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Lipid Removal in Deuterium Metabolic Imaging (DMI) using Spatial Prior Knowledge.

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ABSTRACT

Deuterium Metabolic Imaging (DMI) is a novel method to generate spatial maps depicting dynamic metabolism of deuterated substrates, such as [6,6'-$^2H_2$]-glucose, and their metabolic products, like ^{2}H-lactate. While DMI acquisition methods are simple and robust, DMI processing still requires expert user interaction, for example in the removal of extracranial natural abundance ^{2}H lipid signals that interfere with metabolism-linked ^{2}H-lactate formation. Here we pursue the use of MRI-based spatial prior knowledge on brain and non-brain/skull locations to provide robust and objective lipid removal. Magnetic field heterogeneity was accounted for using DMI-derived surrogate B_0 and B_1 maps, as well as through subdivision of the skull region into smaller compartments. Adequate lipid removal with an average suppression of 90.5 ± 11.4 % is achieved on human brain *in vivo* without perturbation of the metabolic profile in brain voxels, thereby allowing the generation of distinct and reliable metabolic maps on patients with brain tumors.

Key words: Deuterium, Deuterium Metabolic Imaging (DMI), natural abundance lipids, human brain, spatial prior knowledge

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1. INTRODUCTION

Deuterium Metabolic Imaging (DMI) is a recent method to map the spatial distribution of ^{2}H-enriched substrates and their metabolic products in health and disease (De Feyter et al., 2018; Kaggie et al., 2022; Adamson et al., 2023). The most commonly used substrate, [6,6'-$^{2}H_2$]-glucose, has shown promise to offer unique metabolic insights in brain tumors (De Feyter et al., 2018; Adamson et al., 2023), stroke (Straathof et al., 2021), brown adipose tissue (Riis-Vestergaard et al., 2020), heart (Wang et al., 2021), preeclampsia (Markovic et al., 2021) and a range of tumors outside the brain (Kreis et al., 2020; Veltien et al., 2021). Other ^{2}H-enriched substrates, such as $^{2}H_9$-choline and [2,3-$^{2}H_2$]-fumarate, can provide insights into tumor proliferation (Veltien et al., 2021; Ip et al., 2023) and cell death (Hesse et al., 2021), respectively. DMI sets itself apart from other metabolic imaging modalities such as ^{1}H, ^{13}C, hyperpolarized ^{13}C and ^{31}P MRSI, through its simple and robust acquisition methods. The low natural abundance of deuterium eliminates the need for water and lipid suppression, whereas the sparsity of ^{2}H MR spectra reduces the magnetic field homogeneity requirements, thereby enabling the acquisition of 3D DMI across the entire human head with high-quality spectra at all locations (De Feyter et al., 2018; Ruhm et al., 2021; Liu et al., 2022; Seres Roig et al., 2022).

Processing of DMI is generally straightforward, with high-quality quantification achieved using least-squares curve fitting with a limited number of Lorentzian lines (De Feyter et al., 2018). DMI of [6,6-$^{2}H_2$]-glucose metabolism generally requires four signals for ^{2}H-labeled water, glucose (Glc), the combined signal from glutamate and glutamine (Glx) and lactate (Lac). A metabolic map of Lac or a ratio map of Lac/(Lac + Glx) provides high-contrast images of pathological metabolism as described for brain and other tumors (De Feyter et al., 2018), as well as stroke (Straathof et al., 2021). With sufficient sensitivity, as seen near radiofrequency (RF) coil receive elements, natural abundance ^{2}H lipid signals originating from the skull will produce a detectable MR signal. While these small lipid signals do not cause the widespread contamination throughout the brain as seen for ^{1}H MRSI (Tkáč et al., 2021), they can lead to artifactual intensity in Lac and Lac-Glx ratio maps as the Lac and lipids signals share near-identical chemical shifts. Lipid suppression in human brain MRSI studies can be achieved through pulse sequence modifications (inner volume selection, outer volume suppression, longer echo-times), additional hardware (higher-order gradient coils, crusher coils) or post-processing methods. While pulse sequence modifications and hardware solutions can give excellent lipid suppression (Tkáč et al., 2021), the requirements for DMI are generally modest, making post-processing methods a logical choice while still retaining the simple DMI acquisition method. Many post-processing methods utilize MRI-based prior knowledge on the lipid spatial location to achieve lipid removal and include dual density reconstruction (Hu et al., 1994; Metzger et al., 1999), data extrapolation (Haupt et al., 1996), L2 regularization (Bilgic et al., 2014) and Spectroscopic Localization by Imaging (SLIM, (Hu et al., 1988)) and its variants (Liang and Lauterbur, 1991; Von Kienlin and Mejia, 1991; Bashir and Yablonskiy, 2006; Khalidov et al., 2007; Zhang et al., 2012; Passeri et al., 2014; Adany et al., 2016, 2021).

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Here we propose to use the SLIM algorithm (Hu et al., 1988) because it can (1) be applied to standard, 3D phase-encoded DMI without data acquisition modifications, (2) remove extracranial lipids without perturbing the brain metabolic profile and (3) be extended to provide regional brain signals from anatomy-matched compartments. The processing pipeline, including MRI brain/skull segmentation, generation of DMI-based surrogate B_0 and B_1 maps and SLIM-based regional signal removal, can be fully automated and provides a robust and objective tool to accelerate the inclusion of DMI in a clinical MR workflow.

2. METHODS

2.1. Workflow and algorithm

SLIM belongs to a class of post-processing methods that constrains the MRSI reconstruction with spatial prior knowledge derived from anatomical MRIs. The MRSI acquisition is formulated as a linear model whereby the acquired k-space data P is the linear sum of ROI-specific signals C weighted by a gradient and position-dependent factor G according to

$$P = G.C \qquad [1]$$

P is the measured N_{enc} x N_{time} k-space data matrix, with N_{enc} representing the total number of phase-encoding gradient combinations (i.e., number of k-space encodings) and N_{time} representing the number of complex, spectroscopic time domain points. C is an N_{ROI} x N_{time} matrix containing the time-domain signals from each of the N_{ROI} compartments, the sum of which comprises the entire object under investigation (e.g., human head, including brain and skull areas). The shape of the ROIs can be arbitrary with $N_{ROI} \leq N_{enc}$. G is a N_{enc} x N_{ROI} encoding matrix describing the amount of signal dephasing across a given compartment k, during phase-encoding step m according to

$$G_{k,m} = \sum_{r \in ROI_k} e^{2\pi i k_m r} \qquad \text{with } k = 1 \ldots N_{ROI},\ m = 1 \ldots N_{enc} \qquad [2]$$

k_m represents the time integral of phase-encoding gradient m. The SLIM algorithm calculates the ROI-specific signal C from the measured data P according to

$$C = G^{-1}.P \qquad [3]$$

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whereby the inverse of G can be obtained through singular value decomposition (SVD). If the object under investigation can be decomposed into C_{ROI} *homogeneous* compartments, without any requirements on homogeneity *between* compartments, then the SLIM algorithm produces C_{ROI} signals from the ROIs without any contamination from other compartments.

Fig. 1 summarizes how the outlined algorithm can be utilized to achieve lipid removal in DMI. Based on anatomical MRIs (Fig. 1A), the human head can be segmented into N_{brain} ROIs and N_{skull} ROIs (Fig. 1B/C), after which the gradient encoding matrix G can be calculated for each ROI. With the measured DMI data (Fig. 1D) as input P, the ROI-specific signals C can be calculated via Eq. [3] (Fig. 1G). The N_{skull} signals can be used to reconstruct, via Eq. [1], a skull MRSI dataset (Fig. 1H), which can be subtracted from the original MRSI to provide a skull-free, lipid-suppressed MRSI dataset (Fig. 1I).

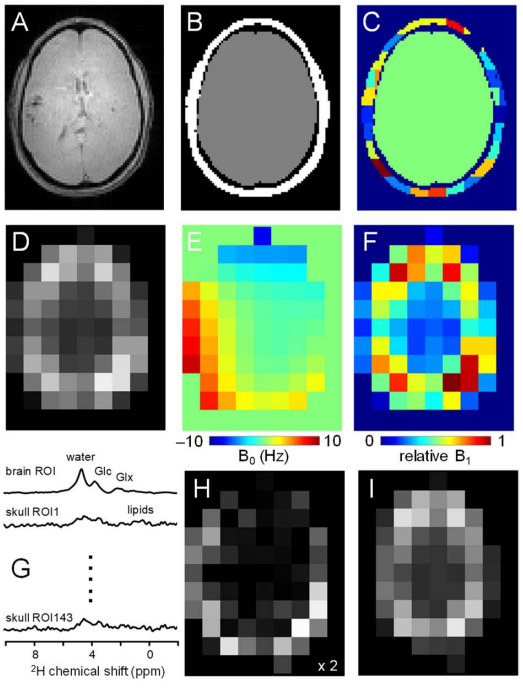

Figure 1 – Lipid removal workflow. (A) Anatomical MRI and (B) brain and non-brain/skull ROIs. (C) To accommodate heterogeneity in the skull ROI, it is sub-divided into 125-175 ROIs of 3.5 – 8.5 mL. (D) ^{2}H-water map obtained through numerical integration of each pixel in a 9 x 13 x 11 DMI dataset. (E) ^{2}H-water line shift map and (F) relative ^{2}H-water intensity map. (G) Compartment-specific signals from one brain ROI and 143 skull ROIs are the primary output of the SLIM algorithm. (H) DMI reconstructed from the 143 skull ROI signals, which can be subtracted from (D) the original DMI to yield (I) a skull (and lipid) free DMI dataset.

When all ROIs are homogeneous, the suppression of skull-based signals is expected to be perfect. Unfortunately, the requirement for homogeneous compartments is rarely encountered experimentally due to variations in metabolic composition and B_0 and B_1 magnetic fields across the sample. This heterogeneity is a violation of the linear model (Eq. [1]) and will lead to contamination (or 'bleeding') between ROIs (Liang and

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Lauterbur, 1993; Von Kienlin and Mejia, 1991) and thus an incomplete removal of skull-based lipids. Several strategies have been developed to address the issue of signal heterogeneity. Multiple methods incorporate prior knowledge on magnetic field heterogeneity from B_0 and/or B_1 map into the SLIM processing pipeline (Bashir and Yablonskiy, 2006; Khalidov et al., 2007; Passeri et al., 2014; Adany et al., 2016). Other methods seek to optimize the k-space encoding scheme to minimize bleeding between ROIs (Von Kienlin and Mejia, 1991; Zhang et al., 2012), whereas another strategy rests on subdividing larger ROIs to decrease the heterogeneity across any one ROI (Adany et al., 2021; Dong and Hwang, 2006).

Here we employ two strategies, namely (1) the subdivision of the non-brain ROI into smaller, more homogeneous compartments and (2) the incorporation of prior knowledge on known B_0 and B_1 magnetic field heterogeneity. Following the segmentation of brain and non-brain ROIs, the latter is sub-divided further (Fig. 1C) by multiplying the ROI with an equidistant 3D grid. A minimum ROI volume is enforced by combining adjacent ROIs for which at least one falls below a minimum threshold. The effect of the ROI size and number of ROIs on the localization performance can be quantitatively evaluated through calculation of the spatial response function (SRF, (Von Kienlin and Mejia, 1991)) according to

$$SRF_k(r) = \sum_{m=1}^{N_{enc}} G_{k,m}^{-1}\, e^{2\pi i k_m r} \qquad \text{with } k = 1 \ldots N_{ROI} \qquad [4]$$

The SRF is a complex function that depicts the spatial extent of each ROI given a set of k-space encodings, whereby the net SRF contribution of a given ROI is zero across all other ROIs.

The incorporation of B_0 and B_1 magnetic field heterogeneity is achieved through a modification of the encoding matrix (Eq. [2]) according to

$$G_{k,m,n} = \sum_{r \in ROI_k} B_1(r) e^{2\pi i k_m r} . e^{2\pi i B_0(r) t_n} \qquad \text{with } n = 1 \ldots N_{time} \qquad [5]$$

Note that G essentially converts from a time-independent N_{enc} x N_{ROI} matrix to a time-dependent N_{enc} x N_{ROI} x N_{time} matrix, providing unique encoding for each (spectroscopic) time point n. In Eq. [5] $B_0(r)$ represents a spatial B_0 magnetic field maps (in Hz) and $B_1(r)$ represents a relative signal intensity (0 … 1) with contributions from the transmit B_1^+ and receive B_1^- magnetic fields. While high-resolution B_0 and B_1 maps can be obtained with routine MR methods for ^{1}H MRSI, the low-sensitivity DMI data prevents a comparable implementation. The calculation of surrogate B_0 and B_1 maps (Figs. 1E and F) from the measured DMI data will be described next.

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2.2. Simulations

To evaluate the effectiveness of extracranial lipid suppression and intracranial metabolite retention, simulations were performed on brain and non-brain ROIs segmented from T_2-weighted MRIs of five human subjects. To limit the overall calculation times, all simulations were performed on a single 2D slice. The brain ROIs were manually segmented into gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF). A pathological ROI (e.g., tumor, stroke) with a random size (72 – 148 % of a nominal MRSI voxel), shape and position was placed inside the brain ROI. With ten random pathology ROI variations per subject, a total of fifty datasets were created for simulation.

Heterogeneity in the B_0 and B_1 magnetic fields can significantly affect the reconstruction performance and simulations were extended with typical distributions found across the human head *in vivo*. As ^{2}H-based B_0 and B_1 maps are not readily available, DMI-derived B_0 and B_1 maps were determined on five subjects by measuring the ^{2}H water line shift and ^{2}H water intensity in each pixel across a 2D slice, respectively. The maps were parameterized with a fourth order 2D polynomial fit to set the B_0 and B_1 distribution average and range. Each of the 50 simulated datasets was constructed with unique B_0 and B_1 distributions, calculated from randomly selected polynomial coefficients characterizing the *in vivo* ranges. To further accommodate B_0 and B_1 heterogeneity, the skull ROI was divided into multiple smaller ROIs. The division was initiated by multiplying the skull ROI by a grid of uniform voxels (e.g., 20 x 20 mm). The resulting skull ROIs were combined with the nearest neighbor ROI when the ROI volume was below a minimum threshold volume (e.g., 40% of a nominal volume). By adjusting the grid size, the number of skull ROIs was varied from 1 to 50 to determine the optimal setting.

Using knowledge on the spatial ROIs, B_0 and B_1 distribution and MRSI k-space encoding, DMI datasets were calculated as a 9 x 13 spatial matrix and 512 complex points acquired over a 1.0 kHz spectral width using a single, well-resolved resonance line per compartment in addition to a water signal present in all compartments. Optional Gaussian noise could be added to the entire 9 x 13 x 512 time domain DMI dataset. SLIM processing (i.e., Eq. [3]) resulted in ROI-specific signals C, from which the non-brain ROI signals were selected to calculate a non-brain DMI dataset. Subtraction of the non-brain DMI dataset from the experimentally measured DMI produced a lipid-free, brain-only DMI dataset. All data analysis is based on numerical integration of the well-separated spectral MR signals representing water, lipids and metabolites.

2.3. Human studies *in vivo*

All human studies were approved by the Yale University Institutional Review Board. All scans were performed on a 4 T Magnex magnet (Magnex Scientific Ltd.) interfaced to a Bruker Avance III HD spectrometer running on ParaVision 6 (Bruker Instruments). The system was equipped with 67-cm-diameter Magnex gradients capable of switching 30 mT/m in 1.1 ms. RF transmission and reception were conducted with a 28.5-cm-diameter transverse electromagnetic (TEM) volume coil tuned to the proton frequency (170.5 MHz) for MRI and shimming.

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Deuterium RF reception at 26.2 MHz was achieved with a four-coil phased array that was driven as a single RF coil during RF transmission. The four 8 × 10 cm rectangular ^{2}H array elements were positioned equidistantly on an 18 × 25 cm elliptical former that was positioned within the ^{1}H TEM coil.

DMI was acquired with a pulse-acquire method, extended with 3D phase-encoding according to a spherical k-space sampling pattern. A total of 491 phase encoding steps were acquired to generate a 9 x 13 x 11 DMI dataset in circa 27 min with 8 mL nominal resolution (TR = 333 ms, 10 averages). All DMI scans were preceded by anatomical MRIs and second-order SH shimming over the entire brain. Natural abundance DMI data was acquired on three subjects without the administration of deuterated substrates. On two subjects, including one patient with an intracranial glioblastoma tumor, [6,6'-$^{2}H_2$]-glucose dissolved in water was administered orally (0.75 g/kg) after which the metabolic profile was sampled with DMI 90 – 120 min later. Brain and non-brain (i.e., skull) ROIs were semi-automatically segmented from 3D gradient-echo MRIs (TR/TE = 25/6 ms).

Processing of the *in vivo* DMI datasets is similar to that described for simulated data with a few noticeable differences. Firstly, whereas all *in vivo* DMI data is acquired as a 9 x 13 x 11 matrix over a field-of-view of 180 x 260 x 220 mm (XYZ), the limited length (80 mm) of the ^{2}H RF elements only provided ^{2}H signal in 3 to 4 planes in the Z direction. As a result, ROIs were only generated for spatial positions where the ^{2}H water intensity was at least 5% of the maximum intensity in the entire 3D dataset. Secondly, the brain ROI was not divided into tissue-specific compartments (e.g., GM, WM, CSF) as simulations (see Results) demonstrated that this step did not affect lipid suppression and metabolite retention. Thirdly, the skull ROI was divided according to a 3D grid of nominal DMI voxels without further optimization. ROIs below a minimum volume threshold (40% of nominal) were merged with nearest neighbor ROIs, resulting in 128-177 skull ROIs across all subjects. Fourthly, signal quantification is based on non-linear least-squares fitting using a linear combination model of Lorentzian-shaped signals for ^{2}H-labeled water, glucose, glutamate+glutamine (Glx) and lactate. ^{2}H MR spectra are fitted with a (fixed) linear phase roll due to the delayed ^{2}H acquisition caused by the phase-encoding gradient. While the overall linewidths are unconstrained to accommodate magnetic field heterogeneity, the linewidth of metabolites are linked (within a [–2 … +5] Hz range) to the water linewidth. All spectral fitting was performed in DMIWizard, a graphical user interface programmed in Matlab (The MathWorks, Natick, MA, USA) and freely available to the MR community. Finally, in the evaluation of metabolite retention, only pure-brain pixels are considered. For lipid suppression, partial skull pixels are also considered even though can lead to an underestimation of the real suppression.

3. RESULTS

Fig. 2A shows the brain and non-brain ROIs used for one of the simulations, together with DMI-derived B_0 (Fig. 2B) and B_1 (Fig. 2D) maps, as well as surrogate B_0 (Fig. 2C) and B_1 (Fig. 2E) obtained by fitting the low-resolution maps in Figs. 2B/D with third order 2D polynomials. The B_0 magnetic field varied between –10 and +10 Hz over

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the areas analyzed, whereby the relative B_1 amplitude varied from 0.15 in the center of the brain to 1.00 near the periphery.

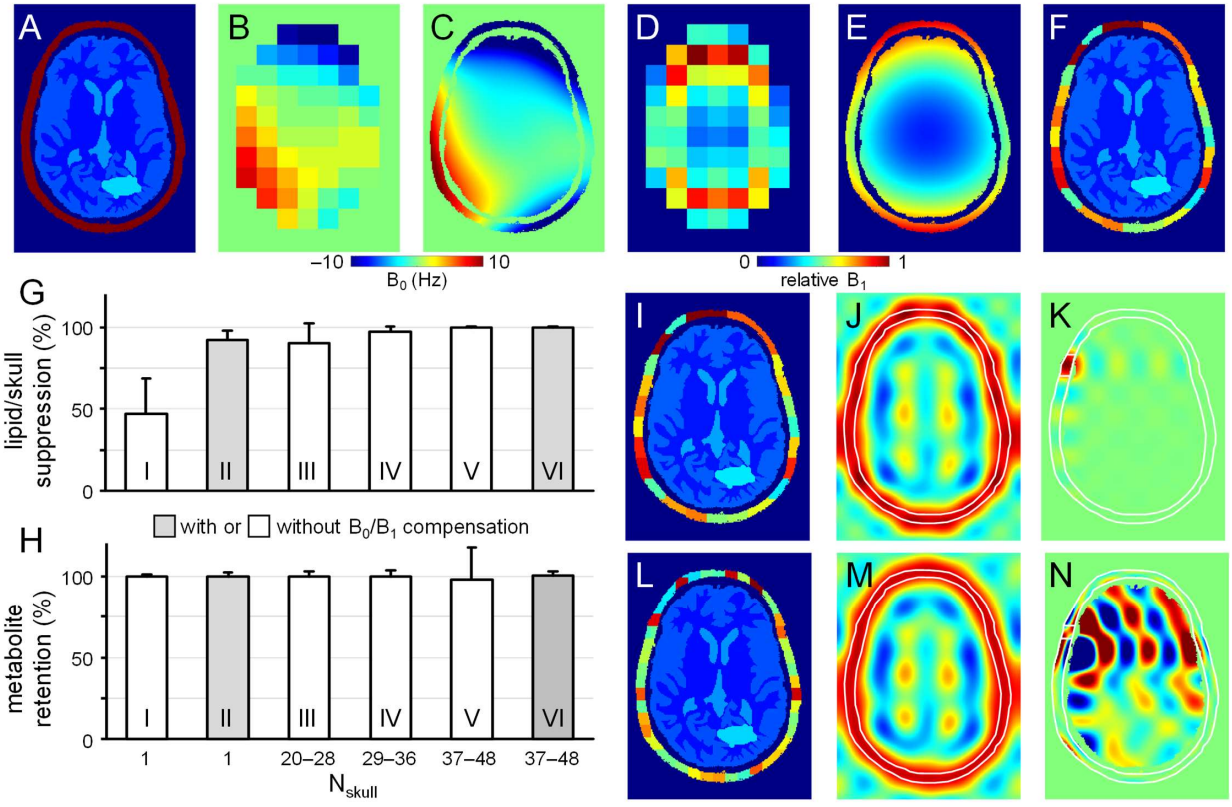

Figure 2 – Performance of SLIM-based lipid signal removal on phantoms *in silico*. (A) Brain and skull tissue constellation for one out of 50 permutations. (B) Water shift and (D) intensity maps as extracted from DMI data, providing (C) surrogate B_0 and (E) B_1 maps following low-order polynomial fitting. (F) ROI map with the skull ROI subdivided into 23 smaller compartments (i.e., N_{skull} = 23) to accommodate signal heterogeneity. (G) Lipid suppression and (H) metabolite retention under different scenarios including N_{skull} = 1 without (column I) and with (column II) B_0 and B_1 compensation, N_{skull} = 20-28 (column III), 29-36 (column IV), 37-48 (columns V and VI) without (columns III-V) and with B_0 and B_1 compensation (column VI). Results for the separate brain ROIs (GM, WM, CSF and pathology) are summarized in Supplemental Figure S2 and essentially minor the whole brain results shown in (H). (I, L) Head constellations with the skull ROI subdivided into (I) 23 and (L) 44 smaller compartments. (J, K, M, N) Spatial response function (SRF) of (J, M) the summed skull ROIs and (K, N) a single skull ROI for N_{skull} = 23 (J, K) and N_{skull} = 44 (M, N). All SRFs have the same vertical scale, spanning -1 to +1. While the integrated, *phase-sensitive* SRF intensity of a single skull ROI is zero across the brain ROI for any N_{skull}, the integrated, *absolute-valued* SRF intensity will be much larger for N_{skull} = 44 (N) compared to N_{skull} = 23 (K). Supplemental Figure S3 gives a summary of the absolute-valued SRF across the brain ROI for N_{skull} ranging from 1 to 50.

Fig. 2F shows the subdivision of the non-brain ROI into 23 smaller ROIs, whereby separate simulations investigated the effect of the number of non-brain ROIs. Supplemental Figure S1 show five additional datasets used for simulation (out of a total of 50 datasets). All simulations achieved 100% skull-based signal removal and 100% brain signal retention in the absence of B_0 and/or B_1 heterogeneity. Even in the presence of B_0 and B_1

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heterogeneity, perfect results were obtained provided that the *exact* B_0 and B_1 spatial distributions were incorporated according to Eq. [5]. However, in the presence of B_0 and/or B_1 heterogeneity, skull-based signal suppression was only 47 ± 21 % when the skull ROI was not subdivided further (Fig. 2G, column I). When the reconstruction was supplemented with DMI-derived surrogate B_0 and B_1 maps, the skull-based signal suppression improved to 92 ± 6 % (Fig. 2G, column II). It was observed that the combined effect of incorporating surrogate B_0 and B_1 maps (6.6 x reduction in residual lipids) was larger than that of the separate B_0 (2.9 x reduction) or B_1 (1.1 x reduction) maps. B_0 compensation becomes less important, and the overall lipid suppression improves, as the spectroscopic linewidths becomes broader. Fig. 2G/H (columns III to VI) explores the effect of subdividing the skull into N_{skull} ROIs, with N_{skull} ranging from 20-28 (column III), 29-36 (column IV) and 37-48 (columns V and VI). Without compensation for B_0/B_1 heterogeneity, the skull suppression increases with increasing N_{skull} as the smaller ROIs exhibit less heterogeneity across their volume (lipid suppression equals 90 ± 12, 97 ± 3 and 99 ± 1% for column III - V). However, for higher N_{skull} the variability in metabolite retention increases from 3% (column III) to 4% (column IV) to 20% (column V). Supplemental Figure S2 summarizes metabolite brain retentions across separate brain ROIs (GM, WM, CSF, and pathology) and essentially mirror the trends seen across the entire brain (Fig. 2H). This effect can be understood by considering the SRF (Eq. [4]) as demonstrated for N_{skull} = 23 (Fig. 2I-K) and N_{skull} = 44 (Fig. 2L-N). In the case of N_{skull} = 23, both the overall skull SRF (Fig. 2J), being the phase-sensitive sum of all N_{skull} ROIs, and an exemplary single skull ROI (Fig. 2K) are well-behaved with the bulk SRF intensity within the intended skull ROI locations. Small contributions inside the brain have a zero net integral due to phase cancelation. In the case of N_{skull} = 44, the overall skull SRF (Fig. 2M) looks like that for N_{skull} = 23 (Fig. 2J). However, the single skull ROI (Fig. 2N) has the bulk SRF intensity inside the brain. Even though the integrated SRF intensity across the brain is zero, the strong reliance on phase-sensitive signal cancellation can lead to alteration of the brain metabolite signal distribution in the presence of compartmental heterogeneity, such as simulated in Fig. 2H (column V). Supplemental Figure S3 summarizes the absolute-valued SRF brain contribution for every skull ROI when N_{skull} varies from 1 to 50. The SRF contribution across the brain ROI for any skull ROI is small and well-behaved for N_{skull} less than circa 35. However, when N_{skull} > 35, the SRF contribution sharply rises, resulting in localization that is highly dependent on phase cancelation – a condition that is violated in the presence of heterogeneity. When the B_0/B_1 heterogeneity is compensated with surrogate B_0/B_1 maps (Fig. 2H, column VI), the metabolite retention variability is greatly reduced (from 20% (column V) to 3% (column VI)) as the large SRF intensity within the brain is properly phase-canceled. Overall, the simulation results in Fig. 2 indicate that the effects of B_0/B_1 heterogeneity can be reduced through (1) compensation with surrogate B_0/B_1 maps, (2) subdivision of the skull region into smaller ROIs, or both, and that the skull ROI subdivision needs to balance improvement in skull suppression with increased variability in metabolite retention. Since the optimal ROI subdivision in Fig. S3 is fairly broad, all 3D human DMI data was divided according to a grid of nominal DMI voxels without further optimization.

Fig. 3 shows the performance of SLIM-based skull removal on a patient with a glioblastoma tumor. Fig. 3A shows a T_2-weighted spin-echo MRI with the approximate tumor location outlined in red. The white dotted lines indicate

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the in-plane DMI grid (8 mL nominal resolution). Fig. 3B shows a grid of ^{2}H MR spectra extracted from the 3D DMI dataset at the location of the green 2 x 2 grid (Fig. 3A).

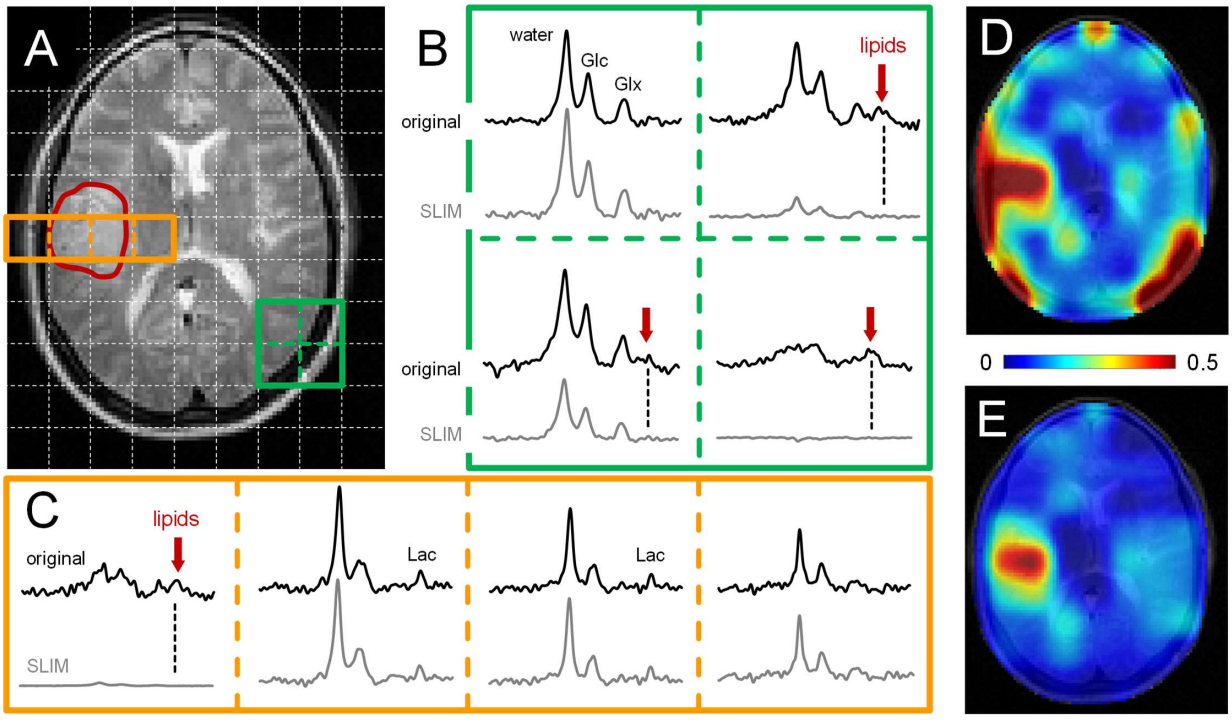

Figure 3 – Performance of SLIM-based lipid signal removal on human brain *in vivo*. (A) T_2-weighted spin-echo MRI of a patient harboring a glioblastoma brain tumor with the approximate location outlined in red. The white dotted lines indicate the in-plane DMI grid (8 mL nominal resolution, circa 30 min total scan time). (B) 2 x 2 x 1 sub-grid extracted from the 9 x 13 x 11 DMI dataset showing the original (black, top) and SLIM-processed (gray, bottom) ^{2}H MR spectra. In three spectra a clear natural abundance lipid signal (red arrow) is present in the original data which is completely removed following SLIM processing. (C) 4 x 1 x 1 sub-grid covering tumor and adjacent skull and brain tissue extracted from the 9 x 13 x 11 DMI dataset. Only the skull voxel shows a pronounced lipid signal that is removed with SLIM processing. While the remaining three spectra looks visually identical with or without SLIM processing, the removal of the extracranial lipid signal has a significant effect on the (D, E) resulting Lac/(Lac + Glx) metabolic maps.

The top spectra (black) represent the original, measured ^{2}H MR spectra, whereas the bottom spectra (gray) are obtained following SLIM-based skull suppression. Signals from the pure skull voxel (lower right) are completely removed, whereas signals from the pure brain voxel (upper left) are fully retained. The two remaining voxel locations have both brain and skull contributions. The extracranial signals (primarily lipids, both also glucose and water) are suppressed, whereas the intracranial signals (glucose, glutamate, and water) are retained. Fig. 3C shows a grid of ^{2}H MR spectra extracted from the 3D DMI dataset at the location of the red 4 x 1 grid (Fig. 3A) through the tumor region. Only the skull voxel shows a pronounced lipid signal that is removed with SLIM processing. The remaining three spectra look visually identical with or without SLIM processing, with the

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increased lactate signal within the tumor region remaining visibly unperturbed. However, the removal of extracranial lipid signal has a significant effect on the resulting Lac/(Lac + Glx) metabolic maps (Fig. 3D/E). Without skull suppression, the lipid signals lead to several hotspots surrounding the brain (Fig. 3D), including an artifactual elevation of the lactate signals within the tumor. After SLIM-based skull removal, the lipid hotspots are removed, resulting in a high-contrast 'Warburg effect' image of aberrant tumor metabolism (Fig. 3E). The lipid suppression across all subjects was 90.5 ± 11.4% with 66% and 99% of all skull pixels achieving suppression factors of at least tenfold and threefold, respectively. The signal retentions for Glc and Glx were 99.8 ± 7.5 and 100.2 ± 7.8 %, respectively.

4. DISCUSSION

The use of spatial prior knowledge in DMI processing allowed the removal of extracranial lipid signals in datasets acquired of human head to below the spectral noise level. Similar approaches have previously been used for lipid signal removal in ^{1}H MRSI (Dong and Hwang, 2006; Adany et al., 2016). However, ^{1}H MRSI requires lipid signal suppression factors well in excess of 100. This puts much higher demands on accurate prior knowledge and signal homogeneity and may ultimately place a limit on the robustness for use on ^{1}H MRSI data. In contrast, the low natural abundance of deuterium leads to much lower amplitude lipid signals in the DMI data which were adequately removed with suppression factors below 10, thereby eliminating ambiguities in detecting elevated lactate levels.

The basic SLIM algorithm that uses two ROIs (one brain, one skull) without compensation for B_0 and B_1 magnetic field heterogeneity only provides modest lipid suppression (47 ± 21 % in simulations). Subdividing the skull ROI into smaller compartments quickly improves the lipid suppression to >90, >97 and > 99.5 % for ~25, ~35 and ~45 ROIs, respectively. However, improved lipid suppression is accompanied by more variable metabolite retention as the SRF outside any given ROI becomes more dominant and localization increasingly relies on phase cancelation. The inclusion of B_0 and B_1 maps greatly improved the lipid suppression (to 92 ± 6 % in simulations for one brain and one skull ROI) without increased variability in metabolite retention. The use of surrogate B_0 and B_1 maps based on the ^{2}H water shift and intensity provide a practical solution to absence of high-resolution maps. Based on these results, it is recommended that B_0 and B_1 compensation should be used whenever possible, ideally in combination with a moderate subdivision of the skull ROI. It should be noted that while B_1 heterogeneity was treated as a nuisance in the current implementation, it is possible to use B_1 receive profiles for signal encoding to accelerate and/or improve data acquisition (An et al., 2011). While the average metabolite retention in the human brain *in vivo* is essentially 100%, the standard deviations on Glc and Glx are somewhat higher than anticipated compared to simulation results (Fig. 2). Several factors can explain the increased variability. Firstly, removal of extracranial signals, including water and Glc, will perturb brain signals as voxel bleeding due to the MRSI point spread function is also removed. Secondly, MRSI voxels with significant partial volume effects will be perturbed as extracranial contributions are selectively removed. Thirdly,

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compensation of B_0 and/or B_1 heterogeneity with DMI-based surrogate B_0 and/B_1 maps will greatly decrease the variability in metabolite retention. However, since the surrogate maps are only an approximation of the actual B_0 and B_1 heterogeneity, the compensation is necessarily incomplete, thus leading to some residual variability. Finally, the SNR of *in vivo* DMI data is generally low, such that small perturbations in signal shape or noise level can lead to large relative changes in fitted signal amplitude.

The SLIM implementation as presented here for DMI can be modified and extended in several ways to enhance the immunity to signal heterogeneity and improve the reliability. Sub-division of the skull ROI can be optimized further. The number of ROIs and ROI shapes can be based on (1) optimizing the SRF contributions, or (2) DMI-based lipid maps or (3) high-resolution MRI-based lipid maps. The SLIM algorithm is also ideally suited to allow regional analysis of brain ROIs during which ^{2}H MR spectra can be obtained from anatomy-matched ROIs without partial volume effects. Development of automated definition of anatomical (GM, WM) and pathological (tumor core, tumor rim, FLAIR-enhanced) ROIs is currently in progress.

Similar levels of lipid suppression could have been achieved with alternative methods, such as dual density reconstruction (Hu et al., 1994; Metzger et al., 1999), data extrapolation (Haupt et al., 1996) or L2 regularization (Bilgic et al., 2014). Whereas L2 regularization and data extrapolation can operate on standard MRSI data, dual density reconstruction requires a modification of the data acquisition scheme, such that high k-space coordinates are sampled in addition to the standard low k-space coordinates typically acquired for MRSI. L2 regularization is based on the conditions of spatial and spectral orthogonality in which the desired and nuisance signals originate from spatially distinct compartments without spectral overlap. As the spectral overlap requirement cannot be fulfilled for lipids and lactate, L2 regularization will remove brain lactate signals, thus making it unsuitable for DMI. Like SLIM, data extrapolation only requires spatial separability of signals and would thus also be applicable to DMI. However, in the current investigation we focused on SLIM-based processing as the algorithm is readily extended to obtain signal from anatomy and/or pathology-based ROIs.

CODE AVAILABILITY

The Matlab code to process 3D DMI data, referred to as DMIWizard, is freely available for download from the Yale website or via GitHub (https://github.com/radegraaf/DMIWizard).

COMPETING INTERESTS

At least one of the (co-)authors is a member of the editorial board of Magnetic Resonance.

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FIGURE LEGENDS

Figure 1 – Lipid removal workflow. (A) Anatomical MRI and (B) brain and non-brain/skull ROIs. (C) To accommodate heterogeneity in the skull ROI, it is sub-divided into 125-175 ROIs of 3.5 – 8.5 mL. (D) ^{2}H-water map obtained through numerical integration of each pixel in a 9 x 13 x 11 DMI dataset. (E) ^{2}H-water line shift map and (F) relative ^{2}H-water intensity map. (G) Compartment-specific signals from one brain ROI and 143 skull ROIs are the primary output of the SLIM algorithm. (H) DMI reconstructed from the 143 skull ROI signals, which can be subtracted from (D) the original DMI to yield (I) a skull (and lipid) free DMI dataset.

Figure 2 – Performance of SLIM-based lipid signal removal on phantoms *in silico*. (A) Brain and skull tissue constellation for one out of 50 permutations. (B) Water shift and (D) intensity maps as extracted from DMI data, providing (C) surrogate B_0 and (E) B_1 maps following low-order polynomial fitting. (F) ROI map with the skull ROI subdivided into 23 smaller compartments (i.e., N_{skull} = 23) to accommodate signal heterogeneity. (G) Lipid suppression and (H) metabolite retention under different scenarios including N_{skull} = 1 without (column I) and with (column II) B_0 and B_1 compensation, N_{skull} = 20-28 (column III), 29-36 (column IV), 37-48 (columns V and VI) without (columns III-V) and with B_0 and B_1 compensation (column VI). Results for the separate brain ROIs (GM, WM, CSF and pathology) are summarized in Supplemental Figure S2 and essentially minor the whole brain results shown in (H). (I, L) Head constellations with the skull ROI subdivided into (I) 23 and (L) 44 smaller compartments. (J, K, M, N) Spatial response function (SRF) of (J, M) the summed skull ROIs and (K, N) a single skull ROI for N_{skull} = 23 (J, K) and N_{skull} = 44 (M, N). All SRFs have the same vertical scale, spanning -1 to +1. While the integrated, *phase-sensitive* SRF intensity of a single skull ROI is zero across the brain ROI for any

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N_{skull}, the integrated, *absolute-valued* SRF intensity will be much larger for N_{skull} = 44 (N) compared to N_{skull} = 23 (K). Supplemental Figure S3 gives a summary of the absolute-valued SRF across the brain ROI for N_{skull} ranging from 1 to 50.

Figure 3 – Performance of SLIM-based lipid signal removal on human brain *in vivo*. (A) T_2-weighted spin-echo MRI of a patient harboring a glioblastoma brain tumor with the approximate location outlined in red. The white dotted lines indicate the in-plane DMI grid (8 mL nominal resolution, circa 30 min total scan time). (B) 2 x 2 x 1 sub-grid extracted from the 9 x 13 x 11 DMI dataset showing the original (black, top) and SLIM-processed (gray, bottom) ^{2}H MR spectra. In three spectra a clear natural abundance lipid signal (red arrow) is present in the original data which is completely removed following SLIM processing. (C) 4 x 1 x 1 sub-grid covering tumor and adjacent skull and brain tissue extracted from the 9 x 13 x 11 DMI dataset. Only the skull voxel shows a pronounced lipid signal that is removed with SLIM processing. While the remaining three spectra looks visually identical with or without SLIM processing, the removal of the extracranial lipid signal has a significant effect on the (D, E) resulting Lac/(Lac + Glx) metabolic maps.