Automatical Adaption of Anatomical Masks to the Neocortex

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Abstract: We describe an image processing chain that is capable of identifying sulci and gyri in MRI brain slices. Contrary to current interactive map fitting schemes it tries to simulate a radiologist's way of image analysis - a process we call *image understanding by landmark detection*. In a nutshell, we detect the entry points of the neocortical sulci by an automated procedure. These entry points are identified as belonging to a specific sulcus by comparison with an anatomical database. From these landmarks a further analysis of the surrounding region can be performed. This algorithm is used for an anatomical mapping facility in a multimodal image editor for medical volume datasets.

1 Introduction

The brain is the most complex organ in the human body. The current available magnetic resonance (MR) imaging techniques give an excellent pictorial description of a patient's brain morphology and pathology. In a normal brain are in the order of 500 locations of interest which are big enough to be detectable by MR techniques. A precise anatomical analysis of a brain MR tomogram requires a working anatomical knowledge and a good understanding of the spatial relationships of the brain locations which is usually only found with a trained neuroradiologist. This process can be eased by fitting an anatomical map to an image slice.

Current approaches of map fitting take a MR slice and adapt it by transformation to a model map [1, 2]. This map is represented as a *geometrical model* which is based on a model brain or a stereotactical atlas [7]. We call this method *example-based map fitting*. This approach works sufficiently in parts of the brain where the anatomy has low individual differences, like in the brainstem and midbrain areas. The neocortical gyri and sulci however display an individual variability so this approach of map adaptation can reach only a moderate degree of accuracy. Pathologic cases with space-consuming properties like tumors or edemas are even harder to handle.

Our approach tries to simulate a radiologist's way of analyzing an image series. One of the first steps in this process is finding any landmarks. Landmarks are well-defined anatomical points that are easily detectable in MR tomograms, f.ex. the eyes, the ventricles and the primary sulci. Once a set of orientation points has been established, a finer analysis of the area „in between" can be performed. In patho-

logic cases either the landmarks are simply displaced or only a subset can be successfully detected. Since our approach uses an algorithm to detect and assign structures (i.e a *symbolic model*) we call this approach in derivation of similar problems in computer vision *map fitting by image understanding*. Another important difference between these two approaches lies in the fact that example-based map fitting is usually an interactive process - i.e. (expert) user-based and thus time-consuming - whereas our approach can be automated.

2 Description of the algorithm

We show how the position of the neocortical sulci can be detected by an automated image processing sequence. In short, we compute the brain contour and its *Voronoi segmentation* figure [5]. The entry point of a sulcus is found at the crossing of the brain's convex hull with the outer segmentation figure. The purpose of the core algorithm in this sequence can be explained for a u-shaped test contour (Fig. 1a). Non-strictly spoken, the outer Voronoi segmentation figure consists of a „crown" around the test contour and a „finger" exploring the sulcus. An outline of the complete sequence is given as follows:

1. Take an MR brain slice with good contrast between liquor and tissue as input
   Comment: Since we want to detect sulci, a good contrast between liquor and brain tissue is necessary. The usual T1-weighted images produced in clinical routine are sufficient. This slice belongs to a volume dataset that has been registered with the stereotactical coordinate system [4]. Note that the current formulation of our algorithm requires a „skull-removed" brain image (Fig. 1b).
2. Compute a polygonal approximation of the brain contour
   Comment: This step approximates the brain contour (preferrably) as a *closed* polygon. We detect the edges in the brain slice by a Canny operator and convert the edge image into a set of line segments by pixel chaining (Fig. 1c).
3. Perform a Voronoi segmentation [5] of the vector image
   Comment: We increase the resolution of the segmentation figure by subdividing long line segments in the input figure. A maximum segment length of 4 pixels yields an optimum between resolution and computation time. The set of Voronoi edges between the bounding rectangle and the brain contour (the exoskeleton) „explores" the sulci (Fig. 1c).
4. Clean out the branches of the segmentation figure („pruning")
   Comment: To include only prominent „fingers" in subsequent steps, a cleaning of the segmentation figure is performed. We determine the adjacency [5] of the Voronoi edges and discard those with an adjacency lower than a predetermined threshold. Usually we prune by a level of 2.
5. Compute the crosspoints of the outer segmentation figure with the hull
   Comment: First we construct a convex hull from the polygon approximation of the brain contour. The cutpoints of the exoskeleton with the convex hull are collected as probable entry points of the sulci. Note that the endoskeleton is disregarded since it lies completely within the hull. Usually 4 to 8 crosspoints per hemisphere are found (Fig. 1d).
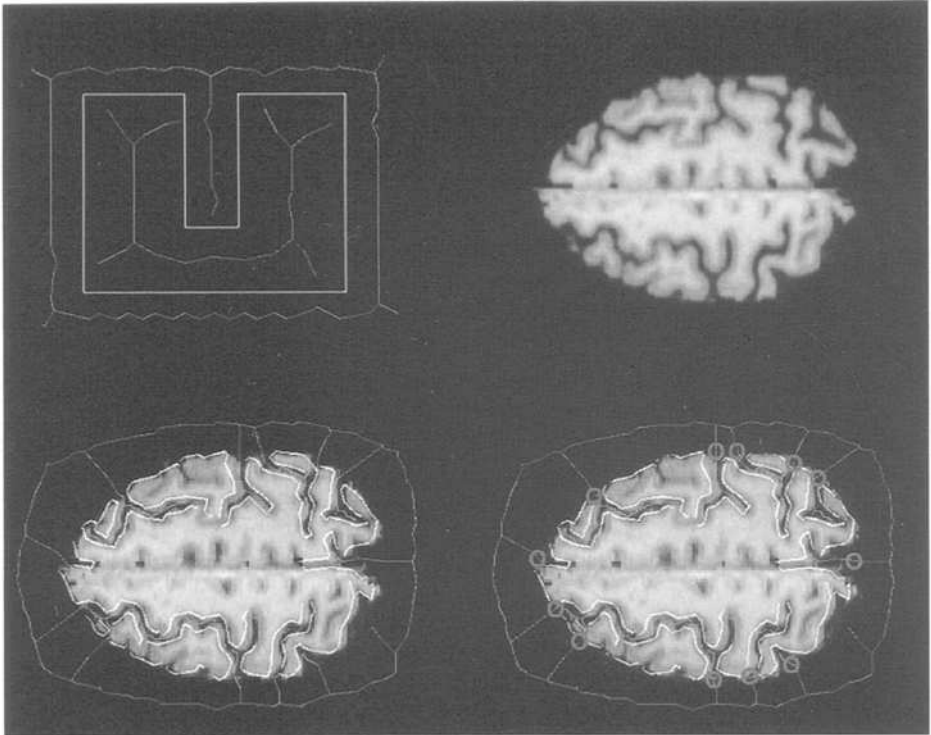
Fig. 1. Top left (a): Test figure „U" and its corresponding Voronoi segmentation. Top right (b): T1-weighted input MR slice 40mm above CA-CP. Bottom left (c): Polygonal approximation of the brain contour and its Voronoi segmentation. Bottom right (d): Crosspoints (shown as rings) with the convex hull are denoted as suspected sulcus entry points.

6. Compare the crosspoints with sulcus locations in the anatomical database (i.e. assign identification probabilities)

   Comment: The z position (slice position) is added to each of the computed crosspoints. The point list is handed to an anatomical database, which contains „usual" positions of the sulci and their variation. These positions were determined initially be manually tracing the sulci in 20 randomly chosen brain MRI datasets. We include sulcus positions successfully assigned by this algorithm (and confirmed by an expert) in a „bootstrap fashion". For all crosspoints we assign probabilities p for belonging to a specific sulcus by comparison with reference locations and their variance using a bivariate normal distribution statistic.

7. Repeat this process for other slices

   Comment: To further enhance the identification process, we perform steps 1-6 for neighbor slices.

8. Define sulci by concatenation of identified crosspoints

   Comment: We collect the crosspoints of all slices including their probabilities for belonging to a specific sulcus and construct a weighted graph (using 1/p) of these points. The path with the lowest cost is accepted as the series of points defining a

specific sulcus. The cost can be used as a quality measurement of the adaptation process. Output is a series of points defining an identified sulcus.

9. Define gyri as structures surrounded by identified sulci

   Comment: The area between two sulci can be identified as a specific gyrus if both limiting sulci are known. Sulci and gyri are shown by name in the dataset currently under investigation by a user of this system (Fig. 2).
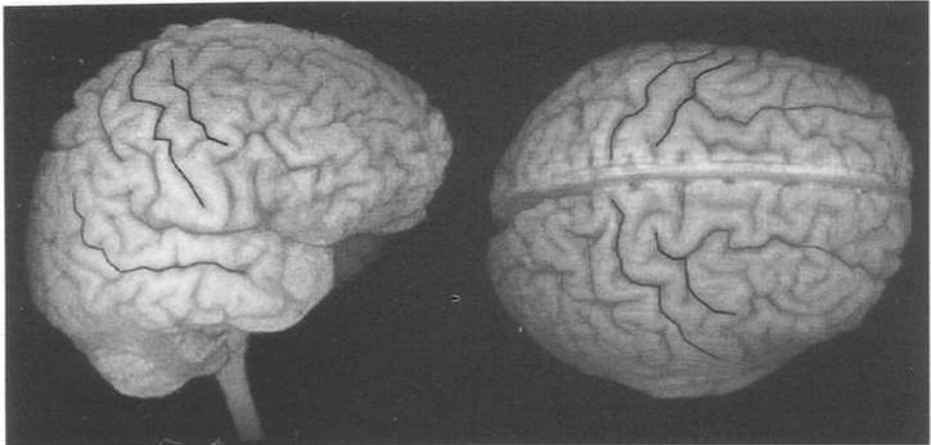

Fig 2. Example of automatically detected sulci in a 3D MR dataset. On the left (L to R): S. temporalis sup., F. Sylvii, S. postcentralis, S. centralis, S. praecentralis. On the right (L to R): S. postcentralis., S. centralis, S. praecentralis, S. frontalis sup.

This algorithm has been implemented as a part of a medical documentation system [3]. It was implemented in about 2000 lines of C++ code. It needs about 10 s per slice on a SGI Indy workstation. Time-consuming steps are the contour formation and the Voronoi segmentation.

Although the details of this algorithm appear complex the whole processing chain can be handled as a black box since the only parameters needed are in the initial edge detection step. Values for these parameters can be supplied by a knowledge database or estimated by histogram analyzation of the slices.

3 Discussion

Several approaches of fitting anatomical maps to MR tomograms have been proposed in the last five years. These approaches use model brains as the base of an anatomical atlas. Former proposals applying rigid matching show adaption problems especially in neocortical structures like sulci and gyri due to their individual variances. Second generation schemes were build on various methods of non-rigid matching [1, 2]. These methods can adapt masks with an accuracy of about 2-3 mm which is sufficient for a physician's orientation but barely acceptable for quantitative volumetric purposes. Furthermore, these adaption schemes work barely in the presence of space-consuming pathologic changes.

In this paper we have outlined a new way of map adaption by feature detection. Our basic idea is to follow a radiologist's way of orientation by finding any landmarks. In our first attempt we identify the primary sulci as landmarks, which are formed first during ontogenesis and develop relatively regular among subjects. By detecting these landmarks, a considerable amount of the interpersonal variability of the neocortical structures can be ruled out. We use a Voronoi segmentation to detect sulci and identify them by comparison with a probabilistic database of their „usual" locations. This distinguishes our approach from static atlases like the one recently introduced by Tiede et al. [7]. Furthermore, by working completely in the „patient space", our scheme does not depend on problems in the adaption of a geometric model as it is the case with non-rigid matching schemes mentioned above.

Our work is related to the study of the neocortical surface topology introduced recently by Mangin et al. [4]. They segment a MR volume dataset to yield a union of gray-matter and cerebro-spinal fluid, which undergoes a skeletonization to form an attributed relational graph that contains a 3D description of the brain's surface topology. This description can be labeled by a neuroanatomist.

While our processing chain appears as a promising approach of map fitting to us, several open problems exist which have to be addressed before this procedure can be applied in an automated system:

1. This algorithm needs a „skull-removed" MR image set. This is currently done by hand editing the original dataset. An automatical algorithm for removing the non-brain parts is under construction in our workgroup.
2. The detection of sulci is depended on a successful edge detection. Most edge detection schemes yield open brain contours, so that the exoskeleton „leaks" into the endoskeleton.
3. Quality measurements of the detection process are not yet available. In a short series using routine MRI slices (20 patients) the primary sulci we correctly assigned in 93%. No incorrect assignments were found.
4. The performance of this algorithm has not been tested with severe distortions of the brain (i.e. large cortical infarcts, malformations).

A possible 3D implementation of this algorithm seems to offer no advantage for us. 3D Voronoi segmentation schemes require high computational efforts, especially due to the amount of boundary planes involved. The resulting topological structures are hard to analyze and to compare. A parallel formulation of this algorithm would be desirable to speed up the computation. In spite of the serial nature of this processing chain, a simple parallelization can be performed by computing several slices in parallel. Candidates for a true parallel formulation are the time-consuming steps 2 and 3.

In the future, we will extend this map adaption scheme to include landmark information of different origin. Through a combination of a region-based growing and a watershed segmentation algorithm [6] we were able to segment deep white-matter structures like the basal ganglia (caudate nucleus, pallidum, putamen and thalamus). This leaves maximum distances of 3 cm to be bridged by patches of conventional

model maps, which are still necessary to locate structures that are (currently) unde-tectable by MRI in terms of their shape or intensity characteristics.

The use of the inner segmentation figure for analyzation of white matter structures appears interesting. The idea of using a Voronoi skeletonization to represent and analyze shapes has recently been published by Mayya and Rajan [5]. The endo-skeletons are reminiscent of the course of the white-matter tracts and thus may re-veal valuable informations about these not directly traceable structures. It seems necessary to include the segmentation of the basal ganglia (as „holes" in the white matter) to restrict the formation of the endoskeleton to the natural compartment of tracts in the brain.

Our map adaption scheme currently undergoes a test phase in the clinical routine. We need to collect experiences when applying this algorithm in the presence of brain pathologies. During the next months we will analyze the performance, accu-racy and failures of our approach under routine conditions. The „gold standard" of an automated analysis is still the approval by an expert. However, we can add suc-cessfully matched sulcus locations to our growing anatomical database and thus yield a more robust assignment.

The implementation enhances a multimodal image editor for the neurologic sci-ences which is currently under development in our clinic.

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