

Combination of Multichannel Single-Voxel MRS Data Using Generalized Least Squares

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Introduction

Multichannel receiver coils are becoming more widely used in single-voxel magnetic resonance spectroscopy (MRS) for shortening scan time or improving signal-to-noise ratio (SNR). However, it remains somewhat unclear how to optimally combine multichannel data to produce the combined spectrum. Two recent methods, nd-comb (noise decorrelated combination) (1) and WSVD (Whitened Singular Value Decomposition) (2), take into account the noise correlation between different channels to improve the SNR of the combined spectrum. In both methods, a linear transformation of the received free induction decay (FID) signals is performed to remove the noise correlation and standardize the noise level. The transformation matrix is obtained by eigen decomposition of the noise covariance matrix. In nd-comb, the transformed FIDs are individually phased and then weighted summed to give the combined spectrum, where the weighting factor for each FID is the SNR of the water signal in water-unsuppressed acquisitions or a large metabolite peak. In WSVD, the combined FID is computed from the transformed FIDs by singular value decomposition. Both methods were tested using 8-channel receiver coils and offered improved SNR performance compared to other methods that ignore the noise correlation between different channels. In this work, we propose to combine multichannel MRS data using a generalized least squares (GLS) approach. The GLS algorithm has been used in parallel imaging and spectroscopic imaging (3,4), and appears to be a natural way for combining multichannel MRS data. However, to our best knowledge, there is no reported work that uses the exact GLS algorithm to combine multichannel single-voxel MRS data. The purpose of this work is to demonstrate that the GLS algorithm is a straightforward and optimal approach for combining multichannel single-voxel MRS data. Results from two in vivo experiments using an 8-channel receiver coil and one phantom experiment using a 32-channel receiver coil will be used to compare the performance of the GLS method with those of the nd-comb and WSVD methods.

Theory

The coil sensitivities S_m ($m = 1, 2, \dots, M$) at the voxel of interest can be obtained from the unsuppressed water signal or a large metabolite peak, where M is the total number of coil elements. The time-domain signal $D_m(t)$ detected by the m th coil element can be written as $D_m(t) = S_m C(t) + \epsilon_m(t)$, where $C(t)$ represents the magnetization vector of the voxel, i.e. the FID, and $\epsilon_m(t)$ is the random noise in the m th channel. In matrix form, we have $D = SC + \epsilon$, where D and ϵ are $M \times P$ matrices with P being the number of data points in the time domain signal; S is an M -element column vector and C a P -element row vector. Assuming that tissue water and metabolites have similar spatial distributions within the voxel, the best linear unbiased estimate (BLUE) of C is given by

$$C = (S^T \Psi^{-1} S)^{-1} S^T \Psi^{-1} D \quad [1]$$

where Ψ is the noise covariance matrix between coil elements, given by $\Psi = \epsilon \epsilon^T$, and T denotes conjugate transpose. Note that $S^T \Psi^{-1} S$ is a scalar, so $(S^T \Psi^{-1} S)^{-1}$ is equivalent to $1/(S^T \Psi^{-1} S)$.

Methods and Results

Two normal volunteers, consented in accordance with procedures approved by our institutional review board, were scanned on a GE 3 T scanner equipped with an 8-channel head coil. Water-suppressed MRS signals were acquired from a $3 \times 3 \times 2$ cm³ voxel in the frontal lobe of the brain using GE PROBE, a point resolved spectroscopy (PRESS) sequence, with TR = 1.5 s, TE = 68 ms, spectral width = 5000 Hz, number of data points = 2048, and number of acquisitions = 256. After the water-suppressed metabolite FIDs were acquired, unsuppressed water signals were acquired with two data acquisitions. The 256 acquisitions with two-step phase cycling were paired up and averaged into 128 sets of FIDs. The three different methods, nd-comb, WSVD, and GLS, were used respectively to compute the combined spectrum for each set of FIDs. For all three methods, the noise covariance matrix was computed using the spectral data of each channel between 8 and 20 ppm where no detectable metabolite peaks exist. For both the nd-comb and GLS methods, the unsuppressed water peak was used as the reference signal. In nd-comb, the noise-whitened signals were phased and weighted summed to give the combined spectrum. The phase correction term for each individual signal is iteratively changed until the real part of the water peak in the spectrum has maximum area. The SNR of the water peak in the real part of the spectrum was used as the magnitude of the weighting factor for each channel. In GLS, the integral of the complex-valued spectral signal over the unsuppressed water peak was used as the coil sensitivity S_m for each channel and the combined spectrum was computed according to Eq. [1]. The combined spectrum of one normal volunteer is displayed in Fig. 1. Coefficient of variation (CV) for the n-acetylaspartate (NAA) peak over the 128 acquisitions was computed for all three methods and are listed in Table 1. For the two normal volunteers, the GLS method has slightly lower CV values than the WSVD method and significantly lower CV values than the nd-comb method.

Phantom experiments using a 32-channel receiver head coil were also performed on a Siemens 7 T scanner. A Braino phantom was scanned with a PRESS sequence (TR = 2.5 s, TE = 100 ms, volumes of interest = $2 \times 2 \times 2$ cm³, spectral width = 4000 Hz, number of data points = 2048, and number of acquisitions = 128). The combined spectrum was computed for each of the 128 acquisitions using the three methods, respectively. For both the nd-comb and GLS methods, the Cr peak was used as the reference signal for computing the weighting factor or coil sensitivity of each channel. The combined spectrum computed using the GLS method is displayed in Fig. 2. The CV values of the NAA peak computed using the three different methods are listed in Table 1. It can be seen that the GLS method has a significantly lower CV value than the nd-comb and WSVD methods.

Discussion

The reduction in CV by using the GLS method becomes more pronounced when the 32-channel coil is used. WSVD decomposes the noise-whitened FIDs into a series of contributions of increasing rank and select the best rank-1 decomposition in terms of two vectors: a column vector containing the coil sensitivities and a row vector containing the combined FID. When the number of channels increases to 32, this rank-1 decomposition seems to become less effective. For nd-comb, the magnitude of the weighting factor for each channel is not optimal for minimizing multi-measurement variations. It would become optimal if the weighting factors were divided by the sum of squares of the SNR values of the reference peak. This small imperfection results in large multi-measurement variations when the number of channels is large.

Conclusions and Future Work

Mathematically, the GLS method gives the unbiased results with maximum SNR. In this work, we have demonstrated that the GLS method has lower CV than the nd-comb and WSVD methods. We expect the use of the GLS method will lead to improved precision in metabolite quantification in multi-measurement MRS studies. As future work, in vivo experiments using a 32-channel coil will be performed to further evaluate the GLS method.

References

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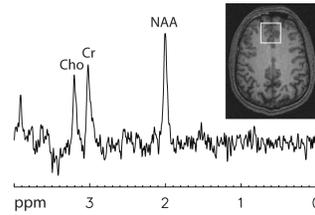


Fig. 1. Combined spectrum of one normal volunteer computed using the GLS method, where 8-channel data from a pair of acquisitions were used.

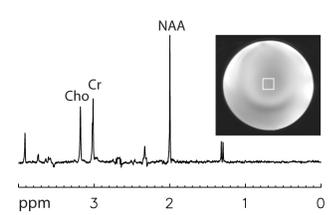


Fig. 2. Combined spectrum of the Braino phantom computed using the GLS method, where 32-channel data from a single acquisition were used.

	Volunteer 1 (8-channel coil)	Volunteer 2 (8-channel coil)	Phantom (32-channel coil)
nd-comb	6.68%	6.09%	6.35%
WSVD	5.54%	4.87%	7.13%
GLS	5.31%	4.36%	2.85%

Table 1. CV values of the NAA peak in the combined spectrum