, which is consistent with the results presented herein. The discrepancies between techniques are not surprising given the reported difficulty of using pulsed saturation to determine k_{mf} (Portnoy and Stanisz, 2007). In terms of the current study, it should be noted that k_{mf} showed the largest variability of the qMT parameters, which is consistent with the results from the Monte Carlo simulations. We do not expect this to be a significant drawback as k_{mf} has been shown to be insensitive to the pathological changes in spinal cord WM (Smith et al., 2009).

While there have been no previous reports of R_{1f} in human brain at 7.0 T, it can be shown that the observed T_1 typically reported is $\approx 1/R_{1f}$. Using this relationship, the mean WM and GM observed T_1 values were 1372 and 1724 ms, respectively, which are within the range of previously reported values in human brain at 7.0 T (Wright et al., 2008). As expected, we noted a significant correlation between R_{1f} and PSR in the healthy human brain (data not shown); however, T_1 is sensitive to overall tissue composition [e.g., water content (Kiricuta and Simplaceanu, 1975)] and is believed to be a less specific marker for myelin in WM.

The increased SNR available at 7.0 T was used here to decrease scan time (\approx 40 s/slice) and increase resolution (2 × 2 × 3 mm³) relative to our 3.0-T protocol. Moving forward, it may be advantageous to look at higher resolution protocols. If we assume that all imaging parameters are the same, increasing the resolution to 1 × 1 × 3 mm³ would result in an approximately two-fold decrease in SNR (\approx 70 at thermal equilibrium, assuming we increase the number of acquired points to hold the field-of-view constant). Based upon previous simulation work (Li et al., 2010) as well as the simulation work presented herein, this would be sufficient to robustly fit qMT parameters over most of the brain. Thus, it appears that high-resolution qMT imaging may be feasible in the human brain in vivo at 7.0 T using a protocol similar to that described herein.

Conclusions

The results of this study demonstrate the feasibility of performing qMT imaging in human brain in vivo at high field. The developed SIR-TFE protocol allowed for whole-brain qMT imaging in less than 20 min. In healthy subjects, intra-subject reliability (i.e., test–retest) was demonstrated despite large $!1B_0$ and B_1^+ variations. Additionally, a high level of inter-subject reproducibility was demonstrated for the qMT parameters. Future work includes investigating high-resolution protocols to look at cortical features of qMT parameters and application of the approach in a cohort of multiple sclerosis patients.

Acknowledgments

This work was supported by NIH/NBIB K01 EB009120 (SAS), NIH T32 EB001628 (JCG), NIH EB00461 (JCG), and Vanderbilt Bridge Funding (DFG).

References

- Berry, I., Barker, G., Barkhof, F., Campi, A., Dousset, V., Franconi, J., Gass, A., Schreiber, W., Miller, D., Tofts, P., 1999. A multicenter measurement of magnetization transfer ratio in normal white matter. J. Magn. Reson. Imaging 9, 441–446.
- Bjarnason, T., Vavasour, I., Chia, C., Mackay, A., 2005. Characterization of the NMR behavior of white matter in bovine brain. Magn. Reson. Med. 54, 1072–1081.
- Bruno, S.D., Barker, G.J., Cercignani, M., Symms, M., Ron, M.A., 2004. A study of bipolar disorder using magnetization transfer imaging and voxel-based morphometry. Brain 127, 2433–2440.
- Catalaa, I., Grossman, R.I., Kolson, D.L., Udupa, J.K., Nyul, L.G., Wei, L., Zhang, X., Polansky, M., Mannon, L.J., McGowan, J.C., 2000. Multiple sclerosis: magnetization transfer histogram analysis of segmented normal-appearing white matter. Radiology 216, 351–355. Cercignani, M., Alexander, D., 2006. Optimal acquisition schemes for in vivo quantita-
- tive magnetization transfer MRI. Magn. Reson. Med. 56, 803–810.
- Constable, R.T., Gore, J.C., 1992. The loss of small objects in variable TE imaging: implications for FSE, RARE, and EPI. Magn. Reson. Med. 28, 9–24.
- Dortch, R.D., Li, K., Gochberg, D.F., Welch, E.B., Dula, A.N., Tamhane, A.A., Gore, J.C. Smith, S.A., 2011. Quantitative magnetization transfer imaging in human brain at 3 T via selective inversion recovery. Magn. Reson. Med. 66, 1346–1352.
- Dousset, V., Grossman, R.I., Ramer, K.N., Schnall, M.D., Young, L.H., Gonzalez-Scarano, F., Lavi, E., Cohen, J.A., 1992. Experimental allergic encephalomyelitis and multiple sclerosis: lesion characterization with magnetization transfer imaging. Radiology 182, 483–491.
- Edzes, H.T., Samulski, E.T., 1977. Cross relaxation and spin diffusion in the proton NMR or hydrated collagen. Nature 265, 521–523.
- Filippi, M., Rocca, M.A., 2004. Magnetization transfer magnetic resonance imaging in the assessment of neurological diseases. J. Neuroimaging 14, 303–313.
- Garcia, M., Gloor, M., Wetzel, S.G., Radue, E.-W., Scheffler, K., Bieri, O., 2010. Characterization of normal appearing brain structures using high-resolution quantitative magnetization transfer steady-state free precession imaging. NeuroImage 52, 532–537.
- Gass, A., Barker, G.J., Kidd, D., Thorpe, J.W., MacManus, D., Brennan, A., Tofts, P.S., Thompson, A.J., McDonald, W.I., Miller, D.H., 1994. Correlation of magnetization transfer ratio with clinical disability in multiple sclerosis. Ann. Neurol. 36, 62–67.
- Gloor, M., Scheffler, K., Bieri, O., 2008. Quantitative magnetization transfer imaging using balanced SSFP. Magn. Reson. Med. 60, 691–700.
- Gochberg, D., Gore, J., 2007. Quantitative magnetization transfer imaging via selective inversion recovery with short repetition times. Magn. Reson. Med. 57, 437–441.
- Gochberg, D., Kennan, R., Gore, J., 1997. Quantitative studies of magnetization transfer by selective excitation and T₁ recovery. Magn. Reson. Med. 38, 224–231.
- Graham, S.J., Henkelman, R.M., 1997. Understanding pulsed magnetization transfer. J. Magn. Reson. Imaging 7, 903–912.
- Henkelman, R., Huang, X., Xiang, Q., Stanisz, G., Swanson, S., Bronskill, M., 1993. Quantitative interpretation of magnetization transfer. Magn. Reson. Med. 29, 759–766.
- Kabani, N.J., Sled, J.G., Chertkow, H., 2002a. Magnetization transfer ratio in mild cognitive impairment and dementia of Alzheimer's type. NeuroImage 15, 604–610. Kabani, N.J., Sled, J.G., Shuper, A., Chertkow, H., 2002b. Regional magnetization transfer ratio changes in mild cognitive impairment. Magn. Reson. Med. 47, 143–148.
- Kalkers, N.F., Hintzen, R.Q., van Waesberghe, J.H., Lazeron, R.H., van Schijndel, R.A., Ader, H.J., Polman, C.H., Barkhof, F., 2001. Magnetization transfer histogram parameters reflect all dimensions of MS pathology, including atrophy. J. Neurol. Sci. 184, 155–162.
- Kiricuta Jr., I.C., Simplaceanu, V., 1975. Tissue water content and nuclear magnetic resonance in normal and tumor tissues. Cancer Res. 35, 1164–1167.
- Koenig, S.H., 1991. Cholesterol of myelin is the determinant of gray–white contrast in MRI of brain. Magn. Reson. Med. 20, 285–291.
- Kucharczyk, W., Macdonal, P., Stanisz, G., Henkelman, R., 1994. Relaxivity and magnetization transfer of white matter lipids at MR imaging: importance of cerebrosides and pH. Radiology 192, 521–529.
- Levesque, I.R., Sled, J.G., Pike, G.B., 2011. Iterative optimization method for design of quantitative magnetization transfer imaging experiments. Magn. Reson. Med. 66, 635–643.
- Li, K., Zu, Z., Xu, J., Janve, V.A., Gore, J.C., Does, M.D., Gochberg, D.F., 2010. Optimized inversion recovery sequences for quantitative T₁ and magnetization transfer imaging. Magn. Reson. Med. 64, 491–500.
- Moore, J., Jankiewicz, M., Zeng, H., Anderson, A.W., Gore, J.C., 2010. Composite RF pulses for B₁⁺-insensitive volume excitation at 7 Tesla. J. Magn. Reson. 205, 50–62.
- Morrison, C., Stanisz, G., Henkelman, R.M., 1995. Modeling magnetization transfer for biological-like systems using a semi-solid pool with a super-Lorentzian lineshape and dipolar reservoir. J. Magn. Reson. B 108, 103–113.
- Mougin, O.E., Coxon, R.C., Pitiot, A., Gowland, P.A., 2010. Magnetization transfer phenomenon in the human brain at 7 T. NeuroImage 49, 272–281.
- Mugler III, J.P., Brookeman, J.R., 1990. Three-dimensional magnetization-prepared rapid gradient-echo imaging (3D MP RAGE). Magn. Reson. Med. 15, 152–157.
- Odrobina, E., Lam, T., Pun, T., Midha, R., Stanisz, G., 2005. MR properties of excised neural tissue following experimentally induced clemyelination. NMR Biomed. 18, 277–284.
- Ou, X., Sun, S.W., Liang, H.F., Song, S.K., Gochberg, D.F., 2009. The MT pool size ratio and the DTI radial diffusivity may reflect the myelination in shiverer and control mice. NMR Biomed. 22, 480–487.
- Pike, G.B., 1996. Pulsed magnetization transfer contrast in gradient echo imaging: a two-pool analytic description of signal response. Magn. Reson. Med. 36, 95–103.
- Portnoy, S., Stanisz, G.J., 2007. Modeling pulsed magnetization transfer. Magn. Reson. Med. 58, 144–155.

- Ramani, A., Dalton, C., Miller, D.H., Tofts, P.S., Barker, G.J., 2002. Precise estimate of fundamental in-vivo MT parameters in human brain in clinically feasible times. Magn. Reson. Imaging 20, 721–731.
- Ropele, S., Seifert, T., Enzinger, C., Fazekas, F., 2003. Method for quantitative imaging of the macromolecular ¹H fraction in tissues. Magn. Reson. Med. 49, 864–871.
- Schmierer, K., Scaravilli, F., Altmann, D., Barker, G., Miller, D., 2004. Magnetization transfer ratio and myelin in postmortem multiple sclerosis brain. Ann. Neurol. 56, 407–415.
- Schmierer, K., Tozer, D.J., Scaravilli, F., Altmann, D.R., Barker, G.J., Tofts, P.S., Miller, D.H., 2007. Quantitative magnetization transfer imaging in postmortem multiple sclerosis brain. J. Magn. Reson. Imaging 26, 41–51.
- Sled, J.G., Pike, G.B., 2000. Quantitative interpretation of magnetization transfer in spoiled gradient echo MRI sequences. J. Magn. Reson. 145, 24–36.
- Sled, J.G., Pike, G.B., 2001. Quantitative imaging of magnetization transfer exchange and relaxation properties in vivo using MRI. Magn. Reson. Med. 46, 923–931.
- Sled, J.G., Levesque, I., Santos, A.C., Francis, S.J., Narayanan, S., Brass, S.D., Arnold, D.L., Pike, G.B., 2004. Regional variations in normal brain shown by quantitative magnetization transfer imaging. Magn. Reson. Med. 51, 299–303.
- Smith, S.M., 2002. Fast robust automated brain extraction. Hum. Brain Mapp. 17, 143–155.
- Smith, S., Golay, X., Fatemi, A., Mahmood, A., Raymond, G., Moser, H., van Zijl, P., Stanisz, G., 2009. Quantitative magnetization transfer characteristics of the

human cervical spinal cord in vivo: application to adrenomyeloneuropathy. Magn. Reson. Med. 61, 22-27.

- Stanisz, G., Kecojevic, A., Bronskill, M., Henkelman, R., 1999. Characterizing white matter with magnetization transfer and T₂. Magn. Reson. Med. 42, 1128–1136.
- Underhill, H.R., Yuan, C., Yarnykh, V.L., 2009. Direct quantitative comparison between cross-relaxation imaging and diffusion tensor imaging of the human brain at 3.0 T. NeuroImage 47, 1568–1578.
- Underhill, H.R., Rostomily, R.C., Mikheev, A.M., Yuan, C., Yarnykh, V.L., 2011. Fast bound pool fraction imaging of the in vivo rat brain: association with myelin content and validation in the C6 glioma model. NeuroImage 54, 2052–2065.
- Viola, P., Wells, W.M., 1997. Alignment by maximization of mutual information. Int. J. Comput. Vis. 24, 137–154.
- Wolff, S.D., Balaban, R.S., 1989. Magnetization transfer contrast (MTC) and tissue water proton relaxation in vivo. Magn. Reson. Med. 10, 135–144.
- Wright, P.J., Mougin, O.E., Totman, J.J., Peters, A.M., Brookes, M.J., Coxon, R., Morris, P.E., Clemence, M., Francis, S.T., Bowtell, R.W., Gowland, P.A., 2008. Water proton T₁ measurements in brain tissue at 7, 3, and 1.5 T using IR-EPI, IR-TSE, and MPRAGE: results and optimization. MAGMA 21, 121–130.
- Yarnykh, V.L., 2007. Actual flip-angle imaging in the pulsed steady state: a method for rapid three-dimensional mapping of the transmitted radiofrequency field. Magn. Reson. Med. 57, 192–200.
- Yarnykh, V.L., Yuan, C., 2004. Cross-relaxation imaging reveals detailed anatomy of white matter fiber tracts in the human brain. NeuroImage 23, 409–424.