Chapter 5

Sulcus Extraction and Automatic Labelling (SEAL): I. Method for Mapping of Sulcal Neuroanatomy

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5.1 Introduction

Several studies have suggested that many major functional areas can be located with respect to the cortical sulci, allowing the construction of an anatomo-functional map of the human brain. However, the main difficulty when establishing such a map based on cerebral sulci comes from high inter-subject variability of the cortical topography which makes the definition of a common standard nomenclature to describe the cortical topography a very tedious task. Only the observation and the recovery of statistical parameters representing the normal anatomical variability allow for the definition of objective criteria for the recognition of these structures. In order to address this problem, we have implemented SEAL (Sulcal Extraction and Automatic Labelling). Our modelling method automatically labels the cortical topography of a particular subject using spatial prior on the distribution of the main cortical folds and may require a minumum human intervention to correct some labellings.

5.2 Methods

The method we have developed to extract and label from 3-D MRI the cortical topography is divided in three steps : **a)** extraction of the exterior trace of the sulci and detection of the connections between these entities. At this level, we extract the superficial structural component of the cortical topography ; **b)** modelling of the deeper cortical infolding by tracking the median surface of each cortical fold (*fig 1.a*). As a result, we obtain a parametric surface representing the 3-D shape of the buried part of each sulcus [2]. Finally, a set of parameters are associated with each extracted fold and junction, and the result is encoded in a graph structure. **c)** labelling of these graphs were then performed by an anatomist through an interactive display interface for 51 subjects in order to study the spatial distributions of the cortical sulci. Data expressed with respect to a standardized brain coordinate system (i.e Talairach-like coordinate system) permits the creation of SP_AMs (Statistical Probability Anatomy Map)[1] of the main sulci (*fig 1.b*). These SP_AMs, representing the normal spatial variability of the neuroanatomy are then used to perform the recognition of these anatomical structures on a new subject (*fig 1.c*)

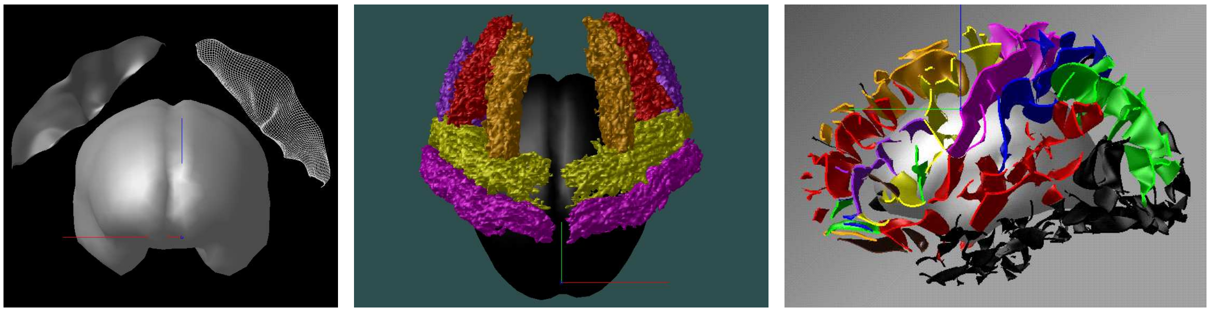

Fig.1 (Left to Right) **1.a** Sulcus extraction (central sulci), **1.b** Spatial distributions from 51 subjects (SPAMs), **1.c** Automatic labelling using spatial priors (grey levels are associated with sulcus names)

5.3 Conclusion

We have developed an algorithm dedicated to sulcal extraction and automatic labelling, SEAL. SEAL can assist the labelling of main cortical sulci by using prior on the spatial distribution of these structures. We have started to labelled and extract statistics for large ensemble of subjects (n=150). In the future, recovered statistics will be re-incorporated into SEAL to improve the labelling given by the use of spatial priors.

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Chapter 6

Sulcus Extraction and Automatic Labelling (SEAL): II. Generation of Frontal Sulci Probabilistic 3D Maps

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6.1 Introduction

Neuroanatomical spatial variability can be quantified in the form of 3-D stereotaxic maps where each voxel expresses the likelihood of finding a particular structure at that location. By averaging the labelling of structure in an ensemble of stereotaxic MRI volumes, a continuous 3-D probability field (0-100% at each voxel) for that structure, termed a statistical probability anatomy map (SPAM), can be constructed [2]. The goal of this study was to generate such a probability field for the main sulci of the dorsolateral prefrontal cortex.

6.2 Methods

We studied *in vivo* the sulcal neuroanatomy of 51 adults who had no previous history of neurological or psychiatric disorders. Magnetic resonance images (MRIs) of the subjects' brains were acquired on a Philips Gyroscan 1.5-T superconducting magnet system using a 3-D fast-field echo-acquisition sequence T1-weighted (Tr = 18 ms, Te = 10 ms, flip angle = 30). In order to account for inter-individual differences in absolute brain size, each brain was separately transformed into standardised (i.e. Talairach-like) stereotaxic space and resampled on a 1 mm^3 voxel grid. This was done using an automatic registration program which uses a 3-D cross-correlation approach to match the single MRI volume with the intensity average of 305 MRI brain volumes previously aligned into standardised stereotaxic space [1].
As manual extraction and labelling of cortical sulci is time-consuming and subject to significant inter- and intra-rater variability when dealing with these complex 3-D folds, we have used a method which permits automatic extraction of an explicit representation of the buried part of the cortical folds and

their arrangement in the form of a labelled graph (SEAL)[3]. Using such extractions, the SPAMs of the superior, middle (i.e. intermediate) and inferior frontal sulci, and of the central sulcus, were calculated.

6.3 Results

Probability maps for these sulci are shown below in standardised space for each of the sulci of interest (fig 1.a, fig 1.b). Moreover, during careful analysis of MRIs we observed that in over 80% of cases there was a clear separation of the superior frontal sulcus into an anterior and a posterior segment (fig 1.c).

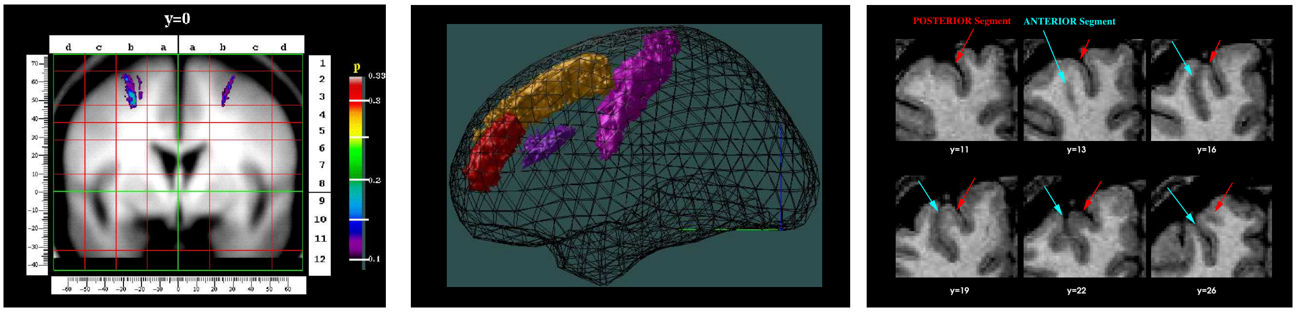

Fig.1 (Left to Right) **1.a** 2D section of superior frontal sulcus SPAM(51 subjects), **1.b** 3D SPAMs of labelled sulci for left hemisphere(51 subjects), **1.c** Example of anterior and posterior frontal sulcus segments.

6.4 Conclusion

the resulting SPAMs, defined in stereotaxic space represent sharable data that can be used by the neuroanatomical community. Several applications (morphometrical analysis, lateralization study, anatomo-functionnal correlations) may take advantage of such data.

Bibliography

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