Simple method for automatic frequency and phase alignment of in-vivo MR spectra

Evita C. Wiegers[1], Bart Philips[1], Hanne M. M. Rooijackers[2], Alan J. Wright[3], Arend Heerschap[1], and Marinette van der Graaf[1,4]

[1]Radiology and Nuclear Medicine, Radboud University Medical Center, Nijmegen, Gelderland, Netherlands, [2]Internal Medicine, Radboud University Medical Center, Nijmegen, Gelderland, Netherlands, [3]Cancer Research UK Cambridge Institute, University of Cambridge, Cambridge, United Kingdom, [4]Pediatrics, Radboud University Medical Center, Nijmegen, Gelderland, Netherlands

Target Audience: Scientists/researchers interested in spectral editing

Purpose Subtraction of MRS data, which is commonly used in J-difference editing techniques, is conceptually easy and relative simple to implement. However, it is of great importance that spectra, which are subtracted, are accurately phase and frequency aligned,[1] especially when the signal of interest is very small, like brain lactate. We present a simple, robust and fast method to align these spectra, based on the scalar product between two spectra.

Methods All data were acquired on a 3.0 T MR scanner (Trio, Siemens) with an interleaved J-editing semi-LASER sequence for brain lactate detection (TE 144 ms, TR 3000 ms, 32 averages in a 2.5 x 5 x 2.5 cm voxel in the supraventricular cortex). J-editing was performed with MEGA-pulses, with a bandwidth of 7 Hz, centered at the lactate quartet at 4.11 ppm. The power of the MEGA-pulse was switched on and off in an interleaved fashion, resulting in spectra where the lactate doublet at 1.33 ppm is negative ('MEGA off') or positive ('MEGA on'). Twenty-six spectra were acquired from one healthy volunteer. The spectra were first zerofilled (from 1024 to 2048 points).

Subsequently, the spectra were phase and frequency aligned. The first recorded spectrum was chosen as the reference spectrum (S_{ref}), to which all other spectra (S_n) were aligned. All spectra have the same line shape function, but are potentially (zero order) phase and/or frequency shifted with respect to the reference spectrum. The alignment algorithm was performed in Matlab (R2014a, The MathWorks), in which the scalar product of S_{ref} with S_n was calculated with varying phase shifts ($\Delta\varphi$, from -30 to 30 degree, with steps of 0.1 degree) and simultaneously varying frequency shifts ($\Delta\omega$, from -29.3 Hz to 29.3 Hz, i.e. 50 data points, with steps of 0.59 Hz) of S_n. Only the spectral region not affected by the MEGA pulses (i.e. from 1.5 ppm to 3.9 ppm) was used in the alignment algorithm. The optimal phase and frequency shifts can be found by maximizing the normalized scalar product (cos(θ)) between both spectra (eq.1), as depicted in Fig.1.

$$\cos\theta = \frac{Re(S_n(\omega+\Delta\omega)e^{-i\Delta\varphi} \cdot S_{ref})}{\|S_{ref}\| \, \|S_n(\omega+\Delta\omega)e^{-i\Delta\varphi}\|} \qquad \text{eq.1}$$

After alignment, 'MEGA on' spectra were subtracted from 'MEGA off' spectra and the average of two difference spectra was used to enable accurate measurement and visualization of the lactate doublet. The AMARES algorithm in jMRUI[2] was used to estimate the amplitude and its standard deviation for the lactate doublet in the difference spectra.

Results In all spectra, one value can be derived for both the phase and frequency shift which results in a maximum of the normalized scalar product. Shifting the phase and frequency of the spectrum with those values results in proper alignment with the reference spectrum for all spectra, as depicted in Fig. 2. The mean value of the maximum normalized scalar product for all spectra was 0.95 (sd: ±0.02, compared to 0.85±0.12 before alignment).

Fig. 3 gives an example of the improvement gained in the subtracted spectra by using our alignment algorithm, compared to aligning only the frequency of the spectra by finding the maximum value of the spectrum (as is done in the automatic alignment algorithm in jMRUI) or no alignment at all. Fitting these three variants of the difference spectra, the standard deviation of the fitted amplitude is 18% using our algorithm but increases to 28% when the automatic alignment algorithm in jMRUI is used. When no alignment algorithm is used, the lactate doublet can not be fitted reliably, in this particular case.

Discussion and Conclusion We have demonstrated a robust and time efficient method for spectral alignment, which is of great importance when subtracting spectra as is done in spectral editing. Comparing our algorithm with more advanced methods,[3,4,5] our method is simple and easy to implement.

Accurate phase and frequency alignment results in a difference spectrum with smaller peak amplitudes left in the residue. This allows a more accurate determination of the metabolite of interest, as shown in the lower standard deviation of the fit.

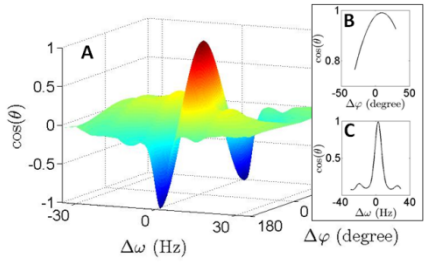

Fig. 1 Normalized scalar product (cos (θ)) between S_{ref} and S_n, for varying phase (Δφ) and frequency shifts (Δω). A clear maximum for cos(θ) can be derived, as shown in A. The alignment algorithm presented here performs a grid search over only a small range of phases and frequencies around this maximum value, as shown in B (phase shift) and C (frequency shift).

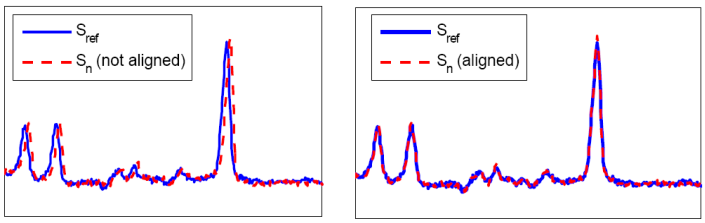

Fig. 2 Two spectra before the alignment algorithm is performed (left) and after applying the alignment algorithm (right). The blue solid line represents the reference spectrum (S_{ref}), the red dotted line represents the spectrum that requires alignment (S_n).

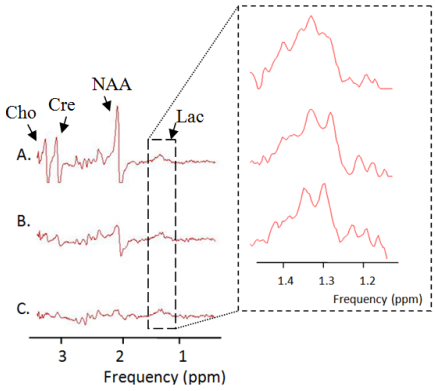

Fig. 3 Difference spectra acquired without using an alignment protocol (A), using the automatic alignment algorithm in jMRUI (B) and with the use of our alignment algorithm (C). Residues of NAA, creatine (Cre) and choline (Cho), visible in A and (to a lesser extend in B), are indicated. The lactate (Lac) doublet at 1.33 ppm is shown (magnified) as insert.

References

1. Waddell K.W., Avison M.J., Joers J.M., Gore J.C. A practical guide to robust detection of GABA in human brain by J-difference spectroscopy at 3 T using a standard volume coil. Magn Reson Imaging. 2007;25:1032–1038.**2.** Vanhamme, L., A. van den Boogaart, and S. Van Huffel, Improved method for accurate and efficient quantification of MRS data with use of prior knowledge. J Magn Reson, 1997. 129(1): p. 35-43 **3.**Vu TN, Laukens K. Getting your peaks in line: a review of alignment methods for NMR spectral data. Metabolites. 2013 Apr 15;3(2):259-76 **4.** Savorani F, Tomasi G, Engelsen SB. icoshift: A versatile tool for the rapid alignment of 1D NMR spectra. J Magn Reson. 2010 Feb;202(2):190-202 **5.**Wright AJ, Buydens LM, Heerschap A. A phase and frequency alignment protocol for 1H MRSI data of the prostate. NMR Biomed. 2012 May;25(5):755-65