

More for Less? Mapping Cortical Metabolites using Multi-Voxel Magnetic Resonance Spectroscopy

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Authors:

Thomas Shaw¹, Zeinab Eftekhari¹, Korbinian Eckstein¹, Bernhard Strasser², Fabian Niess², Wolfgang Bogner², Markus Barth¹

Institutions:

¹The University of Queensland, Brisbane, Australia, ²Medical University of Vienna, Vienna, Austria

First Author:

Thomas Shaw, PhD

The University of Queensland
Brisbane, Australia

Co-Author(s):

Zeinab Eftekhari

The University of Queensland
Brisbane, Australia

Korbinian Eckstein

The University of Queensland
Brisbane, Australia

Bernhard Strasser, Ph.D

Medical University of Vienna
Vienna, Austria

Fabian Niess, Ph.D

Medical University of Vienna
Vienna, Austria

Wolfgang Bogner

Medical University of Vienna
Vienna, Austria

Markus Barth

The University of Queensland
Brisbane, Australia

Introduction:

Concentric ring trajectory-based free induction decay magnetic resonance spectroscopic imaging (MRSI) is a non-invasive technique for generating high-resolution maps of metabolites across the whole brain within reasonable timeframes at both 3T and 7T MRI[1]. Compared to single voxel spectroscopy, MRSI allows for the combination of metabolite maps with segmentations of grey and white matter (GM/WM), allowing for specific metabolite maps of glutamate, glutamine, N-Acetyl-Aspartate (NAA), and creatine

across the cortex and some subcortical regions at 3T and 7T. Previous studies have explored the reproducibility of this technique[2,3], but comparison of MRSI across 3T and 7T in different brain regions have not been performed, which is vital for validation of the technique in GM and WM regions. Considering the improved SNR and spectral resolution at 7T[4], this technique is promising for mapping (sub)cortical metabolite profiles in research settings; while its application in 3T sites lends itself to easy clinical adoption in the future. Here, we show how the upper half of the cortex and white matter can be mapped reliably over time and discuss the implications for future MRS studies.

Methods:

We conducted two scan sessions, 5-9 days apart, on five healthy participants (three female, age: 25-33) using both 7T (Siemens Magnetom 7T+) and 3T (Siemens Prisma) scanners. 3D-FID-MRSI parameters 3T: FOV=220x220x110mm, matrix size=32x32x21 at 6.3 mm³ iso, TA=4:14 min; 7T: FOV=220x220x110mm, matrix size=64x64x31 at 3.4mm³ iso, TA=11:30. A T1-w MP2RAGE was acquired for segmentation using FastSurfer[7] and metabolic maps were interpolated onto the Desikan-Killiany-Tourville (DKT) atlas' cortical surface for visualisation and as proof of concept for cortical metabolic mapping. MRSI spectroscopic quantification was performed in LCModel[6]. Maps were overlaid with T1w DKT segmentations (Fig 1). The FOV of MRSI allowed for quantification of 12 bilateral GM and one WM ROI (25 total). We report on three important metabolite ratios relevant for neurodegenerative diseases: NAA/tCr, Glx/tCr, and Glx/tNAA. Mean concentrations at each ROI and field-strength and the intra- and inter-subject Coefficient of Variation (CV) were calculated to assess reproducibility.

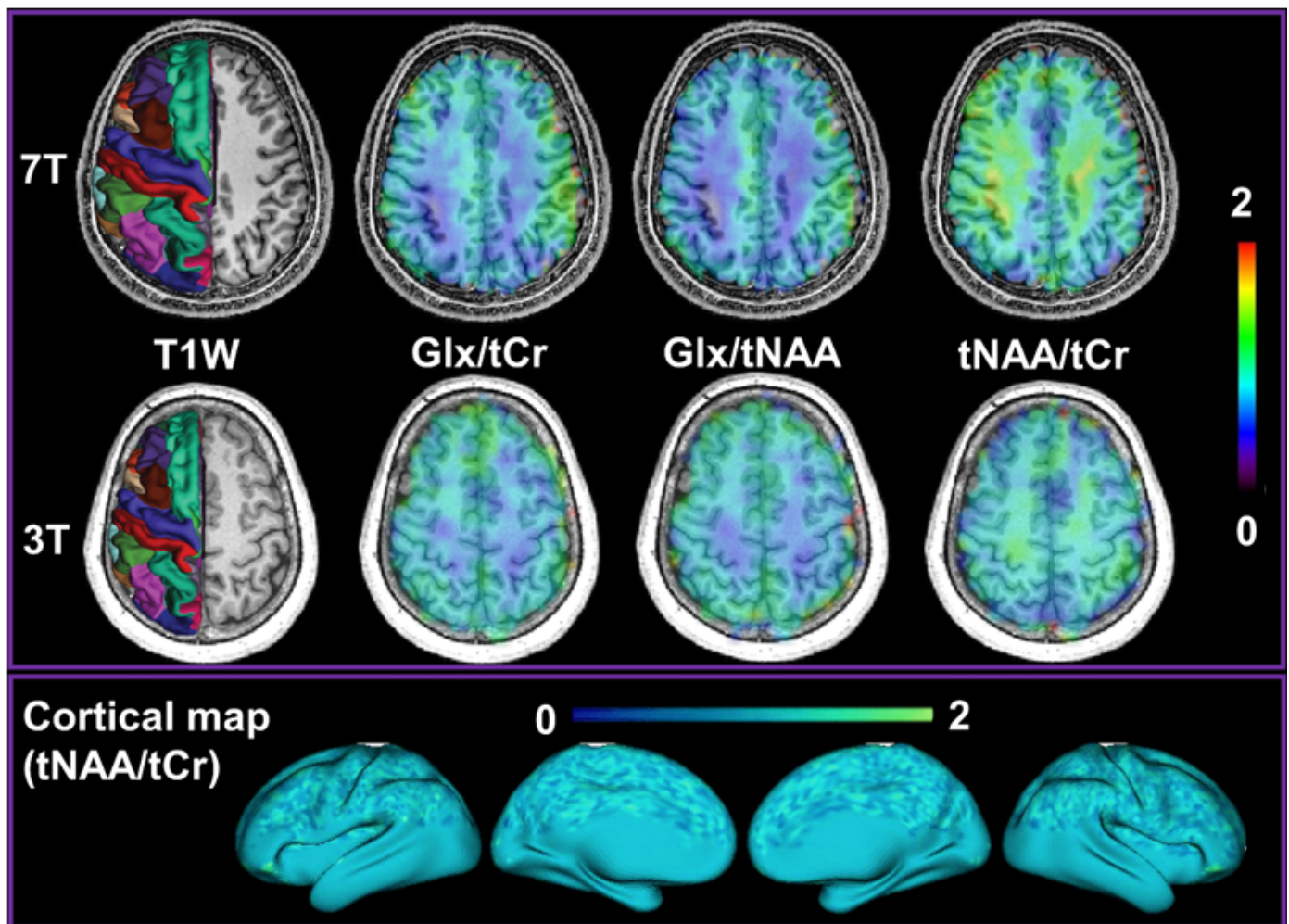


Figure 1: (Top) Metabolic maps of three important metabolites [tNAA = N-acetyl-aspartate (NAA)+ N-acetyl-aspartyl (NAAG); Glx= Glutamate (Glu) + Glutamine (Gln); tCr = Creatine (Cr) + phosphocreatine (PCr)] together with anatomical T1-weighted (T1w) images acquired at 7T (top) and 3T (bottom). DKT parcellations are overlaid on the T1w image. (Bottom) The tNAA/tCr map sampled onto the cortical surface. Colour bars indicate relative concentrations.

·Figure 1

Results:

We examined reproducibility for three metabolite ratios across 25 DKT brain regions using test-retest at 3T and 7T. Across ROIs, the metabolite concentration ratio estimates were stable between subjects and within subject at both fields (Fig 2). Mean \pm SD concentrations were in line with literature[2,3]. The coefficient of variation (CV) for metabolite ratios across most ROIs did not exceed 12% (mean value, 6%; 3T, 7T), which indicated excellent reproducibility for both fields. Metabolic maps were successfully sampled onto FastSurfer cortical surfaces (Fig 1), revealing (for the first time) patterns of metabolic expression over the cortex. We observed higher variability in certain ROIs (e.g., rostral middle frontal) compared to others (e.g., paracentral lobule).

7T Scatterplot of Metabolite ratios

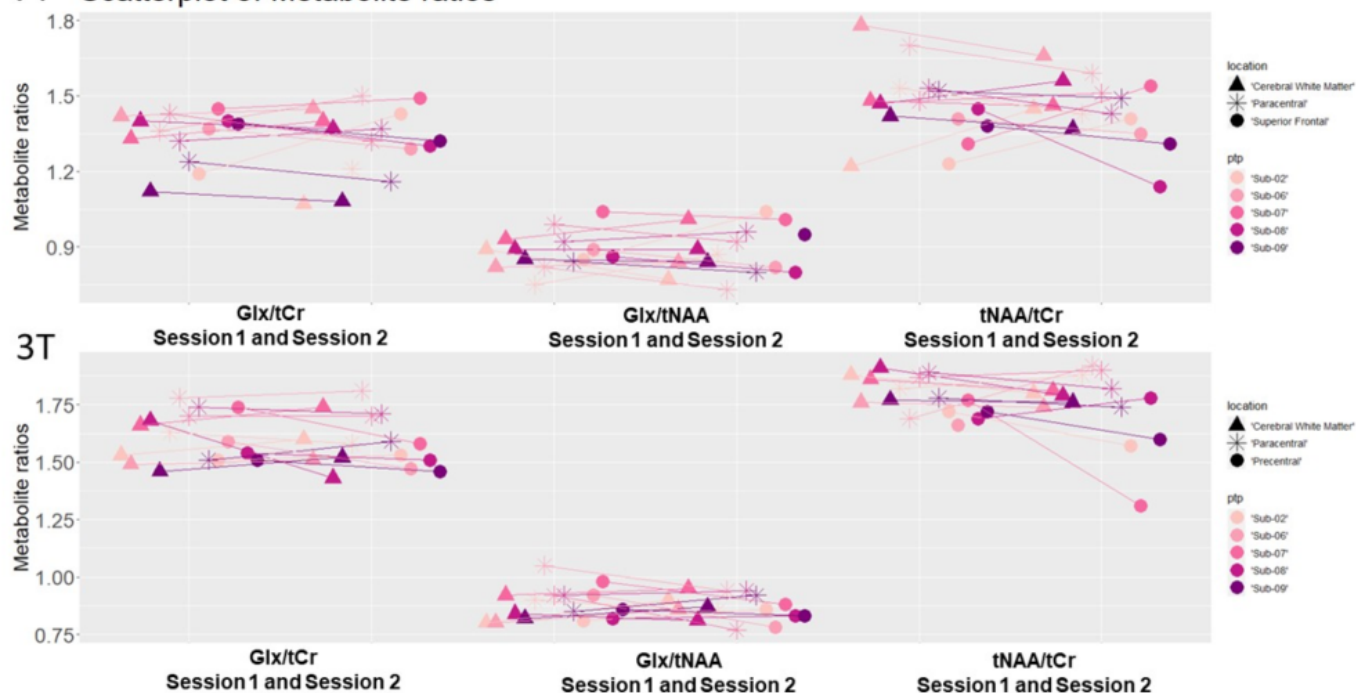


Figure 2: Relative changes of concentration ratios between two sessions with a week apart for three metabolite ratios across select brain regions at both 7T (top) and 3T (bottom). The outlier in the NAA ratios is likely due to a lipid artifact. Points are intentionally jittered.

·Figure 2

Conclusions:

The introduction of a cortical sampling technique for spectroscopy data unlocks the possibility of mapping the metabolic expression of the brain in a reliable, longitudinal manner. Results indicated a high degree of reproducibility for metabolites at both fields, with most ROIs demonstrating higher reproducibility at 3T compared to 7T, likely due to reduced participant movement over the shorter scan time. The variability of NAA/tCr across ROIs was substantial (2.1 CV% to 12 CV%), and besides actual biological variability, this may also be related to lipid contamination in some regions/subjects, warranting further investigation. Our results suggest that ratios of metabolite concentrations can be reproducibly measured with 3D-FID-MRSI at 3T and 7T, and these can be sampled onto the cortex of many brain regions. Scan time is an important factor for variability, and one could test to reduce scan time if lower spatial resolution is not an issue.

Neuroanatomy, Physiology, Metabolism and Neurotransmission:

Cortical Anatomy and Brain Mapping ²

Novel Imaging Acquisition Methods:

MR Spectroscopy ¹

Keywords:

Cortex
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Magnetic Resonance Spectroscopy (MRS)
MR SPECTROSCOPY
Neurotransmitter

¹²Indicates the priority used for review

Abstract Information

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No

Please indicate below if your study was a "resting state" or "task-activation" study.

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Healthy subjects only or patients (note that patient studies may also involve healthy subjects):

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Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.

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Not applicable

Please indicate which methods were used in your research:

Structural MRI

Other, Please specify - Magnetic Resonance Spectroscopy

For human MRI, what field strength scanner do you use?

3.0T

7T

Which processing packages did you use for your study?

FSL

Free Surfer

Other, Please list - LCModel, FastSurfer

Provide references using author date format

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