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Introduction

Recent developments in high field imaging have made possible the acquisition of high quality, low noise relaxographic data in reasonable imaging times. The datasets comprise a huge amount of information ($\gg 1$ million points) which makes rigorous analysis daunting. Here, we present results demonstrating that Principal Component Analysis (PCA) and Bayesian Decomposition (BD) provide powerful methods for relaxographic analysis of T_1 recovery curves and editing of tissue type in resulting images.

Methods

The relaxographic $^1\text{H}_2\text{O}$ image data were acquired from an axial slice of human brain at 4T using PURR¹. The T_1 recovery was sampled at 64 times post-inversion, non-linearly spaced from 30 ms to 17.1 s, with a slice-selective 5° read pulse. The 10 mm slice was spatially encoded over a $(22\text{ cm})^2$ FOV with a 64^2 matrix. The image data were DC corrected and mildly apodized, zero-filled to 256^2 , Fourier transformed, and phased. A second phased dataset was created by reverse Fourier transformation, removal of zero-filling to 64^2 and forward transformation.

PCA was applied to the central 128^2 area of the 256^2 image data (located entirely within the brain) as described previously for CSI data^{2,3} and three significantly different relaxation processes were identified in the data. Thus, the minimum number of solutions BD searched for was three.

Originally BD was developed to analyze spectral data⁴. For this study, BD was modified to convert the underlying model (infinitesimal points of flux called atoms) to exponential recovery curves instead of to Gaussian lineshapes. BD generates acceptable solutions from flat models containing no information and simultaneously finds the distribution of T_1 curves and the time constants for those curves. Since BD is computationally intensive, we limited the analysis to 32^2 pixel ROIs. For the 256^2 dataset, this ROI contained (by visual examination) white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF), and BD searched for three exponential solutions. BD analysis was also done on the central 32^2 ROI (located within the brain) from the 64^2 dataset in order to analyze the entire brain region in reasonable processing time (~ 2 days). Separate analyses searching for three, four, and five solutions were made.

Results

In Figure 1 the BD results for the inner 32^2 section of the 64^2 dataset are shown. The distributions and mean T_1 values for the ROI within the 256^2 dataset (not shown) are consistent with these results. For Figure 1 BD searched for three exponential solutions, which clearly show GM, WM, and CSF.

In Figure 2 the BD results are shown for the same ROI as in Figure 1 with BD seeking four exponential solutions, since the cutoff value for determining independent solutions with PCA is not determined absolutely. Figure 2 gives the results, showing that while WM and CSF are essentially unchanged, the GM splits into two distinct distributions having different T_1 values.

Finally, BD was run seeking five solutions to see if there

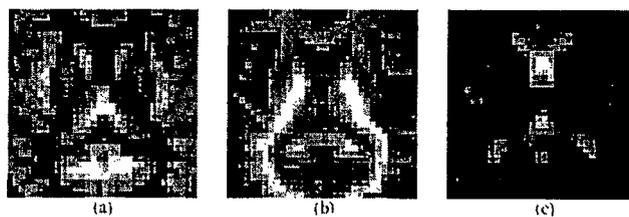


Figure 1: BD results for automatic generation of relaxographic images and mean T_1 values from the 64^2 dataset searching for three separate exponential recoveries; (a) image corresponding to $T_1 = 1.61$ s, (b) image corresponding to $T_1 = 1.06$ s, (c) image corresponding to $T_1 = 3.5$ s.

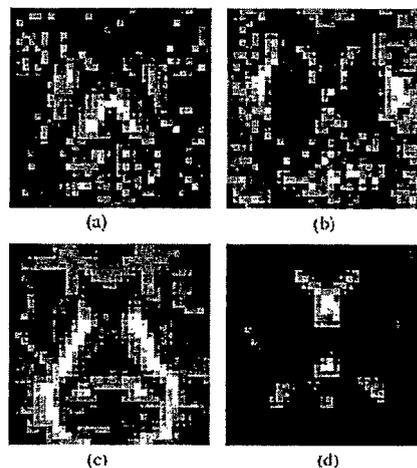


Figure 2: Relaxographic images for four solutions. Note that the gray matter solution (Figure 1a) has split into two solutions (a) and (b) here. Comparison of white matter and CSF solutions (Figures 1b/2c and Figures 1c/2d respectively) show no obvious changes. The mean T_1 values corresponding to these images are (a) 1.35 s, (b) 1.67 s, (c) 1.09 s, (d) 3.5 s.

were any further possible solutions. However, in this case (not shown) BD found the same four exponential solutions and a fifth solution which gave a speckled image and T_1 values which mixed GM and WM values, indicating that BD is unable to recover a fifth independent solution from this data.

Discussion

The T_1 values determined by BD analysis agree closely with those determined by other methods, but it is important to note that BD is unbiased (there are no expected T_1 values or favored pixels) and that BD finds a global solution. Furthermore, the T_1 values of the recovery curves are simultaneously determined with the distribution of the recovery curves, so that the segmentation into GM, WM, and CSF shown in Figures 1 and 2 is automatic and does not require that T_1 values for the tissues be predetermined.

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