Towards Better Management of Cortical Anatomy in Multi-modal Multi-individual Brain Studies

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Abstract–Until recently, low resolution of usual functional data was limiting the interest of using accurate anatomical information in their analysis. Today, different functional modalities have reached a few millimeter accuracy which calls for the design of new analysis methods relying on detailed individual anatomical descriptions. This paper described a project focusing on the automatic detection and identification of cortical structures in a 3D magnetic resonance image (MRI). This project include original anatomical hypothesises allowing us to overcome the large inter-individual variability of cortical topography. A generic probabilistic model of cortical topography is design from these hypothesises which allows recognition of main cortical sulci. New ways of visualizing cortical sulci in 3D are also proposed. Medical applications range from presurgical planning to functional mapping of the human brain.
Keywords–cortical anatomy, brain functional mapping, image segmentation, pattern recognition

1 Introduction

The significant development of ways of in vivo visualizing brain functions (positron emission tomography (PET), single photon emission tomography (SPECT), functional magnetic resonance imaging (FMRI), magneto-encephalography (MEG), electro-encephalography (EEG)...) has induced increasing needs for intra-individual inter-modality registration methods. Usually, anatomical images provided by conventional MRI are involved in this registration step. Indeed anatomy often appears to be the federating information for inter-individual functional data comparison. While satisfactory approaches have been proposed for a lot of intra-individual registration situations [1], inter-individual anatomical matching is still a challenging problem which appears more and more crucial. The first generation of approaches relying on proportional systems like Talairach reference grid (SPM package [2]) has been a great success. Unfortunately, it is today well known that such approaches do not allow an accurate management of cortical anatomy because of a large inter-individual variability. Therefore, a better management of cortical anatomy is required by brain mapping projects relying on high resolution functional modalities like 3D-PET, FMRI or MEG. This paper describes a project which aims at developing robust and reproducible methods to identify automatically various cortical structures, mainly the sulci (cortical folds) and the dual gyri (cortical regions delimited by sulci). In the context of human brain mapping, this project is an important contribution to the design of new inter-individual matching methods and to the creation of anatomy indexed computerized databases which could mediate data communication among laboratories. Indeed, cortical structures are important anatomical landmarks for driving individual adaptation of computerized atlases or individual delineation of volumes of interest. Our project focuses on three main points which will be briefly addressed:

1. The design of a robust method allowing the extraction of a structural representation of the cortex topography from a T1-weighted 3-D MR image [3, 4].

2. The understanding of cortex anatomy inter-individual variability and the constitution of a large database of synthetic cortex representations in which sulci are manually identified [5, 6, 4].

3. The elaboration of a probabilistic structural model of the cortex topography from this database and the design of a method matching this model and any individual cortex representation [7, 4].

2 Cortical fold detection

The structural representation of an individual cortical topography is an attributed relational graph (ARG) [3]. This ARG is inferred from the 3D skeleton of the object made up of the union of gray matter and cerebro-spinal fluid enclosed in the brain hull. In order to increase the robustness of the skeletonization, topological and regularization constraints are included in the segmentation process which provides this object using an original method: the homotopically deformable regions. This method is halfway between deformable contour and Markovian segmentation approaches. The 3D skeleton is segmented in topologically simple surfaces (SS) constituting the ARG nodes (mainly cortical folds) (see Fig. 1). The ARG relations are of two types: first, the SS pairs connected in the skeleton (ρ_T); second, the SS pairs delimiting a gyrus (ρ_C). A third kind of relation (ρ_P) intending to represent fold deformations induced by white matter fiber bundles is under study (see Fig. 2). Semantic attributes like area, orientation or depth of folds, relative positions of folds or gyrus area, are attached to graph nodes and relations. This ARG intends to be a synthetic representation of all the information required by the sulcus and gyrus identification.

3 Generic vision of cortical topography

Unlike the case of monkey, the human cortical anatomy presents large pattern variations between individuals or even between brain hemispheres. Unfortunately, usual anatomical atlases do not provide methodology for overcoming this variability. Therefore, before designing pattern recognition methods dedicated to cortical sulci, we had first to propose a coherent interpretation of this variability. The compilation of various information relying mainly on ontogenesis, phylogenesis, gyrogenesis, cyto-architectonic and myelo-architectonic organization, thalamo-cortical and cortico-cortical tract mapping and anatomo-functional correlations led us to think that the surprising lack of understanding of cortical anatomical variability results from a bad choice of the elementary unit (the sulcus) used for analyzing cortical topography [5, 6]. Indeed, we think that sulci are made up by more fundamental cortical entities related to the first folds appearing in fetus cortex which we call “sulcal roots”. The various phenomena occuring during the following brain growth result then in various connexions between these sulcal roots which explain the different sulcus patterns observed in adult brains. For instance, we think that strong relationships exist between the various sulcal root connexion patterns and the underlying network of white matter fiber bundles. This point of view led us to propose a generic description of cortical topography from which can be understood any individual topography (see Fig. 3 and 4) A second level of variability observed for the various branches of sulci could be related to the underlying functional organization like it has been shown for some animals [8]. Using 3D navigation tools (see Fig. 1), we have constituted a database of ARGs in which each node is identified according to this generic description (a label corresponding to a brain structure is attached to each ARG node).

4 Cortical sulcus identification

The sulcus automatic identification relies on a probabilistic structural model of the cortical topography which is inferred from the learning database mentioned above [4, 7]. This model is a structural prototype (a graph which nodes and arcs represent cortical structures) which nodes can split into pieces according to syntactic constraints. These syntactic constraints rely on a graph grammar which generates the language of possible patterns of a sulcus (related to the sulcal root and fiber bundle point of view). This prototype is endowed with a random graph structure taking into account inter-individual anatomical variability (see Fig. 5). The recognition process is formalized as a consistent labelling problem and the solution is obtained from the maximum a posteriori (MAP) estimator using simulated annealing. This MAP estimator is constructed from a Markovian random field (MRF) model. The main reasons which motivate this choice, which is a key feature of our model, are the following:

1. The contextual information used by a neuro-anatomist to identify a sulcus derives from a confined neighborhood of the sulcus in the brain.
2. The equivalence between MRFs and Gibbs random fields (GRFs) gives a very flexible way of combining syntactic constraints and statistical semantic informations on sulcus and gyrus shapes.
3. It has been proven that stochastic relaxation schemes like simulated annealing (SA) applied to a Gibbs distribution based MAP have very good convergence properties.

First experiments using a learning database of 10 brains have led to very good recognition results for the main cortical sulci. In return, these first results have shown that the current structural representations are insufficient for addressing properly the recognition of more variable sulci of frontal and occipital lobes. Therefore, we try today to improve these representations through the detection of deep white matter fiber bundles and sulcal root fusions (see Fig. 4). Then we will try to discover to which extent the sulcus recognition is well-founded. Indeed, nobody knows if the identification of any cortical fold is possible.

5 Potential applications

Medical applications of the work described in this paper are multiple:

- A first direction of investigation relies in new ways of visualizing cortical anatomy. For instance, in neurosurgical planning, 3D visualization of cortical folds has allowed us to choose natural sulcal pathways to gain access to pathologic structures within the brain, while preserving the integrity of healthy adjacent tissues. In brain functional mapping, the same kind of visualization allows accurate localization of activation foci relatively to individual anatomy (see Fig. 6), which appears especially interesting in MEG which is mostly confined to activation from tangential dipoles usually found in the sulci.
- A second important orientation consists in the design of the next generation of methods dedicated to the analyze of functional data. The goal is a better management of cortical anatomy through for instance a systematic parcelling of the cortex in anatomical volumes of interest or individual image deformations towards a standard atlas guided by identified cortical landmarks.
- A third direction relies in the development of a new generation of computerized databases for brain mapping overcoming the weakness of current approaches with regard to anatomical variability [9].
- Injection of a priori anatomical knowledge in reconstruction algorithms of functional modalities is also one important aim. For instance constraints on dipole localization and orientation could help to solve the difficult inverse problem of MEG.
- Last, the new tools allowing management of cortical topography will result in new anatomical and morphometric studies.

6 Conclusion

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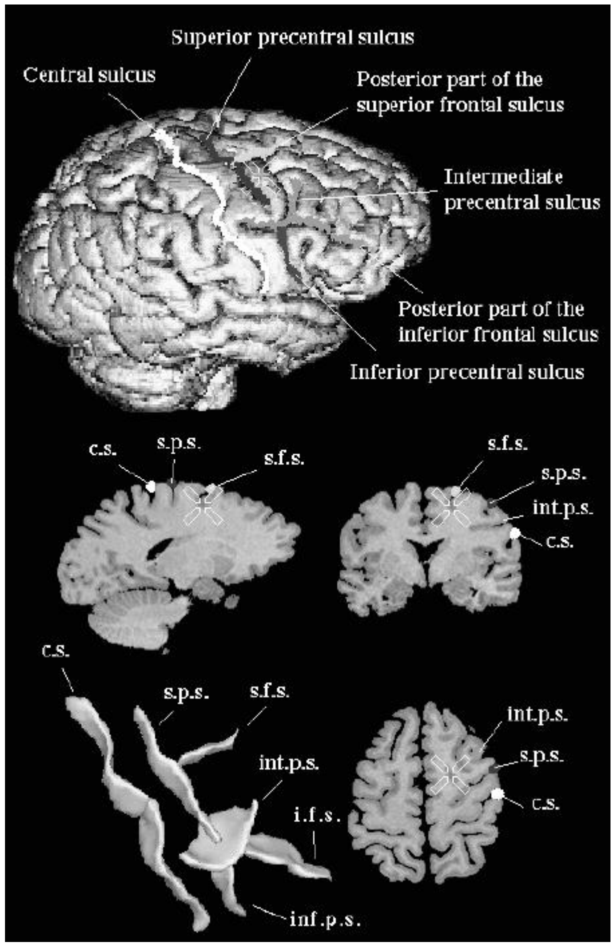


Figure 1: Superimposition of junctions between simples surfaces and brain external surface ($\mathcal{S}_{brain}$) in a 3D rendering of the brain and in 3 orthogonal slices. A 3D rendering of the corresponding simple surface set is also proposed.

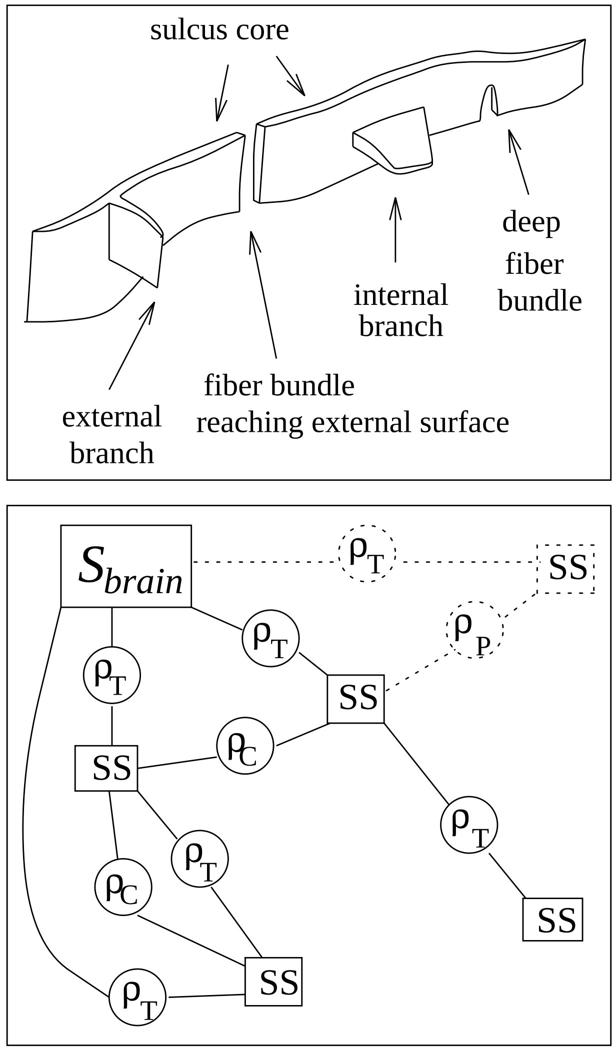
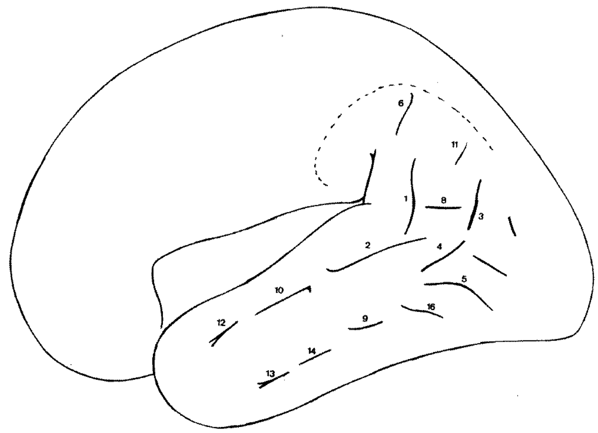
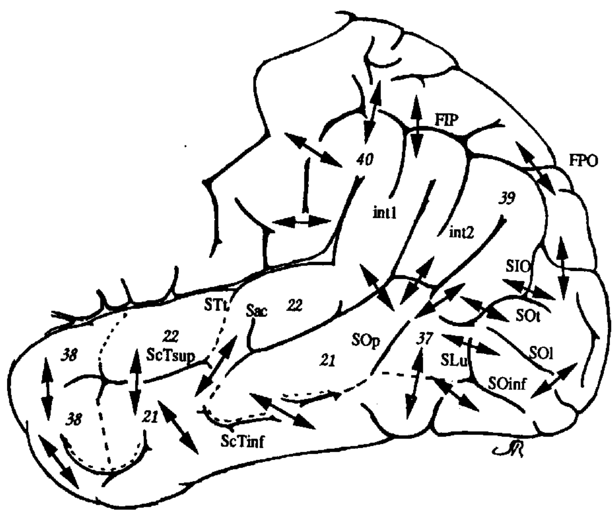


Figure 2: A sulcus of the external face of an hemisphere and its representation in the ARG. This sulcus is interrupted by a white matter fiber bundle allowing communication between the two delimited gyri. A second fiber bundle induces a deformation of the sulcus bottom.



Sulcal roots (fetus)



generic diagram (adult)

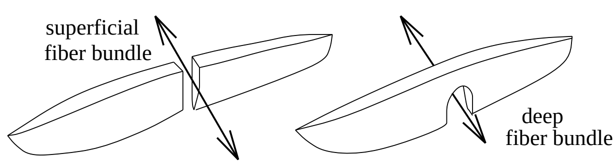


Figure 3: *top:* Sulcal roots of temporal lobe numbered according to their apparition date. *middle:* Simplified generic model of the temporal lobe sulcal topography (arrows denote the presence of white matter fiber bundles between sulcal roots) [5]. *bottom:* According to individuals, a fiber bundle may interrupt or not a sulcus made up by several sulcal roots.

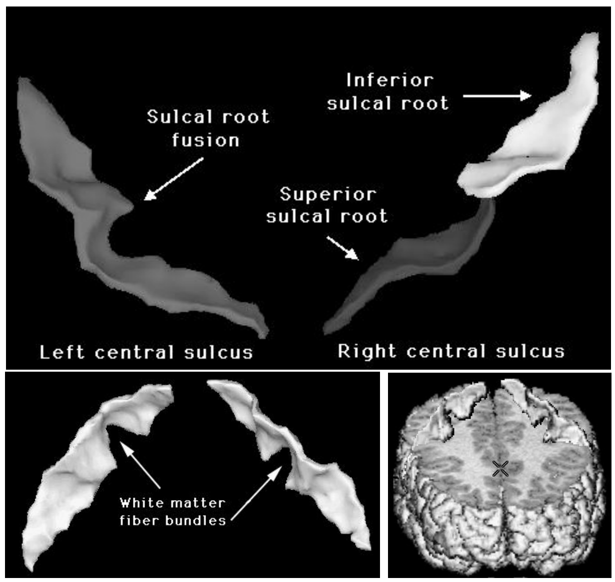


Figure 4: The central sulcus, which mainly delimits motor and sensory cortical areas, is made up by two sulcal roots. *top:* Sulcal roots of right central sulcus have been separated using topological properties. *down:* White matter fiber bundles induce large deformations of both central sulci.

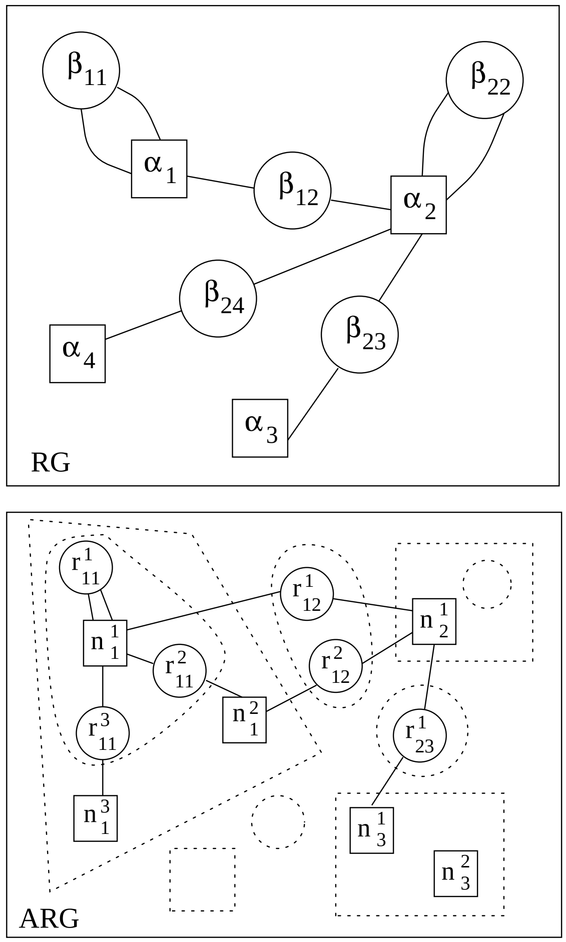


Figure 5: *top:* An instance of random graph (α_i denotes a random vertex and β_{ij} denotes a random arc between α_i and α_j). *bottom:* A realization of the random graph (the realization of α_i is the node set $\{n_i^1, ..., n_i^{n_i}\}$ and the realization of β_{ij} is the relation set $\{r_{ij}^1, ..., r_{ij}^{n_{ij}}\}$).

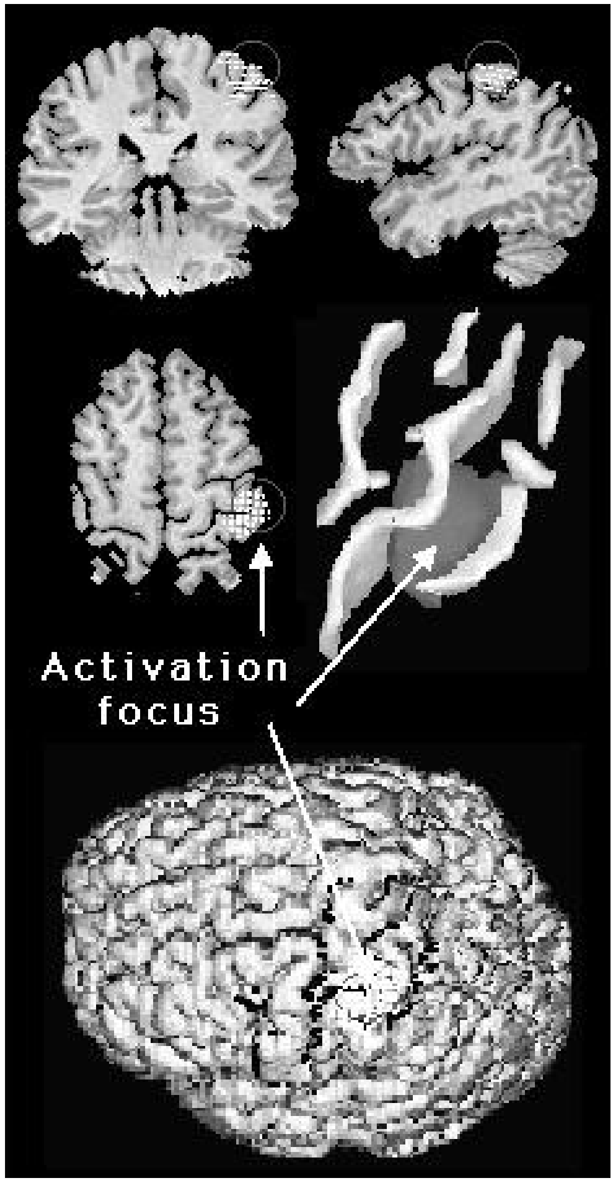


Figure 6: 3D Localization of the focus of activation (functional data from PET) induced by a right hand vibration relatively to sulci of contra-lateral hemisphere (neighborhood of central sulcus).