

Water Lineshape Analysis Identifies Regions of WMH

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Introduction: Magnetic resonance imaging (MRI) of white matter hyperintensities (WMH) has been shown to be associated with structural, functional and psychiatric changes in the brain [1] [2]. Since high-resolution chemical shift imaging (CSI) experiments have shown that water spectra from small voxels in brain carry meaningful information about the heterogeneous subvoxelar magnetic microenvironments [3], it is useful to find out how the water spectrum line shapes change in regions with WMH.

However, CSI acquisitions are very demanding on both data acquisition time and post processing. Echo planar chemical shift imaging (EPCSI) has been reported as a fast CSI method that acquires spatial and spectral signals simultaneously, resulting in significant reduction in scan time compared to conventional CSI [4]. Principal component analysis (PCA) is an efficient method to analyze and correct the entire set of such related spectra and to use the relationships among the spectra to improve the quality of the analysis [5, 6]. Application of PCA to a spectral dataset produces several principle components (PCs), which represent how the spectral shapes vary over the dataset. By calculating the projections of the data set on the subspace of PCs and assuming a Taylor series expansion of the line shape, parameters such as Φ_k (phase), $\delta\omega$ (frequency shift), and $\delta\tau$ (linewidth) can be automatically estimated and can then be used to iteratively correct any unwanted spectral variations that arise from residual field inhomogeneities. The resultant PCs and their scores can be examined to determine how residual line shape variations are distributed over the dataset. Following PCA correction, a constrained Nonnegative Matrix Factorization (cNMF) algorithm can be used to identify underlying spectral shapes and their spatial distributions [7]. In cNMF, the spectral data sets are expressed as $A * S + N$, where A and S are estimated in a maximum-likelihood framework. The columns of A represent the abundance of the spectral shapes in each voxel, the rows in S represent the spectral shapes themselves and N represents additive noise. In cNMF we constrained A and S to be non-negative.

In this work, we studied the water spectral lineshape of a dozen healthy elderly adults with WMH by using a fast spectral lineshape analysis method that combines EPCSI, PCA and cNMF for acquisition, data correction and analysis respectively.

Methods: We acquired high resolution brain CSI of water spectra within a very short time using echo planar (EP) readouts to traverse k-space rapidly enough to achieve sufficient spectroscopic bandwidth. EPCSI brain study *in vivo* was performed after written informed consent was obtained from twelve elderly subjects (75 ± 5 yrs) on a 1.5T Philips Intera scanner (Philips Medical Systems, Best, The Netherlands). We applied a composite 180° inversion pulse with an appropriate inversion time (TI = 606 ms) before the slice-selective RF pulse and the EPCSI readout to suppress the cerebral spinal fluid (CSF) signal. For a single slice 10 mm thick we acquired water signal over a field of view (FOV) of 250 mm with a matrix of 128 x 128. The effective repetition time (TR) of 1500 ms resulted in a scan time of 3m and 12s. Reconstruction was performed using Matlab (Mathworks, Natick, MA) on even and odd echoes by shifting each sampled point to a common temporal origin. Both PCA correction and cNMF analysis were done offline using 3DiCSI, an interactive software program under development in our lab [8].

Results and Discussion: Figure 1 shows the frequency and phase variations before (A and B) and after (C and D) PCA correction. It can be seen that the original frequency shift and phase variation appears to be primarily related to the shimming of the scanner since they followed the same pattern on both phantoms and humans. They need to be corrected before any physiological information can be obtained. After iterative PCA correction to convergence, the PCA showed three main PCs (the PCs and their corresponding score maps are shown in figure 2: (A) to (C)): 1st PC represents the average peak shape (its corresponding eigenvalue equals 98.5%), 2nd and 3rd represent the shapes corresponding to line width variations (eigenvalues equal to 1.15% and 0.35%, respectively). Compared with the FLAIR image (Fig. 2G), the WMH regions are clearly shown in all three score maps. The first PC score map shows the low proton density of WMH. The second and third maps indicate that WMH has higher scores of the corresponding lineshape variations represented by the PCs. cNMF gives us the constituent spectra from the corrected CSI data. Plots (D) to (F) represent three main constituent spectra which represent 98.87% total variance of the dataset. In Fig. 2(D), WMH region is a little darker than normal WM, which coincide with the results of PCA shown in Fig. 2(A). Both results indicate that WMH has lower proton density than normal WM. In the abundance maps of two broader spectra shown in Fig. 2(E, F), WMH completely disappears, the cause of which is under investigation. Similar results are observed in the remaining subjects.

Conclusion: Here we have demonstrated that the EPCSI sequence can be used to acquire CSI data sets with high spatial resolution in a short scan time. Analysis of the spectral information in these large data sets can be done very efficiently using PCA to identify unwanted spectral variations that arise from residual field inhomogeneities. Instead of fitting the spectral dataset to a specific lineshape model, cNMF can be used to find the constituent spectra and abundance maps from the

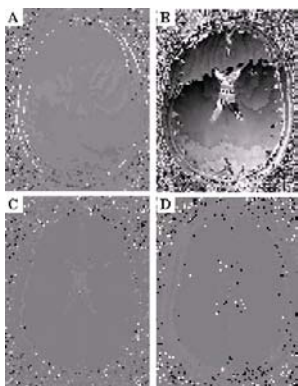


Figure 1: (A) and (B) show the original frequency and phase variation across the slice respectively. (C) and (D) are the resultant frequency and phase variation across the slice after PCA iterative correction.

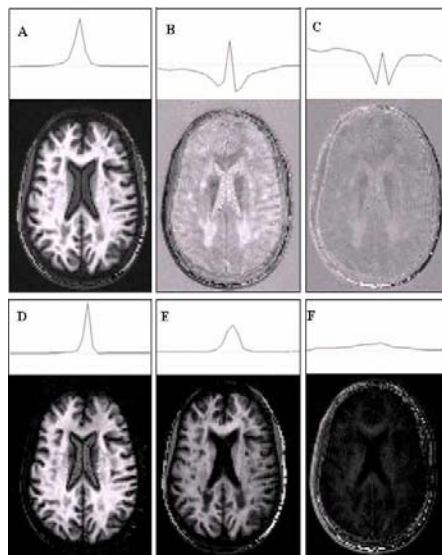


Figure 2: (A), (B) and (C) are the resultant first 3 PCs from these brain water spectra together with their corresponding score maps after PCA frequency and phase correction. (D), (E) and (F) are the resultant 3 constituent spectra and their corresponding abundance maps from cNMF after PCA frequency and phase correction. (G) shows a T2W FLAIR image of the same slice shown in plot (A) to (F).

PCA corrected data. Using cNMF and PCA, we not only can see the clear structure of the WMH, we can also find out the spectral lineshape for every voxel, which reflects variations in local tissue contributions to the water linewidth. The specific causes responsible for these variations are under study.

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