Fast Adiabatic Spin Echo MRSI Sequence for Whole Brain 5mm-isotropic metabolic imaging

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Synposis:
A Proton 3D Adiabatic Spin-Echo (ADISE) MRSI sequence was implemented to measure metabolite distributions over whole brain with 5mm isotropic resolution. MRSI data were measured over volunteers and compare with FID-MRSI sequence. ADISE 3D-MRSI and 3D FID-MRSI acquisitions were accelerated with Compressed-sensing acceleration and reconstructed with a Low-Rank TGV-constrained model.

Introduction:
Free induction decay -MRSI (FID-MRSI) is a fast sequence that allows measurment of metabolic profiles across the whole brain at ultra-short echo-time (TE) and in high spatial resolution in 2D[1,2,3] or 3D[9,10,11]. The simple excite-acquire scheme of the sequence allow to reduce repetition time (TR), and acquisition time significantly by using a low flip angle. In combination with the other acceleration methods [4,5,9], whole-brain high-resolution acquisition is possible in a reasonable time. However, the FID-MRSI is a sequence scheme that might suffer from B_0 field in-homogeneity due to its gradient-echo architecture.
The aim of the research presented here is the implementation of a Fast ADISE MRSI sequence including signal refocusing pulse that would circumvent the T2* susceptibility of FID-MRSI but with the same low flip-angle, same TR, with the shortest TE possible, to match FID-MRSI acquisition time. Also, considering the large excitation slab of a 3D-MRSI sequence, adiabatic full passage (AFP) pulse were chosen to perform the signal refocussing and minimizing the chemical shift artefact in the slab direction.
The 3D Cartesian encoding was undersampled randomely to enable compressed-sensing acceleration[9] with a low-rank total generalized variation (TGV)-constrained reconstruction.
This research aims to compare the MRSI signal resulting from both acquisition sequences and compare the high-resolution 3D metabolite maps. The performance of the techniques is assessed on metabolite images, their respective Cramer-Rao-Lower-Bound (CRLB) values and spectral quality parameters (SNR,FWHM).

Method:

A volume selective 3D ADISE-MRSI sequence including WET water suppression was designed and implemented. The excitation pulse of 0.9 ms was designed with a Shinnar-Le Roux algorithm and set to excite 150% of the slab thickness. The excitation was followed by two adiabatic full-passage hyperbolic-secant pulses of 5ms with slab selective gradients and crushers set to refocus 100% of the slab thickness. This spin-echo sequence was made *Fast* with the shortest possible TE (20ms) and TR (360 ms) (Fig.1 A) and a low excitation flip-angle (35deg). The signal was recorded with 1024 points over a 4 kHz bandwidth.
The 3D FID-MRSI sequence used for the comparison (Fig.1 B) contains the same excitation pulse and has the same spectral resolution bandwidth and TR of 360 ms. The TE (or acquision-delay in this case) was 0.6ms.
The excited slab size was (A/P-R/L-H/F) 210x160x100mm. The 3D encoding volume was set slightly larger to 210x60x110mm to prevent aliasing and the encoding matrix was 42x32x22 resulting in a 125 mul voxel volume (5mm isotropic).
During acquisition, 3D Cartesian encoding for both ADISE and FID-MRSI was performed following a random undersampling pattern with a variable density[8,9] for an acceleration factor of 3.5 and an acquisition time of 20min (Fig.1 C). A water reference measurement was acquired to determine the coil sensitivity and the B0 fieldmap with the same FID-MRSI sequence but with a TR of 31 ms, 48 FID points and a 5-degree flip angle and a full elliptical k-space.

Three healthy volunteers were scanned on a 3T-scanner (Prisma/Siemens/Erlangen/Germany) with 64-channel receiving head coil. A 3D-T1-weighted *MPRAGE* sequence was acquired for anatomical landmarks. The 3D ADISE-MRSI and FID-MRSI were acquired in a row with the same FOV and excitations slab followed by the fast water reference scan.
The acquired undersampled 3D MRSI data were cleaned from skull lipids by *lipid-metabolite spectral orthogonality*[8,9] and reconstructed with low-rank TGV regularized model[7,8,9]. The reconstructed MRSI dataset was them quantified using LCModel[12] into NAA+NAAG (N-acetylaspartate and N-acetyl aspartylglutamate),

Cre+PCr (total creatine), Cho (choline-containing compounds), Ins (myo-inositol) and Glx (glutamate and glutamine).

Results :

In Fig.2, metabolite volumes resulting from the 3D Fast ADISE-MRSI sequence are exhibited with a quality reflected by the anatomical contrast highlighted in all metabolite distributions. Typical contrast for Cre+PCre and Cho metabolite are present but the metabolite signal loss is still present in region of strong B0 inhomogeneity. In Fig.3, the comparison between 3D Fast ADISE-MRSI versus 3D FID-MRSI illustrates the close similarity of the results. Due to longer TE timing, signal of ADISE-MRSI is slightly lower as shown by the sample spectra in Fig.3 and SNR maps presented in Fig.4. The fitting error estimated by CRLB values tend to be slightly higher for ADISE-MRSI than FID-MRSI as depicted by the histograms in Fig.4. Use of ADISE-MRSI doesn't improve much for signal loss due to B0 inhomogeneities. Although metabolite signal is refocussed by the spin echo sequence, the strong T2* relaxation consecutive to the B0 inhomogeneity results in a significant increase of the linewidth, and reduction of detectable metabolite signal. This phenomenon occurs identically in both sequences as illustrated by FWHM maps in Fig.4.

Discussion:

Original results of whole brain 3D Fast ADISE-MRSI were presented with a demonstration of the good quality of the results. Although overall spectral quality and quantification error are better using a FID-MRSI sequence, the results presented here demonstrate the feasibility of performing a spin-echo sequence in a reduced scan time over the whole brain. This paves the way to implementation of the Fast ADISE-MRSI squence with any TE to highlight specific metabolite or the implementation of spectral editing techniques requiring spin-echo. Although metabolite signal is refocussed by the two AFP pulses, there is still a strong signal loss in B0 inhomogeneity regions probably consecutive to T2* relaxation during FID.

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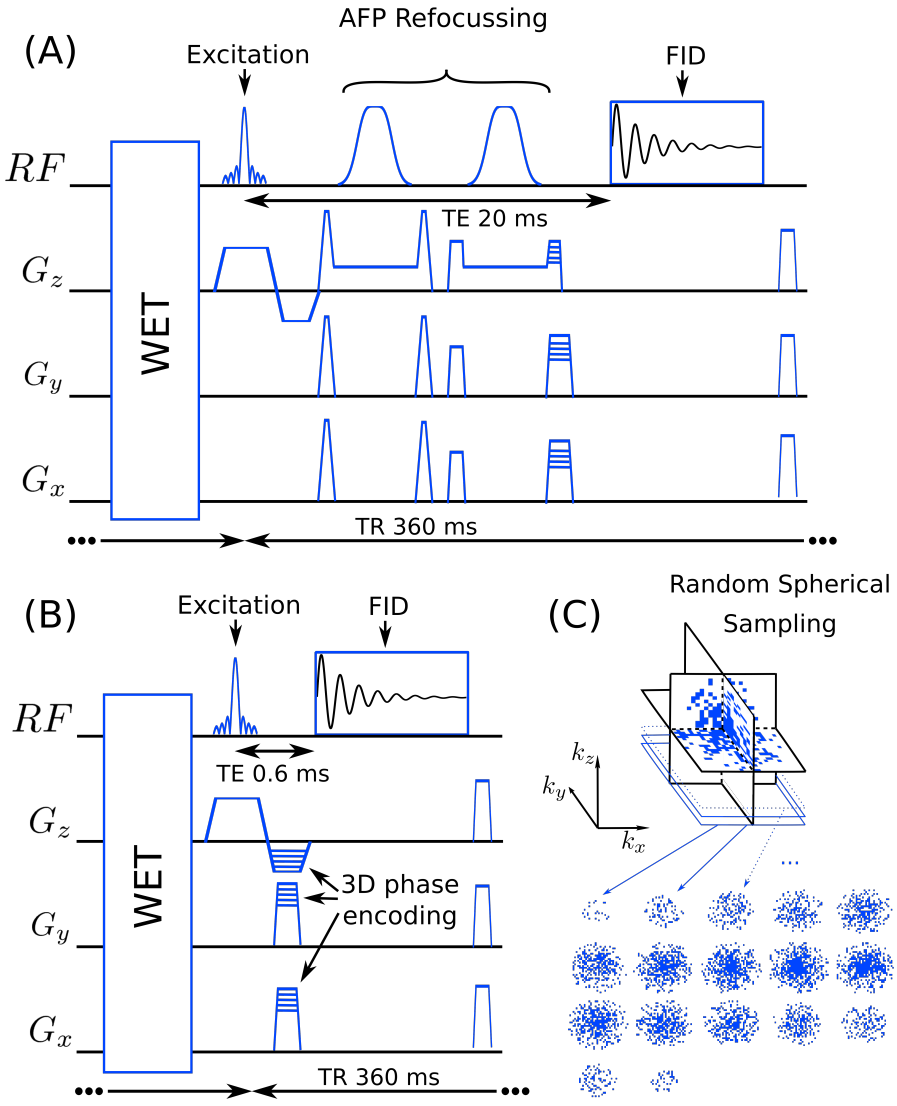

Figure 1: Scheme of the two sequences used for 3D MRSI. (A) The 3D ADISE-MRSI includes 2 adiabatic full passage refocusing pulses. (B) The 3D FID-MRSI consists of only one excitation pulse followed by the acquisition. (C) The Fourier domain encoding was perform with variable density random undersampling for both sequences.

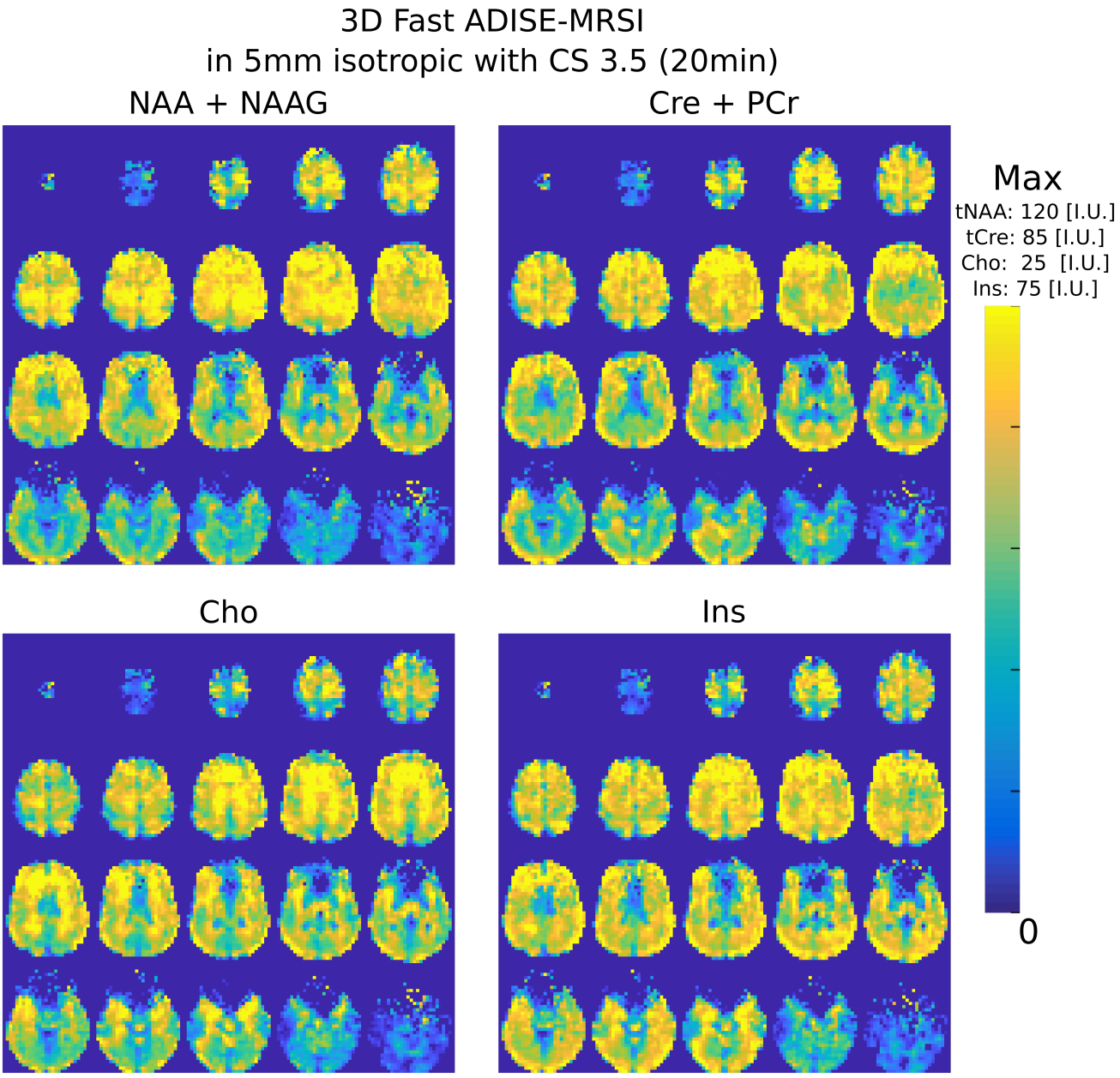

Figure 2: 3D metabolite maps reconstructed from the ADISE-MRSI CS3.5 acquisition. Maximum of the colorbar is expressed in institutional units (I.U.). The MRSI technique enable to measure metabolite distribution throughout the whole brain with a contrast unique to each metabolite.

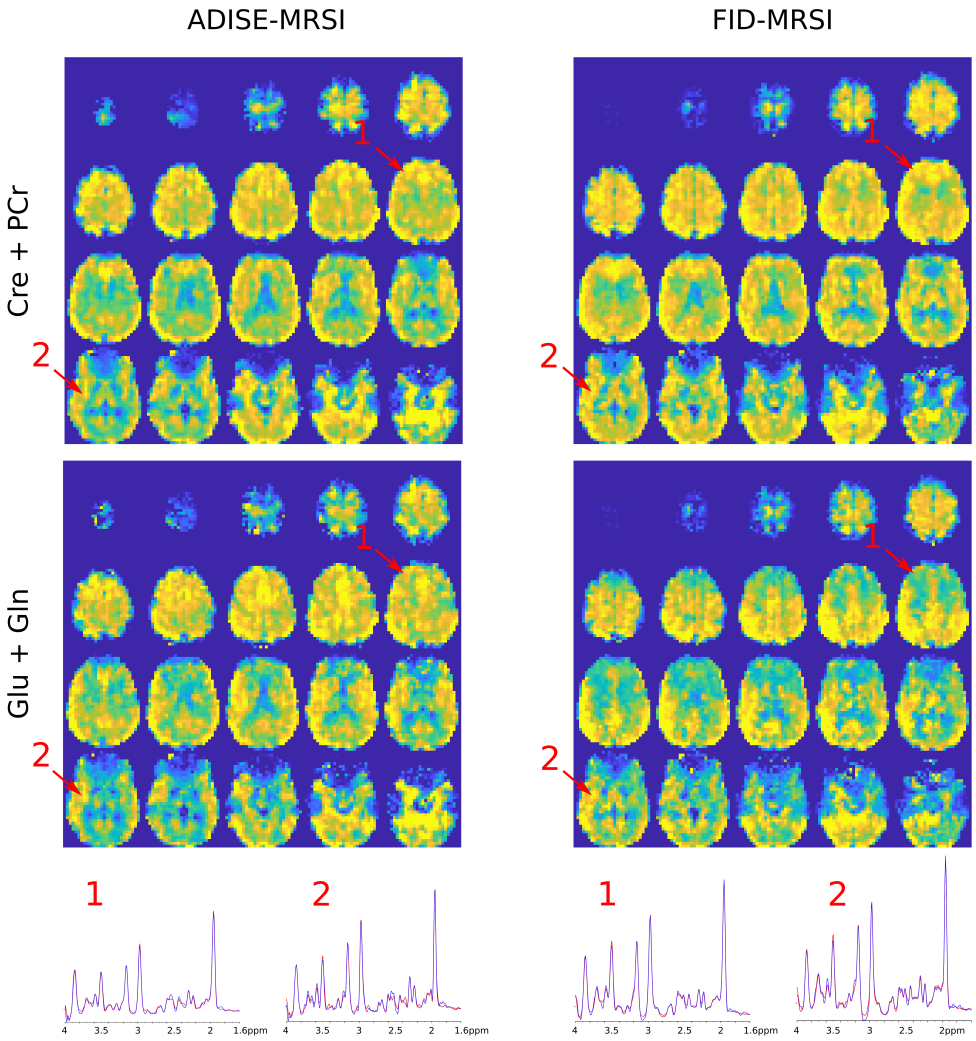

Figure 3: Comparison between 3D metabolite volumes resulting from ADISE-MRSI and FID-MRSI acquisition sequences acquired subsequently in one volunteer. Bottom, two sample spectra at same location for both sequences are shown on the same scale and exhibit a slightly lower signal with ADISE-MRSI sequence, consequence of the longer TE. Signal loss due to B0 inhomogeneity in frontal lobe is present with both sequences.

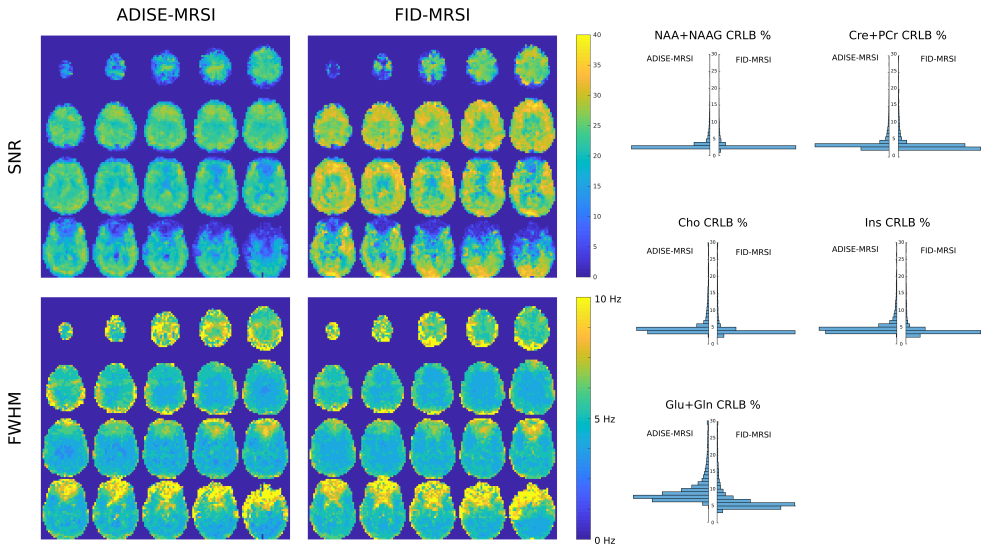

Figure 4: Comparison of spectral quality parameters between Fast ADISE-MRSI and FID-MRSI sequences on the same session. Left, the signal loss due to the longer TE for ADISE-MRSI is visible over the whole brain in the SNR map. FWHM maps exhibits no marked difference. Right, the histograms of the Cramer-Rao Lower Bound (CRLB) from the whole brain LCModel fitting resulting from both sequences are displayed side to side. Although there is no differences for NAA+NAAG, all other metabolites show a slight shift towards higher CRLB values for ADISE-MRSI. This is particularly visible for Glu+Gln that are known to be more difficult to quantify at longer TE due to J-coupling modulations of the signal.