

A freely available Anatomist/BrainVISA package for structural morphometry of the cortical sulci

D. Rivière^{*†}, J. Régis[†], Y. Cointepas^{*†}, D. Papadopoulos-Orfanos^{*†}, T. Ochiai[†], A. Cachia^{*†}, J.-F. Mangin^{*†}

^{*}*SHFJ, CEA, Orsay*

[†]*Service de Neurochirurgie Fonctionnelle et Stéréotaxique, La Timone, Marseille*

[‡]*IFR 49, Paris*

Abstract

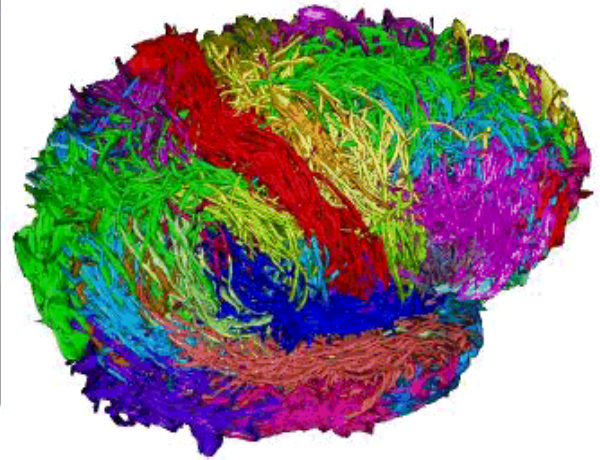
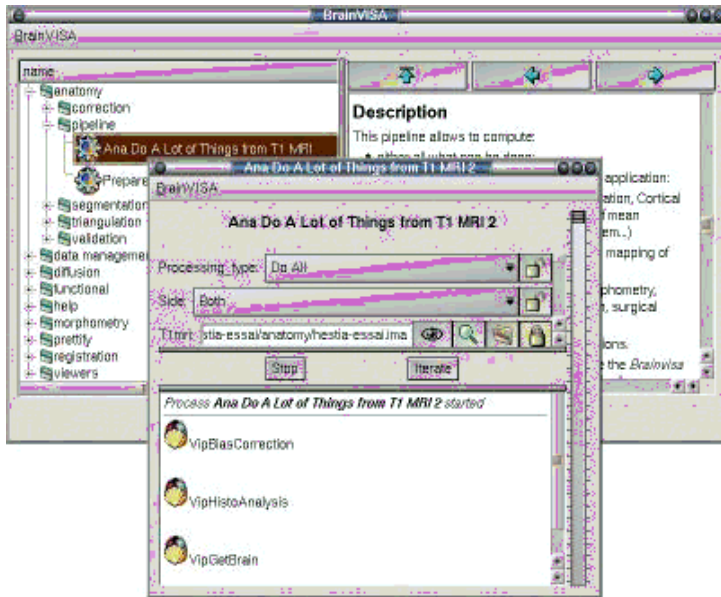
BrainVisa is a software platform designed to make image processing tools easy to use and to chain in a common environment [1]. It is useful both for methodologists who develop algorithms and for end users (clinicians or neuroscientists). BrainVisa is strongly connected to Anatomist, a 3D visualization software able to display anatomical and functional volumes, surfacic meshes of segmented structures, and structural data such as graphs of cortical sulci [2]. Results can be viewed in the most convenient and comprehensive manner. BrainVisa and Anatomist are free and downloadable from (<http://anatomist.info>); they currently run on Unix platforms (Linux, Solaris, Irix, soon on MacOS X). The software package also contains a large set of anatomical MRI processing tools that we have developed during the last 10 years.

Virtually any software can be easily integrated in Brainvisa. Therefore the application field of the platform is extremely wide. It uses a common and easy-to-read script language (Python), so even people who are not specialists of computer science can plug external software into BrainVisa. This paper focuses on such a package dedicated to sulcal morphometry. This package relies on a structure-by-structure analysis. For each subject, each cortical sulcus is assigned a set of descriptors, each representing either a measure (such as length, maximum depth, global size, position and direction, ...) or a more topological aspect (number of unconnected parts, etc...). These descriptors are then compared by statistical analysis across different populations.

These descriptors stem from a complex but fully automatic image processing and artificial intelligence pipeline. The main steps are: bias correction, histogram analysis, brain segmentation, hemispheres and cerebellum separation, gray/white matters segmentation, sulci skeletonization, graph construction (with nodes representing parts of sulcus and relations showing neighbourhoods), sulci identification [3], and sulcus descriptors extraction. BrainVisa can iterate the processing pipeline on a group of subjects (see Fig). A database-like system helps the user to select the set of input T1 MRI images in a few clicks and knows where to write the results. No user intervention is required after the processing pipeline is started. However the difficult step of cortical folds identification is prone to some errors. Manual corrections may be done in a post-processing stage using Anatomist, but we have shown that with a sufficiently large data set, interesting results can be obtained without any correction (see other poster in HBM2003). The figure shows the automatic processing of 50 subjects merged in Talairach referential.

We believe that structural morphometry represents an interesting alternative or complement to voxel based morphometry (VBM) because it allows the study of aspects which are not described by VBM: directions, shape descriptors, structural aspects like numbers of intra-sulcus interruptions, etc... Furthermore, similar studies can also be performed for the relations between sulci through questions like "how are precentral sulcus and superior frontal sulcus connected, how does this connection varies across subjects or across different populations ?".

- [1] Cointepas et al., HBM 2001, NeuroImage 13(6).
- [2] Rivière et al., HBM 2000, NeuroImage 11(5).
- [3] Rivière et al., Medical Image Analysis, 6(2):77-92,2002



Pipelining the automatic recognition of 50 brains