2D & 3D high-resolution whole brain FID-MRSI at 3T accelerated by compressed-sensing

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Introduction

Free induction decay (FID)-MRSI sequence allows acquisition of metabolic profiles across the whole brain slices in 2D at high-resolution[1,2]. However, in clinical setting (3T), low SNR due to small voxel volume and longer FID acquisition time limit the technique. However, using a low-rank reconstruction model with TGV regularization, MRSI datasets can be efficiently denoised and accelerated with compressed-sensing SENSE. This research aimed to optimize both denoising and acceleration to make possible the 2D and 3D high-resolution FID-MRSI on 3T clinical MRI.

Methods

We implemented a 2D and 3D high-resolution (2D: 3.3x3.3x10mm / 3D: 5x5x5xmm) FID-MRSI sequences covering whole brain. Skull-lipid contamination was removed by post-processing[3] then the reconstruction was performed with a low-rank model including total generalized variation (TGV) regularization[4]. The regularized reconstruction including coil sensitivity profiles enable compressed-sensing SENSE acceleration by random k-space undersampling. The low-rank TGV reconstruction model was benchmarked with simulated MRSI data with or without acceleration. 2D & 3D FID-MRSI acquisitions of healthy-volunteer brains were reconstructed with the whole pipeline.

Results

Reconstruction was performed on healthy-volunteer (Fig. 2) and simulated data (Fig. 1). In both cases reconstructed data showed clear improvement with the low-rank TGV model compared to inverse Fourier reconstruction. Also, acceleration by compressed-sensing SENSE up to a factor 4 was feasible with minimal impact on either reconstruction errors and metabolite image quality (Fig.2 & 3).

Discussion

Low-rank TGV reconstruction demonstrates the ability to efficiently denoise and reconstruct FID-MRSI datasets with compressed-sensing acceleration.

Conclusion

The reconstruction presented for 2D & 3D FID-MRSI makes imaging of high-resolution metabolite maps possible on clinical 3T MRI system. This method enables whole brain metabolite mapping with acquisition time compatible with clinical requirements (2D: 10 min, 3D: 22 min).

References

[1]Nassirpour, S *et al.* (2017). NIMG 168, 211–221 [2]Hangel, G *et al.* (2018).NIMG, 168, 199–210
[3]Bilgic, B *et al.* (2014) JMRI, 40(1), 181–191 [4]Kasten, J *et al.*(2013). IEEE Trans.Med.Img 32(10) 1853–1863

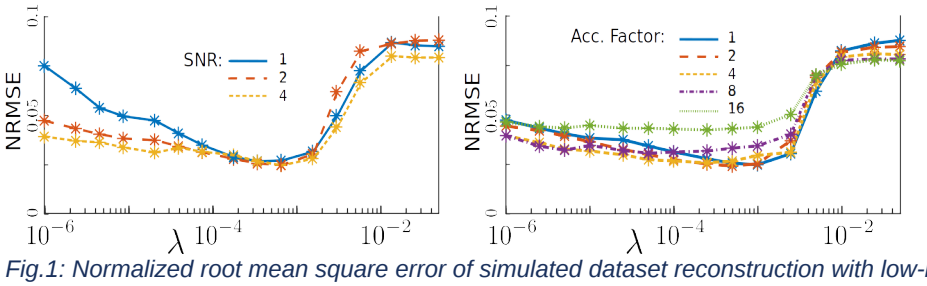

Fig.1: Normalized root mean square error of simulated dataset reconstruction with low-rank TGV model. Left, the error as a function of the regularization parameter (λ) and with three SNR levels. Right, error of the accelerated dataset.

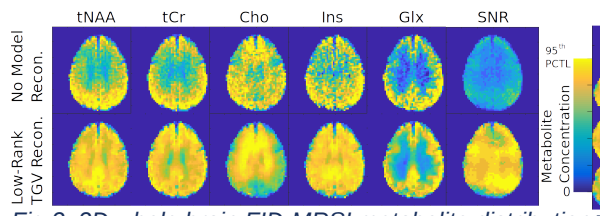

Fig.2: 2D whole brain FID-MRSI metabolite distributions reconstructed either with simple inverse Fourier transform or the low-rank TGV model. Metabolite concentration and SNR were estimated with LCModel

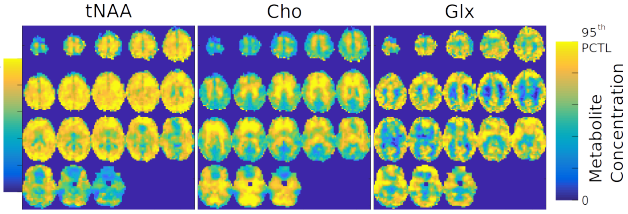

Fig.3: 3D FID-MRSI metabolite distributions reconstructed with low-rank TGV model and accelerated with compressed-sensing factor 3.3 . Concentrations were estimated with LCModel and the total acquisition time was 22 minutes.