Brain Segmentation Based On Multi-Spectral And Corrected Gray-Scale Analysis

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ABSTRACT

This work describes an automated segmentation method based on in vivo corrected multi-spectrum MRI datasets. By optimized TR and inversion recovery time TI, contrast among brain tissues and SNR are optimized to separate CSF, WM and GM in multi-spectrum MRI data sets. Signal intensity inhomogeneities are corrected using transmission and reception maps obtained *in vivo*. The three-Gaussian distribution model is used to fit histogram of the images to find the initialization parameters for Expectation-Maximization (EM) algorithm. Finally, the brain tissues are classified by EM algorithm.

INTRODUCTION

Segmentation based on calculated features (such as T1, T2, diffusion, and perfusion) is restricted by the poor SNR from this non-linear calculation. Features based on pixel intensities are strongly dependent upon inhomogeneities in signal intensity (SI) caused by the RF coil, wave behavior, eddy currents and radiofrequency field penetration. This is especially true for acquisitions using phased array coils where such problems can be more pronounced. Here multi-spectral datasets are corrected by transmission and reception maps acquired *in vivo* in only two minutes [1]. Multi-spectral analysis and the EM algorithm are used to improve segmentation.

METHOD

Both phantom and human studies were conducted on a Siemens 3.0 T Trio system with a body coil and 8 channel phased array coils. The correction matrix used for correcting SI inhomogeneities were obtained using two segmented SE-EPI sequences. Three image acquisitions were used for segmentation: ***I*** ($SI_{CSF} < SI_{GM} < SI_{WM}$) is acquired by MPRAGE with the resolution of 256 x 256 x1 mm^3 at TR/TI/TE=/800/15 ms; ***II*** ($SI_{WM} < SI_{GM} < SI_{CSF}$), and ***III*** ($SI_{GM} < SI_{CSF} < SI_{WM}$) are acquired by inversion recovery TSE with the resolution of 256 x 256x2 mm^3 at TR/TI/TE=/400/15 ms, /1380/15 ms, respectively. TI and TE were selected to first maximize the contrast between tissues, and secondly maximize SNR for each tissue. Preprocessing of the images included removal of low-intensity background noise and non-brain tissues (skull and extra-cranial tissues), registration of multi-spectrum acquisitions, and correction of non-uniformity. Finally, the histograms for the three images are fitted to obtain the initialization parameters for classification, and EM algorithm (Generalized Decomposition Mixture Algorithmic Scheme) is employed to perform segmentation of brain [2].

RESULTS AND DISCUSSION

The conventional multi-spectral datasets include T1-weighted, T2-weighted and PD-weighted images. For PD weighted images, the maximum contrast is ~20%. At the high field (above 1.5 T), the SI inhomogeneities in the brain are more than 20% making segmentation difficult**.** Here, TE is minimized and TR/TI is optimized in our multi-spectrum to acquire the images with high SNR**.** The original multi-spectral images and their images after pre-processing are shown in Fig. 1**a-c** and Fig. 1**d-f**, respectively. The multi-spectral images show excellent contrast among brain tissues (CSF, GM and WM). The images after pre-processing exhibit more homogeneous signal than the original images. Figure. 2 shows histograms of the images after pre-processing. A three-Gaussian mixture model (CSF, GM and WM) is implemented to fit these histograms and to obtain the reasonable initialization parameters of the EM algorithm automatically [3]. The segmentation results of brain tissues with EM algorithm are shown in Figure. 3.

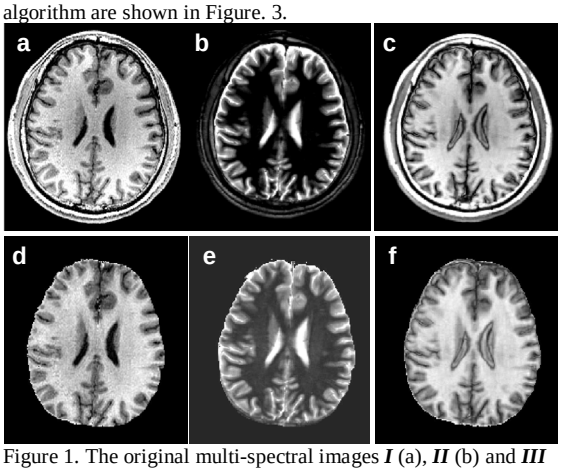

Figure 1. The original multi-spectral images ***I*** (a), ***II*** (b) and ***III*** (c), and the post-processed images (d)-(f), respectively.

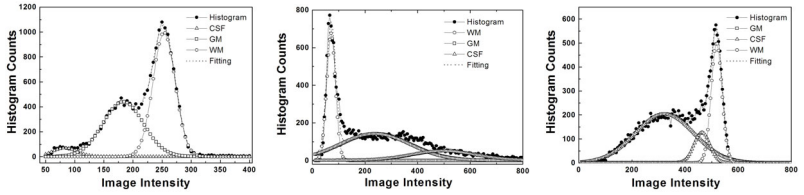

Figure 2. Histograms and their fits, for the images ***I*** (a), ***II*** (b) and ***III*** (c) after pre-processing with Gaussian mixture tissue distribution model.

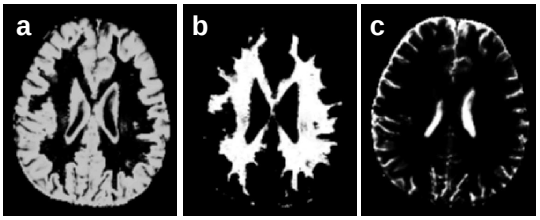

Figure 3. Mapping the spatial distribution of the probabilities of (a) GM, (b) WM, and (c) CSF

CONCLUSION

The paper proposes a rapid and automated brain image segmentation. The key contribution of this method includes: (1) *in vivo* SI inhomogeneity correction of multi-spectral datasets; (2) choice of features for optimizing CNR and SNR among brain tissues.

REFERENCE: 1. Wang et al. (2004). Proc Intl Soc MRM (submitted). 2. Theodoridis S et al. Pattern Recognition, Academic Press, San Diego 1998
3. Kovacevic N et al. Neuroimage. 2002;17:1087

ACKNOWLEDGMENTS: Special thanks for support from NIH NS40497, NS38467, EB00473.