

Metabolic Imaging of Pediatric Brain Tumors Using High-Field MRI

^{31}P -Magnetic Resonance Spectroscopy

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Metabolic Imaging of Pediatric Brain Tumors Using High-Field MRI ^{31}P -Magnetic Resonance Spectroscopy

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Preface

I would like to take this opportunity to express my gratitude to everyone who has contributed to the completion of this master's thesis and supported me throughout this project.

This thesis represents my research on metabolic imaging in pediatric brain tumors, a topic that has both challenged and inspired me. Conducting this research has allowed me to merge technical knowledge with clinical applications. From data analysis to patient-centered perspectives, I have gained a deeper appreciation for the complexities of pediatric neuro-oncology and the evolving role of non-invasive imaging in improving patient care. Working with children facing serious illness has shaped my perspective, reminding me of the real impact of medical research and the importance of advancing non-invasive imaging techniques.

I would like to express my gratitude to my supervisors and colleagues for their invaluable guidance and encouragement. Jannie and Chloe, I am incredibly grateful for the time you dedicated to me despite your busy schedules, always finding a moment to meet with me, answer my emails, ask insightful critical questions, and patiently explain concepts multiple times when needed. Evita, I appreciate your support after returning from your paternity leave, always making time for my questions. Wouter, thank you for providing a medical perspective that enriched my understanding of the clinical application.

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Finally, I am deeply grateful to my family and friends for their unwavering support, patience, and belief in me throughout this journey. Your encouragement from the very first day has meant the world to me.

I hope this thesis contributes to the ongoing efforts to refine metabolic imaging and inspires further research in this field.

*Hilde Roording
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Summary

Introduction

Pediatric brain tumors are the most common solid tumors in children and a leading cause of cancer-related mortality. Magnetic resonance imaging (MRI) is the primary tool for assessing tumor progression and treatment response. However, distinguishing treatment effects from tumor progression remains a challenge, complicating clinical decision-making. Phosphorus-31 Magnetic Resonance Spectroscopic Imaging (^{31}P -MRSI) is a non-invasive technique that provides spatially resolved metabolic information by detecting phosphorus-containing metabolites, such as phosphocreatine (PCr), adenosine triphosphate (ATP), and phosphomonoesters (PME). These metabolites offer insights into energy metabolism, cell membrane turnover, and intracellular pH regulation, which could help differentiate tumor progression from treatment-related changes. A major challenge in ^{31}P -MRSI is its low signal-to-noise ratio (SNR), due to the relatively low gyromagnetic ratio and the low concentration of phosphorus metabolites in tissues. This necessitates large voxel sizes, leading to partial volume effects, where a voxel contains signals from multiple tissue types (e.g., tumor and normal-appearing white matter (NAWM)). To address this, post-processing regridding techniques can be applied to recalculate the spatial position of the ^{31}P -MRSI signal and improve grid alignment with anatomical structures.

Aim

This study investigates post-processing regridding techniques to optimize spatial localization in ^{31}P -MRSI and evaluates longitudinal metabolic changes in pediatric brain tumors and NAWM.

Methods

Phantom and in vivo clinical data were acquired using a 7T MRI scanner. In the phantom experiment, a spherical phantom with inorganic phosphate (Pi) was scanned with different MRSI grid configurations. Two post-processing regridding techniques were evaluated by comparing regridded data to a reference: 1) K-space phase adjustment, which applies a phase shift before Fourier transformation, and 2) Interpolation-based regridding, which estimates spectral data at shifted voxel positions. Correlation analysis was performed with Pearson's correlation. Following phantom validation, the best-performing regridding technique was applied to in vivo pediatric brain tumor data. The impact of regridding was assessed by analyzing metabolic ratio changes (PE/GPE, PCr/ γ ATP, pH, Pi/ATP) in tumors and NAWM, alongside spectral quality metrics such as SNR and linewidth. Additionally, longitudinal data from eight pediatric patients with low-grade glioma were analyzed to assess metabolic ratio changes over time. Patients underwent different chemotherapy regimens, enabling an evaluation of therapy-related metabolic alterations.

Results

K-space phase adjustment performed superior compared to the spatial interpolation, evidenced by higher correlations and more accurate peak intensities in voxels near the Pi bead. In in vivo data, regridding improved voxel alignment with tumor regions, increasing tumor contribution within individual voxels. Spectral quality (SNR and linewidth) remained stable after regridding, and metabolic ratios were not significantly altered. Longitudinal analysis revealed metabolic changes in tumors and NAWM over time. However, normalizing tumor metabolic ratios to NAWM did not produce consistent trends across patients.

Conclusion

Regridding enhances spatial localization in ^{31}P -MRSI without degrading spectral quality, making it a viable post-processing approach. While metabolic alterations in tumors and NAWM were observed, they did not reach statistical significance. Further validation in larger cohorts is required to assess the clinical significance of these metabolic changes.

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Nomenclature

Abbreviations

Abbreviation	Definition
^1H	Proton (Hydrogen-1)
^{31}P	Phosphorus-31
ADP	Adenosine Diphosphate
AP	Anterior–Posterior
APT-CEST	Amide Proton Transfer Chemical Exchange Saturation Transfer
ATP	Adenosine Triphosphate
BL	Baseline
CSI	Chemical Shift Imaging
Cr	Creatine
DLGNT	Diffuse Leptomeningeal Glioneuronal Tumor
DPG	Diphosphoglycerate
DWI	Diffusion-Weighted Imaging
FID	Free Induction Decay
FOV	Field of View
FWHM	Full Width at Half Maximum
FU1	Follow-Up 1
FU2	Follow-Up 2
GPC	Glycerophosphocholine
GPE	Glycerophosphoethanolamine
LGG	Low-Grade Glioma
LR	Left–Right
MITCH	Metabolic Imaging of Tumors in Children
MRSI	Magnetic Resonance Spectroscopic Imaging
NAWM	Normal-Appearing White Matter
NADH	Nicotinamide Adenine Dinucleotide
NSA	Number of Single Averages
PC	Phosphocholine
PCr	Phosphocreatine
PE	Phosphoethanolamine
Pi	Inorganic Phosphate
PME	Phosphomonoesters
PDE	Phosphodiester
ppm	Parts Per Million
PSF	Point Spread Function
RAPNO	Response Assessment in Pediatric Neuro-Oncology
RF	Radiofrequency
RL	Right–Left
ROI	Region of Interest
SNR	Signal-to-Noise Ratio
TE	Echo Time
TR	Repetition Time
UDPG	Uridine Diphosphoglucose
VOI	Volume of Interest

Introduction

An introduction to the clinical background of this research

1.1. Pediatric brain tumors

Brain cancer is the most prevalent solid cancer in children and one of the leading causes of cancer-related death in both children and adults worldwide [1, 2]. Brain tumors vary widely in terms of morbidity and mortality depending on the type, size, location, and rate of tumor growth. For example, pilocytic astrocytoma, a low-grade glioma, has a 10-year survival rate exceeding 95% [1], whereas diffuse midline glioma has a very poor prognosis, with only 10% of the patients surviving beyond two years [3]. Despite advances in diagnosis and treatment, including surgery, radiation therapy, and chemotherapy, brain tumors remain a major clinical challenge [4, 5].

Pediatric brain tumors differ from adult tumors in terms of histopathology, tumor location, and genetic alterations, influencing treatment strategies and prognosis [1]. Given these differences, research on pediatric brain tumors is essential to improve diagnosis and treatment strategies tailored to this population. The most common malignant pediatric brain tumors include gliomas, embryonal tumors, and germ-cell tumors [1]. Symptoms vary based on the tumor location; for instance, cortical tumors may cause seizures, optic pathway tumors can impair vision. Other common symptoms include nausea, headache, ataxia, and hemiparesis [6].

The gold standard for diagnosing tumors is magnetic resonance imaging (MRI) in combination with histopathology [7]. Complete surgical resection offers the best prognosis, but is often infeasible due to the location and invasive nature, necessitating adjuvant chemotherapy and/or radiotherapy [4]. Regular MRI scans are essential to monitor treatment response and disease progression [7].

1.2. MRI assessment

A diagnostic brain MRI typically includes a T1-weighted scan for anatomical assessment; a T2-weighted scan to evaluate the ventricular system, subdural spaces, and edema; a FLAIR sequence to detect white-matter tumor involvement and edema; and diffusion-weighted imaging (DWI) to assess tumor cellularity and cytotoxic edema [8, 9]. In addition, post-contrast T1-weighted images are used to evaluate vascularity and blood-brain barrier disruption [10]. These conventional MRI sequences also provide an initial assessment of tumor composition, such as the identification of cystic components, calcifications, hemorrhagic products, fibrin deposits, or melanin accumulation [9].

The response to therapy for pediatric patients can be evaluated in studies using the response assessment in pediatric neuro-oncology (RAPNO). It evaluates the response of tumors according to different criteria such as the size of the lesion, contrast enhancement pattern, new lesions, and clinical parameters [11, 12]. However, these criteria may be inconclusive in distinguishing true tumor progression from pseudoprogression, which is a therapy-induced contrast-enhanced T2 and/or FLAIR hyperintense region that mimics progression [13, 14, 15, 16]. Tumor progression may require modification of treatment,

while pseudoprogression is a sign of response to treatment. Thus, accurately differentiating the effects of treatment from the effects of progression is critical to ensure timely treatment adjustments and prevent unnecessary therapeutic escalation. From a diagnostic perspective, we lack a tool that can non-invasively identify tumor activity and indicate the aggressiveness of that part of the tumor.

Advanced metabolic imaging techniques are evolving rapidly and are increasingly helpful in understanding tumor biology, tumor characterization, guiding treatment, and predicting patient outcomes, thereby facilitating more personalized care in cancer treatment [17, 18]. Key methods include ^1H and ^{31}P magnetic resonance spectroscopic imaging (MRSI) of various metabolites, chemical exchange-dependent saturation transfer (CEST), and positron emission tomography (PET) [17]. While the MRI techniques are noninvasive, PET requires the administration of radioactive tracers that expose patients to ionizing radiation. In clinical practice, ^1H -MRSI has been widely employed [19, 20], whereas ^{31}P -MRSI is less commonly applied but offers novel insights into phospholipid and energy metabolism, particularly at higher magnetic field strengths where enhanced spectral resolution and improved signal-to-noise ratio further augment metabolite detection [21, 22]. Each modality, therefore, presents unique advantages and limitations regarding sensitivity, spatial resolution, metabolic specificity, and clinical feasibility.

1.3. Aim

This study aims to address key challenges in ^{31}P -MRSI at 7T, focusing on the validation of post-processing techniques for realigning the spectral grid of ^{31}P -MRSI and analyzing in vivo spectra of pediatric patients with brain tumors. By evaluating the accuracy and impact of these realignment techniques, this study seeks to optimize spatial localization, reduce partial volume effects, and ultimately enhance ^{31}P -MRSI for metabolic imaging applications.

³¹P-MRSI Background

An introduction to the technical background of this research

2.1. MRI in general

MRI is an imaging technique that uses a strong static magnetic field, time-varying gradient fields, and radiofrequency (RF) pulses to generate high-resolution images of tissues and organs. Conventional MRI primarily exploits the magnetic properties of hydrogen nuclei (¹H), which are abundant in water and fat molecules [23]. Each nucleus has a unique gyromagnetic ratio γ , representing the ratio of its magnetic moment to its angular momentum. When placed in a static magnetic field (B_0), nuclei align with the magnetic field and resonate at a specific frequency known as the Larmor frequency f , equation 2.1.

$$f = \gamma B_0 \quad (2.1)$$

The application of an RF pulse at this resonance frequency temporarily disrupts the alignment, causing protons to displace their magnetization from equilibrium. As the nuclei return to equilibrium, they emit signals characterized by two relaxation processes: T_1 (spin-lattice) and T_2 (spin-spin). Tissue contrast in MRI arises from differences in these relaxation properties (T_1 and T_2 relaxation time) [23].

Spatial encoding is achieved through gradient fields, which introduce frequency and phase variations across the imaging volume. The acquired signals are sampled in k-space, which is a frequency-domain representation of the MRI signal, and reconstructed into spatial images using an inverse Fourier transform, enabling MRI to provide detailed soft tissue contrast [23].

2.2. Phosphorus magnetic resonance imaging

Although MRI predominantly relies on ¹H due to its high natural abundance and strong signal intensity, other nuclei, such as phosphorus-31 (³¹P), can also be studied using MR techniques [21]. Nuclei resonating at higher frequencies generate stronger signals. At 7T, ¹H resonates at approximately 300 MHz, whereas ³¹P resonates at around 121 MHz, making detection of ³¹P challenging. However, this sensitivity limitation can be partially mitigated by higher magnetic field strengths, which enhance signal intensity and improve spectral resolution. To acquire ³¹P signals, an RF pulse must be applied at its specific resonance frequency [21]. Additionally, since standard MRI coils are optimized for ¹H, a dedicated ³¹P receive coil is required for efficient signal detection.

However, the exact resonance frequency of a nucleus is not solely determined by B_0 ; it also depends on its local electronic environment, an effect known as the chemical shift. This phenomenon arises from electron shielding, where surrounding electron clouds generate an opposing magnetic field (B_e), reducing the local field strength ($B_n = B_0 - B_e$). The extent of this shielding depends on the electronegativity of nearby atoms, leading to small variations in resonance frequency [21]. As a result, different ³¹P-containing molecular groups, even within the same molecule, can exhibit distinct resonance frequencies.

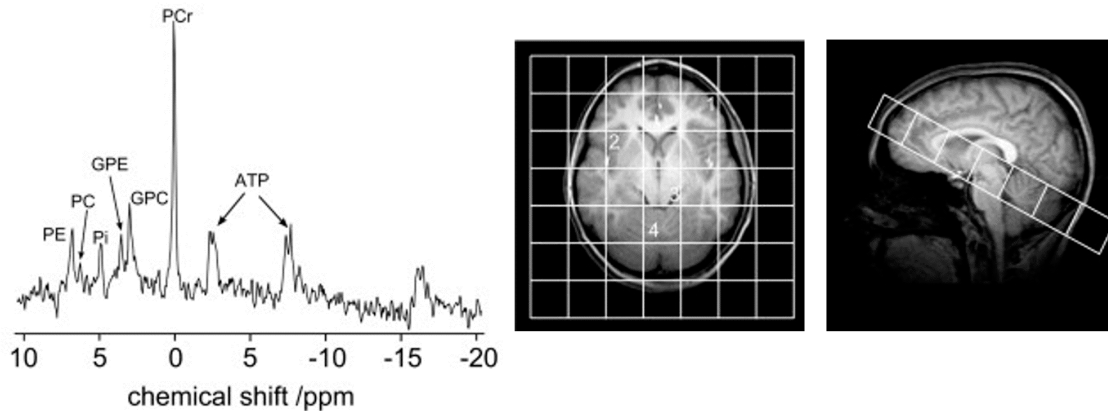


Figure 2.1: ^{31}P -MRSI spectrum obtained from a healthy volunteer. The orientation of the grid is shown on the right. The orientation of the MRSI grid allowed simultaneous metabolic profiling of various regions of the brain [25].

In ^{31}P magnetic resonance spectroscopic imaging (MRSI), this effect allows differentiation of phosphorus-containing metabolites based on their distinct chemical environments [21]. Key metabolites such as phosphocreatine (PCr), adenosine triphosphate (ATP), and inorganic phosphate (Pi) exhibit characteristic chemical shifts, enabling their quantification [24]. Chemical shifts are typically expressed in parts per million (ppm) relative to a reference compound, such as PCr (0.00 ppm) in muscle or brain spectroscopy, an example spectrum is visualized in Figure 2.1. This ppm scale normalizes the resonance frequency differences across different magnetic field strengths, ensuring consistent metabolite identification [21].

2.3. Phosphorus in the human body

Phosphorus plays a central role in cellular function, serving as a key component of energy metabolism, intracellular signaling, and structural integrity.

2.3.1. Cellular energetic state

Phosphorus is essential for maintaining cellular energy homeostasis through ATP and PCr [26, 27, 28, 29]. These molecules enable rapid ATP regeneration to meet fluctuating energy demands (Figure 2.2), particularly in high-energy-consuming tissues such as muscle and brain. The reversible reaction between PCr and creatine (Cr), catalyzed by creatine kinase, facilitates ATP regeneration by transferring a phosphate group from PCr to adenosine diphosphate (ADP) to regenerate ATP (Equation 2.2) [30].



Dysregulated ATP metabolism can disrupt the cellular energy balance, which is particularly relevant in disease conditions such as cancer. The Pi/ATP ratio is used as an indicator of ATP turnover, while the PCr/ATP ratio reflects the overall energetic state of a tissue [31]. Furthermore, the PCr/Pi ratio represents oxidative capacity [32, 33], and the Pi/ATP ratio provides insight into the dynamics of ATP turnover [33].

Beyond energy metabolism, phosphorus also contributes to pH regulation. Intracellular pH homeostasis is maintained through buffering systems and ATP-driven ion transport mechanisms, with inorganic phosphate (Pi) acting as a key regulator [34]. Alterations in pH influence enzyme activity, cell proliferation, and metabolic function [35, 34].

2.3.2. Phospholipid Metabolism

Phosphorus plays a fundamental role in cell membrane integrity, forming the backbone of phospholipids such as phosphatidylcholine (PC) and phosphatidylethanolamine (PE). In ^{31}P -MRSI, phospho-

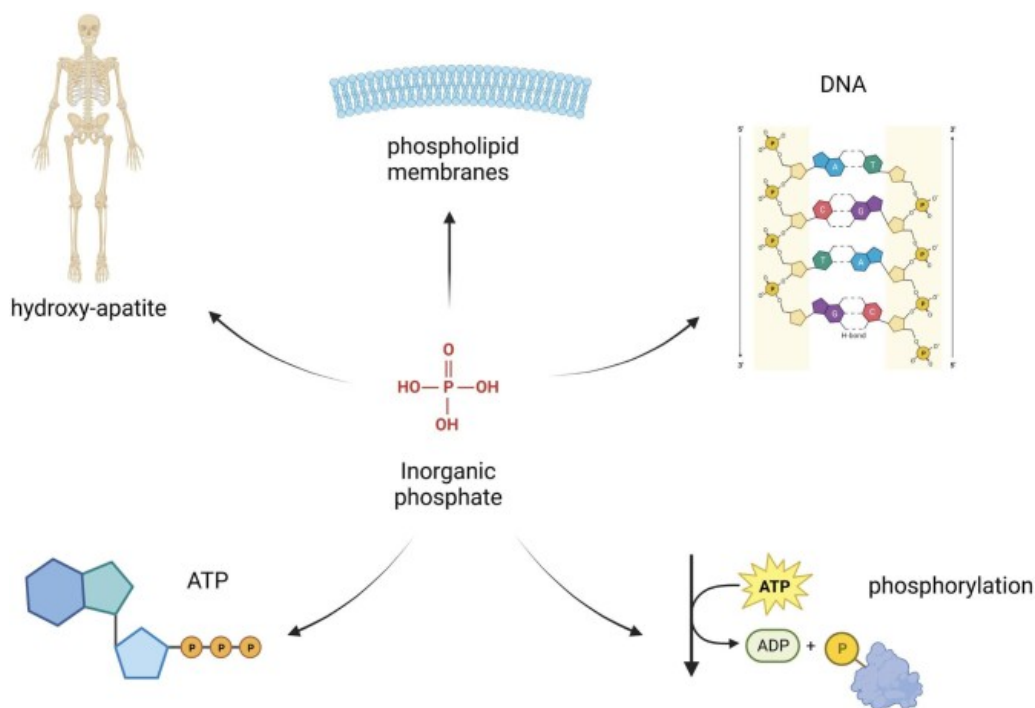


Figure 2.2: Functions of phosphate inside the human body. Inorganic phosphate is a building block for phospholipids in biological membranes, for nucleotides in DNA and RNAs, to form ATP, is involved in intracellular signaling events, and is critical for the stability of bone under the form of hydroxyapatite [26].

monoesters (PME), including PE and PC, serve as markers in phospholipid biosynthesis. Their breakdown products, phosphodiester (PDEs), such as glycerophosphoethanolamine (GPE) and glycerophosphocholine (GPC), reflect membrane degradation and turnover [36].

2.3.3. Brain tumors

Alterations in phosphorus metabolism reflect high metabolic demands, rapid proliferation, and adaptation to hypoxic conditions characteristic of malignant brain tumors [35, 37, 36]. These metabolic disruptions, including dysregulated energy metabolism, pH imbalance, and abnormal phospholipid turnover, drive tumor growth and aggressiveness [35, 34]. Non-invasive metabolic imaging techniques, such as ^{31}P -MRSI, provide a unique opportunity to assess these alterations in vivo. By quantifying phosphorus-containing metabolites, ^{31}P -MRSI enables the evaluation of tumor bioenergetics (PCr/ATP, Pi/ATP), hypoxia-related acidosis (intracellular pH), and membrane turnover (PME/PDE, PE/GPE), offering insight into tumor physiology beyond conventional imaging.

From the literature review on metabolic imaging in response to therapy (Appendix A), key phosphorus-containing metabolic markers relevant to brain tumors include:

- Cellular energetic state: PCr, PCr/ATP, PCr/Pi, PDE/ATP
- ATP turnover: Pi/ATP
- Hypoxia markers: pH
- Cell membrane metabolism: PME/PDE, PE/GPE, PME/PCr, GPE

These markers have been used to assess treatment response in glioblastoma patients receiving bevacizumab and temozolomide, with reductions in hypoxia markers and improved energy metabolism observed post-therapy [35, 38].

2.4. ^{31}P -MRSI challenges

Despite the promising potential of ^{31}P -MRSI in brain cancer, its clinical application remains limited by the variability in study designs and inconsistent findings across different studies.

A challenge with ^{31}P MRSI is the inherently low signal-to-noise ratio resulting from the relatively low gyromagnetic ratio and the low concentration of phosphorus-containing metabolites. This necessitates large voxel sizes that may introduce partial volume effects where tissue boundaries, such as those around tumors, span multiple voxels, Figure 2.3 [39, 22]. This leads to a mixture of metabolic signals from the tumor and adjacent normal tissue [40].

Reducing voxel size improves spatial resolution thus minimizing the partial volume effect, but it requires increased field strength or prolonged acquisition times. As an alternative, post-processing techniques, such as k-space phase correction and interpolation-based re-gridding, can mitigate these effects [41].

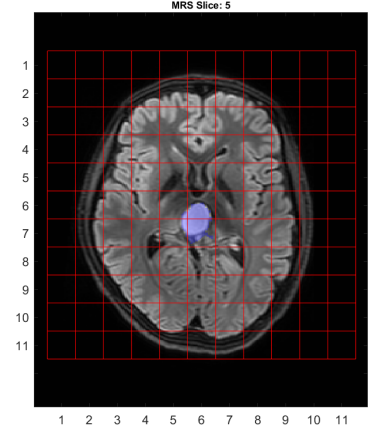


Figure 2.3: Pediatric brain MRI showing a tumor (purple) and a ^{31}P -MRSI grid (red). The tumor spans two voxels, leading to a partial volume effect where each voxel contains signals from both tumor and normal brain tissue.

Experiment

3.1. Introduction

Post processing methods can be used to recalculate ^{31}P -MRSI data. A challenge with ^{31}P -MRSI is the inherently low signal-to-noise ratio due to a relatively low gyromagnetic ratio, and a low concentration of phosphorus-containing metabolites in tissues necessitating large voxel sizes [39]. These larger voxel sizes may introduce a partial volume effect where tissue boundaries, such as those around tumors, span across multiple voxels, leading to a mixture of metabolic signals from tumor and adjacent normal tissues [42]. To address this, post-processing methods can help to realign the MRSI grid to align more precisely with tissue structures. Here we evaluate two methods to recalculate the spatial position of the MRSI signal (1) k-space domain based phase adjustment, and (2) spatial domain based spectral interpolation in a phantom model.

Aim

This experiment examines two post-processing regridding methods —k-space-based using phase-encoding adjustment and spatial-based using linear interpolation— to reduce partial volume effects in ^{31}P -MRSI.

3.2. Methods

Phantom experiments were performed on a 7 Tesla MRI scanner (Achieva, Philips Healthcare, The Netherlands) to assess two post-processing techniques for regridding. The scan parameters are provided in Table 3.1. A spherical phantom containing a bead with 200 mM inorganic phosphate (Pi) was used. Seven datasets were acquired, two references with different resolutions, and five datasets where the grid was repositioned at a shifted location compared to the reference:

1. Reference:

Table 3.1: Scan parameters for a phantom experiment to assess two regridding techniques with FID=Free Induction Decay, MRSI=Magnetic Resonance Spectroscopic Imaging, TR= Repetition Time, TE=Echo Time, NSA=Number of Single Averages

Scan Parameters	Image Sequence	Coil	Acquisition pattern	TR	TE	Flip angle	Matrix size	Voxel size	NSA
Normal resolution	3D-FID-MRSI sequence	Custom quadrature TxRx 1H/31P head coil	Hamming-weighted k-space acquisition	100 ms	0.42 ms	11.4°	11x11x9	20x20x20mm ³	28
Higher resolution	3D-FID-MRSI sequence	Custom quadrature TxRx 1H/31P head coil	Hamming-weighted k-space acquisition	100 ms	0.42 ms	11.4°	12x9x12	10x10x10mm ³	20

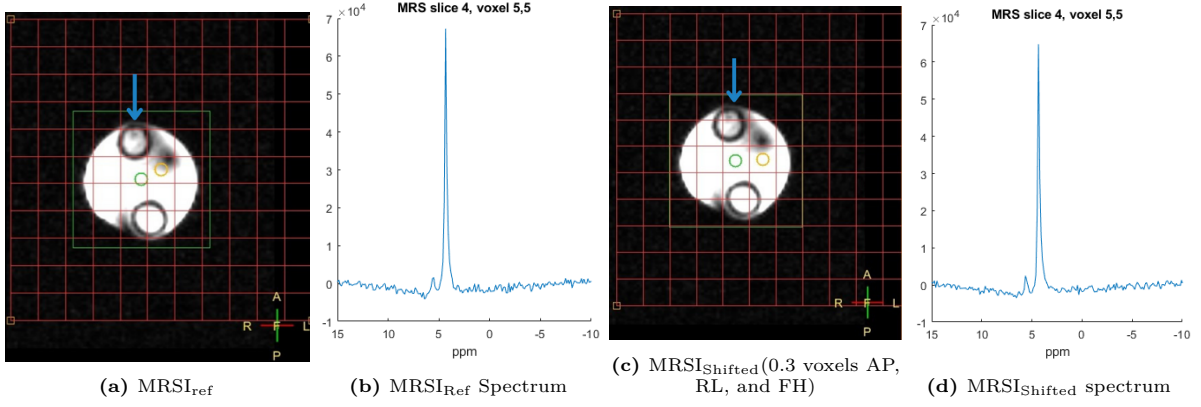


Figure 3.1: Phantom with the inorganic phosphate (Pi) bead, annotated with the arrow, and the MRSI grid superimposed for MRSI_{Ref} where the Pi bead is entered inside a voxel (A) and for (B) $\text{MRSI}_{\text{Shifted}}$ where the grid is shifted 0.3 voxel in Anterior-Posterior (AP), Right-Left (RL), and Feet-Head (FH) directions. For both cases, the ^{31}P spectrum of the MRSI voxel containing the Pi bead is displayed as well.

- (a) **MRSI_{Ref} :** The MRSI grid was positioned so that a voxel was centered on the Pi bead along the anterior-posterior (AP), left-right (LR) and feet-head (FH) axes (Figure 3.1a) for two different resolutions: $20 \times 20 \times 20 \text{ mm}^3$, and $10 \times 10 \times 10 \text{ mm}^3$.

2. Shifted Datasets:

- (a) **$\text{MRSI}_{\text{Shifted}}$:** The MRSI grid from MRSI_{Ref} was shifted in the AP, LR, and/or FH directions, simulating misalignment (Figure 3.1c). Four different grid configurations were acquired for the low resolution: shift of 0.3 voxels (i.e., 6 mm) in the AP, RL, and FH directions, shift of 0.3 voxels (i.e. 6 mm) in the RL direction, shift of 0.1 voxels (i.e. 2 mm) in AP direction, shift of 0.5 voxels (i.e. 10 mm) in FH direction. One shifted grid configuration was acquired for the high resolution: shift of 0.3 voxels (i.e., 6 mm) in the AP, RL, and FH directions.

Two post-processing methods were implemented to recalculate the spatial position of the MRSI signal so that the positions of the voxel coincide more closely with the region of interest and applied to $\text{MRSI}_{\text{Shifted}}$. The first method is based on the shift theorem [40]. A phase shift, $e^{-i\Delta r k}$ is applied to the k-space data, $f(k, t)$ in different directions (AP, RL and/or FH) prior to the Fourier transformation, $F(r, t)$ where Δr represents the spatial shift and k represents a spatial location in the grid (equation 3.1) [40].

$$F(r + \Delta r_{AP}, \Delta r_{RL}, \Delta r_{FH}, t) = FT \left[f(k_{AP}, k_{RL}, k_{FH}, t) e^{i(\Delta r k_{AP}, \Delta r k_{RL}, \Delta r k_{FH})} \right] \quad (3.1)$$

The second method is a linear interpolation of the spectral data in the spatial domain, equation 3.2. For this technique, frequency and phase alignment of the MRSI data across voxels was performed prior to interpolation. Linear interpolation is used to estimate the value of spectral data in a shifted location $(r + \Delta r, t)$ by taking a weighted average (equation 3.3, where f is the fractional shift) of a spectral data point (r, t) and its spatial neighbor.

$$F(r + \Delta r_{AP}, \Delta r_{RL}, \Delta r_{FH}, t) = \sum_{a=0}^1 \sum_{b=0}^1 \sum_{c=0}^1 w_{abc} F(r_{i+a}, j+b, k+c, t) \quad (3.2)$$

$$w_{abc} = (1 - a + (-1)^a f_{AP})(1 - b + (-1)^b f_{RL})(1 - c + (-1)^c f_{FH}) \quad (3.3)$$

The recalculated MRSI datasets are referred to as $\text{MRSI}_{\text{PhaseShift}}$ and $\text{MRSI}_{\text{Interpolated}}$, respectively.

^{31}P -MRSI data were reconstructed using custom MATLAB software with the pipeline described in Appendix B. The Pi signal was fitted as a single Lorentzian line-shape peak with AMARES [43]. The fitted area under the curve (AUC) of the Pi peak of $\text{MRSI}_{\text{Shifted}}$, $\text{MRSI}_{\text{PhaseShift}}$, and $\text{MRSI}_{\text{Interpolated}}$

Table 3.2: Correlation coefficients for ^{31}P -MRSI post-processing techniques— $\text{MRSI}_{\text{phase shift}}$ and $\text{MRSI}_{\text{interpolated}}$ —are presented for conventional and high-resolution data. Four grid shift configurations were applied: a shift of 0.3 in the anterior–posterior (AP), right–left (RL), and feet–head (FH) directions, and individual shifts of 0.3 (RL), 0.1 (AP), and 0.5 (FH).

Correlation coefficient	0.3 AP, RL, FH	0.3 RL	0.1 AP	0.5 FH
$\text{MRSI}_{\text{phase shift}}$	0.960	0.960	0.963	0.960
$\text{MRSI}_{\text{phase shift high resolution}}$	0.915			
$\text{MRSI}_{\text{interpolated}}$	0.939	0.957	0.958	0.954
$\text{MRSI}_{\text{interpolated high resolution}}$	0.935			

was compared voxel-wise to the AUC of MRSI_{Ref} with Pearson’s correlation coefficient. The correlation coefficients were interpreted as follows[44]: <0.5 indicates a weak correlation, $0.5\text{--}0.7$ moderate, $0.7\text{--}0.9$ strong, and >0.9 excellent.

3.3. Results

Figure 3.2 (large voxel) and 3.3 (small voxel) display heatmaps for MRSI_{Ref} and the results after correcting $\text{MRSI}_{\text{shifted}}$, which was repositioned with 0.3 voxels in the AP, RL, and FH direction, (i.e., $\text{MRSI}_{\text{PhaseShift}}$ and $\text{MRSI}_{\text{Interpolated}}$). The heatmaps for all the different grid positions can be found in Appendix C. For all grid positions, phase adjustment in k-space ($\text{MRSI}_{\text{PhaseShift}}$) yielded values closer to MRSI_{Ref} compared to spectral interpolation ($\text{MRSI}_{\text{Interpolated}}$). The correlation coefficients for the AUC between the shifted spectra and MRSI_{Ref} can be found in Table 3.2, demonstrating an excellent correlation (>0.9) for both methods. However, k-space phase adjustment consistently yielded higher agreement with MRSI_{Ref} . The full width at half maximum (FWHM) of the shifted spectra was similar to MRSI_{Ref} .

3.4. Discussion

This study evaluated two post-processing MRSI-regridding methods —k-space domain based using phase-encoding adjustment and spatial domain based using linear interpolation—to address partial volume effects in ^{31}P -MRSI. Both techniques demonstrated strong correlations with the baseline; however, k-space phase adjustment performed better compared to spatial interpolation, evidenced by higher correlations and more accurate peak intensities in voxels near the Pi bead. The lower peak intensities at interpolation are probably due to signal averaging around the peak that diminishes peak height.

Alternatively, interpolation could have been applied to the AUC maps after peak fitting, rather than directly to the spectra, potentially yielding different results. Neither regridding technique achieved a perfect correlation of 1 with the baseline, which was not expected, as repeated ^{31}P acquisitions on the same scanner can exhibit measurement variability. In a previous study on the repeatability of ^{31}P -MRSI in the healthy brain at 7T, the covariance for Pi was 16.2% [45].

In the small-voxel image, both post-processing techniques resulted in higher AUC deviations from the reference compared to the large-voxel images. However, these images exhibited higher noise, which could have arisen due to differences in scan parameters such as the number of single averages.

Although the phantom experiment allowed for controlled comparisons between true and post-processed regridding, it may not fully reflect the complexity of in vivo tumor imaging, where heterogeneous tissue characteristics can impact spectral properties. In the future, the focus should be on implementing the k-space phase adjustment method in clinical data.

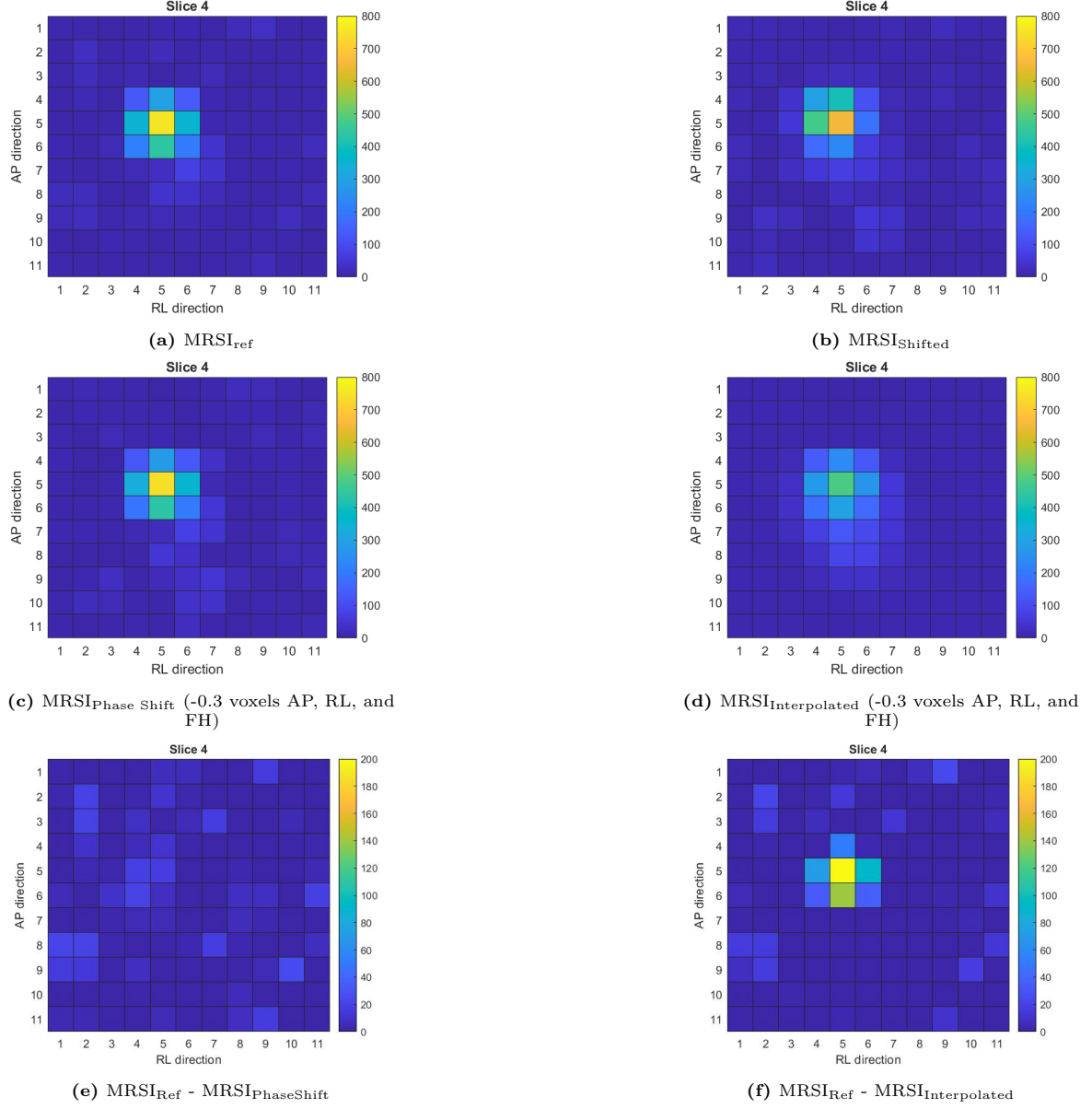


Figure 3.2: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment. Where (a) shows the AUC of MRSI_{ref} , (b) shows the AUC of $\text{MRSI}_{\text{shifted}}$, (c) shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.3 voxels in the Anterior-Posterior (AP), Right-Left (RL), and Feet-Head (FH) directions ($\text{MRSI}_{\text{Phase Shift}}$), (d) shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.3 in AP, RL, and FH direction ($\text{MRSI}_{\text{interpolated}}$), (e) and (f) depict the differences between the shifted AUCs and the MRSI_{ref} for k-space phase adjustment and spatial-based interpolation, respectively.

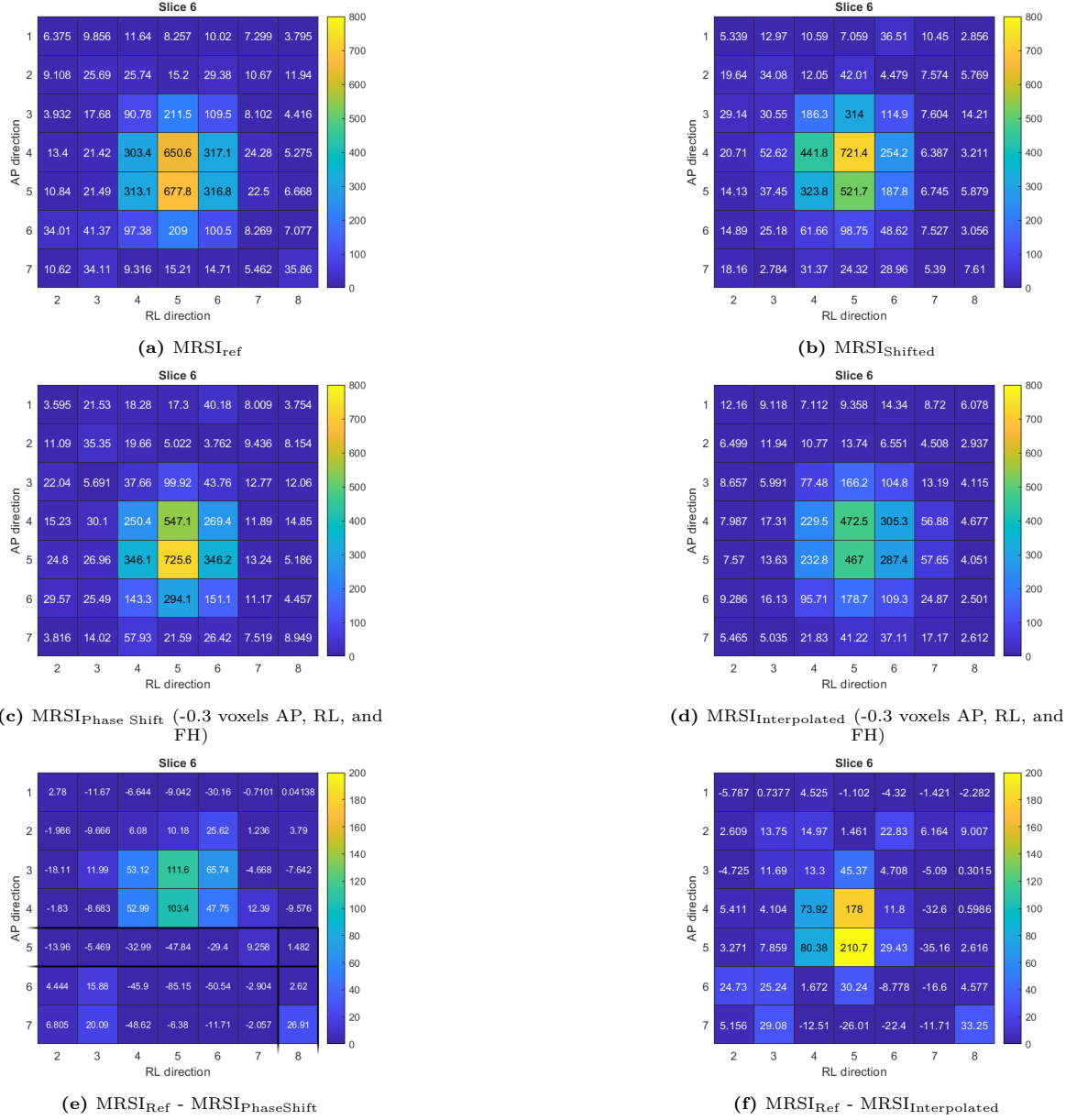


Figure 3.3: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment with the higher resolution voxels. Where (a) shows the AUC of MRSI_{Ref} , (b) shows the AUC of $\text{MRSI}_{\text{shifted}}$, (c) shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.3 voxels in the Anterior-Posterior (AP), Right-Left (RL), and Feet-Head (FH) directions ($\text{MRSI}_{\text{Phase Shift}}$), (d) shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.3 in AP, RL, and FH direction ($\text{MRSI}_{\text{Interpolated}}$), (e) and (f) depict the differences between the shifted AUCs and the MRSI_{Ref} for k-space phase adjustment and spatial-based interpolation, respectively.

4

Regridding in vivo

4.1. Introduction

As established in chapter 3, ^{31}P -MRSI data can be spatially shifted during post-processing by k-space phase adjustment [42]. Optimizing the spatial location of the grid can enhance tumor content within a voxel and reduce partial volume effects, thus improving the accuracy of metabolic analysis. However, this has not yet been evaluated in in-vivo data.

This study assesses k-space phase adjustment in vivo, using data from the Metabolic Imaging of Tumors in Children (MITCH) study. The MITCH study focuses on metabolic imaging of pediatric brain tumors using 7T MRI. Two different coils are used for metabolic imaging: a custom quadrature TxRx $^1\text{H}/^{31}\text{P}$ head coil, specifically designed to acquire ^{31}P -MRSI data, and a Multix Nova head coil, used to acquire amide proton transfer chemical exchange saturation transfer (APT-CEST), a high-resolution FLAIR, and a T1 image. The FLAIR and T1 images serve as an anatomical reference for tumor delineation. Due to patient repositioning between acquisitions, image registration is required to align the different datasets.

Previous projects established methods for registering the low-resolution anatomical ^{31}P -MRSI image with the FLAIR image. However, no method has been developed to quantitatively determine the spatial shift required to maximize tumor coverage within a voxel or to calculate the percentage of tumor inclusion before and after regridding.

4.2. Aim

This study aims to evaluate regridding in k-space in in-vivo scans by: 1) determining the optimal spatial shift to improve tumor alignment within a voxel, 2) quantifying the percentage of tumor inclusion within a voxel before and after regridding, 3) assessing the impact of voxel shifting on the spectrum and metabolic ratio measurements in tumors and NAWM.

4.3. Methods

Twelve registered FLAIR images and ^{31}P -MRSI datasets from the MITCH study were used for regridding and metabolite analysis. Data were acquired using a 7 Tesla MRI scanner (Achieva, Philips Healthcare, The Netherlands). The scan parameters are provided in Table 4.1. Tumors were delineated on FLAIR images by a pediatric neuroradiologist with over ten years of experience using ITK-SNAP (v4.0.1). A control region in normal-appearing white matter (NAWM) was defined superior to the lesion, at least 2 cm away from the tumor, in an area without observable pathology.

The FLAIR grid overlay was used to determine the new grid position in the axial and sagittal views using custom Matlab software R2021a [46]. The exact code can be found in Appendix D. The new grid position was calculated by manually selecting the center of the tumor in the FLAIR image at the voxel with the highest tumor content. The $Displacement_{AP,RL,FH}$ between the center of the tumor

Table 4.1: Scan parameters for the in-vivo protocol to acquire 31-Phosphorus Magnetic Resonance Spectroscopic Imaging (^{31}P -MRSI) data with FID=Free Induction Decay, TR= Repetition Time, TE=Echo Time, NSA=Number of Single Averages

Image Sequence	Coil	Acquisition pattern	TR	TE	Flip angle	Matrix size	Voxel size	NSA
3D-FID-MRSI sequence	Custom quadrature TxRx 1H/ ^{31}P head coil	Hamming-weighted k-space acquisition	100 ms	0.42 ms	11.4°	11x11x9	20x20x20mm ³	28

TumorCenter and the center of the nearest MRSI voxel, *VoxelCenter* was calculated for each direction Anterior-Posterior (*AP*), Right-Left (*RL*), and Feet-Head (*FH*) using equation 4.1.

$$Displacement_{AP,RL,FH} = \frac{(TumorCenter - VoxelCenter)_{AP,RL,FH}}{ResolutionMRSI_{AP,RL,FH}} \quad (4.1)$$

The displacement values were initially determined in the resolution of the FLAIR image and converted to the MRSI resolution. The selection process was iterated until a satisfactory tumor voxel alignment was achieved.

Spectral quality was assessed by the SNR, defined as signal amplitude of PCr divided by the standard deviation of the noise, full width at half maximum (FWHM) of the PCr peak, and the presence of artifacts. Spectra were excluded if the FWHM>25Hz, the SNR<10 or if there were large artifacts assessed by an expert.

^{31}P -MRSI data were and frequency corrected using custom MATLAB software, which fitted the PCr signal as a single Lorentzian peak with AMARES [43]. The spectrum was subsequently corrected with the fitted frequency and phase offset before performing a full AMARES fit for the following metabolites: PCr, ATP, nicotinamide adenine dinucleotide (NAD), GPC, GPE, PC, PE, inorganic phosphate (Pi), extracellular Pi (ePi), uridine di-phosphoglucose (UDPG), membrane phospholipids (MPL), and diphosphoglycerate (DPG).

The following metabolic ratios were calculated for analysis: PE/GPE (cell membrane metabolism), PCr/ γ ATP (energetic state), pH (hypoxia), Pi/ATP (ATP turnover) [Appendix A]. A Wilcoxon signed rank test was performed to evaluate the significance between before and after regridding, with statistical significance set at $p<0.05$. A Pearson's correlation was performed to evaluate the correlation between metabolic change and the increase of tumor inside a voxel. The correlation coefficients were interpreted as follows[44]: <0.5 indicates a weak correlation, 0.5–0.7 moderate, 0.7–0.9 strong, and >0.9 excellent.

4.4. Results

One scan was excluded due to a low SNR (7.4) and excessive linewidth (46 Hz), leaving 11 scans for analysis. Before regridding, the average SNR was 56.78 ± 19.86 , and the average linewidth was 9.62 ± 2.83 Hz. After regridding, the average SNR was 58.78 ± 19.41 , and the average linewidth was 10.44 ± 4.39 Hz. Changes varied across scans, with SNR and linewidth either increasing, decreasing, or remaining unchanged depending on the scan.

Figure 4.1 presents an example of the initial and shifted grid positions for patient 891_{FU2}, along with the corresponding spectra for the tumor and NAWM voxels. The grid was shifted by 0.63 MRSI-voxel in the AP direction, -0.047 MRSI-voxel in the RL direction, and 0.34 MRSI-voxel in the FH direction. Table 4.4 summarizes the percentage of tumor inclusion within the voxel of interest before and after regridding. In all cases, regridding increased the tumor content within the voxel.

Figure 5.2 illustrates the metabolic ratios (PE/GPE, PCr/ γ ATP, and Pi/ATP) before and after regridding. Although regridding caused some changes in metabolite ratios, none were statistically significant.

The changes in metabolic ratios are plotted against the change in tumor volume in Figure 4.2. The correlation between changes in metabolic ratios and tumor content within the voxel was weak for

PCr/ATP (0.18), Pi/ATP (0.56), and PE/GPE (0.36), and moderate for pH (0.64).

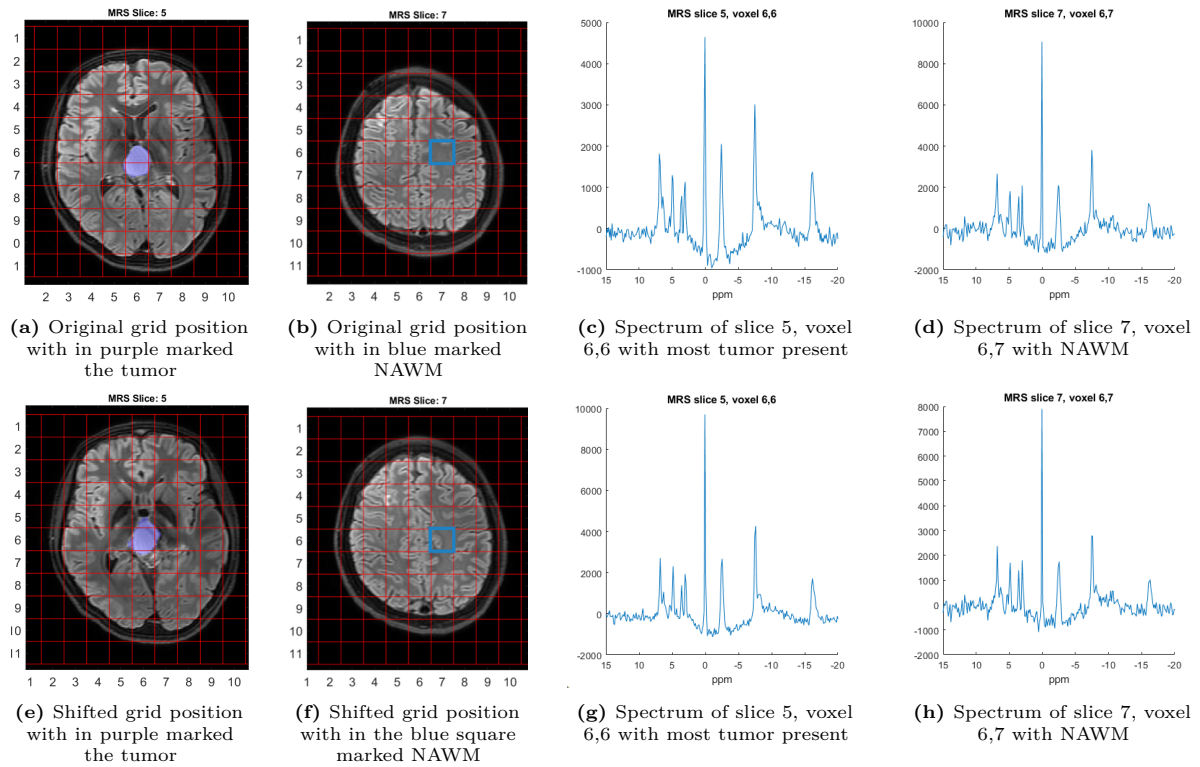


Figure 4.1: Grid position over the brain and normal-appearing white matter (NAWM), along with the corresponding ^{31}P -MRSI spectra before (a-d) and after (e-h) regridding. The tumor is marked in purple, and NAWM is marked in blue. Panels (c) and (g) show the spectrum from slice 5, voxel (6,6), where the tumor is most present. Panels (d) and (h) show the spectrum from slice 7, voxel (6,7), representing NAWM.

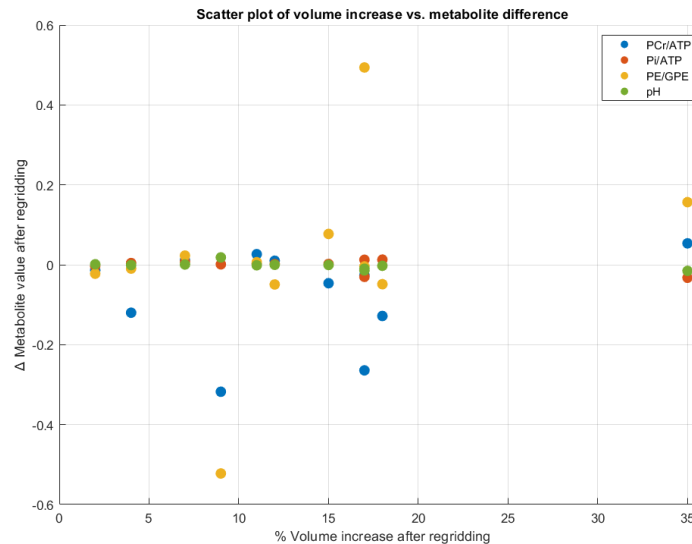


Figure 4.2: Scatter plot showing the relationship between tumor volume increase due to regridding (horizontal axis) and metabolic ratio changes after regridding (vertical axis) for phosphocreatine (PCr) to γ -adenosine triphosphate (ATP), inorganic phosphate (Pi) to ATP, phosphomonoesters (PE) to glycerophosphoethanolamine (GPE), and pH. No correlation is observed between the percentage increase in tumor volume and changes in metabolic ratios. Data points represent all patients at baseline, follow-up 1, and follow-up 2.

4.5. Discussion

A method was developed to reposition the grid to maximize tumor content within a voxel. This approach was applied to in vivo data, leading to changes in metabolic ratios (pH, PE/GPE, PCr/ γ ATP, Pi/ATP) in both tumor and NAWM. Increasing the tumor fraction within the voxel aimed to minimize partial volume effects. However, these effects were not entirely eliminated, as the tumor often remained smaller than the voxel size.

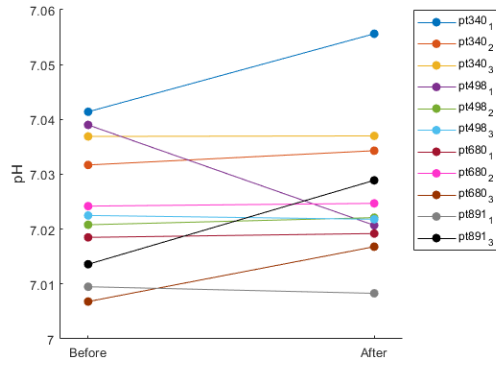
In addition to partial volume effects, other confounding factors influence metabolic ratios and spectral quality. B0 inhomogeneities introduce local variations in resonance frequency. These can be mitigated by shimming, which optimizes magnetic field homogeneity, or by applying localized B0 correction during post-processing [21]. Another factor is voxel bleeding, which results from the Fourier transformation properties described by the point spread function (PSF), leading to signal contamination from adjacent voxels [40]. Voxel bleeding can be eliminated using single-voxel spectroscopy or reduced by increasing phase encoding steps. K-space weighting and filtering (e.g., a Hamming filter already applied in this study) further minimize its impact [47].

Spectral quality, assessed by noise levels and linewidth, remained largely unchanged after regridding, suggesting no significant spectral degradation.

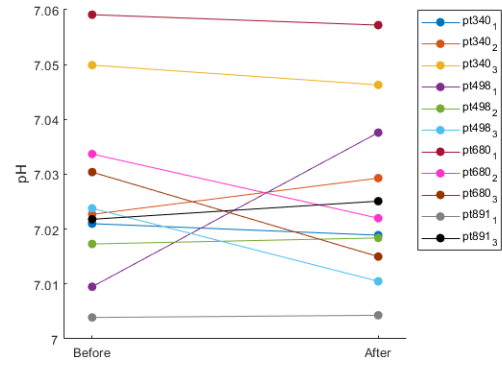
Metabolic changes before and after regridding showed a weak to moderate correlation with the increase in tumor volume in the voxel.

Chapter 3 demonstrated that k-space regridding is possible in phantom data. Although metabolic ratios changed in vivo, their clinical significance remains uncertain due to the small sample size ($n=11$) and the lack of ground truth for tumor and NAWM metabolite levels. This limitation underscores the challenge of confirming the accuracy of voxel-shifting approaches in patient scans.

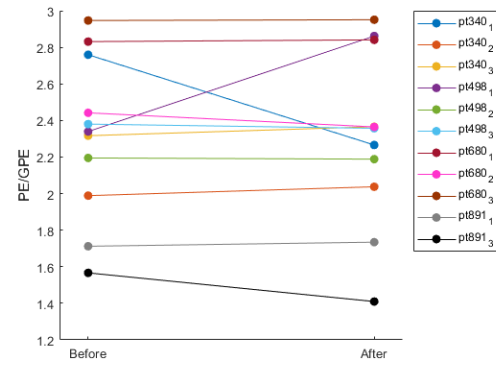
Future research should focus on systematically comparing the evolution of tumor and NAWM metabolic ratios in pediatric patients. Monitoring these metabolic changes could provide valuable insights into tumor biology and behavior. Expanding the cohort size will be crucial to further evaluate these metabolic changes.



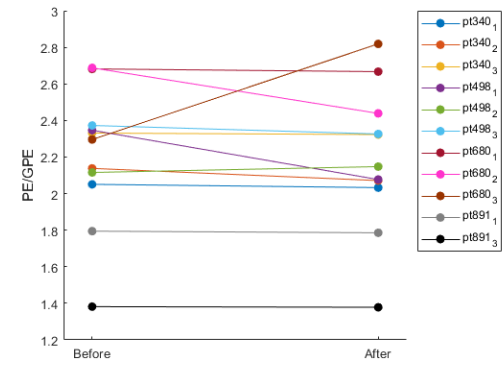
(a) pH in tumor before and after regriding, showing no significant differences ($p=0.25$)



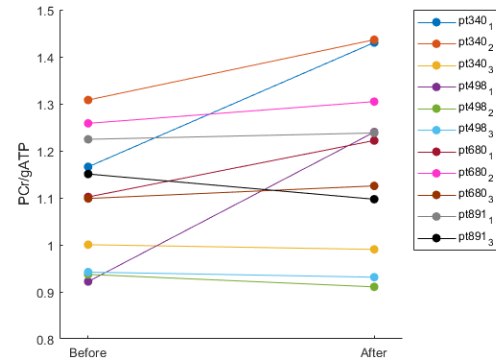
(b) pH in NAWM before and after regriding, showing no significant differences ($p=0.53$)



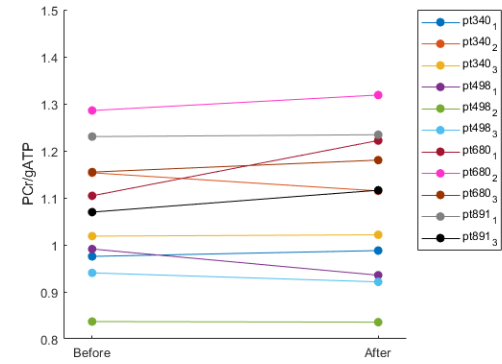
(c) PE/GPE in tumor before and after regriding, showing no significant differences ($p=0.93$)



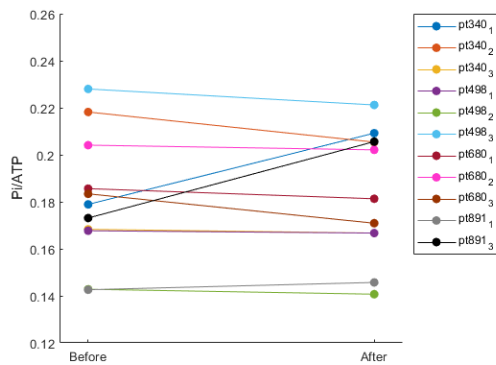
(d) PE/GPE in NAWM before and after regriding, showing no significant differences ($p=0.16$)



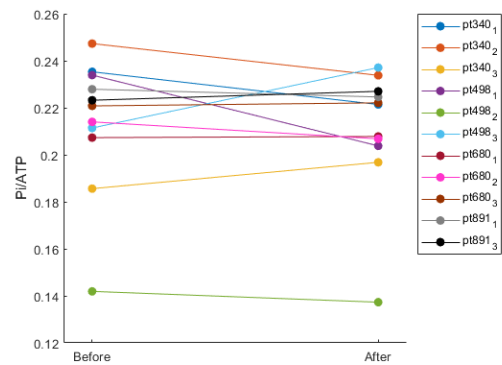
(e) PCr/γATP in tumor before and after regriding, showing no significant differences ($p=0.09$)



(f) PCr/γATP in NAWM before and after regriding, showing no significant differences ($p=0.42$)



(g) Pi/ATP in tumor before and after regriding, showing no significant differences ($p=0.53$)



(h) Pi/ATP in NAWM before and after regriding, showing no significant differences ($p=0.21$)

Figure 4.3: Metabolic ratios in tumor and normal-appearing white matter (NAWM) before and after regriding. The analyzed ratios include pH, phosphomonoesters to glycerophosphoethanolamine (PE/GPE), phosphocreatine to γ -adenosine triphosphate (PCr/γATP), and inorganic phosphate to ATP (Pi/ATP). No significant differences were observed before and after regriding ($p > 0.05$).

31P MRSI in clinical setting

5.1. Introduction

As mentioned in Chapter 1, we lack a tool to non-invasively identify tumor activity. ^{31}P -MRSI provides metabolic insight by detecting phosphorus-containing compounds involved in energy metabolism and cell membrane turnover, which are often dysregulated in malignant tumors [35, 38]. Key metabolic markers in ^{31}P -MRSI, focus on PE/GPE as indicators of membrane turnover, PCr/ATP to assess energy homeostasis, Pi/ATP as a marker of ATP turnover, and intracellular pH to reflect tumor microenvironment acidity. These parameters provide crucial information about tumor metabolism.

5.2. Aim

This study aimed to evaluate ^{31}P -MRSI metabolic ratios in pediatric patients with low-grade glioma over multiple time points to assess treatment response or monitor tumor progression in cases managed with a wait-and-scan approach. By analyzing metabolic changes over time, we sought to assess potential biomarkers for tumor progression and treatment response.

5.3. Methods

5.3.1. Patient Selection

For this study data was used from nine patients included in the MITCH study in which children (6-18 years old) diagnosed with a brain tumor underwent metabolic research scans in addition to their standard clinical imaging protocol. 7 Tesla MRI scans (Achieva, Philips Healthcare, The Netherlands) were performed at three time points: baseline (BL), follow-up 1 (FU-1), and follow-up 2 (FU-2). The baseline scan did not necessarily align with the diagnosis but was acquired at any point during the patient's oncological follow-up. During the research period, patients could receive chemotherapy, radiation therapy, or remain untreated.

This study was approved by the local ethics committee of the UMC Utrecht, and written informed consent was obtained from all patients and their legal guardians. Disease progression was assessed by a multidisciplinary tumor board consisting of at least one oncologist, neurologist, ophthalmologist, surgeon, and radiologist based on clinical and imaging findings. These specialists were blinded to the acquired ^{31}P -MRSI data.

5.3.2. ^{31}P -MRSI Acquisition

^{31}P -MRSI was acquired on a home-build quadrature TxRx $^{31}\text{H}/^{31}\text{P}$ head coil. The MRSI protocol employed a 3D chemical shift imaging (CSI) sequence with a matrix size of [11, 11, 9], a nominal isotropic resolution of $20 \times 20 \times 20 \text{ mm}^3$, a repetition time (TR) of 100 ms and a flip angle (α) of 11.4 degrees. Hamming-weighted k-space sampling was applied to improve the signal-to-noise ratio (SNR). The number of signal averages (NSA) was set to 28.

5.3.3. MRSI Data Processing and Quantification

³¹P MRSI datasets were processed and evaluated using in-house MATLAB software [46]. K-space regridding was performed according to the methods described in Chapters 3 & 4, focusing on the voxel with the largest tumor content. Spectral quantification was conducted in the time domain using a home-built MATLAB implementation of the AMARES algorithm [28]. Quantification was performed in two steps:

- Prefitting: Estimation of the local B_0 shift and zero-order phase correction (ϕ_0) by fitting the phosphocreatine (PCr) resonance as a singlet with a variable frequency range of $[-0.5, +0.5]$ ppm [28].
- Main Quantification: Performed on the phase-corrected MRSI dataset with frequency constraints adapted to the local B_0 estimated in the prefitting step. Residual phase errors were compensated by allowing ϕ_0 to vary within $[-0.09\pi, +0.09\pi]$ [28].

Twelve metabolites were quantified, including PCr, ATP, NAD, GPC, GPE, PC, PE, Pi, ePi, UDPG, MPL, and DPG. UDPG is a sugar nucleotide underlying PE and PC. It was modeled as a pseudo-doublet with a fixed frequency spacing of $\Delta f = 1.6$ ppm following methods described in [28].

Spectral quality was assessed by the SNR, defined as the signal amplitude of PCr divided by the standard deviation of the noise, FWHM of the PCr peak, and the presence of artifacts. Spectra were excluded if the FWHM > 25 Hz, the SNR < 10 , or if there were large artifacts assessed by an expert. Patients were excluded from the analysis if they had only one timepoint available for evaluation, as no metabolic change could be evaluated.

5.3.4. Tumor and Normal-Appearing White Matter (NAWM) Region of Interest (ROI) Analysis

Tumors were delineated on FLAIR images by a pediatric neuroradiologist with over ten years of experience using ITK-SNAP (v4.0.1). A control region in normal-appearing white matter (NAWM) was defined superior to the lesion, at least 2 cm away from the tumor ROI, in an area without observable pathology. The follow-up ROI was chosen at the same anatomical location as the baseline scan ROI.

5.3.5. Analysis

The following metabolic ratios were calculated for the analysis representing different processes: PE/GPE (cell membrane metabolism), PCr/ γ ATP (energetic state), pH (hypoxia), Pi/ATP (ATP turnover) [Appendix A]. To assess whether changes in tumor tissue differed from those in NAWM, relative metabolite ratios were calculated. For each patient, the metabolite value in the tumor voxel at each time point was divided by the corresponding NAWM voxel value. To focus on changes over time, these ratios were further normalized to their baseline value. Metabolite ratios between the tumor and NAWM ROIs were compared. Changes between consecutive time points were analyzed separately for progressors and non-progressors. Comparisons between metabolic ratios of tumors and NAWM were performed using the Wilcoxon signed-rank test, accounting for the non-independence of paired measurements. A significance threshold of $p < 0.05$ was applied.

5.4. Results

Eight patients (six males and two females) with a median age of 7 years were included in this study, patient information can be found in Table 5.1. Two spectra were excluded because of low SNR and large linewidth, leading to the exclusion of one patient because it had only one timepoint available for evaluation. Patient characteristics are summarized in Table 5.1. All patients had a low-grade glioma (LGG), including optic pathway glioma, pilocytic astrocytoma, and diffuse leptomeningeal glioneuronal tumor (DLGNT). The treatment regimens at each time point are detailed in Table 5.2.

Four patients completed the full follow-up, while four had data available only for baseline and the first follow-up. One patient did not receive treatment throughout the study, while the remaining patients underwent various chemotherapy regimens, including bevacizumab, irinotecan, vincristine, and carboplatin.

In patients 340, 498, 224, and 962, the tumor volume within the analyzed voxel remained below 52%. The average metabolic values and their standard deviation for tumors and NAWM in all scans are

Variable	n
Total Patients	8
Age (years)	
Median	7
Range	6-14
Sex	
Male	6
Female	2
Tumor Type	
Low-Grade Glioma	8
Histological Subtype	
Optic Pathway Glioma	5
Pilocytic Astrocytoma	2
Diffuse Leptomeningeal Glioneuronal Tumor	1
Tumor Location	
Optic Chiasm	4
Optic Chiasm + Basal Ganglia + Thalamus + Brainstem	1
Mesencephalon	1
Right Mesiotemporal Lobe	1
Supratentorial and Infratentorial Regions	1

Table 5.1: Summary of patient demographics, including total number of patients, median and range of age, sex distribution, tumor type, histological subtype, and tumor location.

Patient	Baseline (BL)		First Follow-up (FU1)		Second Follow-up (FU2)	
	Treatment at time of the scan	% Tumor volume	Treatment at time of the scan	% Tumor volume	Treatment at time of the scan	% Tumor volume
340	Bevacizumab + irinotecan	27	Bevacizumab + irinotecan	30	Bevacizumab	18
498	Vincristine + carboplatin	13	Vinblastine + bevacizumab	20	Vinblastine + bevacizumab	15
680	No treatment	93	Vinblastine	89	Vinblastine	87
891	No treatment	74	-	-	No treatment	81
162	No treatment	67	Vinblastine	59	Vinblastine	72
224	Bevacizumab	51	Bevacizumab	46	Bevacizumab	-
276	Vinblastine	94	Vinblastine	95	-	-
962	Vincristine + carboplatin	40	Vincristine + carboplatin	45	-	-

Table 5.2: Overview of patient treatments and tumor volume progression at different time points. Treatments administered at the time of each MRI scan are listed along with the percentage of the voxel occupied by the tumor at baseline (BL), first follow-up (FU1), and second follow-up (FU2). Missing values indicate unavailable data.

summarized in Table 5.3. No significant differences were observed between tumors and NAWM for all metabolites.

5.4.1. Tumor metabolite ratios

Figure 5.2 illustrates the changes in the metabolite ratios for tumor and NAWM—pH (a-b), PE/GPE (d-e), PCr/ γ ATP (g-h), and Pi/ATP (j-k)—at different time points for each patient. Panels (c-f-i-l) show normalized differences relative to NAWM and baseline. The multidisciplinary board conclusions are color-coded: red for disease progression, green for response to therapy, and orange for stable disease.

At baseline, three patients (498, 680, and 162) showed progression, leading to a therapeutic switch to vinblastine, with additional bevacizumab for patient 498. Following treatment adjustments, these patients remained stable. During follow-up, minimal pH changes were observed. PE/GPE initially decreased but later increased, PCr/ γ ATP remained largely stable, and Pi/ATP showed minimal changes. When normalizing tumor metabolite changes to NAWM and baseline, no consistent metabolic changes were observed across these patients.

Among patients with stable or responding disease at baseline, treatment regimens remained unchanged. One patient (340) responded to bevacizumab and irinotecan at FU-1, showing decreased pH and PE/GPE, while PCr/ γ ATP and Pi/ATP remained stable, also reflected in the relative NAWM-normalized changes.

Disease progression was observed in two patients (340 and 276) at FU-2 and FU-1, respectively. In both cases, pH and PE/GPE increased, while PCr/ γ ATP and Pi/ATP decreased. The absolute metabolic changes for patient 340 were Δ pH = 0.0027, Δ PE/GPE = 0.33, Δ PCr/ γ ATP = -0.45, and Δ Pi/ATP = -0.034, while for patient 276, these changes were: Δ pH = 0.034, Δ PE/GPE = 0.36, Δ PCr/ γ ATP = -0.23, and Δ Pi/ATP = -0.015. When normalizing tumor metabolite changes to NAWM and baseline, pH

	pH	p	PE/GPE	p	PCr/ γ ATP	p	Pi/ATP	p
Tumor	6.999 ± 0.105		2.115 ± 0.434		1.156 ± 0.214		0.191 ± 0.052	
NAWM	7.021 ± 0.016	0.18	2.098 ± 0.354	0.74	1.105 ± 0.167	0.79	0.212 ± 0.032	0.08

Table 5.3: Metabolite ratios and pH values for tumor and normal-appearing white matter (NAWM). Values are presented as mean \pm standard deviation over all patients and timepoints. p-values are calculated between tumor and NAWM, none showed statistical significance ($p < 0.05$)

remained the only consistent trend in these patients. Patient 276, diagnosed with DLGNT, continued to progress rapidly after FU-1 and could not complete the study due to disease-related mortality.

5.4.2. NAWM metabolite ratios

In patient 891, who did not receive therapy, NAWM showed an increase in pH, a decrease in PE/GPE and PCr/ γ ATP, and stable Pi/ATP levels. When tumor metabolite changes were normalized to NAWM, no additional consistent metabolic changes emerged.

Among the two patients who exhibited disease progression, metabolic alterations in NAWM mirrored those in the tumor, leading to inconsistent relative differences. One patient switched to bevacizumab after discontinuing irinotecan before progression, while the other continued with vinblastine.

No clear metabolic trends in metabolite changes emerged across different therapy types. The most stable NAWM metabolite ratio was PCr/ γ ATP.

5.5. Discussion

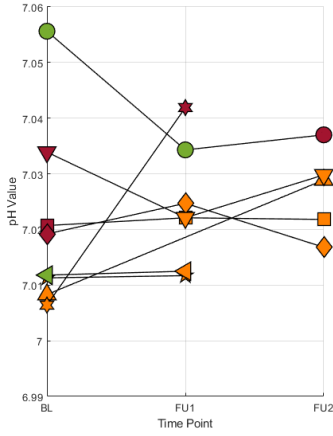
This study investigated metabolic changes in pediatric LGG's over time using ^{31}P -MRSI, focusing on tumor response to therapy and potential biomarkers of disease progression. Our findings highlight metabolic alterations in tumors and NAWM, however no trends in metabolite changes were observed when normalizing tumor metabolic ratios to their NAWM.

5.5.1. Metabolic Alterations in Tumor and NAWM

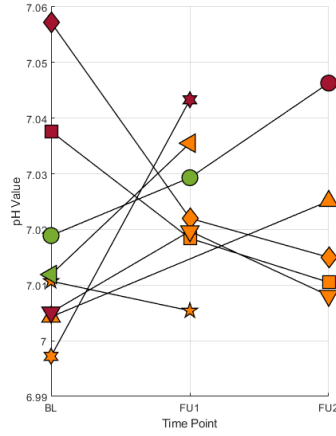
Tumor comparison was challenging due to anatomical variations and differences in treatment regimens. In half of the patients, the tumor was smaller than an MRSI voxel, and even after regridding, it did not fully occupy the MRSI voxel. This led to partial volume effects, where tumor and NAWM signals were mixed, complicating the interpretation of metabolic changes.

The two patients with disease progression exhibited similar metabolic alterations, including increased energy metabolism (pH and Pi/ATP), reduced ATP synthesis (PCr/ γ ATP), and altered phospholipid turnover (PE/GPE). Furthermore, patients with stable disease or response to therapy showed a decrease in phospholipid turnover (PE/GPE) and stable ATP levels (PCr/ γ ATP). These changes align with previous studies on the effects of therapy on phosphorus metabolites in brain tumors [33, 36, 37]. However, none of the changing metabolic ratios remained consistent after normalization to NAWM and baseline, suggesting that they may reflect normal biological variation, incidental findings, or treatment effects that influence both tumor and NAWM metabolism.

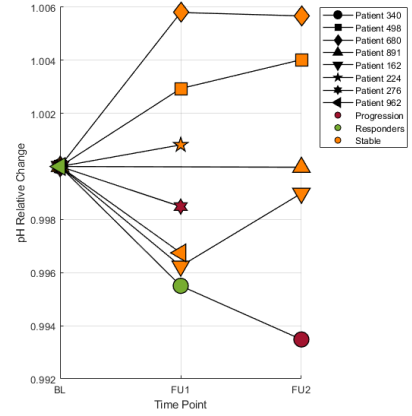
To determine whether the observed metabolic changes fall within the expected biological range, we compared our findings with values reported in the literature. While reference values for adult NAWM are available, data for the pediatric population remain limited. However, pediatric comparisons are essential, as Raz et al. [48] reported significant metabolic differences between children and adults at 3T. The study included 48 children (age 10.6 ± 2.4) and 80 adults (age 69.1 ± 7.3) and they found significantly higher PME, γ ATP, and pH levels in children compared to adults, while PDE and Pi levels were lower. A study by Albers et al. [49] provided absolute values, acquired with a 1.5T MRI scanner, for eight patients (age 7.4 ± 5.1) with aggressive tumors (e.g., primitive neuroectodermal tumors, ependymoma, anaplastic astrocytoma) and six healthy controls (age 6.3 ± 5.3):



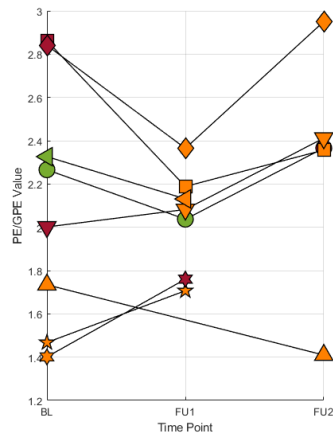
(a) pH in tumor over time



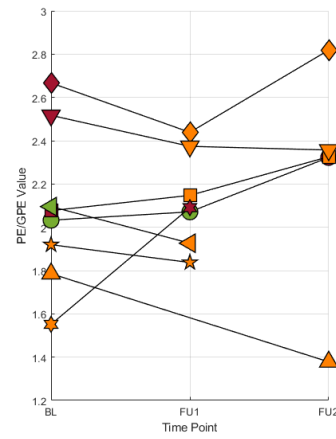
(b) pH in NAWM over time



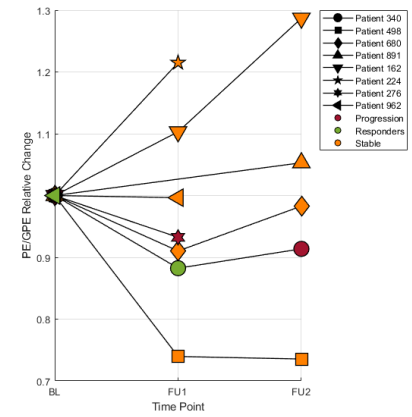
(c) pH tumor relative change



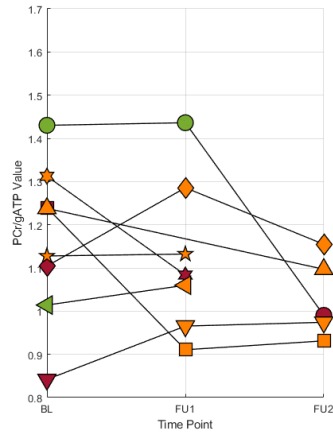
(d) PE/GPE in tumor over time



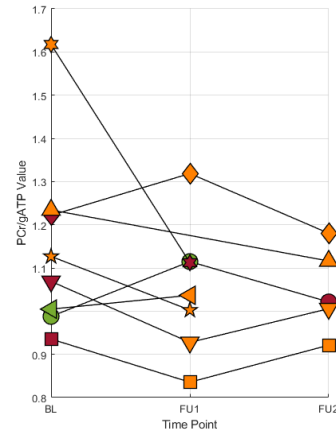
(e) PE/GPE in NAWM over time



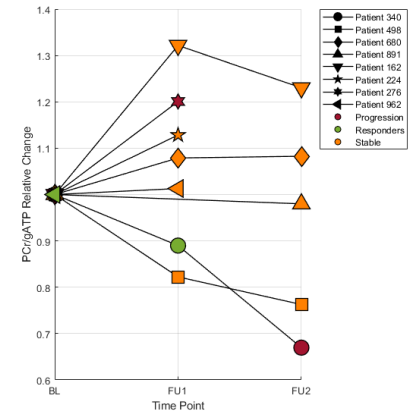
(f) PE/GPE tumor relative change



(g) PCr/γATP in tumor over time



(h) PCr/γATP in NAWM over time



(i) PCr/γATP tumor relative change

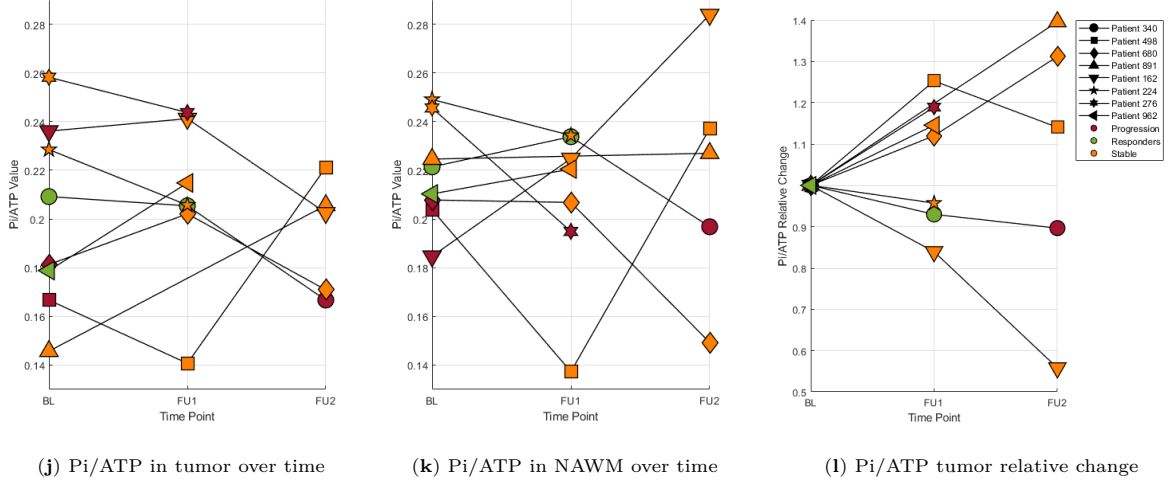


Figure 5.2: Longitudinal changes in tumor and normal appearing white matter (NAWM) metabolism and the relative tumor changes normalized to NAWM for pH (a-c) PE/GPE (d-f) PCr// γ ATP (g-i). The multidisciplinary board conclusions are color-coded: red indicates disease progression, green indicates a response to therapy, and orange represents a stable scan.

- **Tumors:** PCr/ATP = 1.22 ± 0.54 , PE/GPE = 9.23 ± 7.78 , Pi/ATP = 0.39 ± 0.14 , pH = 7.06 ± 0.03 .
- **NAWM healthy controls:** PCr/ATP = 2.07 ± 0.17 , PE/GPE = 3.42 ± 1.62 , Pi/ATP = 0.40 ± 0.14 , pH = 6.98 ± 0.03 .

The differences between tumor and NAWM in the literature and in our data are small, with large confidence intervals. In our study, tumor and NAWM values fall largely within the standard deviation of pediatric NAWM, except for Pi/ATP, which was slightly lower. Similarly, Novak et al. [25] found slightly lower Pi/ATP values in both tumor and NAWM in three patients with LGG. Given that pediatric LGGs are slow-growing and have a favorable prognosis, with a 10-year survival rate exceeding 95% [1], their metabolic profile may not differ substantially from NAWM, supporting the hypothesis that observed metabolic differences may not exceed normal inter-individual variation.

Furthermore, normalizing the metabolic ratios of the tumor to NAWM did not yield distinct differences, raising the question whether the treatment has an effect on both the tumor and NAWM. Previous studies in adults indicate that therapies such as temozolomide and bevacizumab affect phosphorus metabolites in NAWM [36, 50, 37], potentially contributing to the observed variability. In our study, metabolic changes in NAWM were detected in both treated and untreated patients. In patients with tumor progression, NAWM metabolic alterations resembled those in tumor tissue, leading to inconsistent relative differences. No clear metabolic changes were associated with specific therapies, which could be due to the small sample size and the distinct molecular targets of treatments in this cohort. The therapies studied pathways related to angiogenesis, DNA synthesis, and cell division [51], which may explain the absence of a uniform metabolic response across patients.

Finally, another consideration is the repeatability of ^{31}P -MRSI at 7T in vivo. Lagemaat et al. [45] assessed the within-session reliability of a 3D- ^{31}P -MRSI sequence in healthy adults and reported coefficients of variation for different metabolites and brain regions reporting coefficients of variation of <6% for PCr and ATP, <12% for PE, GPE, and GPC, and <20% for PC and PE [45]

5.5.2. Clinical Implications and Future Directions

Patient 680 exhibited metabolic changes similar to those observed in progressive cases, including increased PE/GPE and decreased PCr/ γ ATP and Pi/ATP at FU-2, along with slight tumor growth on clinical imaging. However, the multidisciplinary tumor board classified the patient as stable, as no neurological or visual deterioration was observed. This underscores that tumor growth and metabolic alterations alone may not be sufficient indicators of disease progression when assessed in a clinical context, where functional measures such as vision, motor function, reflexes, coordination, sensation, and

gait pattern are also considered [11].

The metabolic changes observed in this study warrant further investigation as potential biomarkers for disease monitoring. Early metabolic alterations in tumors could aid in treatment planning. If an early biomarker were identified for progression, it could justify initiating treatment before clinical symptoms emerge. However, given the subtlety of metabolic changes and their overlap with normal NAWM variation, the clinical feasibility of such an approach remains uncertain.

Higher-grade gliomas may provide a better model for identifying metabolic differences, as these tumors are metabolically more active they might exhibit more pronounced metabolic alterations [49]. However, the clinical impact of these findings is uncertain. In high-grade tumors, treatment decisions are often guided by the aggressive nature of the disease, and additional metabolic biomarkers may not substantially change clinical management.

Distinguishing between different pediatric brain lesions, such as LGGs, germinomas, or neurofibromatosis type 1 (NF1)-associated lesions, remains a challenge in pediatric radiology. It would be highly valuable if metabolic information from ^{31}P -MRSI could aid in this distinction, potentially reducing the need for invasive biopsies, particularly in cases where surgical intervention poses significant risks.

Similarly, differentiating between active tumor growth and treatment-related effects, such as pseudoprogression or radiation necrosis, is a major challenge in pediatric radiology. More non-invasive methods to assess tumor viability would be highly beneficial, as distinguishing viable tumor tissue from post-treatment changes has significant implications for therapy planning and prognosis. More research is needed to determine whether phosphorus metabolites could provide useful markers in this context.

Imaging was conducted on a 7T MRI scanner, providing high spectral and spatial resolution that is not typically available in clinical settings. While this limits the immediate clinical applicability, it also allows for the most detailed metabolic assessment currently possible. If successful, these findings could inform future studies exploring the feasibility of translating this approach to more widely available 3T scanners.

5.5.3. Limitations

This study has some limitations. The small sample size limits the generalizability of the findings, and the relatively large voxel size increases the likelihood of partial volume effects. Additionally, only a single MRSI voxel was analyzed for NAWM, making it susceptible to contamination of other structures. Future studies could improve accuracy by averaging metabolic values across multiple white matter MRSI voxels for a more representative measure of NAWM metabolism.

5.6. Conclusion

This study found metabolic changes in pediatric low-grade gliomas and normal appearing white matter over time using ^{31}P -MRSI. However, their clinical relevance requires further investigation.

6

Conclusion

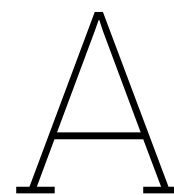
In this study, we demonstrate that applying a phase shift as a post-processing step in ^{31}P -MRSI improves spatial localization by incorporating a greater proportion of tumor tissue within MRSI voxels while preserving spectral quality. Additionally, metabolic ratio analyses over time in pediatric patients with low-grade brain tumors revealed variations in metabolite profiles, which may reflect tumor-specific metabolic activity, normal cerebral fluctuations, or treatment effects. Overall, our findings highlight the potential of ^{31}P -MRSI at 7T, combined with regridding techniques, to enhance spatial localization and mitigate partial volume effects. Further research is needed to validate the clinical utility of ^{31}P -MRSI in pediatric brain tumors.

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Literature Review

A literature review for the course TM30003

Evaluating APT-CEST and ^{31}P MRSI Imaging in Brain Tumors: A Literature Review of Diagnostic Performance, Repeatability, and Therapy Response

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Abstract

Introduction Brain cancer poses significant challenges despite advances in treatment. Advanced imaging techniques, amide proton transfer chemical exchange saturation transfer (APT-CEST), and phosphorus-31 magnetic resonance spectroscopy imaging (^{31}P MRSI) offer potential insights into tumor metabolism. This review updates the role of APT-CEST and ^{31}P MRSI in brain cancer diagnosis and therapy monitoring.

Methods In June 2024, a systematic search of PubMed, Embase, and Scopus was conducted for studies on brain cancer, APT-CEST, and ^{31}P MRSI. Abstracts were screened, and data on imaging parameters, therapy schemas, and patient demographics were extracted.

Results Thirteen studies were included—nine on APT-CEST (229 patients) and four on ^{31}P MRSI (63 patients), all prospective. APT-CEST showed consistent within and between-session repeatability and effective tumor differentiation. It identified therapy response with higher baseline magnetization transfer ratio asymmetry (MTR_{asym}) values predicting early progression. ^{31}P MRSI demonstrated consistent repeatability and metabolic differences between tumors and normal-appearing white matter (NAWM). Changes in pH and metabolite ratios during therapy were noted.

Conclusion This review highlights the potential of APT-CEST and ^{31}P MRSI imaging techniques to enhance brain tumor diagnosis and monitoring, emphasizing the need for standardized protocols and further research to address technical challenges and optimize clinical application.

Keywords: APT-CEST Imaging, ^{31}P MRSI, Brain Tumor, Diagnostic Performance, Therapy Response Monitoring

1. Introduction

Brain cancer remains a major clinical challenge due to its high morbidity and mortality rates despite advances in diagnosis and treatment strategies such as surgery, radiation therapy, and chemotherapy (13, 14). Conventional assessment of diagnosis, resection results, and therapy response relies on structural magnetic resonance imaging (MRI) scans. For example, therapy response can be evaluated using the response assessment in neuro-oncology (RANO) criteria, which categorizes outcomes based on lesion size, new

lesions, and clinical parameters (17). However, differentiating true tumor progression from pseudoprogression—therapy-induced contrast-enhanced or T2/FLAIR hyperintense regions that mimic progression—remains a significant challenge (18-21).

Advanced imaging techniques are increasingly helpful in understanding tumor biology, guiding treatment, and predicting patient outcomes (22). Two modalities, amide proton transfer chemical exchange saturation transfer (APT-CEST) and phosphorus-31 magnetic resonance spectroscopy imaging (^{31}P

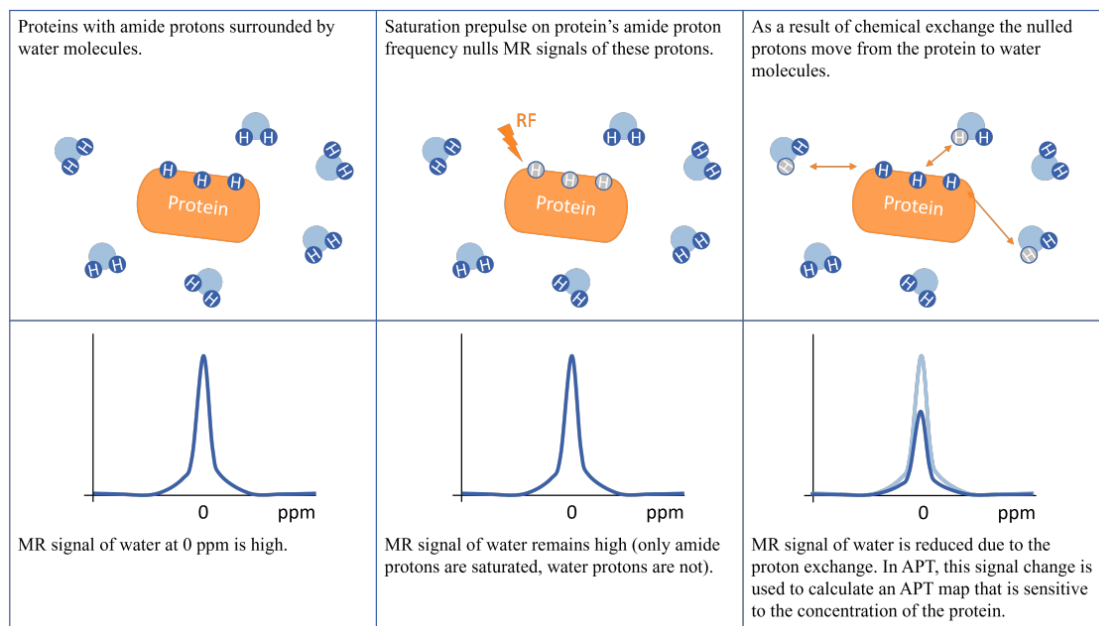


Figure 1: A visual representation of the general principle of chemical exchange saturation transfer (CEST). The bottom row shows the effect of the saturation and magnetization transfer on the proton spectrum (11).

MRSI) offer promising new ways to evaluate brain tumors.

APT-CEST is an MRI technique that detects proton exchanges between endogenous amide groups in mobile proteins and peptides and the surrounding water, enabling visualization of protein concentration and pH changes in tissue (11, 23-25). Using a selective radiofrequency (RF) saturation pulse targeted at 3.5 ppm for APT, a CEST signal is generated by transferring saturated protons to free water protons resulting in a measurable reduction in the water signal amplitude, as explained in Figure 1 (23, 24). This method is sensitive to microenvironmental changes, such as increased protein synthesis and acidity, which are common in malignancies (24, 26-29). APT-CEST has demonstrated potential in differentiating tumor grades, distinguishing tumor recurrence from treatment-related changes, and assessing therapy response (25, 26, 30-33).

³¹P MRSI, on the other hand, offers unique insights into tumor metabolism by measuring phosphorus-containing metabolites, such as phosphocreatine (PCr), adenosine triphosphate (ATP), phosphomonoesters (PME), inorganic phosphate (Pi), glycerophosphoethanolamine (GPE), phosphoethanolamine (PE),

phosphocholine (PC), glycerophosphocholine (GPE), and phosphodiester (PDE), which are involved in energy production, cell membrane synthesis, and cellular pH regulation (34-36). This technique utilizes the magnetic resonance properties of the phosphorus-31 nucleus to detect the chemical shifts of these metabolites in tissues (37). By applying specific RF pulses, ³¹P MRSI generates a spectrum (Figure 2) reflecting metabolite concentrations, offering potential in differentiating tumor types, assessing treatment response, and distinguishing recurrent tumors from radiation necrosis (37-45).

Despite the promising potential of APT-CEST and ³¹P MRSI in brain cancer, their clinical application remains limited by variability in study designs, imaging protocols, and inconsistent findings across studies. A systematic review by Okuchi et al. (46) highlighted the potential of CEST imaging in brain tumor diagnosis and therapy response assessment but noted the need for more evidence to resolve technical challenges and enhance clinical utility. Additionally, an umbrella review by Dagher et al. (47) found promising results for APT-CEST MRI in differentiating tumor progression from

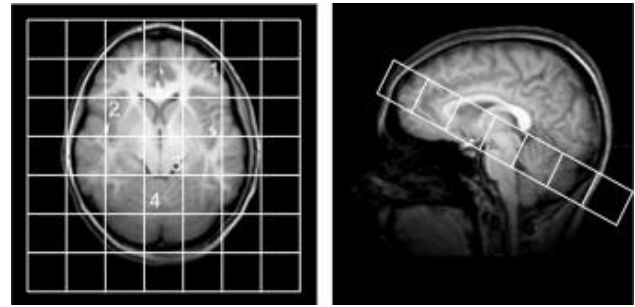
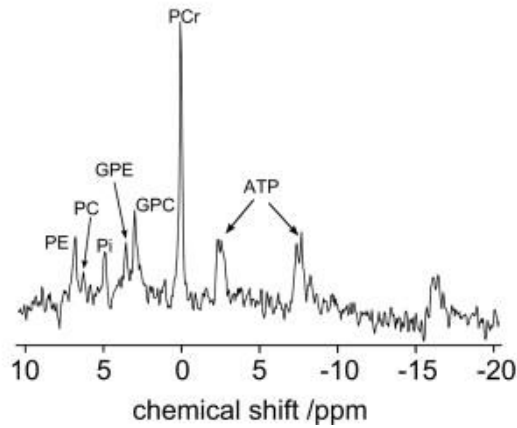


Figure 2: ^{31}P Magnetic Resonance Spectroscopic Imaging (MRSI) spectrum obtained from a healthy volunteer. The orientation of the grid is shown on the right. The orientation of the MRSI grid allowed simultaneous metabolic profiling of various regions of the brain (12).

pseudoprogression and radionecrosis. However, since 2018, no systematic reviews have focused on therapy response assessment with APT-CEST despite significant new research advances.

Likewise, no comprehensive systematic reviews exist on ^{31}P MRSI across various brain tumors and treatments. The limited evaluation by El-Abtah et al. (48) only covered one specific tumor type following chemotherapy; they identified metabolite changes associated with survival outcomes.

The current literature review provides an updated overview of APT-CEST and ^{31}P MRSI in brain cancer patients, focusing on monitoring therapy response. Additionally, it assesses repeatability and diagnostic performance.

2. Methods

2.1 Search Methodology

In June 2024, a systematic search was conducted using PubMed, Embase, and Scopus. The search terms focused on brain cancer, APT-CEST imaging, and ^{31}P MRSI imaging. Further details of the search strategy are provided in Appendix A. For studies involving APT-CEST imaging, only articles published after 2018 were reviewed because of a systematic review that had already covered studies before 2018 on a similar topic (46).

2.2 Selection criteria

Abstracts were screened by one reviewer based on predefined inclusion and exclusion criteria. Studies were included if they involved the ^{31}P MRSI or APT-CEST technique on at least two occasions in patients with brain cancer. Exclusion criteria were: (a) animal or laboratory studies; (b) review articles, case reports with fewer than five cases, letters, commentaries, or conference proceedings; (c) non-English full text; (d) studies utilizing different MRI scanners or field strengths for a single patient. Rayyan, a tool for study selection, was used for the selection (49). Duplicates were extracted using partially automated methods, and manual abstract and full-text screening was performed.

2.3 Data extraction

The extracted data from the included studies encompassed CEST and ^{31}P parameter values, scan intervals, therapy details, country of origin, patient demographics (including age), tumor histologic features, response assessment, MRI field strength, type of CEST contrast, acquisition schemes, acquisition parameters, and the definition of the region of interest (ROI).

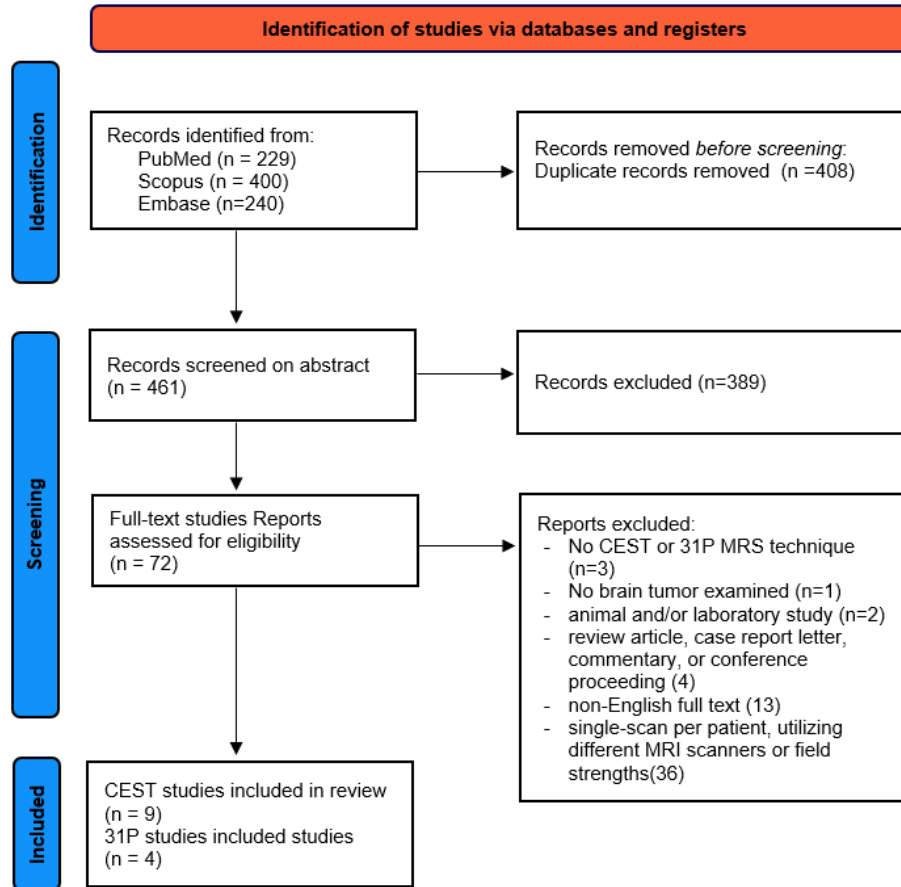


Figure 3: PRISMA flow diagram of the study selection process

3. Results

3.1 Study selection

The systematic search of PubMed, Scopus, and Embase databases yielded 461 unique studies. After screening abstracts, 72 studies met the initial inclusion criteria. Full-text review led to the final inclusion of 13 studies: nine utilizing APT-CEST imaging, involving 229 patients, and four employing ^{31}P MRSI, involving 63 patients (Figure 3). All studies were prospective and observational in design.

3.2 APT-CEST

Three studies assessed the repeatability of APT-CEST on 3T MRI scans, while six studies evaluated therapy responses to chemotherapy (bevacizumab or temozolomide) with or without concurrent radiation therapy across various MRI field strengths (1.5T, 3T, and 7T) (3-10, 50). Most patients included had

glioblastoma (WHO grade IV; 181/229). The scanning parameters varied, including saturation strength (0.5 to 6 μT), saturation time (1 to 3 seconds), and frequency offset range, see Table 1. Detailed information is provided in Appendix B.

Repeatability: Three studies evaluated repeatability across different tumor types and WHO grades (5, 8, 50), all reporting high intersession and intrasession intraclass correlation coefficients (ICC) and low coefficients of variation (COV) for tumors (ICC=0.97; 95% CI, 0.82–1.00 (8), COV within session = 2.64 [1.35–7.00] (50)) and normal appearing white matter (NAWM) (0.99; 95% CI, 0.92–1.00 (8); COV within session = 2.62 [0.94–7.08](50)). However, Lee et al. (5) noted greater session variability in pontine lesions, and both Lee et al. (5) and Wu et al. (50) observed better reproducibility within sessions than between sessions.

Diagnostic performance: Six studies found that before starting therapy MTRasym values were significantly higher and MTRamide and MTRnoe values were lower in tumors compared to NAWM (3-8). Chan et al. (2020-2) (4) identified higher MTRnoe and MTRamide values in high-grade tumors than in low-grade tumors, though this distinction was absent when excluding necrotic or resected regions.

Therapy response: Six studies assessed therapy. Three studies with almost all glioblastomas (80/82 patients) reported higher baseline MTRasym values in early progressors compared to responders or late progressors receiving radiation therapy and temozolomide (3, 6, 7). This is consistent with findings from Yao et al. (10) showing higher baseline MTRasym indicative of shorter progression-free survival (PFS) for patients receiving bevacizumab. Early progression was defined as progression within seven months following therapy. Mehrabian et al. (6) also reported increased baseline MTRnoe, MTRamide, MT, and CESTnoe values in progressors, which was not observed in the other studies (3, 7). No significant differences between progression and non-progression groups were observed immediately after therapy (3, 6, 7, 9). Significant increases in MTRnoe and MTRamide were noted in responders to radiation and chemotherapy during early treatment within 2 weeks (4, 6), with a stable or slight increase in MTRnoe at therapy end (7). Park et al. (9) and Yao et al. (10) observed significant decreases in MTRasym in responders to bevacizumab, correlating with longer PFS.

3.3 ³¹P MRSI

One study evaluated repeatability (15), while three studies assessed therapy response to either temozolomide or bevacizumab (1, 2, 16). Detailed information is provided in Appendix B, with key scanner parameters listed in Table 2. All studies used consistent scanning parameters but with varying voxel sizes (ranging from 5x15x12.5 mm³ to 30x30x25

mm³). All studies focused on glioblastomas (WHO grade IV).

Repeatability: Alcicek et al. (15) found consistent repeatability by comparing scans taken before and after 72 hours of fasting, with consistent full spectral linewidth at the half amplitude of maximum signal (FWHM >0.1 ppm) and no significant differences in relative standard deviation or signal-to-noise ratio.

Diagnostic performance: All studies reported differences in metabolite parameters between tumor and NAWM, with variations in the significant metabolites reported in Table 3. Three studies (2, 15, 16) reported elevated pH values in tumors compared to NAWM.

Therapy response: Three studies assessed changes in metabolites during therapy. Two studies found decreased pH values after bevacizumab treatment (2, 16), with Wenger et al. (16) also noting increased pH during disease progression and no significant changes in NAWM. Hattingen et al. (2) observed increased GPE levels in responders, with no changes in other metabolites. Grams et al. (1) reported increases in PCr/ATP, PCr/Pi, and PDE/ATP ratios, along with decreases in PME/PDE and PME/PCr ratios in tumor tissue after therapy initiation with temozolomide, along with significant metabolic changes in adjacent and contralateral NAWM.

Table 1: MRI protocol details and imaging parameters for different studies of amide proton transfer (APT) chemical exchange saturation transfer (CEST)

Article	MRI scanner	Acquisition	Saturation		Sampling			
		Sequence	uT	s	Steps	Range, equal steps	Nr of slices	Voxel size in mm ³
Chan, 2021 (3)	1,5T Philips	2D imaging pulse sequence	2.5	1.13	64	±6 ppm Yes	1	2.5x2.5x5
Chan 2021-2 (4)	1,5T Philips	2D imaging pulse sequence	2.5	1.13	67	±3,5 ppm No	1	2.5x2.5x5
Lee, 2020 (5)	3T Philips	3D turbo spin echo sequence	2	2.00	7	±4.3 and -1560 No	15	1.8x1.8x5
Mehrabian, 2018(6)	3T Philips	2D fast field echo with multi-shot turbo field echo	0.5	0.97	60	±5.9 ppm Yes	1	1.3x1.3x3
Meissner, 2019 (7)	7T Siemens	2D gradient echo CEST sequence	0.6 & 1.0	2.25	59	± 300 ppm No	3	1.72x1.72x5
Park, 2020 (9)	3T Philips	3D turbo spin-echo sequence	2	2.00	?	?	15	1.11x1.11x5
Wamelink, 2023 (8)	3T Siemens	3D turbo spin echo SPACE APT CEST	2	1.00	7	± 4,0, and 1560 No	85	2.8x2.8x2.8
Wu, 2023 (50)	3T GE	A 3D snapshot CEST image acquisition	1.5	1.60	43	±100 ppm No	14	1.7x1.7 x 3
Yao, 2019 (10)	3T Siemens	2D CEST-EPI or CEST- SAGE-EPI sequence	6	3.00	29	±3,5 ppm No	1	1.9x1.9x4

Table 2: MRI protocol details and imaging parameters for different studies of ³¹P MRSI

Article	Sequence	MRI field strength	TR ms	TE ms	Flip angle (*)	Nr of slices	Thickness mm	Voxel size mm ³	Coil
Alcicek, 2024 (15)	3D ³¹ P FID CSI sequence WALTZ4 1H decoupling	3T Siemens	2000	2.3	60	multi	12.5	5 x15x12.5	Double-tuned 1H/31P volume head coil
Grams, 2021 (1)	3D sequence with WALTZ 4 proton decoupling	3T Siemens	2000	2.3	60	multi	25	30x30x25	Double-tuned 1H/31P volume head coil
Hattinge n, 2011 (2)	3D ³¹ P MRSI; WALTZ4 proton decoupling	3T Siemens	2000	2.3	60	multi	25	15x15x25	Double-tuned 1H/31P volume head coil
Wenger, 2017 (16)	3D ³¹ P MRSI; WALTZ4 proton decoupling shift imaging (CSI)	3T Siemens	2000	2.3	60	multi	25	15x15x25	Double-tuned 1H/31P volume head coil

Table 3: Metabolite parameters and their values for tumor tissue and normal-appearing white matter (NAWM), with standard deviation.

Study	Tumor value \pm SD	NAWM value \pm SD
Alcicek, 2024 (15)	pH=7.08 \pm 0.05 PME/PDE=0.71 \pm 0.41	pH=7.03 \pm 0.01 PME/PDE=0.51 \pm 0.16
Grams, 2021 (1)	No absolute values available	No absolute values available
Hattingen, 2011 (2)	pH= 7.11 \pm 0.56 PE/GPE = 2.14 \pm 0.75 Pi/ATP = 0.94 \pm 0.43 PCr = 1.69 \pm 0.29 GPE = 0.24 \pm 0.24	pH= 7.04 \pm 0.02 PE/GPE = 1.75 \pm 0.31 Pi/ATP = 0.79 \pm 0.26 PCr = 1.88 \pm 0.34 GPE = 0.28 \pm 0.10
Wenger, 2017 (16)	pHi= 7.110 \pm 0.053	pHi = 7.017 \pm 0.026

Tumor before therapy compared to NAWM

Difference between MTRamide and MTRnoe removing direct water saturation and magnetization transfer effects

↑ MTRasym (3-8)

Sum of all saturation effects at 3.5ppm amide proton

↓ MTRamide (3-8)

Sum of all saturation effects at -3.5 ppm nuclear Overhauser effect

↑ MTRnoe (3-8)

Responding tumors post-therapy compared to the baseline

Difference between MTRamide and MTRnoe removing direct water saturation and magnetization transfer effects

↓ MTRasym (9, 10)

Sum of all saturation effects at 3.5ppm amide proton

↑ MTRamide(4, 6, 7)

Sum of all saturation effects at -3.5 ppm nuclear Overhauser effect

↑ MTRnoe (4, 6, 7)

Tumor before therapy compared to NAWM

Cell membrane metabolism

↑ PME/PDE (1, 2)

↑ PE/GPE (2)

↑ PME/PCr (1)

↓ GPE (2)

Hypoxia markers

↑ pH (2, 15, 16)

Energetic state of the cell

↓ PCr/ATP (1)

↓ PCr/Pi (1)

↓ PDE/ATP (1)

↓ PCr (2)

ATP turnover

↑ Pi/ATP (1, 2)

Responding tumors post-therapy compared to the baseline

Cell membrane metabolism

↓ PME/PDE (1)

- PE/GPE (2)

↓ PME/PCr (1)

↑ GPE (2)

Hypoxia markers

↓ pH (2, 16)

Energetic state of the cell

↑ PCr/ATP (1)

↑ PCr/Pi (1)

↑ PDE/ATP (1)

- PCr (2)

ATP turnover

- Pi/ATP (1, 2)

Figure 4: Left: Comparison of metabolites and metabolite ratios between tumor and normal appearing white matter (NAWM) for APT-CEST top row and 31P MRSI bottom row. Right: Changes in tumor metabolites post-therapy compared to baseline for responding tumors for APT-CEST top row and 31P MRSI bottom row.

5. Discussion

This review highlights the potential clinical utility of APT-CEST and ^{31}P MRSI imaging techniques in brain tumors, focusing on their repeatability, diagnostic performance, and therapy response monitoring. While both modalities offer unique insights into brain tumor biology, they differ in their specific applications and findings.

Conventional MRI is essential for diagnosing and monitoring treatment response, though distinguishing between true tumor progression and pseudoprogression, and obtaining a histological diagnosis, remains challenging (10-13). Metabolic MRI has the potential to refine the differential diagnoses and help to differentiate between true tumor progression and pseudoprogression (47). This may reduce the need for invasive biopsies, prevent overtreatment, and enable earlier intervention (25, 26, 30-33).

5.1 APT-CEST

APT-CEST imaging shows high repeatability across various tumor types and grades, which is essential for reliable tumor monitoring. However, session variability in certain anatomical locations, like pontine lesions, underscores the need for careful region of interest (ROI) placement, consistent with Obdeijn's findings in healthy volunteers at 3T (51). Moreover, all studies in this review evaluated repeatability using 3T MRI scanners, but it is known that higher field strengths, like 7T used in the MITCH study (52), suffer from more B0 and B1 field inhomogeneities that could affect repeatability (53). However, other studies also reported excellent reproducibility of inter- and intrasubject APT-CEST at 7T (54, 55). These studies found increased repeatability after correcting for B1 inhomogeneities.

APT-CEST distinguishes tumors from NAWM through higher MTR_{asym} and lower MTR_{amide}/MTR_{noe}, though this distinction adds little diagnostic value beyond conventional imaging. The technique holds more promise in distinguishing high-grade from low-grade

tumors, as shown by a meta-analysis reporting 88% (95% CI, 77–94%) sensitivity and 91% (95% CI, 82–96%) specificity (3, 56), though standardization in ROI placement is needed to fully leverage these capabilities.

In therapy response monitoring, APT-CEST shows potential as an early biomarker for progression. Baseline imaging parameters, such as MTR_{asym}, MTR_{noe}, and MTR_{amide}, demonstrated predictive value for early progression, consistent with previous studies (32, 33). However, heterogeneity in study populations, therapy regimens, and imaging parameters complicates comparisons. Differences in frequency offsets, saturation strength, and saturation duration highlight the need for standardized imaging protocols. A paper by Zhou et al. (57) aimed to achieve this by standardizing APT imaging in a clinical setting on 3T focusing on brain tumors.

Differences in MRI field strengths have contributed to varied results; Chan et al. (3, 4) found no significant changes using 1.5T MRI, while Meissner et al. (7) detected significant changes at 7T MRI, likely due to the higher signal-to-noise ratio achievable at 7 Tesla. These factors underscore the need for larger, multicenter studies to validate the clinical utility of APT-CEST across diverse settings and patient populations.

5.2 ^{31}P MRSI

^{31}P MRSI demonstrates the potential in monitoring metabolic changes and therapy response in brain tumors. Alcicek et al. (15) confirmed its repeatability at 3T MRI, and similar studies in other tissues have shown reliable repeatability at 7T MRI (58-61).

The included studies only assessed glioblastoma, a tumor with mitochondrial dysfunction leading to the preference for glycolysis over oxidative phosphorylation and decreased ATP production (62). Key metabolic markers assessed included PME/PDE, Pe/GPE, and PME/PCr, which reflect increased cell membrane metabolism, decreased energetic states (PCr/ATP, PCr/Pi), and heightened ATP turnover (Pi/ATP), summarized in Table 4.

These markers, in response to treatments with bevacizumab and temozolomide, show a reduction in hypoxia markers and an improvement in energetic states, offering a potential window for early therapy monitoring. Additionally, changes in pH during disease progression (2, 16) provide insight into tumor aggressiveness, consistent with findings linking higher pH to more aggressive gliomas (41, 63).

Despite these promising results, variability in the metabolic ratios used across studies complicates direct comparisons, emphasizing the need for standardized approaches. The observed changes in NAWM and areas beyond the tumor region suggest that ^{31}P MRSI may also capture the broader effects of brain tumors and their treatment, providing a more comprehensive picture of the disease process.

However, technical challenges such as low signal-to-noise ratio (SNR), coarse spatial resolution, and long acquisition times, limit its clinical applicability (48). For instance, in Alcicek et al. (15) nine out of 22 patients were excluded due to poor spectral quality.

A limitation of this review is that the most statistically significant results came from Grams et al. (1), who compared multiple regions and metabolites without applying statistical corrections. Additionally, their use of large voxel sizes raises concerns about the reliability of the findings due to the partial volume effect.

While ^{31}P MRSI can offer valuable metabolic insights, the general clinical applicability requires further optimization and validation.

5.3 Potential application in pediatric brain cancer

Pediatric brain cancer, alongside leukemia, is one of the most prevalent and fatal cancers affecting children (64, 65). These tumors differ significantly from those in adults, predominantly occurring in the posterior fossa and presenting distinct molecular subtypes and pathology (66, 67). Most pediatric brain tumors are low-grade gliomas (LGG), classified as WHO grade 1, with a 10-year overall survival

rate of 90% (66, 68, 69). In contrast, the majority of tumors reviewed in this study were high-grade, with an overall survival of nine months (70).

APT-CEST imaging offers several advantages for pediatric patients, particularly by eliminating the need for intravenous gadolinium contrast. Obtaining intravenous access is invasive, causing discomfort and posing risks such as phlebitis, occlusion, and infection (71). Gadolinium use carries risks of hypersensitivity reactions, including erythema, exanthema, urticaria, angioedema, and respiratory symptoms such as bronchospasm, though these reactions are infrequent (72).

Preliminary studies, including Zhang et al. (73), suggest that APT-CEST can distinguish between high- and low-grade tumors in pediatric patients, similar to findings in adults (46). Obdeijn (51) also observed differences across various tumor types. Early results from 7T APTw imaging in pediatric brain tumors demonstrate its feasibility, with longitudinal APTw changes exceeding intrasubject variability in several cases (51). APTw imaging shows particular promise for tumors with indolent courses, such as optic pathway gliomas, where conventional MRI might not adequately reflect changes in tumor status (19, 47). Moreover, APT-CEST holds promise for other pediatric CNS diseases, offering non-invasive metabolic insights and potentially reducing the use of contrast agents (67). However, further research is required to validate its efficacy in children and establish standardized imaging protocols.

5.4 APT-CEST and ^{31}P : Clinical, Economic, and Environmental Benefits

Using gadolinium contrast agents is invasive and poses risks related to intravenous access and hypersensitivity reactions (71, 72). Reducing the use of these agents directly benefits patients by minimizing these risks and avoiding potential adverse effects. While APT-CEST and ^{31}P MRSI are not yet ready for routine clinical use and require post-processing and specialized expertise, their application

could significantly improve patient quality of life by identifying ineffective therapies early, thereby minimizing exposure to the side effects of unnecessary treatments. Furthermore, this approach could provide substantial economic benefits, as standard therapies can cost between €15,000 and €30,000 per patient, with pediatric cases potentially reaching hundreds of thousands or even millions of euros (74, 75).

Separately, reducing gadolinium usage also offers environmental advantages. Gadolinium is excreted through urine and can accumulate in water bodies, particularly near urban areas, posing risks to aquatic ecosystems due to its toxicity at higher concentrations. Gadolinium is environmentally persistent, raising concerns about its long-term ecological impact and potential effects on human health through water contamination (76)

5.5 Future recommendations

For APT-CEST and ^{31}P MRSI to become clinically viable, several key steps are necessary. First, imaging protocols, post-processing analysis, and signal intensity values need standardization across institutions. This standardization will reduce variability and improve comparability between studies. Second, larger, multicenter studies should be conducted to validate these imaging techniques' findings and establish robust biomarkers for diagnosis, therapy response, and prognosis.

Additionally, research should explore the potential applications of these techniques in pediatric brain cancer, as the unique tumor biology in children may yield different findings from those in adults (66). Given the significant advancements in MRI technology and the increasing understanding of tumor biology, both APT-CEST and ^{31}P MRSI hold substantial promise for the future of brain tumor imaging.

6. Conclusion

This review underscores the potential of APT-CEST and ^{31}P MRSI imaging techniques in enhancing the clinical management of brain tumors. Both modalities offer unique insights

into tumor biology. However, challenges such as variability in imaging protocols and technical limitations must be addressed to fully realize their clinical potential. Future research should focus on standardizing imaging procedures, validating findings through larger multicenter studies, and exploring applications in pediatric brain cancer. Advancing these techniques could significantly improve diagnostic accuracy, therapy monitoring, and overall patient outcomes.

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Appendix A: Detailed search strategy

Search performed 13-06-2024

Pubmed – 229 articles

Phosphorus-31 – 38 articles

((Neoplasms, Neuroepithelial[MeSH] OR Glioma[tiab] OR brain tumo*[tiab] OR brain cancer[tiab] OR brain metastasis[tiab]) AND (P MRS[tiab] OR P MR spectroscopy[tiab] OR P Magnetic Resonance spectroscopy[tiab] OR P MRSI[tiab] OR 31 P spectroscopy[tiab] OR Phosphorus 31 MR Spectroscopy[tiab] OR 31P Magnetic Resonance Spectroscopy[tiab] OR 31P MR Spectroscopy[tiab] OR 31p/1H MRSI [tiab] OR 31p-1H MRSI [tiab]) AND Humans[Mesh])

Amide Proton Transfer chemical exchange saturation -- after filtering from 2018, 191 articles

(Neoplasms, Neuroepithelial[MeSH] OR Glioma[tiab] OR brain tumo*[tiab] OR brain cancer[tiab] OR brain metastasis[tiab]) AND ((magnetic resonance imaging[MeSH Terms] AND CEST[tiab]) OR chemical exchange saturation transfer[tiab] OR APT[tiab] OR amide proton transfer[tiab] OR magnetization transfer[tiab] OR z-spectrum[tiab] OR chemical exchange[tiab] OR exchange transfer[tiab] OR saturation transfer[tiab]) AND Humans[Mesh]

Scopus – 400 articles

Phosphorus-31 – 69 articles

Article title, Abstract, Keywords ((neuroepithelial AND neoplasms) OR glioma OR "brain tumo*" OR "brain cancer" OR "brain metastasis")

AND

Article title, Abstract, Keywords ("31P-MRS" OR "P MR spectroscopy" OR "P Magnetic Resonance spectroscopy" OR "31P MRSI" OR "31P spectroscopy" OR "Phosphorus-31 MR Spectroscopy" OR "31P Magnetic Resonance Spectroscopy" OR "31P-MR Spectroscopy" OR "31p/1H MRSI" OR "31p-1H MRSI")

AND

All fields (humans)

Amide Proton Transfer chemical exchange saturation – 331 articles

Article title, Abstract, Keywords ((neuroepithelial AND neoplasms) OR glioma OR "brain tumo*" OR "brain cancer" OR "brain metastasis")

AND

Article title, Abstract, Keywords (("magnetic resonance imaging" AND cest) OR "chemical exchange saturation transfer" OR apt OR "amide proton transfer" OR "magnetization transfer" OR "z-spectrum" OR "chemical exchange" OR "exchange transfer" OR "saturation transfer")

AND

All fields (humans)

Filter: Limit 2018-2024

Embase – 240 articles

1. 'neuroepithelial neoplasm'/exp OR glioma:ti,ab OR 'brain tumor*':ti,ab OR 'brain cancer':ti,ab OR 'brain metastasis':ti,ab
2. 'p-mrs':ti,ab OR 'p mr spectroscopy':ti,ab OR 'p magnetic resonance spectroscopy':ti,ab OR 'p-mrsi':ti,ab OR 'p-spectroscopy':ti,ab OR 'phosphorus-31 mr spectroscopy':ti,ab OR '31p magnetic resonance spectroscopy':ti,ab OR '31p-mr spectroscopy':ti,ab OR '31p/1H MRSI':ti,ab OR '31p-1H MRSI':ti,ab)
3. 'magnetic resonance imaging'/exp AND CEST:ti,ab
4. 'chemical exchange saturation transfer':ti,ab OR APT:ti,ab OR 'amide proton transfer':ti,ab OR 'magnetization transfer':ti,ab OR 'z-spectrum':ti,ab OR 'chemical exchange':ti,ab OR 'exchange transfer':ti,ab OR 'saturation transfer':ti,ab

31P MRSI – 35 articles

5. 1 AND 2
6. Limit 5 to human

APT CEST – 205

5. 1 AND (3 OR 4)
6. Limit 5 to human AND Date 2018-2024

Appendix B: Detailed information for all included studies

Table 1: Detailed information on the included Amide Proton Transfer (APT) Chemical Exchange Saturation Transfer (CEST) studies.

Article	Goals	Country	Patients	Median age in years (range)	Scan interval & therapy	ROI	Tumor histologic features	Parameters	Response assessment
Chan, 2021	Assess CEST feasibility in GBM at 1.5T; compare early vs. late progression.	Canada	51 (22 female)	56 (19-68)	Pre-radiation, fractions 10 & 20, 1-month post-radiation; in combination with temozolomide.	Tumor GTV, CTV(=GTV+1.5cm), cNAWM	Glioblastoma (51)	MT, MTRasym, MTRamide	Early (<7m) progression vs. late progression (>7m) progression by RANO.
Chan 2021-2	Implement CEST on 1.5T MR-Linac; assess signal changes vs. tumor grade.	Canada	54 (25 female)	54 (26-81)	Pre-radiation, weekly during radiation (6, 3, or 1 time(s)); in combination with chemotherapy.	Tumor GTV, NAWM	Glioblastoma (28), Astrocytoma (10), brain metastasis (7), Oligodendroglioma (3), Ependymoma (1), Schwannoma (1)	MTRasym, MTRamide, MTRNOE	-
Lee, 2020	Assess the repeatability of APTw MRI in the brain across conditions and locations.	South Korea	15 (10 female)	54.6 ± 11.3	Two scans per session, one week apart.	T2 enhancing tumor, cNAWM	Low-grade glioma (6), High-grade glioma (9)	MTRasym	-
Mehrabian, 2018	Monitor CEST changes during chemoradiation; identify earliest response time.	Canada	19 (6 female)	55	Pre-radiation, at 2 and 4 weeks, 1-month post-treatment; in combination with temozolomide.	GD-enhanced tumor, initial GTV, cNAWM	Glioblastoma (19)	MTRamide, MTRnoe, APT, direct effect	Progression/non-progression 3-8m post-therapy assessed with RANO
Meissner, 2019	Assess if CEST MRI enables early chemoradiation response evaluation in glioma.	Germany	12 (5 female)	56± 18	Pre-radiation, 1-week post-radiation, 6 weeks post-radiation; in combination with temozolomide.	Not described	Glioblastoma WHO IV (10), oligodendroglioma WHO II (1), Astrocytoma WHO II (1)	rNOE, dnsAPT, Cho/NAA	Response/progression by MRI, neuro evaluation at 1 & 3 months.
Park, 2020	Predict response and evaluate changes to antiangiogenic treatment in recurrent glioblastoma.	Korea	54 (30 female)	56 (49-64)	Baseline, 6 weeks post-bevacizumab.	FLAIR enhanced tumor, cNAWM	Glioblastoma (54), IDH wildtype (49), IDH mutation (5)	ADC (from DWI), APTw, nCBV (from DSC)	Progression at 12m; PFS until progression/death.

Wamelink, 2023	Test reproducibility of APT-CEST with a clinically feasible scan time in healthy tissue and glioma at 3T.	Netherlands	6 (3 female)	50 ± 17	Two scans in one session, repositioning between scans.	Gd or FLAIR enhanced tumor, cNAWM	Glioblastoma (4), oligodendroglioma (1)	MTRasym	-
Wu, 2023	Evaluate APT-weighted CEST reproducibility across sessions and scanners.	Netherlands	7 (1 female)	69 (57-73)	Two scans in one session, one after 4 days.	Gd enhancing tumor, cNAWM	Glioblastoma (4), lung metastasis (2), oligodendroglioma	MTRasym, MTRrex, Lorentzian difference	-
Yao, 2019	Assess treatment response in recurrent glioblastoma with bevacizumab and pH-weighted APT-CEST.	United States	11 (2 female)	55 (29-75)	Pre- and post-bevacizumab treatment.	Gd or FLAIR enhancing tumor	Recurrent glioblastoma (11)	MTRasym	PFS from the start of treatment; progression defined as >25% increase/new lesion.

Table 2: Detailed information of the included 31 phosphorous Magnetic Resonance Spectroscopic Imaging (MRSI). RANO = Response assessment in neuro-oncology, NAWM=Normal appearing white matter, CE= Contrast-enhanced, FWHM= Full width at half maximum, SNR= Signal-to-noise ratio, SD= Standard deviation, PME= Phospho-mono ester, PDE= Phospho-di ester, ATP= Adenosine triphosphate, PCr= Phosphocreatine, Pi= Inorganic phosphate, PCho= Phosphocholine, GPC= Glycerophosphocholine, GPE= Glycerophosphoethanolamine, PEth= Phosphatidylethanolols,

Article	Goals	Country	Patients	Median age in years (range)	Scan interval and therapy	ROI	Tumor histology	Parameters	Response assessment
Alcicek, 2024	Feasibility, reliability, and repeatability of a multi-voxel, multi-nuclei (1 H/31 P) MRSI protocol	Germany	13 (6 female)	61	Baseline, +72h fasting	CE tumor, NAWM	WHO grade II-IV adult type diffuse gliomas	FWHM, SNR, SD, pH _i , PME/PDE, ATP/PCr	Biopsy or resection
Grams, 2021	Investigate energy and membrane metabolism with bevacizumab for glioblastomas	Austria	20 (7 female)	63 (36-77)	Baseline, +4m temozolomide	CE tumor, adjacent tumor, NAWM (ipsilateral and contralateral)	Glioblastoma	PCr/ATP, PCr/Pi, Pi/ATP, PME/PDE, PME/PCr, PDE/ATP	Neuroradiologist according to RANO
Hattingen, 2011	Energy metabolism after bevacizumab treatment	Germany	16 (5 female)	50 (30-68)	Baseline, +2m bevacizumab	CE tumor, NAWM	Recurrent glioblastoma	Pi/PCr, Pi/ATP, PCho/GPC, PEth/GPE, pH _i , Pi, ATP, PCr, GPE, PEth, GPC, PCho	Neuroradiologist according to RANO
Wenger, 2017	Detect pH changes before structural changes in brain tumors	Germany	14 (3 female)	51(31-67)	Baseline, +2m bevacizumab until further progression	CE tumor, NAWM	Glioblastoma (not methylated(9) methylated(5))	pH _i	Neuroradiologist according to RANO

B

^{31}P -MRSI Pipeline

The ^{31}P -MRSI Pipeline with below the Matlab code for Phase correction and interpolation

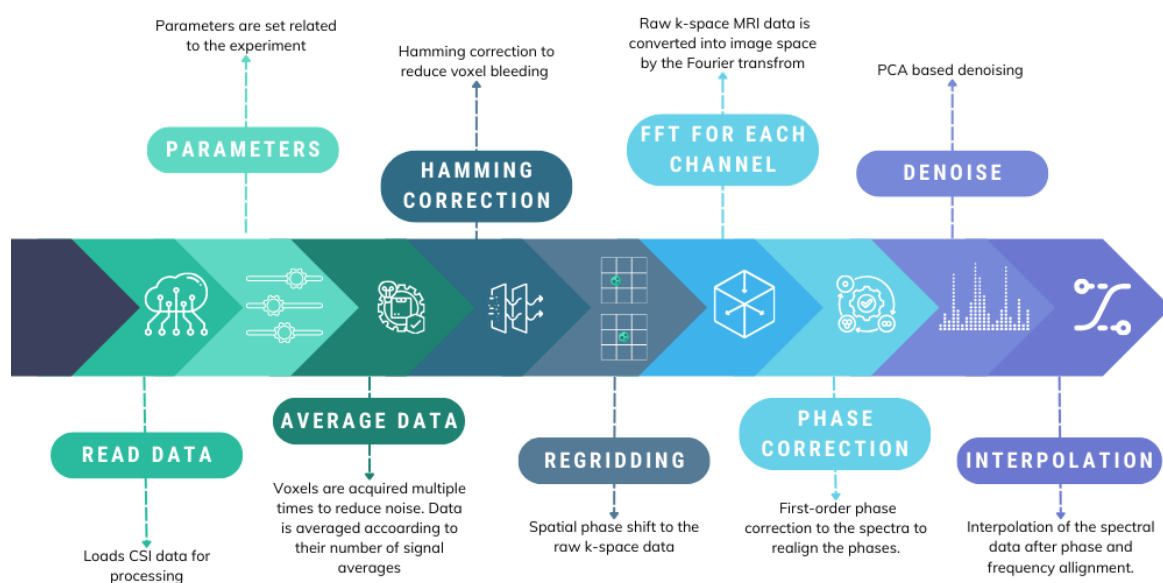


Figure B.1: ^{31}P -MRSI Pipeline for Chemical Shift Imaging (CSI) experiments with multichannel acquisition made in a Philips scanner (7T). In the process of analyzing ^{31}P -MRSI data, either phase correction or interpolation was applied, but not both. PCA = Principal Component Analysis.

```

1 function [spectrum_voxelshift_kspace] = VoxelShiftKSpace(k_space_data, voxel_shift_RL,
2   voxel_shift_AP, voxel_shift_FH)
3   %% This function applies a voxel shift in k-space by introducing a phase shift.
4   % The shift is applied along three spatial directions:
5   % - Right-Left (RL)
6   % - Anterior-Posterior (AP)
7   % - Feet-Head (FH)
8   %
9   % Author: Hilde Roording
10  %
11  % Inputs:
12  % - k_space_data: 4D complex array of k-space data (spectral dimension x spatial
13    dimensions)
14  % - voxel_shift_RL: Shift in voxel units along the Right-Left direction
15  % - voxel_shift_AP: Shift in voxel units along the Anterior-Posterior direction
16  % - voxel_shift_FH: Shift in voxel units along the Feet-Head direction
17  %
18  % Output:
19  % - spectrum_voxelshift_kspace: 4D complex array with voxel shift applied in k-space
20
21  [dimx, dimy, dimz] = size(k_space_data, [2, 3, 4]);
22  [x, y, z] = meshgrid(1:dimy, 1:dimx, 1:dimz); % Grids for x, y, z voxel dimensions
23
24  %Compute phase shifts based on voxel shifts
25  % Phase shift formula:  $\exp(-i * \text{delta}_r * k)$ , where:
26  % -  $\text{delta}_r = \text{voxel shift} * 2 * \pi$ 
27
28  RL_new = x * (voxel_shift_RL * 2 * pi) / dimx;
29  AP_new = y * (voxel_shift_AP * 2 * pi) / dimy;
30  FH_new = z * (voxel_shift_FH * 2 * pi) / dimz;
31
32  % Create complex array  $e^{-ix} = \cos(x) - i\sin(x)$ 
33  phase_shift_complex_RL = complex(cos(RL_new), -sin(RL_new));
34  phase_shift_complex_AP = complex(cos(AP_new), -sin(AP_new));
35  phase_shift_complex_FH = complex(cos(FH_new), -sin(FH_new));
36
37  % Add the spectrum dimension to enable multiplying
38  phase_shift_complex_RL = reshape(phase_shift_complex_RL, [1, dimx, dimy, dimz]);
39  phase_shift_complex_AP = reshape(phase_shift_complex_AP, [1, dimx, dimy, dimz]);
40  phase_shift_complex_FH = reshape(phase_shift_complex_FH, [1, dimx, dimy, dimz]);
41
42  % Multiply with the k-space data
43  k_space_data_shifted = k_space_data .*...
44    phase_shift_complex_RL .* phase_shift_complex_AP .* phase_shift_complex_FH;
45
46  spectrum_voxelshift_kspace = k_space_data_shifted;
47 end

```

```

1 function [spectrum_voxelshift_interpolation] = VoxelShiftInterpolation(spectral_data,
2   voxel_shift_RL, voxel_shift_AP, voxel_shift_FH, interpolation_technique)
3   %% VoxelShiftInterpolation - Apply voxel shift using interpolation
4   % This function applies a voxel shift to spectral data using interpolation.
5   % The shift is applied along three spatial directions:
6   % - Right-Left (RL)
7   % - Anterior-Posterior (AP)
8   % - Feet-Head (FH)
9   %
10  % Author: Hilde Roording
11  %
12  % Inputs:
13  % - spectral_data: 4D array of spectral data (spectral dimension x spatial dimensions)
14  % - voxel_shift_RL: Shift in voxel units along the Right-Left direction
15  % - voxel_shift_AP: Shift in voxel units along the Anterior-Posterior direction
16  % - voxel_shift_FH: Shift in voxel units along the Feet-Head direction
17  % - interpolation_technique: Interpolation method (e.g., 'linear', 'nearest', 'cubic')
18  %
19  % Output:
20  % - spectrum_voxelshift_interpolation: 4D array with voxel shift applied using
21    interpolation
22
23  % Pad data with repeating edge values along each spatial dimension

```

```

22     spectral_data = padarray(spectral_data, [0, 1, 1, 1], 'replicate', 'both'); % pad only
        spatial dimensions
23
24     [dimx, dimy, dimz] = size(spectral_data, [2, 3, 4]);
25
26     % Create original voxel position grids
27     [RL, AP, FH] = meshgrid( 1:dimy, 1:dimx, 1:dimz); % Grids for x, y, z voxel dimensions
28
29
30     % Compute new voxel positions after shifting
31     RL_new = RL + voxel_shift_RL;
32     AP_new = AP + voxel_shift_AP;
33     FH_new = FH + voxel_shift_FH;
34
35
36     shifted_data = zeros(size(spectral_data));
37
38     % Perform interpolation for each spectral point independently
39     for i = 1:size(spectral_data, 1)
40 %       Interpolate for each spectral point
41         shifted_data(i, :, :, :) = interp3(RL, AP, FH, double(squeeze(spectral_data(i, :, :,
            :))), RL_new, AP_new, FH_new, interpolation_technique, 0);
42
43     end
44     % Remove padding to return to original shape
45     shifted_data = shifted_data(:, 2:end-1, 2:end-1, 2:end-1); % crop padded dimensions
46
47     spectrum_voxelshift_interpolation = shifted_data;
48
49 end

```

C

Heatmaps

Heatmaps for the 0.3 voxel shift in Anterior-Posterior (AP), Left-Right (LR), and Feet-Head (FH) direction

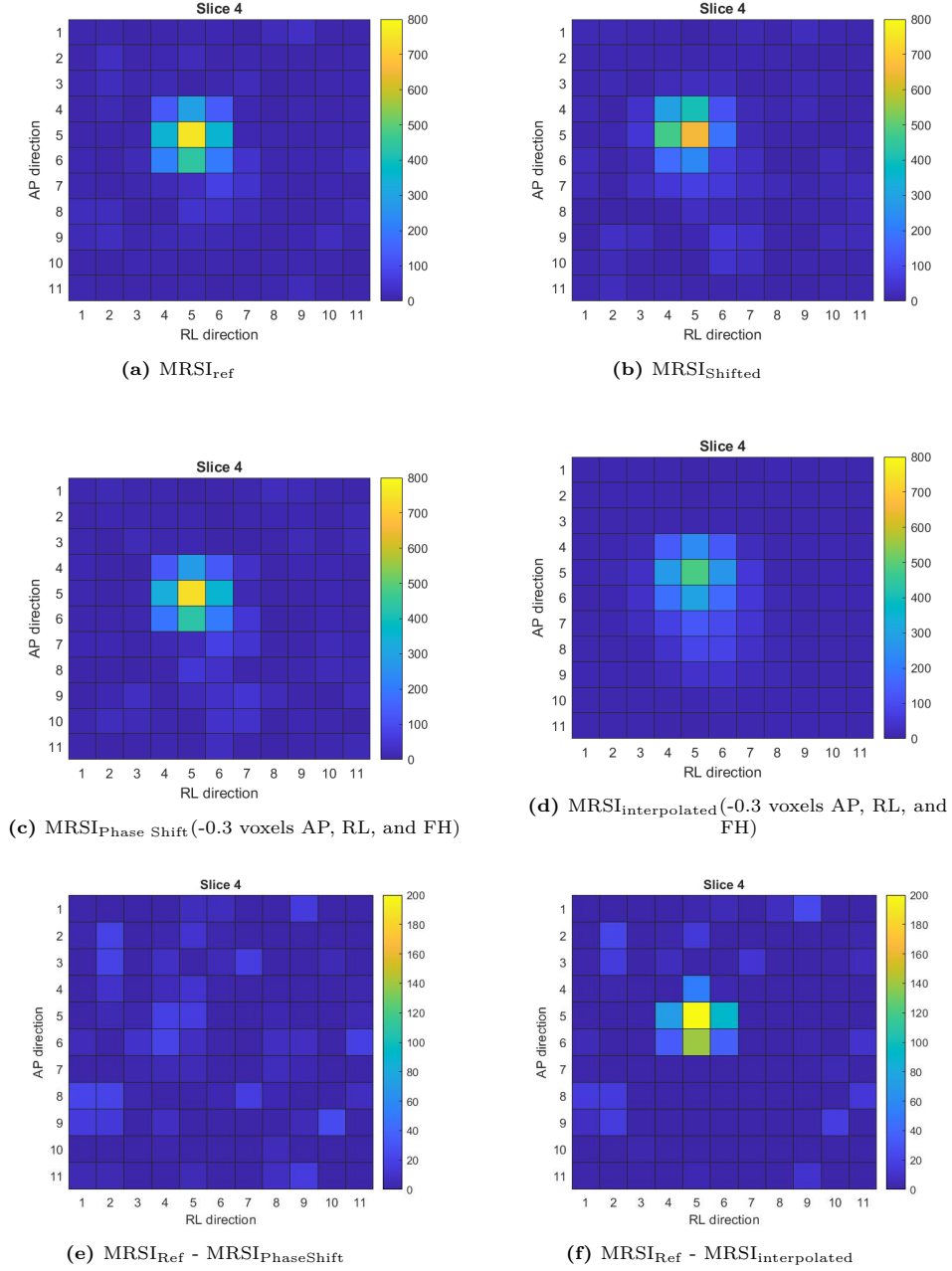


Figure C.1: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment. Where C.1a shows the AUC of MRSI_{ref} , C.1b shows the AUC of $\text{MRSI}_{\text{shifted}}$, C.1c shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.3 voxels in the Anterior-Posterior (AP), Right-Left (RL), and Feet-Head (FH) directions ($\text{MRSI}_{\text{Phase Shift}}$), C.1d shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.3 in AP, RL, and FH direction ($\text{MRSI}_{\text{interpolated}}$), C.1e and C.1f depict the differences between the shifted AUCs and the MRSI_{ref} for k-space phase adjustment and spatial based interpolation, respectively.

Heatmaps for the 0.1 voxel shift in Anterior-Posterior (AP) direction

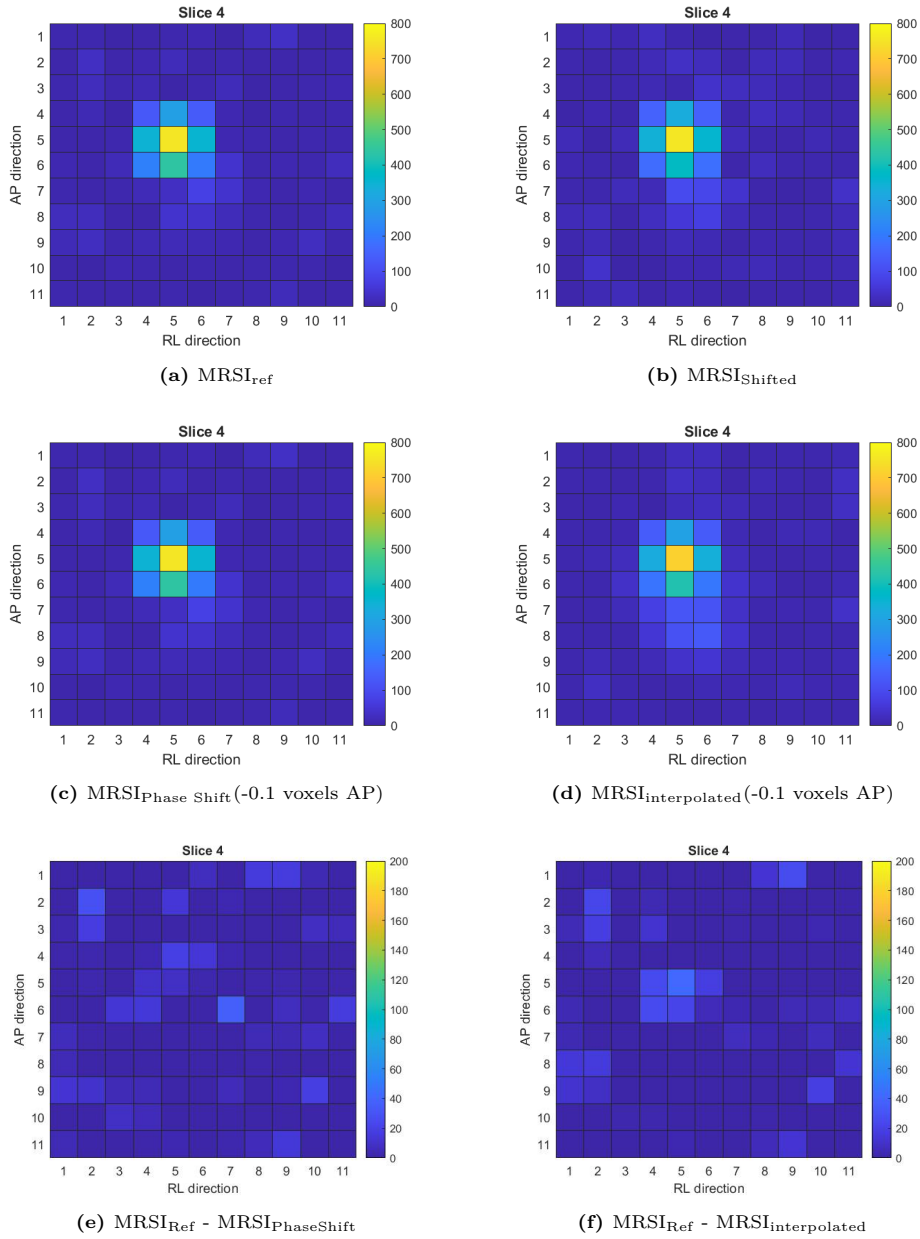


Figure C.2: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment. Where C.2a shows the AUC of MRSI_{Ref} , C.2b shows the AUC of $\text{MRSI}_{\text{shifted}}$, C.2c shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.1 voxels in the Anterior-Posterior (AP) direction ($\text{MRSI}_{\text{Phase Shift}}$), C.2d shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.1 in AP direction ($\text{MRSI}_{\text{interpolated}}$), C.2e and C.2f depict the differences between the shifted AUCs and the MRSI_{Ref} for k-space phase adjustment and spatial based interpolation, respectively.

Heatmaps for the 0.3 voxel shift in Left-Right (LR) direction

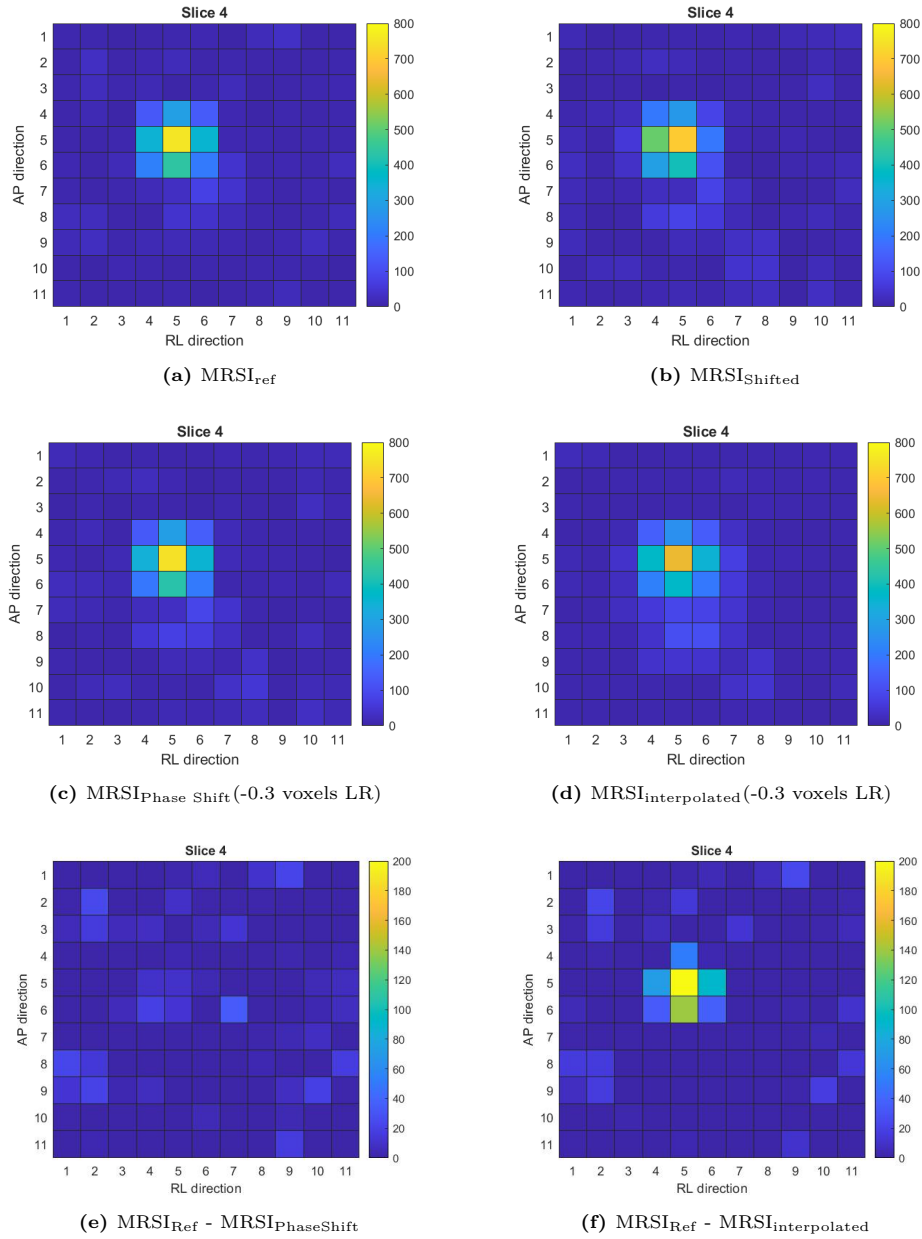


Figure C.3: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment. Where C.3a shows the AUC of MRSI_{ref} , C.3b shows the AUC of $\text{MRSI}_{\text{shifted}}$, C.3c shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.3 voxels in the Left-Right (LR) direction ($\text{MRSI}_{\text{phaseShift}}$), C.3d shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.3 in LR direction ($\text{MRSI}_{\text{interpolated}}$), C.3e and C.3f depict the differences between the shifted AUCs and the MRSI_{ref} for k-space phase adjustment and spatial based interpolation, respectively.

Heatmaps for the 0.5 voxel shift in Feet-Head (FH) direction

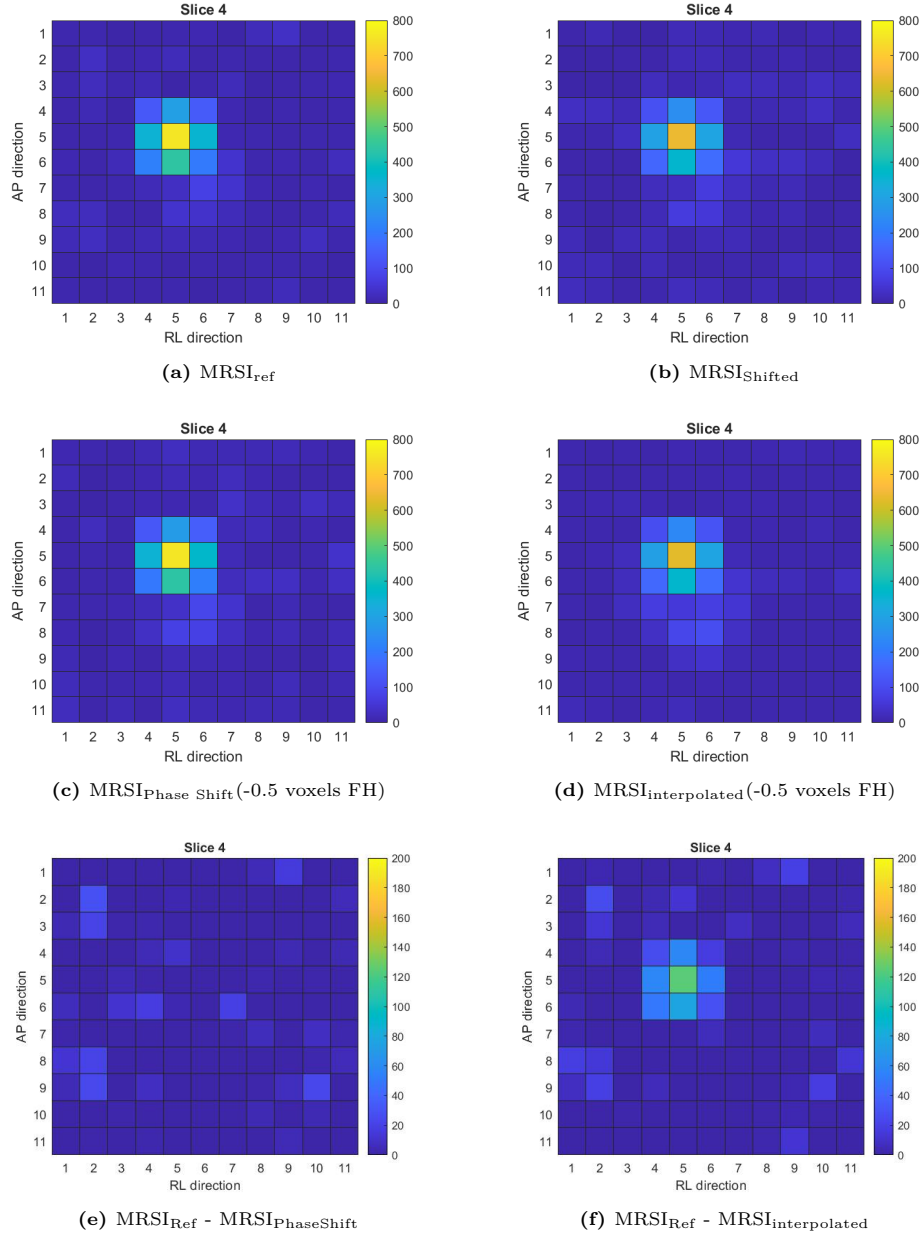


Figure C.4: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment. Where C.4a shows the AUC of MRSI_{Ref} , C.4b shows the AUC of $\text{MRSI}_{\text{shifted}}$, C.4c shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.5 voxels in the Feet-Head (FH) direction ($\text{MRSI}_{\text{Phase Shift}}$), C.4d shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.5 in FH direction ($\text{MRSI}_{\text{interpolated}}$), C.4e and C.4f depict the differences between the shifted AUCs and the MRSI_{Ref} for k-space phase adjustment and spatial based interpolation, respectively.

Heatmaps for the 0.3 voxel shift in Anterior-Posterior (AP), Left-Right (LR), and Feet-Head (FH) direction for voxel size $10 \times 10 \times 10 \text{ mm}^3$

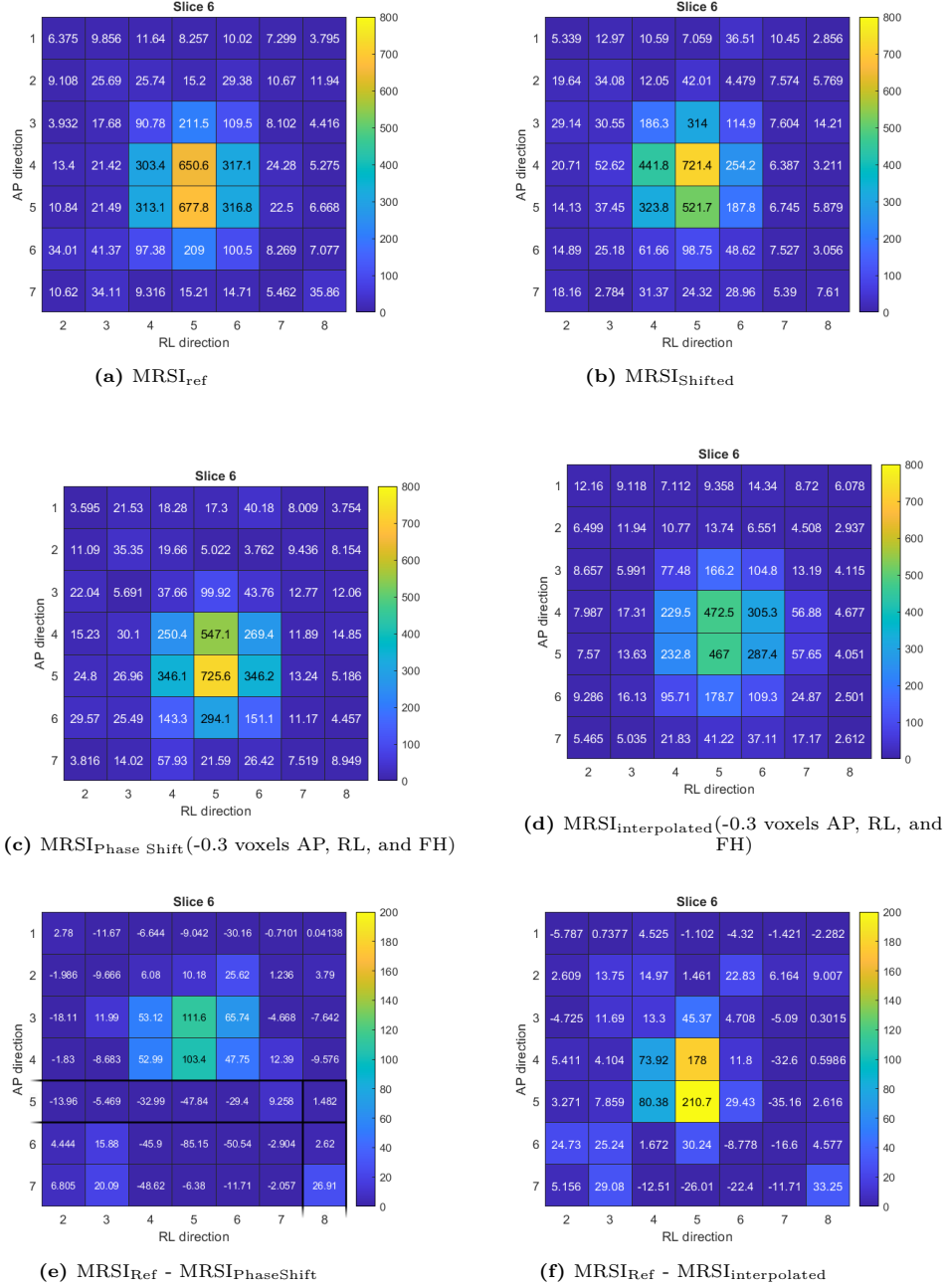
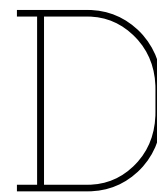


Figure C.5: Heatmaps of the area under the curve (AUC) of the signal of inorganic phosphate (Pi) in the phantom experiment with the voxel size $10 \times 10 \times 10 \text{ mm}^3$. Where C.5a shows the AUC of MRSI_{ref} , C.5b shows the AUC of $\text{MRSI}_{\text{shifted}}$, C.5c shows the AUC of $\text{MRSI}_{\text{shifted}}$ after phase adjustment in k-space by -0.3 voxels in the Anterior-Posterior (AP), Right-Left (RL), and Feet-Head (FH) directions ($\text{MRSI}_{\text{Phase Shift}}$), C.5d shows the AUC of $\text{MRSI}_{\text{shifted}}$ after spatially based interpolation by -0.3 in AP, RL, and FH direction ($\text{MRSI}_{\text{interpolated}}$), C.5e and C.5f depict the differences between the shifted AUCs and the MRSI_{ref} for k-space phase adjustment and spatial based interpolation, respectively.



^{31}P -MRSI code for grid calculations

```
1 %% MRI Data Processing and Tumor Volume Analysis
2 % This script processes MRI and MRSI data for voxel alignment and tumor volume estimation.
3 % It loads patient data, aligns imaging modalities, visualizes voxel grids, and computes
   tumor coverage.
4 %
5 % Author: Hilde Roording
6 %
7 % Key Steps:
8 % - Load subject-specific MRI and MRSI data from predefined directories.
9 % - Align FLAIR and SmartBrain images, ensuring correct spatial dimensions.
10 % - Generate and visualize voxel grids before and after displacement.
11 % - Determine voxel-wise displacement using manual selection and correction.
12 % - Compute the percentage of tumor coverage in each voxel before and after alignment.
13 % - Save results, including displacement values and tumor volume percentages.
14
15 close all
16 clear all
17 clc
18 addpath(genpath('H:\MATLAB\FID-A\FID-A-master'))
19 addpath(genpath('Z:\F_DataAnalysis\ImageRegistration_Dominique'))
20 addpath(genpath('H:\MATLAB\MRS_MRI_libs-master'))% FID-A toolbox
21 addpath(genpath('W:\F_DataAnalysis'))
22 addpath(genpath('W:\G_Output'))
23
24 %% Subject info
25 % subj ID, timepoint, DICOM smartbrain sagittal, spar file original data, slice with tumor
26
27 % subject_info={'MITCH_224', 'Baseline', 'SBSag','RECREATED_DBIEX_7_2_raw_act',5;};
28
29 plotdata.subject_info=subject_info;
30
31 MITCH_dir = '\\ds\data\BEELD\Wetenschap\MITCH\'
32 % MITCH_dir = 'H:\';
33
34 pp=1; % If only one patient is present in subject_info
35
36 % Set paths smart brain, FLAIR registered to smart brain and spar file
37 dirFLAIR_final=[MITCH_dir subject_info{pp,1} '\\' subject_info{pp,2} '\\Classic\Results\x.
   Registration\reg_FLAIR_SB\x.Transformix_FLAIR'];
38
39 dirMask_final=[MITCH_dir subject_info{pp,1} '\\' subject_info{pp,2} '\\Classic\Results\x.
   Registration\reg_FLAIR_SB\x.Transformix_mask'];
40 dirMRS=[MITCH_dir, subject_info{pp,1},'\\', subject_info{pp,2}, '\\Classic\Data'];
41 path_SB = [dirMRS '\\DICOM\' subject_info{pp,3}];
42 spar_info=mrs_readSPAR([dirMRS '\\' subject_info{pp,4}]);
43 % [spar_name,spar_path] = uigetfile({'*.spar'},'Select a file',dirMRS);
44 % spar_info=mrs_readSPAR([spar_path '\\' spar_name]);
45
46 % Directory to save images
```

```

47 plotdata.save_dir = [MITCH_dir subject_info{pp,1}, '\ ' subject_info{pp,2} '\Plots_Grid\
    Grid_BeforeShift_HR_202501'];
48 mkdir(char(plotdata.save_dir));
49 plotdata.save_dir_afterShift=[MITCH_dir subject_info{pp,1}, '\ ' subject_info{pp,2} '\
    Plots_Grid\Grid_AfterShift_HR_202501'];
50 mkdir(char(plotdata.save_dir_afterShift));
51
52
53 % Check if the spar file is the right one it should be-> scan_id : 3D CSI FID FA 11p4 20
    x20x20 NSA 28_MITCH
54 if spar_info.averages~=28
55     error('Warning!\_This\_is\_not\_correct\_spar\_file;\_stop')
56 end
57
58 % Load in FLAIR and MASK, if no mask available create a mask of zeros
59 [rFLAIR, resFLAIR] = ReadRawImage([dirFLAIR_final, '\FLAIR_reg_SB_PV.mhd']);
60 [mask, mask_res] = ReadRawImage([dirMask_final, '\Tumor_reg_SB_PV.mhd']);
61 % mask=zeros(size(rFLAIR));
62
63
64 info_SB = dicominfo([dirMRS, '\DICOM\ ', subject_info{pp,3}]);
65
66 if ~isequal(info_SB.PulseSequenceName, 'T1TFE')==1
67     error('Warning!\_This\_is\_not\_SmartBrain\_7T;\_stop')
68 end
69
70 disp(['Size\_of\_rFLAIR:\_', mat2str(size(rFLAIR))]);
71 disp(['Size\_of\_Mask:\_', mat2str(size(mask))]);
72
73 if ~isequal(size(rFLAIR), size(mask))
74     error('Warning!\_The\_FLAIR\_and\_Mask\_do\_not\_have\_the\_same\_size');
75 end
76
77 % % Visualize all slices
78 % figure(); subplot(1,2,1); montage(rFLAIR,'DisplayRange',[ ]);
79 % subplot(1,2,2); montage(mask,'DisplayRange',[ ]);
80
81 rImage=rFLAIR;
82 plotdata.resImage=resFLAIR;
83 % The spar could be either type 1 or 2 the patient data is type 1 the
84 % phantom data is type 2
85
86
87
88 %% Code for when everything is read in
89 % Extract offcenter smart brain
90 pixelspac_SB = info_SB.PerFrameFunctionalGroupsSequence.Item_1.PixelMeasuresSequence.Item_1.
    PixelSpacing;
91 thickness_SB = info_SB.SpacingBetweenSlices;
92 spacing_SB = [pixelspac_SB(1) thickness_SB pixelspac_SB(2)];
93
94 SB_AP_off = info_SB.Private_2001_105f.Item_1.Private_2005_1078;
95 SB_RL_off = info_SB.Private_2001_105f.Item_1.Private_2005_107a;
96 SB_FH_off = info_SB.Private_2001_105f.Item_1.Private_2005_1079;
97
98 sb_rows=info_SB.Rows;
99 sb_columns=info_SB.NumberOfFrames;
100
101 % Add and remove zeros from the FLAIR to make sure the dimensions are
102 % correct
103 if (size(rFLAIR,1) ~= sb_rows) && (size(rFLAIR,2) ~= sb_columns)
104
105     rImage = padarray(rImage,[0 round((sb_columns*spacing_SB(2)/resFLAIR(2)))-size(rImage,2)
        0],0,'post');
106     plotdata.rImage = rImage(1:(sb_rows*spacing_SB(1)/resFLAIR(1)), :, :);
107
108     rMask = padarray(mask,[0 round((sb_columns*spacing_SB(2)/mask_res(2)))-size(mask,2) 0],0,
        'post');
109     plotdata.mask = rMask(1:(sb_rows*spacing_SB(1)/mask_res(1)), :, :);
110     plotdata.rImage = padarray(plotdata.rImage,[20 20 0],0,'both');
111     plotdata.mask = padarray(plotdata.mask,[20 20 0],0,'both');

```

```

112 else
113     disp('The FLAIR has the same size as the SmartBrain')
114     plotdata.rImage = padarray(rFLAIR,[20 20 0],0,'both');
115     plotdata.mask = padarray(mask,[20 20 0],0,'both');
116 end
117
118 %% Add offcenter information !!!!
119 % Define the spar info type when loading in the images. Patient data is
120
121     plotdata.offcAP = -round(SB_AP_off - spar_info.offcentre(2));
122     plotdata.APpix = plotdata.offcAP/plotdata.resImage(1);
123
124
125     plotdata.offcRL = -round(SB_RL_off - spar_info.offcentre(1));
126     plotdata.RLpix = plotdata.offcRL/plotdata.resImage(2);
127
128     plotdata.offcFH = round(SB_FH_off - spar_info.offcentre(3));
129     plotdata.FHpix = plotdata.offcFH/plotdata.resImage(3);
130
131
132 %% Calculate size of the grid
133 plotdata.inputCSI = [11 11 9];
134 [plotdata.AP, plotdata.RL, plotdata.FH] = size(plotdata.rImage);
135
136 % The grid is centered on the image and has dimensions 20mm*resolution
137 % of the image. The image field of view (FOV) is larger than the grid FOV.
138 % The Halfdif is the distance to the grid as seen from the image.
139 % Halfdif=(FOV-FOV_GRID)/2
140 plotdata.APhalfdif = round((plotdata.AP-((plotdata.inputCSI(1)*20)/plotdata.resImage(1)))/2);
141 plotdata.RLhalfdif = round((plotdata.RL-((plotdata.inputCSI(2)*20)/plotdata.resImage(2)))/2);
142 plotdata.FHhalfdif = round((plotdata.FH-((plotdata.inputCSI(3)*20)/plotdata.resImage(3)))/2);
143
144 % Z halfdif important for what slices of the MRI are displayed for grid slices
145 plotdata.VoxFH = round(plotdata.FHhalfdif-plotdata.FHpix:((plotdata.FH-(2*plotdata.FHhalfdif)
146 )/plotdata.inputCSI(3)):plotdata.FH(end)-plotdata.FHhalfdif-plotdata.FHpix);
147
148 plotdata.VoxRL = round(plotdata.RLhalfdif-plotdata.RLpix:((plotdata.RL-(2*plotdata.RLhalfdif)
149 )/plotdata.inputCSI(2)):plotdata.RL(end)-plotdata.RLhalfdif-plotdata.RLpix);
150
151
152 % Initialize with no displacement
153 Displacement.AP_relative=0;
154 Displacement.RL_relative=0;
155 Displacement.FH_relative=0;
156
157 % Make the sagittal image and mask by permuting, rotating and flipping
158 sag_trans_new=permute(plotdata.rImage, [3, 1, 2]);
159 sag_intermediate = rot90(sag_trans_new, 2);
160 plotdata.rImageSag = flip(sag_intermediate, 2);
161
162 mask_trans_new= permute(plotdata.mask, [3, 1, 2]);
163 mask_intermediate = rot90(mask_trans_new, 2);
164 plotdata.maskSag = flip(mask_intermediate, 2);
165
166 mydlg = warndlg('press "CTRL+C" in command window, do the visualization manually', 'AWarning
167 _Dialog');
168 waitfor(mydlg);
169
170 disp('press "CTRL+C" keys in the Command Window');
171 pause
172
173 %% Visualization
174 % Define before shift as 1 and after shift as 2 to make sure the images are
175 % saved in the right folder
176 no_saving= 0;
177 before_shift=1;
178 after_shift=2;
179
180 % Choose before_shift to save images in the folder defined at the beginning
181 saving_choice=no_saving;
182
183 % Plot middle slice of the FLAIR for each CSI slice
184 k_full_cor=1:plotdata.inputCSI(3);

```



```

180 plot79=PlotGridHR(plotdata,Displacement, k_full_cor,saving_choice);
181 k_full_sag=1:plotdata.inputCSI(2);
182 plot167=PlotGridSagHR(plotdata,Displacement, k_full_sag,saving_choice);
183
184 % Choose an RL slice on the sagittal image where you want to shift in AP-FH direction
185 RL_slice=6;
186 plot300=PlotGridSagHR(plotdata,Displacement, RL_slice,no_saving);
187
188 %Choose an FH slice where you want to shift the coronal image in AP-RL direction.
189 FH_slice=4;
190 plot7=PlotGridHR(plotdata,Displacement, FH_slice,no_saving);
191
192 % Choose a slice where you want to shift in AP-FH direction
193 q=1:9;
194 plot489=PlotGridAllSlicesHR(plotdata,Displacement,q,saving_choice);
195 close all
196
197 %% FH-AP displacement !!First select appropriate RL-slice!!
198 Displacement = FindDisplacementSagHR(plotdata,Displacement,RL_slice);
199 plot300=PlotGridSagHR(plotdata,Displacement, RL_slice,no_saving);
200
201
202 %% AP-RL displacement !!First select appropriate FH-slice!!
203 % First plot all slices of the coronal plane of the slices with tumor as
204 % visualized with the images made above:
205 Displacement = FindDisplacementHR(plotdata,Displacement,FH_slice);
206 plot796=PlotGridHR(plotdata,Displacement, FH_slice,no_saving);
207
208 %% Check the alignment and if neccessary repeat code
209 t=5;
210 plot156=PlotGridAllSlicesHR(plotdata,Displacement,t,no_saving);
211
212
213 %% Calculate the percentage tumor in a voxel
214 Displacement_zeros.AP_relative=0;
215 Displacement_zeros.RL_relative=0;
216 Displacement_zeros.FH_relative=0;
217
218 PercentageTumor_noDisplacement=PercentageTumorInVoxel(plotdata,Displacement_zeros, FH_slice);
219 PercentageTumor=PercentageTumorInVoxel(plotdata,Displacement, FH_slice);
220
221 Results=Displacement;
222 Results.PercentageTumor_noDisplacement=PercentageTumor_noDisplacement;
223 Results.PercentageTumor=PercentageTumor;
224
225 %% Saving all the shifted images, displacement and tumor volume
226 cd([plotdata.save_dir_afterShift]);
227 save('Results.mat','Results')
228
229 saving_choice=after_shift;
230 plot79=PlotGridHR(plotdata,Displacement, k_full_cor,saving_choice);
231 plot167=PlotGridSagHR(plotdata,Displacement, k_full_sag,saving_choice);
232 plot156=PlotGridAllSlicesHR(plotdata,Displacement,q,saving_choice);
233 close all

```