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The rapid and automatic combination of proton MRSI data using multi-channel coils without water suppression

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Abstract

The use of multi-channel coils can efficiently increase the signal-to-noise ratio (SNR) of magnetic resonance spectroscopy data if the signals from multiple channels are optimally combined. Combining multi-channel signals requires proper alignment of the phases of the signals from each of the elements of the coil and then accurately weighting the summation of those signals. We present a procedure for acquiring proton magnetic resonance spectroscopic imaging (MRSI) data using an eight-channel coil without water suppression and a rapid and robust method that uses unsuppressed water signal as a reference both for aligning the phases and for weighting the summation of signals that originate in the multiple coil elements. We use both computer simulation and in vivo proton MRSI data to demonstrate the advantages of our method for optimizing the SNR of the combined signal compared with the SNRs of signals that were acquired either using a standard volume head coil or using an eight-channel coil with a metabolite signal as the reference for combination.

Keywords

Multi-channel coil; Proton magnetic resonance spectroscopic imaging; Water suppression; Signal-to-noise ratio; Brain

1. Introduction

Magnetic resonance spectroscopic imaging (MRSI) non-invasively measures the concentrations and distributions of metabolites throughout the brain. Because the abundance of metabolites is much lower than that of water in the brain, however, the signal-to-noise ratio (SNR) of MRSI is low compared with the SNR of conventional anatomical MR imaging. The SNR of MRSI data can be improved by increasing either the size of the voxels or the measurement time. Increasing voxel size, however, compromises spatial resolution, and increasing measurement time poses problems for many patient populations who have difficulty remaining still for long durations.

An alternative approach to improving the SNR of MRSI data from the brain is to use a multi-channel coil for signal acquisition. A multi-channel coil consists of an array of mutually decoupled, geometrically optimized surface coils, which receive MR signal from the brain simultaneously [1–7]. These multiple signals are then combined mathematically to yield a single spectroscopic signal at each voxel. For multi-channel coils to increase the SNR of MRSI data compared with the SNR of data acquired using a conventional single-channel volume coil,

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the signals from each of the coil elements of a multi-channel coil must be combined optimally through both the accurate alignment of phases and the accurate weighted summation of signals from each of the coil elements. Phase alignment eliminates differences between the phases of the component signals, thereby permitting their constructive summation. The weighting of individual signals during their summation emphasizes those signals that have comparatively higher SNRs, thereby optimizing the SNR of the combined signal.

Both the accurate alignment of the phases of the signals and the calculation of the weighting factors (WFs) for signal summation require the use of a reference signal. One recent approach to phase alignment used the signal in the time domain as a reference to calculate and eliminate phase differences between signals from differing coil elements [2]. Another approach used spectral fitting software to identify in the frequency domain phase differences in metabolite signals that originated in different coil elements [3]. To calculate the WFs required for signal summation, some approaches have employed background noise as a reference to optimize SNR [2,4], whereas others have used as a reference the SNR of a spectrum [5] or the peak area of a particular metabolite [3,6] to calculate the optimal WFs. Each of these approaches used water suppression (WS) during signal acquisition to reduce the dynamic range of the signal, thereby avoiding introduction of noise from the analog-to-digital conversion, and simplifying the post-processing of the MR signal.

The signal from unsuppressed water itself, however, can serve as an ideal reference for the correct alignment of phases and for the calculation of the optimal WFs required for combining signals across multiple coil elements. The phase and amplitude of the dominant water signal in the brain are more easily and rapidly measured against the background noise and baseline distortion of MRSI data than is possible when using a metabolite as a reference, thus permitting a more accurate calculation of phase differences in signals across coil elements and a more optimal calculation of the WFs for signal combination. Reducing error in these measurements and calculations can substantially enhance the combined signal and therefore increase its SNR.

One recent study demonstrated the use of unsuppressed water signal as a reference to combine signals from multi-channel coils in single-voxel proton spectroscopy [7]. Water and metabolite signals were acquired in separate scans, and the metabolite signals were measured after the suppression of water signal. Although measuring water and metabolite signals in separate scans increases only marginally the total measurement time for single-voxel ^1H MRS, use of this same strategy would increase substantially the measurement time for ^1H MRSI. Other recent studies have demonstrated the feasibility and advantages of in vivo ^1H MRS and ^1H MRSI without WS while measuring metabolite and water signals simultaneously [8–11]; these studies used standard volume coils, however, not multi-channel coils. Finally, two recent conference abstracts have reported use of the unsuppressed water signal to generate the sensitivity maps used to unwrap the folded images in sensitivity-encoded spectroscopic imaging (SENSE-SI), images produced by under-sampling k -space data during signal acquisition with parallel imaging [12,13]. The aim of those SENSE-SI studies, however, was to reduce measurement time, not to improve phase alignment during signal combination or to increase SNR, which were the aims of this study.

We describe a method for performing ^1H MRSI without WS using an eight-channel coil in which we use the unsuppressed water signal as a reference to improve the phase alignment and weighted summation of signals across the multiple coil elements, thereby increasing the SNR of the combined images. We then use computer simulations and in vivo ^1H MRSI data to demonstrate the advantages of using unsuppressed water as a reference to align phases and weight the summation of multi-channel signals, compared with the combined multi-channel signals using as a reference a metabolite signal and signals acquired with a single-channel volume coil.

2. Methods

2.1. Data acquisition

We acquired MRI and MRSI data using a whole-body 3-T scanner (Signa 3.0T, GE Healthcare, Waukesha, WI, USA) equipped with a single-channel volume coil for transmission and an eight-channel coil for receiving radiofrequency signals. An axial, T1-weighted scout image was acquired first for localization, prior to MRSI acquisition. MRSI data were acquired using a multi-planar SI pulse sequence (MPCSI) [14]. The parameters used for data acquisition were as follows: TR/TE=2300/288 ms; FOV=24×24 cm²; number of phase encoding (PE) steps=32×32; spectral width=2000 Hz; number of slices=4; slice thickness/spacing=10/2 mm; a full echo was acquired with 512 complex data points. Outer volume lipid signal was suppressed with user-placed saturation bands. The WS option of the pulse program was turned off. Data were acquired in the extended dynamic range mode with an oversampling factor of 62.5 [15] and were saved in 32 bits. The transmitter gain, digital receiver gain (R1) and analogue receiver gain (R2) were identified during an automatic prescan procedure; R1 and R2 were then manually adjusted to their highest possible values without saturating signal. We also acquired in vivo data using the standard single-channel volume coil to compare with the data acquired using the eight-channel coil.

2.2. Subjects

Four healthy adult volunteers participated in the human studies. The protocol was approved by the Institutional Review Board of the New York State Psychiatric Institute.

2.3. Combination of signals from multiple channels

The raw dataset acquired with the eight-channel coil was initially transferred from the scanner to a personal computer. We separated the complete dataset into eight portions, one for each of the individual coil elements. We then used a two-dimensional Hamming window to perform spatial filtering on the k -space data obtained from each coil element. We subsequently applied Fourier transformation to transform those data into the spatial domain on a slice-by-slice basis. We calculated the phases of the signals from each of the coil elements on a voxel-wise basis according to the 256th complex data point of the signals. The first coil was designated as the reference coil against which the relative differences in phases, $\Delta\phi$'s, of the other coil elements were determined. The phases of the signal from each element were aligned to the phase of the reference coil by multiplying their signals with the corresponding terms of their differences in phase, $\exp(i\Delta\phi_c)$, thus compensating for phase differences between the signals of coil elements that arose from their differing spatial positions relative to the locations of the voxels being sampled:

$$S_{v,c,\text{align}} = S_{v,c} e^{i\Delta\phi_c}, \quad \Delta\phi_c = \phi_1 - \phi_c, \quad c = 2, \dots, N. \quad (1)$$

The alignment was applied voxel-wise; therefore, $S_{v,c}$ stands for the signal from voxel v sampled by coil element c .

The WFs were also calculated on a voxel-wise basis from quasi-SNRs calculated in each voxel to take into account both signal amplitude and noise when optimizing the SNR of the combined signal. Quasi-SNR (qSNR) was defined as the ratio of the amplitude of the signal in each voxel, a_v , to the relative overall noise level R_c of that particular coil element:

$$\text{qSNR}_{v,c} = a_v / R_c. \quad c = 1, 2, \dots, 8. \quad (2)$$

The overall noise level for each coil, N_c , was calculated from selected voxels outside of the brain, and the relative noise levels, R_c 's, were calculated using the first coil as a reference (i.e., $R_c = N_c / N_1$). We assumed that the R_c 's did not change with time and could be used as the relative

sensitivities of the coils [2]. For our eight-channel coil, the R_c 's were 1.00, 1.11, 1.38, 1.28, 1.27, 1.33, 1.16 and 1.06. We calculated the normalized WF for voxel v and coil c , $w_{v,c}$, using the following equation:

$$w_{v,c} = \text{qSNR}_{v,c} / \sqrt{\sum_{c=1}^N \text{qSNR}_{v,c}^2}, \quad c = 1, 2, \dots, N; N = 8. \quad (3)$$

The combined signal of the phased array coils at each voxel was calculated as:

$$S_v = \sum_{c=1}^N w_{v,c} S_{v,c,\text{align}}. \quad (4)$$

For the MPCSI data, which were acquired with full echoes, we calculated the amplitude of signal at each voxel (a_v) by Fourier-transforming the signal from the time domain into the spectral domain. We then integrated the area under the water peak in the spectrum for each voxel and obtained the WFs using Eqs. (2) and (3).

These procedures for signal combination were implemented with a fully automated and computationally efficient software program developed in-house and written with Matlab (The MathWorks, Inc., Natick, MA, USA). On a server equipped with a 2.7-GHz processor, the algorithm required approximately 10 s to combine raw SI datasets from eight channels, each with 16×16 PEs and four slices.

2.4. Extraction of water signal

To facilitate the subsequent processing of metabolite signals, we modeled the water components of the combined signal using the Matrix-Pencil Method (MPM) [16]. Signal components with frequencies in the range of -0.5 to 0.5 ppm were classified as water signal and were recombined together to form the total water signal, which was then subtracted from the full signal to yield the retained signal from metabolites. To speed the computational modeling of water signal using MPM, we separated the signal from each voxel into two half-echoes and entered them separately into MPM for detecting the water components. We then combined the first and second half-echoes for water to form its full echo. This approach reduced the processing time by a factor close to 3 and reduced the residual water signal after extraction.

2.5. Computer simulations

We conducted a computer simulation to compare SNRs when using either a metabolite or water as the reference to combine signals from an eight-channel coil. We first generated eight free induction decays (FIDs), each with differing amplitudes and phases of $n\pi/4$ ($n=1, 2, \dots, 8$), representing the differing metabolite signals from individual coil elements. We added to the FID for each channel noise that was Gaussian distributed with a standard deviation (S.D.) of 1. We then combined the 8 signal components using the aforementioned procedures for phase alignment and weighted summation of signals from each coil element. We then measured the SNR of the combined signal. These procedures were repeated 500 times, using a different Gaussian noise set in each trial. We subsequently calculated the means and S.D.'s for the SNRs of the combined signals in the 500 trials. We repeated the above procedure with a second set of eight FIDs, whose amplitudes were set 200 times greater than those in the first set, to approximate the amplitudes of the water signals. We compared the means and S.D.'s obtained from the two datasets.

We also performed a computer simulation to compare the SNRs of the signals combined using two differing weighting mechanisms: one is based on WFs calculated from SNRs of signals from each of the individual coil elements; the other is based on WFs calculated from signal

amplitudes only. We again generated a set of eight FIDs, each with identical phase but differing amplitudes and noise levels that mimicked typical values in vivo. This dataset underwent two combination procedures, using the aforementioned two sets of WFs, respectively. We calculated the SNRs of the two combined signals. We then circularly shifted the signal amplitudes among the eight FIDs while keeping the noise levels unchanged and repeated 160 times the procedures for FID generation, signal combination and SNR calculation. We compared the resulting two sets of 160 SNRs each.

3. Results

We aligned the phases of the signals from each of the elements of the eight-channel coil in the time domain using the signal of the unsuppressed water as a reference. Visual inspection of signals from differing channels in the frequency domain showed that, although their phases differed before alignment, the water signals exhibited identical phases following alignment (Fig. 1). Aligning phases using the water signal in each voxel also aligned metabolite signals (Fig. 1), because the phase differences across coil elements were identical for water and metabolites [3].

The metabolite spectra had lower SNRs and larger noise levels than did the signals from water (Fig. 1). Computer simulations confirmed that the large noise levels seen in the metabolite signals produce errors in the calculation of phases, and, in turn, in the aligning of phases, if a metabolite signal rather than the water signal is used as a reference. In the first simulation, the amplitudes of the eight signals in the time domain were 2.5, 4, 5.5, 7, 8.5, 10, 11.5 and 13, respectively, and the noise level was 1. In the frequency domain, the corresponding SNRs (defined as the ratios of peak heights to the S.D. of real or imaginary parts of data in signal-free regions) for the eight channels approximated 6, 10, 13, 17, 21, 25, 27 and 32, respectively. These values are typical SNRs for metabolites measured using in vivo single-voxel MRS data acquired with multi-channel coils [7]. The theoretical SNR of the combined signal — its SNR if these signals were combined without error in the alignment of phases — was 60.0. In contrast, the simulation demonstrated that the mean±S.D. of the SNR of the combined signal, which included contributions mainly from noise-induced errors in phase alignment, was 56.2±5.08, corresponding to a bias of 6.3% and coefficient of variation (CoV) of 9.0%. However, the bias and the CoV of the combined signal were 0.0 and 1.0% in the second simulation, where the SNR of the signal was 200 times larger than that of the first simulation. In the in vivo situation, the SNR of water in ¹H MRSI without WS is typically three orders of magnitude larger than that of metabolites. Thus, the simulation demonstrates clearly that the use of unsuppressed water as a reference for the aligning of phases across channels is more reliable and more robust than is the use of a metabolite as a reference.

The superiority of the SNR associated with use of unsuppressed water as a reference was further confirmed by comparing it to the SNR obtained using NAA as a reference for in vivo ¹H MRSI datasets reconstructed from eight-channel signals. The use of unsuppressed water as the reference produced spectroscopic images with high SNR in regions of the image where metabolites were present (Fig. 2). The use of NAA as the reference, in contrast, produced low signal and noisy images of metabolite concentrations (Fig. 2). The spectra also demonstrated clearly the improvement in SNR of the combined signal when water was used as a reference compared with the signals from the individual coil elements (Fig. 3). Numerical calculation showed that the SNR of NAA in the combined signal in this example was 144% of the highest SNR present in the signals from the component coils.

Computer simulation and in vivo data showed that the advantage of using SNRs to calculate WFs over using signal *amplitudes* only depended on the number of coils and the differences in their noise levels. In the simulation, the gain of using SNRs against using amplitudes was

1.65% (paired t -test; $P < 10^{-14}$, $N = 160$), for relative noise levels, R_c 's, given in the Methods section. If only the first four coils were used, the gain was 2.2% (paired t -test; $P < 10^{-16}$, $N = 160$). In the in vivo case, the gains varied from <1% to 2% (paired t -test; $P < 10^{-4}$, $N \geq 100$) for different regions and slices. The improvement of SNR is statistically significant, although the value looks marginal.

To assess the improvement in SNR of an eight-channel coil over a standard volume coil throughout the imaging volume, we compared the SNRs of whole-brain MRSIs measured using each of these two coils (Fig. 4). The SNRs of NAA at 2.01 ppm range from 2.0 to 76 for the eight-channel coil, and from 2.3 to 41 for the single-channel volume coil, respectively. The ratios of the highest, the most probable and the average SNRs between the two coils are 1.83, 1.64 and 1.77, respectively. In addition, the histograms demonstrate clearly that the SNRs are right-shifted substantially in the data from the multi-channel coil compared with data from the volume coil. We note that these values may be affected subtly by several factors, such as partial volume effects at the edge of regions of interest (ROIs), different shimming and loading of the two coils and differing anatomical positions of the slices.

4. Discussion

The use of signal from unsuppressed water as a reference facilitates the accurate detection and subsequent alignment of phases in signals from individual coil elements within a multi-channel coil (Fig. 1). We use a straightforward technique for measuring in the time domain the phase of the n th complex data point of the unsuppressed signal (e.g., the midpoint in a full-echo). Although this method of phase alignment works well in the absence of WS, several difficulties arise with the technique if the data are acquired with WS. One is that the phases of residual water signal differ from those of metabolite signals [3]; phase alignment that is based on residual water signal therefore may produce errors in the correction of phases of the metabolite signals. A second difficulty is that J-coupled resonances introduce significant errors into the phases of the signals unless the echo time is either very short (e.g., <20 ms, in which case the effects of J-coupling resonances will be small) or very long (e.g., ≥ 280 ms, in which case the J-coupled resonances will decay to levels below noise). A third difficulty is that when measuring the phase of a complex data point in the FID signals acquired with WS, noise can cause sizable errors in the measurement of the phase of a signal, especially when SNR is low. This noise effect has been shown previously [2] and is evident in the results of our computer simulations.

As an alternative to detecting phases of signals in the time domain, phase detection could be performed in the frequency domain by employing as a reference the signal of a metabolite, such as NAA. In this case, however, contamination by lipid signals can introduce errors into the calculation of phases because the lipid and NAA peaks may overlap. In addition, the effects of noise that are similar to those in the time domain also occur in the frequency domain. Our computer simulations demonstrated that all of these difficulties can be minimized if the unsuppressed water signal is used as the reference for phase alignment.

The results of our computer simulations were further confirmed by in vivo data, which demonstrated a superior SNR for signals that were combined using water as a reference compared with the SNR of signals that were combined using NAA as a reference (Fig. 2). We note that phase alignment using NAA as a reference performed particularly poorly with our algorithm; therefore, it was conducted in the frequency domain, after removing water components from the signal and zero-filling from 512 to 4096 data points in the time domain. We employed this procedure for using NAA as a reference to ensure a fair comparison of its performance with the use of water as a reference. Monte Carlo simulation on signals without noise verified that the bias of phase detection with this approach was close to zero ($\sim 10^{-3}$

degree), with a standard deviation of about 1.5 degrees. This amounts to an error of approximately 1/6 of that caused by the typical noise levels used in the previous computer simulation. Therefore, the reduction in SNR of the combined signal when using NAA as a reference (Fig. 2) was mainly a consequence of noise-induced errors in phase alignment and in the weighted summation of signals from the multiple coil elements. We note further that this simple approach for phase detection of the NAA signal in the frequency domain is only feasible for MRSI data acquired using a long TE, when spectral overlap and baseline distortion are minimal. For MRSI acquired at short TE, other investigators [3] have used the LCModel [17] to estimate the phases and amplitudes of the reference signal, a method that is more robust to the imperfections of spectral overlap and baseline distortion. However, the computational cost of this method is high.

Our approach to calculating WFs, which is based on the SNRs of the water signal of the individual coil elements rather than on the amplitudes of either the water signal or background noise, also helped to optimize the SNR of the combined signal from a multi-channel coil. Improvement in SNR was attributable to the much greater strength of the water signal compared with either noise or baseline distortion. Use of *SNR* of water as a reference also contributed to the improvement of SNR because it accounted both for the amplitudes of the water signals and for the differences in noise levels across coil elements [2,3,5].

Previously, either background noise [2] or signal amplitude [7] has been used as references for calculating WFs. The former amounts to ignoring differences in coil proximity; therefore, signals from all voxels across the ROI have similar WFs. When the size of the ROI is large and the amplitudes of signals from differing voxels vary significantly across the ROI, the SNR of the combined signal using background noise as a WF may be far from optimum [2]. The latter ignores differences in noise levels among element coils and implies that they all have the same sensitivity [7]. We found that noise levels can differ by as much as 30% across coil elements. In this case, our simulations showed that ignoring these differences in noise can reduce the SNR of the combined signal up to 2%, which is statistically significant ($P < 10^{-14}$; paired *t*-test).

We calculated the SNRs of signals from the individual coil elements by averaging noise in regions outside the brain and using that average to characterize the noise level of the coil. This approach in essence disregards the correlations of noise across coil elements, which seems reasonable, given that noise correlations are minimal for decoupled multi-channel coils [18]. A common procedure to determine SNR is to measure the signal and noise in the *same* voxel [5]. In this case, however, water components must be removed from the signal before measuring residual noise in each voxel for each coil element, which can be time-consuming.

The combined eight-channel signals using unsuppressed water as a reference increased the SNRs of the MRSI signals (Fig. 3), significantly when compared with signals acquired using the standard volume coil (Fig. 4). A more accurate comparison of these SNRs is desirable, although difficult. Nevertheless, this general comparison may prove useful when designing pulse sequence parameters that require consideration of SNR trade-offs, such as spatial resolution (in-plane voxel size, slice thickness) and measurement time (TR, TE, number of PEs), for ^1H MRSI studies using an eight-channel coil.

One disadvantage of using ^1H MRSI without WS is that audio vibrations from the gradient coils induce frequency modulations of the water signal that then produce several sidebands in the MR spectra. These sidebands increase noise in metabolite signals [10,19]. Although several methods have been proposed to suppress these sidebands [8,10,19], at present we suggest that our method for signal combination across coil elements should be applied only with data acquired using a long TE, thereby minimizing the presence of sidebands. In our experiment at

TE=288 ms, the noise levels in individual coil elements for MRSI without WS were <3% greater than noise levels in MRSI with WS. In the future, pulse sequences with interleaved water and metabolite acquisitions — i.e., acquisition within a single MRSI scan of both an unsuppressed water signal and a metabolite signal with WS — can be implemented to allow use of a shorter TE [20]. An additional trivial disadvantage of our method is that it may require manual adjustment of the receiver gain in order to extend the dynamic range of the signal and to avoid signal overflow.

5. Conclusion

We have presented a method for performing proton MRSI using multi-channel coils without WS. We combine the signals from the multiple elements of a multi-channel coil using the unsuppressed water signal as a reference in order to align phases of the signals more accurately and to improve the weighted summation of component signals, which together maximize SNR of the combined signal. In addition, this algorithm for phase alignment and the weighted summation of multi-channel MRSI data works rapidly and is robust to the influences of noise, baseline distortion and spectral overlap. We have demonstrated that measuring water and metabolite signals simultaneously, within a single scan, minimizes overall scan time, an important advantage when scanning vulnerable patient populations who may have difficulty tolerating longer scan times. Future investigation will determine whether the water signal can be used as an internal reference for the absolute quantification of metabolite concentrations. Further research should also develop effective methods for reducing the levels of noise that can be induced by the water signal, thereby allowing our approach to be applied to data acquired with a shorter TE.

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Fig. 1.

Spectra for water and metabolites from multiple individual coil elements (each represented in differing colored lines) at a single voxel after phase alignments that were performed using water signal as a reference in the time domain (TD). Water spectra were obtained directly by Fourier transform (FT). The metabolite spectra were obtained by FT after removing the dominant water components in the TD. In both cases, no zero- or first-order phase corrections were made. The three prominent spectral peaks were assigned to NAA (2.01 ppm), total creatine (Cr, 3.04 ppm) and choline-containing compounds (Ch, 3.24 ppm). Note that both water spectra and metabolite spectra are perfectly in phase following use of the high SNR of water signal as a reference for more accurate phase alignment. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Fig. 2.

Spectroscopic images of metabolites (NAA, Cr and Ch) reconstructed from signals combined across coil elements using water as a reference (top row) compared with images reconstructed from combined signals using NAA as a reference (lower row). The dataset was acquired from a healthy human subject using an eight-channel coil without WS. To facilitate the use of NAA as a reference for the combination, we removed the water components from the component element signals and zero-filled the time-domain data from 512 to 4096 points. We then detected and aligned the phases of the NAA peaks in individual voxels in the frequency domain. We further calculated the WFs according to the SNRs of NAA and combined the signals acquired from the eight coil elements. The SIs reconstructed from signals that were combined using NAA as a reference are noisy due to signal loss that was caused by the imperfect alignment of phases and suboptimal combination of signals from the multiple coil elements.

Fig. 3.

Representative spectra from each of the eight coil elements (Panels 1–8) and the combined signal (Panel 9) using water as a reference. The three prominent peaks were assigned to NAA, Cr and Cho, respectively (shown in Panel 3). The spectrum in Panel 9 is scaled by 1/2. Spectral regions above 6 ppm and below 1 ppm are displayed (indicated by arrows in Panel 1) to facilitate comparison of noise levels. The data were acquired as a full-echo using MPCSI, and the spectra are in magnitude mode. The SNR of NAA in the combined signal is 144%, the highest SNR of the NAA signal in any of the individual coil elements (in this instance, shown in Panel 3).

Fig. 4. Histograms showing distributions of SNR of the NAA peak in MRSIs measured using an eight-channel coil (a) and a volume head coil (b), respectively. The voxels are from four slices in both cases. The total numbers of voxels are 1237 and 1123 in (a) and (b), respectively. The histograms show SNR improvements of the eight-channel coil compared to the single-channel volume coil.