

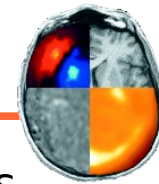
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# BrainVISA advanced Training Introduction

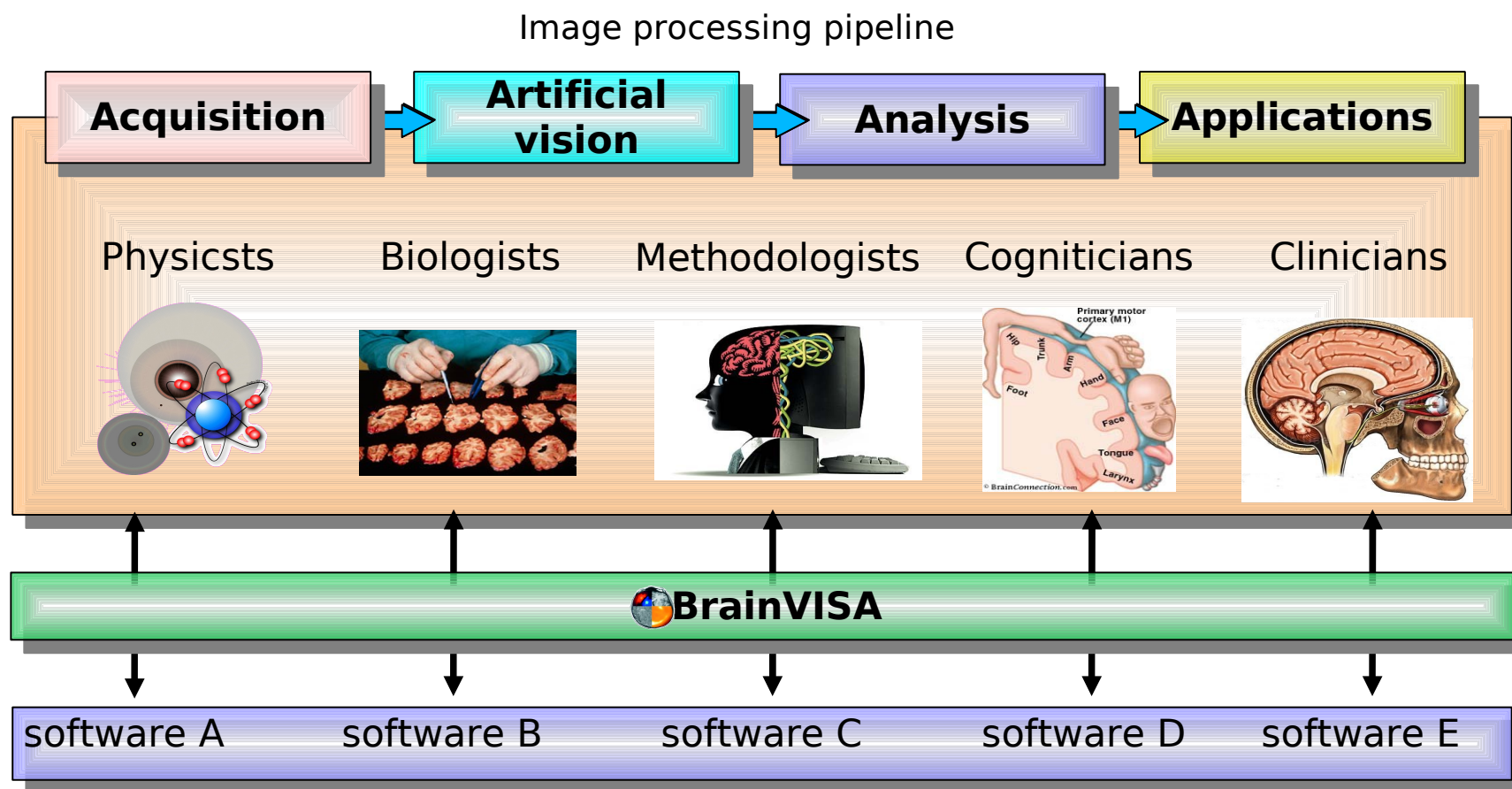
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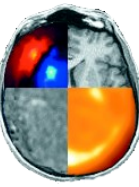


# What is BrainVISA ?



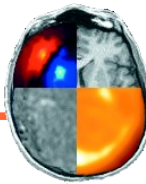
- Modular and customizable software platform built to host heterogeneous tools dedicated to neuroimaging research
- **Aim : help sharing neuroimaging data and processing tools.**
- Free and open-source software -> extensible





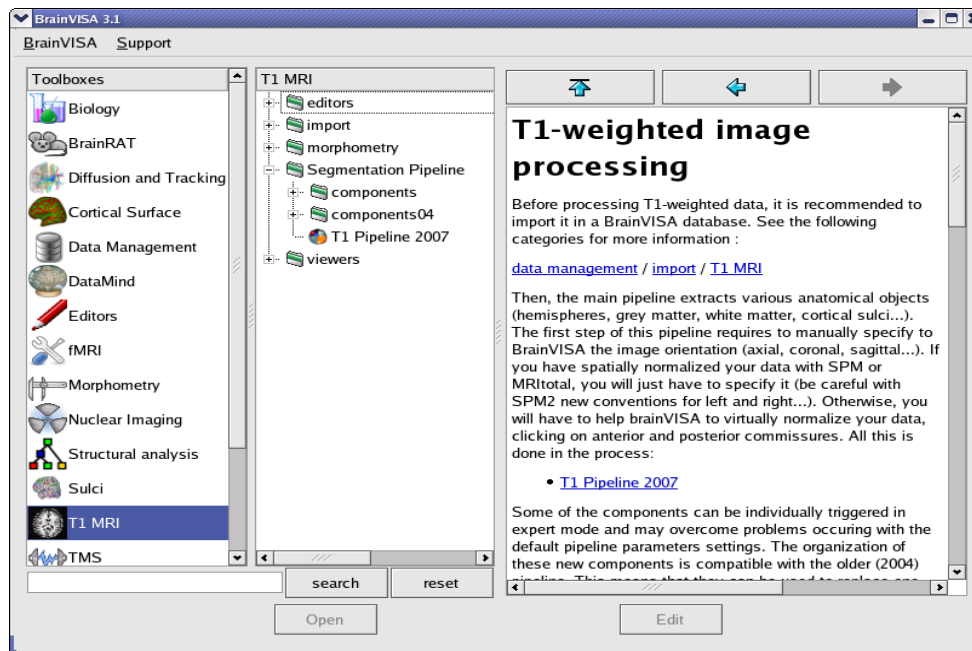
- Overview of BrainVISA package
  - Anatomist
  - BrainVISA
  - Command lines
- BrainVISA toolboxes
- Starting with BrainVISA
- Documentation & Help
- Installation
- Exercises

# Overview of BrainVISA package

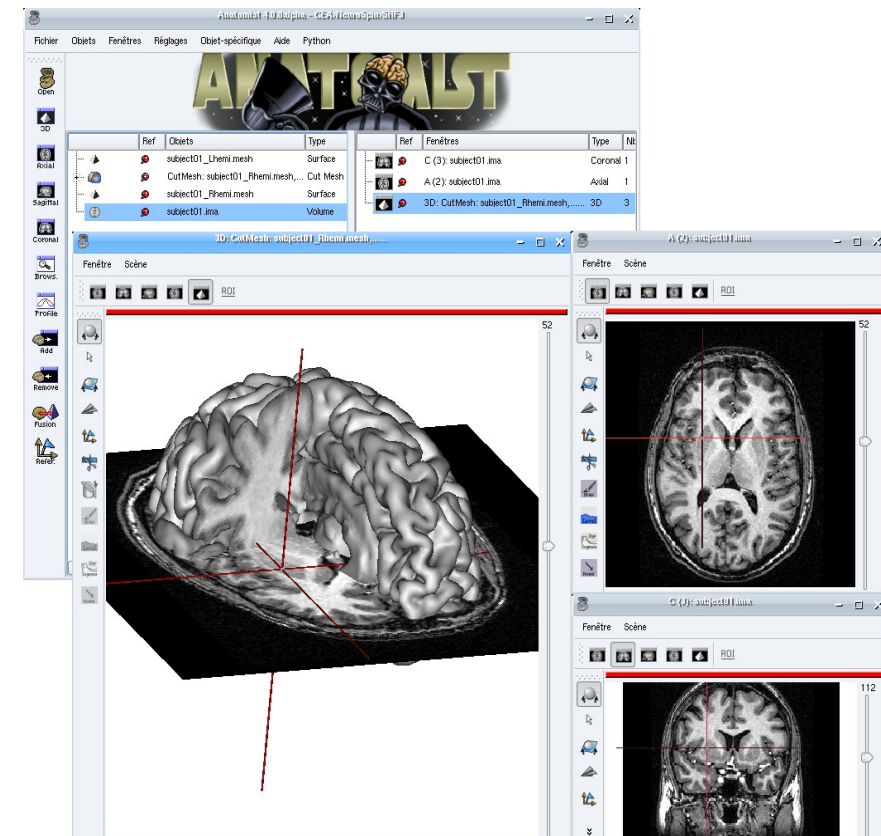


Available for free download on <http://brainvisa.info>

Linux, Windows XP, and MacOS versions



**BrainVISA**

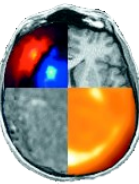


**Anatomist**

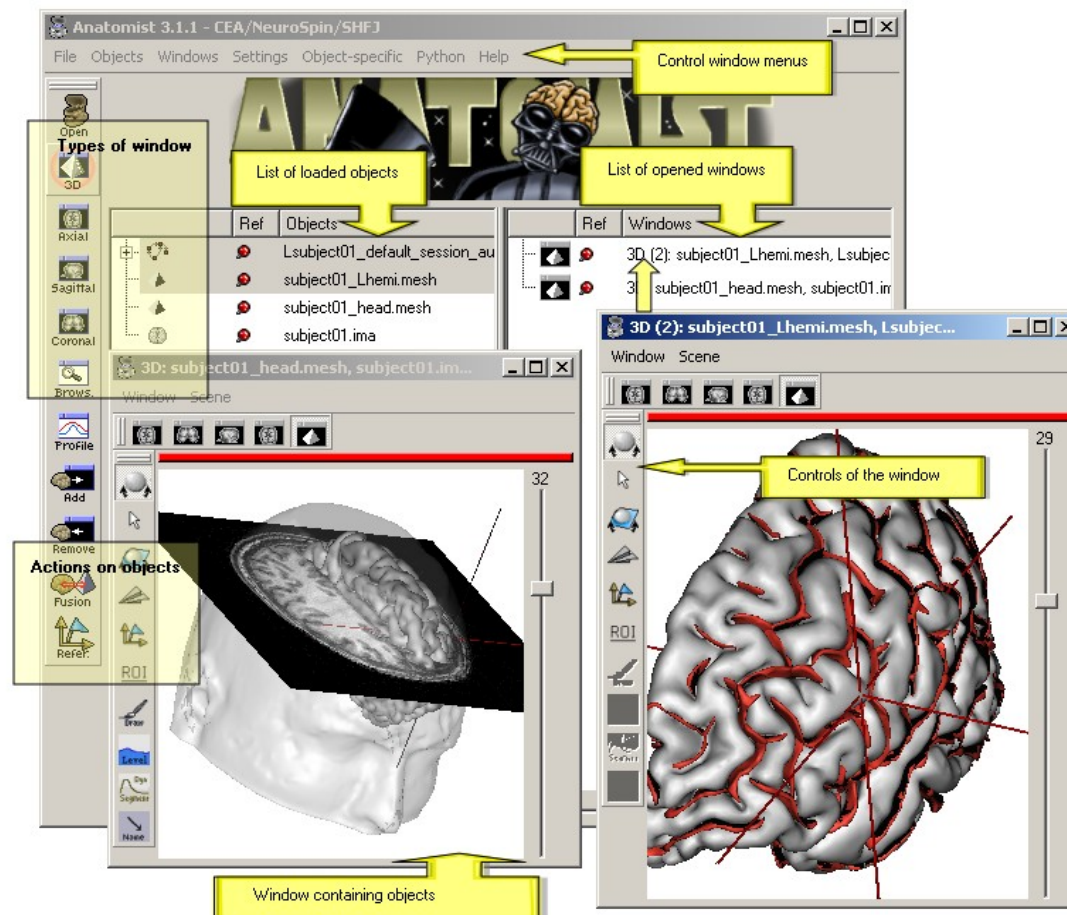
## Aims Commands

```
$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

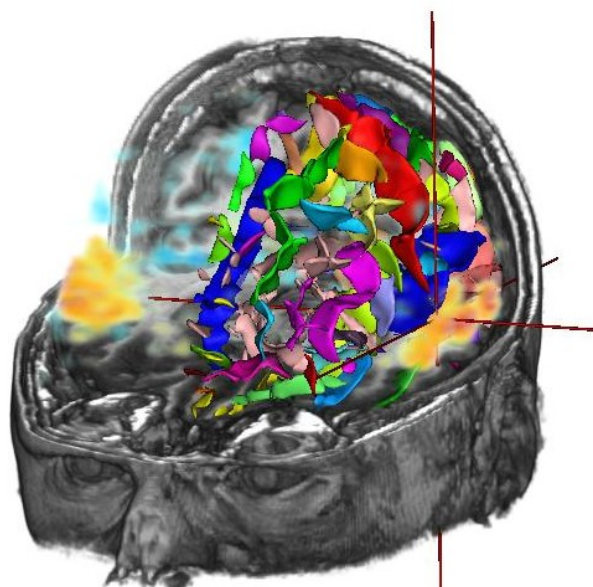
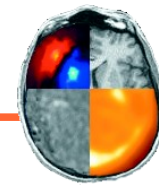


- Visualization of several types of objects : image, volume (3D, 4D), mesh, graph (sulci, ROI)
- Management of coordinate systems and transformations
- Possibility of building complex 3D scenes with several objects (merging, superimposing...).
- A lot of tools : color palettes, region of interest module,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

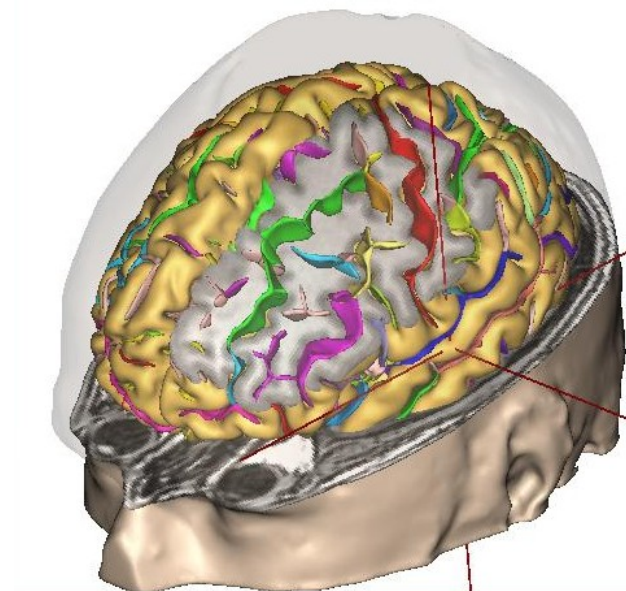




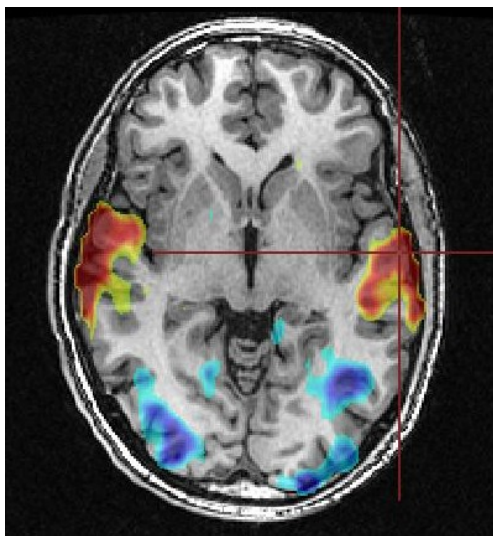
# Anatomist features



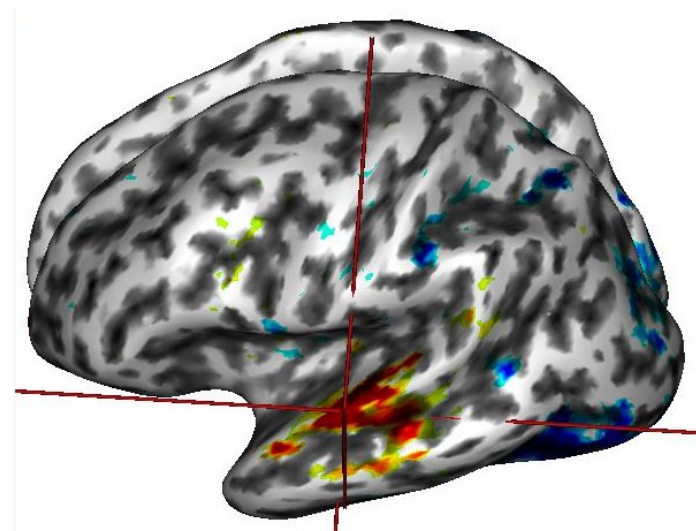
Volume rendering



Cut mesh

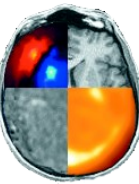


2D fusion

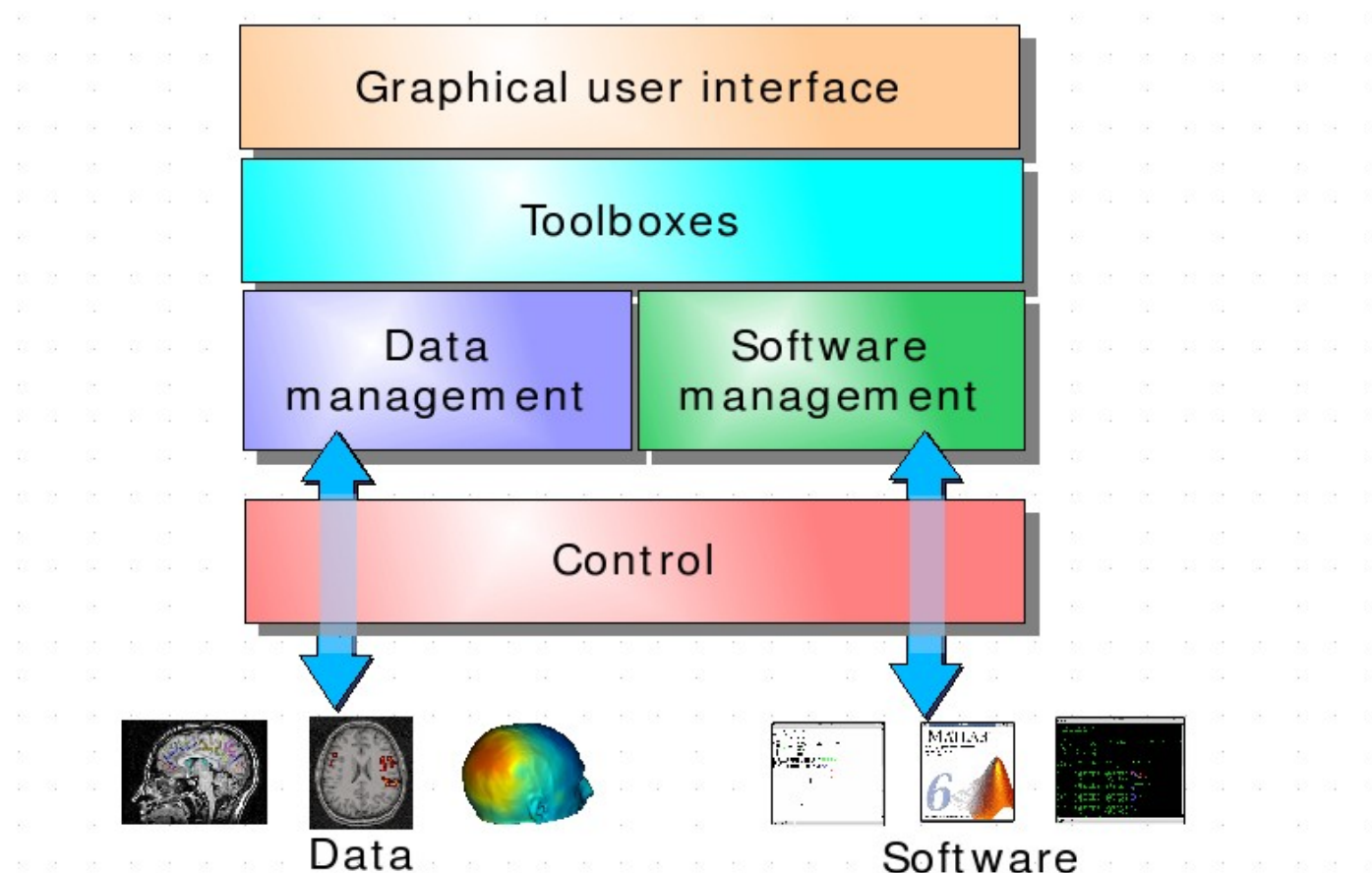


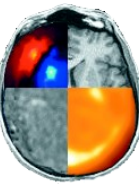
3D fusion

# 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





## 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

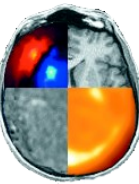
List of all commands on brainvisa website

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

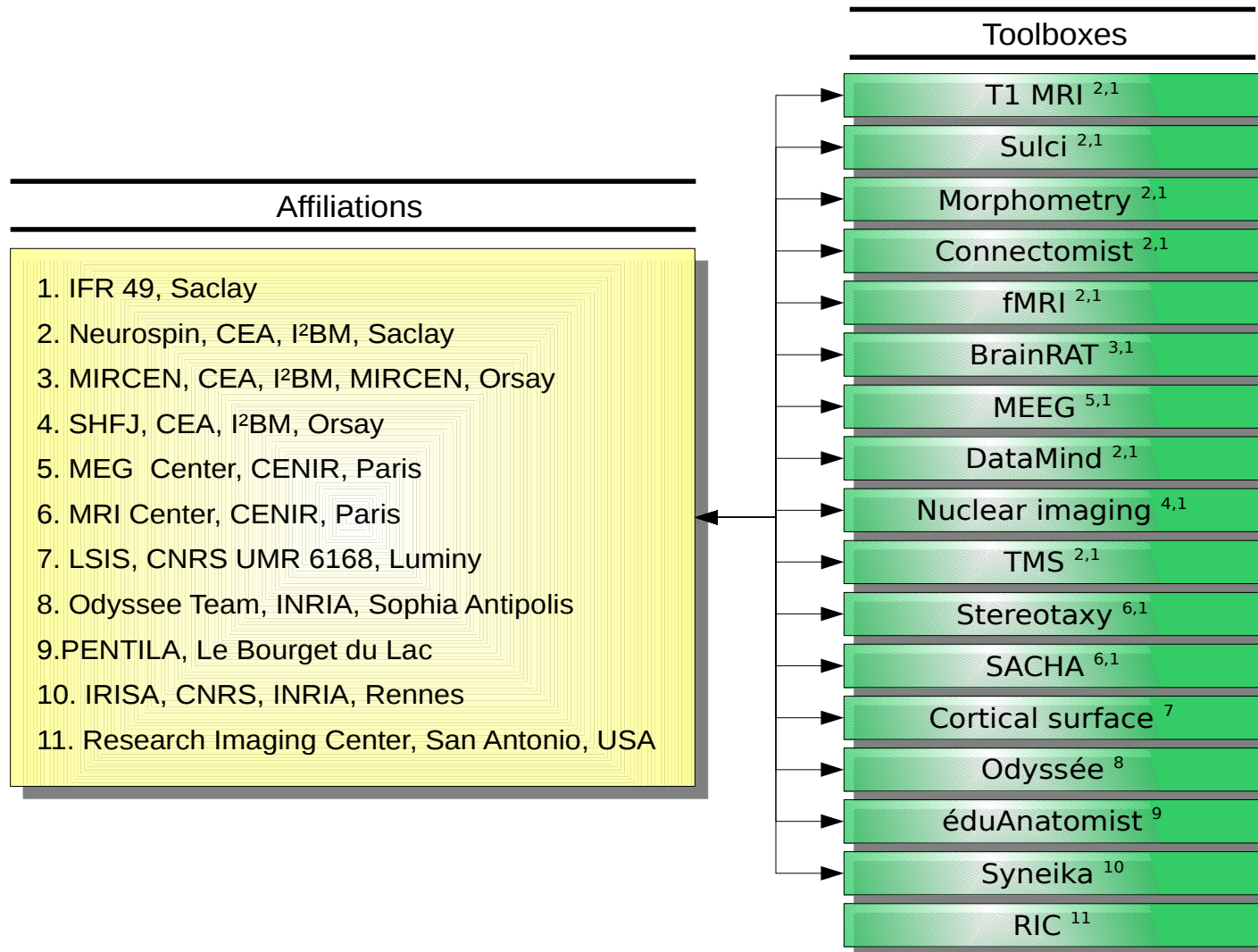
**Python API** enables to write scripts to handle data (volume, mesh, texture, graph...)



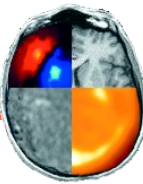
# BrainVISA toolboxes



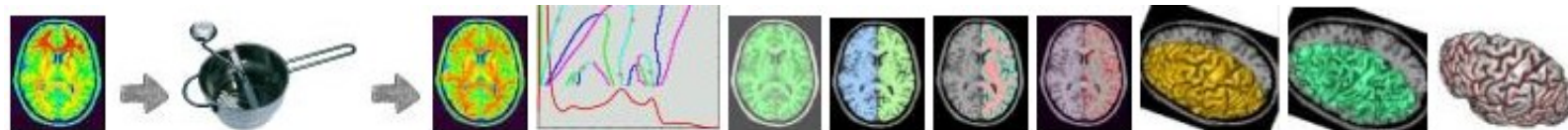
- Currently, there are 17 application toolboxes among which 12 are developed by IFR49 teams.



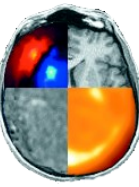
# T1 MRI, Sulci and Morphometry



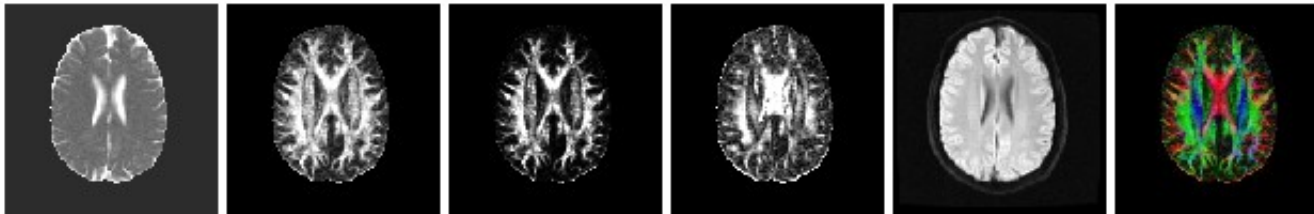
- First tools developed in BrainVISA
- Anatomical T1 MRI processing  
*T1MRI -> Segmentation Pipeline -> **T1 Pipeline 2007***
  - Cortex and white matter segmentation
  - hemispheres and cerebellum separation
  - meshes building
  - cortical sulci segmentation
  - automatic identification of cortical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

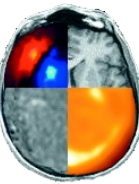


- DWI data processing :
  - Echoplanar distortions correction
  - Diffusion model creation (DTI or Q-Ball)
  - Diffusion maps (ADC, FA, VR...)
  - Fibers tracking and reconstruction
  - Analysis of white matter fibers
- 2 main pipelines :
  - Diffusion model pipeline

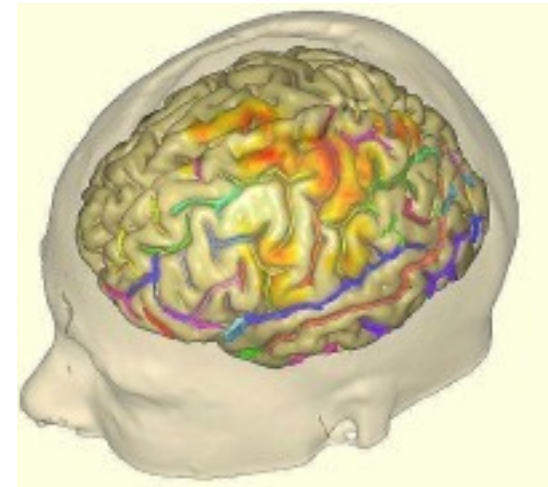
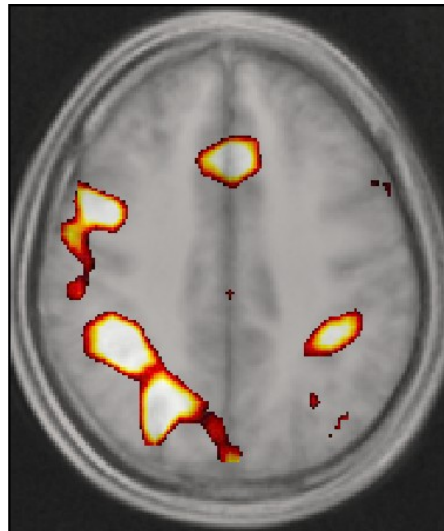


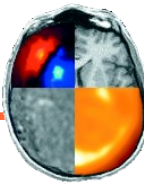
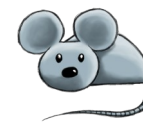
- Fascicles Tracking Pipeline



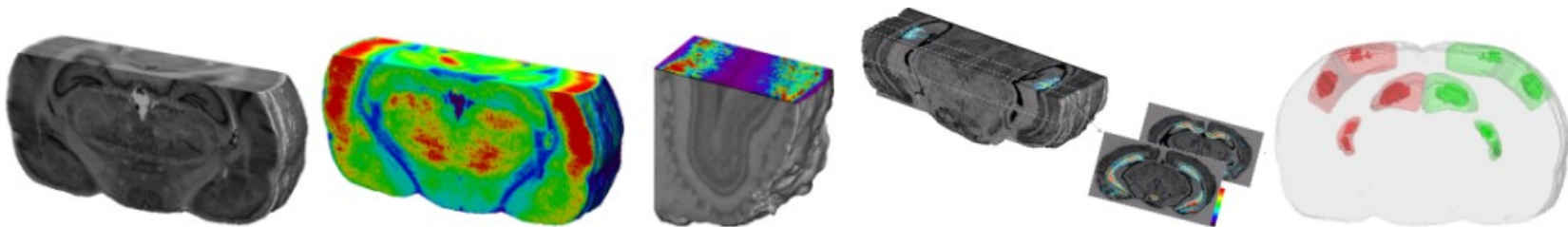


- Aim : to ease neuroimaging studies involving both structural and functional modalities and/or large cohorts, for which automated database management is critical.
- Original algorithms developed at Neurospin/LNAO, INRIA Saclay/Parietal and partners to do univariate analyses a la SPM and less conventional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

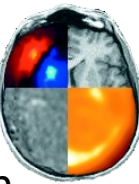




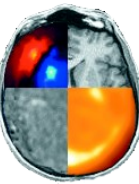
- Aim : Process histological and autoradiographic sections (rodents and monkeys) using 3D information.
- BrainRAT results from collaborative work of image processing methodologists and biologists of MIRCent.
- Features :
  - optimized digitization
  - 3D reconstruction of volume based on a reliable registration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





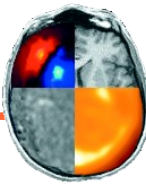


- **Cortical surface:** processing surface-based data. Developed by researchers from the LSIS lab (Marseille).
  - build a coordinate system constrained by sulci on a cortical surface
  - tools for morphometric study of cortical sulci surfaces
  - Surface-based functional data processing
- **Datamind:** 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...

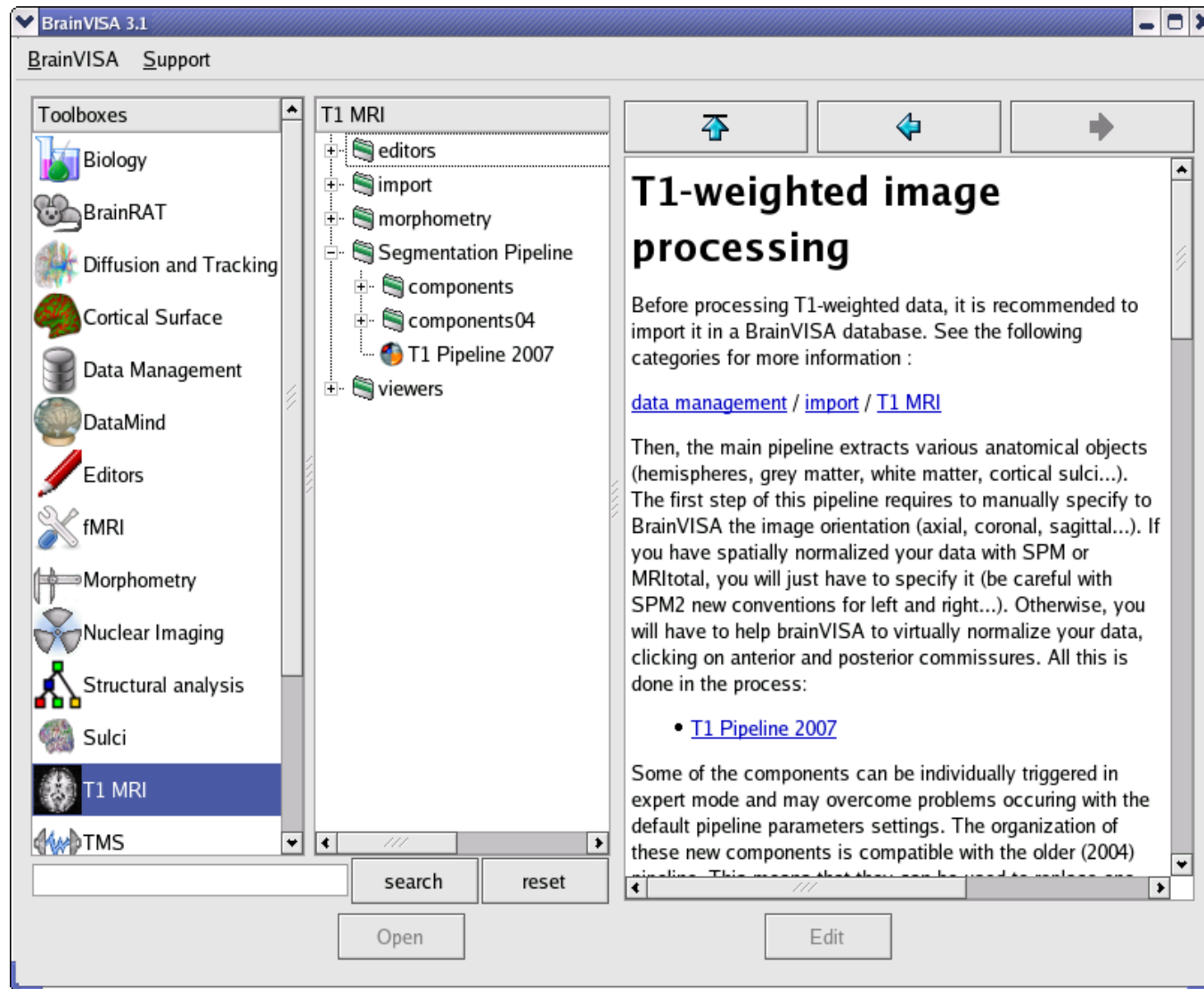


- **MEEG**: MEG / EEG signals processing. Developed on the MEG/EEG Salpêtrière platform, by the LENA lab. Source localization, visualization and statistical analysis.  
<http://cogimage.dsi.cnrs.fr/logiciels/index.htm>
- **Stereotaxy**: help electrode implantation surgery planning by computing stereotaxic 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.
- **Odyssée**: 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

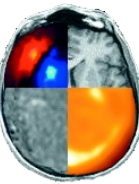


- Run the program by typing *brainvisa* in a terminal
- Processes organized by toolbox

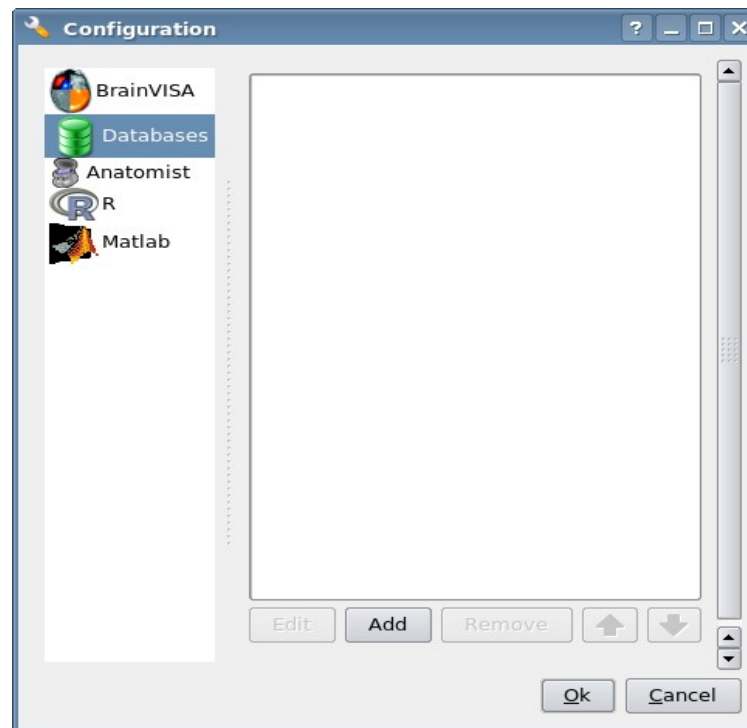


Graphical user interface

# First step : define a database

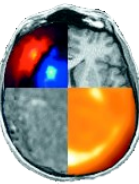



- A directory where all data written by BrainVISA will be stored.
- BrainVISA database is organized to store information in addition to the data files : protocol, subject, modality, acquisition, analysis...
- Data management toolbox : visualization, update, conversion, importation

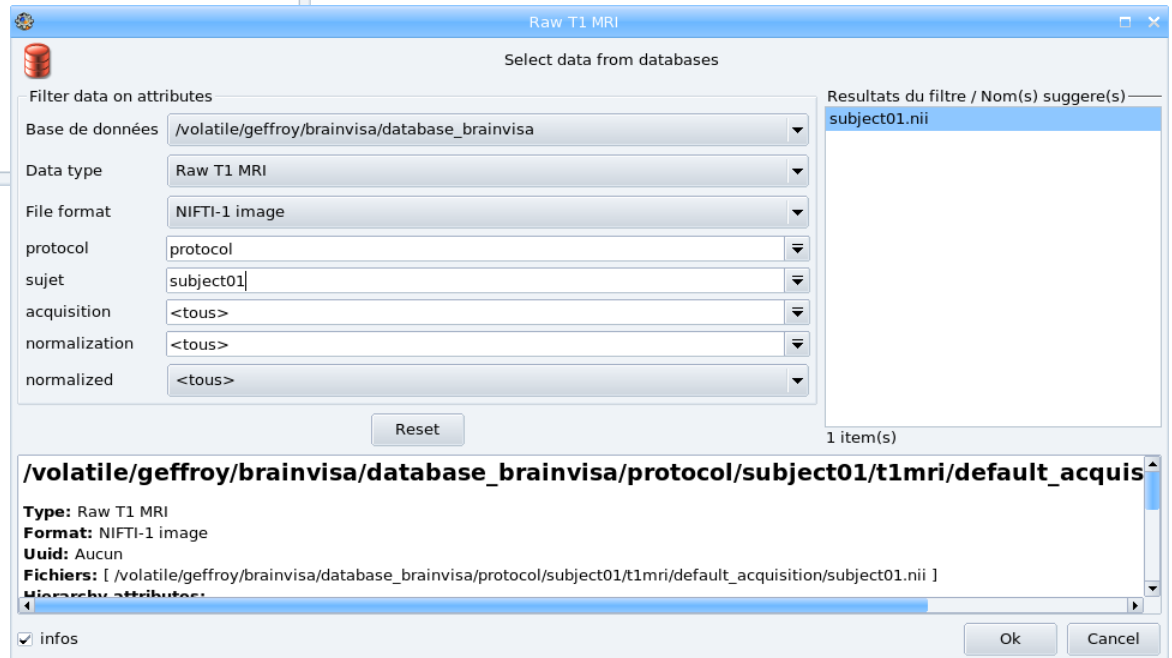
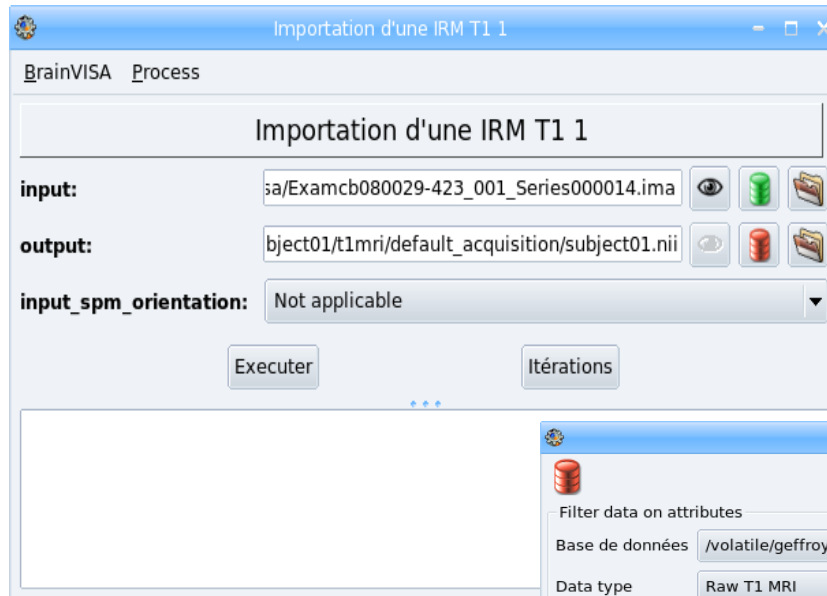


*Menu BrainVISA -> Preferences -> Databases -> Add*

# Second step : Import data

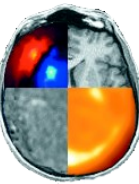




- Import data to process in your BrainVISA database : you enter information about data with BrainVISA copy it in the database. 
- Different **importation processes** exist according the type of data (T1 MRI, Diffusion MRI, fMRI...)

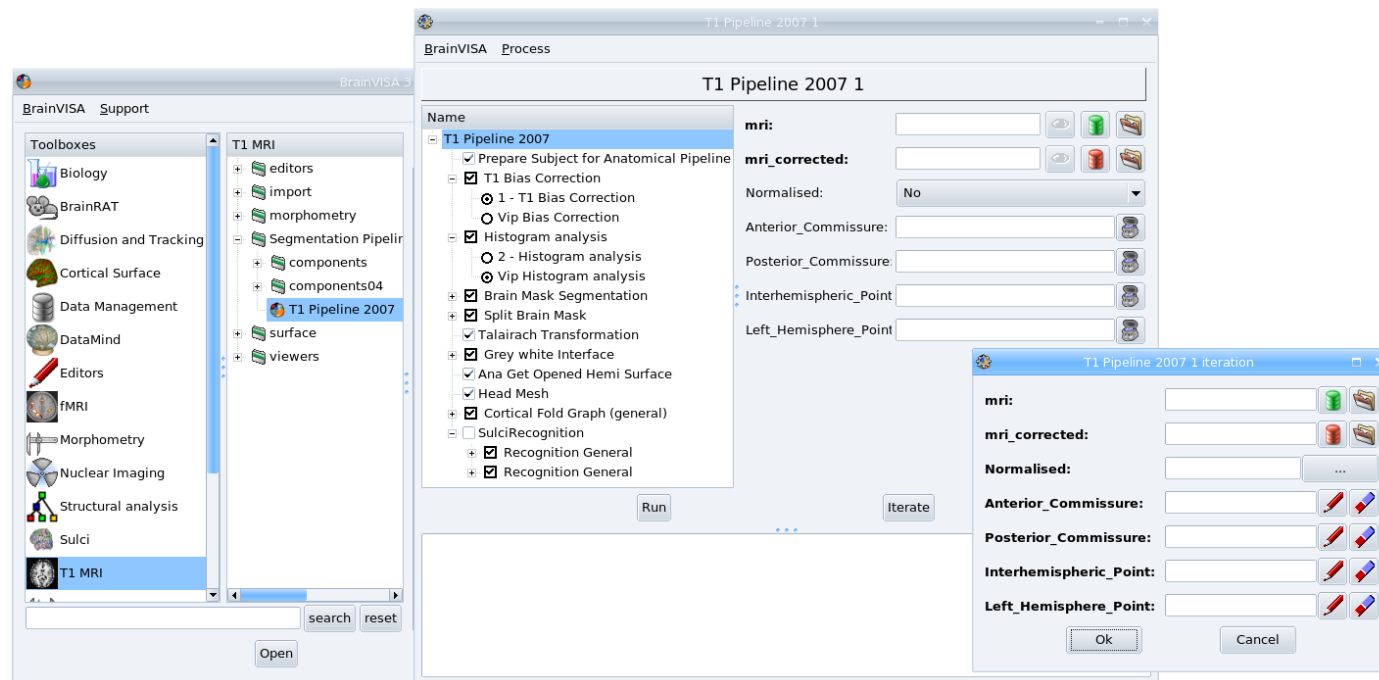


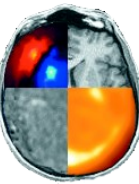


# Process data

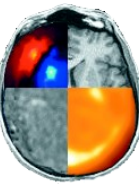


- Select a process and open it (double click or open button)
- Enter input parameters by selecting them in the database using the button 
- BrainVISA automatically complete as many parameters as possible. Output data will be written in the database.
- Data visualization with 
- Iteration of a process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





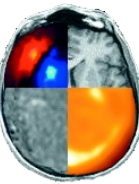
- Manuals and tutorials available on BrainVISA website :  
<http://brainvisa.info/documentation.html>
- Document of the JIRFNI 2008 training course about Anatomist and BrainVISA with associated data.  
[http://brainvisa.info/doc/jirfni\\_bv-2008/jirfni\\_bv\\_training/fr/html/index.html](http://brainvisa.info/doc/jirfni_bv-2008/jirfni_bv_training/fr/html/index.html)  
<http://brainvisa.info/downloadpage.html#data>
- Inline BrainVISA documentation about toolboxes and processes in the right panel of BrainVISA main window
- Forum to ask questions : <http://brainvisa.info/forum/>



- Steps to install:
  - Download an archive according to the system on:  
<http://brainvisa.info/downloadpage.html>
  - Uncompress the file
  - Go into the created directory
  - Execute the setup file
  - 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>

# Exercise



- Run BrainVISA

/tsi/medikit/tp-data/brainvisa/BrainVISA

- Create a new empty database in

/scratch/<login>/<databaseName>

- Import a Raw T1 MRI

/tsi/medikit/tp-data/brainvisa/data\_unprocessed/sujet01/anatomy/sujet01.ima

- Browse the database with the DatabaseBrowser process.

- Visualize data.

- Anatomist tutorial : [http://brainvisa.info/doc/anatomist-3.2/ana\\_training/en/html/index.html](http://brainvisa.info/doc/anatomist-3.2/ana_training/en/html/index.html)