BrainVISA: a complete software platform for neuroimaging

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BrainVISA is a modular and customizable software platform built to host heterogeneous tools dedicated to neuroimaging research. It aims at helping researchers in developing new neuroimaging tools, sharing data and distributing their software. It is developped by research organizations (mainly CEA, INSERM, INRIA, CNRS) grouped in a federative research institute (IFR 49) founded by the french government. It is a free and open-source software written in Python language and can be downloaded from: **http://brainvisa.info.**

BrainVISA offers numerous features in several domains of neuroimaging software:

Data management

As most neuroimaging software deal with neuroimaging data as files, BrainVISA keeps data files on the filesystem, and is using a database to index them. BrainVISA database system is based on a customizable **ontology** that defines the data types handled by the software, associated key attributes for indexation, and filename patterns to make the link between the filesystem and the database schema. There is a bijection between the files organization and the database which makes it possible to get an input or output file name from data attributes values through a simple database request.

BrainVISA currently uses **SQLite** as a SQL database engine because it is simple, easy to use and does not need any server. Moreover, SQLite can be directly used from the Python language. The database is stored in a single file that can be copied from one computer to another, making sharing databases easier for users.

Workflows and pipelines

BrainVISA offers several neuroimaging processing pipelines. A pipeline is a combination of reusable executable components called *processes*, it groups together several processing steps.

Developping new pipelines for BrainVISA is a matter of writing small scripts in Pyhton (Fig. 1). They may jointly use home-made algorithms, software contained within the core BrainVISA package, or third-party software. Some existing BrainVISA pipelines use for example SPM, FSL, Freesurfer, etc.

Graphical user interface

BrainVISA graphical user interface has been developped with PyQt, the python bindings of the Qt library. A view is automatically generated for each pipeline to allow the user to fill in the parameters. This view is created from a simple python description of the process input and output parameters. It also shows a panel to monitor the execution of the pipeline. Of course, it is possible to customize the default user interface if it does not fit the user needs.

BrainVISA may also work as batch and without graphical interface, to run a specific process or pipeline. This thus allows for instance, batch scripting or parallel distribution, and the use of BrainVISA components from custom software.

Visualization

BrainVISA offers a way to define viewers which may use any visualization software. A viewer is a processes dedicated to the visualization of data of a specific type. Most of BrainVISA existing viewers use **Anatomist,** a powerful software for 3D visualization and manipulation of structured objects. Anatomist, controled through its python API by BrainVISA, provides an interactive visualization, suitable for any kind of data.

Massive computation facilities

In order to ease the processing of large neuroimaging databases, BrainVISA provides a feature to **iterate** a process or a pipeline on whole or part of a database. Input data are selected through a request to the database and all generated results will be written automatically at a suitable location on the filesystem and indexed in the database thanks to the ontology.

Since the 4.1 version, it is also possible to submit BrainVISA pipelines or iterated processes to parallel computing ressources thanks to the **Soma-workflow** software. Soma-workflow is an independent software component of the BrainVISA environment, which provides a homogeneous and single way to submit and monitor parallel computing to various computing resources (laptops, workstation farms, clusters...). See its home page on http://brainvisa.info/soma/soma-workflow/ for more information.

Toolboxes

As BrainVISA is designed to be extensible, it is possible to create a custom toolbox which includes a set of processing tools, an ontology definition, documentation, and any needed software and data. Toolboxes may be distributed as separate add-on packages.

Thus, BrainVISA infrastructure advantages have encouraged several teams to develop their own toolboxes. A lot of neuroimaging tools are already available in **BrainVISA toolboxes**. For example, it is possible to perform automatic segmentation of brain hemispheres and sulci from T1 MR images with **Morphologist** toolbox, automatic sulci identification and object-based morphometry with **Sulci** toolbox, cortical surface geometry analysis and functional data projection with **Cortical Surface** toolbox, diffusion MR images analysis and fiber tracking with **Connectomist**, automated processing of

histological and autoradiographic sections with **BrainRat**, functional MRI data analysis with **fMRI** toolbox, etc.

Conclusion

BrainVISA has now many years of maturity and has been successfully used by various research groups. See http://brainvisa.info/biblio/en/index.html for a list of publications involving BrainVISA. BrainVISA has been chosen by several research centers and collaborative projects as the backbone infrastructure for data management, neuroimaging tools development and software distribution.

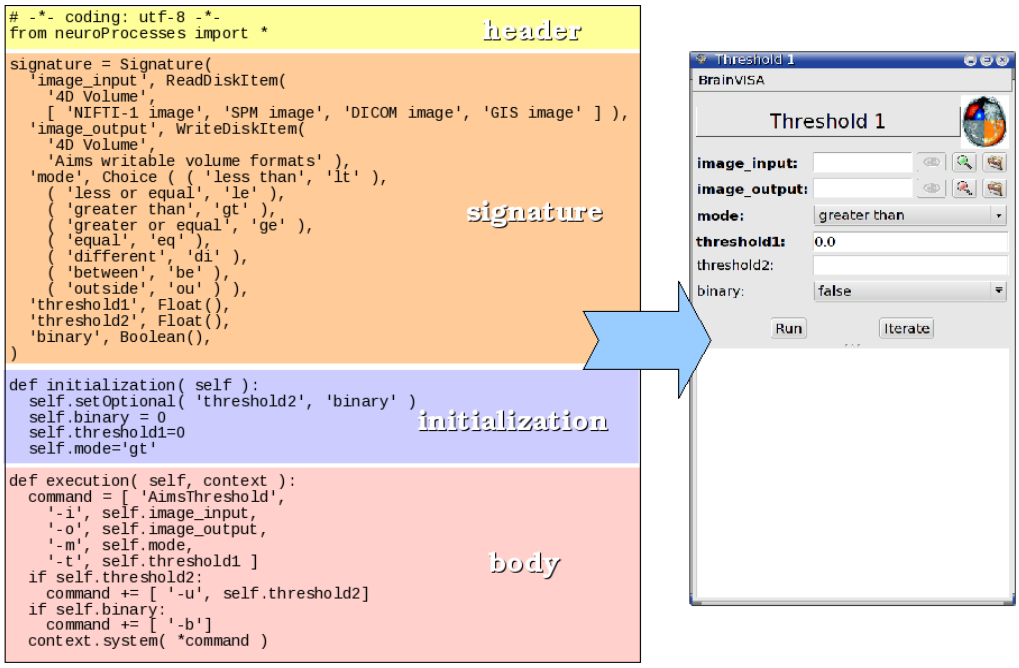

Fig. 1: A simple BrainVISA process: source code and default GUI