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# Introduction to BrainVISA

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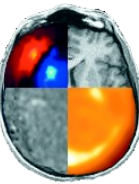
**Inserm**



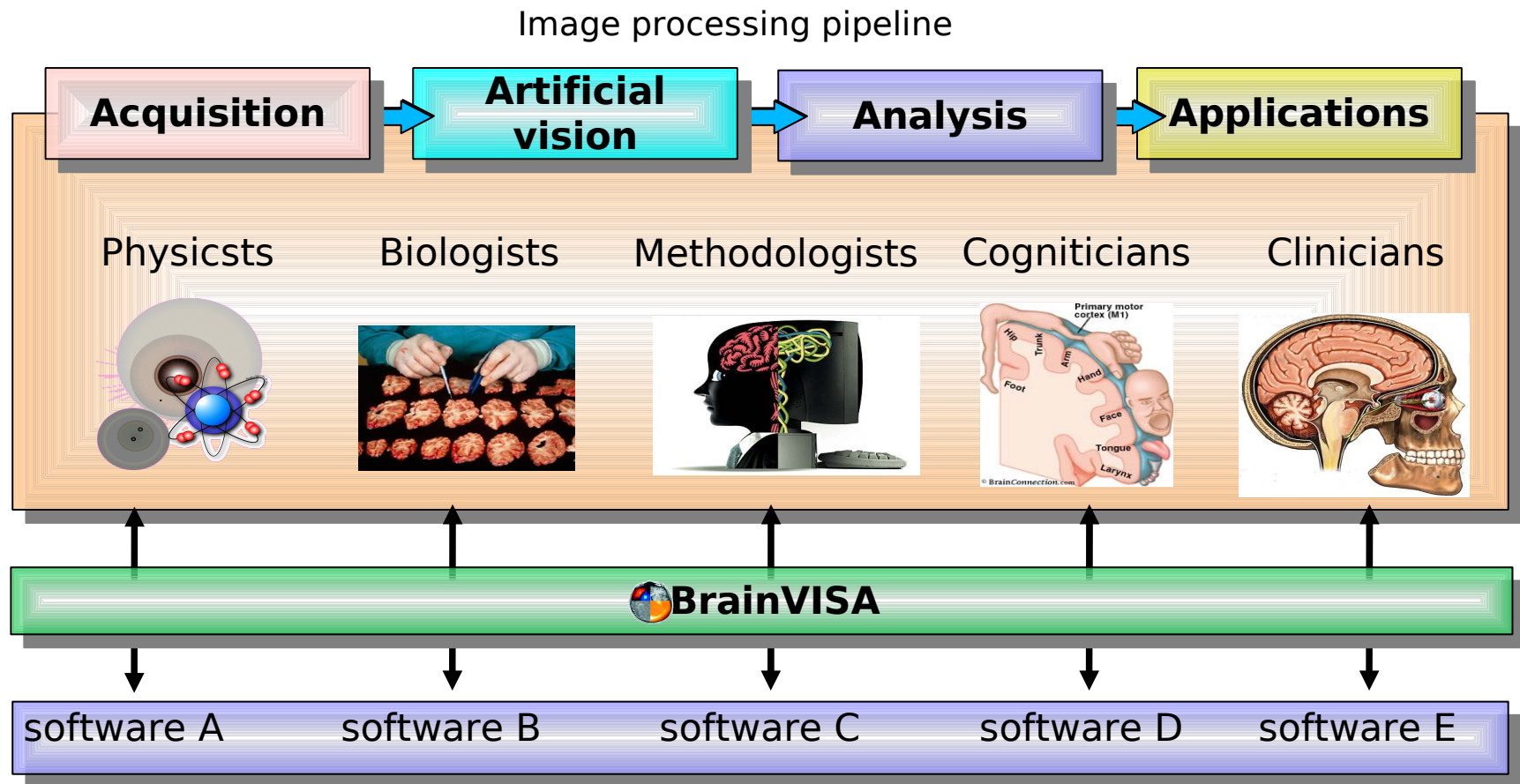
**INRIA**

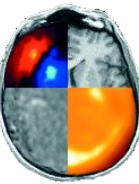


# What is BrainVISA ?



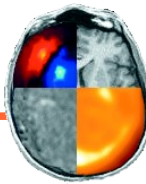
- Modular and customizable software platform built to host heterogeneous tools dedicated to neuroimaging research
- **Aim : help sharing neuroimaging data and processing tools.**
- Free and open-source software -> extensible





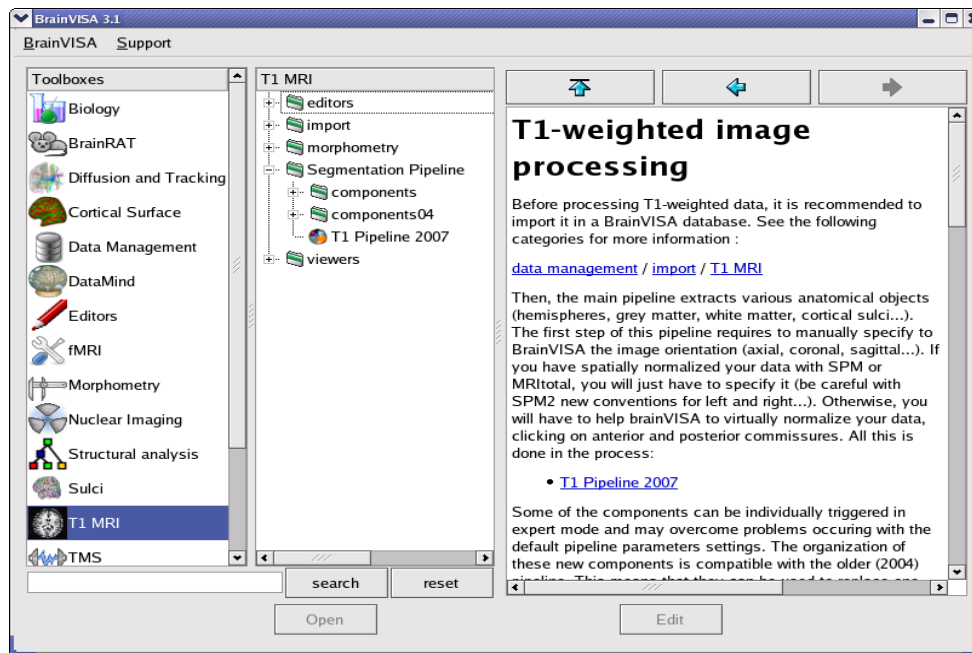
- Overview of BrainVISA package
  - Anatomist
  - BrainVISA
  - Command lines
- BrainVISA toolboxes
- Starting with BrainVISA
- Documentation & Help
- Installation

# Overview of BrainVISA package

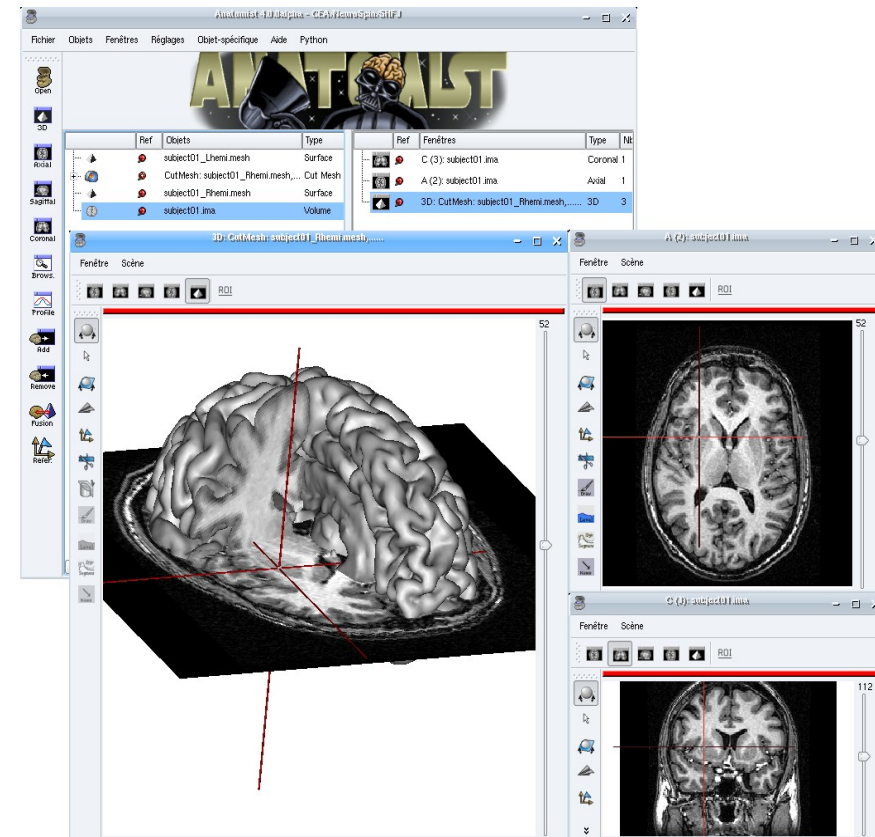


Available for free download on <http://brainvisa.info>

Linux, Windows XP, and MacOS versions



**BrainVISA**

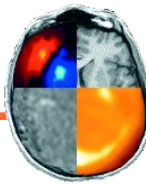


**Anatomist**

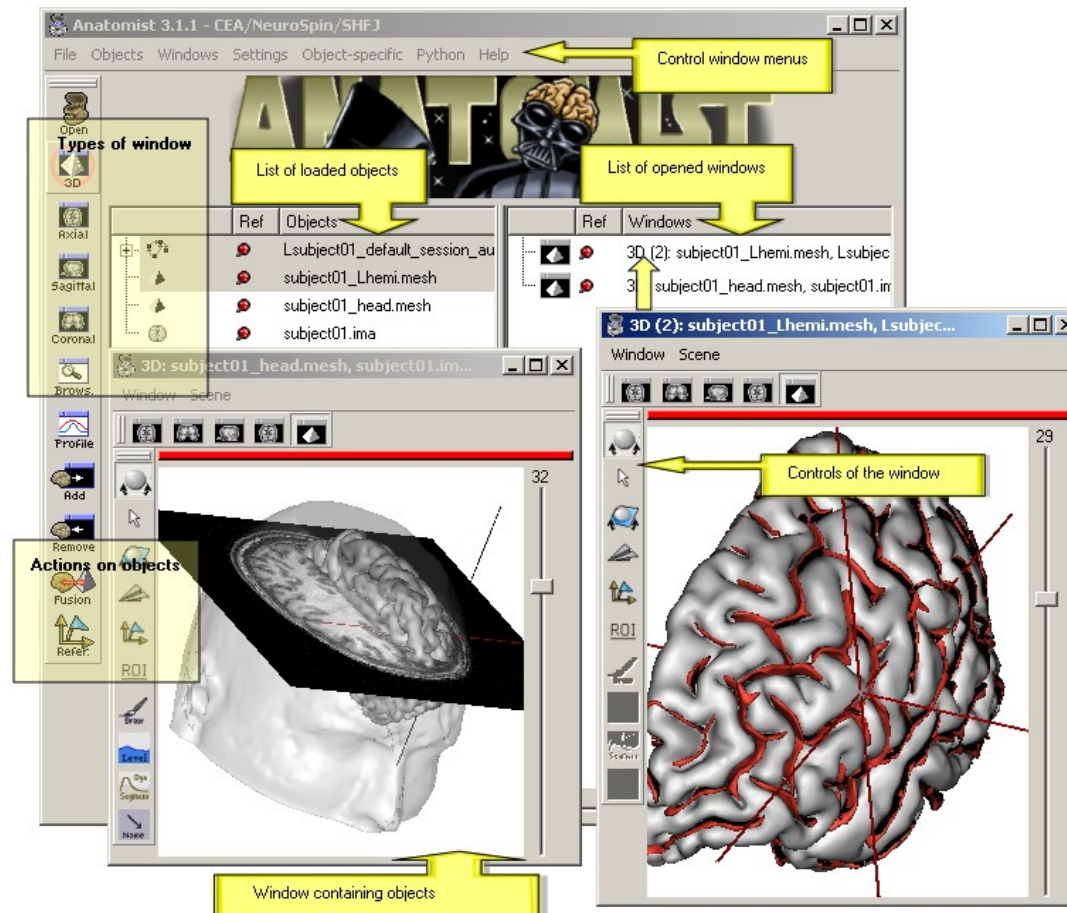
## Aims Commands

```
$AimsSubVolume -i diff_data.ima -o t2.ima -t 0 -T 0  
$AimsThreshold -i voronoi_lesson1.ima -o hemi_only.ima -m lt -t 3  
$AimsGraphConvert -i label_image.ima -o label_graphe.arg -bucket ...
```

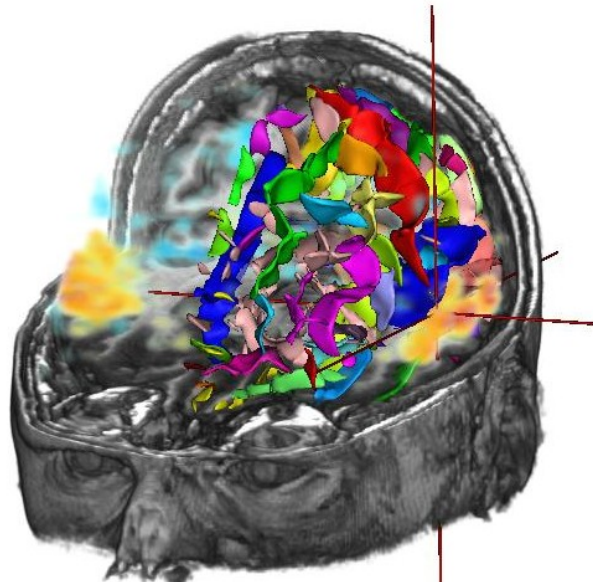
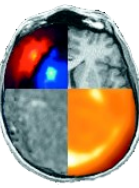
# Anatomist



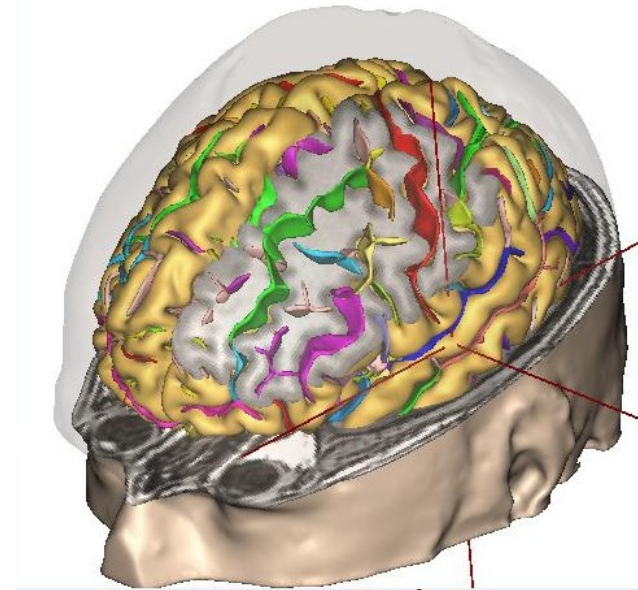
- Visualization of several types of objects : image, volume (3D, 4D), mesh, graph (sulci, ROI)
- Management of coordinate systems and transformations
- Possibility of building complex 3D scenes with several objects (merging, superimposing...).
- A lot of tools : color palettes, region of interest module, manual registration



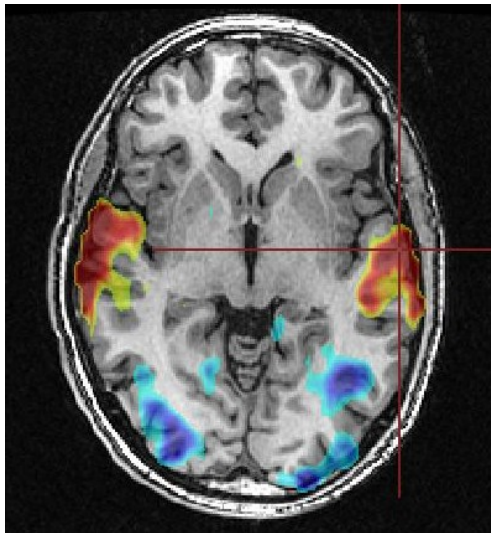
# Anatomist features



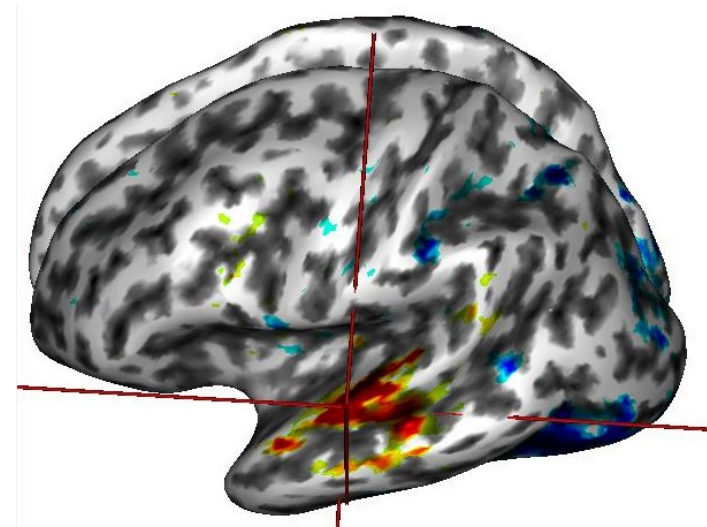
Volume rendering



Cut mesh

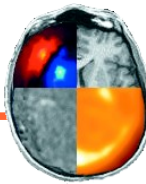


2D fusion

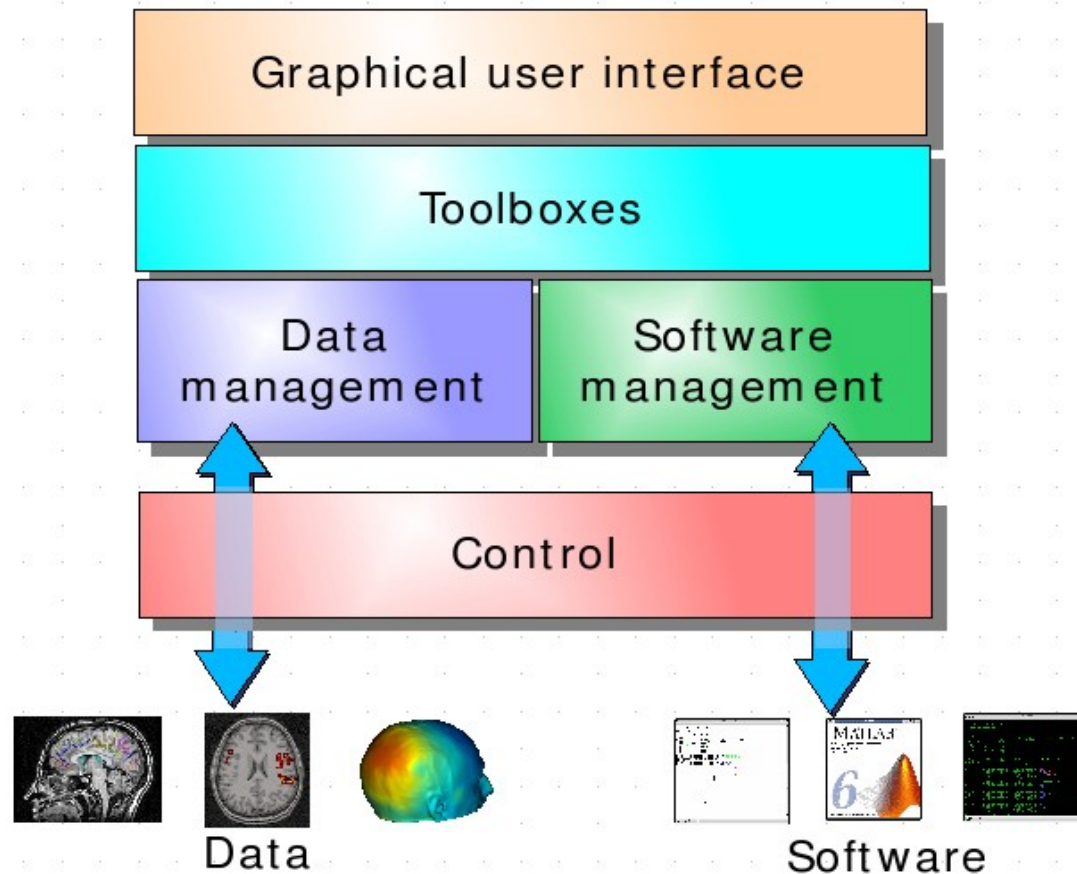


3D fusion

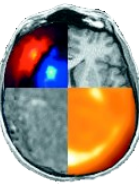
# BrainVISA features



- Data management system allows database sharing
- Harmonization of communications between different software
- Interactive visualization of multimodal data
- Automatic generation of graphical user interface
- Workflow monitoring : processes, pipelines, iterations



# Aims Commands



## Commands for many purposes

- File information and conversion: *AimsFileInfo*, *AimsFileConvert*, *AimsGraphConvert*, *AimsSetMinf*, *AimsAttributedViewer*
- Cut / cat / merge and other simple operations: *AimsTCat*, *AimsSubVolume*, *AimsOverVolume*, *AimsFlip*, *AimsMerge2RGB*, *AimsSplitRGB*, *AimsGraphMerge*, *AimsMergeLabel*
- Simple, basic processing: *AimsThreshold*, *AimsAverage*, *AimsMassCenter*, *AimsMeshArea*
- Coordinates transformations: *AimsComposeTransformation*, *AimsInvertTransformation*, *AimsGraphExtractTransformation*
- Labels selection (ROI): *AimsLabelSelector*, *AimsSelectLabel*
- Mathematical morphology: *AimsErosion*, *AimsDilation*, *AimsOpening*, *AimsClosing*, *AimsVoronoi*, *AimsChamferDistanceMap*, etc.
- Statistics on ROI and images: *AimsRoiFeatures*, *AimsVoiStat*.
- Mesh operation: *AimsMeshGenerate*, *AimsMeshCut*

Inline help with *--help* option

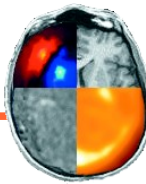
List of all commands on brainvisa website

<http://brainvisa.info/doc/documents-3.1/shfjcommands/commands.html>

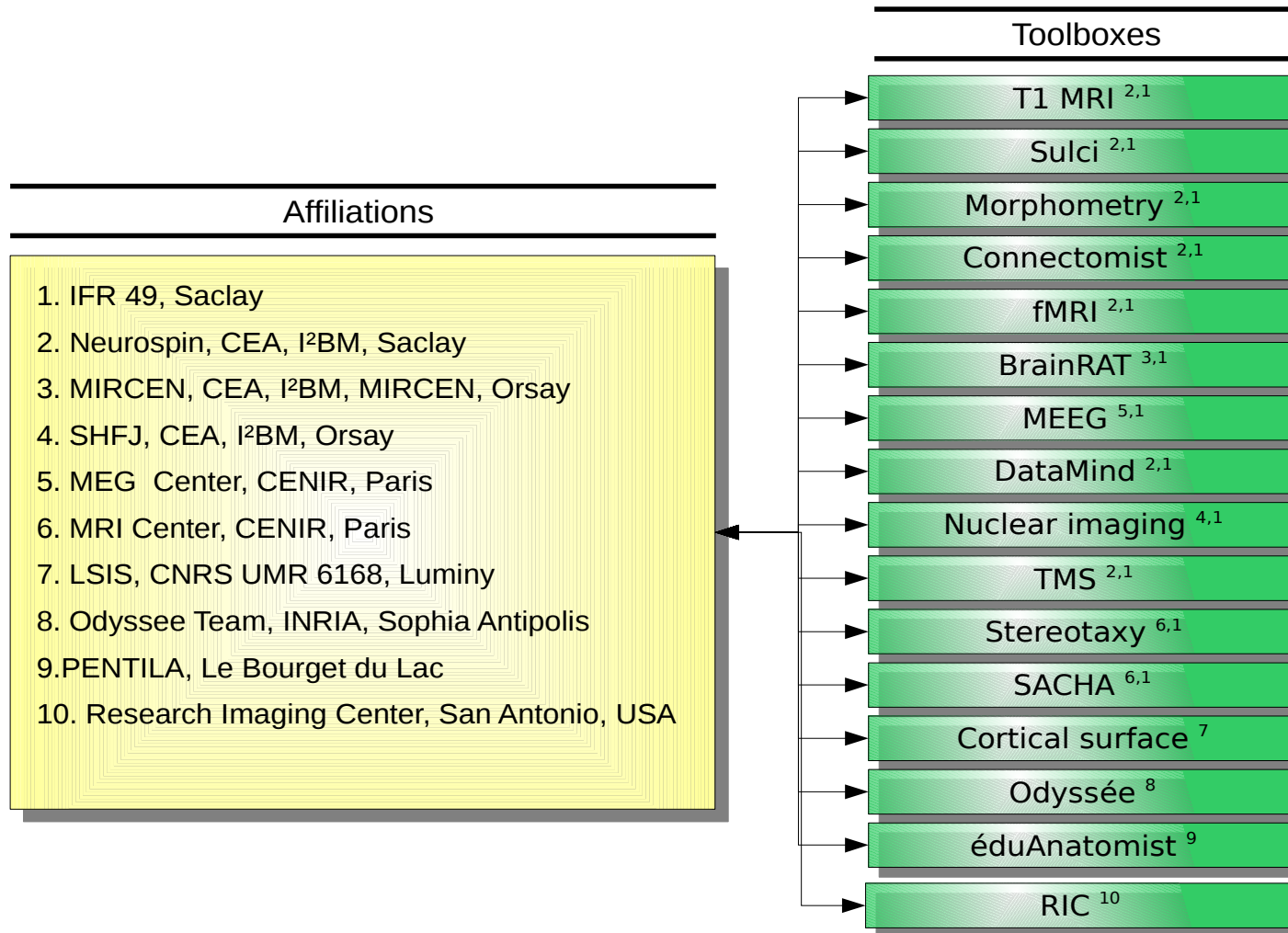
**Python API** enables to write scripts to handle data (volume, mesh, texture, graph...)



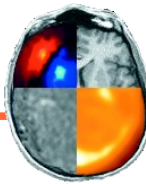
# BrainVISA toolboxes



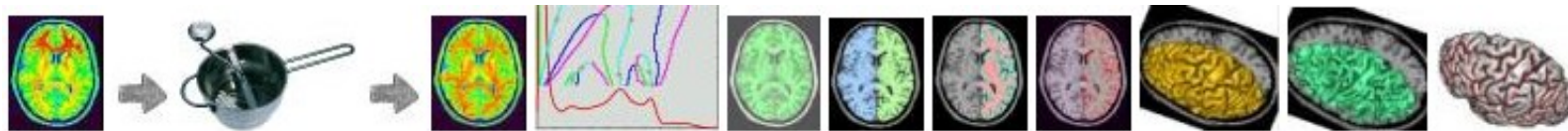
- Currently, there are 16 application toolboxes among which 12 are developed by IFR49 teams.



# T1 MRI, Sulci and Morphometry

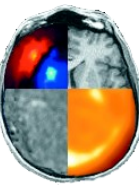


- First tools developed in BrainVISA
- Anatomical T1 MRI processing  
*T1MRI -> Segmentation Pipeline -> **T1 Pipeline 2007***
  - Cortex and white matter segmentation
  - hemispheres and cerebellum separation
  - meshes building
  - cortical sulci segmentation
  - automatic identification of cortical sulci

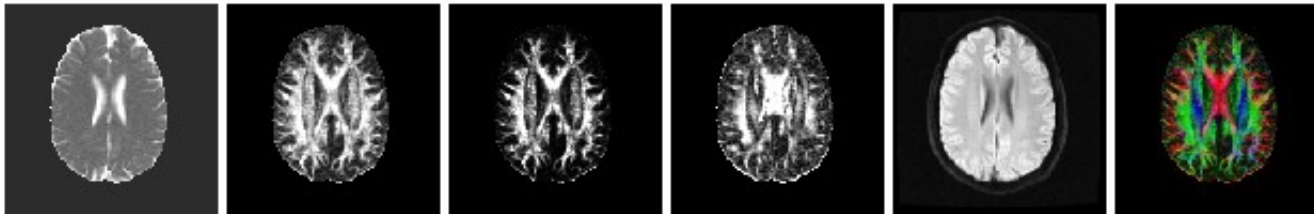


- **Sulci** toolbox : sulci recognition processes, recognition models creation tools (to learn a model from a database of manually identified brains)
- **Morphometry** toolbox : measurements on identified sulci or named ROIs (size, length, depth, barycenter position, orientation...)

# Diffusion and Tracking

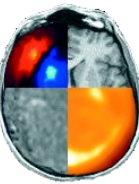


- DWI data processing :
  - Echoplanar distortions correction
  - Diffusion model creation (DTI or Q-Ball)
  - Diffusion maps (ADC, FA, VR...)
  - Fibers tracking and reconstruction
  - Analysis of white matter fibers
- 2 main pipelines :
  - Diffusion model pipeline

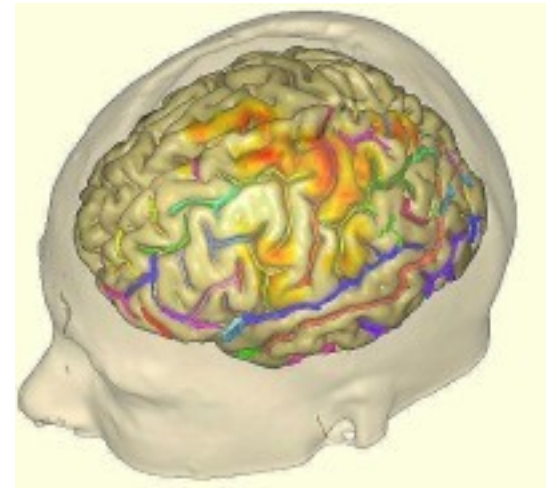
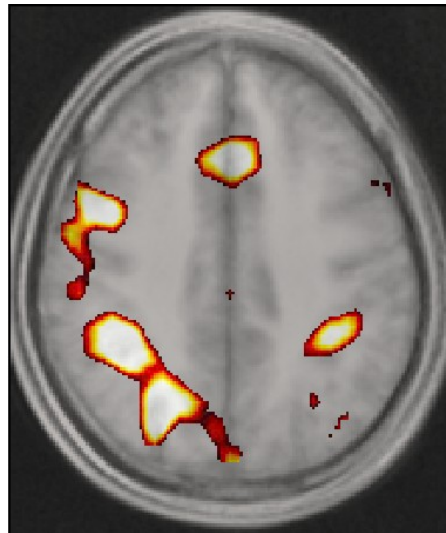


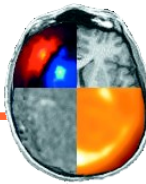
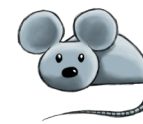
- Fascicles Tracking Pipeline



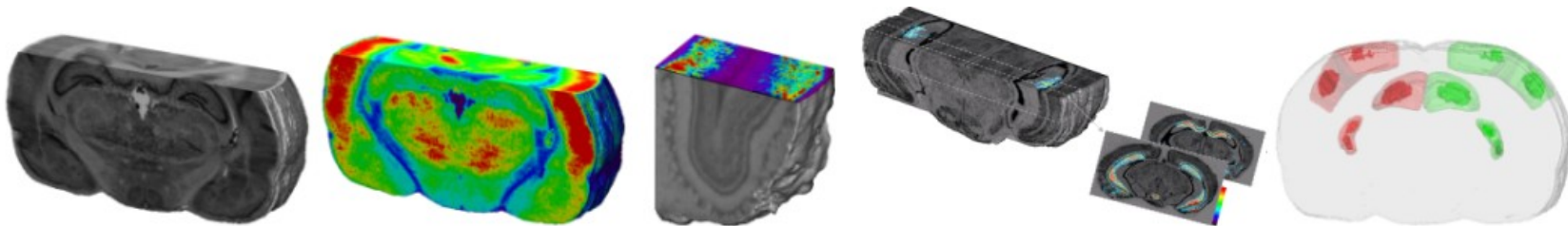


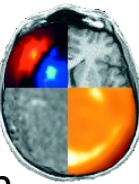
- Aim : to ease neuroimaging studies involving both structural and functional modalities and/or large cohorts, for which automated database management is critical.
- Original algorithms developed at Neurospin/LNAO, INRIA Saclay/Parietal and partners to do univariate analyses a la SPM and less conventional multivariate analyses.
- Features
  - Pre-processing using SPM or FSL
  - First level analysis (intra-subject)
  - Group analysis (inter-subject)
  - Advanced visualization tools using Anatomist





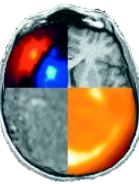
- Aim : Process histological and autoradiographic sections (rodents and monkeys) using 3D information.
- BrainRAT results from collaborative work of image processing methodologists and biologists of MIR Cen.
- Features :
  - optimized digitization
  - 3D reconstruction of volume based on a reliable registration method
  - analysis





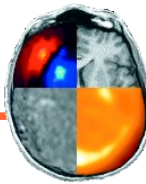
- **Cortical surface:** processing surface-based data. Developed by researchers from the LSIS lab (Marseille).
  - build a coordinate system constrained by sulci on a cortical surface
  - tools for morphometric study of cortical sulci surfaces
  - Surface-based functional data processing
- **Datamind:** analysing features over multidimensional arrays. Classification, data mining...
- **Nuclear Imaging:** processing of Positron Emission Tomography images. Developed in the SHFJ.
- **TMS:** Transcranial magnetic stimulation toolbox provides tools helping positioning a stimulation target in a subject specific referential.
- **Tools:** internal toolbox containing common image processing tools like thresholding, resampling, linear combination, conversion...

# External toolboxes

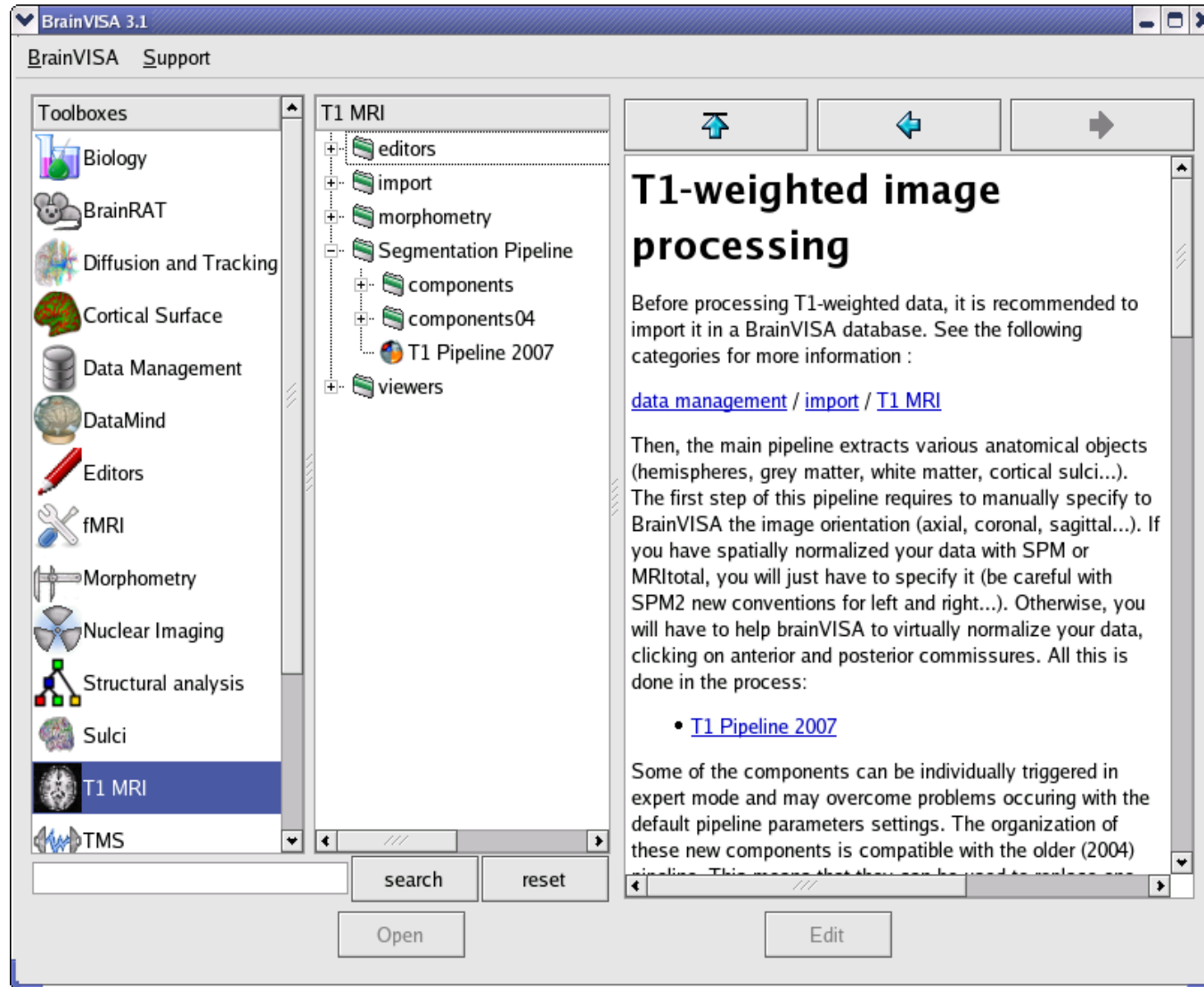


- **MEEG**: MEG / EEG signals processing. Developed on the MEG/EEG Salpêtrière platform, by the LENA lab. Source localization, visualization and statistical analysis.  
<http://cogimage.dsi.cnrs.fr/logiciels/index.htm>
- **Stereotaxy**: help electrode implantation surgery planning by computing stereotaxic coordinates for a target in the brain. Developed in the Pitié-Salpêtrière hospital.
- **SACHA**: automatic segmentation of the hippocampus and the amygdala from clinical MRI scans.
- **Odysée**: visualization and analysis of diffusion MRI data. Developed at INRIA Sophia Antipolis.
- **RIC**: processes to compute cortical thickness maps, gyrification index, sulcal length and depth, and also NIFTI and NEMA formats converters. Developed by P. Kochunov (Health Science Center at University of Texas).  
<http://ric.uthscsa.edu/personalpages/petr/genetics.html>

# Starting with BrainVISA



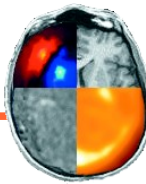
- Run the program by typing *brainvisa* in a terminal
- Processes organized by toolbox



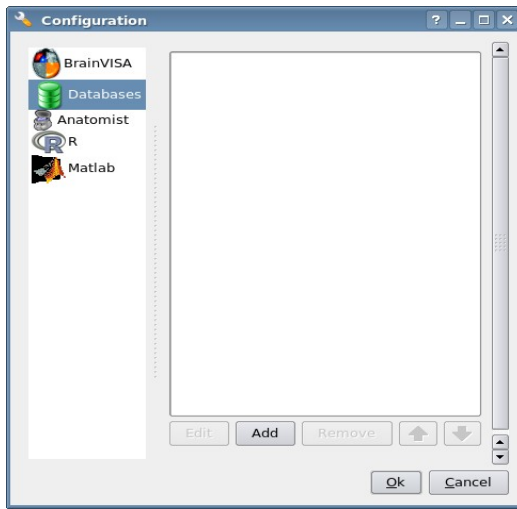
Graphical user interface



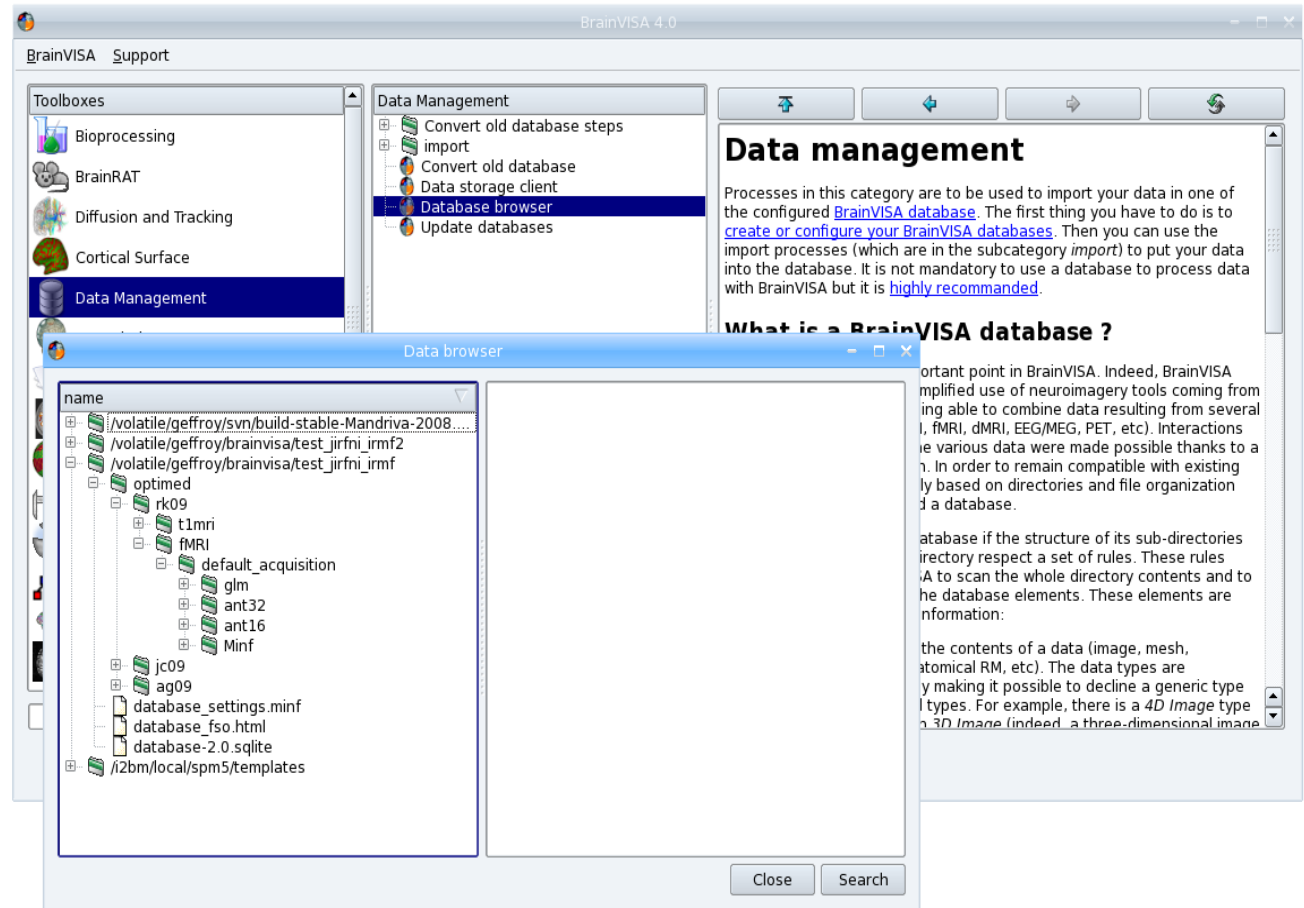
# First step : define a database



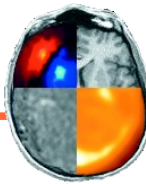
- A directory where all data written by BrainVISA will be stored.
- BrainVISA database is organized to store information in addition to the data files : protocol, subject, modality, acquisition, analysis...
- Data management toolbox : visualization, update, conversion, importation




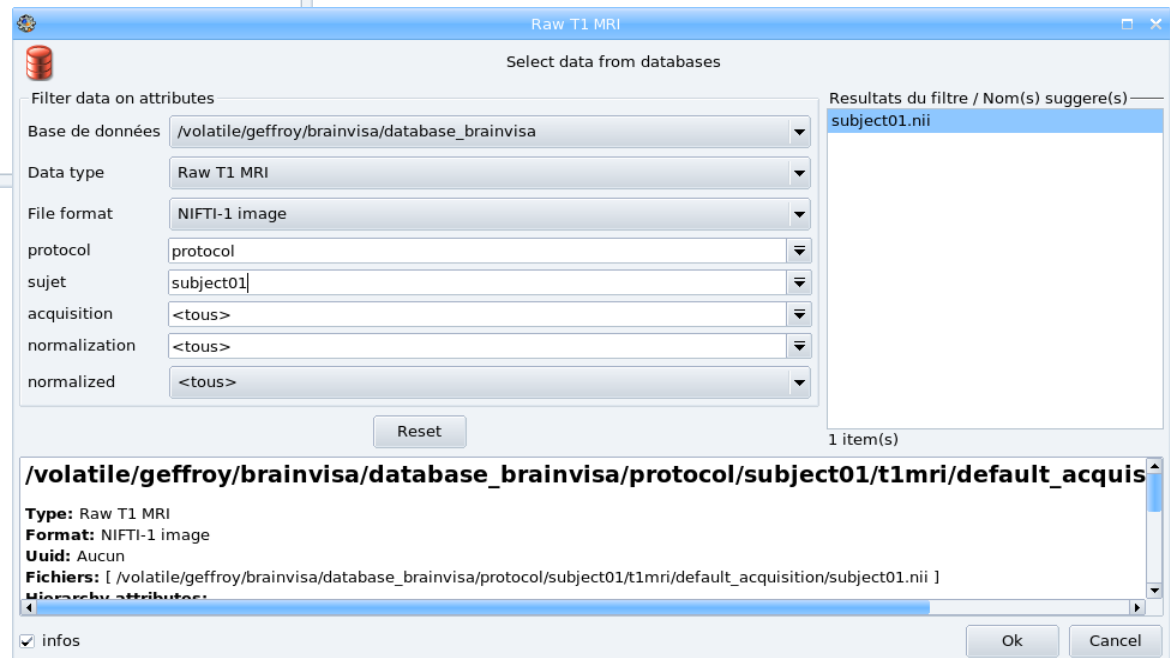
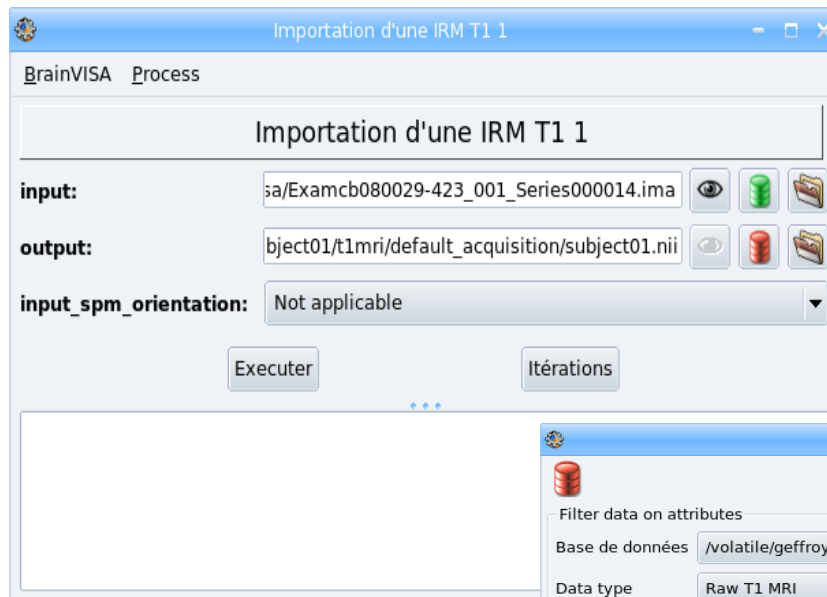
Menu BrainVISA ->  
Preferences -> Databases -> Add



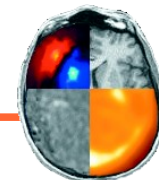
# Second step : Import data





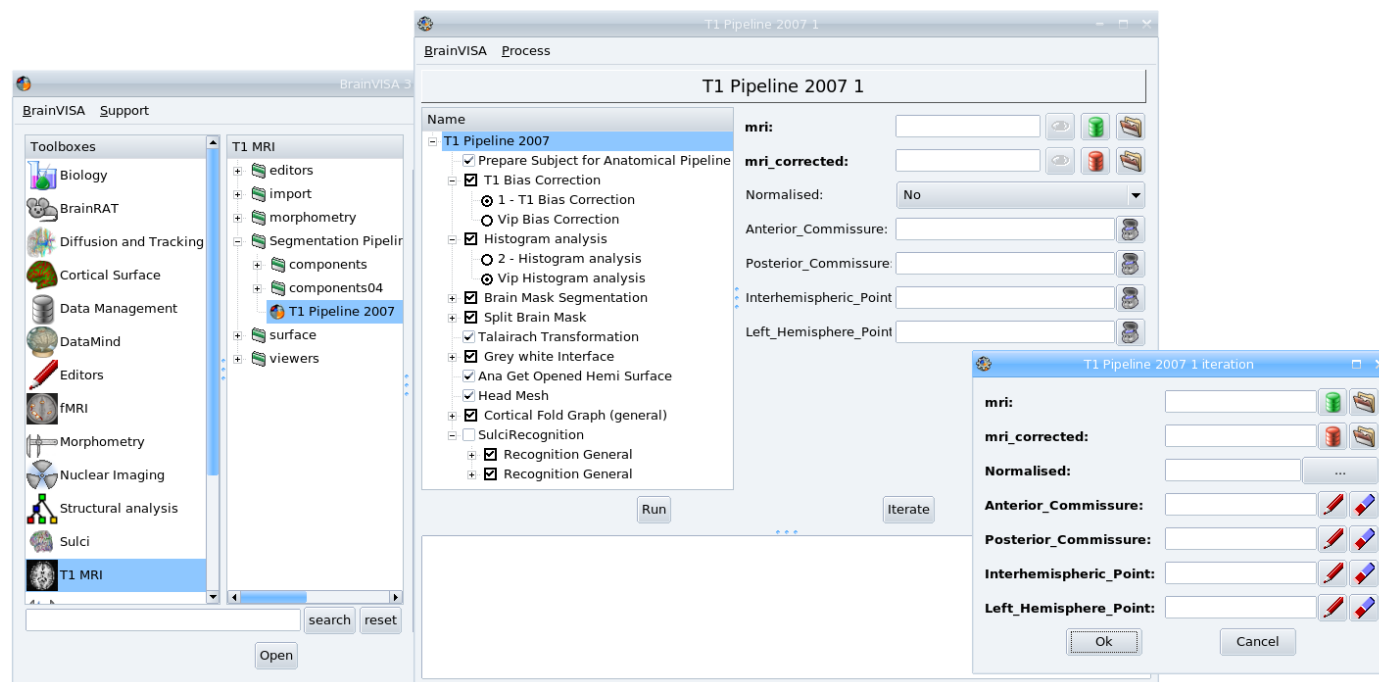
- Import data to process in your BrainVISA database : you enter information about data with BrainVISA copy it in the database. 
- Different **importation processes** exist according the type of data (T1 MRI, Diffusion MRI, fMRI...)



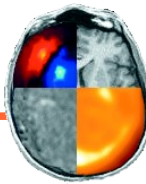
# Process data



- Select a process and open it (double click or open button)
- Enter input parameters by selecting them in the database using the button 
- BrainVISA automatically complete as many parameters as possible. Output data will be written in the database.
- Data visualization with 
- Iteration of a process on several data.
- Execution log : Menu BrainVISA -> Show log
- Pipeline : set of processes (serie, choices)




# Documentation & Help



- Documentation and forum on the website : <http://brainvisa.info/>

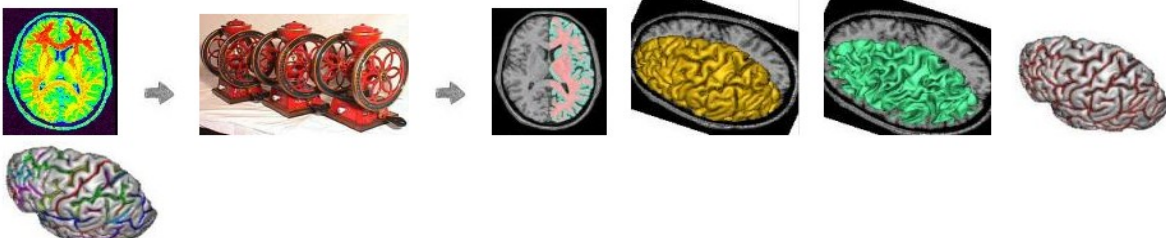
The screenshot shows a web browser window with the title "BrainVISA/Anatomist Home Page - Konqueror". The address bar shows "http://brainvisa.info/". The page content includes a navigation menu with links for CONTRIBUTORS, NEWS, TOOLBOXES, DOWNLOAD, DOCUMENTATION, PUBLICATIONS, and SUPPORT. A cartoon brain character is on the left. The main text area contains news items and a description of BrainVISA as a software image processing factory. Below the text is a sequence of images showing the processing pipeline from raw MR data to 3D brain renderings. A final paragraph describes the Anatomist visualization software.

**BrainVISA / Anatomist**  
(français )

**CONTRIBUTORS**   **NEWS**   **TOOLBOXES**   **DOWNLOAD**   **DOCUMENTATION**   **PUBLICATIONS**   **SUPPORT**

- ▶ **New:** (05/11/2009) BrainVISA/Anatomist version 3.2.0 is available.
- ▶ **New:** (25/11/2009) fMRI toolbox version 3.2.0 is available.
- ▶ *BrainVISA* is a software, which embodies an image processing factory. A simple control panel allows the user to trigger some sequences of treatments on series of images. These treatments are performed by calls to command lines provided by different laboratories. These command lines, hence, are the building blocks on which are built the assembly lines of the factory.

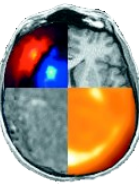
*BrainVISA* is distributed with a toolbox of building blocks dedicated to the segmentation of T1-weighted MR images. The product of the main assembly line made up from this toolbox is the following: grey/white classification for Voxel Based Morphometry, Meshes of each hemisphere surface for visualization purpose, Spherical meshes of each hemisphere white matter surface, a graph of the cortical folds, a labeling of the cortical folds according to a nomenclature of the main sulci:



A glimpse of the package content is proposed in *BrainVISA* help pages.  
[About BrainVISA.](#)

- ▶ *Anatomist* is a visualization software, which main originality is a generic module dedicated to structural data, namely sets of objects linked one another into a graph structure. These objects may be cortical folds inferred from T1 weighted MR data, fiber bundles inferred from MR diffusion weighted data, activated clusters inferred from Statistical Parametric Maps, etc... This module includes a nomenclature control panel, which can drive several brains simultaneously. *Anatomist* provides also some tools to easily map Statistical Parametric Maps on 3D renderings of the brain, inflated meshes of the cortical surface, etc... Finally, a manual drawing toolbox can be used for various purpose.

# Installation



- Steps to install:
  - Download an archive according to the system on:  
<http://brainvisa.info/downloadpage.html>
  - Uncompress the file
  - Go into the created directory
  - Run the executable « BrainVISA »
- Installation instructions available in a README file
- Visualization problems can occur on some computers because of the 3D graphical card. Solutions can be found on the forum.

<http://brainvisa.info/forum/viewtopic.php?f=6&t=1131&p=3880>