Skeleton-based Region Competition for Gray/White Matter Segmentation and its Application on Analysis of Regional Brain Atrophy

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Purpose

Segmentation of brain tissues in MRI is essential for quantitative analysis in studies of structural-functional relationship. Different brain regions are responsible for certain functions and may have specific implication for diagnosis. Differentiation between gray matter and white matter may provide useful information for understanding disease progression in various pathological conditions, such as development of dementia. While gray matter atrophy is a direct indicator for loss of brain function, abnormality in white matter may disturb the brain connection and also lead to loss of function.

Region competition [1] has been recently proposed as an effective method for medical image segmentation by minimizing a generalized Bayes/MDL criterion. However, it is sensitive to initial conditions – the "seeds", so an optimal choice of "seeds" is necessary for accurate segmentation. In this study, we propose a new skeleton-based region competition algorithm for automated gray and white matter segmentation. Skeletons can be considered as good "seed regions" since they provide the morphological a priori information, thus guarantee a correct initial condition. This algorithm was first evaluated using simulated MRI images from a realistic digital brain phantom. Then it was applied to assess gray matter atrophy in two groups of subjects, patients with Mild Cognitive Impairment (MCI, N=13) and Normal healthy controls (N=13). The percentage of gray matter in lateral temporal lobe was measured and compared between these 2 groups.

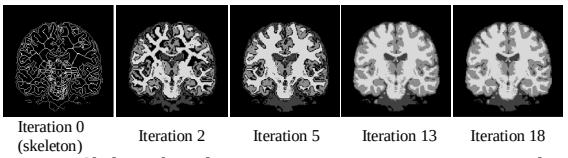

Figure 1 Skeleton-based region competition segmentation results for coronal slice No.-110, at iterations- 0, 2, 5, 13, and 18.

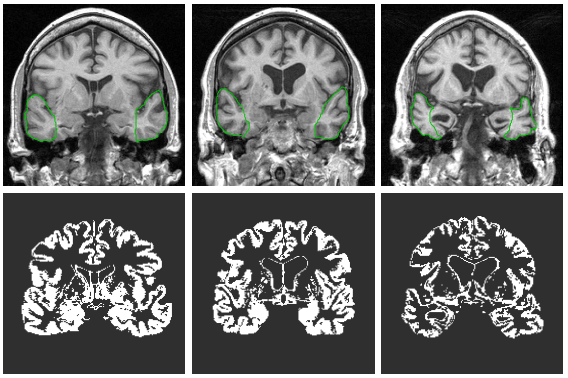

Figure 2 The outlined temporal lobes and gray matter segmentation results in one coronal slice for (a) Normal Control (b) MCI without severe atrophy (c) MCI with severe atrophy.

Methods

Three steps were required in execution of the skeleton-based region competition segmentation. Step I- CSF, gray matter and white matter were roughly segmented using a shape-based histogram algorithm. Step II- the Hildith sequential thinning algorithm [2] was used to extract the skeletons of segmented regions. Although the boundaries between regions might be not accurate, skeletons should correctly represent the corresponding regions. Step III- the region competition algorithm is started with the skeletons as the initial condition. When the algorithm converged, gray matter and white matter were successfully segmented. The iteration process is demonstrated in Figure 1. The method was first tested using digital brain phantom images, developed by the Montreal Neurologic Institute [3], to determine the accuracy (true positive % and true negative %), then applied to analyze images obtained from subjects. Temporal lobes were first extracted from MNI template and then mapped to T1-weighted images of each subject using deformation matrix. The deformation matrix was obtained from co-registration of subject's MR images to MNI template using statistical parametric mapping (SPM). The extracted temporal lobe ROIs were further modified manually by a radiologist using an image analysis program ROITOOL developed in our lab. Finally the gray matter percentage in temporal lobe was calculated for each subject. The results in MCI group were compared to normal controls.

Results

The simulated T1-weighted MR images of MNI digital brain phantom were used to quantitatively validate the proposed algorithm. The segmentation results were compared to the gold-standard gray matter and white matter volumes in the digital brain phantom to evaluate the performance. The results for the whole brain are summarized in Table 1. Regional performance of this algorithm was also evaluated using nine regions, as shown in Table 2. In general, this method worked well with a 96% accuracy, although the performance varied in different regions. Figure 2 shows images from 3 subjects, a normal control (a), a MCI with mild atrophy (b), and another MCI with severe atrophy (c). The original images with the outlined lateral temporal lobe, and the segmented gray matter maps are shown. It can be seen that the MCI with severe atrophy(c) had the lowest gray matter, but there was no substantial difference between the MCI with mild atrophy (b) and the normal control (a). The percentage of segmented gray matter in the lateral temporal lobe was only 29% for subject (c), compared to 48% for subject (a) and 45% for subject (b). The MCI group had a lower gray matter percentage than normal controls, but did not reach a significance level in group comparison.

Table 1 Performance of skeleton-based region competition segmentation in the MNI digital brain
(TP: True Positive, TN: True Negative)

Tissue type	True tissue volume	Segmented tissue volume	TP (%)	TN (%)
GM	901.7 ml	908.0 ml	95.8	95.8
WM	674.8 ml	687.6 ml	97.3	97.6

Table 2 Performance of skeleton-based region competition segmentation in various brain regions

Brain Regions	Gray Matter (%)		White Matter (%)	
	TP	TN	TP	TN
Lateral Frontal	94.9	96.9	96.6	97.8
Parasagittal Frontal	94.0	96.5	97.4	95.1
Lateral Parietal	96.2	95.3	95.2	97.9
Parasagittal Parietal	96.2	95.8	98.4	97.5
Lateral Temporal	96.9	95.9	96.6	98.2
Medial Temporal	93.1	95.6	97.4	94.0
Occipital	91.9	97.4	98.5	93.6
Basal Ganglia Region	96.7	95.8	98.6	97.8
Cerebellum	96.2	97.2	98.2	97.9

Discussion

We presented a new skeleton-based region competition scheme for automated gray matter and white matter segmentation. In this method, the skeletons, which were extracted by using Hildith sequential thinning algorithm from the thresholding-segmented result, were used as the seed regions. Since a correct initial condition is guaranteed, it is efficient and can avoid the problems associated with manual seed selection. The algorithm is especially useful for the segmentation of complex structures such as gray and white matter, where manual seeds placement is difficult. The algorithm worked well for gray and white matter segmentation in different brain regions, with approximately 96% accuracy. We further demonstrated that the algorithm could be applied to segment brain images from MCI subjects and normal controls. Combined with automatic lobe segmentation as demonstrated here, it may provide an efficient tool for investigation of regional atrophy in various brain diseases.

References

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Acknowledgments:

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