

Fast Segmentation of MR Brain at 3T using Phase Sensitive Inversion Recovery Images

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Introduction: Changes in individual tissue volumes in brain provide important information about pathologic processes and help in objective evaluation of clinical status in a number of neurological disorders, such as Multiple Sclerosis and Alzheimer's disease. However existing segmentation techniques for tissue classification involve relatively long computation times. Fast tissue classification allows the estimation of tissue volumes close to real time and can be implemented on the MRI scanner. We present a vector orthogonalization based approach for fast and robust segmentation of gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) using phase sensitive inversion recovery (PSIR) images [1] of brain. This approach exploits the significantly different contrasts in tissues in the magnitude and phase sensitive reconstructed PSIR images. The method was tested on data acquired on normal volunteers.

Methods: Data acquisition: PSIR images covering the entire brain were acquired on a Philips 3T Intera scanner with the following parameters: TR/TI/TE=4300ms/400ms/8ms, number of slices=44, slice thickness=3.0mm, slice gap=0.0, FOV=240x240, image matrix=256x256, acquisition time=4 min 9 sec. Images were reconstructed in both magnitude and phase sensitive mode.

Tissue segmentation: Brain mask was generated automatically as suggested by Ji et al. [2]. Let \mathbf{r} and \mathbf{m} represent phase sensitive reconstructed and magnitude image vectors respectively. These two vectors can be orthogonalized by Gram Schmidt process [3]. Let

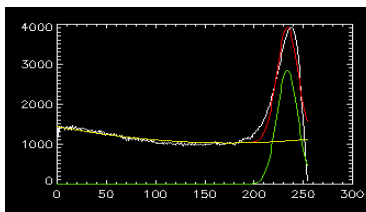
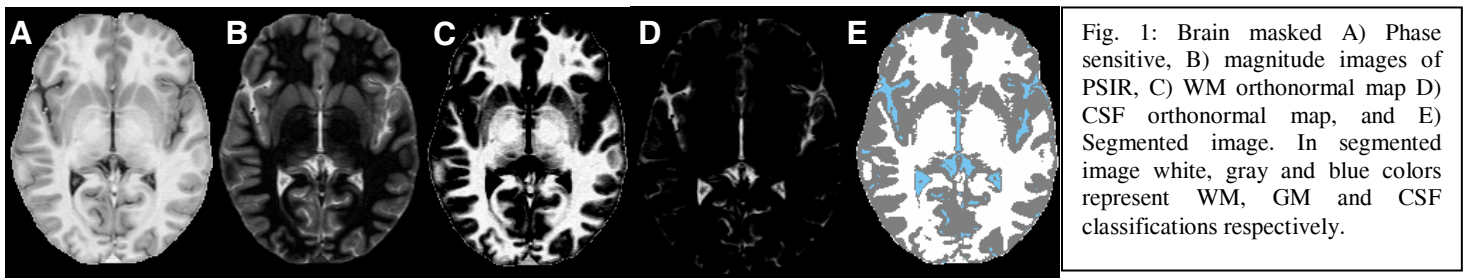
$\mathbf{p}_1 = \mathbf{m}$ and $\mathbf{p}_2 = \mathbf{r} - \left(\frac{\mathbf{m}^T \mathbf{r}}{\mathbf{m}^T \mathbf{m}} \right) \mathbf{m}$ where T represents the *transpose*. The normalized vectors can be written as $\mathbf{q}_i = \mathbf{p}_i / \|\mathbf{p}_i\|$. The

orthonormalization produces an image that has significant contribution from WM. The histogram of this image was fitted to a function which is a linear combination of Gaussian and quadratic. The intersection of the quadratic and Gaussian function provides the necessary threshold for WM segmentation (Fig. 2). The WM regions were masked out from \mathbf{r} and \mathbf{m} . Now, orthogonalization of \mathbf{r} relative to \mathbf{m} produces the CSF only map. CSF hard segmentation was realized by thresholding this map. The remaining brain parenchyma was classified as GM.

Results & Discussion: The segmentation results on one volunteer are shown in Fig.1. Excellent suppression of GM and CSF in Fig. 1C and WM and GM in Fig. 1D can be observed. Figure 2 shows the histogram of the orthogonal map for WM. The non-linear fit separates the WM from the partial volume and background. For CSF, a fixed threshold on CSF only map has produced consistent and accurate segmentation as other two tissues were almost completely suppressed on this map. The major advantages of this technique are: 1) total computation time for whole brain segmentation is less than 40 sec; 2) it uses images acquired with only a single sequence; 3) since both phase sensitive and magnitude images are reconstructed from the same raw data, no image registration is required; 4) bias field correction is not necessary because both images are derived from the same data set; 5) this approach is not very sensitive to variations in tissue T1 values. With all these advantages the present approach could evolve as one of the fastest algorithms for brain tissue segmentation and can be implemented on the MR scanner for almost real time results.

Conclusion: A fast and robust algorithm for whole brain tissue segmentation based on PSIR images is presented. This approach should be helpful in providing information about brain tissue volumes close to real time.

Acknowledgements: This work is sponsored by NIH Grant Nos: EB02095 and S10RR19186. Authors thank Vips Patel for his technical help in acquiring the MRI data on normal subjects.



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