Improving Spectral Resolution of Proton MRSI by Deconvolving Field Inhomogeneities

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Introduction

The spectral resolution of in vivo ^{1}H MRSI spectra is inherently poor because of the narrow range and severe overlap of the spectra. Spectral resolution is further degraded by inhomogeneities of the magnetic field. Scanning at high magnetic fields increases chemical shifts, but the the exaggerated susceptibility effects that accompany imaging at high fields can offset this advantage almost entirely [1,2]. The usefulness of high order shimming is limited for MRSI in a large volume across the brain. A postprocessing method that uses internal water as a reference to eliminate the lineshape broadening caused by the field inhomogeneity is useful for single voxel ^{1}H MRS [3]. Acquiring a water SI in addition to the metabolite SI is time-consuming, however, and impractical for clinical applications. Herein we propose a method that uses spectral lineshapes reconstructed from field maps as references to deconvolve the effects of field inhomogeneities. We have designated this method "Spectral Resolution Amelioration by Deconvolution" (SPREAD). We demonstrate the performance of the method in both phantom and in vivo ^{1}H MRSI datasets.

Methods

SPREAD The principle of SPREAD is based on the fact that the spectrum from a sampling volume can be regarded as a combination of many spectral lines originating from tiny sub-volumes of the sample, each of which has its own natural linewidths, but with frequencies that are altered slightly by the small differences in strength of the local field where the sub-volumes are located. The effects of spatial variation of the magnetic field on the spectrum can be modeled by the spectral lineshape, which can be reconstructed from the field map. By de-convolving the lineshape function from the measured data, the effects of field inhomogeneities can be eliminated, and the intrinsic linewidth and lineshape can be recovered. The implementation of SPREAD entails the following steps: (1) Obtain high-resolution field maps for the entire volume of the MRSI; (2) Reconstruct the lineshape of the MRSI from the field maps by simulating the real world MRSI scan of the water, whose frequencies were determined from the field maps. The phase encodings of the simulation are the same as those of the metabolite MRSI scan; (3) Divide the measured metabolite signal by the lineshape signal $s_V^0(t_d) = s_V(t_d) \cdot w(t_d) / L_V(t_d)$, where $s_V(t_d)$ and $L_V(t_d)$ are the time domain measured signal and the lineshape signal in voxel V, respectively, and $w(t_d)$ is the window function to suppress noise and transform the lineshape [5].

MR Measurements We acquired MR data on a phantom and on human volunteers using a whole body 3T scanner (Signa 3.0T, GE Healthcare, Waukesha, WI). MRSI data were acquired using a multiplaner MRSI pulse sequence [4] (Number of slices = 4; Slice thickness = 10 mm; Nominal number of phase encoding = 16 x 16; TR/TE = 2300/144 ms.). Immediately following the MRSI scan, high resolution MR images for field mapping were acquired using a commercial 3D MRI sequence, "Incoherent Radio Frequency Spoiled Gradient Echo" (SPGR), with the same field shimming as used for the MRSI scans. The slices of the 3D SPGR image were exactly parallel to those of the MRSI data. The volume of the 3D SPGR image was slightly larger than that of the MRSI. The TEs of the two sets of MR images were 8 and 10.5 ms, respectively. Therefore, each MRSI slice covered 5 high-resolution MRI slices, and each MRSI voxel consisted of 1280 high-resolution MRI voxels. All the protocols were approved by the IRB of the New York State Psychiatric Institute.

Numerical Evaluation We evaluated performance of the method by comparing the spectral linewidths and the asymmetry of lineshapes of unsuppressed water signals before and after application of SPREAD. The linewidths were measured at the full width at half maximum and full width at tenth maximum the asymmetry of a peak was defined as $\gamma = |a_L - a_R| / (a_L + a_R)$, where a_L and a_R are the left and right half areas, respectively, when dividing the spectral line from the top of the peak.

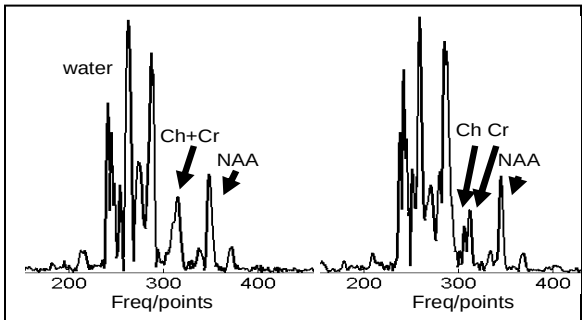

Fig. 1 Phantom spectra from a voxel near water-air interface before SPREAD (left) and after APREAD (right). The field Broad water residues are shown.

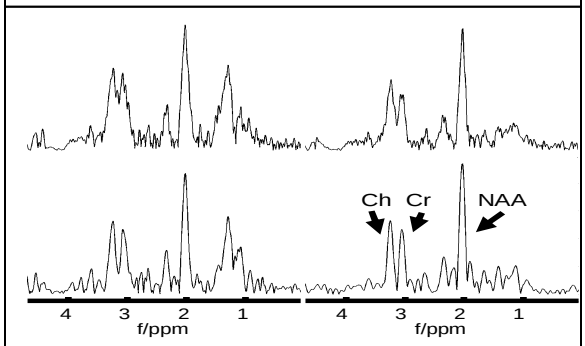

Fig. 2. In vivo human brain spectra before (upper) and after SPREAD (lower panel).

Results and Discussion

Numerical results show that the FWHM of water was reduced 30-50% and the FWTM 3-55% after SPREAD. The asymmetries of the peaks were reduced 75-99%. Overlapping peaks of total Creatine and total Choline were resolved after SPREAD, due to reduced linewidth and improved lineshape (Fig. 1 and Fig.2). Although the examples were from ^{1}H MRSI of the human brain, the technique can be applied to MRSI data of other nuclei, such as ^{31}P and ^{13}C, and to MRSI data from other parts of the human body and from other species.

References

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