Fast whole brain quantitative proton density mapping to normalize 1H MR Spectroscopic Imaging

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Target audience: MR spectroscopy community

Purpose: To obtain normalized signal CSI maps that can be compared directly between subjects, MR spectroscopic images have to be normalized for water content. One normalization method, initially proposed by Maudsley et al. [1], aims at correcting non-water suppressed CSI by proton-density (ρ) MRI. We present in this study a very fast way to generate ρ-maps. ρ-mapping is based on equations describing signal intensity of SPGR sequence at equilibrium [2]. However, additional parameters such as relaxation times T1 and T2*, distortions of the transmitted ($B1^+$) and received ($B1^-$) radio-frequency (RF) fields are required for absolute ρ-map computation. To minimize the acquisition time, only three sequences were combined: a conventional T2* mapping, XEP [3] for $B1^+$-mapping and DESPOT1 [2,4], an optimized variable flip angle method for T1 mapping used both for $B1^-$-mapping and M0 calculation. We first validated this method on phantom, and determined proton density maps in three healthy volunteers also explored by CSI technique.

Methods: Data were acquired at 3T (Siemens, Verio system) using a 32-channel receiver head coil. A 240mm-FOV was acquired covering by 44 contiguous slices (thickness 3mm) for all sequences except for XEP sequence (22 slices with a thickness of 3.43 and a gap of 75%). ***T2* mapping*** was performed by acquiring GE data sets with different echo times (TE). The parameters were acquisition time =4.5 min, a matrix of 256x256 and TR/TE1/TE2/TE3/TE4/TE5/TE6 =1920/4.4/11.9/19.4ms/27/34.5ms and α=17°. The ***$B1^+$-mapping*** was calculated using the XEP sequence. Based on a 3-D GE-EPI**,** XEP parameters were TR/TE=20000/21ms with an acquisition matrix of 64x64. This sequence lasted 40s. The relaxation time ***T1 mapping*** was based on a 3-D gradient echo (SPGR) with 2 different values of the nominal excitation angle α. The imaging parameters were TR/TE=20/4.9ms, α_{N1}/α_{N2}=2°/13°, matrix size =256x256. The duration of this sequence was 4.1min. The ***$B1^-$-mapping*** was calculated using the low-pass-filter method [2] applied on the lower nominal excitation angle α images acquired on the previous step. The total acquisition was about 9.3 min. The additional 2D ***CSI*** acquisition parameters were a FOV=220mm², a VOI=160 mm², a thickness =20mm, TR/TE=1600/135ms and 6 OVS.

M0 measurements were based on spoil gradient echo steady state equation [5] using the equilibrium signal, the flip angle and the T1 relaxation time.

First measurements were assessed on a phantom. Mean, standard deviations and profiles were analyzed for T1 and M0 maps. Three healthy volunteers (mean age=33±12 years, age range=26-47, 2 women and 1 man) were also scanned using the same protocol. All subjects gave their consent to participate to the study, which was approved by the local committee on ethics. Absolute relaxation time T1 and proton density values of different cerebral regions were compared to data from the literature. Lower resolution 64x64 matrix T1 and M0 images more compatible with clinical exam durations were also generated. This allowed decreasing acquisition time to 6:29 min. Lower resolution images derived from the first study and from lower resolution $B1^+$, $B1^-$, and T1 sequences were compared.

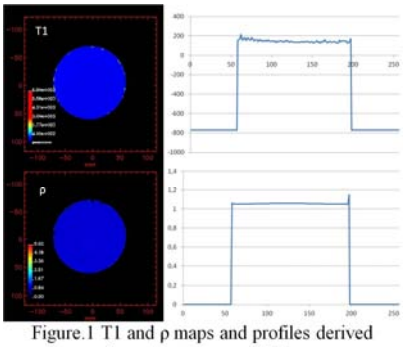

Figure.1 T1 and ρ maps and profiles derived from phantom acquisition

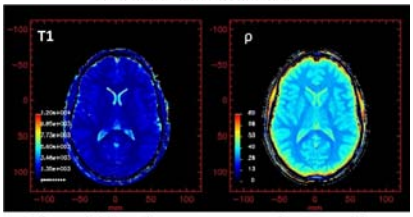

Figure.2. T1 and ρ maps on one volunteer with a 256x256 matrix

Results: 1-Phantom T1 maps and profiles (Figure.1) show a good homogeneity within slices. Within the central slice, in a ROI corresponding to 75% of the phantom diameter, the T1 and ρ standard deviations were 5.5% of the T1 mean and 0.9% of the ρ mean respectively. ρ values were stable at the center of the phantom but sometimes not in the periphery due to the applied filter. These ρ variations observed on the edges could be corrected by other filters. Nevertheless, applied to CSI acquisitions, most of the large ρ variations involved regions where signal was suppressed by OVS (all around the skull), minimizing thus the importance of this pitfall.

2-Good agreement was achieved between T1 [6,7,8] and ρ [9,10,11,12] published values and mean values (Figure.2) found on volunteers in different regions. The observed mean T1 were 1684±50 ms in the gray matter (GM), 1015±10 ms in the white matter (WM), 1399±30 ms in the putamen, 1493±16 ms in the caudate nucleus, 967±17 ms in the genu and in the splenium. Water contents ρ were found to be 82.1±2.2% in the GM, 68.3±1.3% in the WM, 78.9±1.4% in the putamen, 78.5±3.0% in the caudate nucleus, 68.3±1.0% in the genu and 66.9±0.2% in the splenium.

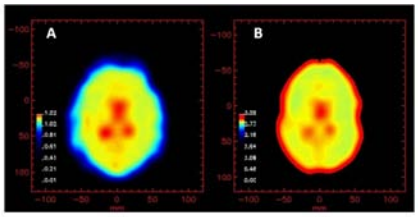

Figure.3. CSI resolution (25x25 matrix) ρ maps for one volunteer (A) generated from high resolution M0 maps, (B) calculated from CSI resolution B1+, B1-, T1 images.

3- In order to be able to apply this technique for clinical protocols by reducing acquisition time, two sorts of lower resolution ρ images were generated down to the CSI resolution : ρ images obtained by down-sampling high resolution ρ images (Figure.3 A) , and ρ images obtained with previous down-sampling high resolution B1+, B1-, T1 and T2* images (Figure.3 B). Those were found to be qualitatively similar in terms of correction performances relative to CSI maps (Figure.3).

4- CSI maps obtained with a homemade software [13] were corrected using T1, T2*, $B1^+$ and $B1^-$ maps previously presented. Pseudo-absolute NAA maps generated without and with correction for one volunteer are presented on figure.4. Only metabolite map with correction allowed a good definition of brain structures (lenticulate, insula, thalamus, corpus callosum) with good intra-structure homogeneity.

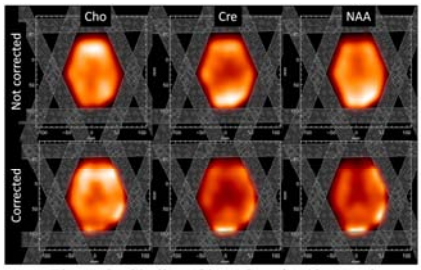

Figure.4. Choline (Cho), Creatine(Cre) and N-Acétyl-Aspartate (NAA) maps from CSI technique without and with B1+, B1-, T2* and T1 corrections.

Conclusion: The combination of XEP, DESPOT1 and multi-echo GE sequences allows fast generation of quantitative ρ-mapping to be used to normalize CSI maps. In that case, this combination yields to a real benefit for water spectrum correction and could be applied in clinical protocol to obtain signal normalized maps of metabolites even in the presence of macroscopic brain lesions such as tumor for which water content cannot be directly known. However, acquisition time could be much lower if T2*sequence, which is resolution dependent, could be acquired faster.

References: [1] Maudsley et al, NMR Biomed. 19: 492-503 (2006), [2] Deoni et al, MRM 51: 194-199 (2004), [3] Amadon et al. ISMRM, p.2828 (2010), [4] Wang et al. MRM 53:666-674 (2005) [5] Handbook of MRI pulse sequence, p.587 [6] Lu et al, MRM, 52(3):679-682 (2004), [7] Gelman et al, MRM, 45:71-79 (2001) [8] Wansapura et al, JMRI, 9:531-538 (1999) [9]Volz et al, MRM, 68 :74-85 (2012), [10] Neeb, Neuroimages, 42(3) :1094-1109 (2008), [11] Whittall et al, MRM, 37(1) :34-43 (1997), [12] Warntjes et al, MRM, 57(3):528-537 (2007) [13] Le Fur et al, Magma, 23(1):23-30, 2010