Automatic Brain MRI Segmentation in Very Preterm Infants

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INTRODUCTION

Premature birth and secondary perinatal-neonatal insults profoundly alter brain development and functional outcomes. Accurate gray and white matter tissue quantification of neonatal brain MRI scans can enhance our understanding of this developmental trajectory and serve as diagnostic and prognostic biomarkers. However, accurate quantification remains an extremely challenging task due to a combination of factors, including lower image contrast (due to incomplete myelination at this isointense stage), lower signal-to-noise ratio (shorter scan times), greater motion artifacts, and lower spatial resolution (smaller head size) as compared to adult brain scans[1, 2]. Most segmentation algorithms run in an interactive/semi-auto manner, which are subjective and labor-intensive, while other automatic segmentation programs may need prior input from training data sets [2]. Atlas-based methods have the potential to improve neonatal brain tissue segmentation. High quality atlases are usually difficult to develop, however because of the need for high levels of inter/intra operator reproducibility as well as robust registration algorithms [3]. In this paper, we present a fully automated and computational efficient spatial fuzzy segmentation algorithm via Markov Random Fields (MRFs), which we first proposed to detect activation regions in functional MRI [4]. A significant challenge in newborn brain segmentation is the lack of construction of a gold standard for validation. We simulate ground truth neonatal T2 weighted images based on a normal anatomical model from BrainWeb [6]. The segmentation method is validated both qualitatively and quantitatively on simulated and in-vivo extremely low birth weight (ELBW; BW ≤ 1000g) infant brain MRI scans at term-equivalent age.

THEORY AND METHODS

We encode spatial regularization through the mutual influences of neighboring voxels into a fuzzy segmentation framework. By imposing such constraints, we expect that the probability of a given voxel belonging to a certain class is influenced by the probabilities of all voxels in its neighborhood. A brain image is considered as an MRF and a fuzzy neighborhood energy function is defined to describe the interaction between neighboring voxels; and then the segmentation is determined by a joint fuzzy membership containing two components to balance the statistical and spatial information: one helps to preserve isolated voxels having high statistical values and the other tends to eliminate them by considering local neighborhood interactions. Based on a normal anatomical model from BrainWeb [6], neonatal T2 weighted images with different contrast to noise ratios (CNRs) was simulated. The CNR was defined as the ratio of mean interclass contrast to the standard deviation of the noise. Rician noises were considered and the intensities of WM and GM were interchanged. Heuristically, we found that for preterm brain images, the CNRs of GM vs. WM and CSF vs. WM could be as low as 3 and 4, respectively. For two tissue segmentations (ground truth T vs. auto segmented S), the accuracy was measured by Dice similarity index, Dice = $2|T \cap S| / (T \cup S)$, whose value ranges from 0 to 1, corresponding to "no agreement" to "full agreement" between the segmentations. The resolution of the simulated images was 1 x 1 x 2 cm^3. A preliminary study bases on five in-vivo ELBW infant brain MRI scans was also conducted. Parental informed consent was obtained for brain MRI scans and the study was institutional review board approved. The scans are on a 3 Tesla Philips scanner. Dual echo spin echo sequence parameters for PD and T2 weighted images are: TE 17/175 ms; TR 10000 ms; Flip angle 90°; matrix 256 x 256; resolution 0.7 x 0.7 x 2 cm^3. Intensity inhomogeneities were corrected [5].

RESULTS AND DISCUSSIONS

Very high Dice index values of GM, WM and CSF at each CNR level over ten random Monte Carlo realizations are shown in Fig.1. It also shows that the segmented results have very high agreement with ground truth in Fig.2. To evaluate the proposed method, manual segmentations by an expert was considered as golden standard. Figs. 3 and 4 show high segmentation accuracy of GM and WM. Relatively low CSF segmentation accuracy is predominantly caused by the white matter signal abnormalities, which were observed in most of our ELBW preterm infants. The problem can be solved by considering an extra tissue class, as we are currently pursuing. In summary, we present a fully automated and accurate method for preterm brain segmentation. It is a data-driven approach without any training data sets needed and very computationally efficient.

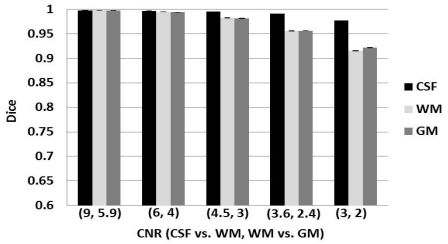

Fig1. Dice similarity index of CSF, WM and GM on simulated data with different CNRs

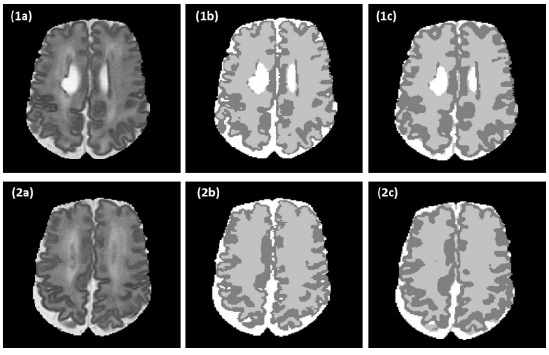

Fig.4 **(a)** ELBW T2-weighted images; segmentations by **(b)** manual expert; and **(c)** proposed method.

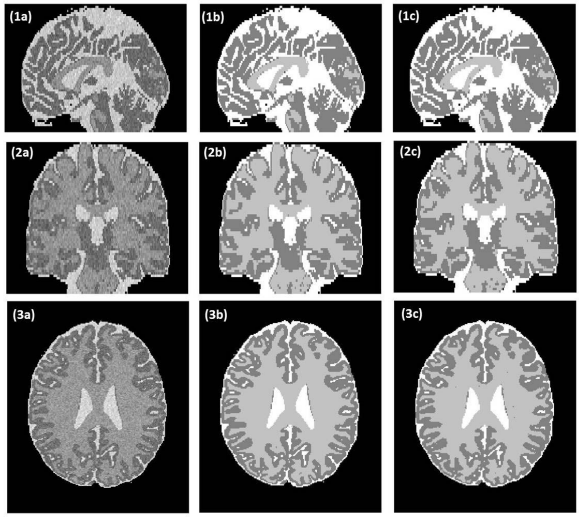

Fig2. Segmentations on simulated data. Rows 1, 2 and 3 are sagittal, coronal and axial views of the whole brain. **(a)** CNR of CSF vs. WM is 4.5 and CNR of WM vs. GM is 3; **(b)** ground truth; and **(c)** segmentation by proposed method

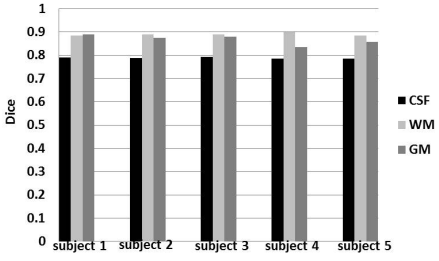

Fig3. Dice similarity index of CSF, WM and GM on real ELBW data.

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