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AUTOMATIC COMPARTMENTAL DECOMPOSITION FOR 3D MR IMAGES OF HUMAN BRAIN

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ABSTRACT

A new method is developed to automatically decompose human brain MR images into cerebrum, cerebellum and brainstem. It utilizes the partial differential equations based shape bottlenecks algorithm to segment an interior brain tissue region into three compartmental seeds. Then the compartmental decomposition is obtained by reconstructing the compartments from the seeds according to the compartment boundary knowledge defined with partial volume information. This method was validated against manual segmentations of 35 T1-weighted MR images. It was demonstrated to be accurate and robust, and the mean Dice coefficients for cerebrum, cerebellum and brainstem were 0.99, 0.98 and 0.82, respectively.

***Index Terms*—** Partial volume effect, partial differential equations, shape bottlenecks algorithm, cerebrum, cerebellum, brainstem

I. INTRODUCTION

Decomposing the human brain volume into cerebrum (CBR), cerebellum (CBL) and brainstem (BS) compartments in 3D magnetic resonance (MR) images is required for various medical and neuroscientific applications. Our motivation to solve this task stems from the studies of human brain asymmetry: CBR and CBL, whose interhemispheric asymmetry is interesting, need to be extracted from MR brain images before the brain hemisphere segmentation [1] can be applied to them separately. In addition, it would be beneficial to discard BS to eliminate its contribution to the brain asymmetry analysis.

Automatic techniques based on graph cuts [2], mathematical morphology [3], and fuzzy logic [4] have been developed for compartmental decomposition in 3D brain MR images. Although these approaches can be considered successful, they have some restrictions. Firstly, the partial volume effect (PVE), i.e. the phenomenon that a voxel can contain more than one tissue types, is an inevitable property of MR images. All the techniques mentioned above use hard brain tissue classification into the three primary tissue types [grey matter (GM), white matter (WM) and cerebrospinal fluid (CSF)] and do not take the PVE (CSF/GM, GM/WM and CSF/background) into account. The accuracy of brain (consisting of only GM and WM essentially) extraction is therefore suspectable. More specifically, in the graph cuts based algorithm [2], the searched segmentation boundary, segmenting cerebral hemispheres and cerebellum+brainstem (CBB), is supposed to be located in the CSF-filled space. Ignoring the existence of PVE between CSF and GM can cause errors on the boundary detection. It is also difficult for the other two methods [3], [4] to locate the boundary between CBR and CBL with distance or intensity criteria, which is essentially an area of GM, because of the mixture of GM and WM at that region. Furthermore, the graph cuts based approach is not able to separate BS from CBL. The mathematical morphology based method is not completely automatic [3] as the location of anterior and posterior commissures needs to be specified manually. Some assumptions and parameters used by the fuzzy logic based technique [4] might be data set specific, so its applicability appears to be seriously restricted.

We present a novel and completely automatic method to decompose human brain volume into CBR, CBL and BS in 3D MR images. This method extracts the brain volume and defines the skeleton of the compartment boundary based on the partial volume voxel classification (into GM, WM, CSF, GM/WM, CSF/GM and CSF/background) acquired using a partial volume estimation approach [5]. The partial differential equations (PDEs) based shape bottlenecks algorithm [6] is utilized to segment the WM+GM/WM region into compartmental seeds, from which the shapes of the compartments are reconstructed according to the compartment boundary knowledge defined with partial volume information.

II. METHODS

The basic strategy of our method is to find compartmental seeds in an interior brain tissue region for the wanted compartments and reconstruct the brain volume from the seeds as a generalized Voronoï diagram. This is similar with the mathematical morphology based method's basic strategy [3], which obtains the seeds by eroding a hard extracted

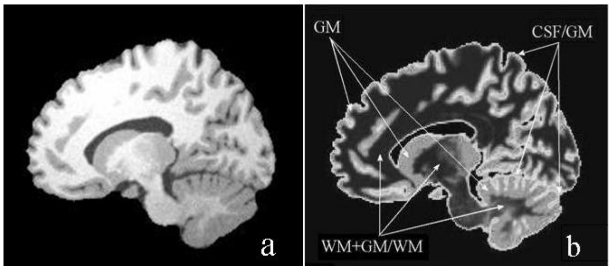

Fig. 1. Skull-stripped brain volume from a T1-weighted MR image (a) and its partial volume voxel classification map (b), where the pure CSF is discarded. CSF/GM and GM are white and light grey respectively. WM+GM/WM is dark grey.

WM mask to disconnect the compartments at bottlenecks and produces the generalized Voronoï diagram with conditional dilation. The sizes for erosion and dilation are controlled by a virtual affine normalization to a template image already compartmentally decomposed. Differently, we obtain the compartmental seeds by segmenting the WM+GM/WM region into parts corresponding to CBR, CBL and BS. As illustrated in Fig.1-b, the WM+GM/WM region is the largest tissue area inside the brain with the simplest compartmental adjacencies (in this region, only BS is connected with CBR or CBL, and no connection between CBR and CBL) so that the PDEs based shape bottlenecks algorithm [6] is applicable for segmentation. No voxel is discarded during this segmentation procedure. Thus the generated seeds are maximal and can preserve the shapes of the compartments more accurately than an eroded WM mask. Moreover, it is reasonable to consider the CSF/GM region as the skeleton of the compartment boundary because the PVE of CSF/GM mostly occurs on the borders of CBR, CBL and BS (see Fig.1-b). Especially, voxels of CSF/GM build a thin interface between CBR and CBL. Therefore, we produce the generalized Voronoï diagram by reconstructing the compartments from the seeds restricted by the region of CSF/GM. No brain image registration is needed in the whole algorithm.

II-A. Preprocessing

Initially, the skull, scalp and other extraneous tissues are removed from a MR brain image using the Brain Surface Extractor (BSE). The intensity non-uniformity, which can significantly degrade partial volume voxel classification, is compensated for with the Bias Field Corrector (BFC). Both BSE and BFC are implemented in the BrainSuite software [7].

The partial volume voxel classification is done for the skull-stripped volume by using an partial volume estimation approach based on trimmed minimum covariance determinant parameter estimation and Markov Random Fields based tissue classification [5]. With the acquired PVE information, the voxels that contain only CSF or CSF/background are discarded, and the retained volume will be processed as the brain volume to decompose.

II-B. Compartmental seeds

The WM+WM/GM region is segmented into three compartmental seeds using the PDEs based shape bottlenecks algorithm [6]. The PDEs based shape bottlenecks algorithm is a model simulating a steady state of the information transmission process between two parts of an object with PDEs. The information source and terminal are defined with the *Dirichlet* boundary condition, i.e. the information is supposed to be propagated from a boundary subset H with high information potential value (IPV) h towards another boundary subset L with low IPV l. The rest of the boundary is defined with a more complicated *Neumann* boundary condition, the detailed description of which is given in [6]. The information transmission process inside the object is assumed to have a conservative flow, and the interior domain is modeled as a Laplace equation whose consistent second order discrete form is:

$$\begin{aligned} &\frac{1}{\delta_x^2}[i(x-1,y,z)-2i(x,y,z)+i(x+1,y,z)] \quad (1)\\ &+\frac{1}{\delta_y^2}[i(x,y-1,z)-2i(x,y,z)+i(x,y+1,z)]\\ &+\frac{1}{\delta_z^2}[i(x,y,z-1)-2i(x,y,z)+i(x,y,z+1)]=0, \end{aligned}$$

where $i(x,y,z)$ is the IPV at point (x,y,z), and δ_x, δ_y, δ_z correspond to voxel dimensions in x,y and z directions. This linear system is solved with an iterative successive over relaxation scheme [6]. When the convergence is achieved, an information potential map (IPM) of the object is produced, which represents the steady state of the information transmission process.

We segment the WM+GM/WM region at the two interfaces between BS and the other two compartments, since CBR and CBL are not connected in this region. The numerical implementation here is the same as in [1], where we applied the algorithm for brain hemisphere segmentation, except for the definition of the information source H and terminal L. At first, the WM+GM/WM region is segmented into CBR and CBB parts. H and L, respectively, are supposed to be located at the top and bottom (superior and inferior) of the WM+GM/WM region. Then, the segmentation into CBR and CBB parts is performed by classifying the voxels in the generated IPM into two clusters using the k-means clustering. Secondly, the CBB part is segmented into parts of CBL and BS in a similar way. In this case, H and L are located at the front and back (anterior and posterior) of the CBB part. The segmented three parts of WM+GM/WM region are the wanted compartmental seeds. Fig.2 illustrates the produced IPMs and the compartmental seeds in 2D.

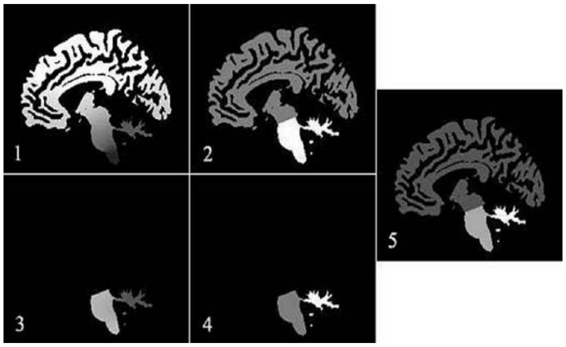

Fig. 2. Seeds detection in the WM+GM/WM region. 1. IPM for separating CBR and CBB parts; 2. segmented CBR and CBB parts; 3. IPM for separating CBL and BS parts; 4. segmented CBL and BS parts; 5. compartmental seeds.

II-C. Compartment reconstruction

The original shapes of the compartments are grown from the seeds towards the region of CSF/GM. This process is similar with the seeded region growing algorithm that determines whether to add new voxels to a specific region or not according to a similarity criterion. Differently, we employ a compartment boundary closing indicator, $P_{boundary}$, to control the growing. For each brain voxel $\mathbf{v}$, the value of $P_{boundary}$ is computed as

$$P_{boundary}(\mathbf{v}) = P_{background}(\mathbf{v}) + P_{CSF/GM}(\mathbf{v}). \quad (2)$$

$P_{background}$ and $P_{CSF/GM}$ are calculated based on the Euclidean distance to the image background, denoted by D, and the Euclidean distance to the CSF/GM region, denoted by J, as:

$$\forall \mathbf{v} \in \Gamma, \quad P_{background}(\mathbf{v}) = 1 - \frac{D(\mathbf{v})}{D_{MAX}}; \quad (3)$$
$$\forall \mathbf{v} \in \Gamma, \quad P_{CSF/GM}(\mathbf{v}) = 1 - \frac{J(\mathbf{v})}{J_{MAX}},$$

where D_{MAX} and J_{MAX} are the maximal values of D and J throughout the brain domain Γ. These two feature values represent how close $\mathbf{v}$ is to the compartment boundary.

The growing criterion is as follows. Let $\mathbf{v}_{seed}$ denote a voxel on the boundary of one compartmental seed, and $\mathbf{v}_{neighbor}$ denote one of the 26 neighbors of $\mathbf{v}_{seed}$ that is in the target volume and not labeled. The region, where $\mathbf{v}_{seed}$ is, grows by enclosing $\mathbf{v}_{neighbor}$ if $P_{boundary}(\mathbf{v}_{neighbor}) > P_{boundary}(\mathbf{v}_{seed})$.

The growing procedure is implemented iteratively. During each iteration, the whole domain Γ is scanned with the breadth first search scheme. Instead of visiting the voxels in the lexicographical order, the horizontal search is conducted from the left and right sides of Γ towards the middle simultaneously so that the left and right compartmental hemispheres can be reconstructed in parallel. This iterative procedure is repeated until the whole target volume is filled. The growing processes for the three compartmental regions are implemented simultaneously to restrict each other around the adjacent areas of the compartments. The highest values of $P_{boundary}$ are mostly possessed by the region of CSF/GM defined as the skeleton of the compartment boundary. Therefore the compartmental growing processes will stop when the region of CSF/GM is reached so that CBR and CBL are segmented from each other in the reconstructed brain volume. The compartmental segmentation in the WM+GM/WM region ensure that BS, containing mainly WM+GM/WM voxels, is separated from CBR and CBL in the final result. The CSF/GM voxels are enclosed in the closest compartmental regions in the end. After the region growing, there may exist small holes, i.e. missed voxels, as in the classical seeded region growing algorithm. They are filled by labeling each missed voxel with the dominating compartmental label among its 26 neighbors.

Severe longitudinal intensity non-uniformity remaining after non-uniformity correction can cause an area of WM+GM/WM located at the lower part of BS to be misclassified as GM. If the misclassified area is connected with CBL, the compartment boundary knowledge represented with $P_{boundary}$ would be not sufficient for separating this area from CBL. For this specific problem, we insert one more CBB segmentation stage into the reconstruction procedure. When GM region is filled from the initial seeds obtained in the WM+GM/WM region, the grown region of CBB is segmented into parts of CBL and BS using the PDEs based shape bottlenecks algorithm once more. Differently from segmenting the CBB part described in Sec.II-B, the initial seeds for BS and CBL are set to be the information source and terminal respectively. After that, the growing is continued to fill the CSF/GM region from the grown CBR region and the newly segmented regions of CBL and BS.

III. EVALUATION

The LONI Probabilistic Brain Atlas (LPBA40) database [8] was employed to evaluate the method proposed in this paper. This database contains 40 T1-weighted MR images of human brain ($256\times124\times256$ voxels, voxel size: $0.86\times1.50\times0.86$ mm^3) and manually delineated anatomic regions for each MR image. 5 images of the database were rejected from the evaluation because the intensity non-uniformity occurring in them was too severe to be corrected by BFC so that the following partial volume voxel classification clearly failed. The proposed method was applied to segment the remaining 35 images, and the segmentation result (Fig.3) for each image was compared quantitatively with the corresponding manual segmentation. The decomposition accuracies for each compartment were calculated as Dice coefficients. The Dice coefficient is a similarity measure for two sets X and Y defined as $(2|X \cap Y|)/(|X| + |Y|)$. The evaluation results are provided in Fig.4. Our method could extract CBR and CBL precisely (mean Dice coefficients

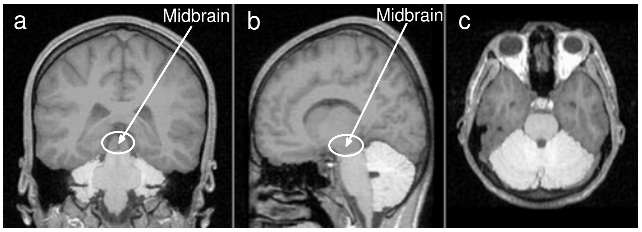

Fig. 3. Decomposed brain image sample shown in coronal (a), sagittal (b) and transverse (c) views. The original brain image is overlayed with the corresponding decomposed brain volume.

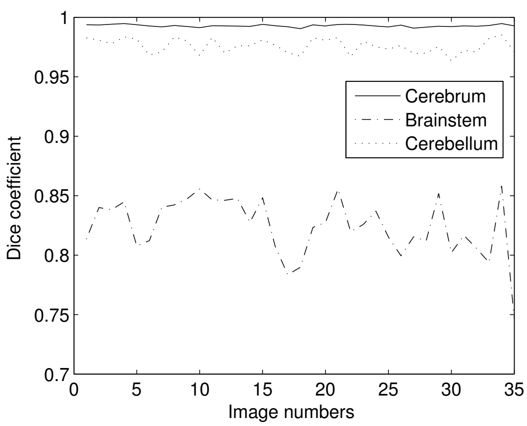

Fig. 4. Quantitative evaluation results for proposed method.

for CBR and CBL were 0.99 and 0.98 respectively). The decomposition accuracies for BS (mean Dice coefficient for BS was 0.82) were slightly lower. The primary reason for this is that the definition of BS in our method does not include the midbrain as shown in Fig.3. This is different from the traditional BS definition (midbrain+lower brainstem) applied in the manual delineations of the LPBA40 database. However, we do not consider this difference as a problem because our motivation to extract BS is to eliminate its contribution to the MR brain image analysis and extracting only the lower brainstem is sufficient for this aim. The actual decomposition accuracy for the lower BS should be close to the high accuracies for CBR and CBL considering the volume proportion of the midbrain in the traditionally defined BS is around 10% [9].

IV. CONCLUSIONS

A novel and fully automatic compartmental decomposition method for human brain MR images was introduced in this work. The method relies on the classification of the voxels in the brain volume to the three primary tissue classes and their PVE mixtures. The PDEs based shape bottlenecks algorithm is applied to segment the WM+GM/WM region into compartmental seeds. The compartmental decomposition is completed by reconstructing the brain compartments from the seeds with compartment boundary knowledge based on a simultaneous region growing algorithm. The LPBA40 database was employed to evaluate this method. The high decomposition accuracies obtained from the quantitative evaluation demonstrated that this method can robustly and accurately decompose brain volume into CBR, CBL and BS in MR images.

V. ACKNOWLEDGMENT

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