Automated Positioning of Multiple Spatial Saturation Planes for Non-Cuboidal Voxel Prescription in MR Spectroscopy

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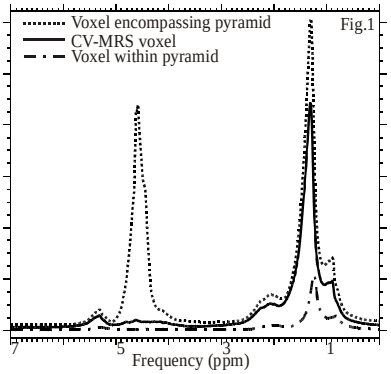
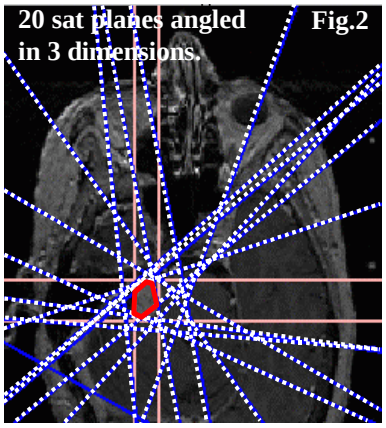
Introduction: No lesions within the body are of cuboid shape. However, current methodology for *in vivo* MRS is essentially limited to cuboid volumes due to the use of three intersecting slice-selective RF pulses (eg. STEAM, PRESS), with minor voxel-shaping using several user-defined spatial saturation planes. We describe here a method of conformal voxel MR spectroscopy (CV-MRS) which utilizes the base localization sequence (e.g. PRESS) in conjunction with a larger number of Very Selective Saturation (VSS) RF pulses[1] with spatial positions automatically determined to shape a cuboid excitation volume to conform to a given convex volume. This method does not require modifications to the base localization sequence, as in a previously proposed conformal acquisition technique[2]. Benefits of this technique are - 1) greatly reduced scan times due to the increased lesion volume included in the voxel; 2) a spectrum more representative of the lesion volume rather than a subjectively placed sub-section of the lesion, with implications to MRS classification[3]; and 3) reduced graphic prescription time with computer-optimized, automated positioning of both the excitation voxel and multiple spatial saturation bands. This technique has applications to MRS of brain tumours, breast lesions, prostate cancer, and all applications where a spectrum from a defined tissue-of-interest is needed.

Methods: The CV-MRS technique involves the automated, optimized placement of a large number (6 to 20 in the current application) of VSS bands to "sculpt" the cuboid excitation voxel to conform to a volume-of-interest (VOI). VSS pulses, with their extremely sharp transition band, are well-suited to define a sharp voxel, as compared to standard outer volume saturation (OVS) pulses. The standard PRESS pulse sequence was modified to include up to 20 VSS pulses with rotations and spatial offsets defined in an external file - graphic prescription was not required. The external file was created by a separate computer program which analyzed the input MR scout images – first the tissue-of-interest (TOI) was defined by a simple region-growing algorithm, a boundary-detection algorithm, or by a user-defined boundary; then the position of up to twenty planes was optimized in three dimensions to conform to the TOI such that the volume of TOI encompassed by the saturation planes was maximized and the volume of non-TOI was minimized. All experiments were performed on a GE (Waukesha, WI) 1.5T Signa LX MR scanner equipped with Echospeed actively-shielded gradient coils (22 mT/m, 120 T/m/s) using the standard transmit/receive head coil. Total spatial saturation time was increased from 48ms for the standard sequence to approximately 120ms, requiring adjustment of water suppression to account for the increased delay between suppression and acquisition. Phantom experiments were performed on different shaped oil-filled phantoms inside a larger water-filled jug. Testing of the CV-MRS program was performed on 6 brain tumour MR datasets.





Results: For a spherical TOI with a cubic excitation voxel placed entirely within the TOI, only 37% of the TOI is sampled. With the cubic excitation voxel entirely encompassing the spherical TOI, 100% of the TOI is sampled, but 91% of the total signal is "contaminated" from adjacent normal tissue. By adding 20 VSS pulses using CV-MRS, 90% of the TOI is sampled with only 3% contamination from non-TOI signal. Further reduction of non-TOI signal is possible with a slight reduction in TOI signal. For a pyramidal-shaped oil-filled phantom within a large water-filled jug, the spectrum (Fig.1) from the voxel encompassing the entire phantom (dashed line) represents full signal from the TOI with significant contamination (note the large water peak at 4.7 ppm). If the voxel is reduced to be entirely within the phantom (dash-dot line) only 17% of the lipid signal remains. The CV-MRS voxel (solid line) shows 73% lipid signal with minimal contamination from outside the TOI (seen as a very low water peak at 4.7 ppm). Use of CV-MRS on a brain tumour MRI dataset is shown in Fig.2 (saturation planes angled in three-dimensions shown in dashed lines, conformed voxel shown in solid red). Table 1 shows results of using CV-MRS on 6 brain tumor datasets showing an average 23% tumor volume enclosed by the cuboid vs 56% for CV-MRS, resulting in a 6-fold reduction in scan time for equivalent SNR.

Patient #	Tumor Volume[1]	CV-MRS %Tumor[2]	Cuboid %Tumor[2]	Ratio CV/Cube[3]	Time Reduction[4]
1	15.4	58.0	18.6	3.1	9.8
2	57.1	69.1	24.3	2.8	8.1
3	2.8	36.3	25.1	1.4	2.1
4	31.6	79.3	25.9	3.1	9.3
5	5.7	51.3	27.5	1.9	3.5
6	3.1	40.7	18.5	2.2	4.8
AVG	19.3	55.8	23.3	2.4	6.3

[1] Volume in cm^3; [2] Percent of tumor included in voxel

[3] Ratio CV-MRS to Cuboid signal; [4]CV-MRS vs Cuboid scan time reduction factor for equivalent SNR

TABLE 1 – CV-MRS versus Standard MRS with cuboid volumes for 6 brain tumor cases

Discussion: CV-MRS reduced scan-time for equivalent SNR compared to standard cuboid MRS due to the larger fraction of total TOI signal acquired. Scan time reductions depend on lesion-shape but are 6-fold and 16-fold for the spherical and pyramidal TOI, respectively, and an average 6-fold reduction in 6 sample brain tumor datasets. The CV-MRS spectrum is more representative of the tumor than the standard cuboid acquisition in which only an average of 23% of the tumor was sampled. In the simplest implementation of CV-MRS, the user points-and-clicks on a lesion, and the program automatically finds the boundaries in three-dimensions, places a voxel to fully encompass the lesion, and automatically positions up to 20 saturation planes to conform to the lesion, within approximately 10 secs in our Java/C++ implementation. The CV-MRS technique could also be used to improve outer volume suppression in MRSI applications such as whole brain MRSI and prostate MRSI.

References: [1] T.C.Tran, *et al.*, *MRM* **43**, 23-33. [2] Sharp JC *et al*, *MRM* **23,** 386-393. [3] Ricci *et al*, *AJNR* 21:367-374.