MEDICAL UNIVERSITY OF VIENNA

Creating an RF Pulse Simulation Model for Whole Brain MRSI at 7 T

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Purpose

Like all magnetic resonance applications, whole brain magnetic resonance spectroscopic imaging (*MRSI*) requires excitation pulses (radio frequency pulses or *RF* pulses) in order to generate measurable signals. When an RF pulse is applied, lipids around the brain can significantly affect the subsequently measured signals, so their excitation should be avoided by using optimized pulse shapes and positions. The purpose of this work was to create a simulation model capable of evaluating different RF pulses with regards to the generation of artifacts.

Methods

A simulation model based on a numerical brain phantom was created. The numerical phantom contained a brain region and a surrounding lipid region and its shape was based on volunteer measurements. A combination of representative metabolite spectra and lipid spectra, which had been simulated in jMRUI[1], were then copied into their respective voxels.[2] Subsequently, an RF pulse was simulated using VeSPA[3], moved to a desired position in the brain phantom and applied to the model by point-wise multiplication. Spatial and spectral shifts due to B_0 inhomogeneities were calculated and a measurement process was modeled by truncating k-space, resulting in artifacts identical to the ones in real MRSI measurements. The resulting spectral data was evaluated by integrating over a region of interest around the N-acetylaspartate (NAA) peak (1.9-2.1 ppm) and in a region containing lipid signals (0.7-1.5 ppm) (figure 3). This process was performed in every voxel, enabling the creation of maps such as the ones in figures 2 and 4. The sum of all voxel signals inside a volume of interest (VOI) could then be compared for different simulations.
The simulation was conducted at different resolutions (28x32x20 and 56x64x40), with different model compositions (lipids only, metabolites only, both lipids and metabolites) and for different pulse shapes (ideal *binary* pulse, realistic *sinc* pulse, figure 1), vertical positions and rotations.

Overview of Simulations	
Shape	Sinc, Binary
Signal Source	Metabolites, Lipids, Metabolites and Lipids
Resolution	56x64x40, 28x32x20
Vertical Position	Positions 0, 1, 2 and 3
Rotation	0°, 20°

Results

The model composition had a significant effect on the measured signal in the region of interest. Especially in regions close to the modelled lipid regions, the signal in the NAA range inside the VOI increased significantly (figure 4). When the numerical phantom consisted just of metabolites, no such effect was observed.
On the other hand, increasing the resolution decreased the signal inside the brain. This effect was most pronounced in lipid-containing phantoms as well (figure 4).
The pulse position played a role insofar as the signal in the VOI in lipid-containing models increased for pulse positions 2 and 3 (figures 4 and 5).
The local B_0 field influenced the signal, too, with regions with more severe B_0 inhomogeneities being visible in the resulting maps (figure 2).[4]
The pulse shape (*binary* or *sinc*) did not seem to have a significant influence on the aforementioned effects.

Conclusions

Lipids appear to be a significant contributor to the signal inside the brain. Higher resolutions correspond to decreased signal contamination inside the brain, which would be expected due to the larger number of phase encoding steps in the higher resolution model.
There are suboptimal pulse positions that excite lipids more than necessary, resulting in an increase of the total measured signal in a VOI. Most notably, this happens when the excitation pulse is placed further up in the brain due to the lipids there. With regards to lipid artifacts, an idealized *rectangular* pulse does not appear to be better than realistic *sinc* pulses which are currently in use in MRSI.

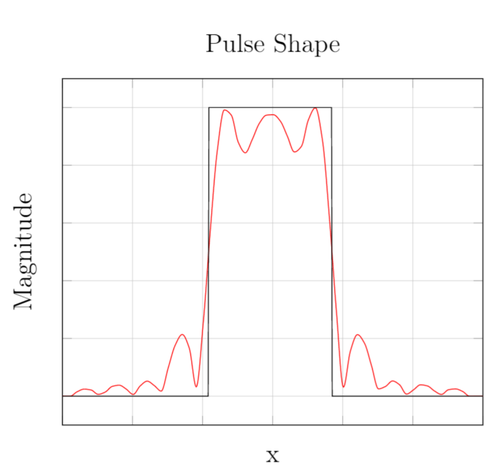

Figure 1: Comparison of a binary pulse (*black*) and a sinc pulse profile (*red*) in the spatial domain.

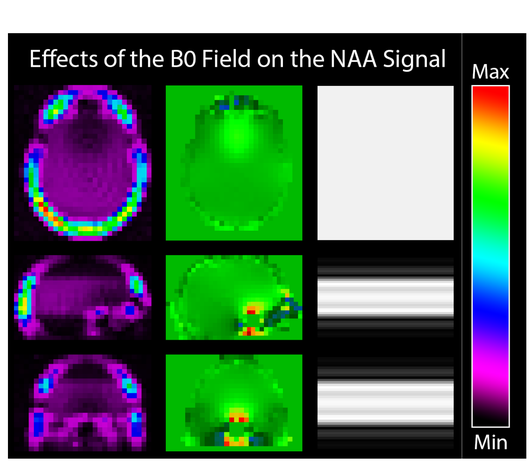

Figure 2: Transversal, sagittal and coronal view of the effects of the B0 field (*middle*) on the NAA map (*left*). The sinc pulse used is also illustrated (*right*).

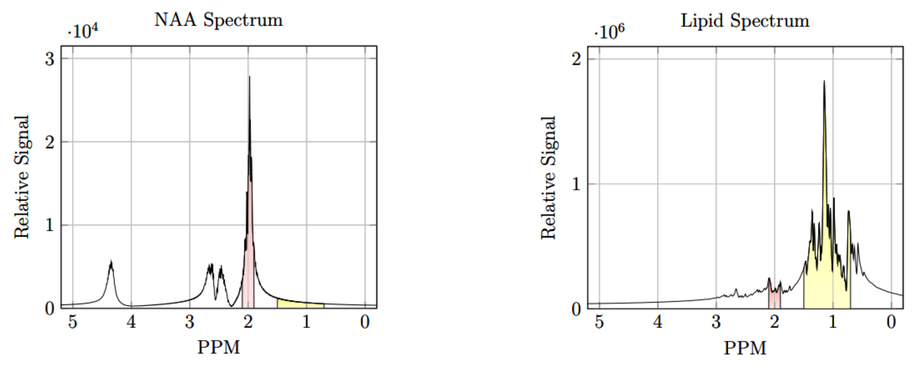

Figure 3: Spectra of NAA (*left*) and lipids (*right*) together with the later used analysis ranges from 0.7 to 1.5 ppm (*yellow*) and 1.9 to 2.1 ppm (*red*).

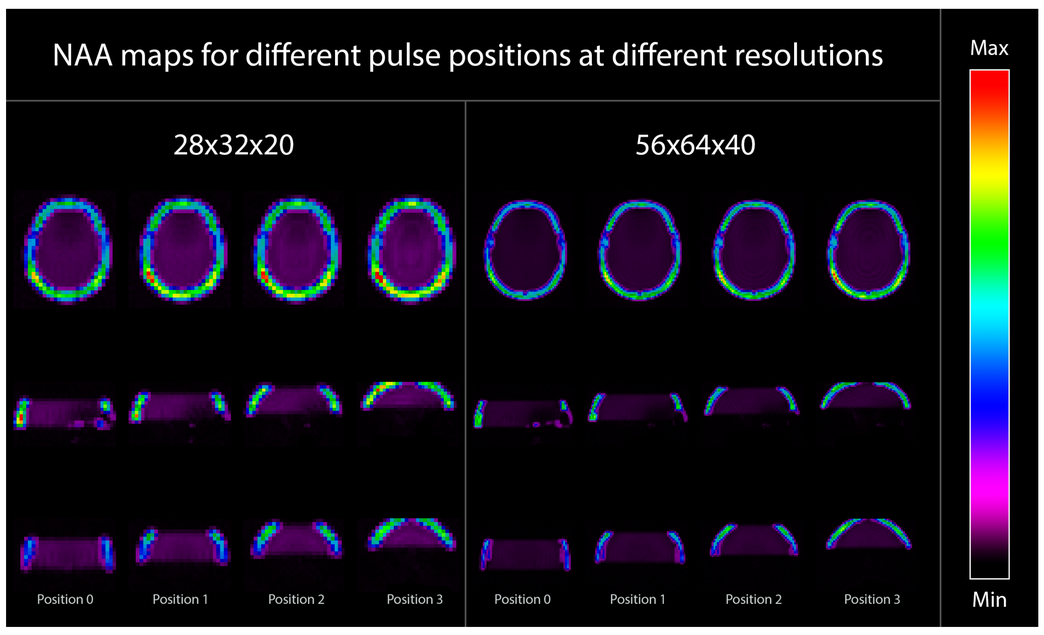

Figure 4: Transversal, sagittal and coronal views of NAA maps for different pulse positions at two different resolutions. In this simulation, the numerical phantom contained metabolites and lipids. The higher signal inside the brain for the lower resolution simulation is clearly visible. For this simulation, a binary pulse was used.

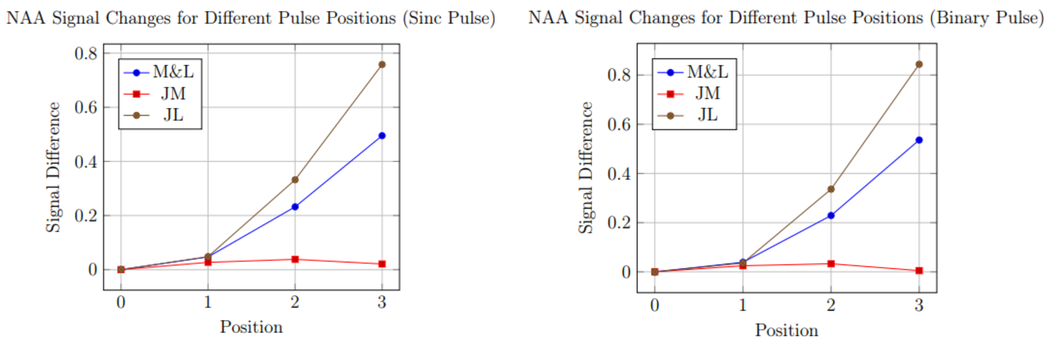

Figure 5: Changes of the NAA signal in a volume of interest for four different vertical pulse positions, plotted for a numerical phantom containing just lipids (*JL*, *brown*), just metabolites (*JM*, *red*), or both metabolites and lipids (*M&L*, *blue*). There is little qualitative difference between the sinc pulse (*left*) and the binary pulse (*right*). This shows clearly that the influence of the lipids above the head increases significantly

References

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[4]Christoph Juchem, Cristina Cudalbu, Robin A. de Graaf, Rolf Gruetter, Anke Henning, Hoby P. Hetherington, and Vincent O. Boer. B0 shimming for in vivo magnetic resonance spectroscopy: Experts' consensus recommendations. NMR in Biomedicine, Special Issue Review Article, Epub Ahead Of Print, June 2020. doi: 10.1002/nbm.4350t.