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P1

FID backward linear prediction with two autoregressive algorithms for full compensation of acquisition delays

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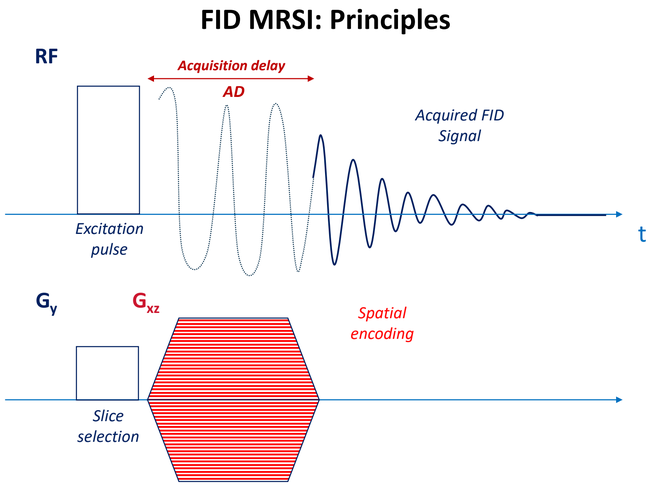
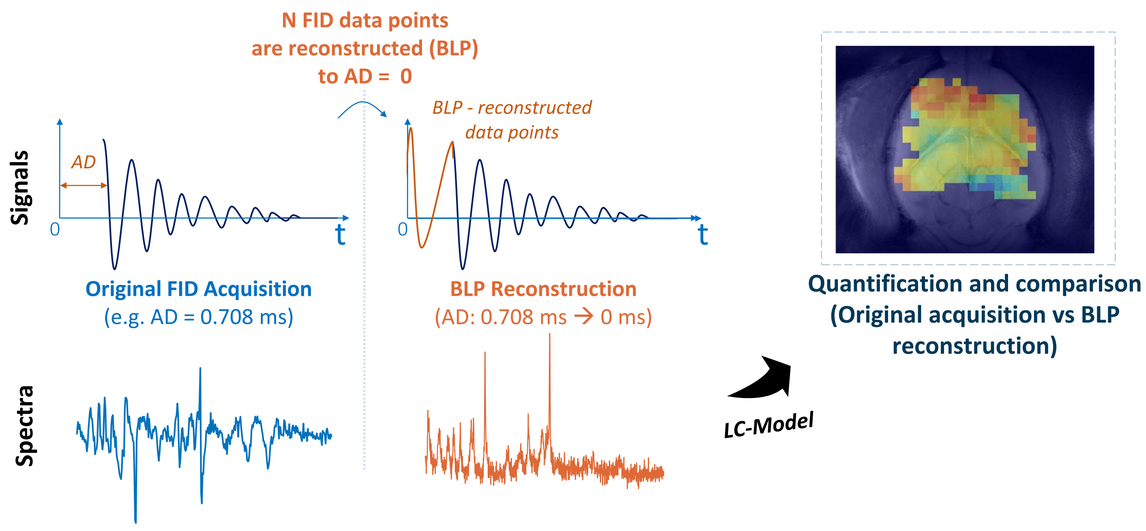
BACKGROUND

Despite their great potential[1-3], the main disadvantage of ^{1}H-FID-MRSI acquisitions at ultra-high field is the delay required between the excitation pulse and the FID acquisition signal (between 0.7 and 1.5 ms). Signal quantification was proposed either by adapting the basis-set simulation by removing the first points of all FIDs[2], or by prediction of the missing points at the beginning of FIDs using a backward linear prediction (BLP) autoregressive algorithm[3].



METHODS

Backward Linear Prediction (BLP) Autoregressive Methodology: Steps



***In-vivo* data (rat brain)**:

- 2D FID ^{1}H-MRSI (14.1 T, AD = 0.708 and 1.300 ms, time-domain sampling = 1024 points, slice thickness = 2 mm, FOV = 24x24 mm^2, matrix size = 31x31, 1 average, n = 4 rats)
- HLSVD, lipid suppression, denoising, LCModel fitting
- BLP back-calculation of missing points (5 for AD = 0.708 ms case and 9 for AD = 1.300 ms) up to AD = 0 ms, metabolites quantification and comparison with original acquisition
- Focus on metabolites of interest Glu, Gln, Ins, Tau, tCho and tNAA.

Monte-Carlo FID ^{1}H-MRSI simulations:

- 1000 realisations on a single voxel based on reference spectra (AD = 0.708 and 1.300 ms, SNR = 12, absence of water and lipids, 1 voxel)
- Analogous acquisition parameters as *in-vivo*
- Realistic concentrations values for 24 metabolites
- BLP back-calculation of missing points (5 for AD = 0.708 ms case and 9 for AD = 1.300 ms) up to AD = 0 ms, metabolites quantification and comparison with original simulations
- Focus on metabolites of interest Glu, Gln, Ins, Tau, tCho and tNAA.

AIMS

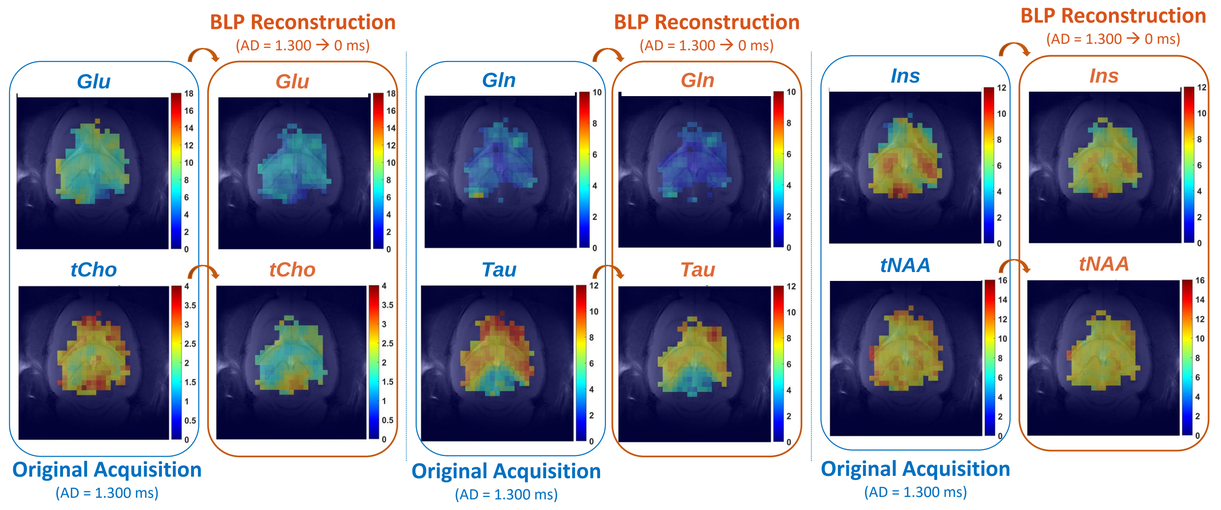
To investigate **two Backward Linear Prediction (BLP) auto-regressive** methods (*fillgaps* and *arburg*) on **full reconstruction of FID signals up to AD = 0** and to evaluate their consistency on metabolites concentration estimation in two situations:

- On ***in vivo* acquisitions** with common acquisition delays (AD), e.g. 1.300 ms and 0.708 ms
- On **Monte-Carlo simulations,** to replicate the *in-vivo* approach in ideal conditions

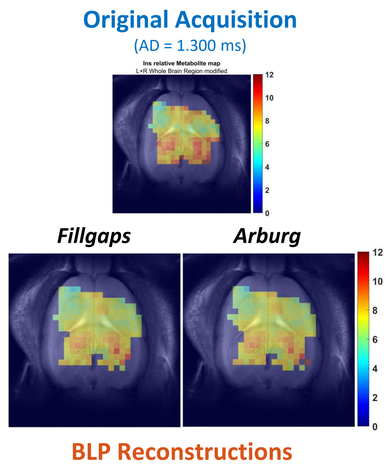
RESULTS

In-vivo concentration maps show:

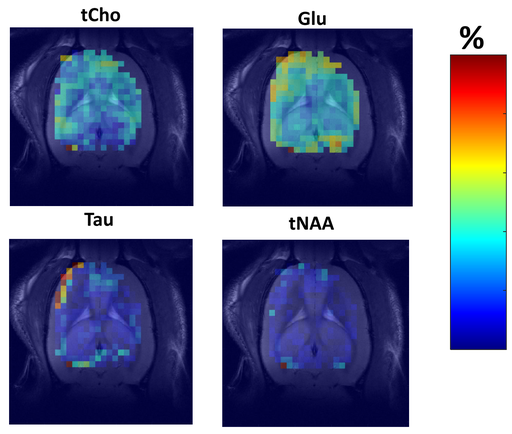
- Good consistency between BLP (AD = 0) results and original acquisitions for metabolites as Gln, Ins, Tau, tNAA with slice-averaged relative errors respectively below < 6.9 %, < 11.3 %, < 7.5 %, < 4.2 %.
- A biased quantification for Glu and tCho only, related probably to induced baseline distortions
- Consistency between *fillgaps* and *arburg* quantification results for all the quantified metabolites



Fillgaps **vs** ***arburg***

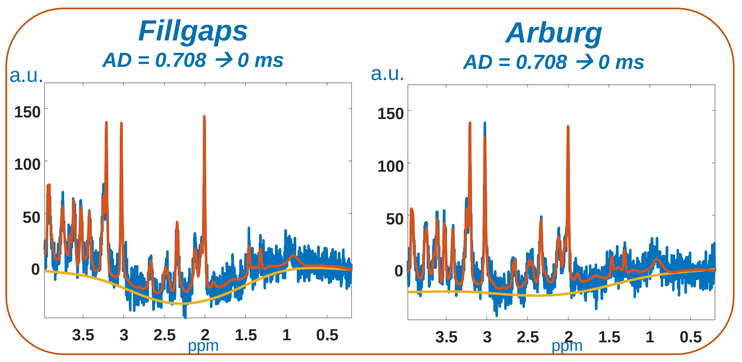


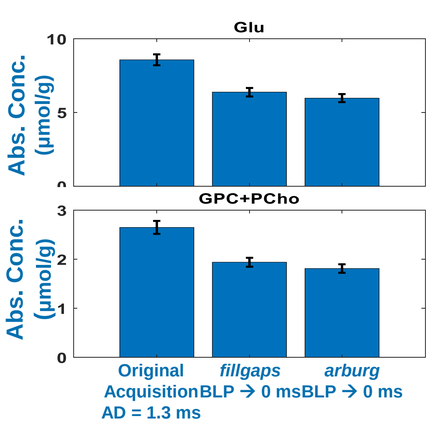
BLP reconstruction vs original acquisition: relative errors



Monte-Carlo analysis*:*

- Confirmed the *in-vivo* detected biased quantification for Glu and tCho and baseline distortions
- Consistency between *fillgaps* and *arburg* quantification results was also observed for all the metabolites





CONCLUSION

- The **two** tested **BLP autoregressive methods** show a **great potential** for accurate ^{1}H FID MRSI **full back-predictions to AD = 0**
- An optimized processing pipeline of BLP and metabolic quantification to avoid baseline distortions is yet to be developed

References:

1. *Simicic D, et al. Fast high-resolution metabolite mapping in the rat brain using 1H-FID-MRSI at 14.1T. 2023;(arXiv:2307.03261). doi:10.48550/arXiv.2307.03261;*

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3. *Henning A. Proton and multinuclear magnetic resonance spectroscopy in the human brain at ultra-high field strength: A review. NeuroImage. 2018;168:181-198. doi:10.1016/j.neuroimage.2017.07.017*

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