A STEP-BY-STEP GUIDE TO MANUAL B_0 SHIMMING FOR IN VIVO PROTON MRS OF THE BRAIN

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Abstract — ***In vivo*** **proton magnetic resonance spectroscopy (MRS) has been around for nearly thirty (30) years and has proven itself to be an indispensable tool at the hands of an experienced practitioner. However, in certain occasions such as when there are hemorrhagic foci inside the volume of interest, the spectral resolution is hindered, due to paramagnetic effects. In these cases, spectra acquired with automatic shimming of the static magnetic field B_0 field may present broad linewidths and overall poor spectral quality. In such a scenario, the MRS practitioner must perform a manual shim, by appropriately adjusting the strengths of the gradient coils. The purpose of this study was to provide a step-by-step guide for manually shimming the B_0, to improve spectral resolution of acquired spectra and, thus, to potentially increase the diagnostic power of the method. Furthermore, the effect of spectral resolution on the signal-to-noise ratio (SNR) of metabolite peaks was also investigated in a phantom study at two field strengths, where all acquisition parameters and conditions were identical, with the exception of the spectral linewidth which ranged from 1 Hz to 8 Hz (at 1.5T), or equivalently from 2 Hz to 16 Hz (at 3.0T).**

Keywords — ***in vivo*** **proton MRS, manual shimming, spectral resolution, metabolite signal-to-noise ratio.**

I. Introduction

Proton magnetic resonance spectroscopy (MRS) has played an important role in the clinical environment since the early days of its introduction to the clinical practice [1-9]. Nowadays, most commercially available MRS sequences are based on a saturation-recovery (SR) scheme, thereby employing either three slice-selective 90° – 180° – 180° pulses (i.e., PRESS) or three 90° slice-selective pulses (i.e., STEAM). Both techniques have advantages and disadvantages, but a comparison between them is beyond the scope of this study.

In the clinical setting, *in vivo* brain MRS has shown tremendous capabilities in oncology [10-16] and has provided notable contributions in the fields of neuropsychiatry [17] and neurology [18], among others.

However, spectra are not acquired under identical acquisition conditions, and on many occasions the acquisition conditions are far from optimal. For example, acquired spectra may suffer from a low signal-to-noise ratio (SNR) due to poor acquisition parameter adjustments, while the spectral lines of the metabolites might be broad, due to static field inhomogeneities. Spurious artifacts might arise due to suboptimal eddy current compensation or patient motion. Other issues include ineffective water suppression and various reproducibility issues. There is, therefore, an imperative need for optimization of the acquisition procedure and conditions. Additionally, the implementation of the post-processing steps, as well as the interpretation of the spectra, may also be proven very tricky.

All current MR systems used in the acquisition of *in vivo* MRS spectra are equipped with an automatic shimming scheme which takes place during acquisition preprocessing, during which, the gradient strengths across all spatial directions get adjusted automatically, and the main water peak is identified. In our experience so far, automatic shimming is sufficient for approximately 75% of MRS acquisition conditions, in a clinical setting.

If the practitioner wants to ensure robust and repeatable spectral quality, therefore maximizing the amount of relevant and pertinent clinical data, allowing an accurate interpretation of the acquired spectra, leading to a correct differential diagnosis, sometimes, the static B_0 field homogeneity must be improved in a non-automatic way, through a process which is commonly known as *manual shimming*.

II. Materials and methods

Presented spectra were acquired with either a 1.5T GE Signa HD28 system or a 3.0T GE Signa Premier V.29.0 scanner, both equipped with PRESS [19] and STEAM [20] spectroscopic pulse sequences. A step-by-step practical guide is provided, with screenshots taken directly from the MR consoles while using the manufacturer's spectroscopy reference phantom, which is designed for quality assurance assessments in in vivo proton MRS.

All single-voxel spectra were acquired with the commercially available pulse sequence known as PROBE-P [21] which acquires both water-suppressed, and water-unsuppressed MR spectra. PROBE stands for PROton Brain Examination, and the -P at the end stands for PRESS. Similarly, one can use PROBE-S, which uses a STEAM-based pulse sequence.

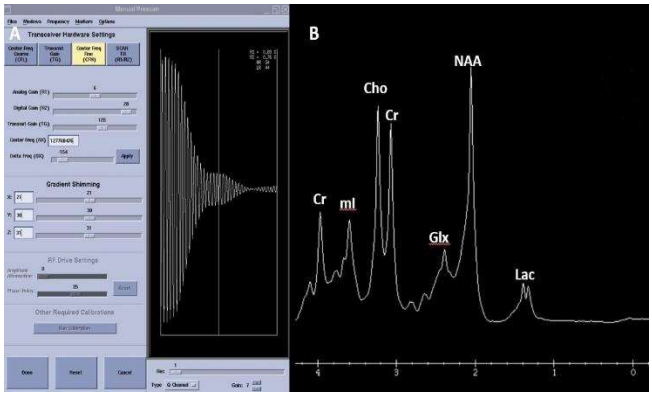

Fig. 1 Screenshot of the manual pre-scan submenu on a GE 3.0T scanner console with the respective poorly shimmed FID signal on the left sub-window **(A)**, and the produced low-resolution post-processed spectrum on the right **(B)**.

Metabolite signal intensities in the PROBE-P pulse sequence package are evaluated through the product of each peak's linewidth with its height (area-based). The height itself is computed with reference to the creatine metabolite peak, and the metabolite peaks that are automatically reported are myoinositol (mI), choline (Cho), creatine (Cr), and N-Acetylaspartic Acid (NAA). Automatic peak reporting follows the Rose criterion [22, 23], wherein a peak must have at least five (5) times more signal than the background noise, for it to be accurately distinguished from noise, and thus be reported back to the practitioner as a measured metabolite peak.

Finally, all phantom spectral acquisitions were run consecutively to minimize inter-day variations. The same voxel size was used in all acquisitions to eliminate SNR differences due to voxel dimensions. Furthermore, spectra were obtained from the same area of the phantom (at its center) to eliminate metabolite differences due to phantom inhomogeneities. Finally, the same transmitter and receiver gains (to obtain the same scale-up factors) were used across all spectral scans. Therefore, any potential differences observed would result from the influence of spectral resolution on the overall spectral quality.

Table 1 Average signal-to-noise ratio (SNR_{av}) values with corresponding standard deviations (SD) for the four major metabolites (per spectral group) measured at 3.0T

	First Group (2 Hz)				Second Group (10 Hz)				Third Group (16 Hz)			
	NAA	Cho	Cr	mI	NAA	Cho	Cr	mI	NAA	Cho	Cr	mI
SNR_{av}	*65.9*	*40.8*	*44.0*	*14.1*	*37.7*	*26.2*	*27.7*	*11.0*	*22.0*	*16.2*	*15.5*	*7.8*
±SD	*5.33*	*3.15*	*3.32*	*1.59*	*1.81*	*1.81*	*1.43*	*0.66*	*1.41*	*0.87*	*1.02*	*1.34*

III. Results and Discussion

In Figure 1A, the manual pre-scan menu on the console of the 3.0T system is shown. Upon selecting the option "manual pre-scan", the user is directed to the window shown in Figure 1A, on the "Center Frequency Coarse" channel, of the submenu "Transceiver Hardware Settings". The user must then select the third option in the submenu, namely, the "Center Frequency Fine". Following this, the user must change the channel at the bottom of the page, from the P-channel (or Absorption channel) to either the Q-channel or the I-channel. The Q and I channels are precisely identical, with the exception that the I-channel corresponds to the same free induction decay (FID) signal as in the Q-channel, multiplied by a 90° phase factor (representing the imaginary portion of the signal received at the phased array coil elements).

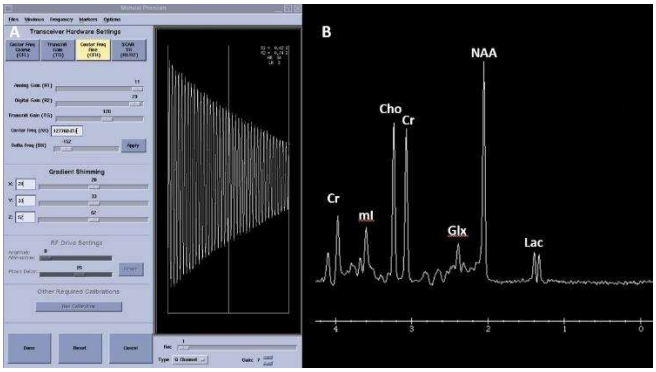

Fig. 2 Screenshot of the manual pre-scan submenu on a GE 3.0T scanner console, with the respective well-shimmed FID signal on the left sub-window **(A)**, and the produced high-resolution post-processed spectrum on the right **(B)**.

After selecting the appropriate coil channel, the user must amplify the FID by adding more "Gains" on the bottom right side of Figure 1A. Following appropriate signal amplification through the option "Gains", the user must then go to the Delta Freq (DX) option and move away from the central water frequency by approximately 100 Hz (at 1.5T), or about 150 Hz at 3.0T. This enables the visualization of the FID wiggles [24, 25], which allows the user to visualize the FID signal received on the coil element representing the collective voxel signal inside the PRESS-box. The FID for GE's quality assurance MRS phantom, which contains known concentrations of metabolites commonly found in a healthy adult brain, is shown in the right sub window of Figure 1A. If no manual shimming is performed, this FID signal, will yield the MR spectrum presented in Figure 1B, which is characterized by a linewidth of approximately 16-17 Hz at 3.0T (or equivalently 8-9 Hz at 1.5T).

After reaching the submenu shown in Figures 1A and 2A, the process of manual shimming can be initiated. The entire goal of the process of manual shimming is to apply different gradient strengths across all three dimensions for the decay of FID wiggles to appear smooth (right sub window in Figure 2A). Since the z gradient is the biggest one, it is safe to assume that it might produce the largest effects on our FID signal. Therefore, one can routinely start the process of shimming by adjusting the z gradient first.

Table 2 Average signal-to-noise ratio (SNR_{av}) values with corresponding standard deviations (SD) for the four major metabolites (per spectral group) measured at 1.5T

	First Group (1 Hz)				Second Group (5 Hz)				Third Group (8 Hz)			
	NAA	Cho	Cr	mI	NAA	Cho	Cr	mI	NAA	Cho	Cr	mI
SNR_{av}	*27.1*	*16.3*	*19.0*	*9.04*	*18.6*	*11.3*	*13.1*	*6.3*	*13.0*	*8.3*	*9.4*	*6.1*
±SD	*1.96*	*1.67*	*2.03*	*0.83*	*1.58*	*1.67*	*2.03*	*1.09*	*2.3*	*1.63*	*2.27*	-

By choosing a specific direction (left or right), the user is advised to continue in the same direction until it becomes apparent that the FID either definitively improves or definitively deteriorates. Then, the process is repeated for other gradient directions (x and y). When the FID gets the desired shape, we return our central frequency (Delta Freq) back to the original position (at the center of the water peak at 4.8 ppm), where the FID wiggles are no longer visible. However, since the total magnetic field inside our PRESS-box will not be the same as it was in the beginning (i.e., the effect of shimming), one would have to further adjust by a few Hz either to the right or to the left. The user can then confirm the choices made by selecting "Done" and start the acquisition. Figure 2B presents the MR spectrum of the quality assurance phantom following manual shimming, which is characterized by a linewidth of approximately 2 Hz at 3.0T (or equivalently 1 Hz at 1.5T).

Figure 3 shows representative spectra of a quality assurance phantom by the scanner manufacturer at two field strengths, with a linewidth of 1 Hz (A) at 1.5T, linewidth of 2 Hz (B) at 3.0T, 8 Hz (C) at 1.5T, and 16 Hz (D) at 3.0T.

The average SNR for creatine across the 1 Hz spectra was 47.5 a.u. The average SNR for creatine across the > 5 Hz spectra was 16.4 a.u. This means that by shimming the B0 field prior to acquisition the practitioner may achieve a considerable increase in SNR. Equivalently, the root mean square (RMS) across the high-resolution spectra was 3.5 arbitrary units, whereas the RMS across the lower resolution spectra was 13.8 a.u.

In a more detailed experiment, additional forty-two (42) MR spectra of the phantom were acquired. Acquisition parameters for all spectra can be found in Table 1. The spectra spanned three groups of fourteen (14) spectra per group, which were acquired at 1.5T with (a) a linewidth of 1 Hz, (b) a linewidth of 4 Hz, and (c) a linewidth of 8 Hz. The voxel (20x20x20 mm^3) was placed at the center of the phantom, which was positioned at the center of a 16-channel neurovascular (head and neck) phased-array coil. Transmit and receive gains were identical across all spectral acquisitions.

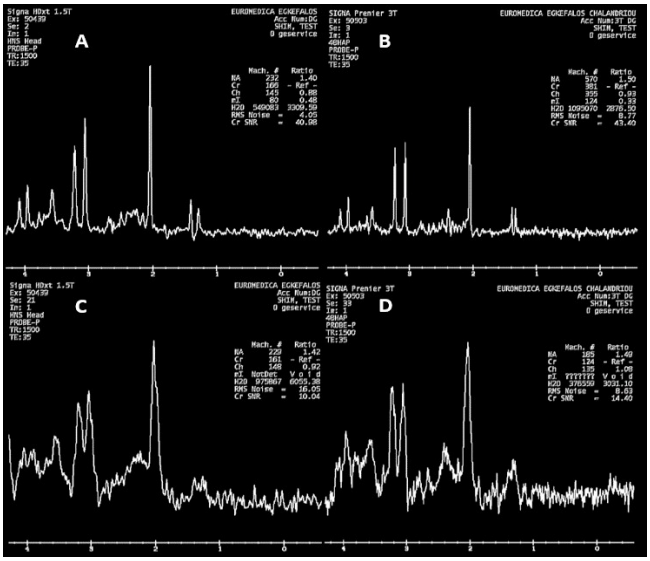

Fig. 3 Representative MR Spectra acquired at 1.5T from 8 cm^3 voxel sizes, located at the center of the same phantom, with transmit/receive gains equal to 13×30×131, and linewidths **(A)** 1 Hz, and **(C)** 8 Hz. Similarly, 3.0T Spectra with linewidths **(B)** 2 Hz, and **(D)** 16 Hz.

The SNR of the four major metabolites as a function of linewidth (1 Hz, 5 Hz, and 8 Hz) can be found in Table 1. Similarly, from measurements performed at 3.0T, the corresponding metabolites' SNR as a function of linewidth (2 Hz, 10 Hz, and 16 Hz) can be found in Table 2. Myo-inositol, being a small peak, together with being closest to the main water peak (at 4.8 ppm), suffered the most out of all other main metabolites, with increasing linewidth.

This study, nevertheless, suffers from several limitations. The step-by-step procedure described above pertains to GE MR systems. To our knowledge, this practical guide also may also apply to Siemens MR scanners (similar interface and signal visualization options). However, Philips MR scanners do not provide the option of manual shimming. Instead of that, the user is given the option to upload preparatory scripts on the MR console, whose purpose is to do baseline corrections and advanced compensation of eddy currents.

Furthermore, due to raw MRS data (p-files with software versions > 28.0) incompatibility with external offline software packages (i.e., SIVIC [26], INSPECTOR [27] and TARQUIN [28]), we were unable to cross-validate our findings pertaining to the extent of the effect of spectral linewidth on the overall metabolite SNR.

IV. Conclusions

In conclusion, B_0 shimming is a very important aspect associated with the acquisition of highly diagnostic MR spectra and should not be skipped under any circumstances. When the automatic pre-scan yields large water spectral linewidths (e.g., > 12 Hz at 3.0T, or > 6 Hz at 1.5T), the practitioner must shim the B_0 field manually, to obtain robust

spectra of high diagnostic accuracy, with sharp peaks. Furthermore, the improvement of spectral resolution prior to the acquisition of in vivo MR spectra has a definitive and positive impact on metabolite SNR. Therefore, we believe that manual B_0 shimming inside the PRESS-box must be performed even for borderline cases (e.g., linewidth = 12 Hz at 3.0T). A minimum 50% increase in metabolite SNR can be realized by manually shimming the B_0 field. Thus, the SNR benefit is deemed worth the time spent for manual shimming (approx. 2 minutes), in addition to the spectral resolution benefit from the same process. Exception may be cases with increased paramagnetic effects, either from the volume of interest or from an external source (e.g., prosthetics).

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