A Novel Automatic Algorithm for Selecting a Target Brain using a Simple Structure Analysis in Talairach Coordinate System

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Abstract: It is one of the most important issues to determine a target brain image that gives a common coordinate system for a constructing population-based brain atlas. The purpose of this study is to provide a simple and reliable procedure that determines the target brain image among the group based on the inherent structural information of three-dimensional magnetic resonance (MR) images. It uses only 11 lines defined automatically as a feature vector representing structural variations based on the Talairach coordinate system. Average characteristic vector of the group and the difference vectors of each one from the average vector were obtained. Finally, the individual data that had the minimum difference vector was determined as the target. We determined the target brain image by both our algorithm and conventional visual inspection for 20 healthy young volunteers. Eighteen fiducial points were marked independently for each data to evaluate the similarity. Target brain image obtained by our algorithm showed the best result, and the visual inspection determined the second one. We concluded that our method could be used to determine an appropriate target brain image in constructing brain atlases such as disease-specific ones.

INTRODUCTION

Human brain anatomy shows significant variations in size, shape and position among different subjects. These variations are a fundamental problem in a group study and have been widely studied to reveal clinical importance using computational morphometry analysis [1]. One of the most promising approaches to this problem is to use a probabilistic atlas of the human brain (Statistical Probability Anatomy Map: SPAM) [2], which was first developed by Evans et al. [3]. In this approach, large ensembles of brain data are manually individual dataset into the stereotaxic space. A probability map is constructed for each segmented structure, by determining the proportion of subjects at each voxel position after assigning a given anatomic label in the stereotaxic space. This map is useful in designing automated tissue classifiers and constraining the search space for significant activations in functional imaging studies using PET and SPECT [4, 5]. Although it seems to give better results when all the brain data are manually segmented, the manual segmentation is very labor-intensive and apt to lack reproducibility. Therefore, it can be considered as a useful approach to segment a target brain only, to spatially normalize it into all the other data using non-linear registration routines for automatic parcellation, and to spatially transform again them into Talairach coordinate system. While the main advantage in this approach is the handling of one manually segmented brain data, the possible disadvantage is the inclusion of a bias according to the selected brain data. It is a critical issue to adopt an appropriate target brain that is, in general, classified into average or individual. The MNI-305, which was created by averaging MR images from 305 young normal subjects following global spatial normalization to a Talairach-like brain space [6, 7], has been widely used as an average target. Although such an average target brain is usually not affected by the biases that can arise from using an individual brain, it is quite blurred losing much detailed structural information [8]

The atlas of Talairach and Tournoux, which is an example of an individual target brain, is widely used in the neuroimaging field. Although this kind of an individual target brain has detailed information of the brain, it can be affected severely by biases such as age, sex, ethnic or disease [9]. Therefore, an individual target brain that is selected among the group can give the most appropriate common space to find out the inherent characteristics of them. Previously, the individual target brain was selected manually through visual inspection. This approach gives some acceptable result, but it takes quite a few times and has a risk of inter-rater variability.

In this paper, we proposed an automatic and reproducible algorithm using a simple quantitative factor measurement of brain structure for determining a target individual brain image in a specific group.

MATERIALS AND METHODS

Subjects

T1-weighted MR images of 20 healthy young volunteers were acquired from the Seoul National University Hospital for this study. They consisted of 14 males and 6 females (male: 27.23 ± 10.10, female: 29.40 ± 6.46). MR imaging was performed on a 1.5T GE SIGNA scanner (GE Medical System, Milwaukee, USA) using a 3D-SPGR T1-weighted spoiled gradient echo pulse sequence with the following parameters: 1.5 mm sagittal slices; TE = 5.5 ms; TR = 14.4 ms; number of excitations = 1; Flip angle = 20°; FOV = 21×21 cm; matrix = 256×256.

Preprocessing

Images were resampled to 1.0 mm^3 voxels and filtered using anisotropic diffusion methods to improve the signal-to-noise ratio. These procedures were processed using the commercial software-ANALYZE 3.0 (Mayo Foundation, USA). Cerebrospinal Fluid (CSF) and skull structure, which are not a region of interest in the brain analysis, were removed using the conventional region growing method following morphological operations such as dilation and erosion [10]. The Talairach coordinate system is a stereotaxic space to quantify the size and location of the brain, and the transformation process consists of 1) manually defining anterior commisure (AC) and posterior commisure (PC), 2) aligning the line which includes AC and PC horizontally, 3) defining the boundary box to divide the image into a set of 1,056 grid cells, centered

upon AC and PC. The skull-stripped data were transformed into Talairach coordinate system automatically except the defined AC and PC (Fig. 1).
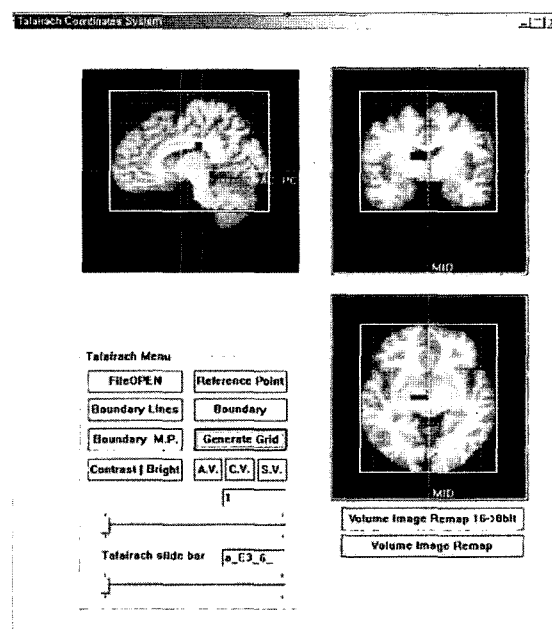

Fig. 1. Generated grid cells based on the Talairach space. Transformation process consists of 1) manual defining anterior commisure (AC) and posterior commisure (PC), 2) aligning the line which includes AC and PC horizontally, 3) defining the boundary box to divide the image into a set of 1,056 grid cells, centered upon AC and PC [9]. Note that all the steps were performed automatically except defining AC and PC.

Characteristic Vector

Eleven lines were selected as components of the characteristic vector from 1,056 grid cells to reflect the variability of each brain's inner structure. They are distributed over the whole brain area in order to represent the structural variation of each brain as follows: most anterior point and AC point, most posterior point and PC point, AC point and PC point, AC (PC) and upper (lower) vertical boundary in the sagittal direction, AC point and left (right) horizontal boundary, PC point and left (right) horizontal boundary in the coronal direction. We obtained the average characteristic vector of the group and the difference vectors of each characteristic vector from the average. Finally, the individual data that has the minimum difference vector was determined as the target brain.

Table 1. Eighteen anatomical fiducial points defined by clinically trained technician.

In the midline sagittal slice	In the sagittal slice of (midline + 5)
1. AC (Anterior Commissure) 2. PC (Posterior Commissure) 3. Anterior tip of the corpus callosum 4. Posterior tip of the corpus callosum	12. Anterior tip of the left cingulated sulcus at the level of 3 13. Posterior end of the left cingulated sulcus 14. Anterior end of the left parietooccipital sulcus 15. Posterior end of the left parietooccipital sulcus
5. Posterior tip of the 4th ventricle 6. Posterior end of the cerebellum at the level of 5 7. Inferior notch of the pons	**In the transverse slice at the level of ACPC**
	16. Right posterior end of the sylvian fissure (or insula) 17. Left posterior end of the sylvian fissure (or insula)
In the sagittal slice of (midline − 5)	**In the transverse slice at the level of 3**
8. Anterior tip of the right cingulated sulcus at the level of 3 9. Posterior end of the right cingulated sulcus 10. Anterior end of the right parietooccipital sulcus 11.Posterior end of the right parietooccipital sulcus	18. Anterior end of the right lateral ventricle 19. Posterior end of the right lateral ventricle 20. Anterior end of the left lateral ventricle 21. Posterior end of the left lateral ventricle

Correlation Analysis

To evaluate the results quantitatively, we defined the 18 anatomical fiducial points that were independent of the characteristic vector (Table 1). They were marked manually through visual inspection by human experts. We assumed that the target brain resembles all the other brains more than any other brain does in the group, and that it could be measured by the registration error. We, therefore, used an affine registration method based on intensity similarity [11]

Fig. 2. Target registration error. we defined the 18 anatomical fiducial points that were independent of the characteristic vector (Table 1). They were marked manually through visual inspection by human experts. We assumed that the target brain resembles all the other brains more than any other brain does in the group, and that it could be measured by the registration error. We, therefore, used an affine registration method based on intensity similarity [13] to measure registration error from each brain image to the target

to measure registration error from each brain image to the target as shown in Fig. 2 [12, 13]. We obtained all the registration errors from each brain to all the other brains. Human experts determined manually the target brain in the same group by visual inspection in order to see if it produces consistent result with the suggested method.

RESULTS

The results of vector analysis method for 20 healthy young subjects were shown in Table 2. When all the data were ranked according to the magnitude of difference vectors, the manually selected one was ranked as 2nd in the same group (Table 2). This result shows our method is consistent with human visual inspection. Each target images determined by our method and by visual inspection are shown in Fig. 3.

The registration errors were calculated when each brain was the target, and the means and the standard deviations are plotted in Fig. 4. Subject 1, which was selected as the target brain by our algorithm, showed the best result with the smallest mean and the relatively small standard deviation. Note that Subject 2, which was selected by visual inspection, also showed better result than others.
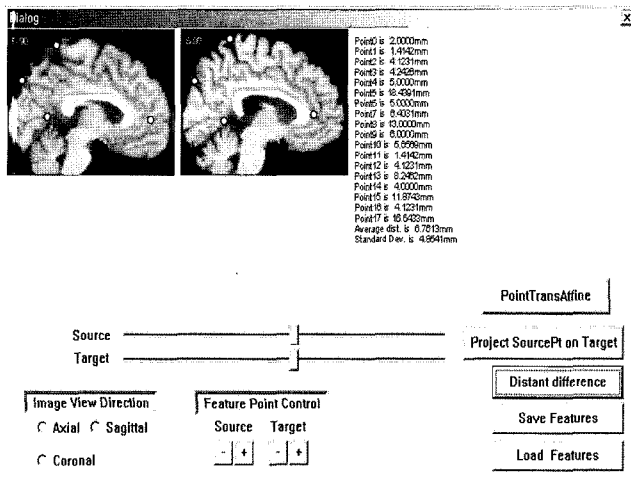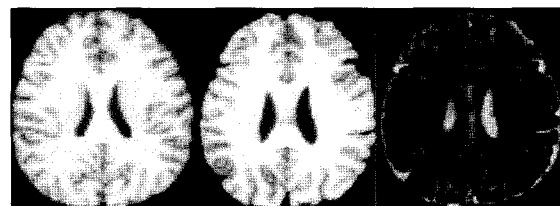

Fig. 3. Selected standard brain image from the vector analysis (left) and manual selection (middle) method. The difference of these two images is shown in the right.
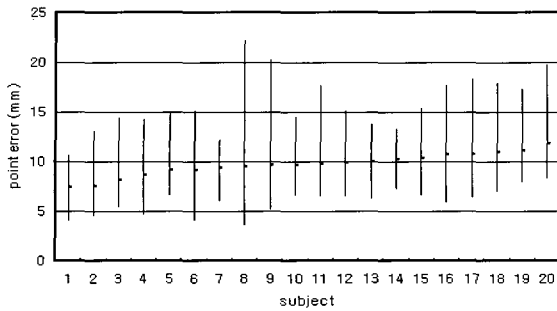
Fig. 4. Distribution of registration errors from each target brain to all the other brain in the group.

Table 2. Vector analysis method and registration error analysis method. Note that the Subject 2 is selected by visual inspection as the target brain.

Subject number	Vector analysis	Point_error(mm)	
		Mean	S.D.
1	7.95	8.66	2.83
2	8.18	7.44	1.53
3	9.68	9.52	3.75
4	9.99	9.11	2.10
5	10.33	8.12	2.19
6	10.47	9.39	1.97
7	10.67	7.55	1.92
8	12.07	9.97	2.10
9	12.78	9.16	2.47
10	13.01	9.67	2.08
11	13.05	11.77	2.64
12	13.10	10.69	3.64
13	14.06	10.34	2.57
14	14.41	10.20	1.92
15	15.41	9.79	3.23
16	18.66	10.67	3.22
17	19.46	9.59	3.61
18	21.18	11.02	2.85
19	21.26	9.93	2.31
20	23.28	11.06	2.51

DISCUSSION

When constructing a statistical probabilistic anatomical map of the human brain, it is one of the most important issues to choose an appropriate individual target brain. Our method gave highly correlated result with the conventional visual inspection method. While the visual inspection method is generally accepted in many clinical applications, it is apt to give inter-rater variability. The result showed that our method could be substituted for the conventional manual method. Because there is usually no gold standard in brain selection, our method can be used as a fast and robust selection method. Our proposed method can be used in many clinical applications such as clinical diagnosis, disease specific

group studies and an optimal template in statistical and probabilistic anatomical mapping studies. We used this approach in developing the Korean statistical and probabilistic anatomical brain template.

This paper introduces a novel automatic method for selecting a target individual brain in a data set. Our method uses simple and reproducible analysis in Talairach coordinates system and give good results based on quantitative evaluations. In the future, we will compare our method with nonlinear registration process and modify our method for nonlinear registration process.

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