Using Peak-Enhanced 2D-Capon Analysis with Single Voxel Magnetic Resonance Spectroscopy to Estimate T2* for Metabolites

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Introduction

Single voxel proton *magnetic resonance spectroscopy* (MRS) is typically used in a clinical setting to quantify metabolites in the human brain. By convention, an MRS absorption spectrum shows the relative concentration of certain key metabolites, including NAA, choline, creatine and others. Stoica and Sundin have shown that other nonparametric techniques in addition to *Fourier* transformation may be used for MRS analysis (1). One such technique, *2D-Capon analysis*, can be used effectively to estimate the damping associated with each metabolite. This is useful since it is related to T2*, the total transverse relaxation time, for each metabolite.

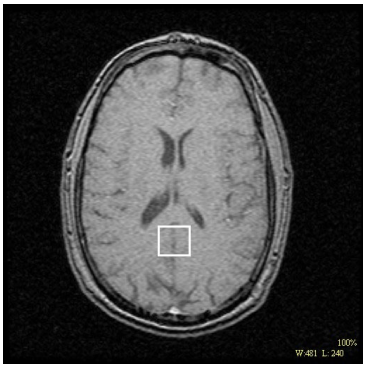

Fig. 1. MR image of human brain.

Methods

Data was collected using a 1.5 T Signa MR scanner (GE Medical Systems, Waukesha, Wisconsin, USA) equipped with a high bandwidth (1MHz) data acquisition subsystem and a TwinSpeed gradient coil capable of switching 40 mT/cm at a maximum slew rate of 150T/m/s. Conventional *point resolved spectroscopy* (PRESS) was used with a single-channel quadrature head coil to acquire the data. For each single-voxel MRS scan, a set of non-water-suppressed reference data was collected along with a corresponding set of water-suppressed data for which water was suppressed using a *chemical shift selective* technique. Raw data from each experiment was saved and processed off-line using MATLAB. Parameters for the scan were: TE: 35 msec., TR: 1500 msec., 8 cm^3 voxel, 16 reference frames, 128 water-suppressed frames, with a scan time of 3 minutes and 48 seconds. Each data set was phase corrected using a phase-correction vector created from the reference data. Residual water was removed from the phase-corrected water-suppressed data by subtracting an appropriately scaled and phase-corrected reference data set.

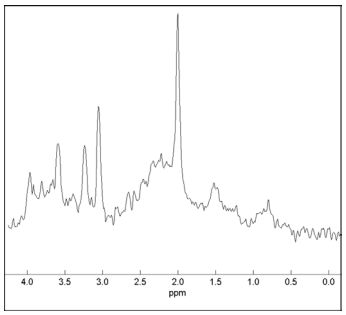

Fig. 2. MRS absorption spectrum of region indicated in Fig. 1.

Results

A Fourier transformation of the windowed, phase-corrected water-suppressed data set with residual water removed was used to generate the MRS absorption spectrum as shown in Fig. 2. 2D-Capon analysis was performed on the same phase-corrected water-suppressed data with residual water removed to generate the result shown in Fig. 3. This result is a "peak-enhanced" version of 2D-Capon analysis for which local peaks are plotted as *Dirac* delta functions. A contour plot of the surface shown in Fig. 3 is shown in Fig. 4. From this contour plot, damping factors for choline, creatine and NAA can be clearly identified.

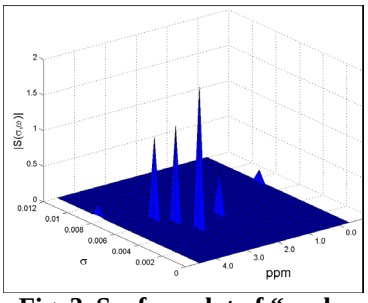

Fig. 3. Surface plot of "peak-enhanced" 2D-Capon Analysis.

Discussion and Conclusion

Peak-enhanced 2D-Capon analysis simplifies the interpretation of the results of conventional 2D-Capon analysis and facilitates determining the damping factor, σ, which may then be used to provide an estimate of T2* for each metabolite. 2D-Capon analysis is somewhat more computationally intensive than techniques based on Fourier transformation. The example shown in Fig. 4 with 2048 complex data samples, a filter length of 256, and 30 different values of σ took approximately 5 seconds to execute using a standard PC with MATLAB.

Determination of T2* for metabolites has been studied (2),(3) and has been shown to have clinical value for certain pathologies including cancer (4). Using 2D-Capon analysis in conjunction with single voxel proton MRS studies provides an effective method for estimating T2* for each metabolite.

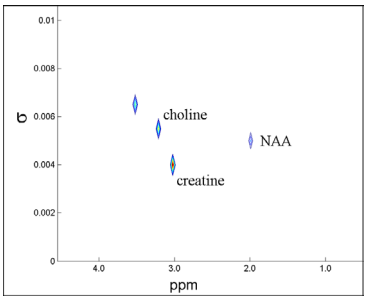

Fig. 4. Contour plot of "peak-enhanced" 2D-Capon Analysis providing estimates of T2*.

References

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