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Journal of Magnetic Resonance 159 (2002) 151–157

JMR Journal of Magnetic Resonance

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Automated correction of unwanted phase jumps in reference signals which corrupt MRSI spectra after eddy current correction

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Received 14 May 2002; revised 30 September 2002

Abstract

A commonly applied step in the postprocessing of gradient localized proton MR spectroscopy, is correction for eddy current effects using the water signal as a reference. However, this method can degrade some of the metabolite signals, in particular if applied on proton MR spectroscopic imaging data. This artifact arises from the water reference signal in the presence of a second signal which resonates close to the main water resonance. The interference of both resonances will introduce jumps in the phase of the reference time domain signal. Using this phase for eddy current correction will result in a ringing artifact in the frequency domain of the metabolite signal over the whole frequency range. We propose a moving window correction algorithm, which screens the phase of reference signals and removes phase jumps in time domain caused by interference of signals from multiple spin systems. The phase jumps may be abrupt or gradually distributed over several time data points. Because the correction algorithm only corrects time data points which contain phase jumps, the phase is minimally disrupted. Furthermore, the algorithm is automated for large datasets, correcting only those water reference signals which are corrupted. After correction of the corrupted reference signals, normal eddy current correction may be performed. The algorithm is compared with a method which uses a low-pass filter and tested on simulated data as well as on in vivo proton spectroscopic imaging data from a healthy volunteer and from patients with a brain tumor.

Keywords: Magnetic resonance spectroscopic imaging; Eddy current correction; Data processing; Reference deconvolution; Artifact

1. Introduction

In proton magnetic resonance spectroscopy, eddy current correction (ECC) [1–5] is a standard correction method [6] which requires a metabolite signal as well as a reference signal. In in vivo MR studies, the reference signal normally consists of the unsuppressed water signal. Theoretically, ECC corrects for time dependent eddy current phase effects in the free induction decay (FID). Besides, it resets the zero-order phase and resets the water frequency to 0 Hz. However, ECC may lead to a severe ringing artifact in the metabolite spectrum [7–9] if the envelope of the water reference time domain signal crosses zero, causing the phase of the water reference signal to flip 180° at a specific time point. The zero crossing of the envelope may occur because the single water reference peak has acquired some doublet character because of poor shimming or due to susceptibility effects [7,9]. Generally, these artifacts appear more frequently in magnetic resonance spectroscopic imaging (MRSI) data than in single voxel data because of the much larger volume of interest. In addition, signals with slightly different water frequencies originating from different voxels in the MRSI dataset may be mixed as a result of the point spread function [10]. The eddy current division will introduce the 180° phase jumps into the metabolite time domain signal, causing severe ringing in the frequency domain after Fourier transformation.

A solution to this problem has been presented by Wild [7], who used low-pass filtering of the total phase of the water reference time domain signal to remove unexpected phase jumps. They tested the efficiency of two low-pass filters, an infinite impulse response Butterworth filter and a finite impulse response filter. The Butterworth filter was found to be more effective.

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PII: S1090-7807(02)00102-7

This paper also deals with the implementation of a correction algorithm which detects phase jumps in the phase of reference time domain signals, but instead of filtering the whole phase our algorithm has a local nature. It searches for specific features in the magnitude and the phase of the reference time domain signal, and only corrects time points when specific conditions are met. The advantages of our method are: (a) only the time points at a phase jump are altered; (b) reference signals which do not contain phase jumps remain unchanged and therefore the correction algorithm can be applied on large datasets like MRSI data; (c) the correction algorithm identifies abrupt changes as well as more gradual distributed transitions, which also induce ringing in the frequency domain of a metabolite signal.

In order to validate the correction algorithm, we tested it on simulated data, compared it with the filter described by Wild [7] and used it to screen brain MRSI datasets of a volunteer and several patients with a brain tumor. In 93% of the cases the unwanted phase jumps in the reference time domain signal were identified by our method, resulting in substantial improvement of the metabolite spectrum after ECC.

2. Theory

2.1. Eddy current correction

The theory of ECC has been frequently described in literature [1–5,8] and will therefore be discussed concisely. To perform ECC, the metabolite time domain signal is point-wise divided by the phase factor of the reference signal in the time domain. Practically, the phase of the reference signal is calculated by taking the arctangent of the quotient of the imaginary and real part of each time point.

The correction only holds when the reference signal contains a single dominant component. If this is not the case, one should use other techniques like described by Barjat et al. [9].

However, in the correction of large sets of data, as in MRSI, which only contain few reference signals with some doublet character, ECC is still very effective. Correction of the largest artifact introduced in the metabolite spectrum, i.e., the ringing due to phase jumps in the phase of the reference time domain signal, ensures that the metabolite spectrum can still be of use.

2.2. The ringing artifact

The origin of the ringing artifact is explained in Fig. 1. As an example we have simulated a metabolite and two reference signals. The metabolite signal contains two resonances. The first reference signal contains one resonance and the second two. These two resonances are close together, in order to simulate a water reference signal with some doublet character. Information about the signals can be found in Table 1.

The left column in Fig. 1 gives an example if the reference signal only contains 1 resonance. Figs. 1a and b show the magnitude and phase of the reference time domain signal. Both magnitude and phase do not show any irregularities. When the phase is used to perform ECC on the metabolite signal (Fig. 1c), this results in a phase corrected spectrum (Fig. 1d) which has shifted 10 Hz to the left due to the offset frequency of the reference to the detector.

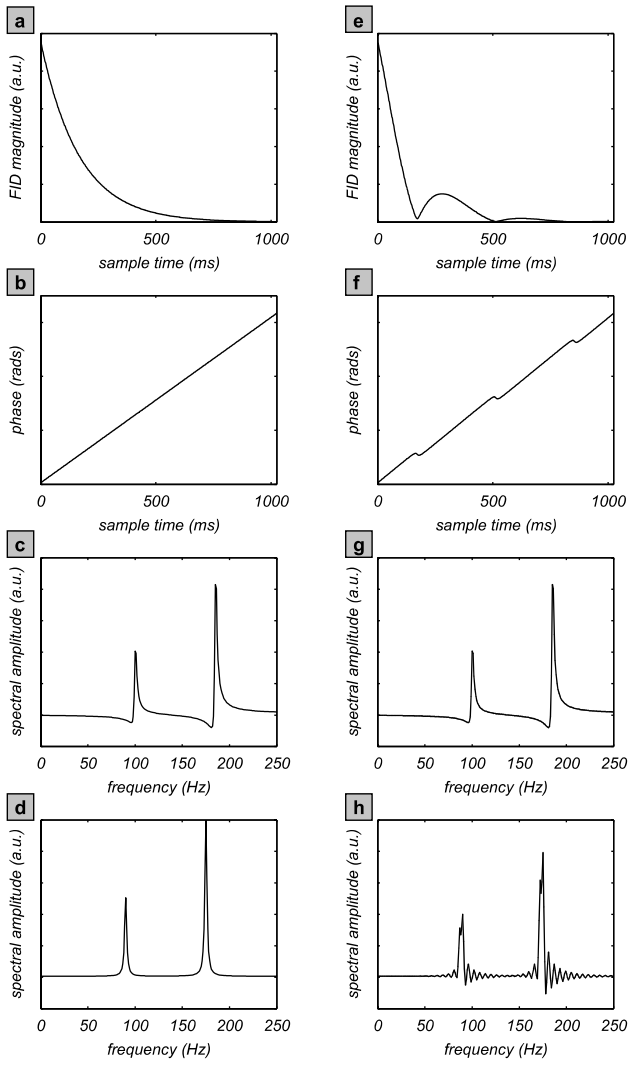

Fig. 1. Example of ECC and the ringing artifact. Parameters for the simulated data can be found in Table 1. (a) Magnitude of the simulated reference time domain signal containing one resonance. (b) Phase of this reference signal. (c) Frequency domain of the simulated metabolite spectrum. (d) ECC-corrected metabolite spectrum. The zero-order phase is corrected and the two resonances are shifted 10 Hz to the left. (e) Magnitude of the simulated reference signal containing two resonances. (f) Phase of this reference signal. The phase jumps are gradually distributed but will nevertheless introduce ringing in the metabolite spectrum (g) when ECC is performed (h).

Table 1
Parameters for the simulated data presented in Fig. 1[a]

	Metabolite signal	Reference signal 1	Reference signal 2
ω_1 (Hz)	100	10	10
ω_2 (Hz)	185		13
$d_{1,2}$ (Hz)	8	6	6
$\Phi_{1,2}$ (°)	35	35	35
A_1 (a.u.)	1	95	50
A_2 (a.u.)	2		45

[a] Each signal is constructed using the following equation: $\mathrm{FID} = \sum_k A_k * \exp(\mathrm{i}2\pi/360\Phi_k) * \exp(-\pi d_k + \mathrm{i}2\pi\omega_k)t_n$, with A_k the amplitude, Φ_k the phase, d_k the damping and ω_k the frequency of resonance k. t_n is the time instance.

In the right column of Fig. 1 the same metabolite spectrum is used (Fig. 1g), but in this situation the reference signal contains two resonances which are only 3 Hz apart. Because of interference, the magnitude (Fig. 1e) of the reference signal shows beats at specific points in time domain. The phase of the reference signal contains phase jumps which are gradually distributed and not exactly 180°, because the amplitudes A_1 and A_2 are not the same (Fig. 1f). ECC of the metabolite FID with the phase of this reference signal will introduce severe ringing in the spectrum (Fig. 1h). This ringing is asymmetrical around the tops of the resonances, because the phase jumps are distributed over a certain number of points. If the phase jump occurs over one time point the ringing is symmetrical, but in practice this hardly ever occurs.

2.3. Outline of the correction algorithm

To remove the jumps in the phase of the reference time domain signal, we have developed a correction algorithm which moves along it, correcting it if certain conditions are met. If one of the conditions fails, the reference signal is not changed. A flow-chart of the steps in the correction algorithm is presented in Fig. 2.

Step a: If the reference signal contains two interfering resonances, its magnitude will contain one or more minima. Normally only one minimum occurs in the signal-containing part of the magnitude of the FID. However, if necessary it is possible to search in a successive way for more minima and investigate if the phase at that point also needs a correction. Each minimum can be found by searching for a change in the sign of the first derivative of the magnitude signal from negative to positive. Reference signals from in vivo experiments normally have a large signal to noise ratio, therefore finding a zero crossing in the first derivative is straightforward. If the signal is noisy, smoothing of the magnitude can be applied.

Step b: A minimum in the magnitude must coincide with a sigmoidal shape in the phase of the reference signal. This shape can be found in the first derivative of the phase, by searching for a successive number of data points which are above or below the baseline.

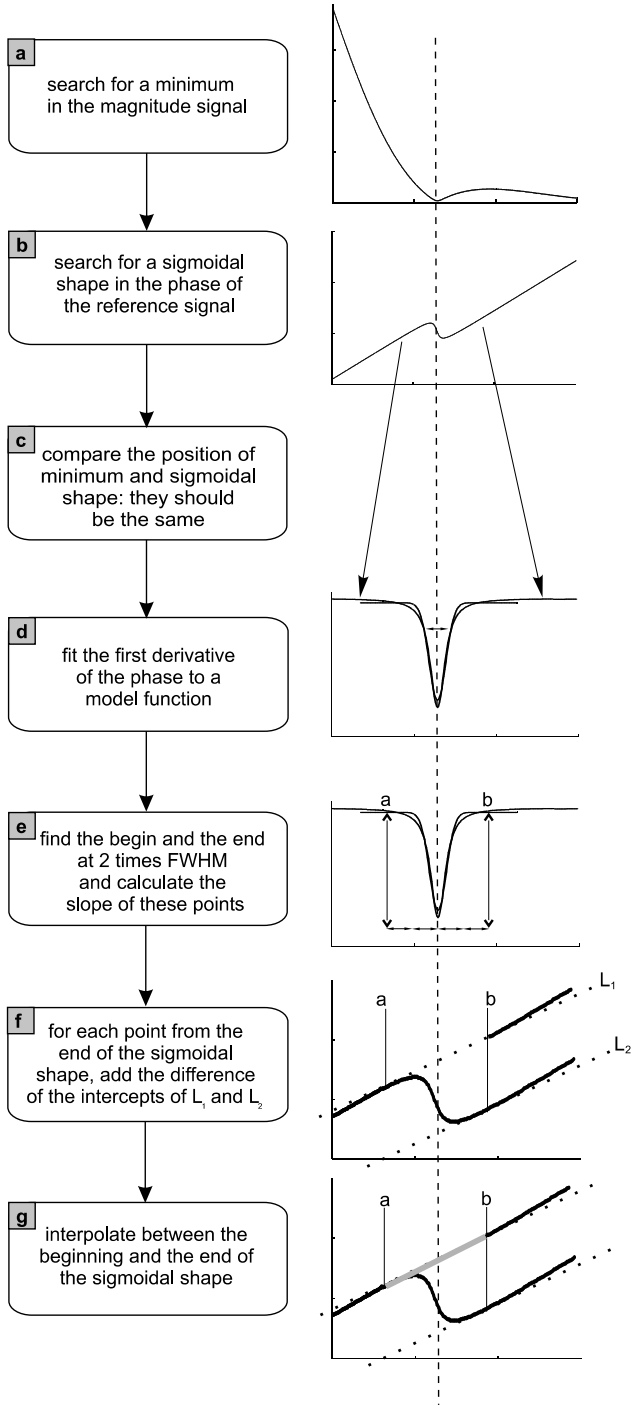

Fig. 2. Flow-chart of the correction algorithm.

Step c: The location of the minimum in the magnitude is compared to the location of the sigmoidal shape. They have to be at the same time point. If there is no minimum, no sigmoidal shape or the two do not coincide, then there is no phase jump due to interference and the correction algorithm is aborted.

Step d: To find the beginning and the end of the phase jump, the first derivative of the phase is fitted to a model function (e.g., Gaussian). This can be done in a robust way, because the position and maximum are known and the width is rather small for phase shifts which corrupt the metabolite spectrum after ECC. There is no theoretical basis for fitting to a Gaussian, but in practice this works fine.

Step e: From the fitted first derivative of the phase, the beginning and the end of the part of the phase which needs to be corrected can be found. The first point of this region can be found by subtracting twice the FWHM from the x-value belonging to the maximum of the first derivative of the phase. The last point is found by adding twice the FWHM to the x-value belonging to the maximum. The factor of two ensures that all corrupted points are corrected.

Step f: The slope of the phase at the start and end point is set equal and is approximated by taking the offset of the fitted first derivative. This slope is used to plot two lines (L_1 and L_2) which are parallel and go through the begin and the end point. The part of the phase after the end point is corrected by adding the difference of the intercepts of L_1 and L_2 for each point.

Step g: Finally, the part between the begin and the end point is interpolated, resulting in a straight line with the slope of L_1 between these points. This part of the phase is approximated and replaces the incorrect sigmoidal shape.

If one of the steps a–d fails, the original phase of the reference signal will be used. This ensures that only appropriate corrections are performed. Although the correction algorithm is assumed to be robust for data acquired using several acquisition protocols (e.g., PRESS, STEAM), some parameters have to be checked and adjusted. The phase of the reference signal may become noisy when the magnitude approaches zero. Correcting it in this part of the signal will become difficult, but is also not necessary because it is more probable that a phase jump in that area is introduced due to the noise in the signal than due to interference of resonances. Therefore we only screen the phase of the reference signal until its magnitude has decreased to 1% of its maximum. A second parameter which can be adjusted concerns the maximum width of the fitted model function in step d of the correction algorithm's design. When the width increases, the total number of time data points which are interpolated will also increase. This may prevent a good correction. Furthermore, a large width of the fitted model function indicates a slowly changing phase, which will not introduce ringing. Therefore, a maximum should be set for this parameter. If the fitted model function exceeds this maximum, the correction algorithm is not triggered. For our in vivo data we found a width of 40 ms to be convenient.

3. Experimental

In order to compare our algorithm with the filter implemented by Wild, we copied his simulated data, which consisted of the metabolite and reference signals listed in Table 2.

In addition, water suppressed and unsuppressed 2D ^{1}H MRSI datasets of the human brain were acquired from one healthy volunteer as well as from patients with a brain tumor. The measurements were performed on a 1.5 T Siemens Vision whole body MR system, with the following parameters: 16×16 matrix size, STEAM volume pre-selection and outer volume suppression, a repetition time of 2500 ms, an echo time of 20 ms, a slice thickness of 15 mm and a field of view of 200 mm. The number of time points sampled was 1024 with a dwell time of 1 ms.

The acquired metabolite- and reference-data were first Fourier transformed in the direction of the spatial axes only. Mild Hamming smoothing was applied prior to Fourier transform to lower the ripple effect [10] introduced by the point spread function. Only mild smoothing was used to prevent significant broadening of spatial structures. Before ECC, all reference signals within the STEAM box of each MRSI dataset ($\sim$80 time domain signals) were automatically screened and corrected for phase jumps—if present—as described. After ECC of all metabolite signals, the residual water in the metabolite signal was removed. This was performed by HLSVD filtering [11] of a region between 4.3 and 5.1 ppm in the spectrum, with 10 singular values. The HLSVD filtering enables a better comparison of the relevant part of the spectrum. Finally, each metabolite time domain signal was Fourier transformed to get ^{1}H MR spectra.

4. Results and discussion

The use of our correction algorithm on the simulated data (Table 2) and the comparison with the one Wild presented is visualized in Fig. 3. The phase of the ref-

Table 2
Parameters for the simulated data presented in Fig. 3[a]

	Metabolite signal	Reference signal
ω_1 (Hz)	8.1	8.1
ω_2 (Hz)	97.3	16.2
ω_3 (Hz)	110.6	
ω_4 (Hz)	176.0	
d_1 (Hz)	22.2	2.2
$d_{2,3,4}$ (Hz)	3.2	2.2
$\Phi_{1,2,3,4}$ (°)	0	0
A_1 (a.u.)	20	1000
$A_{2,3,4}$ (a.u.)	2	1000

[a] For explanation of the parameters we refer to Table 1.

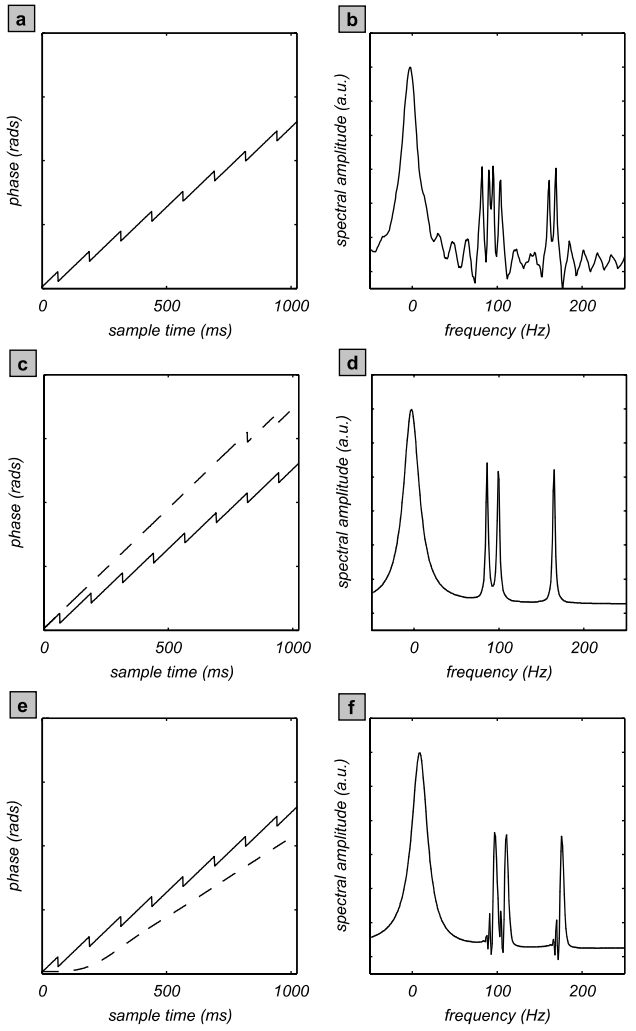

Fig. 3. Comparison of ECC corrected simulated spectra. When the non-corrected phase in (a) is used, the metabolite spectrum is heavily corrupted (b). When the phase is corrected with our algorithm (dotted line in c), the metabolite spectrum (d) is virtually uncorrupted. In (f) the metabolite spectrum after correction with the phase filtered by Wild's method (dotted line in e) is shown.

erence signal, which is plotted in Fig. 3a, shows eight phase jumps. When this phase is used to perform ECC on the metabolite signal, the result is a heavily corrupted spectrum (Fig. 3b). In Fig. 3c, the corrected phase using our correction algorithm is shown (dotted line). The jumps in the corrected phase are totally removed, except for the two last ones. At that location the amplitude of the FID magnitude is below 1% of its maximum, causing the moving window algorithm to stop. After ECC of the metabolite signal, this results in a virtually uncorrupted spectrum (Fig. 3d). The effect of low-pass filtering the phase of the reference signal using Wild's method is presented in Fig. 3e. The phase steps have been removed effectively (dotted line), although a delay has been introduced and the phase is curved at the first 200 points. The resulting spectrum after ECC (Fig. 3f) is much better than the original, but still some artifacts are visible at the base of the peaks. Wild has shown that mild smoothing of the frequency domain will effectively remove the artifacts at the base.

In in vivo MRSI data, the moving window correction algorithm was found to be very effective and robust in correcting data in batch mode. In one volunteer and several patients, the screening resulted in correction of up to 10% of the reference signals. Of this 10%, some of the reference signals are erroneously corrected due to supposed phase jumps in the last (noisy) part of the phase. However, these erroneous corrections are not harmful, because they occur in the noise.

In Fig. 4 an example is given of one corrected time domain signal from the volunteer. Figs. 4a and b show the magnitude and phase of the reference signal. Fig. 4c shows the ECC-corrected metabolite spectrum if the phase shown in Fig. 4b is used. Ringing is especially visible in the residual water signal, but is present over the whole frequency range. In Fig. 4d, the first derivative of the phase is plotted together with its fitted function (dotted). Information from the fit is used to correct the phase of the reference signal as described (Fig. 4e), and this phase is used for ECC of the metabolite signal. The resulting ECC-corrected metabolite spectrum is plotted in Fig. 4f and is virtually free of ringing.

Fig. 5 gives examples of corrected spectra from which the water residual has been removed by HLSVD. The upper spectrum of each subplot has been ECC-corrected with the uncorrected phase of the water reference signal. In the middle of a subplot, spectra are depicted which have been corrected by our method. It is clearly visible that: (a) in the uncorrected cases a lot of residual water remains after removal of the water resonance by HLSVD; (b) The metabolic resonances in the corrected spectra have narrower lineshapes and have higher amplitudes, since line broadening by ringing is removed; (c) in cases of severe ringing or low signal to noise ratio some resonances are completely flooded in the uncorrected case, thus making it impossible to quantitate these resonances in the frequency domain [12]. Also quantitation in the time domain [13] will be difficult, because the metabolite FID contains an unexpected phase jump. The lower spectrum of each subplot shows the corrected spectrum using Wild's filter. After manually setting the filter parameters, it performs under visual inspection equally well as ours.

Robustness of the correction algorithm is based on the fact that reference signals are only corrected when they satisfy three criteria: (a) a local minimum in the magnitude reference signal; (b) a sigmoidal shape in the phase of the reference signal; (c) the possibility to fit a model function through the first derivative of the phase with a low error and a relatively small width. When one of these criteria is not met, it is assumed that correction is not needed. Next to robustness, these criteria also ensure that only phase jumps caused by two interfering

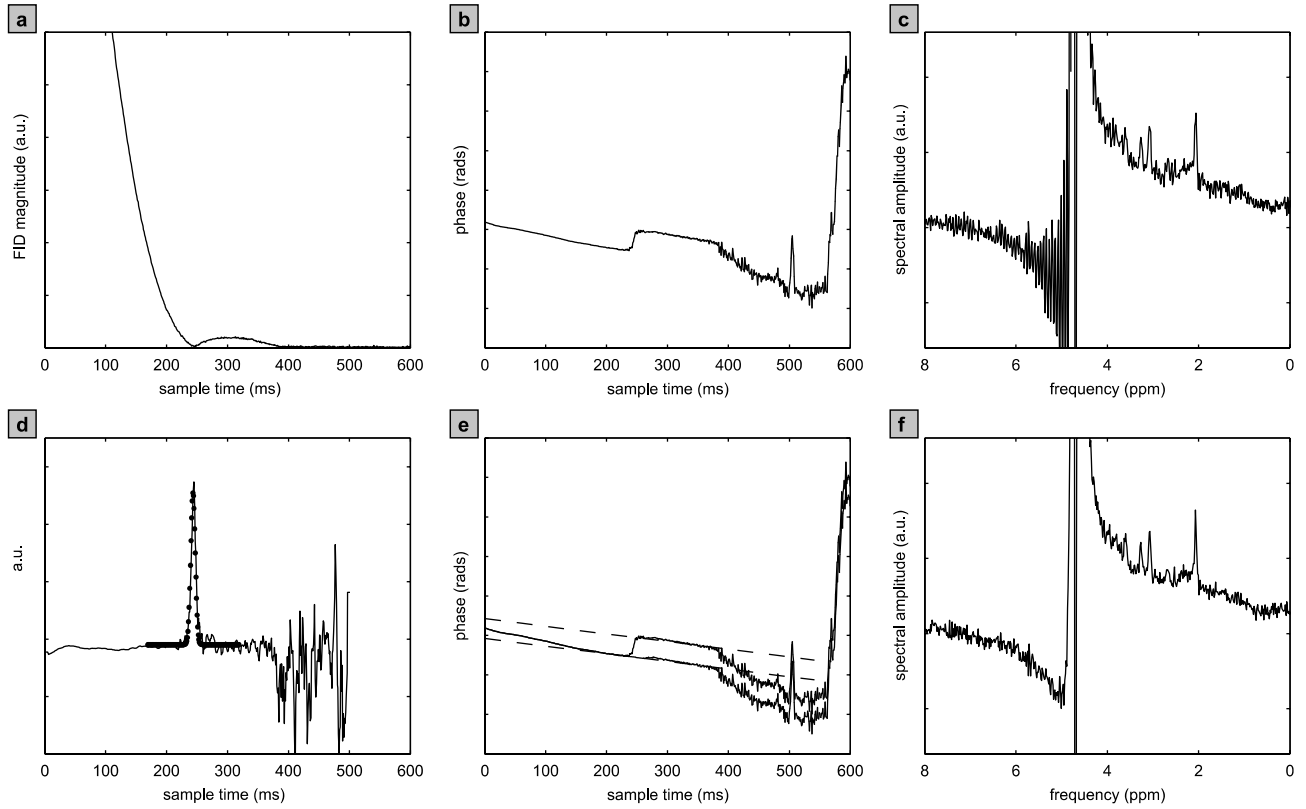

Fig. 4. Example of the application of the correction algorithm on MRSI data from a volunteer. (a) Magnitude and (b) phase of the reference time domain signal. (c) The metabolite spectrum after ECC correction with the phase shown in (b). (d) The first derivative of the phase locally fitted to a model function. (e) Correction of the phase as explained in the theory section. (f) The metabolite spectrum after ECC correction with the corrected phase.

resonances are corrected, therefore the algorithm can be applied on large datasets.

The algorithm also takes the steepness of the phase jump in the reference signal into account; when the discontinuities in the magnitude and phase are large (and ringing is severe), they are easily detected. If the discontinuities are more gradual, they will be more difficult to correct, but this is not a problem because the ringing will be less.

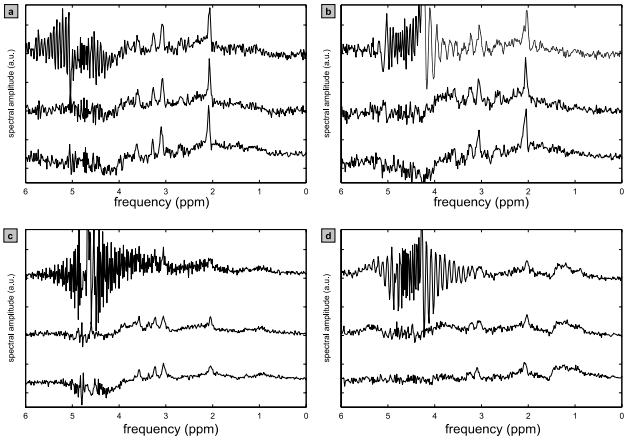

Fig. 5. Examples of spectra which were collected from a volunteer (a) and several patients (b, c, and d). The upper spectrum is ECC-corrected without correcting the phase of the reference signal, the middle spectrum is ECC-corrected using the presented correction algorithm, the lower with Wild's filter.

5. Conclusion

We have presented a method to locally remove jumps in the phase of water reference time domain signals. The removal of these jumps prevents the metabolite signal to become corrupted after ECC by severe ringing, which may completely obscure all resonances. The correction algorithm only corrects specific regions of the phase and is able to do so for sharp as well as gradually distributed transitions, which both can occur if the water reference obtained some doublet character.

In contrast to low-pass filters, our method uses features within the reference time domain signal which are related to the artifact. Using these features ensures a robust correction and enables the application of the algorithm in an automated manner on large datasets like MRSI, because only reference signals which need to be corrected are changed. Moreover, taking into account these features may prevent erroneous corrections of phase jumps which were induced by eddy currents.

Acknowledgments

The authors thank J.M. Wild for discussions and providing his software. This research is partly funded by the EU: INTERPRET project, IST-1999-10310.

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