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Introduction

Standard analysis methods for processing inversion recovery MR images traditionally have used single pixel techniques. In these techniques each pixel is independently fit to an exponential recovery, and spatial correlations in the data set are ignored. By analyzing the image as a complete dataset, improved error analysis and automatic segmentation can be achieved. Here, we apply principal component analysis (PCA) to a series of relaxographic images. This procedure decomposes the 3-dimensional data set into three separate images and corresponding recovery times. We attribute the 3 images to be spatial representations of gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF) content.

Methods

The relaxographic ¹H₂O image data was acquired from an axial slice of human brain at 4T using PURR¹. The T₁ recovery was sampled at 64 times post-inversion, non-linearly spaced from 30 ms to 17.1 s. The 10 mm slice was spatially encoded over a (22 cm)² FOV.

PCA identifies common patterns (the principal components (PCs)) in large, multivariate datasets². The PCs are orthonormal and the data can be represented in the nonphysical coordinate system, defined by the PCs, i.e.:

$$D = S \times P, \quad [1]$$

where D is the data matrix, P are the PCs and S contains the projections (also called scores) of the data along the PCs.

The PCs are ordered by the decreasing amounts of variance in the data they explain. In this way differentiation between significant (signal-related) and non-significant (noise-related) PCs is naturally achieved. If k is the number of significant PCs for the entire image, then the subset P_k containing the significant PCs, together with their corresponding scores, S_k can represent the data without loss of information. Consequently, applying PCA to an arbitrary region in the relaxographic image can determine the number of relaxation processes in that region. Thus, exploring the data by applying PCA to regions with different numbers of pixels, regions with only one significant PC can be identified and the relaxation times in these regions can be estimated by fitting an exponential to the only significant PC in that region. Once the relaxation curves of the underlying different tissues are determined (E_k), a transformation matrix R can be estimated, such that:

$$E_k = R \times P_k. \quad [2]$$

Using the SOLVER utility in MS Excel the exponential fits, as well as R are determined. From Eqs. [1] and [2]:

$$D \sim S_k \times P_k = S_k \times R^{-1} \times R \times P_k = F_k \times E_k, \quad [3]$$

where the F_k (= S_k × R⁻¹) effectively contains the images of the different relaxation processes, which we interpret as images of different brain tissues.

Results

PCA was applied to the entire image data (256×256×64) and 4 significant PCs were determined. Presenting their scores as images it was apparent that the 4th PC was related to artifacts in the posterior region of the skull. In order to avoid this artifact, we focused our investigation on the central 128×128 pixels located entirely within the brain and only three significant PCs were identified from this data. The central image was subdivided in 32×32 squares of 4×4 pixels. PCA was applied to each square, and 10 squares were identified that had only one significant PC. There were two groups of relaxation times (means 0.85 and 1.23 s), determined by an exponential fit of the first PCs from these 10 squares. Based on the locations of the squares in the brain, we concluded that the T₁'s were associated with WM and GM, respectively. At this resolution a region containing only CSF was not identified. However, using the GM T₁ and the data from the ventricles we estimated a T₁ of 4.25 s for CSF. Using these three relaxation times the global PCs were combined to make single exponential recovery curves yielding the matrix R. Figure 1 presents the resultant images and the spatial distribution shown is the one expected for GM, WM and CSF.

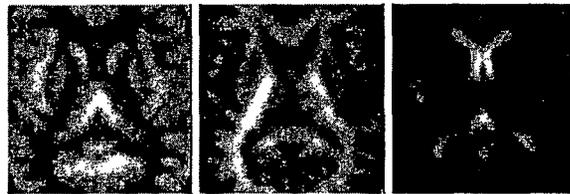


Figure 1. Images of GM (T₁ = 1.23 s), WM (T₁ = 0.85 s), and CSF (T₁ = 4.25 s).

Discussion

The method achieves representation of relaxographic image data as a product of the three relaxation curves and their respective magnitudes, which we attribute to GM, WM and CSF. This method uses the first PC of regions in the data containing only one recovery component, thereby improving the accuracy of the fits over individual pixel fitting.

The results from the PCA application to these images compare favorably with results, obtained by CONTIN and Bayesian Decomposition (presented at this meeting).

The presented procedure is fast, robust and straight forward to implement. PCA is available as a standard procedure on number of software packages (IDL, SAS). The procedure can be used to investigate the number of underlying variations contained in images, acquired under different conditions.

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References

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