

Quantification of Human Brain Metabolites with Different RF Coils

Harald E. Möller^{1,2}, Timm Wetzel¹ & Marc Tittgemeyer¹

¹Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany

²Department of Radiology, University Hospital Münster, Münster, Germany
email: moeller@cbs.mpg.de



MAX PLANCK INSTITUTE FOR HUMAN COGNITIVE AND BRAIN SCIENCES LEIPZIG

Introduction

When interpreting quantitative magnetic resonance spectroscopy (MRS) studies of pathology, knowledge of the intra- and inter-subject variations is important, especially if deviations from normal mean values are measured in a single patient. In multi-center trials, use of different hardware may be an additional source of variation.

For further analysis of such issues, 12 healthy human volunteers (male 4, female 8, age 28 ± 3 y) were investigated by single-voxel MRS in repeated sessions using two different types of radiofrequency (RF) coils.

Methods

- 3 T MAGNETOM Trio (Siemens, Erlangen, Germany).
- ¹H PRESS (TR 5 s, TE 30 ms, 128 acq.).
- Single 3-mL voxel in the fronto-parietal white matter (WM; Fig. 1).
- 6 spectra recorded in separate sessions from each subject using either a transmit/receive birdcage (3 spectra) or an 8-channel array receive-only head coil (3 spectra).
- Absolute metabolite concentrations with LCModel [1] and unsuppressed water signal as a reference.
- Four strategies for combining the array-coil data:
 - (I) Exclusive consideration of spectrum from the coil element yielding the maximum signal-to-noise ratio (SNR).
 - (II) Summation of spectra from all coil elements with weighting factors, w_k , proportional to the individual SNR [2-4]:

$$w_k = \frac{\text{SNR}_k}{\sum_{i=1}^8 \text{SNR}_i}, \quad k \in [1, \dots, 8].$$

- (III) Summation of spectra above an SNR threshold:

After arranging the spectra from the coil elements according to their SNR (i.e., $\text{SNR}_1 \geq \text{SNR}_2 \geq \dots \geq \text{SNR}_8$), the summation is terminated if

$$\frac{\sum_{i=1}^{n+1} \text{SNR}_i}{\sqrt{n+1}} \leq \frac{\sum_{i=1}^n \text{SNR}_i}{\sqrt{n}} \Rightarrow \frac{\sqrt{n}}{\sqrt{n+1} - \sqrt{n}} \text{SNR}_{n+1} \leq \sum_{i=1}^n \text{SNR}_i.$$

- (IV) Combination of strategies (III) and (IV); i.e., weighted summation of spectra above an SNR threshold.

- Inclusion criteria for the final analysis [5]:
 - (a) Absence of significant artifacts in the residuals.
 - (b) Full linewidth at half height (FWHH) < 0.08 ppm.
 - (c) Concentration estimates with Cramer-Rao lower bounds (CRLB) < 50%.

1

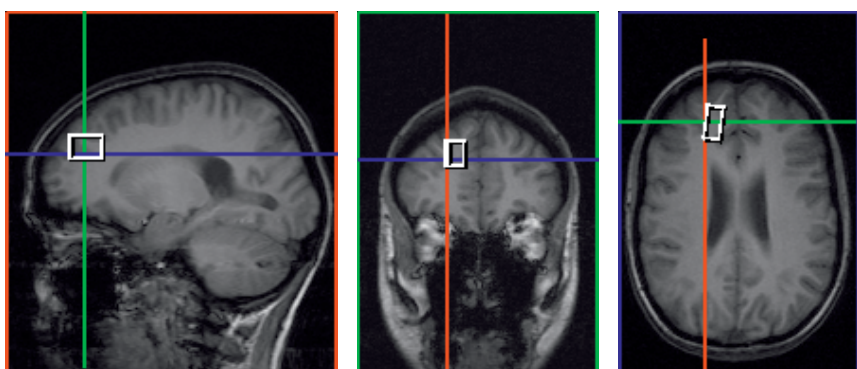


Figure 1. Typical position of the 10x20x15mm³ voxel in fronto-parietal WM.

Results & Discussion

LCModel outputs of spectra recorded with the two coils in a 26-year-old female volunteer are shown in Fig. 2.

If compared to Strategy I (consideration of only one coil element), the SNR of the array data improved by 17% if all spectra from the 8 coil elements were averaged (Strategy II) and by 23% for Strategy IV (Fig. 3). Consistently, smaller CRLB's of the major peaks were obtained with Strategy IV (Fig. 4). A comparison of Strategies III and IV demonstrates the beneficial effect from using weighting factors (Fig. 3, 4). The difference between Strategies II and IV is indicative of phase and baseline errors of fitted spectra recorded with distant coil elements and, hence, rather poor quality. Strategy IV was used in the final analysis.

Average metabolite concentrations (mean values and standard deviations, SD) and CRLB's are shown in Fig. 5 and Table 1 for both RF coils. The SNR almost doubled, and the CRLB's decreased by 9-16% for the major peaks (i.e., total N-acetylaspartate, tNAA; total creatine, tCr; total choline, tCh; and myo-inositol mI) when using the array instead of the birdcage coil indicating a higher fitting precision. This improvement did not lead to consistent differences of the standard deviations of the pooled data for both coils, which seemed to be dominated by biological variability and errors in repositioning the voxel. Highly significant differences in the absolute concentration estimates included an overestimation of glutamate plus glutamine (Glx) by 19% mostly due to an overestimation of glutamine (Gln) and an overestimation of mI by 7% when using the birdcage coil. This confirms previous reports of a tendency to overestimate these metabolites in low-SNR spectra [4] and may be related to residual baseline errors. As additional trends, the separation of N-acetylaspartate (NAA) and N-acetylaspartylglutamate (NAAG) was improved in the array-coil spectra, and a more reasonable estimate of the normal resting-state lactate (Lac) concentration (below 1 mM) was obtained. Inter-subject variation was of the order of 6% for tNAA.

2

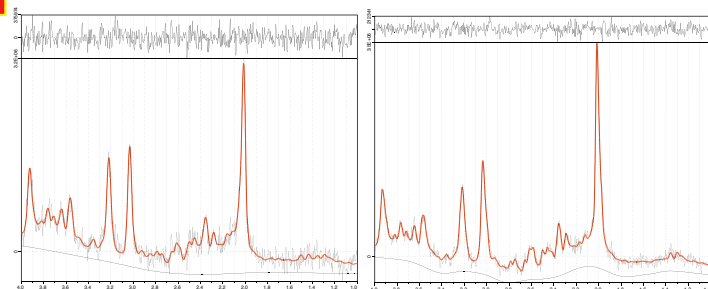


Figure 2. WM spectra recorded in the same subject with the birdcage (left) and the array coil (right) and results from LCModel fitting.

3

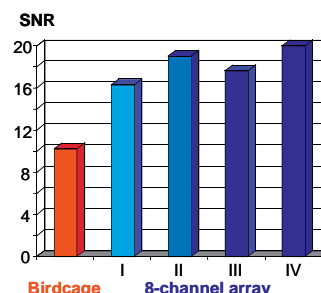


Figure 3. Average SNR from LCModel fitting of all spectra recorded with different coils (processing strategies I, ..., IV for the array data are explained in the Methods section).

4

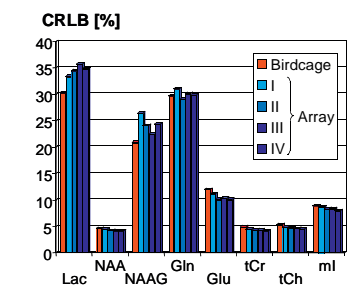


Figure 4. Cramer-Rao lower bounds obtained with LCModel for individual metabolites.

5

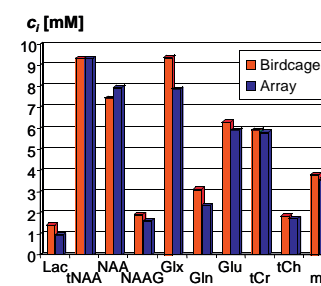


Figure 5. Average metabolite concentrations obtained with the two coils in the same group of subjects.

Table 1

Metabolite	Birdcage coil		8-channel array coil	
	Conc./mM	CRLB	Conc./mM	CRLB
Lac	1.42 ± 0.31	30.3%	0.95 ± 0.31	34.9%
tNAA	9.33 ± 0.35	3.3%	9.33 ± 0.82	2.8%
NAA	7.45 ± 0.42	4.6%	7.94 ± 0.59 [†]	4.1%
NAAG	1.93 ± 0.46	20.9%	1.62 ± 0.74	24.4%
Glx	9.37 ± 0.94	9.1%	7.87 ± 1.08 [†]	11.0%
Gln	3.12 ± 0.85	29.7%	2.34 ± 0.66 [*]	29.9%
Glu	6.31 ± 0.80	12.0%	5.92 ± 0.73	10.1%
tCr	5.92 ± 0.40	4.9%	5.82 ± 0.59	4.1%
tCh	1.85 ± 0.26	5.3%	1.73 ± 0.36	4.5%
mI	3.81 ± 0.72	8.8%	3.56 ± 0.57 [*]	8.0%
FWHH/Hz	6.2 ± 3.8		5.3 ± 1.3	
SNR	10.2 ± 2.9		20.0 ± 3.9 [†]	

Table 1. Average metabolite concentrations (mean ± SD).

Conclusions

Use of a standard phased-array headcoil for single-voxel MRS offers a significant SNR benefit and yields improved precision in the fitting of signals from strongly coupled spin systems such as Glu and Gln. Alternatively, the scan time may be reduced by more than 50% even when studying WM voxels. Regarding systematic differences in the estimated concentrations of selected metabolites, care must be taken when pooling data recorded with different types of RF coils.

REFERENCES:

- [1] S.W. Provencher, Magn. Reson. Med. 30: 672-9 (1993);
- [2] L.L. Wald et al., Magn. Reson. Med. 34: 440-5 (1995);
- [3] T. Prock et al., Phys. Med. Biol. 47: N39-46 (2002);
- [4] O. Natt et al., Magn. Reson. Med. 53: 3-8 (2005);
- [5] R. Kreis, NMR Biomed. 17: 361-81 (2004).