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P3

Optimizing rosette spectroscopic imaging for mapping neurotransmitters at 7T

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BACKGROUND

Magnetic resonance spectroscopic imaging (**MRSI**) enables the measurement of maps of brain metabolite, but:

- is limited by temporal and spatial resolution, long acquisition times, and low signal to noise ratio (SNR)[1]

In this work we aim to demonstrate:

- **a 2D rosette MRSI (RSI) sequence employing SLOW editing [2] and accelerated k-space sampling[3]**
- **a reconstruction pipeline involving k-space and phase distortion corrections**
- **measurements of brain neurotransmitter maps (Glu, GABA) within 5min**

METHODS

- measurements were conducted in 2 healthy subjects (1 female; 24/26yrs) on a 7T Terra.X MR scanner (~20min per subject)
- MP2RAGE images were used for slice adjustment **[Fig. 3]**

Edited RSI:

- an MRSI sequence based on the GABA SLOW[2] editing was implemented and extended by a rosette trajectory readout[5] (BW: 2.5kHz, G_{max}: 13.5mT/m, $Slew_{max}$: 206.4T/m/s) **[Fig. 1, left]**
- an optimized Five variable Angle gaussian pulse with ShorT duration (FAST[4]) scheme was used for water suppression (WS)
- the resolution was set to 7.5 x 7.5 x 20mm³ (FoV: 240 x 240mm²)
- a water reference scan was used for coil combination and k-space trajectory correction (1:15min, 50 RSI petals)
- edited ON/OFF scans were acquired interleafed (4:30min, 100 RSI petals, TR/TE 1300/68ms, TE_1=TE_2, 2 prep scans)

Data reconstruction & processing:

- reconstruction used a nonuniform FFT[5] and included k-space distortion and phase correction steps **[Fig. 2]**
- ON/OFF scans were frequency/phase aligned and subtracted to obtain EDITED spectra
- L_2 regularization was used for lipid suppression[6]
- to evaluate SNR and spectral quality improvements reconstruction was repeated without k-space and phase correction using only the first petal half – common approach[7]

Analysis & fitting:

- linear combination modelling was performed in LCModel[8] including 17 metabolites (Asp, Cr, GABA, GPC, GSH, Glc, Gln, Glu, Gly, NAA, NAAG, PCho, PCr, PE, Tau, mI, sI) for editing OFF and 4 metabolites (NAA, Glu, Gln and GABA) for EDITED spectra

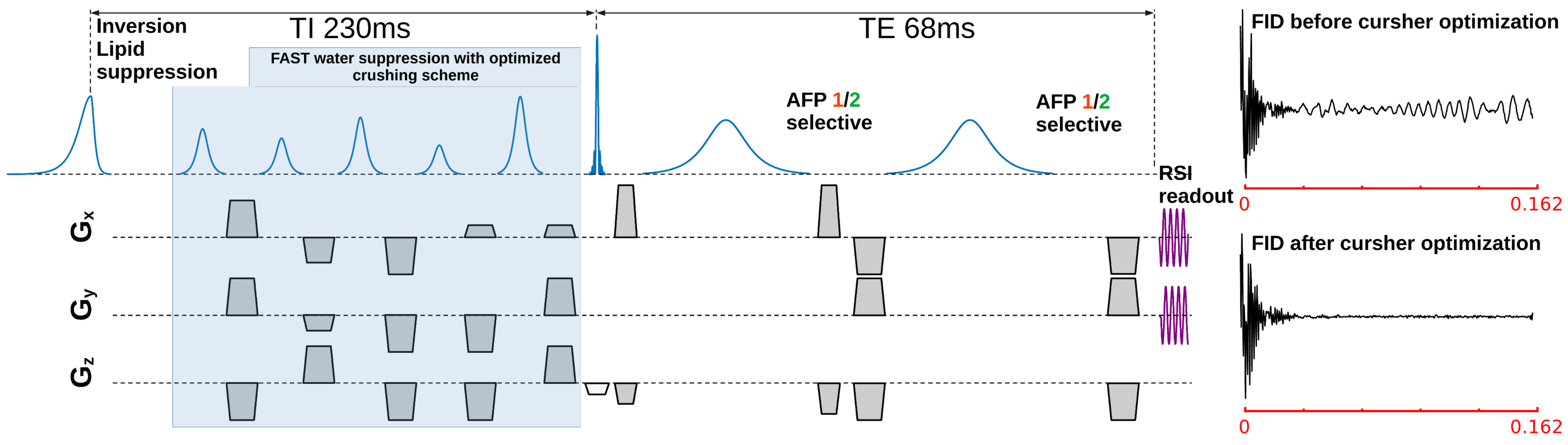

Fig. 1: Left: Sequence design including: lipid suppression, FAST water suppression, frequency selective adiabatic refocusing (AFP) editing pulses and rosette (RSI) readout. Right: FID signal from pixel in prefrontal cortex before and after crusher optimization.

RESULTS

- the crushing scheme optimized for FAST WS[9] largely reduced spurious echoes **[Fig. 1, right]**
- if k-space trajectory remains uncorrected noticeable image shrinkage and blurring was observed **[Fig. 2, top-left]**
- k-space correction enables to mitigate image distortions and recover image scaling **[Fig. 2, bottom-left]**
- linear phase evolution was corrected by phase alignment of spectra reconstructed from the first and second petal halves **[Fig. 2, right]**
- SNR increased from 6.0 to 7.5 and 4.2 to 4.9 for edited OFF and EDITED spectra, respectively **[Fig. 3]**
- CRLBs decreased for all metabolites **[Fig. 3]**
- CRLBs are highest in the frontal lobe (strong B_0 distortions) **[Fig. 3]**
- anatomical features are clearly visible in the tCho maps [10] **[Fig. 3]**
- metabolite concentrations are in line with literature[11,12]

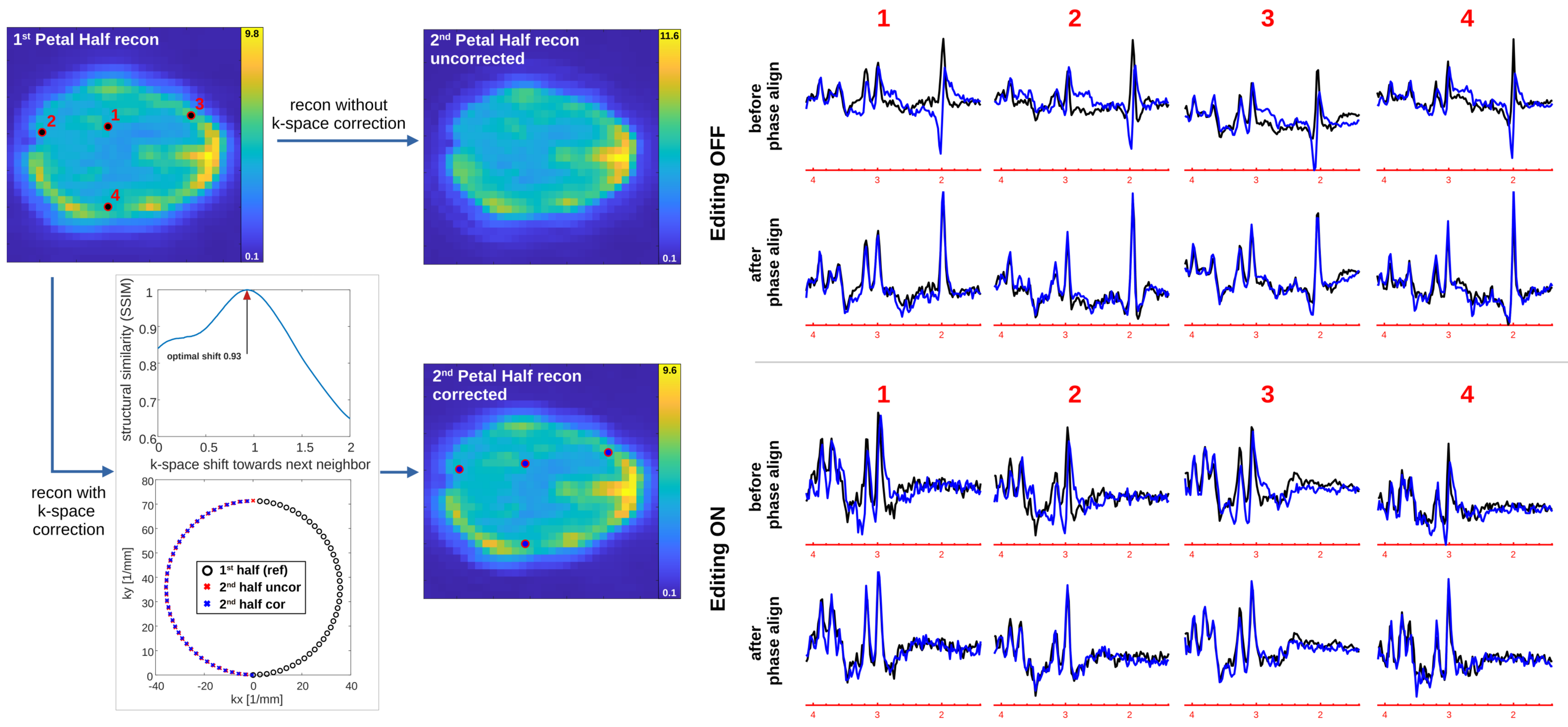

Fig. 2: Left: Correction of k-space trajectory compensates for image shrinkage. Right: Zero and first order phase correction of edited ON and edited OFF enables coherent averaging (particular with phase distortions for NAA).

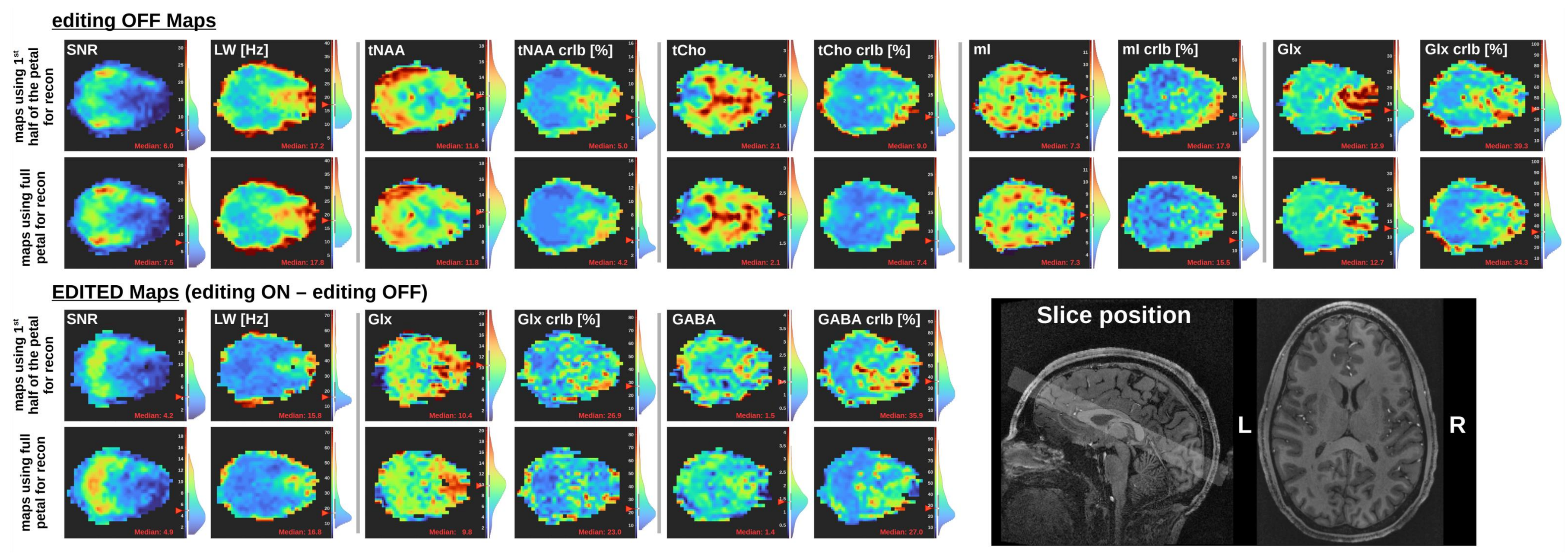

Fig. 3: Metabolite maps and CRLBs estimated for using only the 1st half of the RSI petals for reconstruction (upper row) or the full RSI petals (lower row). Right corner: Anatomical position of the slice tilted to cover prefrontal cortex, thalamic nuclei, and visual cortex.

DISCUSSION & CONCLUSION

- by employing an RSI sequence with an optimized full k-space reconstruction (k-space correction and phase alignment) we demonstrate improvements in SNR, spectral quality, and CRLBs of brain metabolite maps
- we introduce an optimized FAST water suppression scheme (5 pulses / tailored crushing scheme) to achieve a robust water suppression

These results can pave the way for implementing RSI combining real-time k-space measurements (e.g., using a field camera) with compressed sensing to achieve temporal resolution of ~3min.

References: [1] Bogner W, et al. NMR Biomed. 34:e4314 (2021); [2] Weng G, et al. MRM. 88:53–70 (2022); [3] Schirda CV, et al. JMRI. 29:1375-85 (2009); [4] Huang Z, et al. ISMRM Workshop on MRS, Boston MA USA (2024); [5] Fessler JA, et al. IEEE. 51:560–74 (2003); [6] Bilgic B, et al. MRM. 69:1501–11 (2013); [7] Schirda CV, et al. MRM. 76:380-90 (2015); [8] Provencher SW. NMR Biomed. 14:260-4 (2001); [9] Landheer K, et al. NMR Biomed. 81:1–13 (2019); {10] Shah C, et al. Front. Neurosci. 12:1–11 (2018); [11] Mekle R, et al. MRM. 61:1279–85 (2009); [12] Emir UE, et al. NMR Biomed. 25:152–60 (2012); **Acknowledgements:** This work is supported by the Swiss National Science Foundation (#213769).