An Optimal Excitation Scheme for ^{1}H-MRS? Insights from Magnetic Resonance Fingerprinting Monte Carlo Simulations

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Introduction

Brain metabolite concentrations and relaxation values (T_1, T_2) can change in various pathologies. Not only do such changes carry diagnostic value [1], but accurate per-subject knowledge of T_1, T_2, and transmit inhomogeneity (B_{1+}) is necessary for absolute quantification. Our recently proposed spectroscopic fingerprinting (MRSF) framework [2] can simultaneously quantify concentrations, T_1, T_2 and B_{1+} values within clinical scan times. Previous work had shown that reducing schedule length in favour of SNR can improve estimation accuracy [3]. Our aim was to numerically optimize the MRSF schedule and schedule length to further improve T_1, T_2 and concentration estimation.

Methods

To estimate the effect of trading schedule length and SNR we tested eight MRSF schedules lengths: N=5, 10, 15, 20, 25, 50, 60 and 100. For all schedules the total measurement time (TA) was set to 6 min. Flip angles (30°≤FA≤150°), repetition times (550ms≤TR and $\sum_n TR_n = N \cdot 0.6\,(sec)$) and echo times (40ms≤TE≤150ms) were optimized using MATLAB's genetic algorithm toolbox (GA, The Mathworks 2017a) to minimize the mean CV: $CV \equiv \min_{FA_n TR_n TE_n} \sum_{i=1,j=1}^{4,3} CV\left(T_1^i\right) + CV\left(T_2^j\right)$,with

$CV(T_1) = \sqrt{\left(T_1^{variance}\right)^2 + \left(T_1^{bias}\right)^2}/\bar{T}_1$ and $CV(T_1) = \sqrt{\left(T_2^{variance}\right)^2 + \left(T_2^{bias}\right)^2}/\bar{T}_2$. $\bar{T}_1, \bar{T}_2$ are averaged across a range of in-vivo values. Bias and variance were calculated using Monte-Carlo simulation, keeping the same SNR per unit time. Monte-Carlo simulations were used to assess the performance of each schedule (SNR per single, fully relaxed, 90° pulse excitation = 10), averaging T_1 and T_2 coefficients of variation (CVs) over $T_1 \in [750{,}1650]$ ms and $T_2 \in [125, 350]$ ms.

Results

Fig. 1 plots the average CV as a function of schedule length, showing optimal schedules require only a relatively small number (10-25) points. The optimized FAs and TEs for all schedules (N=5, 10… 100) are plotted in Fig. 2, where they naturally form four distinct clusters around FA=30°, 109° and TE=40, 120 ms, regardless of schedule length.

Discussion

Our computer simulations indicate short MRSF schedules are preferable in an RMSE sense. Such short schedules can be more easily combined with spectroscopic imaging or J-coupling encoding. Furthermore, the clustering of schedule flip angles and echo times indicates the parameter space of MRS is, in fact, discrete, due to some yet-unknown underlying structure. This can be used to considerably speed up subsequent optimizations.

Conclusion

We have shown that reducing schedule length in favor of SNR can reduce T_1 and T_2 estimation errors, with optimal schedule lengths of N=15 points, with a CV of 8.7% (Averaged over a range of typical in-vivo T_1 and T_2 values).

References

[1] II Kirov et al, Radiology 254(3):858-866 (2010); [2] A Kulpanovich, NMR in Biomed (in print); [3] A Kulpanovich, Poster #1329, Intl. Soc. Mag. Reson. Med., Paris (2018)

Acknowledgements

This work was supported by the Minerva Foundation. Assaf Tal acknowledges the support of the Monroy-Marks Career Development Fund and the historic generosity of the Harold

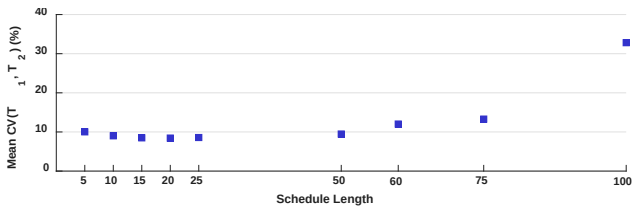

Figure 1. Schedule root mean square error (RMSE) as a function of its length (total number of excitations).

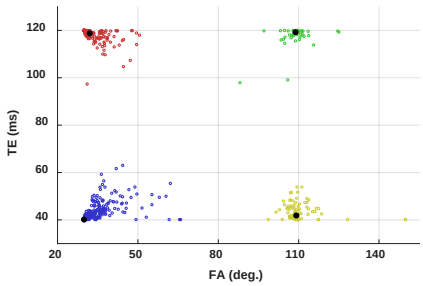

Figure 2. Flip angle and echo time clusters. Black dot marks the centre of the cluster.

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