A Fast and Automatic Approach to Extract the Brain and Midsagittal Lines from FDG-PET Head Scans

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Abstract—A fully automated approach is presented to extract brain areas efficiently from FDG-PET head scans. A threshold value is automatically calculated from the histogram graph of the brain images, followed by region growing and morphological operations, to segment brain areas from these images. Next, the midsagittal lines on axial slices are detected to separate the brain into two hemispheres. The proposed approach has been applied to 226 cases of normal controls and patients with neurological diseases. The average processing time is about 3 seconds on a standard personal computer. The experiment has shown promising results.

Keywords—image processing; brain extraction; midsagittal line

I. INTRODUCTION

Positron emission tomography (PET) is a powerful, non-invasive tool used to study the biochemistry and physiology of the living organs like human brain [1]. It is a nuclear medicine imaging technique to produce a three dimensional (3D) image of functional processes in the body. After a tracer is injected into a patient, a PET scanner can form images of the tracer distribution. Fluoro-deoxy-glucose (FDG) is a commonly used tracer to distinguish the high-glucose-consuming cells from the other parts of the body. Usually it is used for assessment of glucose metabolism mainly in the brain, heart, and kidney. This imaging technique is widely used for tumor detection and diagnosis of the neurological diseases, e.g. Alzheimer's disease (AD).

Identification of the brain volume from PET images is a basis for many applications, e.g. registration with the images of other modality like magnetic resonance imaging (MRI) or computed tomography (CT), quantitative analysis of brain cortex, etc. Due to the poor spatial resolution and the low signal-noise ratio of PET images, automated brain extraction from those images is still a challenging task, as well as the identification of a midsagittal line (MSL) which separates the brain image into two hemispheres.

Brain extraction from PET images can be manually done by an experienced physician or radiologist. Such a time-consuming work produces a subjective and unrepeatable result. Alternatively, the registration tools such as Analyze [2] and Statistical Parametric Mapping (SPM) [3] are applied to extract physiological information from PET images by registration with a brain template or another structural modality (e.g. MRI) which has anatomical information to be used as a reference. These tools need the user to load images and operate several

steps on them for registration. There are also a few automated methods of brain extraction from PET images including thresholding [4] that needs user interventions, cluster analysis and pattern classification methods [5, 6] which are sensitive to noise and patient movement during the study.

A separation plane, i.e. midsagittal plane (MSP), of two hemispheres in the brain is an important landmark for further volumetric symmetry analysis, such as registration, quantification, and pathology detection. It can be the first step to automatically detect the anterior commissure and posterior commissure [7], and other landmarks [8]. Those landmarks are used in functional neurosurgery [9], brain mapping [10], and other neuroradiology applications [11]. There are several methods to locate the MSP in MRI or CT images [12-15]. Those methods may not apply to PET images.

In this paper, a fully automated approach to extract two hemispheres of the brain from FDG-PET images is presented. Histogram graph, thresholding, region growing, and morphological operations are applied to extract the brain from a volumetric FDG-PET dataset. Our method, which was earlier successfully applied to extract the MSP from MR images, is extended to locate the MSL in PET images. A total of 226 cases of FDG PET images including normal controls, and patients with mild cognitive impairment (MCI) and AD, were tested. The proposed approach requires no user intervention, and needs only a few seconds processing time.

II. MATERIALS AND METHOD

A. Materials

The proposed approach of brain extraction and MSL detection was evaluated with the FDG-PET images from Alzheimer's Disease Neuroimaging Initiative (ADNI) database. Each case has 6 dynamic frames with scanning every 5 minutes from 30 to 60 minutes after FDG injection. Those scans were preprocessed by the following steps: 1) registered to the first frame, 2) averaged, 3) reoriented into a grid of 160×160×96 voxels with voxel size 1.5×1.5×1.5mm [16]. The preprocessed images have their horizontal axis paralleled with the anterior commissure and posterior commissure. Figure 1 shows the examples of images from a patient with MCI. Figure 1a is one slice of the original baseline images; Figure 1b is another original image co-registered with baseline images; Figure 1c is an averaged image of 6 dynamic scans; and Figure 1d is a slice after reorientation.

Figure 1. ADNI images: (a) a slice of original baseline images; (b) a co-registered image; (c) averaged image of dynamic scans; (d) reoriented image.

Figure 2. A flowchart of brain extraction and MSL detection.

B. Method

In FDG-PET images, the regions of the cerebrum and cerebellum are much brighter than the areas around or outside the crania. The proposed method automatically calculates an intensity value as a threshold to segment the images into brain and non-brain areas, followed by the MSLs detection on selected axial slices. The flowchart in Figure 2 shows the processing steps and the components of the brain extraction and the MSL detection. The brain extraction component is to: 1) generate a histogram graph from the volumetric dataset, 2) select two peak values and a threshold value from the graph, 3) generate the mask images based on the threshold value, and 4) apply region growing operation and morphological operations. The MSL detection component is firstly to generate the candidates of the MSL, and then calculate the symmetry index for each of them in order to finally select the MSL.

C. Brain Extraction

1) Intensity histogram and peak points

The histogram graph is created by counting the number of voxels with same intensity values in the whole volumetric images. Figure 3 shows the graphs with smoothed histogram by cutting off the highest peak of background for illustration purpose. Besides a highest peak of the image background, there are two situations about the peak points in the histogram graph: 1) two peaks to indicate the areas inside the crania and the areas around the crania (Figure 3a), 2) one peak to indicate the areas inside the crania (Figure 3b). For both situations, the peak points are selected by calculating the intensities gap G at each intensity value. For example at the histogram graph of Figure 3, let us consider X as the horizontal axis of intensities and Y as the vertical axis of the number of voxels which have same intensity values. The intensity gap value G is defined as

Figure 3. Histogram graphs: (a) with two peaks; (b) with one peak.

Figure 4. Selection of threshold value: (a) smoothed histogram graph, (b) highest point on the convex border.

$$G_i = x_i - \max(x_j), \text{ where } j < i \text{ and } y_j = y_i \quad (1)$$

where i and j are the positions on X axis, x_i is the intensity value of i , y_i is the vertical height of i on the histogram graph, $\max$ is to calculate the maximum value of all x_j values which meet the defined conditions.

The points with larger G values are the peaks of the graph. As the histogram graph has one peak or two peaks only, the points with the largest and the second largest G values are selected as the peak points.

2) Pick threshold value and generate binary images

The peak point at the rightmost hand of the histogram graph (point p_1 in Figure 4a) indicates a class of pixels with higher intensity values, i.e. the pixels of brain cells. Another peak point p_2 indicates the non-brain or background pixels. In order to largely segment two classes of brain and non-brain pixels, the deepest point in the valley (point p in Figure 4a) is selected as the threshold value. The point p is also the highest point of the convex (Figure 4b), as well as the longest distance towards two peak points (p_1 and p_2). To locate the highest point of convex, the orthogonal lines of the peak line ($L_{p_1 p_2}$) are drawn to have two intersection points p and p' . The point p is the intersection with the histogram graph, and the point p' is the intersection with $L_{p_1 p_2}$. The set of all the distances between p and p' , for all the points on the line $L_{p_1 p_2}$, is defined as

$$D = \{d(pp'), x_1 < i < x_2, p' \in L_{p_1 p_2}, \text{ and } L_{pp'} \perp L_{p_1 p_2}\} \quad (2)$$

Figure 5. Extracted brain images: (a) original images; (b) extracted areas.

where $d_i(pp')$ is the distance between the points p and p' , x_1 and x_2 are the x -axis positions of point p_1 and p_2 , $L_{p_1p_2}$ and $L_{pp'}$ are the lines of points p_1 and p_2 , and points p and p' .

The corresponding x value of the point, whose $d_i(pp')$ value is maximum in the set D , is the threshold value to segment the FDG-PET image into two parts: brain area and non-brain area. Based on the selected threshold value, the binary mask images are generated.

3) 3D region growing and filling the holes inside the brain

Thresholding segmentation may leave some isolated points or small areas and may have holes inside the brain area. It is necessary to remove those isolated areas and fill those holes to complete the areas or volume inside crania. 3D region growing algorithm is applied to do so as the brain area is considered as a largest connected component. The seed point for region growing is the center of the volume. If it happens to be the non-brain voxel, one of its brain voxel neighbors is automatically selected. The growing goes to three directions at the same time and complete until no more brain voxel added. Figure 5 shows the examples of three slices and their extracted areas from inferior slice (left) to superior slice (right).

D. MSL Detection

The brain areas are extracted and non-brain parts are removed from the FDG-PET images by applying the binary images generated from previous steps. Since the most inferior slices do not have detectable MSL, they are excluded from the calculation. About two-third superior slices of whole brain are selected for MSL detection. For example, if the most inferior slice is 5 and superior slice is 84 (80 slices in total), there 53 slices are calculated for MSLs from slice 30 to slice 82.

We introduced earlier a symmetry index (SI) [12] for MSP detection from MR images. For detection MSL on FDG-PET images, it needs to be modified and extended to calculate the symmetry of brain cortex rather than the areas near the interhemispheric fissure, in order to avoid the areas (e.g. ventricles) which have less glucose uptake than brain cells. There are three steps to detect the MSL on an axial slice: 1) to choose the candidates, 2) to calculate the SI, and 3) to determine MSL.

Figure 6. Detection of MSL: (a) the candidate lines; (b) calculation of SI.

Figure 7. MSLs on: (a) inferior slice; (b) middle slice; and (c) superior slice.

1) MSL candidates

MSL is supposed to be an almost vertical line with some rotations and shifts. The range of rotations or shifts has their limits, e.g. the rotation not more than 40° . The candidates of MSL are chosen from those lines generated by the following step (Figure 6a):

1. the middle vertical line is the first candidate ($N_v = 1$)
2. rotate the middle vertical line to the left by θ degree (e.g. $\theta = 2$) for N_r times (e.g. $N_r = 10$)
3. rotate the middle vertical line to the right θ degree for N_r times
4. shift the line to the left by λ pixels (e.g. $\lambda = 1$) for N_s times ($N_s = 10$)
5. shift the line to the right by λ pixels for N_s times

A total of $N_v + (2 \times N_r) \times (2 \times N_s)$ candidates are generated to calculate the SI.

2) SI calculation

For each candidate line (CL), SI is defined as an average of the sum of the difference between the left and the right of the CL. The calculation of SI is defined as (Figure 6b),

$$SI(\theta, \gamma, k) = \frac{1}{H} \sum_{k=1}^{N_c} |V(P_L) - V(P_R)| / (N_c \times H) \quad (3)$$

where H is the height of the image, N_c (e.g. $N_c = 5$) is the number of pairs of the parallel lines which have same distance (γ) to the CL. $V(P_L)$ and $V(P_R)$ are the intensity values of the mirrored points P_L and P_R on the parallel lines (Figure 6b). Their coordinates are defined as,

$$P_{L,R}(x, y) = (Px \mp \gamma \cos \theta, Py \mp \gamma \sin \theta) \quad (4)$$

3) MSL selection

The line with minimum SI from a group of candidates is selected as the MSL. Figure 7 shows the results of brain extraction and MSLs on an inferior slice, a middle slice and a superior slice.

TABLE I. TEST RESULTS OF BRAIN EXTRACTION

Case	Manual (cm ³)	Auto (cm ³)	Sensitivity (%)	Specificity (%)	DI (%)
1	1143.86	1316.99	99.53	98.87	96.66
2	1234.17	1393.21	99.91	97.73	93.86
3	1305.84	1488.07	99.26	97.25	92.78
4	1426.10	1709.43	99.96	95.87	90.93
5	1443.07	1503.79	94.76	98.01	92.81

TABLE II. TEST RESULTS OF MSL DETECTION

Case	Angular difference (°)	Center displacement (mm)
1	1.09 ± 0.87	0.43 ± 0.01
2	1.25 ± 0.89	0.41 ± 0.01
3	0.87 ± 0.48	0.23 ± 0.01
4	0.95 ± 0.93	0.58 ± 0.15
5	1.47 ± 1.12	0.05 ± 0.03

III. RESULTS

The proposed approach was implemented in C++ running on a standard personal computer with 2.4GHz CPU. The average processing time was 3.03 seconds per case. A total of 226 cases with a resolution of 160×160×96 voxels of size 1.5 mm³ were tested. Five of the datasets have the brain areas manually extracted and the MSLs manually drawn for comparison with the results of the automatic method. The other cases were visually checked with satisfactory results.

Table I provides the segmented results with sensitivity, specificity and Dice's index (DI). Sensitivity is the ratio of the number of true positives to the sum of true positives and false negatives. Specificity is the ratio of the number of true negatives to the sum of true negatives and false positives. DI is the ratio of the overlap, between the automatically extracted areas and manually extracted areas, and the sum of them [17].

Table II provides the mean values and the standard deviations of the angular difference and the center displacements of comparing the automated MSL detection and the manual method. No significant statistical difference was observed. The angular difference (Da) is defined as the angle between two lines L , $ax+by+c=0$ a detected MSL line, and L' , $a'x+b'y+c'=0$ the line manually drawn (5). The center displacement (Dc) is defined as the distance of the center points of lines L and L' (5).

$$Da = \left| \arccot\left(-\frac{b}{a}\right) - \arccot\left(-\frac{b'}{a'}\right) \right| \times 180 \div \pi, \quad a \neq 0 \text{ and } a' \neq 0 \quad (5)$$

$$Dc = \left| \left(\frac{b \times H + 2 \times c}{2 \times a} - \frac{b' \times H + 2 \times c'}{2 \times a'} \right) \right|, \quad a \neq 0 \text{ and } a' \neq 0$$

where H is the height of the image.

IV. DISCUSSION AND CONCLUSION

A fast and fully automatic approach to extract the brain areas from FDG-PET images and detect MSLs from selected axial slices is presented. It has been applied to hundreds of cases and shown promising results. However, if the images have serious partial volume effect, those affected voxels are difficult to be classified into brain or non-brain areas. It may also face problems even for an experienced expert to manually segment the low resolution images like FDG-PET. To speed up the processing time, the proposed approach makes use of the

histogram of the whole volume. However, for the cases with serious inhomogeneity between the slices, this method may cause false segmentation results. In such cases, the histogram of each slice may be helpful.

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