# Improving the Spectral quality of Magnetic Resonance Spectroscopy using Multi-Taper Methods (MTM)

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## Introduction

*In vivo* MRS is characterized by the low SNR due to the low concentrations of metabolites. Several time-domain filtering methods also known as apodization are usually used to improve the spectral SNR for better metabolite analysis and quantification. However, these filters improve the SNR at the expense of increasing spectral line width (FWHM). Multiple-Taper Methods (MTM) has been proposed by Thomason [1] for the consecutive spectral estimation of time series data with poor SNR, which has been widely used in the analysis of EEG and MEG [2]. The advantage of MTM is that it is designed to improve the estimation of spectrum and also minimize the spectral leakage [2]. In this study, we apply the MTM on in vivo MRS data to improve spectral SNR of MRS data without increasing the FWHM. MRS data at different SNR levels were compared by SNR, FWHM and goodness-of-fitting before and after the application of MTM. In addition we also investigate the optimal number of taper functions for *in vivo* MRS.

## Theory and Methods

In MTM, FID is multiplied by several orthogonal taper (window) functions before Fourier transformed to the spectral domain [3]. A particular choice of these taper functions with the optimal spectral concentration properties, which means to prevent bleeding of power to neighboring frequencies, is given by the Discrete Prolate Spheroidal Sequences (DPSS) [4]. An unbiased spectrum can be produced by averaging these uncorrelated taper functions, which yields a better and more stable estimation of spectrum. The first seven taper functions available are graphed below (Figure 1). By adjusting the relative weights on the contributions from each of the tapering functions, a leakage-resistant spectral estimate can be obtained [3]. The appropriate choice of number of tapering functions is critical for the application, depending on the feature of data set. It is better to try iteratively and judge by errors indexes [2]. The optimal choice of number of taper functions for *in vivo* MRS has been investigated in this study.

All experiments were performed on healthy volunteers on a 3T scanner (Tim Trio, SIEMENS Medical Solutions, Erlangen, Germany). For SVS experiments, a 2x2x2 cm$^3$ volume was prescribed at the parietal lobe using PRESS (TR/TE = 2000/40 ms, bandwidth = 2KHz, sample points = 2048, number of measurement = 128). 8 healthy subjects were enrolled. The first 1, 4, 16, 64 and 128 measurements of the SVS data were averaged generate spectra with different SNR level. Spectral-time domain transformation was carried out using Fourier Transform only and Fourier transform with MTM using 3, 5, 7, 9, 11 taper functions, respectively. Therefore for each subject, each of the spectra with different number of averages was processed using six different ways, termed as FFT, MTM-3, MTM-5, MTM-7, MTM-9, MTM-11. For the MRSI experiments, Proton Echo Planar Spectroscopic Imaging (PEPSI) [3] data were acquired from a para-axial slice above the ventricles with voxel size of 0.95 ml (matrix size = 32x32, FOV = 220mm, slice thickness= 20mm, NEX=1). The above listed spectral-time domain transformations were applied. N-acetyl-aspartate (NAA), Creatine (CRE), Choline (CHO),myo-Inositol (mI) and the sum of Glutamate and Glutamine (Glx) were quantified using LCModel [4] fitting with simulated basis sets. The following metrics for spectral quality were evaluated: SNR, FWHM, Cramer-Rao Lower Bound (CRLB), which is the lowest bound of the standard deviation of estimated metabolite concentration expressed in %.

## Results

| SVS | | FFT | MTM-3 | MTM-5 | MTM-7 | MTM-9 | MTM-11 |
|---|---|---|---|---|---|---|---|
| SNR | avg128 | 21 | 23 | 24 | 25 | 26 | 26 |
| | avg64 | 17 | 19 | 21 | 22 | 22 | 24 |
| | avg16 | 10 | 13 | 15 | 16 | 17 | 17 |
| | avg4 | 6 | 7 | 8 | 9 | 10 | 10 |
| | avg1 | 3 | 4 | 5 | 5 | 5 | 6 |
| FWHM | avg128 | 0.0440 | 0.0375 | 0.0385 | 0.0405 | 0.0435 | 0.0440 |
| | avg64 | 0.0435 | 0.0380 | 0.0385 | 0.0390 | 0.0405 | 0.0435 |
| | avg16 | 0.0425 | 0.0385 | 0.0390 | 0.0400 | 0.0420 | 0.0450 |
| | avg4 | 0.0460 | 0.0395 | 0.0385 | 0.0405 | 0.0435 | 0.0435 |
| | avg1 | 0.0505 | 0.0390 | 0.0395 | 0.0380 | 0.0410 | 0.0435 |
| PEPSI | | | | | | | |
| SNR | | 4.16 | 5.90 | 7.04 | 7.69 | 8.20 | 8.57 |
| FWHM | | 0.0574 | 0.0474 | 0.0507 | 0.0559 | 0.0596 | 0.0618 |



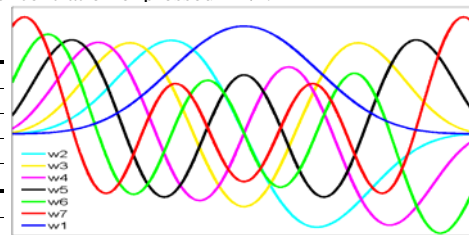**Figure 1** the first 7 DPSS tapering functions.



**Table 1** Summarized SNR and FWHM in SVS and PEPSI experiments. Results shown are averaged from 8 subjects in SVS experiments and from whole brain slice in PEPSI experiment. SNR increases with the application of MTM in both PEPSI and SVS at all SNR levels (P<0.01). These gains increase with the number of taper functions. The FWHM was found to decrease (P<0.05) with the application of 3, 5 and 7 taper functions (MTM-3, MTM-5, MTM-7) and increased when more taper functions were used (MTM-9 and MTM-11).

**Figure 2** Whole slice averaged CRLBs from LCModel fitting for NAA, CRE, CHO, mI and Glx in the PEPSI experiment. Lower CRLBs are found with the application of MTM compared with FFT
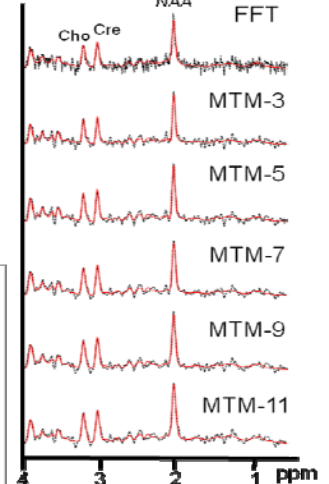


**Figure 3** Six spectra processed by FFT and MTM (up to bottom) selected from a voxel in PEPSI experiment. Note that the reduction in noise can be clearly visualized with the application of MTM spectrum.
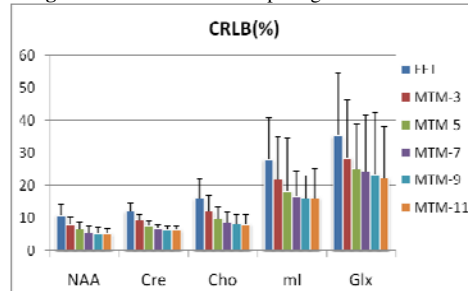
## Discussion

In this study, we have demonstrated that MTM can significantly improve the spectral quality including the SNR and FWHM and it is beneficial for the metabolic quantification for *in vivo* SVS and PEPSI data. Based on the measured SNR and FWHM, we conclude that the optimal numbers of tapering functions for in vivo MRS are between 5 to 7 (MTM-5 and MTM-7). While SNR increases when more tapering functions are used, the FWHM didn't show the similar decreasing trend when more tapering functions are included (Table 1). The CRLBs also decrease with the application of MTM, which is reasonable due to the gain in SNR and reduction in FWHM. However, the CRLB is not significantly lower in MTM-9 and MTM-11 than MTM-7.

## References

**1.** Thomoson, DJ., Proc IEEE, 1982;70:1055-96 **2.** Mitra, PP., et al., Biophys J, 1999;76:691-708 **3.** Perceval, DB., Walden, WT., Cambridge University Press 1993 **4.** Slepian, D. et al., Bell Syst Tech J,1961;40:43-63 **5.** Posse, S., et al., MRM, 1995,33:34-40 **6.** Provencher, SW., et al., MRM, 1993,30:672-79.