Robust Quantitative Magnetization Transfer Magnetic Resonance Imaging in the Presence of Radiofrequency Field Inhomogeneities

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December 15th, 2017

A thesis submitted to McGill University in partial fulfillment of the

requirements for the Degree of Philosophy

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Acknowledgements

First and foremost, I would like to express my sincerest gratitude to my PhD advisor, Professor Bruce Pike, for all his guidance and support over the course of this degree. The mentorship you offered me was an invaluable experience that I will carry with me throughout my career. Thank you for letting me be increasingly autonomous as this project progressed, and for guiding in the right direction when I sometimes veered off track. I’d like to also thank the other members of my PhD committee, Dr. Douglas Arnold and Professor Robert Funnell, for your guidance and advice at every stage of this thesis work.

I am indebted to all the staff who I’ve leaned on during a variety of circumstances throughout these years. Thank you to Prof. Pike’s administration coordinators (Naomi Takeda, Jennifer Chew, and Christa Collie) for all the hard work and rapid problem-solving you’ve done for me, whether I was aware of it or not at the time. Thank you to the staff of McGill’s Department of Biomedical Engineering, particularly Pina Sorrini, Daniel Caron, and Nancy Abate. Thank you to the McConnell Brain Imaging Center’s research assistants, Ilana Leppert and Michael Ferreira, for all the technical support you provided me throughout the years, and most importantly for the assistance you gave me during my initial transition into the lab.

Thank you to all the past and present members of our research group, for creating a rich learning environment full of fruitful ideas, and who were always open to sharing their expertise and insights: Eva Alonso-Ortiz, Silvain Beriault, Avery Berman, Jennifer Campbell, Halleh Ghaderi, Ye Gu, Ives Levesque, Yuhan Ma, Ethan MacDonald, Clarisse Mark, Erin Mazerolle, Melany Mclean, Nikola Stikov, Christine Tardif, and Marika Wallenburg. Special thanks to my deskmate, Yuhan Ma, for your patience while entertaining all my questions, debugging session, general comments, and ideas. Sincere thanks to Prof. Nikola Stikov, a close collaborator on several projects within (and beyond) this thesis work, for all your great insights, your contagious enthusiasm for collaboration, and your strong encouragement to contribute to the world of open science. Lastly, thank you to Marika Wallenburg, a close colleague and friend, who passed away while also pursuing her PhD in our lab.

This work could not have been possible without the following sources of funding: the Natural Sciences and Engineering Research Council of Canada (NSERC) Alexander Graham Bell Canada Graduate Scholarship (CGS-D3), the McGill Biomedical Engineering Department Recruitment Award, the International Society for Magnetic Resonance in Medicine (ISMRM) Educational Stipend, the endMS Summer School program, and the McGill Biomedical Engineering Department Travel Award. This research was also funded by my PhD advisor’s (Bruce Pike) research and operating grants from NSERC and the Canadian Institutes of Health Research (CIHR).

Last but not least, thank you to all my family and friends who supported me throughout this journey. I am immensely grateful to my wife, Gabrielle Lapointe, for your patience, support, and encouragement all these years. To my father, for igniting my passion of experimental science at an early age, by sharing your skills and time with me when I participated in science expos as a kid. And to my mother, for noticing and nourishing my interest in mathematics and physics, purchasing several math and logic exercise books for me when we would visit bookstores, and for getting me a career day visit to the Physics and Astronomy Department of l’Université de Moncton while in high school.

Mathieu Boudreau

December 15th, 2017

Preface

The original research presented in this Ph.D. thesis is composed of the following three peer-reviewed international journal articles:

1. **Mathieu Boudreau**, Christine L. Tardif, Nikola Stikov, Wayne Lee, John G. Sled, G. Bruce Pike, “*B1 Mapping for Bias-correction in Quantitative T1 Imaging of the Brain at 3 Tesla Using Standard Pulse Sequences*”, Journal of Magnetic Resonance Imaging, 46:1673-1682 (2017)
2. **Mathieu Boudreau**, Nikola Stikov, G. Bruce Pike, *“B1-Sensitivity Analysis of Quantitative Magnetization Transfer Imaging”*, Magnetic Resonance in Medicine, doi:10.1002/mrm.26673 (2017).
3. **Mathieu Boudreau** and G. Bruce Pike, *“B1-Sensitivity Analysis of Quantitative Magnetization Transfer Imaging”*, Submitted to Magnetic Resonance in Medicine.

This thesis was written with the assumption that its readers already have a good fundamental background of MRI theory, the details of which are not presented here. Additional material to bridge the gap between basic MRI physics and the advanced quantitative MRI concepts required for understanding the original research work reported in this thesis is presented in the background chapter (Chapter 2).

Contribution of Authors

I am the first author of the three manuscripts included in this thesis. As such, I designed the studies, acquired the data, processed and analyzed the data, wrote (or customized) the majority of the simulation and analysis code needed, and wrote the manuscripts. The contributions of the co-authors of these articles are listed below.

* **Christine L. Tardif, PhD:** Previously implemented some of the quantitative imaging pulse sequences used (Actual Flip angle Imaging and spoiled Variable Flip Angle) as well as some data analysis code (for the Bloch-Siegert shift technique). Provided guidance during the planning stage of the study (Chapter 3). Edited the manuscript prior to submission (Chapter 3).
* **Nikola Stikov, PhD:** Provided general guidance throughout the studies (Chapters 3 and 4), and some data analysis code (Variable Flip Angle and Actual Flip angle Imaging). Edited the manuscripts prior to submission (Chapter 3 and 4).
* **John G. Sled, PhD:** Assisted in the implementation of the echo-planar imaging double angle B1 mapping sequence on our scanner (Chapter 3). Edited the manuscript prior to submission (Chapter 3).
* **Wayne Lee, MSc:** Assisted in the implementation of the echo-planar imaging double angle B1 mapping sequence on our scanner (Chapter 3). Edited the manuscript prior to submission (Chapter 3).
* **G. Bruce Pike, PhD:** Overall supervision, mentorship, guidance, assistance, and feedback throughout each stage of all three projects presented in this thesis. Edited all manuscripts and the thesis as a whole prior to submission.

Other Publications

The following list of peer-reviewed articles and conference presentations were also produced over the course of this PhD degree, but are not included in the thesis. In addition to the three first-authored manuscripts included this thesis, these other publications total five co-authored peer-reviewed journal articles, five first-authored peer-reviewed conference presentations, and three peer-reviewed co-authored conference presentations.

* J.S.W. Campbell, I.R. Leppert, S. Narayanan, **M. Boudreau**, T. Duval, J. Cohen-Adad, G.B. Pike, N. Stikov, *“Promise and pitfalls of g-ratio estimation with MRI”*, NeuroImage, doi:10.1016/j.neuroimage.2017.08.038 (2017).
* M. Mclean, M.E. MacDonald, R.M. Lebel, **M. Boudreau**, B. Pike, *“Accelerated z-Spectrum Imaging”*, Oral, International Society for Magnetic Resonance in Medicine Meeting (2017).
* J. Campbell, I.R. Leppert, **M. Boudreau**, S. Narayanan, T. Duval, J. Cohen-Adad, G.B. Pike, N. Stikov, *“Myelin g-ratio imaging: promises and pitfalls”*, Poster, International Society for Magnetic Resonance in Medicine Meeting (2016).
* J.-F. Cabana, Y. Gu, **M. Boudreau**, I.R. Levesque, Y. Atchia, J.G. Sled, S. Narayanan, D.L. Arnold, G.B. Pike, J. Cohen-Adad, N. Stikov, *“Quantitative Magnetization Transfer Imaging Made Easy with qMTLab: a Software for Data Simulation, Analysis and Visualisation”*, Concepts in Magnetic Resonance Part A, 44A: 263–277 (2016).
* N. Stikov, J.S.W. Campbell, T. Stroh, M. Lavalée, S. Frey, J. Novek, S. Nuara, M.-K. Ho, B.J. Bedell, R.F. Dougherty, I.R. Leppert, **M. Boudreau**, S. Narayanan, T. Duval, J. Cohen-Adad, P.-A. Picard, A. Gasecka, D. Côté, G.B. Pike, *“In vivo histology of the myelin g-ratio with magnetic resonance imaging”*, NeuroImage, 118:397-405 (2015).
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* N. Stikov, **M. Boudreau**, I.R. Levesque, C.L. Tardif, J. Barral, G.B. Pike, “*On the Accuracy of T1 Mapping: Searching for Common Ground.*” Magnetic Resonance in Medicine, 73:514-522 (2015).
* **M. Boudreau**,N. Stikov, G.B. Pike, *“B1-Sensitivity Analysis of qMT”*, Poster, International Society for Magnetic Resonance in Medicine Meeting (2015).
* N. Stikov, J. Campbell, **M. Boudreau**, S. Narayanan, T. Stroh, S. Nuara, J. Novek, S. Frey, M.-K. Ho, B. Bedell, G.B. Pike, “*In vivo histology of the myelin g-ratio”*, Poster, Organization for Human Brain Mapping Annual Meeting (2014).
* **M. Boudreau**, N. Stikov, G.B. Pike, *“A B1-Insensitive qMT Protocol”*, Poster, International Society for Magnetic Resonance in Medicine Meeting (2014).
* **M. Boudreau**, C. Tardif, N. Stikov, G.B. Pike, *“A Comparison of B1 Mapping Methods for T1 Mapping at 3T”*, Electronic Poster, International Society for Magnetic Resonance in Medicine Meeting (2014).
* **M. Boudreau**, N. Stikov, G.B. Pike, *“Effect of Different T1 Mapping Techniques on a Quantitative Magnetization Transfer MRI Biomarker for Myelin Density”*, Poster, endMS Conference (2013).
* **M. Boudreau**,N. Stikov and G.B. Pike, *“T1 Mapping: Should We Agree To Disagree?”*, Poster, International Society for Magnetic Resonance in Medicine (2013).

Abstract

Quantitative magnetization transfer (qMT) imaging is a quantitative magnetic resonance imaging (MRI) technique that has demonstrated considerable promise for multiple sclerosis (MS) research. qMT improves on conventional imaging by probing the macromolecules present in myelin, providing a quantitative estimate called the pool-size ratio which correlate strongly with myelin density. qMT requires several other quantitative MRI map for calibration purposes: the main magnetic field (B0), of the radiofrequency amplitude (B1), and the longitudinal relaxation time (T1). These maps can also depend on each other (e.g. some T1 mapping techniques require B1), meaning that the impact of B1-inaccuracies on the fitted pool-size ratio may depend on the choice of T1 mapping technique. The focus of this thesis is to characterize and optimize the B1-sensitivity of qMT.

The first aim of this thesis was to compare several whole-brain B1 mapping techniques, their potential sources of inaccuracies, and their impact on a B1-sensitive T1 mapping technique (variable flip angle – VFA). This study was done in the context of validating a B1 mapping technique using a standard MRI pulse sequence, compared against two other advanced techniques. The second aim was to characterize the B1-sensitivity of qMT for two different T1 mapping techniques: B1-dependent (VFA) and B1-independent (inversion recovery– IR). qMT data were simulated and fitted for a wide range of B1-inaccuracies, and in vivo qMT data were acquired in healthy subjects using both VFA and IR T1 mapping and different B1 mapping techniques. The final aim was to develop an optimization framework for qMT protocols to further improve the robustness against B1-inaccuacies. A sensitivity-regularized Cramér-Rao lower bound expression was theoretically developed as an iterative optimization condition, and was validated for a wide range of conditions (signal-to-noise ratios, B1-inaccuracies, tissue types) using Monte Carlo simulations. Overall, this thesis presents a characterization and optimization of the robustness of qMT to B1-inaccuracies, and suggests that it may be possible to develop an imaging protocol that could omit B1 maps altogether without substantially impacting the pool-size ratio estimates.

Résumé

* Traduction française. (To be translated only after the English abstract is finalized)

Original Contributions

The original contributions of the thesis are:

1. Demonstration that rapid whole-brain B1 mapping using a standard product sequence provides sufficient quality B1 maps to produce accurate variable flip angle T1 maps in white matter, of similar quality to other widely used advanced B1 mapping methods that require pulse sequence programming implementations.
2. Characterization of the sensitivity of quantitative magnetization transfer (qMT) imaging to B1-inaccuracies, and its dependence on the choice of T1 mapping method.
3. Discovery and demonstration that a robust measurement of the qMT biomarker for myelin density (pool-size ratio) can be maintained in the presence of large B1 inaccuracies if the variable flip angle T1 mapping method is used in the qMT processing pipeline.
4. Development and validation of an iterative optimization strategy of qMT acquisition protocols for minimized sensitivity to B1-inaccuracies, potentially eliminating the requirement of B1 maps from qMT acquisition protocols.

# *Introduction*

## Motivation

Quantitative magnetic resonance imaging (MRI) is a subset of MRI techniques which measures specific properties about the subject, or physical quantities of the imaging environment. Although the majority of acquired MRI images are qualitative in nature, meaning that the signal intensity of a pixel is due to a combination of several factors that aren’t all precisely known and likely vary between scanners or subjects, quantitative MRI promises more specificity, accuracy, and reproducibility for estimates of biological or system properties, which is particularly of interest in a research setting. If clinical MRI is imagined to be a camera capable of non-invasively capturing pictures of inside the body, quantitative MRI should be interpreted to be the scientific instrument analogue of this camera.

Most diseases for which clinical MRI is used as a diagnostic tool could benefit from quantitative MRI to study their biological origin, progression, and treatments. In particular, one disease that has widely benefited from the advent of MRI is multiple sclerosis (MS), an autoimmune disease of the central nervous system that results in the destruction of myelin which wraps around axons. This loss of myelin, which acts as an electrical insulator, inhibits signal transmission between neurons, resulting physical and cognitive impairments. MS is a disease that has benefited significantly from MRI, both for diagnostic purposes and to study the disease in a research setting. However, clinical imaging techniques of MS are not specific only to myelin loss and can have confounding factors, such as edema. Several quantitative MRI techniques have emerged to provide better specificity and quantification of myelin density, one of which is called quantitative magnetization transfer (MT) imaging. Quantitative MT (qMT) improves on clinical MRI techniques by probing the myelin content which is typically unobservable using conventional imaging techniques due to its rapid signal decay. Providing several quantitative values, one qMT parameter, the pool-size ratio, has been shown to correlate strongly with myelin density in post-mortem histological studies.

Magnetization transfer is the phenomenon where energy that is selectively sent using radiofrequency (RF) pulses to hydrogen in macromolecules (“restricted” pool) is transferred to nearby hydrogen in water molecules (“free” pool) through dipolar interactions or chemical exchange. Image voxels containing a high density of myelin (mostly composed of macromolecules) will see greater signal loss in the presence of an MT effect. To estimate quantitative tissue values (e.g. pool-size ratio) from qMT data, several MT images must be acquired (typically 10 or more, varying in frequency and amplitude of the MT pulse) to fit the data for all the parameters in the mathematical model (3 to 5 independent fitting parameters). Three additional calibration measurements are also necessary: a B0 map to account for main magnetic field inhomogeneity, a B1 map for radiofrequency amplitude inhomogeneity, and a T1 map to constrain a subset of the fitting parameters. In general, the absence or inaccurate estimate of any of these additional measurements will also result in an error of the estimate of one or more of the quantitative MT fitting parameters. Because the calibration measures do not have perfect accuracy and can be sensitive to different error sources (which varies between the techniques used to measure these maps), it should be desirable to reduce the sensitivity of the qMT experiment to inaccuracies in calibration techniques (e.g. from noise or small artifacts). However, some of the calibration methods required for qMT can also require calibration maps. For example, the widely used whole-brain T1 mapping technique Variable Flip Angle (VFA) also depends on B1 maps as a calibration measurement, unlike other T1 mapping techniques which are B1-independent, such as inversion recovery (IR). Therefore, the error propagation due to inaccuracies in B1 maps likely impacts the qMT fitting parameters differently depending on which T1 mapping technique is chosen: B1-dependent (e.g. VFA) or B1-independent (e.g. IR).

## Objectives

**The broad objective of this thesis is to improve the robustness of qMT against potential inaccuracies in measured B1, the amplitude of transmitted radiofrequency electromagnetic fields, in order to improve the estimates of the pool-size ratio, a promising biomarker for myelin density.** The rational is that lower B1-sensitivity of the pool-size ratio will improve estimates of the myelin density comparisons between space and time, since B1 maps can have regional inaccuracies such as artifacts, and could also differ between scanning sessions in longitudinal studies. If the B1-sensitivity of the pool-size ratio is sufficiently lowered, it could even be possible to develop a protocol in which the B1 map could be entirely omitted, reducing the total acquisition time. The three core objectives of this thesis are:

1. To identify and compare potential sources of B1-inaccuracies amongst common whole-brain B1 mapping methods, and investigate the impact of B1-inaccuracies on a B1-dependent T1 mapping method. This will be explored in the context of a study comparing state-of-the-art whole-brain B1 mapping techniques with a technique capable of being implemented using standard MRI pulse sequences that are typically available on clinical scanners, having a target audience of researchers who do VFA T1 mapping in their studies but omit B1 correction due to unavailability of modern whole-brain B1 mapping pulse sequences at their disposal.
2. To fully characterize the sensitivity of qMT parameters to B1-inaccuracies, and compare between the use of B1-dependent (e.g. VFA) and B1-independent (e.g. IR) T1 mapping techniques. qMT benefits from B1 maps to correct the MT-sensitizing RF pulse and excitation pulse flip angles for fluctuations in B1 amplitude that naturally occur in a loaded coil. However, T1 maps, which are required to constrain model parameters in qMT, can also depend on B1 as a flip angle correction factor, meaning that B1-error propagation to qMT will behave differently depending on the choice of T1 mapping technique. The aim of this study is to determine the T1 mapping technique that results in the lowest B1 sensitivity of the qMT pool-size ratio estimate for a given qMT acquisition protocol.
3. To develop aqMT acquisition protocol optimization algorithm to further improve the B1-insensitivity of the pool-size ratio estimate. Having determined the optimal T1 mapping technique for a given qMT acquisition protocol in objective ii), this objective will use consider that choice in T1 mapping technique and will vary optimize qMT acquisition protocol itself (e.g. off-resonance frequencies, MT flip angles). A theoretical framework for an iterative optimization algorithm for B1-insensitivity will be developed, and validated using simulations for a wide range of specified conditions (e.g. B1 error, signal-to-noise level, tissue types).

## Thesis Outline

This thesis is written in a manuscript-style format and contains three completed manuscripts, which as of the time of initial submission, two have been accepted and one has been submitted to peer-reviewed international scientific journals. Chapter 2 contains a brief review of relevant background material about MS and several quantitative MRI techniques relevant to the later chapters. This thesis is written with the assumption the reader has a solid foundation in the basics of MRI physics, and this chapter looks to bridge the knowledge gap required to understand the manuscripts, which deals with more advanced MRI techniques. Chapter 3 contains the first manuscript titled “B1 Mapping for Bias-Correction in Quantitative T1 Imaging of the Brain at 3T Using Standard Pulse Sequences”, which was published in the *Journal of Magnetic Resonance Imaging*. This works presents a comparison in B1 and resulting VFA T1 map quality between modern whole-brain B1 mapping pulse sequences typically not available to most researchers/clinicians, with a B1 mapping technique implemented using only the standard pulse sequences conventionally available on most MRI scanners. Chapter 4 contains the second manuscript titled “B1-Sensitivity Analysis of Quantitative Magnetization Transfer”, which was accepted and is currently available in Early View in the journal of *Magnetic Resonance in Medicine*. This work presents a characterization of the B1-sensitivity of qMT fitted parameters using simulations and in vivo measurements, and in particular does a comparison between using B1-dependent and B1-independent T1 mapping techniques. Chapter 5 contains the last manuscript titled “Sensitivity-Regularization of the Cramér-Rao Lower Bound to Minimize B1 Nonuniformity Effects in Quantitative Magnetization Transfer Imaging”, which was submitted and is currently under review in the journal of *Magnetic Resonance in Medicine*. This work proposes a sensitivity-regularized approach of the Cramér-Rao lower bound as an optimization condition, and uses Monte Carlo simulations to compare several qMT acquisition protocols to determine their robustness under several conditions (B1 error range, signal-to-noise level, tissue type). Lastly, Chapter 6 presents a summary of the three manuscripts, and briefly explores potential future work topics.

# *Background*

## Multiple Sclerosis

### Overview

Multiple sclerosis (MS) is an autoimmune disease that attacks the central nervous system. Canada has one of the highest prevalence of MS in the world [1]; approximately 1 in 340 Canadians have MS [2]. Affecting women disproportionately relative to men (3:1), the rate of incidence has also been observed to increase disproportionally for women in the last century [3]. There is no cure for MS. The exact cause of the disease remains unknown, both environmental and genetic factors have been shown to increase the risk of getting the disease [4-6]. People living in countries at higher latitudes have a higher incidence rate of MS [7-9], and are at a higher risk if an immediate family member also suffers from the disease, up to a 25% chance for identical twins [10]. Clinical onset of MS mostly begins between the ages of 15 and 40 [11]. Typical physical and cognitive symptoms include vision problems, incoordination, fatigue, difficulty speaking and/or swallowing, pain, spasms, depression, and impaired information processing speed [12,13]. For most people with the disease, symptoms will initially be temporary ( called “attacks” or “flare-ups”, lasting between days up to several months [14]) with partial or complete recovery during the relapse-remitting multiple sclerosis (RRMS) stage of the disease, followed by the secondary progressive multiple sclerosis (SPMS) stage where there is a gradual increase in disability over time. There is no cure for MS. Treatment strategies mostly involve drug therapies to reduce the frequency of attacks (e.g. interferon beta) or hasten recovery after an attack has already begun (e.g. using corticosteroids) [15]. A particularly promising recent Canadian study demonstrated that stem-cell treatment after immunoablation was effective at suppressing long term inflammatory activity in a population with early-aggressive MS [16]. Development of drug therapies that promote remyelination is also an active area of research [17,18], however one of the important challenges in this field is accurately quantifying the myelin regeneration in vivo. Clinical MRI techniques used for diagnosing MS are not specific enough to myelin density for this purpose; quantitative MRI techniques are expected to emerge as a useful tool for remyelination quantification in clinical trials [18,19].

The mechanisms regulating damage in MS are still not fully understood. Broadly, demyelination in white matter (WM) lesions is believed to be a result of an immunologically mediated attack on myelin and oligodendrocytes [20,21]. In active MS lesions, T-cells mistakenly recognize myelin antigens as a foreign body and responds by emitting cytokines, attracting more lymphocytes to the site that disrupts the blood-brain barrier and amplifies the immune system response. Macrophages responding to the released cytokines attack the myelin. Following this immune-mediated attack, if local oligodendrocytes are still present, some level of remyelination may occur [22]. However, after repeated attacks irreversible damage will set, such as axonal degeneration and axon bisection. Several other characteristic phenomena occur over the course of the disease progression, such as gliosis (scarring), degeneration of the distal segment of transected axons (Wallerian Degeneration), abnormalities in the non-lesion WM (normal appearing white matter - NAWM), brain atrophy, and cortical lesions. Although MS has mostly been described as a WM disease, post-mortem histological evidence has shown many abnormalities in cortical GM of MS patients. GM lesions are characterized by demyelintation, axonal and dendritic transection, neuronal apoptosis and limited inflammatory cell content compared to WM lesions [23,24].

### Role of MRI in MS

The gold standard criteria for diagnosing MS with MRI since 2001 has been the McDonald Criteria [25], subsequently getting two revisions in 2005 and 2010 [26,27], and with a most recent update in 2016 by the European group MAGNIMS (Magnetic Resonance Imaging in MS) [28]. These criteria require that hyperintense lesions in T2-weighted MRI images be observed to have a dissemination in space (three out of the following lesions: at least 3 periventricular, 1 cortical/juxtacortical, 1 infratentorial, 1 optic nerve, or 1 spinal cord) and display a dissemination in time (new lesions relative to a previous scan). In addition, these can both be determined in a single imaging session if a gadolinium-enhancing T1 lesion is observed instead of the dissemination in time condition above (suggesting a disruption in the blood-brain barrier of an early lesion). It’s important to note that the presence of a lesion in one part of the brain does not always predict a symptom in the corresponding anatomical/physiological region [29], meaning that the criteria above is not sufficient in itself for diagnosing MS. MRI provides an additional tool for the diagnostics of MS when supplementing the patient’s history and a physical exam done by a neurologist [30].

Beyond clinical MRI, there are a broad range of other techniques which are widely used to study MS in research settings, of which we will mention a select few here. Brain atrophy in MS has been shown to correlate more with disability than clinically identified lesions [31,32], and can be estimated with manual or automated tissue segmentation using structural images like T2-weighted fluid attenuated inversion recovery (FLAIR) [33,34]. Magnetization transfer and diffusion tensor imaging have both demonstrated better sensitivity to abnormalities in NAWM [35,36], widespread throughout the brain and in regions preceding lesion formation. In post-mortem studies, diffusion and magnetization transfer metrics have both been shown to correlate with myelin content and axonal count [37-39]. Blood-oxygen-level dependent (BOLD) functional MRI (fMRI) used in MS to study cognitive dysfunctions and phenomenon like motor and cognitive reorganization during the disease progression [40,41]. Lastly, the role of GM pathology in MS has been increasingly investigated as a possible role in cognitive dysfunction that become evident during the progressive stage of the disease. Although cortical GM has low myelin content relative to WM, magnetization transfer techniques have demonstrated sensitivity to demyelination in cortical GM lesions [42,43], and are useful to investigate and/or segment cortical lesions and atrophy [44-46].

## Quantitative MR Imaging

Prior to presenting the theory behind qMT imaging, which is the focus of this thesis, several other quantitative imaging techniques must be discussed, as qMT requires these measurements for calibration and to constrain fitting parameters in certain fitting models. The following section briefly presents the relevant tissue and field properties of interest for qMT, and explains select measurement techniques for these which are widely used, particularly in the manuscripts of the later chapters of this thesis. Countless other measurement techniques of these properties exist, but are not presented here.

### Tissue Properties (T1, T2)

*Longitudinal Relaxation Time (T1)*

The longitudinal (or spin-lattice) relaxation time (T1) is a value that describes how rapidly longitudinal magnetization (Mz) returns to its thermal equilibrium values (M0) after excitation, which typically behaves mono-exponentially for liquids. The relaxation rate (R1 = 1/T1) is sometimes defined instead of T1. For the simplest case (e.g. liquids), this behavior is mono-exponential. At clinical field strengths, T1 is approximately several seconds for liquids, near one second for soft tissues, and between one and several seconds for solids (which has multi-exponential behavior). Unlike T2, T1 is highly dependent on field strength (proportionally) for the range commonly to image humans (1.5 to 7 Tesla), because higher energy level differences of the spins (Zeeman effect) are needed to be bridged by the magnetic fields from fluctuating nearby spins. For example, one study measured T1 values at 1.5/3.0/7.0 Tesla to be 650/840/1,130 ms for WM and 1200/1600/1940 ms for GM. Knowledge of T1 values for tissues is important in several areas, such as optimizing pulse sequences for signal-to-noise (e.g. in steady-state pulse sequences), for maximum contrast (e.g. FLAIR), and for estimating other quantitative parameters (e.g. dynamic contrast enhancement – DCE [47,48]). For qMT, T1 is a necessary parameter to constrain several fitting parameters in the model which will be discussed later.

The most widely known T1 mapping pulse sequence which is typically considered the gold standard is Inversion Recovery (IR) [49,50]. A simplified pulse sequence diagram for IR is presented in Figure 2‑1. The longitudinal magnetization is initially inverted with an inversion pulse (180°). After allowing a time interval (inversion time – TI) for the longitudinal magnetization relaxes towards its equilibrium state, a saturation excitation pulse (90°) is applied and k-space data is acquired. By repeating this experiment for several TI values (allowing for a wide range of different longitudinal relaxation amounts to occur), an estimate of T1 can be determined by fitting the data voxel-wise for each TI. There are several forms of fitting equations to fit IR data, and an overview of them are covered in depth by Barral et al. [51]. For complex data (magnitude & phase), the fitting equation that has been shown to be most robust inaccuracies of the inversion and saturation flip angles and to shorter TRs (shorter than the TR ≈ 5T1 needed for full recovery [51,52]) is the following 5-parameter model, assuming a single tissue type within the voxel:

|  |  |
| --- | --- |
|  | **(2-1)** |

where *a* and *b* are complex fitting parameters and *In* is a complex voxel-wise signal value for the TIn measurement. If only magnitude data is available, a modified version of Eq. (2-1) must be used but is too cumbersome to be explained here (see Eqs. 20-24 of Ref. [51] ). Note that IR fitted using this form, unlike alternative forms of Eq. 2-1, is very robust against flip angle-inaccuracies/B1-inaccuracies. Inversion recovery is typically limited to a single-slice technique in practice, requiring long TR relative to other steady-state techniques (TR > T1). Some modified inversion recovery methods exist to accelerate the acquisition, such as Look-Locker [53,54], which acquires several TIs within a single TR using a small flip angle and is a more B1-dependent technique than IR. Another inversion recovery-based T1 mapping technique that has become increasingly used due to its availability as a standard MRI scanner pulse sequence over the course of this thesis work is Magnetization Prepared 2 Acquisition Gradient Echo (MP2RAGE) [55]. MP2RAGE simultaneously acquires a T1-weighted map and a T1 map, is a B1-independend measurements like IR, and has potential applications for MS research [56].



Figure ‑. Simplified pulse sequence diagrams of two T1 mapping techniques: Inversion Recovery (IR) and Variable Flip Angle (VFA).

Variable Flip Angle (VFA) is alternative T1 mapping technique that is capable of mapping T1 throughout the brain in a clinically feasible acquisition time [57,58]. VFA also sometimes goes by the name DESPOT1 (Driven Equilibrium Single Pulse Observation of T1) [59]. A simplified pulse sequence diagram for VFA is presented in Figure 2‑1. VFA is a steady-state technique that uses a spoiled gradient echo (SPGR) pulse sequences. VFA takes advantage of the fact that the SPGR acquisition signal for short TR (TR T1, in the tens of ms range) is very sensitive to the flip angle (α) and T1. By acquiring d SPGR images using different small flip angles, the T1 values within a voxel can be estimated by fitting the magnitude data to the steady-state SPGR signal equation:

|  |  |
| --- | --- |
|  | **(2-2)** |

where K is a constant that includes tissue density and receiver coil sensitivity information. Although T1 could be estimated by a fitting Eq. (2-2) using non-linear fitting algorithms, which could be time-consuming for high-resolution whole-brain scans, the terms can be rearranged so that a solution can be found in terms of a linear equation of the form y = mx + b:

|  |  |
| --- | --- |
|  | **(2-3)** |

Because and TR are known values, this equation can be solved for T1 rapidly by linear fitting for a minimum of two flip angles (slope = ). However, one caveat of this method is that due to its sensitivity to the flip angle, it is a B1-dependent T1 mapping method, meaning that a B1 map must be acquired to correct the nominal flip angles for accurate estimation of T1 values using this technique. One advantage of VFA T1 mapping is that SPGR is a standard pulse sequence on most MRI scanners, making whole-brain T1 mapping accessible to a wide range of researchers and clinicians if they also acquire a B1 map, which is not always the case [60], particular for DCE studies [48,61,62].

*Transversal Relaxation Time (T2)*

The transverse (or spin-spin) relaxation time (T2) is a value that describes how rapidly transverse magnetization (Mxy) returns to its thermal equilibrium values (0) after excitation in the absence of magnetic field inhomogeneities, which typically behaves mono-exponentially for liquids. T2 is always smaller or equal to T1, otherwise it would be feasible for the length of the total magnetization vector to exceed the equilibrium values (M0) under certain circumstances. In general, T2 is longer in liquids (~ seconds) than in solids (~ microseconds), and tissues have an intermediate T2 range of 25-100 ms [63]. Macromolecules, such as proteins and lipids in myelin, have T2 values closer to solids (~10 microseconds) [64], due to a longer rotational correlation time of hydrogen in these molecules [65]. In general, T2 does not have a strong dependence on field strength (unlike T1); however, T2\* – the apparent T2 in the presence of static field inhomogeneities ­ does have a strong dependence on main magnetic field strength (inversely proportional) [66].

qMT does not require a quantitative T2 map for calibration or to be a constraint. However, most qMT models do inherently fit the data for T2 values. In the two-pool qMT model (to be discussed in detail later), qMT models typically have two different T2 fitting parameters: T2 of the “free-pool” (T2,f, on the order of milliseconds) and T2 of the “restricted pool” (T2,r, on the order of microseconds). Some groups choose to fix the T2,r values to the average whole-brain value in their fitting models [67], in part because histopathology studies have not observed a correlation between T2,r and myelin density [39]. Nevertheless, quantitative T2 mapping is an important technique for MS, as it is used to estimate the myelin water fraction (MWF) [68,69], a measure that has been shown to correlate with myelin content [70,71]. MWF is calculated as the ratio of T2 distribution of water trapped between the myelin layers (~40-50 ms) over the T2 distribution of intra/extracellular water (~100 ms). These T2 distributions are typically estimated by fitting multi-component T2 signal decay curves with multi-echo spin-echo pulse sequences; a comprehensive technical review of MWF acquisition methods is presented in Alonso-Ortiz et al. 2015 [72].

### Field Properties (B0, B1)

*B1 Mapping*

The transmit radio-frequency (RF) amplitude (“B1+”, but often written simply as “B1” in the context of qMRI imaging) is a quantity that directly impacts the actual flip angles magnetization in a voxel rotates due to an on-resonance RF pulses and energy that is absorbed by the tissue. Spatial inhomogeneity of B1 leads to different spins across the sample to experience different flip angles, which can lead to differences in image contrast throughout the sample. Although B1 can refer to the actual RF magnetic field amplitude (on the order of microteslas [73]), it is more commonly referred to as a normalized correction factor of the nominal flip angle that is set by the user at the scanner (α = B1·αnominal). B1 maps are often measured as a calibration measurement for quantitative MRI techniques, however some interesting parameters can be derived directly from B1 maps, such as the electrical conductivity and permittivity of tissues[74], and the local spectral absorption rate (SAR) [75]. Even B1 is calibrated to a high degree of homogeneity in an empty scanner using pickup coils, electrodynamic interactions with tissue (loading/boundaries) will impact and distort the B1 amplitude profile [76]. For a human head, this pattern is generally elliptical [77]. B1 inhomogeneity is also heavily influenced by field strength due to the lengthening of the RF wavelength, worsening at higher field strengths. B1 inhomogeneity is particularly a challenge at ultra-high fields (7T+) due to the RF wavelength being approximately the dimensions of the human head, leading to constructive/destructive interference of the RF wave [78].



Figure ‑. Three widely used B1 mapping methods.

One of the simplest ways to map B1 in vivo is to acquire two images using different excitation flip angles. The actual voxel-wise flip angles can be then estimated with simple trigonometry, by calculating the ratio in expected signal amplitudes. Using the Double Angle (DA) method, one image is acquired with double the excitation flip angle than the other, which results in a very simple equation for a spin-echo acquisition pulse sequence (Figure 2‑2) [79,80]:

|  |  |
| --- | --- |
|  | **(2-4)** |

Another implementation of the DA method uses a spin-echo pulse sequence where the inversion pulse is 2α instead 180°, since some MRI scanner manufacturer set their spin-echo pulse sequence to be α-2α. The equation for the DA B1 differs from the one above and can be found in Wang et al 2005 [81]. DA B1 mapping is easy to implement using pulse sequences available on most scanner, however to completely reduce the influence of T1 relaxation in the region of interest, it requires a long TR (at least longer than a few T1’s [80], but ideally TR≥5T1), usually limiting the pulse sequence to a single-slice technique. Other pulse sequence variations of the double angle technique exists, to improve acquisition properties like acquisition time [81,82] and slice profile effects [83].

Numerous rapid whole-brain B1 mapping techniques have been developed over the years. The popular techniques to have emerged in the past decade is Actual Flip angle Imaging (AFI) [84] and Bloch-Siegert (BS) shift [85] B1 mapping (Figure 2‑2). AFI is a 3D technique implemented using a steady-state imaging approach, whereas BS is a phase-based imaging technique. The AFI pulse sequence is a SPGR-based technique, in which in a single TR two acquisitions occur with different delays before the next excitation pulse (TR1 and TR2, TR1 ≠ TR2). The steady-state signal for each acquisition will be different because of the different time allowed for relaxations relative to the previous excitation pulse. If TR1 and TR2 are both very short relative to T1, and B1 for this experiment can be calculated from the following equation [84]:

|  |  |
| --- | --- |
|  | **(2-5)** |

where *r* = and *n* = . B1 calculated from AFI is very insensitive to T1 values [84], however it can be sensitive to incomplete RF and gradient spoiling [86,87]. The AFI pulse sequence is currently not typically available by default on most MRI scanners, and must be implemented on-site by an MRI pulse sequence programming expert. Despite this, it is used in a wide array of applications, particularly for B1 mapping at very high fields strengths [88-91].

BS is a phase-based B1 mapping technique that uses the Bloch-Siegert shift effect. The Bloch-Siegert shift is a change in experienced precession frequency of spins in the presence of an off-resonance RF with a frequency far off-resonance, sufficiently far so that no excitation occurs. Conceptually, the spins in the rotating frame at the off-resonance frequency of the RF pulse experience a non-zero Bz vector, and far off-resonance this vector component will dominate over the B1 vector component in transverse plane, such that the spins will precess about Bz at a rate proportional to the B1 amplitude. This results in a phase accruement which also is dependent to the B1 amplitude of the off-resonance RF pulse. Typically, BS B1 mapping is implemented by acquiring two images each using symmetrically off-resonance RF pulses (Δ=±), applied between the excitation pulse and readout. B1 values can be calculated from this experiment using the following equations [85]:

|  |  |
| --- | --- |
|  | **(2-6)** |
|  | **(2-7)** |

where is the voxel-wise phase image for the Δ=+ acquisition, is the voxel-wise phase value for the Δ=- acquisition, and is the gyromagnetic ratio of the spin population, T is the total duration of the off-resonance pulse, is the excitation pulse flip angle, and is the pulse profile of the off-resonance B1 pulse. The off-resonance RF pulse is typically very long (~10 ms) relative to the excitation pulse and has a wide Fermi or Gaussian profile so that the spins experience a very small frequency band in practice (due to Fourier theory). BS also exhibits minimal sensitivity to T1 effects [85], however it depends on reliable phase unwrapping, which can be challenging in the presence of artifacts such as fringe lines and phase poles [92]. Conventional BS imaging has very high SAR, which is a potentially limiting factor for high field applications, however some modifications to the technique have been proposed to make BS accessible for high field quantitative MRI [88,93].

*B0 Mapping*

The local main magnetic field (B0) influences the resonant precession frequency of spins at that location. In principle, it is very simple to quantify B0 relative to other quantitative MRI parameters. Most scanners come equipped with at least one pulse sequence to acquire B0 or a field map; this information is needed during the shimming process of MRI scanners. The simplest pulse sequence used acquire it is a simple SPGR pulse sequence, and two images are acquired at different TEs. Using a phase subtraction technique, B0 – which in quantitative MRI is usually terms of a frequency – can be simply calculate using the following equation [94]:

|  |  |
| --- | --- |
|  | **(2-8)** |

If B0 or is too large, the phase () can exceed ±π radians, and the phase images will require phase unwrapping prior to calculating the differences, which can also have some challenges as briefly mentioned in the BS discussion above (e.g. fringe lines & poles). Also, the B0 field inhomogeneity can be cause pulse sequence-varying factors, for example Eddy currents induced in the MRI hardware as a result of strong time-varying magnetic field gradients. Thus, for B0 correction of other quantitative MRI techniques, it may be desirable to use a B0 mapping pulse sequence that more closely reproduces the field environment of the quantitative MRI sequence that will use the B0 calibration.

## Magnetization Transfer Imaging

### Two-Pool Model of MT

The largest contribution of signal from conventional MRI experiments originate from hydrogen in water molecules, which is plentiful and dense in human organs (except the lungs) and generally have a slow signal decay (~10s to 100s ms) which allows time for an imaging experiment to occur. Hydrogen is also present in numerous other molecules, such as macromolecules (lipids and proteins) which myelin are comprised of. However, MRI signal from hydrogen in these molecules decay very quickly (T2 ~ µs) due to their semi-solid nature and long rotational correlation times, making it very challenging to image myelin directly. Concomitantly, a consequence of this very short T2 is a very broad spectrum of resonant frequencies for these macromolecules (~10’s of kHz). In the 1970s and 1980s, researchers discovered that by selectively exciting the macromolecular hydrogen with off-resonance RF pulses prior to an NMR/MRI acquisition pulse sequence, some longitudinal magnetization from water hydrogen will be transferred to nearby macromolecules through a process called cross-relaxation, resulting in a lower MRI signal in regions where there is an abundant quantity of macromolecules near water [95-97]. This discovery lead to the development of the two-pool model of magnetization transfer (Figure 2‑3), in which magnetization from hydrogen in water of a voxel is referred to as the “free-pool”, and macromolecular hydrogen is referred to as the “restricted-pool”.



Figure ‑. Two-pool model of the magnetization transfer effect.

Conceptually, the magnetization transfer effect as discussed above and presented in Figure 2‑3 can be difficult to comprehend, because of the following questions: (1) a magnetization vector is not a conserved physical property (e.g. a 90° pulse followed by a crusher gradient converts a [M0, 0, 0] magnetization vector to [0, 0, 0], thus why in MT is it “transferred” from one pool to another (like momentum, energy)?, (2) what underlying mechanism allows magnetization get “transferred” from the free-pool to the restricted pool, (3) why is excitation of the restricted pool needed to initiate this process? The answer to all these questions lies in the fact that it is more specifically *energy* of the spin populations between the two pools that is being transferred during the MT process, and magnetization changes as a result of differing energy level populations of the spins. To illustrate this, Figure 2‑4 shows the energy level diagrams at three different stages of a magnetization transfer experiment. For simplicity, the relaxation rates of each pools (which in reality are present) are neglected in this diagram.

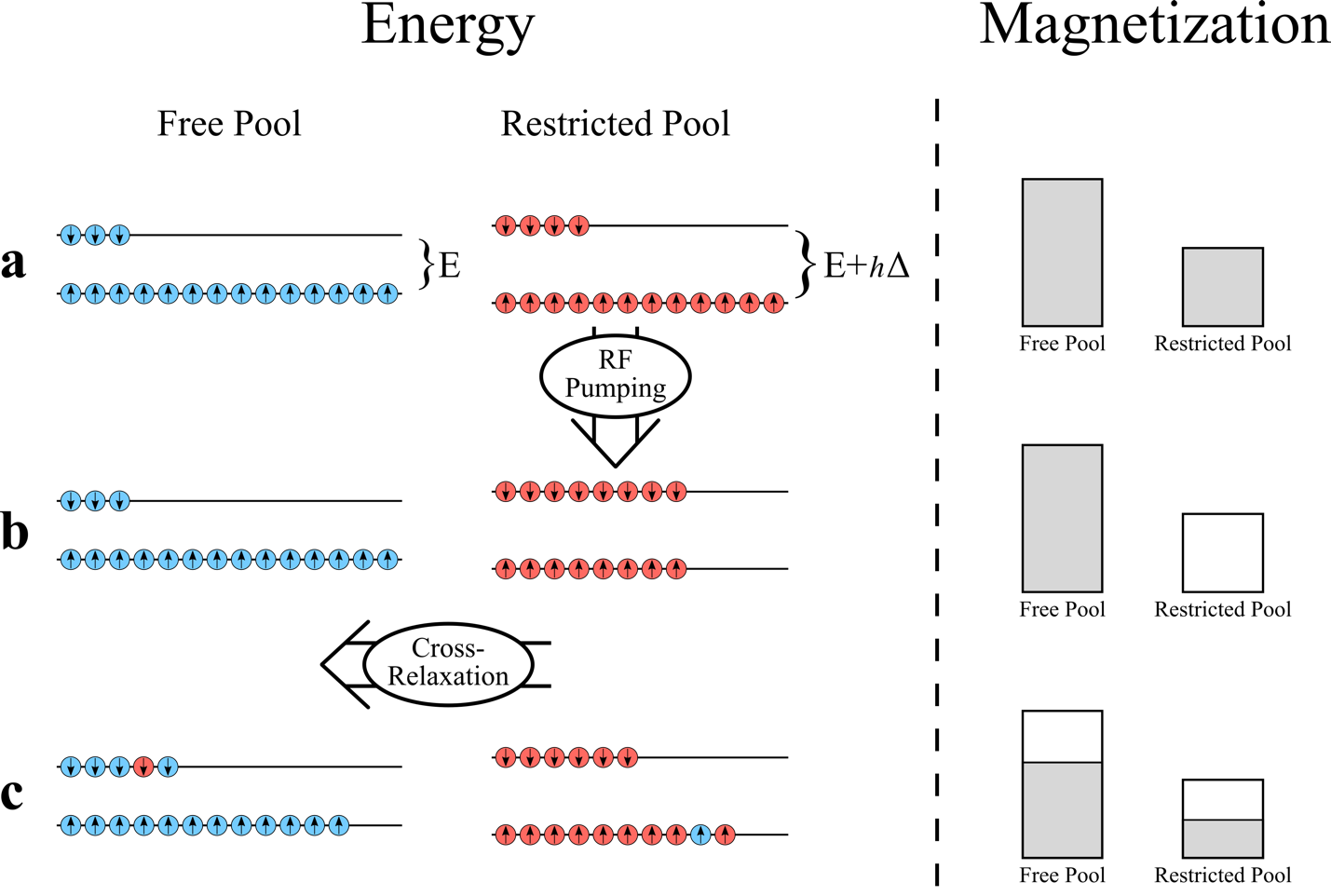


Figure ‑. Energy level (left) and magnetization (right) diagrams of restricted and free pool hydrogen a) at thermal equilibrium, b) after an off-resonance pulse, and c) after cross-relaxation/MT-exchange.

Considering an initial condition of thermal equilibrium, the spin populations for both pools will be distributed unevenly between the two energy levels caused by the Zeeman effect of spins in an external magnetic field, and an excess of spins in the low energy levels will result in total longitudinal magnetization vectors (Mz) of M0,f and M0,r for the free and restricted pools (Figure 2‑4a). By using an off-resonance pulse, the restricted pool can be selectively saturated, without impacting the energy levels of the free pool (Figure 2‑4b; in practice, there is some saturation of the free pool that needs to be modeled). The excess energy provided to the restricted pool in this example reduces the total longitudinal magnetization vector of the spins to 0. Lastly, over time the excess energy pumped into the restricted pool will dissipate nearby hydrogen spins in the free pool by a stochastic process, through phenomena such as dipolar-coupling and chemical exchange. The excess energy loss by the restricted pool results in an increase in longitudinal magnetization, while the excess energy gain by the free pool results in a reduction in longitudinal magnetization, giving rise to an apparent magnetization exchange from the free pool to the restricted pool. The two-pool model is a simplified version of the phenomenon; a four-pool model (myelin water, intra/extra cellular water, myelin semi-solids, non-myelin semi-solids) has also been proposed, as it modeled in MWF imaging. However, it’s been shown that the two-pool model is sufficient to model quantitative MT phenomenon in WM [98].

### MTR and MTsat

*Magnetization Transfer Ratio (MTR)*

The simplest and most widely used measure of the magnetization effect is the magnetization transfer ratio (MTR). In this experiment, two images are acquired with (*IMT*) and without (*I0*) an off-resonance RF pulse preceding the imaging pulse sequence, and MTR is the normalized difference of these two images calculated in terms of a percentage:

|  |  |
| --- | --- |
|  | **(2-9)** |

As discussed in the previous section, the greater the MT effect (e.g. more macromolecular content), the less *IMT* values will be, thus leading to higher MTR values. In the context of MS, demyelinated lesions are expected to have higher MTR voxel values relative to NAWM. An example MT imaging pulse sequence (MT-prepared SPGR) is shown in Figure 2‑5. In this pulse sequence, a typical short-TR SPGR pulse sequence is preceded by a long off-resonance RF pulse with a Gaussian pulse envelope. Prior to the excitation RF pulse (on-resonance) of the SPGR imaging sequence, a spoiler gradient is applied to eliminate any potential free-pool (long T2) magnetization that was excited by the MT pulse and rotated into the transverse plane as well as any residual transverse magnetization from the previous excitation pulse. For the MT-off image (*I0*), the same pulse sequence timing and gradients would be used but without the off-resonance RF pulse.



Figure ‑. Pulse sequence diagram for a pulsed MT-weighted spoiled gradient echo (SPGR) pulse sequence with a Gaussian MT pulse shape. RF: radiofrequency pulse, SS: slice-selecting gradient, PE: phase-encoding gradient, RO: readout gradient, AQ: data acquisition.

MTR pulse sequences are available on most clinical MRI scanners, making it an accessible imaging tool for researcher and clinicians. Due to its simplicity in implementation and computation, it is possible to produce a whole-brain high-resolution MTR maps in a clinically feasible time. However, MRI manufacturers often impose a fixed off-resonance frequency, effective MT pulse flip angle, and MT pulse shape envelope, all of which have an influence on the MT effect, thus on the MTR value. Because the values for these parameters are not standardized between MRI manufacturers, the MTR values for tissues/lesions can differ substantially between imaging sites. One large multi-center study previously observed MTR values at 1.5T in WM ranging between 9% and 51% [99], and as a result standardized protocols have been proposed [100,101]. MTR is not solely sensitive to macromolecular density; it groups all the factors that impact the MT-prepared SPGR steady-state signal into a single value, such that MTR is also sensitive to effects such as B1 inhomogeneity and local T1 values. Thus, MTR is typically referred to as a semi-quantitative MRI measure. Researchers have proposed corrective factors for MTR maps, in particular for B1 inhomogeneity [82,102]. However, requiring a B1 map increases the acquisition time, and B1 mapping pulse sequences are always available on most scanners as a default setting, reducing the accessibility of B1-corrected MTR for researchers and clinicians. The impact of T1 on MTR is also an important consideration, as it varies not only between tissues by also due to other biological processes, such as inflammation and edema which occur in MS lesions [103], and disassociating these effects with demyelination can be challenging for a single measure like MTR. Despite some drawbacks, MTR has been shown to correlate significantly with myelin density and axonal count in MS brains using post-mortem immunohistopathology [38,104], and has been widely used for in vivo MS research studies to infer on de/re-myelination monitoring [19,105-107], diffuse NAWM/NAGM and GM pathology [45,108-114], and therapeutics clinical trials [115-118]. Beyond MS applications, several other diseases with neurological manifestations are studied using MTR, such as schizophrenia [119,120], HIV [121], Alzheimer’s disease [122], and major depressive disorder [123].

*Magnetization Transfer Saturation (MTsat)*

Another semi-quantitative measure of the MT effect is the magnetization transfer saturation (MTsat) value [124]. MTsat is an emerging MT technique with inherent compensation for B1 profile effects and lower sensitivity to T1 differences, and might have all the same potential applications for MS research as were listed above for MTR. Unlike MTR, which is the normalized difference of the steady-state signal with and without an MT-preparation RF pulse, MTsat is an estimate of the fractional longitudinal magnetization reduction caused by the MT pulse within a single TR (after a steady-state has been established). MTsat only requires one additional measurement to two SPGR-MTR acquisitions; one T1-weighted SGPR scan with different TR/α values (↓/↑, respectively) and no MT pulse. From these three measurements (: MT-off SPGR, : MT-on SPGR, : T1-weighted SPGR), MTsat can be calculated directly with the following equations [124,125]:

|  |  |
| --- | --- |
|  | **(2-10)** |
|  | **(2-11)** |
|  | **(2-12)** |

where is the excitation flip angles in radians, and TR is the repetition times in seconds. MTsat calculated in Eq. (2-10) is a fractional value (~10-2), which is sometimes expressed in percentage units (as is done with MTR) by multiplying by 100. Because both MTR and MTsat can both be expressed as percentage units, there is a risk of confusion in interpreting MTsat values relative MTR. MTsat is substantially lower than MTR in tissues, because it represents the fractional signal saturation from a single MT pulse and not the overall steady-state signal differences like MTR. One other caveat to MTsat is that it is somewhat proportional to the effective flip angle of the MT pulse, making it challenging to interpret MTsat values reliably between sites if they use different acquisition protocols. Nonetheless, MTsat is very simple to implement, only requires one additional measurement relative to MTR, and could be an accessible alternative to MTR for researchers in need of a semi-quantitative MT measure with more robustness against B1 and T1. MTsat has been shown to correlate better with MS disability levels than MTR in NAWM and the spinal cord [126] and to have a more linear correlation with the pool-size ratio (restricted/free) than MTR [127]. It has been used in other applications such as g-ratio measurement (ratio of the inner/outer diameter of the myelin sheath of an axon) [127,128], segmentation of deep grey matter structures [129], and hypomyelinating disorders [130].

### Quantitative Magnetization Transfer Imaging

Quantitative measurement of the magnetization transfer effect requires a mathematical model describing the evolution of magnetization/signal throughout an MT experiment. For a two-pool model of exchange (Figure 2‑3 and Figure 2‑4), the Bloch differential equations describing the coupled cross-relaxation of the magnetization vector components of the free and restricted pools are [96,131-135]:

|  |  |
| --- | --- |
|  | **(2-13)** |
|  | **(2-14)** |
|  | **(2-15)** |
|  | **(2-16)** |
|  | **(2-17)** |

where is frequency of the RF pulse, = is a complex and time-varying function of the RF pulse amplitude, is the magnetization exchange rate from the free pool to the restricted pool, is the magnetization exchange rate from the restricted pool to the free pool, is the equilibrium longitudinal magnetization of the free/restricted pool, and *W* is the transition rate to the restricted pool in the presence of an off-resonance RF pulse (see Figure 2‑4a to b) and assumes a shaped RF pulse with a narrow bandwith (a more general expression for *W* is presented in Ref. [134]). Note that the transversal components (x/y) of the restricted pool are omitted above, as *T2,r* is much shorter than the typical experimentation time, thus studies have shown these terms can be safely neglected [134,136]. An important quantitative MT parameter that is implicitly included in the equations above is the pool-size ratio, , where by definition =. In Eq (2-17), G is the spectral lineshape function of the restricted pool (e.g. Figure 2‑3a). Common spectral lineshape use in MT are Gaussian for solids and gels (e.g. imaging phantoms) and super-Lorentzian for in vivo tissues [136]. Lastly, note that the measured longitudinal relaxation rate (R1,obs = 1/T1) in the presence of macromolecules differs from the free pool longitudinal relaxation rate R1,obs, and the relationship between the two is described by:

|  |  |
| --- | --- |
|  | **(2-18)** |

Equations (2-13) to (2-16) cannot be solved analytically for most quantitative MT pulse sequence experiments. One exception is the case where Eqs. (2.15) and (2.16) are driven to a steady-state using a continuous-wave (“hard” pulses) MT-preparation RF pulse (1 to 5 seconds) within a single TR prior to data acquisition [133]. However, this technique does not lend itself well to in vivo quantitative MT imaging experiments due to its long acquisition times and high SAR. Pulsed MT pulse sequences, initially proposed using binomial RF pulses with zero net flip angle on-resonance [137,138] followed by shaped off-resonance pulses [134,135,139] (e.g. Figure 2‑5), were demonstrated to be practical alternative to CW for in vivo quantitative MT imaging. One caveat of using a pulsed approach to qMT is that solving these equations for a pulsed-MT pulse sequence are numerically very difficult, which would require exceedingly large computation times to process the several thousand (single-slice) up to several hundred thousand voxels (whole-brain). Several numerical approximations have been proposed to solve Eqs (2.13) to (2.16) in order to fit qMT data for the unknown model parameters: F, kf, R1,f, R1,r, T2,f, and T2,r. several methods developed to find approximate solutions [135,140,141]. Most pulsed off-resonance qMT models share two features: (1) R1,r is fixed to 1 s-1, as these types of qMT experiments are largely insensitive to R1,r [133], and (2) a T1 map (1/R1,obs) is required to constrain the fitting parameters R1,f, F, and kf using Eq. (2-18) [133,135]. Thus, only four free model fitting parameters remain to be solved in a qMT experiment (F, kf, T2,f, and T2,r).



Figure ‑. Pulsed MT-weighted spoiled gradient echo (SPGR) pulse sequence for a Gaussian MT pulse shape. (\*\*From Sled 2001. Either make a similar figure or get Wiley rights for thesis use\*\*).

The first qMT fitting model approximation proposed for in vivo imaging of all quantitative fitting parameters was introduced in 2001 for a pulsed-MT SPGR experiment [135], often referred to as the Sled and Pike model after its authors. The Sled and Pike model has been shown to produce the most accurate estimations of qMT fitting parameters compared to other techniques [142], and is the model used throughout this thesis. Figure 2‑6 present the approximations used in this model, which is for a pulse-MT SPGR experiment (Figure 2‑5). The effect of both the excitation and MT pulse on the free pool is approximated as an instantaneous saturation, which is precomputed by solving the equations in the absence of relaxation or exchange between pools for a wide range of effective MT flip angles, Δ, and T2,f. The second approximations of the Sled and Pike model is in neglecting the effect of the excitation pulse on the restricted pool, and approximating the shaped MT pulse to a CW pulse of equivalent power and offset frequency. With these assumptions, the evolution of the magnetization can be broken down in event blocks of free precession, CW irradiation at an off-resonance frequency, and instantaneous saturations of the free pool, which simplifies solving the steady-state Bloch equations in a closed-form [134] instead of numerically, substantially improving the fitting time. Fitting the qMT parameters to the model is then done using several MT-weighted SPGR images acquired at several different off-resonance frequencies (Δ) and effective MT-pulse flip angles (FAMT, related to ), in addition to one image without an MT pulse (*I0*) for data normalization. Plots of normalized MT-weighted data as a function of off-resonance frequencies for each FAMT are conventionally referred to as “Z-spectrums”. In addition to the MT data and a T1 map for constraining the model parameters, B0 and B1 maps are typically acquired as corrective factors for Δ and , respectively. Open-source software to simulate and fit qMT data using the Sled and Pike model (and several others) has recently been released online [143].

The qMT parameter that has demonstrated the most potential for inferring information about tissue abnormalities is the pool-size ratio F, which is a measure of the restricted pool size of macromolecular content relative to the local water content. In post-mortem MS brains, F has been shown to have a significant correlation with myelin content [39], and significant differences in F were measured between in WM lesions and NAWM, de- and re-myelinated lesions, and between remyelinated lesions and NAWM. This study also suggested that F may be a more specific biomarker for myelin loss than MTR, particularly in NAWM. Several studies have reported significant difference in F in vivo between MS lesions and NAWM/controls [135,140], and in the longitudinal evolution of acute MS lesions [144]. In healthy brains, regional variations of F across different WM/GM regions of the brains have be reported [145], and great scan-rescan reproducibility has been demonstrated [146]. F has also been a good predictor of de/re-myelination in animal models of MS [147,148]. Beyond MS, other potential applications of qMT have been explored, such as Alzheimer’s [149], breast imaging [150], cartilage imaging [151], g-ratio imaging [127,152], and characterization of dry-cured hams [153].

Fitting qMT data for the four quantitative parameters requires several MT and calibration measurements. Initially, 60 MT-weighted measurements were used (with different TRs, FAMT, Δ values) in addition to one normalization measurement with no MT pulse (for each TR). Subsequent studies demonstrated that the four qMT parameters could be fitted reliably using at least 10 MT-weighted measurements by using protocol-design optimization [154,155]. These MT-weighted SPGR measurements, in addition to the three supporting measurements (B0, B1, T1), historically made qMT limited to a single-slice or low-resolution 3D technique [156]. However, with the development of parallel imaging and compressed sensing rapid acquisition techniques [157,158], high-resolution whole-brain is rapidly becoming accessible. This means that the calibration measurements (B0, B1, T1) used for qMT must also switch from single-slice to whole-brain techniques, which may have unintended impact on qMT parameter estimates. For example, early single-slice qMT studies used single-slice T1 mapping techniques such as Look-Locker or Inversion Recovery, which are B1-independent T1 mapping methods. For whole-brain qMT, VFA is a likely candidate for T1 mapping, however it is a B1-dependent technique. Because qMT is also a B1-dependent technique, inaccuracies in the B1 map may impact the qMT fitting estimates differently depending on if a B1-independent (e.g. IR) or B1-dependent (e.g. VFA) T1 mapping technique is used. Using IR/LL T1, an error in B1 will only propagate to qMT through the FAMT and excitation flip angles in the model. Using VFA T1, an error in B1 propagate through this pathway, but also through the F/kf parameter constraint in Eq. (2-18) through an error in the R1,obs estimate. Sled and Pike [135] first reported that at 1.5T using LL, a 10% error in B1 would result in a 20% error in the estimate for F. Levesque et al. [146] also reported very high coefficient of variations for most qMT parameters in the absence of B1 and B0 maps, but they also used the LL methods which is less B1-sensitive than VFA. Underhill et al. [159] briefly mentions that B1 mapping is particularly important for their whole-brain qMT implementation at 3.0T, in particular because they chose to use VFA T1 mapping, noting that it also depends on B1. To the best of our knowledge, a comprehensive study aimed at characterizing the B1-sensitivity of qMT under these different circumstances has not been reported, which raises the following two questions: (1) what are some potential sources of B1-inaccuracies and how sensitive is VFA to them?, (2) are B1-dependent or B1-independent T1 mapping methods better for robust qMT pool-size ratio estimate?, and (3) can qMT acquisition protocols be optimized for reduced sensitivity to B1-inaccuracies. These questions are the focus of the manuscripts which are explored in the following three chapters, and of this PhD thesis as a whole.

# *B1 Mapping for Bias-Correction in Quantitative T1 Imaging of the Brain at 3T Using Standard Pulse Sequences*

## Preface

B1 maps are an essential component of VFA T1 mapping acquisition protocols. In this context, B1 maps are used as a voxel-wise flip-angle scaling factor for the nominal flip angles that are specified at the scanner for the VFA image acquisitions. Because VFA is typically used to map T1 in the entire brain value, whole-brain B1 mapping techniques that have a short acquisition time are needed for this task. Several rapid whole-brain B1 mapping techniques have been proposed, and the two most popular techniques developed in the last decade are AFI and Bloch-Siegert, both boasting several advantages (e.g. T1 insensitivity). The major drawback of the techniques however is that they are not easily accessible on most clinical scanners; these pulse sequences must be programmed manually on-site, a time-intensive procedure requiring expertise that may not be available.

The following manuscript, published in the *Journal of Magnetic Resonance Imaging*, describes the comparison of an EPI-based double angle (EPI-DA) whole-brain B1 mapping technique against AFI and Bloch-Siegert, and comparing the VFA T1 maps using each B1 mapping technique. EPI-DA has the advantage of requiring no pulse sequence programming; it can be implemented using standard MRI pulse sequences available on most scanners. Unlike the two later manuscripts, this manuscript’s target audience are researchers who may not have quantitative MRI pulse sequence programming expertise, but require a B1 map for another technique such as VFA T1 mapping, which is also easily implementable using standard MRI pulse sequences. To the best of our knowledge, it is the first paper quantitatively compare the B1 maps (and their resulting VFA T1 maps) with a whole-brain B1 mapping technique that can be implemented with a standard MRI pulse sequence, benefiting researchers such as those using dynamic contrast-enhanced (DCE) imaging who need whole-brain T1 maps but often omit B1 maps from their acquisition protocols. In addition, this manuscript that compares all B1 mapping methods both with and without B1 filtering, a post-processing step that is typically done because the B1 profile is expected to be a slowly varying function and is often done to reduce noise. Because B1 maps are usually also acquired at a low resolution, these may both be a source of voxel-wise B1 inaccuracies in a qMT experiment, in addition to larger visible artifact which are also reported in this manuscript.

**B1 Mapping for Bias-Correction in Quantitative T1 Imaging of the Brain at 3T Using Standard Pulse Sequences**

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**Journal of Magnetic Resonance Imaging, DOI: 10.1002/jmri.25692, 2017**

## Abstract

**Purpose:** B1 mapping is important for many quantitative imaging protocols, particularly those that include whole-brain T1 mapping using the variable flip angle (VFA) technique. However, B1 mapping sequences are not typically available on many magnetic resonance imaging (MRI) scanners. The aim of this work was to demonstrate that B1 mapping implemented using standard scanner product pulse sequences can produce B1 (and VFA T1) maps comparable in quality and acquisition time to advanced techniques.

**Materials and Methods:** Six healthy subjects were scanned at 3.0T. An interleaved multislice spin-echo echo planar imaging double-angle (EPI-DA) B1 mapping protocol, using a standard product pulse sequence, was compared to two alternative methods (actual flip angle imaging, AFI, and Bloch-Siegert shift, BS). Single-slice spin-echo DA B1 maps were used as a reference for comparison (Ref. DA). VFA flip angles were scaled using each B1 map prior to fitting T1; the nominal flip angle case was also compared.

**Results:** The pooled-subject voxelwise correlation (*ρ*) for B1 maps (BS/AFI/EPI-DA) relative to the reference B1 scan (Ref. DA) were *ρ* = 0.92/0.95/0.98. VFA T1 correlations using these maps were *ρ* = 0.86/0.88/0.96, much better than without B1 correction (*ρ* = 0.53). The relative error for each B1 map (BS/AFI/EPI-DA/Nominal) had 95th percentiles of 5/4/3/13%.

**Conclusion:** Our findings show that B1 mapping implemented using product pulse sequences can provide excellent quality B1 (and VFA T1) maps, comparable to other custom techniques. This fast whole-brain measurement (~2 min) can serve as an excellent alternative for researchers without access to advanced B1 pulse sequences.

## Introduction

Radiofrequency transmit field (B1+) maps, typically termed “B1 maps” for brevity, are necessary in several quantitative magnetic resonance imaging (MRI) applications, such as specific absorption rate (SAR) estimation, magnetization transfer (MT) imaging, and quantitative T1 mapping. Electrical properties tomography (EPT) relies on quantitative B1 maps to calculate the conductivity (*σ*) and permittivity (*ε*) of tissue in vivo [74], and is an essential step in the estimation of local SAR [75]. MT techniques probe the macromolecular content of tissue, and are often used as an index of myelination in diseases such as multiple sclerosis [39]. Unaccounted B1 inhomogeneity in certain MT experiments can be an important source of error. For example, B1-correction has been shown to improve the quality of MT ratio (MTR) maps [102], due to the sensitivity of MTR to the MT preparation RF pulse power. The longitudinal relaxation time (T1), one of the fundamental quantities in MRI, is an important input for several other data processing pipelines, such as dynamic contrast enhancement (DCE) imaging [48,62] and quantitative MT [135]. Although some whole-brain T1 mapping methods boast first-order insensitivity to RF field inhomogeneities [55], others—notably the variable flip angle (VFA) method [160]—are inherently sensitive to inaccuracies in the excitation flip angles (FA). B1 maps can greatly benefit the accuracy and precision of VFA T1 maps at high clinical field strengths, (eg, 3T), where large B1 amplitude variations are typical in loaded coils [77] (eg, ±30% for the human brain). The broad range of B1 applications highlights the need for accurate B1 mapping techniques, while also balancing other competing interests such as acquisition speed and ease of implementation, particularly in the context of multisite studies.

Substantial efforts have been made to develop rapid whole-brain B1 mapping techniques in the last decade. Previously, conventional B1 mapping was done using some variations of the double angle (DA) method, which consists of two separate gradient-echo or spin-echo measurements with longitudinal magnetization recovery in which the second measurement is performed with double the excitation pulse flip angle [79]. However, conventional DA requires very long repetition times, and was mostly used for single-slice imaging. Advanced pulse sequences have been developed to accommodate whole-brain B1 mapping. Two of the most popular techniques are actual flip angle imaging (AFI) [84] and Bloch-Siegert shift (BS) mapping [85]. AFI is a steady-state 3D spoiled gradient echo (SPGR) B1 mapping method based on a dual-TR acquisition (TR2 = N\*TR1, where N is typically an integer on the order of 5), and has been shown to be T1-insensitive for most tissues. BS is a phase-sensitive slice-selective B1 mapping method using a modified SPGR sequence; a high amplitude off-resonance RF pulse between the excitation and readout events induces a phase-shift proportional to the B1 amplitude. Currently, an important limitation of these methods is their lack of widespread availability as a standard product sequence on clinical scanners. These pulse sequences are typically implemented onsite, a time-consuming process that require pulse sequence programming expertise, and is susceptible to site-specific implementation issues.

The lack of a readily available whole-brain B1 mapping pulse sequence is a challenge to many researchers, particularly in the context of multi-center studies, resulting in the omission of B1 mapping in quantitative imaging protocols that would significantly benefit from its inclusion. One such quantitative MRI method is VFA T1 mapping, which estimates T1 by fitting the gradient echo images to a function of flip angles, making it inherently sensitive to B1 inaccuracies. For example, using a VFA sequence with a 15 msec TR and two flip angles (3° and 20°) [52], an underestimation of the nominal flip angles by 1/5/10/20% results in an overestimation of the fitted T1 by 2/11/24/57%. Thus, errors in B1 induce at least twice as large errors in T1, and the error increases nonlinearly. Notably, DCE imaging protocols that use VFA T1 mapping often omit B1 correction [48,61], even though B1 maps have been shown to substantially improve the accuracy of DCE [47,62]. Citing the unavailability of advanced B1 mapping sequences at their site, other researchers have developed techniques to simulate B1 maps by normalizing the VFA T1 image [60] using postprocessing image analysis algorithms [161]. However, a systemic bias in B1 values (of unknown size) could still be present using this type of image analysis approximation, so measuring B1 directly should improve the accuracy of the T1 maps.

The purpose of this work was to evaluate the quality of a fast and simple whole-brain B1 mapping protocol implemented using a standard EPI pulse sequence. An interleaved multislice spin-echo EPI readout standard product pulse sequence was used to map B1 with the DA method (EPI-DA) [58,81,162] in a group of healthy human subjects. EPI-DA has not gained as much attraction in comparison to AFI and BS, due to their demonstrated robustness against specific characteristics (eg, large T1 values, B0 inhomogeneity) and their compatibility with higher fields systems that use parallel transmit coils. Yet the ease of implementation of EPI-DA or other similar techniques (eg, fast spin-echo DA [82]) may make them a good alternative to advanced B1 methods, which require custom implementations and pulse sequence programming expertise.

## Materials and Methods

All measurements were performed on a 3.0T whole-body MRI scanner (Magnetom TIM TRIO, Siemens, Erlangen, Germany) using a 32-channel phased-array receive-only head coil and whole-body transmit coil.

### Measurements

Healthy adult volunteers were scanned in compliance with the guidelines of the Institutional Ethics Committee, and gave written informed consent prior to being scanned for this study. Six healthy adult volunteers were scanned (three females, three males, 29 ± 3 years old). Axial slices were acquired (for 2D measurements) or extracted (from 3D/multislice measurements, with orientations matching the single-slice 2D measurements) parallel to the anterior and posterior commissure (AC-PC) plane, superior to the corpus callosum.

Quantitative analyses of the B1 and T1 maps were limited to voxels comprised of white matter (WM), consistent with previous work [82,152]. Two reasons factored into this decision. First, as B1 maps are typically acquired at low resolution, partial volume effects occur near cortical gray matter (GM) regions and areas adjacent to ventricles. Therefore, there is an insufficient number of voxels that contain pure GM. Second, the partial volume effects in regions containing cerebrospinal fluid (CSF) result in substantially longer mean T1 values (2–5 sec), so T1-sensitive artifacts will vary in severity between B1 methods that have different intrinsic sensitivity to long T1 and CSF flow. Adequately comparing B1 methods in GM and CSF is a specialized topic that requires higher resolution and/or longer scan-times, which is beyond the scope of this work.

Whole-brain T1-weighted magnetization-prepared rapid gradient-echo (MP-RAGE) 3D volumes (1 × 1 × 1mm3) were acquired: repetition time (TR) = 2300 msec, echo time (TE) = 3.32 msec, inversion time (TI) = 900 msec, iPAT factor = 2 (GRAPPA), bandwidth (BW) 5230 Hz/Px, 5 min 30 sec scan time. Tissue classification maps (WM, GM, CSF) were obtained via Intensity Normalized Stereotaxic Environment for the Classification of Tissue (INSECT)24 using the MP-RAGE data with the ICBM-152 atlas. All necessary preprocessing steps (nonuniformity correction, skull-stripping, etc.) were done using the standard pipeline of the MINC Tool Kit (v. 1.9.11, McConnell Brain Imaging Center, Montreal Neurological Institute, Montreal, Canada). Tissue percentage maps (WM, GM, CSF), at the low resolution (2 × 2 × 5mm3) for which the quantitative maps (B1, T1) were acquired, were estimated by calculating the ratio of high-resolution INSECT tissue-classified voxels (1mm3) that had the center of their voxels located within the corresponding 2 × 2 × 5mm3 voxels. using a majority voting analysis (75% threshold). Figure 3‑1 shows a tissue classification maps of WM, GM, and CSF for a healthy subject. The classification maps show that for a 2 × 2 × 5mm3 resolution, very few voxels consisted of single-tissue GM or CSF, reaffirming our reasoning to exclude these areas in our study. To generate the WM masks for each subject, a >75% binary threshold was applied to the tissue percentage maps; since there can be 20 high-resolution voxels (1mm3) that have their centers located in a low-resolution voxels (2 × 2 × 5mm3), a >75% threshold represents the case that no more than four non-WM INSECT tissue classified voxels (out of 20) are located within a voxel of the WM mask. Lastly, note that the WM mask were only used to mask-out non-WM voxels after the B1 maps were calculated, and are not required to calculate any of the B1 maps described in the following section.



Figure ‑.Tissue classification maps (black = 0%, gray = 100%) of a healthy subject calculated from INSECT [163] using MP-RAGE T1w data (1 × 1 × 1mm3) and resampled to 2 × 2 × 5mm3. Tissue percentages were estimated by calculating the ratio of INSECT tissue-classified voxels (1mm3) for a given tissue type (WM, GM, CSF) that were located inside the corresponding low-resolution voxels (2 × 2 × 5mm3), for which the quantitative maps (B1, T1) were acquired.

### B1 Mapping

Three rapid B1 mapping techniques (Bloch-Siegert shift, BS; actual flip angle imaging, AFI; echo planar imaging double angle, EPI-DA) were acquired with acquisition protocols that matched their original publications values as closely as possible. A single-slice double angle B1 map was acquired as a reference (Red. DA), as is typical [85,164]. Lastly, a uniform B1 map of value 1 normalized units (n.u.), noted in short-hand as “Nominal,” was generated to represent the case when VFA T1 values are fitted using the nominal flip angles of its acquisition protocol.

*BLOCH-SIEGERT (BS).* Single-slice BS B1 maps [85] were acquired using an in-house-developed pulse sequence: TE/TR = 15/100 msec, excitation flip angle (*α*) = 25°, field-of-view (FOV) = 25.6 × 17.6 cm2, 2 × 2mm2 in-plane resolution, 128 × 88 matrix (readout/phase), 5mm slice thickness, 1 slice, 8 msec Fermi Pulse of 500° at 64 kHz off-resonance and phase-shift constant KBS = 74.01 rad/G2, 19 sec scan time.

*ACTUAL FLIP ANGLE IMAGING (AFI).* AFI B1 maps were acquired using an in-house-written slab-selective 3D AFI pulse sequence with optimal RF and gradient spoiling [84,87]: TE/TR1/TR2 3.53/20/100 msec, *α* = 60°, BW = 260 Hz/pixel, FOV = 25.6 × 17.6 × 16.0 cm3, 2 × 2 × 5mm3 resolution, 128 × 88 × 32 matrix (readout/phase/3D), spoiling gradient moment (AG) = 450 mT∙ms/m and RF phase increment (*ψ*) = 39°, 5 min 38 sec scan time.

*EPI DOUBLE ANGLE (EPI-DA).* Interleaved multislice spin-echo EPI-DA B1 maps with whole-brain coverage were acquired using a standard product EPI pulse sequence with a protocol similar to that of Wang et al [81], except with 180° refocusing pulses (the scanner default for this sequence). Since our sequence used (*α*, 180°) and (2*α*, 180°) excitation-refocusing pulses, instead of (*α*, 2*α*) and (2*α*, 4*α*) in the original article, the equation used to calculate EPI-DA B1 was [79,82]:

|  |  |
| --- | --- |
|  | **(3-1)** |

where *α* is the nominal flip angle (double for the second measurement), *α*corr is the true flip angle experienced by the tissue at that voxel location, *I1* and *I2* are the image voxels magnitudes for *α* and 2*α* acquisition, respectively. The EPI-DA acquisition protocol was: TE/TR = 46/4000 msec, *α*/2*α* = 60°/120°, FOV = 25.6 × 25.6 cm2, 2 × 2mm2 in-plane resolution, 128 × 128 matrix (readout/phase), 5mm slice thickness, 27 slices, EPI factor = 9 (15 shots of 9 k-space readout line acquisitions), echo spacing = 4.18 msec, fat saturation on, BW = 250 Hz/px, 2 min 16 sec scan time. Standard automated shimming was performed as with all other sequences (shim currents adjusted using a 3D phase map); no additional adjustments of the static or gradient fields were necessary.

Fast EPI sequences, such as the widely used single-shot implementations, can be susceptible to a wide range of artifacts that lead to a degradation of image quality. Several strategies are incorporated in this protocol to mitigate these artifacts, while still using a readily available scanner sequence and maintaining rapid overall acquisition. A segmented multishot EPI approach increases the effective BW in the phase-encode direction, which reduces distortion artifacts that are typically prevalent in areas of high B0 inhomogeneity such as near the sinuses. Blurring is also reduced, due to decreased T2\* modulation in each acquired echo train. Acquiring the B1 map at a low in-plane resolution (2 × 2mm2) also means smaller readout gradient amplitudes are used, reducing potential eddy current artifacts (eg, ghosting). Other fast imaging techniques, such as fast spin-echo, have also been adapted for whole-brain double angle B1 mapping [82]. These methods could offer different imaging benefits as alternatives to EPI; however, such a comparison is outside the scope of the present work.

*REFERENCE DOUBLE ANGLE (REF. DA).* Single-slice double angle B1 maps were acquired using a spin-echo sequence as a reference measurement for the other B1 mapping techniques: TE/TR 12/1550 msec, *α* = 60°/120°, FOV = 25.6 × 17.6 cm2, 2 × 2mm2 in-plane resolution, 128 × 88 matrix (readout/phase), 5mm slice thickness, 1 slice, slice-selective excitation and 180° refocusing pulses, and BW = 130 Hz/pixel, 4 min 28 sec scan time. The flip angles were chosen to match the EPI-DA sequence. As Ref. DA is the most time costly of all the compared methods (4 min 38 sec), a shorter TR was chosen to reduce the acquisition time of the entire protocol while maintaining sufficient accuracy in WM [52]. The TR is sufficiently long to allow almost complete relaxation of the WM signal, which we are evaluating.

Overall, each pulse sequence had the following effective acquisition time per slice: Ref. DA: 4 min 38 sec/slice, BS: 19 sec/ slice, AFI: 11 sec/slice (3D measurement), EPI-DA: 5 sec/slice (interleaved multislice sequence produced 27 slices in 68 sec per flip angle acquisition).

### T1 Mapping

VFA is a widely used T1 mapping technique; spoiled gradient echo images are acquired using multiple (usually 2–5) excitation flip angles, each using the same TR. VFA T1 maps were acquired using a standard product spoiled 3D gradient echo pulse sequence: 2 × 2 × 5mm3 resolution, 128 × 88 × 32 matrix (readout/phase/3D), TE/TR 2.89/15 msec, *α* = 3°/20°, BW = 390 Hz/pixel, default manufacturer slab-selection and RF spoiling modes, 1 min 28 sec scan time.

### Data Analysis

B1 and T1 maps were processed from the MRI data using custom MATLAB code (MathWorks, Natick, MA). Each B1 map was used to scale the VFA nominal flip angles voxelwise prior to fitting for T1. T1 maps were estimated from linear least square fitting to the SPGR equation [52].

The B1 amplitude is expected to be a smooth slowly varying function, particularly in the brain [161]. As such, B1 maps are commonly filtered to reduce noise and minor artifacts [84,164]. Subjective assessment of the images was performed by two of the coauthors (coauthors #3 and #6) who were blinded to the acquisition method used for each dataset. They provided a brief subjective evaluation of any artifacts they observed. A consensus opinion was then formed via discussion between all coauthors. In addition to comparing unfiltered (raw) B1 maps (as well as in the VFA T1 analysis), we repeated the data analysis using filtered B1 maps. Single slice B1 maps were filtered (prior to WM masking) using the MATLAB function *roifilt2* and skull-stripped brain masks (all tissues). A Gaussian kernel (*fspecial*) was used with a full-width-half-maximum of 10 × 10mm2 (sigma = 4.2466) and a 7 × 7 voxel kernel matrix.

The voxelwise WM B1 and T1 data for each method (Ref. DA, BS, AFI, EPI-DA) and the nominal flip angle case (Nominal) were pooled together (all subjects) for data analysis. Histograms of the unfiltered B1 maps and accompanying fitted T1 values were calculated to investigate the presence of potential systemic biases or spreading between methods [52,82]. Linear regression analysis of B1 and T1 (Pearson correlation and linear fit values) was performed for each B1 method relative to the Ref. DA B1 values. The linear regression analysis was performed using both the unfiltered and the Gaussian filtered B1 data.

## Results

Pooled-subject histograms of unfiltered B1 map values from WM regions are shown in Figure 3‑2a. There is an overlap between the different B1 histograms; the differences in statistical modes (ΔMode) for each method relative to Ref. DA were 3.6/1.5/3.8% (BS/AFI/EPI-DA). EPI-DA is the only method for which a small B1 histogram shift is qualitatively observable, which suggests the presence of a small systemic bias. The unfiltered B1 maps for a single subject are shown in Figure 3‑3b, along with their accompanying acquisition images in Figure 3‑3a. The signal-to-noise ratio (SNR) in a region-of-interest of WM was estimated across all subjects to be 240 ± 45 for Ref. DA, 98 ± 11 for BS, 170 ± 35 for AFI, and 130 ± 30 for EPI-DA. Linear regression statistics computed using the pooled voxelwise data for each unfiltered B1 map (BS, AFI, EPI-DA) relative to the Ref. DA measurement is presented in Table 3‑1. EPI-DA had the highest Pearson correlation coefficient relative to Ref. DA (*ρ* = 0.96) and a near-unity slope (*β* = 0.99); the BS B1 maps had the lowest correlation out of the three (*ρ* = 0.88). Table 3‑2 lists the mean and SD of voxelwise differences (%) in WM for each B1 method relative to Ref. DA. Overall, EPI-DA had a lower voxelwise percent differences SD than other methods for all subjects, except subject #6, where BS had a lower value.



Figure ‑. Normalized histograms of single-slice unfiltered B1 (a) and T1 (b) map values masked for WM in six healthy subjects. The abbreviation “n.u.” stands for normalized units.



Figure ‑. a: Acquisition images for each acquired B1 method: Ref. DA (reference single-slice double angle), AFI (actual flip angle imaging), BS (Bloch-Siegert shift), and EPI-DA (double-angle using an interleaved multislice EPI acquisition). b: Unfiltered single-slice B1 maps, and corresponding WM-masked VFA T1 maps fitted using flip-angles scaled voxelwise using each B1 map. The “Nominal” column represents VFA T1 fitting using no B1 correction (B1 = 1 n.u.).

The pooled-subject histogram analysis of WM T1 values is shown in Figure 3‑2b. Each measured B1 map resulted in narrower WM T1 histograms than for the Nominal case. The differences in statistical modes (ΔMode) for WM T1 between Ref. DA and BS/AFI/EPI-DA/Nominal were 2.5/ 1.0/5.0/5.0%, respectively. The width of the WM T1 distributions had more relative variation between methods than observed for the B1 histograms. EPI-DA had the largest ΔMode value (5%), but did not experience noticeable broadening relative to Ref. DA. However, BS clearly did suffer from broadening, yet much less severe than the Nominal case. The small reduction in EPI-DA WM T1 histogram statistical mode (Figure 3‑2b) is attributed to the small increase in the corresponding B1 histogram statistical mode (Figure 3‑2a). T1 correlations were lower relative to their respective B1 correlations, which was to be expected due to the B1-sensitivity of the VFA technique. Overall, EPI-DA T1 maps had the highest correlation relative to Ref. DA (*ρ* = 0.92), which was substantially better than for the Nominal case (*ρ* = 0.53). WM-masked T1 maps are shown for a single subject in Figure 3‑3. Large overestimations of T1 at the center of the slice are clearly seen for the Nominal case, unlike those using each measured B1 map.

Table ‑. Linear Regression Analysis of the Pooled WM-Masked B1 and T1 Values (Six Subjects) for Each Rapid B1 Method Relative to the Ref. DA Method

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | Unfiltered B1 Maps | | | Gaussian Filtered B1 Maps | | |
|  |  | Ref. DA | Nominal | BS | AFI | EPI-DA | BS | AFI | EPI-DA |
| B1 | **Pearson *ρ*** | --------- | N/A | **0.88** | **0.92** | **0.96** | **0.92** | **0.95** | **0.98** |
| Slope *β* | --------- | N/A | 0.97 | 1.01 | 0.99 | 0.96 | 0.99 | 1.01 |
| Intercept *y0* | --------- | N/A | 0.04 | -0.01 | 0.03 | 0.05 | 0.00 | 0.01 |
| T1 | **Pearson *ρ*** | --------- | **0.53** | **0.79** | **0.81** | **0.92** | **0.86** | **0.88** | **0.96** |
| Slope *β* | --------- | 0.95 | 0.99 | 0.89 | 0.94 | 0.97 | 0.92 | 0.98 |
| Intercept *y0* | --------- | 0.07 | 0.00 | 0.12 | 0.02 | 0.00 | 0.09 | -0.02 |

Table ‑. Mean and Standard Deviations of Voxelwise Percent Differences (%) of B1 and T1 Values in WM Relative to the Ref. DA Method for All Subjects

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Mean ± SD Voxel-wise Percent Differences (%) in White Matter | | | | | | |
|  | Subject # | Ref. DA | Nominal | BS | AFI | EPI-DA |
| B1 | 1 | --------- | N/A | 0.31 ± 3.47 | 0.47 ± 1.83 | 1.67 ± 1.43 |
| 2 | --------- | N/A | 3.34 ± 2.46 | -1.46 ± 2.40 | 2.41 ± 1.32 |
| 3 | --------- | N/A | 0.95 ± 2.24 | -0.44 ± 2.22 | 1.87 ± 1.49 |
| 4 | --------- | N/A | 1.57 ± 2.43 | -1.28 ± 3.12 | 0.15 ± 1.66 |
| 5 | --------- | N/A | -0.01 ± 3.61 | 0.63 ± 2.09 | 2.37 ± 1.45 |
| 6 | --------- | N/A | 2.07 ± -0.69 | -0.69 ± 3.07 | 1.76 ± 2.08 |
| T1 | 1 | --------- | -2.11 ± 12.12 | -0.30 ± 6.83 | -0.85 ± 3.78 | -3.27 ± 2.70 |
| 2 | --------- | 2.86 ± 10.96 | -6.25 ± 4.67 | 3.17 ± 5.07 | -4.64 ± 2.50 |
| 3 | --------- | 0.46 ± 10.64 | 2.10 ± 4.69 | 1.03 ± 4.66 | -3.72 ± 2.59 |
| 4 | --------- | 10.27 ± 14.19 | -3.01 ± 4.84 | 2.69 ± 6.60 | -0.54 ± 2.60 |
| 5 | --------- | 3.40 ± 11.01 | 0.32 ± 7.02 | -1.09 ± 4.16 | -4.53 ± 2.72 |
| 6 | --------- | -2.70 ± 10.54 | -3.86 ± 4.93 | 1.56 ± 6.70 | -3.39 ± 4.36 |

Artifacts in the unfiltered B1 maps differ between methods due to their differing acquisition pulse sequences (Figure 3‑3b). The sulci are visible in the B1 maps of both DA methods (Ref. DA and EPI-DA), unlike BS and AFI. In the ventricles, lower B1 values are present for Ref. DA and EPIDA relative to the other methods (Figure 3‑3b, Figure 3‑5). An open-ended fringe line (pole) was present in the Bloch-Siegert phase maps (Figure 3‑3a), due to out-of-phase multichannel image recombination [165], and may have caused some inhomogeneity in the Bloch-Siegert B1 maps in the posterior left hemisphere (Figure 3‑3b). This phase image artifact was present in all subjects. For BS, the inhomogeneities near the phase pole along with noisier B1 maps were likely contributing factors in the broadening of the WM T1 distribution (Figure 3‑2b). A ringing artifact affected the AFI B1 maps (Figure 3‑3b), although it is not easily seen in the raw AFI acquisition images themselves (Figure 3‑3a). However, by carefully adjusting the window/level (not shown), a small ringing artifact is present in both AFI MRI images. We observed this ringing in both the raw data and B1 maps of all subjects. If the ringing between both images is out-of-phase, the resulting B1 artifact may be amplified due to the nature of the AFI calculation, which requires a division of the two images. The original AFI work only presents their B1 maps postfiltering (8 × 8 × 16mm3 median filter); however, ringing can also be seen in their axial and coronal TR1 images (fig. 10a in Ref. [84]). Overall, these artifacts and noise in the unfiltered B1 maps likely contributed to lower correlations of B1 and T1 relative to the reference maps.



Figure ‑. Unfiltered (a) and Gaussian filtered (b) B1 maps of a single subject. (c) Relative differences between unfiltered and filtered maps shown as percent difference maps.

The unfiltered and Gaussian filtered B1 maps are shown for a subject in Figure 3‑4a,b, and the relative difference (%) between the two is shown in Figure 3‑4c. The Gaussian filter was effective at reducing noise in the maps, as well as in attenuating minor artifacts (eg, sulci in DA maps, “ringing” in AFI). The correlations and linear regression analysis of B1 (and VFA T1) relative to the reference (Ref. DA) were recalculated using the filtered B1 maps (Table 3‑1). The correlations improved postfiltering; for BS/AFI/EPI-DA, B1 correlations (*ρ*) were 0.92/0.95/0.98, and for T1 they were 0.86/0.88/0.96. The 95th percentiles of the absolute relative differences between the reference B1 map and BS/AFI/EPIDA (in WM) were equal or lower than 5% (5/4/3%, respectively), while the nominal flip-angle case had a relative difference (to Ref. DA) 95th percentile of 13%.



Figure ‑. Whole-brain coverage of axial MP-RAGE T1w slices, unfiltered AFI B1 maps, and unfiltered EPI-DA B1 maps in one subject.

The raw images used to calculate an EPI-DA B1 map for a subject are shown in Figure 3‑3a. The image quality of the EPI images is comparable to the Ref. DA method, and no observable distortions or ghosting were present in the brain for either the acquisition images or the B1 map. This observation was consistent in all subjects for the slice used in the data analysis. In addition to the single-slice measurements, two of the B1 mapping protocols were acquired with whole-brain coverage (AFI and EPI-DA). Axial slices for both B1 methods are shown in Figure 3‑5. EPI-DA B1 maps throughout the brain were free of severe susceptibility-induced distortions. However, the ventricles can be clearly identified in the EPI-DA maps (lower values) unlike for AFI, as AFI is well known to be very robust for a wide range of T1 values [84].

## Discussion

Our findings demonstrate that B1 mapping implemented using a standard product EPI pulse sequence (EPI-DA) can provide quality whole-brain B1 maps with a short acquisition time (~2min). The B1 maps were comparable or superior in WM to other well-regarded rapid acquisition B1 methods (AFI and BS) at 3T. Unfiltered B1 maps correlated with our reference single-slice measurement (Ref. DA), and we observed an improvement in those correlations after applying a Gaussian filter to the images to reduce noise and attenuate small artifacts. Pooled-subject voxelwise B1 correlation values (relative to Ref. DA) ranged between 0.88 ≤ *ρ* ≤ 0.96 for unfiltered maps, and 0.92 ≤ *ρ* ≤ 0.98 for filtered maps. The 95th percentile of the relative errors of filtered B1 maps (compared to Ref. DA) were ≤ 5%, nearly three times lower than for the nominal flip-angle case (13%). VFA T1 maps using Gaussian filtered B1 maps correlated with those using Ref. DA (0.88 ≤ *ρ* ≤ 0.96,), unlike for the case using uncorrected (nominal) flip-angles (*ρ* = 0.53). The peak of the WM T1 histograms varied slightly between methods (1 to 5%), much less than the differences reported between different T1 [52] mapping techniques themselves (20–30%). Our results demonstrate that double angle B1 mapping using a standard product EPI sequences can produce whole-brain B1 maps comparable in quality to rapid techniques (eg, AFI and BS) in a clinically acceptable scan time (~2min). While our work was based on a multishot EPI protocol [81], double angle imaging using other fast k-space acquisition strategies could also be considered (eg, double angle using a fast spin-echo readout [82]). Implementing standard product pulse sequence protocols for B1 mapping avoids time-consuming on-site pulse sequence programming (sequences similar to the one used in our study are commonly offered by other manufacturers [81]), improves accessibility of whole-brain B1 mapping to researchers without access to custom pulse sequences, and could facilitate protocol standardization between sites.

Other groups have also presented comparison studies of existing B1 methods. Lutti et al [164] optimized and compared the following methods at 3.0T: AFI, a 3D stimulated-echo B1 mapping method with EPI readouts, a 2D stimulated echo acquisition mode (STEAM) B1 mapping method, and single-slice DA as a reference. The two stimulated-echo-based methods required additional quantitative pulse sequences for calibration: the 3D stimulated-echo with single-shot EPI B1 mapping technique used B0 maps to correct for distortions, and the 2D STEAM method was calibrated against AFI using a separate measurement on a gel phantom to correct for nonlinearities of the slice-selective pulse. Each method demonstrated good reproducibility, and the largest deviation relative to the reference (DA) was observed with the stimulated-echo EPI method (4%), which is in the range of deviation we observed with our standard product EPI-DA pulse sequence (5% relative to Ref. DA for WM). Despite the benefits of these optimized rapid B1 methods, wide-scale use is limited, as all methods require pulse sequence programming expertise and additional quantitative measurements. Another important source of B1 inaccuracies, noise, has been characterized for different B1 methods (Ref. DA, AFI, and BS) using Monte Carlo simulations and phantoms [166,167]. The authors demonstrated that SNRs as low as 50 can be sufficient for accurate flip angle estimation for the range observed in the brain at 3T, and all of the methods compared in our work had SNRs above this threshold in WM.

Optimal flip angles for VFA are in the low FA range (1–30°) due to short TRs required for whole-brain VFA T1 mapping.21 All B1 methods compared in this work used larger flip angles to map the B1 intensity (Ref. DA and EPIDA: 60°/120°; AFI: 60°; BS: 25° and 500°), consistent with the published values in the original articles. Thus, RF amplifier nonlinearities could result in inaccurate low FA estimations. RF amplifier nonlinearity can vary substantially between scanner hardware manufacturers, which may lead to a bias of the corrected low flip angles used for VFA [168]. VFA pulse sequence optimization techniques have been proposed to minimize the impact of RF nonlinearity on T1 mapping [169]. A modified DA B1 method has also been proposed to map low flip angles accurately [168], which could possibly be adapted to use fast k-space readout acquisition pulse sequences, such as EPI or fast spin-echo.

For the purpose of our study, a simple single-slice DA method measurement was considered to be our “reference” method, as is often the case in B1 mapping studies. The Ref. DA acquisition is itself sensitive to sources of inaccuracies, as the typical pulse sequence protocols for Ref. DA render the B1 maps sensitive to long T1, particularly in voxels containing CSF. The TR used for this pulse sequence was shorter than conventional implementations; however, it was validated against another robust DA method [83] using a TR = 3000 msec and demonstrated very high voxelwise correlation in WM (*ρ* = 0.98, y = 0.99x + 0.03). Longer TRs could be used for improved accuracy; however, such a protocol requires 20+ min for a single slice scan [85], and motion would become an increasing concern with longer TRs. Slice-select RF pulse profiles may also impact B1 map accuracy, as nonrectangular RF profiles result in a range of flip angles within a slice (and voxel), particularly for large flip angles. Some techniques have been developed to correct for slice profile effects [170]; however, they add additional complexity in postprocessing and require RF pulse waveform information, which may not always be accessible from the scanner. Single-slice DA imaging can mitigate slice profile inaccuracies by using nonselective excitation pulses [83] or refocusing pulses, yet undesired signal from outside the slice can be a problem if incompletely crushed [171]. All B1 methods compared in this work used pulse sequences that differ greatly in their mechanism and analysis (saturation recovery: DA; steady-state: AFI; phase: BS), yet still produced voxelwise B1 values highly correlated with the reference measurement (Ref. DA). Each B1 method, even considering their imperfections, produced much better T1 maps than for the case of omitting B1 correction altogether (Nominal).

Smoothing or blurring filters are typically applied to B1 maps [84,164,172], as the B1 variation in the brain is expected to be smooth and spatially slowly varying [161]. There is no well-established consensus on which filter is ideal for B1 maps. The types of filters used in the literature are numerous: Gaussian convolution, median filters, spline interpolation, etc. In addition, the size of the blurring kernel used varies widely between studies; ranging from 3mm [84] to 10 mm [172]. Although filtering the B1 map is often considered a good practice when used in subsequent B1-correction applications, unfiltered B1 maps should also be reported when using, developing, or comparing new B1 methods. B1 methods are often only compared postblurring [84,164], thus not all artifacts (or noise level) may be clearly identifiable, only those not fully attenuated by the filters. Unfiltered B1 maps display valuable information about scanner and pulse sequence artifacts, which is particularly useful when developing or evaluating new methods. For example, even though the ringing artifact in our AFI measurements can be attenuated in the B1 maps using filtering methods, it may be preferable to use preprocessing techniques to eliminate the ringing in the acquisition images before the B1 map is calculated [173]. Although blurring B1 maps can attenuate local artifacts, it can also spread inaccuracies (eg, ventricles in our EPI-DA maps). If tissue masks are available, specific tissues known to produce inaccurate B1 values (eg, for the multislice EPI-DA case, cerebrospinal fluid) could be masked, and B1 values could be interpolated in these regions to approximate the missing values.

The specific scope of this work is limited to applications at clinical field strengths. B1 mapping at ultrahigh field strengths must be robust against more B0 inhomogeneity, longer T1 values, and faces additional hardware challenges, such as parallel transmit [174]. Accelerating B1 mapping methods using an EPI-based acquisition scheme can be prone to significant susceptibility distortions and signal dropouts at ultrahigh fields [88]. However, Bloch-Siegert at 7T requires additional acceleration techniques like EPI due to its high SAR RF pulses [175]. Supplementary scans (eg, B0 map) can be used in EPI-based B1 mapping to correct the distortions [176], but at the cost of a longer total scan time. Investigating structural characteristics of the cortex is also a topic of great interest in high-field MRI, due to its capability to image at very high resolutions (≤1mm3). High-resolution VFA T1 mapping of the cortex must use B1 maps acquired using a method that has a good robustness against the long T1 of CSF that neighbors the cortical regions [177], such as AFI, BS, or other advanced B1 mapping techniques.

This study had some limitations. The decision to use single-slice B1 for a reference limited the quantitative comparison between methods to a single slice of the brain. Although using a single-slice DA B1 map as a reference is common for validating whole-brain methods [85,164], one solution could be to acquire two more slices in perpendicular planes. Another limitation was that the low resolution of the reference scan restricted the quantitative assessment of B1 and T1 values to WM. To quantitatively compare B1 maps in the cortex, a faster reference acquisition allowing for higher resolution (~1mm3) is needed.

In conclusion, we report that B1 mapping at 3T implemented using standard product pulse sequences (eg, interleaved multislice EPI double angle) can serve as a sufficient alternative to advanced B1 methods (eg, actual flip angle imaging, Bloch-Siegert), which are not readily available on most MRI systems. The EPI double angle protocol produced whole-brain B1 maps in a clinically acceptable scan time (~2min), shorter than the AFI and BS’s protocols that were compared (although these methods can be further accelerated by implementing fast acquisition strategies, eg, EPI, fast spin-echo, or spiral). All investigated B1 mapping methods correlated well with a reference measurement, and produced substantially better VFA T1 maps than in the absence of B1 correction. The agreement between B1 maps and resulting T1 maps were improved by filtering the B1 maps to reduce noise and minor artifacts. B1 mapping implemented with standard product pulse sequences can provide an excellent alternative for researchers without custom rapid whole-brain B1 methods and is much preferred to omitting B1 correction altogether.

## Acknowledgments

Contract grant sponsor: National Sciences and Engineering Research Council of Canada with the Alexander Graham Bell Canada Graduate Scholarships-Doctoral program (to M.B.); Contract grant sponsor: CIHR and Campus Alberta Innovates grants (to G.B.P.)

# *B1-Sensitivity Analysis of Quantitative Magnetization Transfer Imaging*

## Preface

Chapter 3 demonstrated that acquiring good quality whole-brain B1 map is feasible using a standard MRI pulse sequence, which is valuable to researchers unable to implement pulse sequences such as AFI and Bloch-Siegert. In addition, that chapter presented several potential sources of voxel-wise inaccuracies of B1 maps (e.g. noise, artifacts, filtering) and did some comparisons of VFA T1 maps in the presence of all of these imperfections, as well as for the complete omission of a B1 map. Because qMT requires both a B1 and a T1 map, inaccuracies in B1 values will propagate to the qMT fitting parameters differently depending on if the T1 mapping method used is B1-independent (e.g. Inversion Recovery) or B1-dependent (e.g. VFA). For the B1-independent T1 case, errors in B1 value would propagate to qMT fitting parameters through the calibration of the nominal MT pulse and excitation flip angles; for the B1-dependent T1 case, errors in B1 value would propagate to qMT through this same pathway, but also through errors in T1 (used as a constraint for qMT parameters) as a result of B1-errors. The purpose of this chapter is to examine the B1-sensitivity of qMT for these two categories of T1 mapping, and to determine which T1 mapping method results in the least B1-sensitivity of qMT parameters, particularly for the pool-size ratio.

The following manuscript, published in the journal *Magnetic Resonance in Medicine*, describes a B1-sensitivity analysis of qMT, considering IR and VFA T1 maps. The impact on fitted qMT parameters (F, kf, T2,f, T2,r) due to errors in B1 were first explored using simulations. A sensitivity analysis of the qMT Z-spectrums using simulated values was also done to look into the origin of the differences in sensitivity characteristics between T1 mapping methods. In vivo measurements were used to study the sensitivity of the pool-size ratio for a wide-range of B1 errors by analyzing the values in the absence of any B1 correction; qMT values were also compared using B1 maps originating from 3 different B1 mapping techniques. Overall, this manuscript establishes a foundation for how to study the B1-sensitivity of a qMT acquisition protocol, informs qMT researchers of the substantial differences in B1-sensitivity that exist for the fitted parameters depending on which T1 mapping technique is used, and discovers that under the right circumstances it may be possible for the pool-size ratio to be robustly estimated using qMT even if a B1 map is omitted.

**B1-Sensitivity Analysis of Quantitative Magnetization Transfer Imaging**

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**Magnetic Resonance in Medicine, 10.1002/mrm.26673, 2017**

## Abstract

**Purpose:** To evaluate the sensitivity of quantitative magnetization transfer (qMT) fitted parameters to B1 inaccuracies, focusing on the difference between two categories of T1 mapping techniques: B1-independent and B1-dependent.

**Methods:** The B1-sensitivity of qMT was investigated and compared using two T1 measurement methods: inversion recovery (IR) (B1-independent) and variable flip angle (VFA), B1-dependent). The study was separated into four stages: 1) numerical simulations, 2) sensitivity analysis of the Z-spectra, 3) healthy subjects at 3T, and 4) comparison using three different B1 imaging techniques.

**Results:** For typical B1 variations in the brain at 3T (±30%), the simulations resulted in errors of the pool-size ratio (F) ranging from -3% to 7% for VFA, and -40% to>100% for IR, agreeing with the Z-spectra sensitivity analysis. In healthy subjects, pooled whole-brain Pearson correlation coefficients for F (comparing measured double angle and nominal flip angle B1 maps) were *ρ* = 0.97/0.81 for VFA/IR.

**Conclusion:** This work describes the B1-sensitivity characteristics of qMT, demonstrating that it varies substantially on the B1-dependency of the T1 mapping method. Particularly, the pool-size ratio is more robust against B1 inaccuracies if VFA T1 mapping is used, so much so that B1 mapping could be omitted without substantially biasing F.

## Introduction

Quantitative magnetization transfer (qMT) imaging is a powerful MRI technique used to investigate macromolecular content not typically detectable with conventional MRI. MR properties of macromolecular hydrogen are measured with qMT by indirect means: the magnetization of the macromolecular pool is saturated, and energy is exchanged with nearby water molecules via cross-relaxation processes and chemical exchange [97,133]. In imaging brain white matter (WM), the pool-size ratio (F), the ratio between the equilibrium magnetization of hydrogen in macromolecules versus hydrogen in water, has been shown to be a good marker of myelin density [39,178]. In particular, the pool-size ratio has been used to study multiple sclerosis lesions [144,179,180]. Several methods have been developed to estimate qMT parameters from the mathematical model that describes the exchange processes [134,140,141,181,182].

Commonly, off-resonance qMT imaging uses a magnetization transfer (MT)-prepared spoiled gradient (SPGR) echo pulse sequence [183]. It is a standard SPGR sequence preceded by an off-resonance radiofrequency (RF) pulse that varies in amplitude and frequency offset between measurements; 10 measurements or more are generally required to fit this Z-spectrum (normalized MT signal vs. off-resonance frequencies) [155], and one additional measurement without the MT-preparation for signal normalization. These qMT techniques also require three additional measurements: B0, B1, and T1. In postprocessing, B0 maps calibrate the off-resonance frequency of the MT pulse in each voxel. B1 maps are used to scale the SPGR excitation flip angle and MT-pulse saturation power. A T1 map is necessary to constrain certain fitting parameters of the two-pool MT fitting model [133]. For a given voxel, the measured T1 (T1,meas) is a function of the T1 of the water molecules (T1,f, “f” is for “free pool”) and of the T1 of the macromolecules (T1,r, “r” is for “restricted pool”), and two other parameters (F, ratio of the two pool sizes in the voxel, and kf, the exchange rate constant). The large number of measurements required to sample the Z-spectrum and additional quantitative maps make qMT a time-costly technique.

Increasingly, whole-brain qMT imaging has been achieved via a reduction in qMT measurements [156,159] and new rapid techniques to measure the required quantitative calibration maps [84,85,87]. However, integrating new methods into quantitative imaging studies can introduce unintended effects. For example, transitioning from single-slice T1 mapping techniques (i.e., inversion recovery [IR]) to three-dimensional [3D] techniques, variable flip angle [VFA]) also results in transitioning from B1-insensitive [51,52] to B1-sensitive [60] T1 mapping. If VFA is used in the qMT imaging protocol, inaccuracies in B1 will propagate into fitted qMT parameters through two pathways instead of just one (Figure 4‑1): from errors induced in T1, used to restrict the fitting parameters, and from errors in scaling the MT saturation powers with the B1 maps. The potential effect of B1-uncorrected qMT on the fitted parameters has been noted in previous work [135,184]; however, these were limited in scope to B1-insensitive T1 techniques. To our knowledge, no comprehensive characterization of the B1- sensitivity of qMT (and notably, comparing different T1 mapping methods) has previously been performed.

This work focuses on answering the following three questions: 1) How sensitive is each qMT parameter to B1-inaccuracies? 2) How does the B1-sensitivity of qMT parameters differ between protocols using B1-independent (IR) and B1-dependent (VFA) T1 mapping methods?; and 3) Which T1 mapping method results in the most robust measure of the pool-size ratio in the presence of B1-inaccuracies? To explore these questions, we first focused on simulations under ideal measurement conditions for a single tissue type, and then used this framework to perform a sensitivity analysis of the signal curves. We then measured qMT maps in healthy human volunteers using both T1 mapping methods (IR and VFA), and compared measured B1 maps with fictitious maps generated to have a large range of potential inaccuracies. Finally, we compared the relative agreement of qMT fits between three different B1 mapping methods (double angle, actual flip angle imaging, Bloch-Siegert) using both T1 mapping methods (IR and VFA).

## Methods

All measurements were performed with a 3.0T whole-body MRI scanner (Magnetom TIM TRIO; Siemens, Erlangen, Germany) using a 32-channel phased-array receive-only head coil and whole-body transmit coil. Healthy volunteers were scanned after providing informed consent, in compliance with and approved by the institutional ethics committee. The total scan time for the entire acquisition protocol described in the B1-Sensitivity of qMT in Healthy Subjects and B1 Method Comparison sections was 28 minutes and 58 seconds.

### Simulations

The coupled Bloch-McConnell differential equations describing two-pool magnetization exchange were solved numerically (MATLAB 2011a; MathWorks Inc., Natick, MA) for a pulsed MT-prepared SPGR pulse sequence using the Sled and Pike model [135,142]. The pulse sequence was decomposed into event blocks of instantaneous saturation of the free pool, constant irradiation of the restricted pool, and free precession. Prior to simulating exchange, the fractional saturation of the longitudinal magnetization induced by direct saturation was computed numerically in the absence of exchange and T1 recovery. The steady-state solution was approximated analytically using the assumption that the magnetization at an arbitrary time t should be equal to that of time *t*+prepetition time (TR), as described in detail in the appendix of Sled and Pike [134]. The signal was simulated with the following pulse sequence parameters [155,156]: TR = 25 ms, excitation flip angle (FA) = 7º, MT pulse flip angle = 142 º and 426 º, MT pulse duration = 10 ms, 10 offresonance frequencies ranging between 423.9Hz and 17.2354 kHz in logarithmic steps. The envelope of the MT-preparation RF pulse was a Gaussian-Hanning function, and a super-Lorentzian lineshape function was used for the transition rate of the restricted pool to approximate the behavior observed in tissues [142]. qMT tissue parameters for all simulations were set to healthy white matter values measured in a previous scan: F = 0.122 n.u. (normalized units), magnetization exchange rate (kf) = 3.97 s-1, free-pool longitudinal relaxation rate (R1,f = 1/T1,f) = 1.12 s-1, restricted-pool longitudinal relaxation rate (R1,r = 1/T1,r) = 1.00 s-1, free-pool transverse relaxation time (T2,f) = 27.2 ms, restricted-pool transverse relaxation time (T2,r) = 10.96ms.

SPGR qMT experiments require three additional quantitative measures: B0, B1, and T1. B0 measurement methods typically do not require B1 or T1 calibration; thus, ideal B0 homogeneity was used in the simulations. MT signal values were simulated using B1 (to scale the MT saturation powers and excitation flip angles) and T1,meas (to constrain the fitting parameters) that were fixed to their ideal values (1 n.u. and 0.9 s respectively). The MT signal was subsequently fitted using the Sled and Pike method [135]. As per convention, R1,r was fixed to 1 s-1. R1,f was calculated during the fitting algorithm from an analytical expression of F, kf, R1,r, and T1,meas. To investigate the effect of inaccuracies in B1 and T1,meas on the fitted qMT parameters, the simulated MT signal values were fitted using a large range of B1 and T1,meas values. Four qMT parameters (F, kf, T2,f, T2,r) were explicitly fitted for each pair of 100 B1 and 100 T1,meas values (10,000 combinations). The set of B1 values varied linearly from 0.5 to 2 n.u., and T1,meas varied from 0.1 s to 4 s. For this stage, B1 and T1,meas varied independently of each other. We investigated the qMT parameter sensitivities due to B1 inaccuracies for two T1 mapping techniques: IR, approximately B1 independent [52], and VFA, inherently B1-dependent [60]. The IR case was interpreted to be a linear subset of the B1-T1 combination discussed above by a fixed T1 (T1,IR = 0.9 s, constant). The VFA signals from a two flip angle experiment were calculated for T1 = T1,true =0.9 s from the analytical steady-state SPGR equation (TR = 25 ms, FA = 3º and 20 º). T1,VFA values were subsequently estimated by linear least-square fitting of the VFA data with flip angle calibration [57] using the set of 100 B1 values (0.5 to 2 n.u.). The fitted VFA T1,meas values were then used in conjunction with their respective B1 values to fit the qMT parameters to the simulated MT signal.

### Sensitivity Analysis

To provide further insight into the behavior of fitted parameters in the presence of B1 inaccuracy, a sensitivity analysis of the qMT signal was performed [185]. For each qMT parameter, the following definition of sensitivity was used (cf. Appendix A):

|  |  |
| --- | --- |
|  | **(4-1)** |

where the index *i* describes a specific qMT acquisition point, *Mi* is the normalized signal of the ith qMT measurement, and *Sp,i* is the sensitivity of the MT signal with respect to *p* for the *i*th qMT acquisition. The sensitivity *Sp,i* represents the change in normalized MT signal induced by a slight change in fitting parameter value or model input value (e.g., B1). A large absolute *Sp,i* value signifies that, to a linear approximation, a large change in MT signal will occur (at that Z-spectrum value) for a small variation of *p*. In the context of fitting data to measurements using an inaccurate B1 value, the following relationship can be shown (cf. Appendix A):

|  |  |
| --- | --- |
|  | **(4-2)** |

Thus, the sensitivity values can provide an insight as to why certain fitting parameters are more likely to have large errors due to inaccurate B1 values. When comparing two measurement protocols, the following metrics can be expected to provide insight into which fitting parameters *p* are more/less sensitive to B1 inaccuracies (cf. Appendix A):

|  |  |
| --- | --- |
|  | **(4-3)** |
|  | **(4-4)** |

where ***S*** is the vector of sensitivity values for a set of N measurements, is its norm, and is its unit vector. If the sensitivity values of a parameter *p* and B1 have very similar curves (Eq. (4-3) ≈ 1), then *p* is likely to be most sensitive to B1 inaccuracies compared to other parameters. The relative error of *p* will then be proportional to the ratio in Eq. (4-4).

The qMT measurement protocol and tissue parameters from the Simulations section were used to simulate normalized MT signal values. Partial derivatives with respect to qMT parameters (and B1) of the MT signal were evaluated at each point of the Z-spectrum [186]. B1 sensitivity values were calculated for two cases: T1,meas independent of B1 (which for consistency with the other sections we designate as IR), and T1,meas with VFA B1-dependency. As T1,meas is primarily used to constrain R1,f, R1,f was modified in addition to B1 accordingly for the VFA case. The derivative steps were fixed to a 10-5% relative increase of the parameter denominator value, sufficient for the convergence of the partial derivative at each Z-spectrum point of our qMT protocol.

### B1-Sensitivity of qMT in Healthy Subjects

Three healthy adult volunteers were scanned (two males, one female, 30 ± 4 years old). All quantitative imaging sequences were acquired at a resolution of 2 × 2mm2 in-plane × 5mm slice thickness. Single slices were acquired parallel to the anterior commissure–posterior commissure (AC-PC) line, superior to the corpus callosum.

*T1 Maps:* VFA T1 maps were acquired using a spoiled 3D gradient echo sequence [87]: echo time (TE) = 2.89 ms, TR = 15 ms, FA = 3º and 20 º, spoiler gradient moment (AG) = 280 mT ∙ ms/m, RF phase increment (*φ*) = 169º, 1 m 28 s scan time. Prior to fitting the data for T1, the nominal flip angles were scaled voxel-wise with each B1 map. The VFA T1 values were then estimated from linear least-square fitting. Inversion recovery T1 data were collected from a four-inversion-time (TI) spin-echo sequence [52]: TE/TR = 11/1550 ms, TI = 30, 530, 1030, 1530 ms, 9 m 16 s scan time. An open-source software package for robust inversion recovery fitting was used to fit the IR T1 maps [51].

*qMT Maps:* qMT data were acquired according to the 10-point MT-prepared SPGR acquisition protocol described in the Simulations methods section, which for our single slice has a 2 m 38 s scan time. B0 maps were acquired for off-resonance frequency correction using a two-point phase-difference gradient measurement [187]: TE1/TE2/TR = 4/8.48/25 ms, FA = 7º, 30 s scan time. qMT parameter maps were produced by fitting the normalized qMT data voxel-wise using the Sled and Pike fitting model [143].

*B1 Maps:* Two categories of B1 maps were compared: 1) in vivo measured B1 maps and 2) B1 maps that had a single value assigned to all voxels (B1,Flat). B1,Flat maps were used to investigate the sensitivity of qMT to B1 inaccuracies for in vivo conditions (e.g., noise, tissue partial volume, a broad range of qMT tissue parameter values). Single-slice double angle (DA) B1 maps (B1,DA) were acquired using a spin-echo readout: TE/TR = 12/1550 ms, FA = 60º/120º, with slice-selective excitation and 180º refocusing pulses, 4 m 28 s scan time. A set of B1,Flat maps were generated for a range of values (B1,Flat = 0.5, 0.75, 0.9, 1, 1.1, 1.25, 1.5, 2 n.u.), where B1,Flat = 1 n.u. represents the nominal flip angle case. Prior to fitting the qMT data, each B1 map (B1,DA and the set of B1,Flat) was used as a corrective factor for the VFA nominal flip angles, MT excitation flip angles, and MT saturation powers.

*Data Analysis:* qMT parameter maps (F, kf, T2,f, T2,r) were fitted voxelwise using four sets of B1 and T1 combinations: B1,DA and B1,Flat used with IR and VFA T1 maps (Figure 4‑1). Voxel data of each qMT parameter map were pooled (across all subjects) for each B1 and T1 set, and linear regression analysis was performed (comparing B1,DA and each B1,Flat).



Figure ‑. Quantitative measurements used in our magnetization transfer (MT)-prepared spoiled gradient quantitative MT study. Solid arrows are used for required measurements; dotted arrows are used for specific methods of a particular measurement. The double angle (DA) method is an explicitly measured B1 map. B1,Flat maps are generated using a single value in all voxels. Variable flip angle (VFA) is a T1 mapping methods that also requires B1 as a support measurement, unlike inversion recovery (IR).

### B1 Method Comparison

Several techniques exist to measure B1 maps, and each method can be prone to unique sources of systemic biases or local artifacts [176]. To probe the robustness of the B1-sensitivity of qMT between different B1 measurement techniques, two additional B1 maps were acquired and compared against the DA B1 maps in all three subjects from the B1-Sensitivity of qMT in Healthy Subjects section. Actual flip angle imaging (AFI) [84], a two-TR steady-state SPGR-based pulse sequence, was applied to produce B1 maps with a 2 × 2 × 5mm3 whole-brain 3D spoiled acquisition (19): TE/TR1/TR2 = 3.53/20/100 ms, FA = 60º, AG = 450 mT ∙ ms/m, *φ* = 39º, 5 m 38 s scan time. Bloch-Siegert shift (BS) B1 mapping [85], an SPGR-based method with an off-resonance RF preparation pulse, produced B1 maps using a single-slice 2 × 2 × 5mm3 acquisition: TE/TR = 15/100 ms, *α* = 25º, 8 ms Fermi Pulse of 500º at 64 kHz off-resonance, phase-shift constant (KBS) = 74.01 rad/G2, 19 s scan time.

At the resolution of our data (2 × 2 × 5mm3), partial volume effects near cortical grey matter (GM) and adjacent to ventricles can be significant. The partial volume effects can make the analysis of in GM challenging. Preliminary data (not shown) suggested that an insufficient number of voxels exist containing only GM, for a reliable analysis to be performed, and including all voxels containing at least some GM would include a significant bias in the qMT parameters from cerebrospinal fluid (CSF). As such, the images were masked solely for WM. Whole-brain T1-weighted magnetization-prepared rapid gradient-echo (MP-RAGE) 3D volumes (1 × 1 × 1mm3) were acquired: TE/TR/TI = 3.32/2300/900 ms, parallel imaging acceleration factor = 2, bandwidth (BW) = 230 Hz/Px, 5 m 30 s scan time. Tissue classification maps (WM, GM, CSF) were estimated via Intensity Normalized Stereotaxic Environment for the Classification of Tissue [163] using the MPRAGE data with the International Consortium for Brain Mapping-152 atlas. WM tissue masks were resampled to match the AC-PC 2 × 2 × 5mm3 single slices using a majority voting analysis (75% threshold). The histograms of WM qMT parameters were calculated for all three B1 maps, using both VFA and IR T1 maps in the processing pipeline. Chi-square (*χ*2) of the histogram differences was calculated to quantify how well the histograms matched between the DA case versus AFI and BS.

## Results

### Simulations

The error (%) in F calculated after fitting the simulated qMT signal using each B1 and T1 value-pair is displayed in Figure 4‑2. T1 curves as a function of B1 inaccuracies are superimposed with solid (IR) and dotted (VFA) lines. The error in F (%) is a smooth nonlinear function of B1 and T1, with some speckling in values occurring far from the true B1 and T1 intersection (where they are both grossly inaccurate). IR T1 is set to be constant, resulting in a wide range of errors in F (<-100% to 50%) for the B1 inaccuracy range evaluated. B1 underestimation resulted in an overestimation of VFA T1, and the error in F for this case overlaps near the 0% error contour line (green).



Figure ‑. Simulated differences (%) in fitted quantitative magnetization transfer (qMT) F values in the presence of a wide range of B1 and T1 errors (B1,true = 1 n.u., T1,true = 0.9 s). The superimposed lines plot the T1 distribution for a B1-independent T1 mapping method (inversion recovery [IR], solid line, and variable flip angle [VFA], dashed line). n.u. = normalized units.

At 3T, the B1 amplitude varies approximately ±30% in the brain. The errors in the four qMT fitted parameters are shown for this range of B1 inaccuracy in Figure 4‑3, for both the IR and VFA T1 cases. Note that Figure 4‑3a corresponds to the values superimposed by the IR and VFA T1 lines in Figure 4‑2. Relative to IR, errors in F due to B1 inaccuracies are substantially reduced using VFA. For VFA, the errors in F ranged between -3% and 7% (blue line) for ±30% B1 inaccuracy; for IR, the errors ranged between -40% and >100% (red line). kf exhibits the inverse trend; errors in kf are larger for VFA relative to IR (Figure 4‑3b) for all B1 values. No advantage in either T1 method is identified for T2,f; the slopes of the curves flip between both T1 methods with approximately the same magnitude. T2,r is insensitive to B1 inaccuracies for both T1 mapping method (Figure 4‑3d).



Figure ‑. Simulated errors (%) in fitted quantitative magnetization transfer (qMT) parameters for ±30% B1 errors (a: pool size ratio [F], b: magnetization exchange rate [kf], c: free pool T2 [T2,f], d: restricted pool T2 [T2,r]). Fits using a B1-independent T1 measure (inversion recovery [IR]) are shown in red, and those using variable flip angle (VFA) T1 mapping are shown in blue. The IR curve in d) is underneath the VFA line. Note: The solid and dashed lines in Figure 4‑3 to show the dependence of IR and VFA T1 on B1. n.u. = normalized units.

For IR, a 10% underestimation in B1 produced a 23% error in F, 6% error in kf, 12% error in T2,f, and 0.78% error in T2,r. For VFA, a 10% underestimation in B1 produced a 1.5% error in F, 25% error in kf, 6.7% error in T2,f, and 0.78% error in T2,r. Thus, switching from IR to VFA reduces B1-sensitivity of F by a factor of 15 for a 10% error in B1. The error in F for the IR case (23%) produced from a 10% error in B1 is consistent with the value calculated by Sled and Pike using a 60-point protocol (20%) [135].

### Sensitivity Analysis

The plots of the sensitivity values for our qMT protocol are shown in Figure 4‑4, and the sensitivity metrics (from Eqs. (4-3) and (4-4)) are calculated in Table 4‑1. The curve similarity metric informs us of how well changing a particular fitting parameter *p* (F, kf, T2,f, and T2,r) can correct the expected signal change due to an error in B1. For a B1-independent T1 measurement (e.g., IR), we see from Table 4‑1 that the values have the following trend: (F ≈ 1) > kf > T2,f ≫ T2,r, for VFA: (kf ≈ 1) > F ≈ T2,f ≫ T2,r. This suggests that F has a higher sensitivity to B1 inaccuracies for IR than VFA, with a reverse relationship expected for kf, both in agreement with the simulations results from the Simulations section. Figure 4‑4 illustrates these relationships; the sensitivity curves for B1IR (Figure 4‑4a) have a similar pattern to those for F (Figure 4‑4c), whereas the sensitivity curves for B1VFA (Figure 4‑4b) have a similar pattern to those for kf (Figure 4‑4d). For these respective cases, is greater for kf than F (Table 4‑1), suggesting that larger relative errors in kf are required to compensate B1VFA inaccuracies than F for B1IR, consistent with our simulation observations. Lastly, note that the minima observed in is due to a zero-crossing of , a characteristic that was also reported in a previous study [188].

Table ‑. qMT Z-Spectra Sensitivity Comparison Metrics for B1 (Accounting for the B1-Sensitivity of Each T1 Method, IR, and VFA) and Each Fitted qMT Parameter

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | |  | |
|  |  |  |  |  |
|  | **0.975** | 0.754 | **2.05** | 1.07 |
|  | 0.815 | **0.951** | 6.02 | **3.12** |
|  | 0.704 | 0.776 | 4.67 | 2.43 |
|  | 0.482 | 0.552 | 3.08 | 1.61 |

**Note: corresponds to the qMT sensitivity values relative to B1 assuming a B1-independent measure of T1, whereas considers a qMT protocol using a VFA T1 measurement, which inherently is B1-dependent. IR = inversion recovery; qMT = quantitative magnetization transfer; VFA = variable flip angle.**

****

Figure ‑. Sensitivity analysis of the magnetization transfer signal relative to B1 (a, b) and fitting variables (c–f). The plots (note scale changes) show the magnitudes of the sensitivity values (Eq. (4-2)).

### B1-Sensitivity of qMT in Healthy Subjects

Noise, partial volume effects of tissue, and a wide range of different qMT tissue parameters were not considered in the previous sections, all of which could potentially impact the B1-sensitivity of the qMT fits. In vivo data were acquired to investigate whether the B1-sensitivity features identified in our simulations hold under real-world conditions. Single-slice qMT parameter maps are shown in Figure 4‑5, fitted using VFA (a) and IR (b), for either DA B1 maps or the nominal flip angle assumption (B1,Flat = 1). For VFA and B1,Flat, the elevated T1 at the center of the brain counteracts the underestimated B1 values, resulting in minimal errors in the qMT F maps relative to the IR F maps. At the perimeter of the brain where B1,Flat overestimates the measured values, the VFA case results in nearly no qMT F bias. Regions of very high T1, suggesting presence of CSF, do exhibit speckling of large errors in F. qMT F fitted with the combination of IR and B1,Flat resulted in large errors, where the B1 profile is clearly distinguishable in map of errors in F.

Table 4‑2 lists the correlation and linear regression slope (B1,DA vs. B1,Flat = 1) for all fitted qMT parameters, using both T1 methods. qMT F using VFA had the best correlation (*ρ* = 0.97, slope = 0.97), as opposed to IR (*ρ* = 0.81, slope = 0.57). T2,f also demonstrated good correlations (*ρ* = 0.97), but with an underestimation of the slope (slope = 0.86). Based on our simulations, the low correlation of kf for the IR case (*ρ* = 0.26) was unexpected. Upon further investigation of the raw kf scatter plots (not shown), the linear assumption for fitting the kf scatter plot was violated. Thus, for conditions exhibited in vivo (i.e., noise, multi-tissue voxels), the kf parameter fits were not stable in the presence of large B1 errors, resulting in kf voxel values diverging substantially in the scatter plot data.

Table ‑. Pooled (All Subjects) Pearson Correlation Coefficients and Linear Regression Slopes for qMT Values Comparing Measured DA B1 Maps and Fictitious B1,Flat = 1 Mapsa

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **(B1,DA) vs. (B1,Flat = 1)** | | | |
|  | **T1,VFA** | | **T1,IR** | |
| **qMT** | **Pearson *ρ*** | **Slope** | **Pearson *ρ*** | **Slope** |
| F | **0.97** | **0.97** | 0.81 | 0.57 |
| kf | 0.27 | 0.24 | 0.26 | 0.25 |
| T2,f | 0.97 | 0.86 | 0.93 | 0.90 |
| T2,r | 0.81 | 0.78 | 0.89 | 0.82 |

**aB1,Flat = 1 is equivalent to the nominal flip angle assumption DA = double angle; qMT = quantitative magnetization transfer.**

****

Figure ‑. Single-subject comparison of quantitative magnetization transfer parameter maps fitted using double angle and B1,Flat = 1 maps using (a) variable flip angle (VFA) T1 maps corrected using the corresponding B1 map, and (b) inversion recovery (IR) T1 maps independent of B1.

Expanding the correlation analysis of F to a larger B1,Flat set of values (ranging from 0.5 to 2 n.u.), F was more robust against B1 overestimations than underestimations (Figure 4‑6a). The correlations break down rapidly for B1,Flat values below 0.75, yet are near unity for most values ranging between 1 and 2. The same trend is true for the fit slope for F; it is near unity for slight B1 underestimations and for large B1 overestimations (Figure 4‑6b).



Figure ‑. Pooled (all subjects, voxel-wise) whole brain Pearson correlation coefficients (a) and linear regression slopes (b) for qMT F values between the measured double angle B1 maps and generated B1,Flat maps. IR = inversion recovery; n.u. = normalized units; VFA = variable flip angle.

### B1 Mapping Method Comparison

Three B1 maps (DA, AFI, BS) are shown for one subject in Figure 4‑7. The DA B1 map, which was used in the previous section, was set as the reference measurement that the two other methods are compared against. AFI and BS displayed heterogeneous inaccuracy patterns relative to DA; voxel-wise relative errors were ±10%. In this subject, B1 in the frontal lobe was overestimated by both methods, whereas the left and right posterior regions showed different bias patterns for both techniques. Relative to DA, the voxelwise Pearson correlation and linear regression coefficients for all three subjects were *ρ* = 0.904 (y = 1.035 x – 0.034) for BS and *ρ* = 0.912 (y = 0.960 x + 0.038) for AFI. Despite variations in voxelwise accuracy between B1 methods, the histograms of WM qMT F matched very well for the VFA case (Figure 4‑8b, same subject as Figure 4‑7). The excellent overlap of histogram curves for this case resulted in low *χ*2 values for this subject (*χ*2AFI = 1.24, *χ*2BS = 1.41), unlike to the IR case for F (*χ*2AFI = 5.45, *χ*2BS = 6.40). Consistent with our simulations, the inverse relationship was true for kf in WM (Figure 4‑8c,d). The mean *χ*2 values of F for all subjects also had low standard deviations for VFA (*χ*2AFI = 1.24 ± 0.33, *χ*2BS = 1.41 ± 0.12) relative to IR (*χ*2AFI = 9.25 ± 5.81, *χ*2BS = 9.17 ± 3.94; Figure 4‑8a). For kf, the means for all subject for VFA were *χ*2AFI = 6.10 ± 1.81, *χ*2BS = 9.00 ± 3.45, and for IR were *χ*2AFI = 1.44 ± 0.42, *χ*2BS = 2.44 ± 1.21. These results demonstrate the robustness of VFA for qMT F, even in the presence of local inaccuracies acquired in similar B1 maps, and that B1 maps containing minor artifacts can be used without degradation in quantitative F value precision.



Figure ‑. B1 map comparison in a single subject using three different acquisition techniques: double angle method, actual flip angle imaging (AFI), and Bloch-Siegert shift. n.u. = normalized units.



Figure ‑. Single-subject white matter pool-size ratio (F) (a, b) and magnetization transfer (MT) exchange coefficient (kf) (c, d) distributions for three B1 mapping methods, using inversion recovery (IR) T1 mapping (a, c) or variable flip angle (VFA) T1 mapping (b, d). *χ*2 values of the actual flip angle (AFI) and Bloch-Siegert shift (BS) histograms were calculated relative to double angle.

## Discussion

Our findings demonstrate that the B1-sensitivity of off-resonance MT-prepared SPGR qMT parameters is strongly influenced by the T1 mapping method used. We showed that the robustness of the fitted qMT parameters is impacted by the choice between a B1-independent and a B1-dependent T1 mapping method impacts. Overall, the pool-size ratio F was shown to be most robust against B1 errors when VFA T1 mapping is used. Using simulations, we found that a 10% overestimation in B1 results in a 1.5% error in F if VFA is used for T1 mapping. This B1-induced error in F was 15 times less than for B1-independent methods such as IR (23% error in F). Although possibly a counter-intuitive prediction, the increased robustness in F against errors in B1 for a B1-dependent T1 method is made possible due to other fitting parameters (particularly kf) being more compatible to compensate the expected signal errors for this case. In vivo measurements were in agreement with our simulations; the F maps fitted using the nominal flip angle assumption (B1 inaccuracy ranging between -10% and 25%) and VFA T1-mapping correlated strongly with the case using a measured B1 map (*ρ* = 0.97). Histogram comparisons of WM qMT F between three different B1 mapping methods showed that VFA could result in four to five times better histogram matching (*χ*2 values) in the presence of B1 inaccuracies compared to IR.

Although most B1 mapping methods are designed to be robust to common sources of potential artifacts (i.e., tissues with long T1), there is no well-accepted gold standard method for accurately imaging B1. Our comparison between three well-accepted B1 imaging methods showed that ±10% in voxel-wise differences between B1 maps can be reasonably expected, resulting in inevitable B1 inaccuracies regardless of which technique is chosen. In addition, B1 maps are typically filtered with large blurring kernels (10mm3) [84,164,172], because B1 maps are expected to have a smoothly varying profile [161]. In the presence of local highly inaccurate voxels, blurring filters can have the unintended effect of biasing nearby voxels. Blurring filters can also be less effective in cortical grey matter due to edge effects, an area that is already sensitive to inaccuracies due to partial volume effects with CSF. Resampling low-resolution B1 maps for higher resolution qMT applications means that some inaccurate B1 information will inevitably be used in qMT postprocessing. Overall, some inaccuracies in B1 maps must be considered when planning the qMT acquisition protocol to minimize the sensitivity of the qMT parameter(s) of interest to this source of error.

The B1-sensitivity characteristics reported here are limited to the qMT imaging method and model that were used. Several other qMT techniques could benefit from a similar analysis; well-established pulsed SPGR qMT alternatives include the Ramani [140] and the Yarnykh [84] models. A key difference between these three MT models is in how they approximate the MT pulse power [142]. As B1 is primarily used as a corrective factor for the MT pulse power, B1-sensitivity will likely vary between these methods and could be explored in future work. Our sensitivity analysis results may also suggest that the B1-sensitivity will vary depending on certain key Z-spectrum acquisition choices, particularly dependent on how many MT powers are used. The number of MT powers is conventionally limited to two; however, optimized acquisition schemes have used anywhere between one [67,188] and eight MT pulse powers [155].

Despite the fact that VFA T1 mapping benefits qMT by improving the robustness of F, even for the extreme case of no B1 correction at all, certain limitations must be carefully taken into consideration prior to integration into a protocol. As shown with simulations and in vivo, the increase in robustness of one qMT parameter for a certain choice of T1 method (e.g., IR or VFA) results in a reduction in robustness of the other fitted parameters. For instance, a study whose aim is to compare all the qMT parameters should refrain from omitting B1 mapping, even if VFA is used, as kf will be inaccurate in several regions. Accurate T1 maps, which are valuable to many studies because they correlate with disease characteristics, would also be compromised if measuring B1 is omitted in a qMT protocol that uses VFA. However, for circumstances where the certain qMT parameters have been well-characterized for the disease of interest (e.g., multiple sclerosis), choosing to improve the accuracy and robustness of one parameter (e.g., F) at the expense of others may be justified. Reducing the number of measurements to benefit one qMT parameter at the expense of others has been reported previously; for example, constraining multiple fitting parameters was used to achieve a single off-resonance qMT measurement technique of the pool-size ratio [67,188].

## Conclusion

In summary, our work revealed the strong dependency of qMT B1-sensitivity on the choice of T1 mapping. Choosing carefully between a B1-independent and B1-dependent T1 mapping method can greatly improve the precision of certain qMT parameters. Our results showed that, for a pulsed SPGR qMT sequence with uniform Z-spectrum sampling, using VFA T1 mapping is preferable if the parameter of interest is the pool-size ratio F parameter. The robustness against B1 inaccuracy is so strong for this case, that B1 mapping could be omitted altogether without resulting in large differences in fitted qMT F maps. Omitting this measurement could help accelerate lengthy qMT acquisition protocols, at the expense of losing quantitative T1 information. B1-sensitivity of qMT could be further improved by optimizing the Z-spectrum sampling scheme, similar to how qMT acquisition schemes have been optimized for noise performance [155].

## Appendix A

Let us assume an experiment consisting of N measurements *M*i,meas (i = 1, 2 ..., N). Fitting the data to a mathematical model, the algorithm is expected converge to a state where |*Mi,meas - Mi,fi*t| is minimized at each point, such that ideally:

|  |  |
| --- | --- |
|  | **(4-A1)** |

*Mi,fit* depends on a set model parameters (k = 1, 2, .., L). For a small error in an measured model parameter (i.e., a calibration measurement, such as B1 in qMT), the change in each *Mi,fit* is approximated by a Taylor expansion:

|  |  |
| --- | --- |
|  | **(4-A2)** |

The fitting algorithm will nonetheless aim at producing a good fit (Eq. (4-A1)); thus, the following approximations are expected:

|  |  |
| --- | --- |
|  | **(4-A3)** |
|  | **(4-A4)** |

A first order approximation of the Taylor series for small and substituting for *Mi* condenses Eq. (4-A2) to:

|  |  |
| --- | --- |
|  | **(4-A5)** |

The *Mi* terms cancel, thus any error caused by must be compensated by errors propagated to the remaining fitting parameters for k ≠ j:

|  |  |
| --- | --- |
|  | **(4-A6)** |

For the Sled and Pike model of qMT, the calibration measurement we are interested in as a possible source of error in this work is B1, and the explicitly fitted parameters are F, kf, T2f and T2r:

|  |  |
| --- | --- |
|  | **(4-A7)** |

The sensitivity of a measurement *Mi* relative to a model parameter pk is defined as [185]:

|  |  |
| --- | --- |
|  | **(4-A8)** |

For a set of N measurements, Eqs. (4-A7) and (4-A8) simplify to matrix form:

|  |  |
| --- | --- |
|  | **(4-A9)** |

For a given error in B1 (), Eq. (4-A10) could be minimized to estimate the errors in each fitting parameter (, , , ) having known sensitivity values, which can be calculated analytically or through numerical simulations. However, to simplify the analysis, we chose to compare each fitting parameter *pk* independently to find possible easy-to-understand metrics to compare fitting parameter sensitivity to B1 inaccuracies. For each fitting parameter of interest (, we set all other values to 0. Equation (4-A9) now simplifies to a vector equation:

|  |  |
| --- | --- |
|  | **(4-A10)** |

where is the column vector for the parameter of interest *p* in Equation (4-A9), similar to . This equation is solved for by doing the scalar product of on both sides of the equation, and separating the norm of the vectors ( and their unit vectors (. Also, because and are absolute errors, they are scaled by the parameter values (, where is the relative error). To better compare each parameter, the relative error is preferred:

|  |  |
| --- | --- |
|  | **(4-A11)** |

Thus, for a given relative error in B1 , the parameter *p*, which maximizes for a given measurement protocol, will likely have larger inaccuracies than the other fitting parameters. This can be visualized easily, because ≈ 1 means that the sensitivity curves for B1 and *p* nearly match, and any change in the Z-spectrum expected by an inaccurate B1 can be nearly completely compensated solely by adjusting that fitting parameter. The error induced () will then proportional to the ratio of overall sensitivities .

## Acknowledgements

Funding for M.B. was provided by the National Sciences and Engineering Research Council of Canada with the Alexander Graham Bell Canada Graduate Scholarships – Doctoral program. Funding to G.B.P. was provided by the Canadian Institutes of Health Research, and Campus Alberta Innovates Program also supported this research.

# *Sensitivity-Regularization of the Cramér-Rao Lower Bound to Minimize B1 Nonuniformity Effects in Quantitative Magnetization Transfer Imaging*

## Preface

In the last chapter, we reported differences in the sensitivity of qMT fitting parameters in the presence of B1 inaccuracies between different T1 mapping methods, and investigated these differences for a fixed qMT measurement protocol (“uniform”). We concluded that VFA T1 mapping provides the best robustness of the qMT pool-size ratio against B1-inaccuracies. The next logical step is to investigate how the B1-sensitivity of qMT will change for a fixed T1 mapping method between different qMT measurement protocols. Or, more broadly, can the qMT acquisition protocol be optimized for reduced B1-sensitivity?

The following manuscript, submitted to the journal *Magnetic Resonance in Medicine*, describes a new approach to optimizing qMT for B1-insensitivity by sensitivity-regularizing the Cramér-Rao lower bound (CRLB) in an iterative optimization algorithm. A short theoretical derivation of the regularization condition is presented, as the fundamentals of it is described in detail in Section 4.8 (Appendix A of the previous manuscript). The regularization term was optimized using simulations to minimize the error in the pool-size ratio all while reducing the least impact on the CRLB (a marker for the sensitivity to noise). Using Monte Carlo Simulations, three protocols were compared (Uniform (same as Chapter 4), CRLB, and CRLB with B1-sensitivity regularization) f for a wide range of conditions (SNRs, B1-inaccuracies, different tissues). All the code developed for this project wraps around an open-source quantitative MRI Matlab package available online (a project I was also involved with and resulting in a publication which is not included in this thesis – Cabana et al. 2015), and the optimization code I developed has also been released as an open-source package.

**Sensitivity-Regularization of the Cramér-Rao Lower Bound to Minimize B1 Nonuniformity Effects in Quantitative Magnetization Transfer Imaging**

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**Submitted to Magnetic Resonance in Medicine**

## Abstract

**Purpose:** To develop and validate a regularization approach of optimizing B1-insensitivity of the quantitative magnetization transfer (qMT) pool-size ratio (F).

**Theory and Methods:** An expression describing the impact of B1-inaccuracies on qMT fitting parameters was derived using a sensitivity analysis. To simultaneously optimize for robustness against noise and B1-inaccuracies, the optimization condition was defined as the Cramér-Rao lower bound (CRLB) regularized by the B1-sensitivity expression for the parameter-of-interest (F). qMT protocols were iteratively optimized from an initial search space, with and without B1-regularization. Three 10-point qMT protocols (Uniform, CRLB, CRLB+B1-regulatization) were compared using Monte Carlo simulations for a wide range of conditions (SNR, B1-inaccuracies, tissues).

**Results:** The B1-regularized CRLB optimization protocol resulted in the best robustness of F against B1-errors, for a wide range of SNR and for both white and grey matter tissues. For SNR = 100, this protocol resulted in errors of less than 1% in mean F values for B1-errors ranging between -10 to 20%, the range of B1 values typically observed in vivo in the human head at field strengths of 3 T and less. Both CRLB-optimized protocols resulted in the lowest σF values for all SNRs, and did not increase in the presence of B1-inaccuracies.

**Conclusion:** This work demonstrates a regularized optimization approach for improving the robustness of auxiliary measurements (e.g. B1) sensitivity of qMT parameters, particularly the pool-size ratio (F). Predicting substantially less B1-sensitivity using protocols optimized with this method, B1 mapping could even be omitted for qMT studies primarily interested in F.

## Introduction

Quantitative magnetization transfer (qMT) imaging is a class of techniques that indirectly probe tissue macromolecular content, which is not directly observable using conventional MRI due to their inherently short T2\*. Most qMT techniques quantify properties of macromolecular hydrogen (“restricted pool”) relative to nearby liquid water molecules (“free pool”) by solving the Bloch-McConnell equations, which describes the magnetization exchange between these two interacting pools [134]. Particularly, the pool-size ratio F (ratio of equilibrium magnetization between both pools) is a qMT parameter that correlates strongly with myelin content [39,178]. As such, the pool-size ratio has been proposed as a potential biomarker for lesion monitoring in multiple sclerosis (MS) patients [144,180], and has been shown to correlate with de- and remyelination in a mouse model of MS [148].

Several techniques have been developed to acquire and model qMT data. Most commonly, qMT data are acquired using pulsed off-resonance MT-prepared spoiled gradient echo (SPGR) pulse sequences [135], however techniques using inversion recovery [182] and balanced steady-state free precession have also been proposed [181]. Analytically solving the Bloch-McConnell equations is challenging unless a long continuous-wave MT pulse is used [133], which is impractical for in vivo measurements. Several fitting models have been developed to estimate quantitative parameters from pulsed SPGR qMT data [135,140,141], each with unique sets of experimental assumptions and approximations. In addition, SPGR qMT techniques require several additional quantitative measurements, such as main field (B0) mapping, transmit radiofrequency (RF) field (B1) mapping, and longitudinal relaxation time (T1) mapping. In this context, B0 mapping is used to calibrate the off-resonance frequency values in the presence of main field inhomogeneity [187], B1 mapping to correct the RF field amplitude variations [76,189], and T1 mapping to constrain the magnetization transfer fitting parameters [133,135,190]. These three measurements, in addition to the 10+ qMT measurements typically required to fit the full set of model parameters [155], makes it a challenge to acquire qMT data in a clinically feasible acquisition time.

Several strategies have been developed to shorten the SPGR qMT acquisition time, which originally consisted of over 60 qMT measurements [135] and limited the technique to single slice acquisitions. The first three-dimensional qMT brain scan was achieved using a “uniform” acquisition protocol by reducing the number of off-resonance frequencies (Δ) to 5 (uniformly ranging between 400 Hz and 20 kHz) and MT flip angles (FAMT) to 2 (high and low values), for a total of MT-weighted 10 measurements [156]. Other studies went further, optimizing the protocol Δ and FAMT values using the Cramér-Rao lower bound (CRLB) as an optimization condition to minimize estimated parameter variances, using simulated annealing [154] or an iterative protocol reduction algorithm from an initial search space [155]. Rapid k-space readout techniques such as echo planar imaging have also been proposed to improve acquisition times [191]. The choice of B0/B1/T1 mapping techniques have evolved over time, with researchers typically choosing the most rapid and reliable technique available at their disposal. For example, the evolution from single-slice qMT imaging to whole-brain imaging required a switch from single-slice T1 mapping techniques (e.g. inversion recovery – IR, Look-Locker – LL) to 3D techniques (e.g. Variable Flip Angle – VFA). However, recent work has shown that this transition may impact the robustness of the fitting parameters, since IR is a B1-insensitive technique [51], whereas VFA is a B1-sensitive technique [60]. For a uniform 10-pt SPGR qMT protocol, it has been demonstrated that the pool-size ratio F is much less sensitive to B1-inaccuracies if the qMT protocol uses VFA T1 mapping, relative to B1-insensitive T1 mapping techniques [192]. Since that work used a fixed “uniform” qMT sampling protocol to demonstrate the benefit of using VFA T1 mapping for F, it raises an interesting question: is it possible to further improve the robustness of F against B1 inaccuracies by optimizing the qMT acquisition protocol itself for B1-insensitivity?

The aim of this work is to develop a method to incorporate B1-sensitivity considerations into the optimization of qMT data acquisition, by regularizing the CRLB optimization condition with a B1-sensitivity term. We first derived a B1-sensitivity expression that was used to regularize the CRLB condition. Using simulations, we then explored the B1-sensitivity of qMT for several different uniform sampling protocol configurations. The optimal regularization term for the pool-size ratio was determined, and a sample qMT protocol was iteratively optimized using the CRLB condition both with and without the regularization term. The robustness of three protocols (uniform, CRLB, CRLB + B1 regularization) were then investigated using Monte Carlo simulations for a range of signal-to-noise ratios (SNR), B1-inaccuracies, and tissue values. Lastly, the qMT optimization framework developed and presented here is released as an open-source package.

## Theory

In the presence of a small inaccuracy of a measurement parameter, such as B1 in qMT, this error will propagate to the fitting parameters of the model. The behavior of how this propagated error will impact each fitting parameter can be explored through a sensitivity analysis, by expanding the fitted signal in the presence of a ΔB1 with a Taylor expansion [185]. Assuming a small ΔB1 and a good fit (*M*(*B1*+ ΔB1) ≈ *M*(*B1*) ≈ *M*meas, where *M* is the signal generated by the fit), a first-order approximation of the Taylor expansion of the fitted signal results in the following matrix equation [192]:

|  |  |  |
| --- | --- | --- |
|  |  | **(5-1)** |

where *p* are the model fitting parameters (e.g. for the Sled and Pike[134] model of qMT: F, kf, T2,f, T2,r), is the column vector of errors in fitted parameters [ΔF, Δkf, ΔT2,f, ΔT2,r]ʹ, and are matrices with sensitivities values elements relative to *pi* or *B*1 (columns) for each measurement *n* (rows). can also be interpreted as being the Jacobian of the measurement for the fitting parameters, which we’ll call the Jacobian sensitivity matrix.

Given a known ΔB1 value and Jacobian sensitivity matrices for *p* and *B*1, Eq. (5-1) can be solved for . However, since Eq. (5-1) is typically an overdetermined system of linear equations (), the optimal solution is found by minimizing the following 2-norm for :

|  |  |  |
| --- | --- | --- |
|  |  | **(5-2)** |

Although Eq. (5-2) provides an estimate of the error propagated to the fitting parameters by an error in B1, it alone is insufficient to be used for optimal protocol design. qMT protocols must also be designed for robustness against noise that naturally occurs in measured signals. For this purpose, the Cramér-Rao lower bound (CRLB) has been shown to be an adequate and sufficient estimate to minimize the variance in fitted qMT parameters due to experimental noise [154]. Consider the Fisher information matrix (FIM) **J**, which has elements:

|  |  |  |
| --- | --- | --- |
|  |  | **(5-3)** |

where σ is the standard deviation of the noise, and **x***n* is the acquisition protocol for the *n*th measurement out of N unique measurements. The CRLB is defined as the diagonal elements of **J**-1, and the trace of this matrix provides an overall estimate of the minimum variance of a model. However, because the qMT fitting parameters differ largely in their order of magnitudes, the parameter-normalized CRLB (*V*) is defined instead [154]:

|  |  |  |
| --- | --- | --- |
|  |  | **(5-4)** |

In this work, we propose a regularization approach to simultaneously optimize against both noise (Eq. (5-4)) and B1-error propagation (Eq. (5-2)), using an iterative optimization approach for the acquisition protocol design [155]. Particularly, we are interested in minimizing the propagation of B1-error to the pool-size ratio *F* (Δ*F*) because of its demonstrated potential as a biomarker for myelin content. Thus, to optimally reduce an acquisition protocol of N unique measurements to N-1 measurements, each iteration evaluates:

|  |  |  |
| --- | --- | --- |
|  |  | **(5-5)** |

where λ is the regularization parameter constant, and **x**N-1 is the N-1 optimal qMT subset protocol of **x**N for a given iteration. The regularization parameter λ value controls the tradeoff between CRLB (noise) and *F* sensitivity to B1-inaccuracies during the optimization.

## Methods

The core qMT functions and routines used in the simulations and fitting of this work are from qMRLab (http://github.com/neuropoly/qMRLab), an open-sourced quantitative MRI software packaged that evolved from qMTLab [143] and is written in MATLAB (MATLAB 2017a; MathWorks Inc., Natick, MA). The additional source code developed in this work, particularly for numerically estimating the Jacobians matrices of the system, the protocol optimization algorithms, and the Monte Carlo simulations, is released as its own open-source package (http://github.com/mathieuboudreau/qMTLab\_Tabs). The code was developed to wrap around the qMRLab code, so that it may also be easily adaptable with other qMT software packages or in-house code.

### Uniform Protocols

The regularization term in Eq. (5-5) proposed for optimizing qMT parameters against B1-inaccuracies was derived using a first-order approximation of a Taylor series. To test this approximation, **Δ*p*** values (ΔF, Δkf, ΔT2,f, ΔT2,r) were calculated by solving Eq. (5-2) for a range of ΔB1 typically observed in vivo (±30%, with an actual B1 = 1.0 n.u.), and were compared to values estimated by fitting the signal to the Bloch-McConnell equations [135]. A “uniform” qMT measurement protocol was used, meaning a protocol with logarithmically uniform off-resonance frequencies for each MT flip-angle (αMT) preparation pulse. Jacobian sensitivity matrices calculations for Eq. (5-2) (and) were estimated from numerical partial derivatives (10-2 % relative increase in parameter values). Two different qMT cases were considered for : B1-independent T1 measurements (IR) and B1-dependent T1 measurements (VFA). Signal simulation details (protocol and tissue parameters) matched those described in full detail in a recent study [155].

Prior to protocol optimization, we were also interested in investigating values (from Eq. (5-2)) for other uniform qMT protocols with different numbers of MT flip angles and off-resonance values. MT-prepared SPGR (TR = 25 ms, α = 7°) pulse sequence protocols using every combination of three αMT values (150°, 400°, 650°) were used (each unique αMT, each combination of two αMT values, and all three). Logarithmically-uniform offset frequencies for each αMT values ranged between 300 Hz and 20 kHz. To fairly assess all uniform protocols, the total number of acquisitions were limited between 8 and 30 by varying the number of offset values per αMT sets. For example, a single-αMT 10-point protocol would have 10 off-resonance frequencies, and a two-αMT 10-point protocol would have the same 5 off-resonance frequencies for both αMT. qMT signals were simulated for tissue values within the typical white matter range (Table 5‑1). A 5% overestimation in B1 value (ΔB1 = +0.05 n.u.) relative to the expected value (B1 = 1 n.u.) was used for all protocols to solve Eq. (5-2) for , and a VFA T1 mapping method was assumed (TR = 15 ms, α = 3° and 20°).

### Protocol Optimization

qMT protocols were iteratively optimized [155] from a large initial search-space set of potential αMT and Δ protocol values, for fixed TR and α (25 ms and 7°). The most time-intensive component of the optimization algorithm is computing the Jacobian sensitivities ( and ). The Jacobian sensitivities were precomputed using parallel processing and cached for rapid access during the optimization algorithm execution. Note that both terms in Eq. (5-5) require element values from the Jacobian sensitivity matrices (through Eqs. (5-4) and (5-3)). The optimization search-space consisted of 312 points; each combination of 12 αMT values (ranging between 150° to 700°, in 50° increments) and 26 Δ values (ranging between 300 Hz and 20 kHz, with logarithmically uniform steps). A few (<5%) protocol points resulted in outlier numerical partial derivative values (non-smooth Jacobian sensitivity curve at those points), which may be due to signal simulation rounding errors or imprecise free-pool saturation fraction interpolations in the open-source software used. Those protocol points were replaced with the nearest-neighbor points calculated from a higher-resolution search-space (101 Δ values). The Jacobian sensitivity matrices were calculated for white matter tissue values (Table 5‑1).

Prior to protocol optimization, an optimal value for the regularization parameter λ was determined. The iterative optimization algorithm using Eq. (5-5) was executed for a range of λ values (λ = 0, 0.01, 0.1, 0.5, 1, 2, 5), assuming ΔB1 = 0.05 and VFA T1 mapping (TR = 15ms, α = 3° and 15°). Since TR, TE, and α were fixed for all protocol points, the standard deviation of the noise in Eq. (5-3) (σ) was arbitrarily set to 1 during the optimization calculations. The ΔF values and variance-efficiency curves ([variance × # acq. points]-1/2, where the variance is interpreted to be the parameter-normalized CRLB *V*) were compared for each N during the iterative optimization procedure. Two sets of 10-point protocols were optimized by iteratively finding the N-1 protocol subset that minimized Eq. (5-5) for ΔB1 = 0.05 (and assuming the VFA as above) and with and without regularization (CRLB and CRLBλ).

### Monte Carlo Simulations

Ideal (noiseless) MT-prepared SPGR signals were simulated for three 10-point protocols (Table 5‑2: Uniform, CRLB, and CRLBλ) and two tissue types (Table 5‑1: white matter, grey matter). Rician noise was added to each simulated MT signal and an MT-off signal, for normalization (*M*MT/*M*MT-off). Six different SNR levels were considered (SNR = 25, 50, 75, 100, 150, 200). Sets of 10,000 noisy MT signals were independently generated and compared for each combination of qMT protocols, tissues, and SNR. Each dataset was subsequently fitted for qMT parameters (F, kf , T2,f, and T2,r) considering a range of B1 errors (±30% in increments of 5%) and a two-FA VFA T1 mapping method (TR = 15ms, α = 3° and 15°).

Table ‑. qMT tissue parameters used to simulate white matter and grey matter tissue values in the Monte Carlo simulations. The parameter definitions are: F ­ pool-size ratio, kf  – exchange rate constant, T1,f – longitudinal relaxation time of the free pool, T1,r – longitudinal relaxation time of the restricted pool, T2,f – transverse relaxation time of the free pool, T2,r – transverse relaxation time of the restricted pool. The fitting parameters for qMT are F, kf, T2,f, and T2,r; T1,f is calculated from the observed T1 and the fitting parameters, and T1,r is conventionally fixed to 1 s.

|  |  |  |
| --- | --- | --- |
| Parameter | White Matter | Grey Matter |
| F | 0.15 n.u. | 0.075 n.u. |
| kf | 4.0 s-1 | 2.5 s-1 |
| T1,f | 0.9 s | 1.3 s |
| T1,r | 1.0 s | 1.0 s |
| T2,f | 30 ms | 55 ms |
| T2,r | 12 μs | 11 μs |

Table ‑. qMT protocols used in the Monte Carlo simulations. The repetition times, excitation flip angles, and number of acquisitions were matched for all protocols. The Uniform protocol is a two MT flip-angle with logarithmically uniform off-resonance frequencies. The CRLB protocol was optimized using Eq. (5-5) with the regularization parameter set to 0, and CRLBλ=0.5 was optimized using a regularization parameter of 0.5.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Uniform | | | CRLB | | | CRLBλ=0.5 | | |
| Acq. # | TR/α | αMT | Δ (Hz) | TR/α | αMT | Δ (Hz) | TR/α | αMT | Δ (Hz) |
| 1 | 25ms/7° | 142° | 432.9 | 25ms/7° | 200.0 | 300.0 | 25ms/7° | 200.0 | 300.0 |
| 2 | 1 087.5 | 250.0 | 1 903.9 | 250.0 | 1609.5 |
| 3 | 2 731.6 | 700.0 | 1 609.5 | 700.0 | 1609.5 |
| 4 | 6 861.6 | 700.0 | 12 083.6 | 700.0 | 12 083.6 |
| 5 | 17 235.5 | 700.0 | 1 903.9 | 700.0 | 2 252.2 |
| 6 | 426° | 432.9 | 250.0 | 2 252.2 | 200.0 | 1 903.9 |
| 7 | 1 087.5 | 150.0 | 300.0 | 650.0 | 300.0 |
| 8 | 2 731.6 | 700.0 | 1 360.6 | 200.0 | 1 360.6 |
| 9 | 6 861.6 | 200.0 | 1 609.5 | 700.0 | 1 903.9 |
| 10 | 17 235.5 | 700.0 | 2 252.2 | 150.0 | 300.0 |

## Results

### Uniform Protocols

Figure 5‑1 shows the simulated errors in each fitting parameter (ΔF, Δkf, ΔT2,f, ΔT2,r) estimated from the first-order approximation of the Taylor expansion in Eq. (5-2) (solid lines) and from the relative error in fit using the Sled and Pike model (dash line) in the presence of B1 errors (±30%). Data was simulated for a B1-independent T1 measure (IR, red) and a B1-dependent T1 measure (VFA, blue) separately. The overall trends in the error curves produced by model fits reproduced well similar simulations that were reported recently [192] (Boudreau et al 2017, Figure 3) even though they don’t share the same core qMT simulation and fitting software, establishing confidence in the use of this open-source qMTLab software [143] for this work.



Figure ‑. Simulated qMT parameter errors due to B1-inaccuracies (-30% < ΔB1 < 30%) considering a B1-independent T1 measurement (red: IR – inversion recovery) and a B1-dependent T1-measurement (blue: VFA – variable flip angle). Solid lines are parameter errors calculated from minimizing Eq. (5-2) (first-order approximation of the Taylor expansion), and dashed lines are parameter errors calculated from fitting the qMT signal according to the Sled & Pike model. The tissue parameters (white matter) and qMT protocol (uniform) were matched to those presented in Boudreau et al. 2017 (see Fig. 3 of the paper).

For B1 errors within ±5%, the errors in all parameters calculated from Eq. (5-2) approximated well the fitted estimates. For VFA T1 mapping and ΔB1 = 0.05 n.u. (+5 %), the Δ*p* values (Eq. (5-2), Fit) were: ΔF = (-0.94 %, -1.06 %), Δkf = (14.77 %, 16.88 %), ΔT2,f = (-2.56 %, -1.97 %), and ΔT2,r = (-0.51 %, -0.65%). Both ΔF (for VFA) and ΔT2,r showed linear trends for the “Fit” case, which resulted in an overall better agreement with Eq. (5-2). Resulting from these analyses, a ΔB1 of 0.05 n.u. was selected for the iterative optimization calculation (Eq. (5-5)) later in this work.

Figure 5‑2 shows the simulated errors of fitting parameters for a 5% ΔB1 (assuming VFA T1), using a wide range of uniform qMT acquisition protocols varying in number of FAMT, number of off-resonance frequencies per FAMT, and total number of acquisitions points. While most curves (sets of FAMT combinations) trended asymptotically with increasing number of acquisition points, they did not trend towards 0% parameter error values (except for a few ΔT2,r cases, # FA > 1 protocols that contain 650°). For ΔF, the three # FA = 1 curves (dark blue, orange, yellow) resulted in the largest ΔF values overall, demonstrating the benefit of including at least two flip angles in your qMT protocol in the context of lower B1-sensitivity. The three # FA > 1 protocols that included FA=650° (green, light blue, red) resulted in ΔF curves that overlapped and intercepted ΔF = 0 % values near 10 and 15 acquisition points, but increased in error for larger # of acquisition points.



Figure ‑. Simulated qMT parameter errors estimated from Eq. (5-2) for ΔB1=0.05 for a wide range of logarithmically-uniform (offsets) qMT protocols. Single (blue, orange, yellow), dual (purple, green, light blue), and triple (red) flip angle combinations of 150°, 400°, and 600° were compared. The number of offset frequencies were uniformly distributed between 300 Hz and 20 kHz, and matched for the total number of acquisition points (# offsets × # flip angles).

### Protocol Optimization

Figure 5‑3 displays the values of the Jacobian sensitivity matrices (**a-d** are the columns of , **e** is , and **f** is ). Each plot represents the sensitivity of the Z-spectrum relative to each parameter-of-interest (i.e. the change in Z-spectrum signal value due to a small increase in each parameter). The magnitude of the sensitivity values is shown to simplify interpretations; the sign of the sensitivity curves represents the direction (increase/decrease) that the Z-spectrum changes for small variations of each parameters, while we are mainly concerned in how large of an overall change occurs. A peak of the sensitivity curve for F occurs at off-resonance frequencies an order of magnitude higher for high FAMT (>500°) than for low FAMT values (~150-300°). For all FAMT values, the peak sensitivity for kf remained near Δ = 1-2 kHz. The peak sensitivity of also remained constant near Δ = 1-2 kHz, which may explain why kf has the largest errors due to ΔB1 (Eq. (5-1)) for the VFA case in Figure 5‑1. The higher sensitivity of F at high off-resonance (>10kHz) values (Figure 5‑3a), relative to (Figure 5‑3f), likely contributes to the greater robustness against B1 observed in the previous section.



Figure ‑. Sensitivity values (magnitudes) for each qMT fitting parameters (F, kf, T2,f, T2,r) and B1 measurement values considering a B1-independent T1 measure (IR – inversion recovery) and a B1-dependent T1 measure (VFA – variable flip angle). The 312-point protocol shown (12 flip angles x 26 offset frequencies) represents the initial search-space used for protocol optimization. The sets of sensitivity values for each fitting parameter (a–d) consists of the matrix columns of the Jacobian sensitivity matrix (S*p* in Eqs. (5-2) and (5-5)).

The optimal variance-efficiency and ΔF values (for ΔB1 = 5%) calculated at each iteration of the optimization algorithm using the 312-point initial search-space are shown in Figure 5‑4 for a wide range of regularization parameter (λ) values. The highest-valued variance-efficiency curve occurs for λ=0 (i.e. unregularized parameter-normalized CRLB) and λ = 0.01. For these values, the magnitude of ΔF steadily increased to 1% as the protocol was iteratively reduced to ~150 acquisition points, and then proceeded to decrease to ~0.5% for N < 25. Increasing the regularization parameter by an order of magnitude (λ = 0.1) substantially reduced ΔF values for N > 25 by up to a factor of two, while keeping the variance-efficiency relatively unaffected. However, for this case, ΔF returned to ~-0.5% abruptly for N < 25. A regularization parameter of 0.5 was the lowest value tested which succeeded in ΔF achieving values near 0% for small protocols; for N = 10, λ = 0.5 resulted in ΔF = -0.04% compared to -0.53 % for λ = 0, a factor of 13 in relative improvement of the B1-insensitivity of F. A small reduction in variance-efficiency accompanied the improvement of ΔF for λ = 0.5; for N=10, the variance-efficiency decreased by 6.3% for λ = 0.5 relative to λ = 0. For higher λ values, the regularization term in Eq. (5-5) dominated early in the iterative optimization at the cost of lower variance-efficiencies, which never recover to their unregularized values. For intermediately-high λ values (λ = 1, 2), a second region where the regularization term in Eq. (5-5) dominates the iterative optimization can be seen near N = 60 and 120 respectively, substantially reducing the variance-efficiency. Overall, a λ value of 0.5 showed the best compromise between decreasing ΔF (insensitivity of F against B1 errors) and maximizing variance-efficiency.



Figure ‑. Variance-efficiency (a) and ΔF (b) (Eq. (5-2), ΔB1 = 5%) values during the iterative optimization of the sensitivity-regularized Cramer-Rao Lower-Bound equation (Eq. (5-5)). Variance-efficiency is defined here as (variance × # acq. points)-1/2, where the variance is interpreted to be the parameter-normalized Cramer-Rao Lower Bound (*V*, Eq. (5-3)).

The 10-point protocols optimized using λ = 0 (CRLB) and λ = 0.5 (CRLBλ=0.5) are shown in Figure 5‑5, overlaid on the 312-point protocol search-space (displayed as line plots for better visibility of the optimized protocols). The details of these protocols are listed in Table 5‑2. Overall, both optimized protocols share 7 out of 10 (Δ, FAMT) pairs, with only three acquisition points changing if the regularization term is included in Eq. (5-5) (λ = 0.5). Both protocols have coverage of low, medium, and high off-resonance values, as well as low and high FAMT values.



Figure ‑. Comparison between the 10-point protocols iteratively optimized from a 312-point search space using solely the parameter-normalized CRLB (λ = 0) and regularized CRLBλ=0.5. The different flip angle Z-spectrums of the initial optimization search-space are displayed in blue to emphasize the 10-point protocols. The flip angle Z-spectrums (150° to 700°, in 50° increments) range from the highest MT-signal values curve (150°) to lowest (700°).

### Monte Carlo Simulations

Distributions statistics (mean, σ) of the Monte Carlo simulations of the fitted parameter-of-interest F are shown for a range of ΔB1 values (SNR = 100) in Figure 5‑6 and a range of SNR values (ΔB1 = 0 and 15 %) in Figure 5‑7, for the three protocols listed in Table 5‑2. Figure 5‑6a and b displays the difference (%) in mean F relative to the mean F value for the ΔB1 = 0 case, whereas Figure 5‑7a and b displays the difference (%) in mean F relative to the ideal (noiseless) fitted F value.



Figure ‑. Means (a, b) and standard deviations (c, d) of the distribution of pool-size ratios (F) for sets of Monte Carlo simulations (10,000 runs, SNR = 100) fitted using a range of B1 errors (ΔB1 = ±30%, B1 = 1 n.u.) and for two sets of qMT parameters (white matter – a,c; grey matter – b, d). Mean F values (% error) shown here were compared relative to the accurate B1 value case (ΔB1 = 0), and the grey region represents the region of ±1% relative error. Simulated signal values were generated and fitted for three different 10-point qMT protocols: Uniform (blue) – two-FA protocol with logarithmically-uniform off-resonance frequency values, CRLB (red) – protocol optimized by iteratively minimizing the increase in the parameter-normalized Cramer-Rao Lower-Bound of the system, and CRLBλ=0.5 (yellow) – protocol optimized similar to CRLB, regularized by the estimated error of F (ΔF) in the presence of a B1 error (Eq. (5-5)).



Figure ‑. Means (a, b) and standard deviations (c, d) of the distribution of pool-size ratio values (F) for sets of Monte Carlo simulations (10,000 runs) fitted using a range of SNR values (25, 50, 75, 100, 150, and 200) and for two sets of qMT parameters (white matter – a,c; grey matter – b, d). Mean F values (% error) shown here were compared relative to data fitted for an ideal SNR case (noiseless), and the grey region represents the region of ±1% relative error. Data was fitted assuming ideal B1 values (B1 = 1 n.u., solid lines) and a 15% overestimation in B1 (B1 = 1.15 n.u., dotted lines). Simulated signal values were generated and fitted for three different 10-point qMT protocols: Uniform (blue) – two-FA protocol with logarithmically-uniform off-resonance frequency values, CRLB (red) – protocol optimized by iteratively minimizing the increase in the parameter-normalized Cramer-Rao Lower-Bound of the system, CRLBλ=0.5 (yellow) – protocol optimized similar to CRLB, regularized by the estimated error of F (ΔF) in the presence of a B1 error (Eq. (5-5)).

For the CRLBλ=0.5 protocol, values were less than 1% (grey area) for ΔB1 between -10% and 20% (Figure 5‑6, for both WM and GM). The same was true for ΔB1 between -5% and 10% for the CRLB protocol, and between -5% and 5% for the Uniform protocol. CRLB and CRLBλ=0.5 protocols resulted in standard deviations of fitted F substantially lower (by a factor of ~1.75) than the Uniform protocol. Although CRLBλ=0.5 σF values were slightly different than the CRLB values (6.7% higher), both curves nearly overlapped for all ΔB1 values.

In the absence of B1 errors (ΔB1 = 0), values for both optimized protocols (CRLB and CRLBλ=0.5) were below 1% for datasets with SNR values greater than 75 (Figure 5‑7, WM and GM). The Uniform protocol needed a minimum SNR of 100 to result in values below 1%. In the presence of a 15% overestimation of B1, the vs. SNR curve for CRLBλ=0.5 remained largely unchanged for WM. For GM, the values for CRLBλ=0.5 resulted in slight increase, although remained within 1% for SNR > 100. In contrast, even at high SNR values (>100), values for the CRLB and Uniform protocols resulted in greater bias (>1%) for the ΔB1 = 15% case. The σF curves increased rapidly for SNR values lower than 75 for all protocols. For all cases, σF did not vary substantially between both ΔB1 values evaluated (0% and 15%). For CRLB and CRLBλ=0.5, no substantial differences in their σF vs. SNR curves were observed, and both had lower standard deviations relative to the Uniform protocol.

## Discussion

This work describes a qMT protocol optimization methodology for reduced B1-sensitivity of the pool-size ratio F by regularizing the CRLB with a first-order sensitivity analysis. Using Monte Carlo simulations we found that, for a protocol optimized using regularized CRLBλ=0.5, errors propagated to fitted F were below 1% for B1-errors ranging between -10 and 20%, consistent with the B1 values typically observed in the human brain at 3T [193]. Both regularized and conventional CRLB optimization resulted in an improvement of pool-size ratio B1-insensitivity relative to a two-FAMT uniform protocol. Sensitivity analyses of uniform protocols suggested that, if using VFA T1 mapping, acquiring data at both small and large MT flip angle acquisitions (at mid and high off-resonance frequencies) may be an important contributing factor in designing a B1-insensitive acquisition protocol, where F likely has a higher robustness against B1 errors. These simulations demonstrate for a range of SNRs, B1-inaccuracies, and brain tissues, the effectiveness of a regularized approach of designing qMT for B1-insensitivity. This work suggests that if the pool-size ratio is the primary parameter-of-interest, it may be possible to design a qMT protocol robust enough to omit B1 map acquisition altogether, without substantially biasing estimates of F.

Our study considered a specific qMT fitting model (Sled and Pike[135]) that fitted quantitative MT data for four parameters of the Bloch-McConnell equations (F, kf, T2,f, T2,r). Several other qMT fitting models for MT-prepared SPGR data exist, such as Yarnykh’s model [141], which neglects direct saturation effects, and Ramani’s continuous wave power equivalent model [140]. Each qMT fitting model makes different approximations or assumptions, and differ in fitting parameters. For example, Yarnykh’s model suggests acquiring data only at off-resonance frequencies greater than 1 kHz, and has a different set of fitting parameters (e.g. T2,f is neglected and their pool-size ratio parameter is defined as *f* = M0,r / (1+ M0,r), instead of Sled and Pike’s F = M0,r / M0,f parameter). The different range in off-resonance frequencies will reduce the available Jacobian sensitivity values during optimization, which may impact the optimization against auxiliary measurements (e.g. B1) errors. Different sets of fitting parameters between models could also change the fitting behavior in the presence of B1-error propagation, even if the same SPGR qMT acquisition protocols are used. The single-point qMT fitting model [67,188] may provide additional challenges for optimizing against auxiliary measurement error-sensitivity. This fitting model imposes several fitting parameter restraints, which would provide additional limitations when solving Eq. (5-2). The analysis of uniform protocols and Jacobian sensitivity matrices also suggests that B1-insensitivy of F may be a result of including both small and large MT flip angle acquisitions in a protocol at mid and high off-resonance frequencies, a configuration that cannot be done using single-point measurement protocol.

We proposed a regularization approach to add an auxiliary measurement (e.g. B1) error-sensitivity component to the CRLB in our optimization algorithm. An alternative approach could have been to do a formal statistical analysis of the error propagation using the CRLB instead as the optimization algorithm condition. Lankford and Does [194] recently presented such a treatment and applied it to study T2 mapping. Their statistical analysis of the error propagation from parameter constraints demonstrated that, under certain practical circumstances, it can be beneficial (in terms of variance and full mean-squared error of fitted T2) to include a B1 measurement for multi-echo T2 mapping. Their framework was presented to be generalizable to other quantitative techniques that require auxiliary measurements such as qMT; however, their analysis was only developed for a single-level of parameter constraints. Although this may be applicable for a B1-error propagation analysis of qMT when using a B1-independent T1 mapping method (e.g. IR), a B1-dependent T1 mapping method (e.g. VFA) complicates the error propagation analysis beyond what is presented in Lankford and Does, as there are two interacting constraints within the qMT model (e.g. qMT(B1, T1(B1)). In contrast, one benefit of the sensitivity-regularization approach we presented here is its conceptual simplicity and ease of implementation for optimization applications, particularly for this case. Nonetheless, a formal propagation of error analysis would likely be a good choice moving forward to compare the sensitivity to errors in constraints between different qMT fitting models, as discussed above.

Several limitations should be considered when interpreting this work. An iterative optimization approach was chosen to estimate optimal acquisition protocols from a larger initial search space, however this approach is not guaranteed to result in the global minima of the optimization condition. Global optimization using simulated annealing [154] could have been another valid approach to optimize our qMT protocol using Eq. (5-5). However, iterative optimization approaches benefit from an ease of implementation, rapid computation, and the flexibility to choose the number of measurements in the protocol after the optimization is complete. In contrast, simulated annealing approaches optimize for a fixed pre-determined number of protocol points. We also opted for Monte Carlo simulations instead of an in vivo study to validate the regularized approach to B1-sensitivity protocol optimization. This gave us the flexibility to accurately know and control the system conditions (e.g. tissue values, B1 error values, and noise level). In vivo evidence of the benefits of qMT protocol optimization using CRLB has already been reported in several studies [154,155,191]. In addition, Eqs. (5-1) and (5-2) (used to establish the regularization term) were developed from a recent comprehensive B1-sensitivity analysis of qMT study [192] that compared and validated simulations with in vivo measurements of F in the absence of B1 maps (for a uniform protocol). Lastly, the optimization algorithm investigated here only considered a single tissue type (WM) during the protocol optimization procedure. Although the resulting protocol was also evaluated for another tissue type in the Monte Carlo simulations (GM) and both were restricted to errors below 1%, even though the B1-sensitivity of F in GM varied more than for WM. If desired, the optimization condition (Eq. (5-5)) could be adapted to consider multiple tissue types in a similar manner as proposed by Cercignani et al [154], by instead minimizing for the tissue which results in the maximum value of Eq. (5-5) at each iteration.

Overall, this work presents a framework for designing qMT acquisition protocols optimized for robustness against inaccuracies of auxiliary measurements (e.g. B1) by regularizing the Cramér-Rao lower bound with fitting parameter-sensitivity information. We demonstrated this methodology by optimizing a qMT protocol for robustness of the pool-size ratio (F) against B1-inaccuracies, and studied simulations using this protocol for a wide range of signal-to-noise ratios, B1-inaccuracies, and tissue types. These findings imply that B1 mapping possibly be omitted from such a qMT optimized acquisition protocol with minimal impact to the fitted pool-size ratio (< 1% error). Potential future work may include optimizing protocols for reduced sensitivity of other or multiple auxiliary measurements, and compare this optimization between other qMT fitting models. Another interesting approach could be to combine Z-spectrum compressed sensing [195] with this optimization technique, to maximize the auxiliary measurement insensitivity by increasing the number of measurements while reducing the total acquisition time.

# *Conclusion*

## Summary

Quantitative magnetization transfer imaging is an important quantitative MRI technique for quantifying demyelination in multiple sclerosis over the progression of the disease, and is a promising technique for studying remyelination during the development of therapeutics. However, qMT is dependent on a number of other quantitative MRI techniques, and imperfections in these measurements can affect the estimates of qMT biomarkers, negatively impacting myelin density estimates in the brain. This situation is further complicated when multiples of these measurements that qMT requires also depend on each other, as can be the case for T1 mapping potentially depending on B1. This thesis investigated how to achieve robust quantitative magnetization transfer imaging estimation of the pool-size ratio (myelin biomarker) in the presence of radiofrequency field inhomogeneities and/or inaccuracies. In Chapter 3, several whole-brain B1 mapping techniques were compared along with the VFA T1 maps produced using them, and several method-dependent sources of B1 inaccuracies were reported. In Chapter 4, the B1-sensitivity of the qMT pool-size ratio was investigated for different T1 mapping methods (B1-dependent and B1-independent) with a fixed qMT acquisition protocol (uniform), and VFA T1 mapping was discovered to result in a substantially lower sensitivity of the pool-size ratio to B1-inaccuracies. In Chapter 5, an qMT acquisition regularized-optimization approach to reduce the sensitivity of the pool-size ratio to B1-inaccuracies was presented, and demonstrated using Monte Carlo simulations good robustness of the pool-size ratio for a wide range of conditions (SNR, B1-inaccuracies, tissues) relative to other qMT acquisition protocols (uniform, non-regularized optimization).

*B1 Maps for Quantitative T1*

Chapter 3 compares the quality of B1 maps produced using the double angle method with a standard MRI pulse sequence (EPI) against two others widely-established whole-brain B1 mapping techniques, as well as their resulting T1 maps using the variable flip angle technique. The results from this work demonstrate that for researchers without access to novel B1 mapping techniques on their scanner, or without the ability to implement them using pulse sequence programming, B1 mapping using double angle EPI from standard pulse sequences may be a sufficient alternative to produce good quality whole-brain B1 maps, particularly for VFA T1 mapping applications. In addition, this chapter reports the local variabilities in B1 values which can be expected when choosing between different mapping techniques, establishing that the occurrence of B1-inaccuracies is unavoidable and should be expected in the current state of the quantitative MRI field. Sources of B1-inaccuracies range from large-scale artifacts to voxelwise noise, as well as for regional inaccuracies due to the lower resolution of B1 maps relative to the quantitative maps that depend on B1 or the pre-processing filter that’s often applied to the B1 maps prior to further use.

*B1-Sensitivity Analysis of qMT*

Having established several probable sources of B1 inaccuracies and investigated the relationship between VFA T1 maps and B1 maps, Chapter 4 sought to explore the sensitivity of qMT to B1 inaccuracies between two categories of T1 mapping techniques: B1-independent techniques (e.g. inversion recovery) and B1-dependent techniques (e.g. variable flip angle). Using simulations and then confirming these results with in vivo measurements, this work demonstrated a substantial reduction in B1-sensitivity of the pool-size ratio if a B1-dependent T1 mapping technique is used instead of a B1-independent technique. The robustness we observed is so strong for this case, the results suggest it may be possible to acquire qMT without a B1 map at all without substantially biasing the pool-size ratio estimates in white matter. Although in the last decade there has already been a switch within the qMT field from using B1-dependent T1 techniques such as inversion recovery and Look-Locker to variable flip angle for whole-brain T1 mapping, the advent of new whole-brain T1 mapping sequences that are becoming easily available on clinical scanners (such as MP2RAGE, a B1-independent technique) leads us to believe that some researchers may switch back to using B1-independent T1 mapping techniques in their qMT protocols. Although the results from this work should not automatically discourage researchers to use such techniques in their protocols, they should be mindful of the consequences that this choice can have on their pool-size ratio estimates if their B1 map contains potential inaccuracies, such as artifacts.

*B1-Sensitivity Regularization of the CRLB for qMT Optimization*

Building on the promising results of the previous chapter, the aim of Chapter 5 was to minimize the B1-sensitivity of qMT even further by optimizing the qMT acquisition protocol simultaneously for noise and B1-insensitivity. A regularization term for B1-sensitivity of qMT parameters was derived, and the regularization term was optimized for the pool-size ratio with simulations by minimizing the bias created by an error in B1 during the iterative optimization, while also minimizing the impact on the Cramér-Rao lower bound. Using Monte Carlo simulations, the sensitivity-regularized Cramér-Rao lower bound demonstrated better B1-insensitivity of the pool-size ratio (relative to two other optimized protocols: uniform and unregularized Cramér-Rao lower bound) for a wide range of signal-to-noise values, B1-inaccuracies (typical range observed in vivo if a B1 map was omitted) and tissue types (white matter and grey matter). This work describes a detailed methodology and framework for optimizing qMT protocols to be B1-insensitive, and the algorithms and code that were developed in this project have been released as an open-source package for other researchers to use.

## Future Work

The work presented in this thesis in which the B1-sensitivity of qMT was investigated and optimized only considered a subset of qMT acquisition pulse sequence (SPGR) and fitting model (Sled and Pike). There exist several other qMT fitting models for the SPGR qMT pulse sequence, such as Yarnykh’s model [141], Ramani’s model [140], and Yarnykh’s single-point constrained qMT model [67,188]. Although it may be redundant to do separate B1-sensitivity studies for each fitting model, it would be interesting to do a comparative B1-sensitivity study of these SPGR qMT fitting models. Such a study could follow the same sensitivity analysis and/or optimization framework presented in chapters 4 and 5, or a more formal statistical analysis approach of the error-propagation could be done, by adapting for qMT the theory recently proposed by Lankford [194]. The benefit of the latter approach would be that, instead of investigating the B1-sensitivity for a single abstract source of inaccuracy, the impact of the SNRs of the B1, T1, and qMT measurements on the qMT fitting parameters statistics could be explored in addition to local or systemic biases of B1. For alternative qMT pulse sequences, Gloor’s steady-state free precession method is another pulse sequence approach requiring both B1 and T1 maps that could also be of interest to do a B1-sensitivity study [181], whereas Dortch’s selective inversion recovery method of acquiring qMT has already shown to be B1(and B0)-insensitive [182].

Out of the three qMT calibration measurements (B0, B1, T1), the sensitivity of qMT was only investigated for B1 inaccuracies in this work. Doing additional sensitivity analyses for B0 and T1 would certainly also be of interest, although none of the other measurements are typically dependent on these besides qMT (unlike for B1, which T1 can often depends on). Although not thoroughly investigates, the impact of inaccurate T1 on the pool-size ratio can be seen using simulations in Figure 4‑2, suggesting that overestimations in T1 values will lower the estimated pool-size ratio values, and we reported preliminary results demonstrating this impact in vivo at a conference (Boudreau et al 2013, endMS Conference, see Other Publications section). In vivo, there can be a large variation in T1 values estimated by different T1 mapping methods (±100 ms), relative to inversion recovery (considered the gold standard). These differences measured between several T1 mapping pulse sequences were reported in a paper for which I co-authored during the course of this degree (Stikov et al 2015 [52], see Other Publications section). Using simulations, we proposed that the ~100 ms overestimation in VFA T1 (relative to IR) observed by some groups may be due to only partial spoiling of the transverse magnetization during the steady-state pulse sequence. A paper very recently published proposes a correction to account for the unspoiled magnetization effect in VFA [196], which results in a reduction in T1 estimation relative to the uncorrected values. Another potential research project opportunity could be simultaneously optimizing for reduced sensitivity of all three calibration measurements using regularization by adding B0 and T1 terms in Eq. (5-5), each with unique regularization parameters. For this to potentially work well for all three calibration parameters, it may be needed include additional pulse sequence optimization parameters, such as the repetition time, the excitation flip angle, and the echo time.

One of the major challenges of qMT is in its conventionally long acquisition times, largely limiting it to research applications and rarely included in larger acquisition protocols used clinical studies. Although omitting the B1 map from the qMT acquisition protocol, as suggested to be possible by the last manuscript, will reduce the acquisition time of the overall protocol, it won’t substantially reduce it enough to acquire high-resolution (1 mm3) whole-brain qMT data in a clinically feasible time (5-10 minutes). Other groups have proposed different approaches at measuring qMT biomarkers rapidly, such as constraining the relationships between fitting parameters for reducing the number of qMT measurements [67,188] and using fast k-space readout techniques such as EPI [191,197]. One other potential largely unexplored technique for accelerating qMT is compressed sensing [157,158], a non-linear image reconstruction technique for sparse datasets by randomly acquiring a subset of k-space data. In recent years, there has been a rapid growth of the use of compressed sensing in the MRI community, quantitative MRI applications such as diffusion spectrum imaging [198], quantitative T1 and T2 mapping [199-201], and chemical exchange saturation transfer (CEST) imaging [202,203] (an MT-based spectroscopy technique). Several of these compressed sensing approaches could also be well-suited for qMT, such as low-rank constrains and orthogonal matching pursuit, by taking advantage of data information redundancy in the parameter domain in addition to the k-space domain to further accelerate the acquisition measurements. The reduced acquisition time could be used either for a faster protocol acquisition, or to measure an increased number of qMT protocol points if desired, for example to use an increased number of points for B1-insensitivity of qMT (e.g. see Figure 5‑4). Lastly, MR Fingerprinting is an MRI technique which has also shown promise in simultaneously acquiring several quantitative MRI parameters (e.g. T1, T2, B0) using random pulse sequence parameters during the k-space acquisitions and modelling the images using a pre-computed dictionary of signal values for a large range of qMRI parameters [204]. A recent paper proposed a quantitative CEST MRI Fingerprinting acquisition [205], thus it may be possible also explore implementations of quantitative MT using this technique.

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