Automatical Adaption of the Stereotactical Coordinate System in Brain MRI Datasets

F. Kruggel, G. Lohmann

Max-Planck-Institute of Cognitive Neuroscience
Inselstrasse 22-26, 04103 Leipzig, Germany

Abstract: Neuroanatomical and neurofunctional studies are often referenced to a high resolution MR brain dataset. To allow intersubject comparisons of cortical structures, one needs to remove the outer hulls of the brain, align the dataset with a coordinate system and introduce a spatial normalization. We describe an image processing chain that combines all these steps in a single, interaction-free procedure.

1 Introduction

The structural variability and complexity of the human brain has led to different attempts to define a common reference system in which an individual brain may be described. While today's most common approach was developed by Talairach 40 years ago [1], the high spatial resolution of recent neuroimaging techniques call for more precise methods of comparing individual brains. Most notably this has justified the foundation of a joint project to develop a computerized multimodal brain atlas, the "Human Brain Project" [2]. Common to all these approaches is the registration within a coordinate system and a method for the spatial normalization of the individual brain dataset. The "stereotactical coordinate system" has found the most widespread acceptance. It uses the anterior (AC) and posterior commissure (PC) as reference structures. Their midpoint defines the origin of a right-handed coordinate system. Much less agreement exists which method of spatial normalization will best serve the demands of the problem. First-order normalization methods like the system suggested by Talairach (the so-called Talairach space) have found widespread use [3,4]. Due to their limited accuracy, they will probably be superseded in the near future by second order methods like elastic or viscuous transformations [5] or symbolic atlases [6].
Today, high resolution MR brain datasets often serve as a reference system to which results of functional methods (like fMRI, PET, EEG or MEG) are mapped. They provide sufficient detail to allow the detection of AC and PC. In this article, we describe how a sequence of image processing steps and a few neuroanatomical heuristics work together to yield a stable procedure to detect these reference structures and adapt the stereotactical coordinate system automatically. In addition, this procedure can be comfortably combined with the removal of the non-brain parts ("brain peeling") in the dataset, which requires otherwise tedious manual work.

2 Details of the Procedure

For studying the individual brain anatomy as well as comparisions between brain structures of different subjects, it is advantageous to have a high resolution MR dataset, in which the non-brain parts are removed and which is aligned to a standard co-

ordinate system. Such a dataset is stored in a "brain database" and available for further anatomical or functional studies. For the adaption, we need to (i) find and apply a binary mask to extract the brain, (ii) determine and apply an affine transform to align the brain with the coordinate system, and (iii) apply any method of spatial normalization. We cover only the analysis of single echo T1-weighted images, which commonly serve as a base for neuroanatomical analysis and are easily available on recent MR scanners within 15-30 minutes. In the context of this study, we also require that the MR scans of the head do not contain any pathologies. Most of the steps in this processing chain involve standard algorithms, so we simply refer to the literature for the algorithmic background. Only key processing steps and anatomical heuristics are discussed in more detail. Complete information is given in a technical report, which is available from the authors.

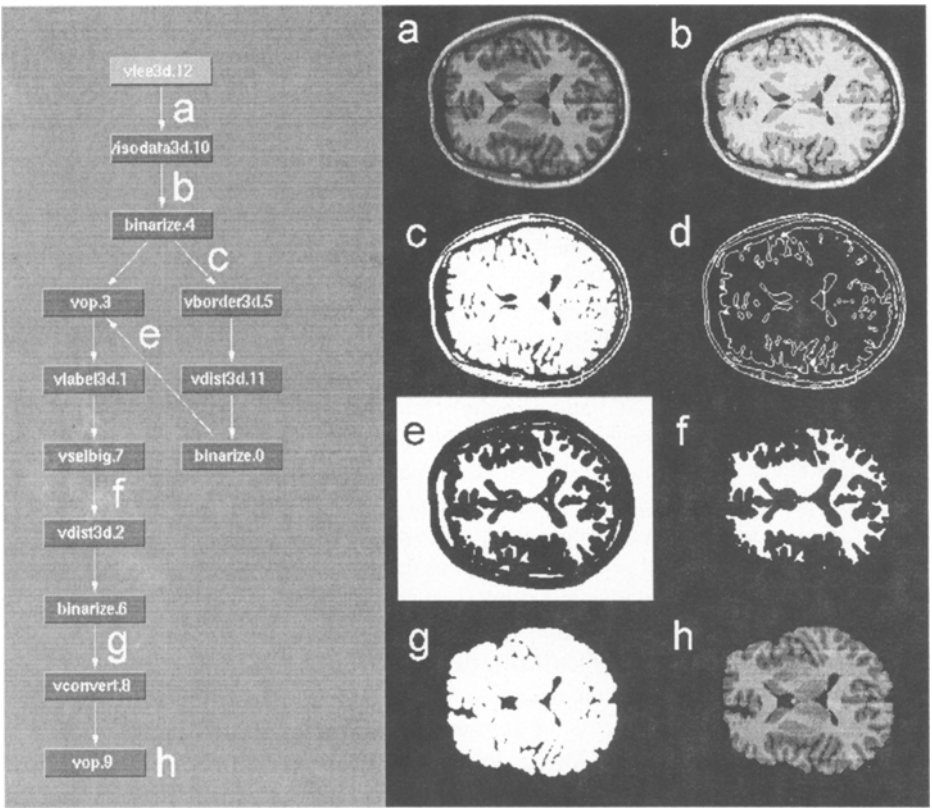

Fig. 1: Schematic overview over the peeling procedure and its intermediate results.

2.1 Brain Peeling

The first part of the processing chain will remove the non-brain parts in the MR tomogram, which is commonly referred to as "brain peeling". Our method is comparable to that of Brummer [7], who suggests a distance transform for the separation of

the brain and its hulls. An overview of our chain and intermediate results are shown in Fig. 1. The dataset is preprocessed with a Lee filter to remove noise (Fig. 1a). A fast k-means algorithm segments the image into 5 classes, of which classes 2 and 3 typically contain grey matter, facial muscles, white matter, and connective tissue. Classes 2 and 3 are combined and binarized to form mask A (Fig. 1c). The set of border voxels is formed (Fig. 1d) and an Euclidean distance transform of this border image is computed (Fig. 1e). We threshold by a distance d1 to exclude all voxels too close to the border. We combine this image (binary 'and' operation) with mask A and select the largest connected component to form mask B (Fig. 1f). This mask is expanded by computing an Euclidean distance transform and thresholding with distance d2. We combine this image (binary 'and' operation) again with mask A. We fill the ventricles (which fall into class 1) by a morphological closing operation with a large spherical structuring mask (Fig. 1g). The final mask is cut with the original (unfiltered) image to extract the brain (Fig. 1h). This processing chain provides only two parameters, d1 and d2. The first distance specifies the separation between the brain and the outer hulls. Typical values range between 1.6mm and 3.0mm with a standard setting of 2.0mm. The distance d2 is used to enlarge the first mask and is usually set to 4.0mm.

2.2 Finding the Origin of the Coordinate System

The anterior and posterior commissure are small fiber bundles that connect both hemispheres and thus cross the mid-sagittal plane of the brain. To detect these fiber bundles and to register the dataset with the coordinate system, we need to perform the following steps: (i) determine the mid-sagittal plane, (ii) detect the anterior and posterior commissures, (iii) find the crossing between the plane and both commissures, (iv) compute the center and the axes, and (v) compute an affine transform for the peeled image and apply it.

Finding the mid-sagittal plane. The mid-sagittal plane is defined as a plane separating both brain hemispheres. It is often mistakenly identified as the interhemispheric cleft or the brain symmetry plane. In most individuals, the left hemisphere is slightly larger (especially in the posterior portions), so the interhemispheric cleft is bent to the right side. So the adoption of a "symmetry plane" is just a first order approximation. In this context, we are interested in a small area of this plane in the core brain and may thus introduce only a small error by assuming planarity.
One could think of two options for approximating the mid-sagittal plane: (i) detect the interhemispheric cleft by minimization of tissue voxels in a plane, (ii) determine a symmetry plane between tissue voxels in both hemispheres. We have tested both approaches and found that the desired plane does not lie in the global minimum of the parameter space. So we have to restrict the search space by introducing constraints.
An initial estimate for the mid-sagittal plane is determined most easily by segmenting the center of both eyes and defining a symmetry plane between them: For the detection of the vitrous body of the eyes, we select the class 1 voxels from the k-means classification in the brain peeling step. A morphological opening separates small bridges between the eyes and the skin. We label connected components and filter

spherical objects of a certain size. If more than two components are found, we select the two most similar which are between 50 and 75 mm apart. The symmetry plane between both eyes is used as an estimate for the mid-sagittal plane. With this initialization we can restrict the rotation range to ± 5 degrees and the translation range to ± 10 mm. Then, we approximate the mid-sagittal plane by finding a symmetry plane between tissue voxels in both hemispheres. A Newtonian optimization scheme was found to be most stable here. This algorithm converges within 5-10 iterations and needs about 2 minutes computation time on a standard workstation.

Detecting the anterior and posterior commissures. The next and crucial step in the adaption of the stereotactical coordinate system is the detection of the two reference structures. Both commissures may be regarded as "shape bottlenecks". If we span a constant gradient field between both hemispheres, these bottlenecks are detectable in the steady state as regions of high flow [8]. Among other structures connecting both hemispheres, we find the anterior and posterior commissures as peak flow regions (Fig. 2). For a complete dataset this algorithm needs about 2h of computation time.

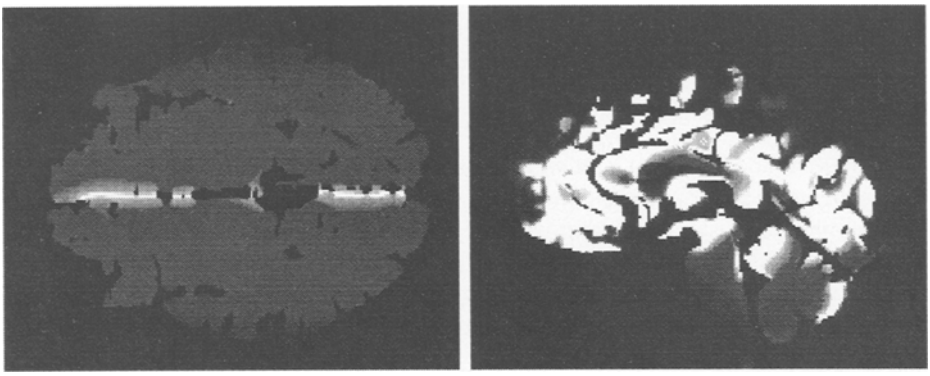

Fig. 2: Flow rate image computed from a binarized peeled dataset. Shown are an axial slice (left) in the AC-PC plane, and the mid-sagittal plane (right). One can easily detect AC and PC as flow maxima in this image.

To detect AC and PC only, it is advantageous to limit the search space to a small subvolume. We have tested several heuristics to define this subvolume. The center of mass in a peeled brain is found quite robustly in the area between the splenium of the corpus callosum, the habenula, and the adhesio interthalamica. On a line between the center of the eyes **CE** and the center of mass **CM**, the anterior commissure **AC** is found close to a point

(1) $\mathbf{a} = \mathbf{CE} + 0.7 * (\mathbf{CM}-\mathbf{CE})$,

where an estimate for the posterior commissure **PC** is given by

(2) $\mathbf{p} = \mathbf{CM} - 0.1 * (\mathbf{CM}-\mathbf{CE})_z$.

These heuristics were found to be valid in all available datasets with a deviation of less than 3mm. One can now limit the search space for **AC** and **PC** to a small subvolume of 50x50x30 voxels computed from **CM** and **CE**. The computation time of the flow algorithm on this grid is in the order of 2 minutes. We cut this flow rate image with the mid-sagittal plane and search for flow maxima using **a** and **p** as starting

points. From these flow maxima, we adjust the coordinates to find the lower margin of AC and the upper margin of PC. We define the line passing through **AC** and **PC** as the x axis of the stereotactical coordinate system. The midpoint between **AC** and **PC** denotes the center. The y and z axis are found by introducing a right-handed system. We compute an affine transform to map the peeled brain image into this reference system which includes rescaling in 3D to form an isotropic resolution. We finally obtain a peeled brain dataset with isotropical resolution and registered to a standardized coordinate system. One should note that the steps to detect AC and PC are parameter-free and do not need any user interaction.

3 Implementation and Results

The image processing sequence outlined above was implemented and intregrated within the BRIAN environment [9]. The performance and robustness of this processing chain were tested with 26 high-resolution MR brain datasets, which were measured on 8 different MR scanners (Siemens Impact at 1.0 T, Siemens Vision at 1.5 T, Phillips Gyroscan at 1.5 T, GE Signa at 1.5 T, and Bruker at 3.0 T) at 5 different locations (see Acknowledgements). We used T1-weighted 3D sequences, including 3D GRE FLASH (16), SE FLASH (7), and MDEFT (3). Each dataset contained 128 sagittal (or axial) slices with an in-plane resolution between 0.86mm and 1.0mm and a plane-to-plane distance between 1.4mm and 1.5mm. All datasets were checked visually by an expert to exclude gross artifacts (motion, folding), developmental abnormalities, or the presence of pathologic structures.
In 17 of 23 cases (74%), this processing chain succeded on the first run. In the remaining 6 cases, the peeling was incomplete with parts of the neck still attached to brain structures. Raising the distance d1 from the default value of 2.0 mm to 2.5 mm resolved this problem in another 5 cases. A sufficient peeling was not achievable in one single case, where the left temporo-mesial cortex was attached to the meninges and thus was not separable. The higher the value of d1, the greater is the chance that portions of the cortical layer will be removed during peeling process. This will be noticable with values of d1 above 3.0 mm, so one should choose d1 to be small enough to warrant a successful peeling. In all successfully peeled cases (96%), the reference structures AC and PC were detected without problems and likewise a coordinate system adapted. To assess the quality of the procedure, we compared the position of the origin and orientation of the axes with reference alignments, which were manually generated. The deviation between the manually and automatically determined origin was 1.2mm (±0.4mm, range 0-2.5mm). The maximal rotational deviation before aligment were 4 degrees around x, 10 degrees around y and 8 degrees around z. After alignment, the deviation between the manually and automatically rotated axes were 0.8 degrees (±0.5 degrees, range 0-1.5 degrees).

4 Discussion

We have described an interaction-free procedure to remove the non-brain parts in an MR tomogram of the head and to adapt the stereotactical coordinate system. By adjusting only one parameter, we were able to segment 22 of 23 high resolution datasets

measured on 8 different MR scanners within a few minutes. To our knowledge, no other algorithms to automatically detect the reference structures of the stereotactical coordinate system have been published so far. Minoshima et al. [10] have designed a two stage registration process that begins by identifying the interhemispheric cleft and then uses empirical rules to automatically locate four points along the AC-PC line. However, because this procedure was designed for PET experiments, these rules are dependent on the tracer distribution applied. Collins et al [4] use a multiscale cross-correlation for the registration of a sample dataset with an averaged MR brain volume that has been aligned with the Talairach space. They do not detect the reference structures directly and are thus dependent on a succesful registration with their model. The primary research focus of our institute is the study of cortical activity in the human brain. Our evaluations are based on a precise anatomical analysis of an *individual* brain. The first step in this analysis is the removal of the outer hulls of the brain and the alignment within a reference system. The procedure described in this paper performs this step automatically and with a high degree of accuracy.

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