Quantitative tissue analysis in MRS using many element coils.

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Introduction

Reliable, absolute quantitative spectroscopy requires knowledge about the compartmentation of the volume elements, as different tissue types like white and gray matter have different metabolite concentrations contributing to the final spectrum [1,2]. In an experiment with phased-array coils, the signal contributions of various tissue types will be additionally weighted by the spatially inhomogeneous B_1-fields of the individual coil elements, as shown in fig. 1. This abstract will discuss a theoretical approach to determine individual metabolite concentrations of tissue types that can be differentiated by means of image-based segmentation.

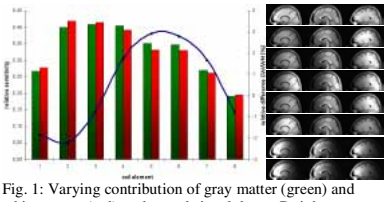

Fig. 1: Varying contribution of gray matter (green) and white matter (red) to the total signal due to B_1 inhomogeneities of individual coil elements shown on the right.

Theory

The signal S of metabolite M in the predefined volume VOI acquired by a RF coil in a MR spectroscopy experiment is proportional to the local concentration C of metabolite M. For phased-array coils, the signal of an individual coil from inside the volume VOI will be weighted by its local sensitivity $g(dV)$. Thus, the signal $S_{M,R}$ from metabolite M acquired by coil R can be written as:

$$S_{M,R}(VOI) = c * \int_{VOI} g_R(V) * C_M(V)dV \qquad (1)$$

To simplify, we define the scaling factor $c=1$, accepting that the results will be presented in arbitrary units. In the case of healthy brain tissue principal contributing compartments will be white matter, gray matter and CSF. The metabolite concentrations in these compartments are expected to show little or no variations, which allows to convert equation (1) into an overdetermined system of R linear equations:

$$S_{M,R}(VOI) = \left\{C_{M,GM}(VOI_{GM}) * \int_{VOI_{GM}} g_R(V)dV\right\} + \left\{C_{M,WM}(VOI_{WM}) * \int_{VOI_{WM}} g_R(V)dV\right\} + \left\{C_{M,CSF}(VOI_{CSF}) * \int_{VOI_{CSF}} g_R(V)dV\right\}, \; R = [1 \ldots \text{number of coils}] \qquad (2)$$

The weighting factors $g_R(V)$ can be determined using commonly applied B_1 mapping approaches, while suitable segmentation algorithms can automatically outline the individual sub-volumes corresponding to the respective compartments VOI_{GM}, VOI_{WM}, VOI_{CSF}, yielding for this specific example individual metabolite concentrations C for gray matter, white matter and CSF.

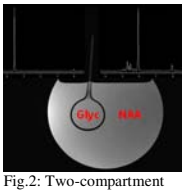

Fig.2: Two-compartment phantom filled with NAA and Glyc.

Materials & Methods

All experiments were performed on a GE Signa Excite 1.5T (GE Healthcare, Milwaukee, WI, USA), MRI scanner using an eight-channel clinical head array (MRI Devices, Waukesha, WI, USA). MR spectroscopy and imaging data were acquired from a healthy volunteer and a custom made phantom as shown in fig.2, consisting of an inner and an outer sphere filled with NAA (outer sphere) and Glycine (inner sphere). Single voxel PRESS spectra at three different positions covering both spheres in the phantom were acquired (fig.3). Due to the homogeneity of the phantom, B_1-maps of the individual coil elements could be derived from proton-density weighted images.

All spectroscopy raw data were processed off-line using the LCModel [3] to determine individual $S_{M,R}(VOI)$, while images were segmented using MRICro (http://www.sph.sc.edu/comd/rorden/mricro.html) with a manually adjusted threshold.

Overdetermined linear equations were solved with Matlab (The MathWorks, Inc.) using linear least square fitting with non-negativity constraints. Only the signals of the four coils with highest SNR were taken into consideration for the fit.

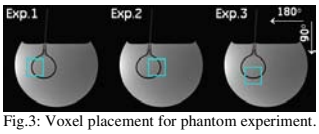

Fig.3: Voxel placement for phantom experiment.

Results

Healthy brain tissue images were successfully segmented into white matter (WM), gray matter (GM) and CSF (Fig. 4). As shown in fig. 1, the contribution of the different tissue types to the total signal varies from coil to coil. As metabolite concentrations are different in WM and GM, the resulting total metabolite ratio will be dependent on the algorithm used to average spectroscopy data from individual coil elements, and will thus become less reliable and reproducible. While this experiment has shown the principle problem of phased-array spectroscopy, the quantitative analysis was initially performed using phantom data with known metabolite concentrations.

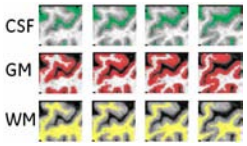

Fig. 4: Segmentation of healthy brain tissue into WM, GM and CSF.

Table 1 shows the results of the quantitative analysis of the spectroscopy data from the three SV acquisitions. The individual analysis of the compartments provided metabolite concentrations as shown on the right side of the table. Out of the twelve different resulting concentrations (three experiments times two compartments times two metabolites), two of the determined values are not in agreement with the known concentrations. Some of the potential reasons for this wrong results are the voxel displacement due to the different chemical shift of NAA and Glyc, low SNR of the individual spectra, inaccuracies of the segmentation process or the least square fitting routine. On the other hand, ten concentrations were correctly assigned to the compartments with an error of less than 10%, demonstrating the potential use of the introduced method.

	Known Concentrations [a.u.]		Estimated concentrations [a.u.] Least square fits with non-negativity constraints					
	NAA	Glyc	NAA-1	NAA-2	NAA-3	Glyc-1	Glyc-2	Glyc-3
Inner Sphere	0	150	19	0	28	144	157	160
Outer Sphere	30	0	30	31	30	0	2	0

Tab.1: Estimated metabolite concentrations of NAA and Glycine from three experiments compared to known concentrations inside the spatially separated inner and outer spheres. Ten out of twelve estimated concentrations were close to the expected values, while two results marked in yellow significantly miss the expected results.

Discussion

Even though the basic concepts for this method are similar to those used for accelerated spectroscopy using parallel imaging techniques [4,5], it cannot be considered an unfolding of spectroscopy data in real or k-space. Additionally to the B_1-maps required for parallel spectroscopy, this method uses image segmentation, quantitative analysis of the spectra of each individual coil and uses specific physiological properties of the tissue under examination.

Further phantom and in vivo studies are required to confirm the usability of this method in a clinical environment, i.e. if the inherently low SNR of in vivo MRS will allow for significant quantitative results. A crucial point is the solution of equation (2), where an overdetermined system of linear equations has to be numerically solved and optimized such that the amount of noise introduced into the solution by low SNR coil elements will be kept at a minimum.

One of the big strengths of the formalism is its flexibility: The compartmentation into GM, WM and CSF was used as a clinical example, but there are several other applications, like e.g. segmentation into active tumor, necrosis and/or healthy tissue, or e.g. inside hippocampus versus outside hippocampus. The number of available coils limits the maximum number of compartments. Still, preferably one would assign fewer compartments than coils to get a more reliable result.

In conclusion, this new method can be seen as a trade-off between SNR gain in recombined phased-array spectra [6,7] and implicitly increased "spatial resolution" due to resolving principal metabolite compartments.

References

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