BrainVisa release plans and planned evolutions

Version 4.2: january 2012

FEATURES:

- Soma-workflow integration in BrainVisa

- FreeSurfer toolbox:
  Process "Import From FreeSurfer to T1 pipeline" is available at user level 1.
  All other processes are available at user level 2.

- lock files:

  Please to refer   Issue #3427 to read the beginning of the discussion.
   To sum up the short implemenation of locked files, it seems better:

    - to lock at the file level with an empty .lock file
    - the lock don't be transmitted when you copy files

  How to lock/how to unlock files entry in the menu by right-click on the parameter
    - by right-click on the parameter

  Lock action:
  When you press "run" to launch a process or a pipeline, BrainVISA must check if data are locked (if there is a .lock). If yes, BrainVISA stops the process.
  When a process launch a command with context.system, BrainVISA must check too.
  context.runProcess and context.system
  But do ALL processes use a context.sytem when they launch a command ?

  Further features:

    - lock all output files of a pipeline or a process
    - add an option in BrainVISA -> preferences : to lock always/never output files

version 4.3: september 1, 2012

- Feature freeze (and svn branches creation): **august 1, 2012**

- Axon:
    - Processing **history management** in databases: (/) **done**
    - GUI: docs viewer is now a "real" web browser: (/) **done**
    - Axon libs can now really be used as standard python libraries: import brainvisa.axon: (/) **done**
    - Anatomist control goes to the "direct" mode, allowing more sophisticated viewers (BV/Anatomist combined interfaces): (/) **done**
    - **reorganization of axon source tree**: files in the "brainvisa" directory should go in the "python" tree. (/) **done**
      Old python modules have been moved to brainvisa.processing, brainvisa.data and brainvisa.configuration sub-modules. Older top-level modules (directly used in processes, such as neuroProcesses) are still reachable directly via a proxy module, which will import from the new location (brainvisa.processing.neuroProcesses for instance). Modules which should not be commonly used from processes (like neuroLog) have been removed from the brainvisa directory.
    - fixes in configuration options (it aborted when a non-existing (or moved away) file was referenced in the config: (/) **done**
    - reusable anatomist windows in Brainvisa: **done** but could be extended to windows blocks: (/) **done**

- Morphologist:
    - Reorganization of the toolbox, now including the sulci and morphometry toolboxes: (/) **done**
    - Greg's **"snapbase"**, large scale snapshot tools

- Anatomist:
    - Replacements for old histogram and profile windows, with more features: (/) **done**
    - "BrainVisa Sulci Atlas" plugin: **may be posponed to release 4.4**
    - some new features in manual sulci splitting: (/) **done**
    - sulci annotations reimplemented in C++, a lot faster now: (/) **done**
    - new fusion modes: (/) **done**

- fibers rendering using shaders light models: (!) delayed, implemented in 4.5

- Aims:
  - AimsRoiFeatures should replace AimsVoiStat: it should thus implement all features of AimsVoiStat (like timesteps features), and make AimsVoiStat issue a deprecation warning

- Soma-workflow:
  - compatibility with Pyside: (/) **done**

- Documentations:

  Document new features: **TO DO**...

Most important features are almost ready.
Still needs:

- testing
- a pass on open bug tickets.
  Please check / confirm / status bugs:
  - anatomist: [#4293](#), [#4264](#)
  - axon: [#4965](#), [#4964](#), [#4528](#), [#4420](#), [#4358](#), [#4303](#), [#4292](#), [#4260](#), [#5068](#), [#2056](#)
  - commuincation / build: #4379 -> delete already done in [#2721](#)
  - brainrat: #3886
  - morphologist: [#4861](#)
  - soma-workflow: [#4608](#)
  - soma-base: [#4107](#), [#2319](#)
  To do sulci: [#1649](#)
  - aims: [#5016](#), [#4744](#), [#5086](#)
  - anatomist: [#5063](#)
  - axon: [#5064](#), [#5065](#)
  - cortical_surface: [#4887](#)
  - development: [#5072](#)

Later, version 4.4? and / or 5.0

Most of the following features have been aborted and postponed. Version 4.4 (released in nov. 2013) was mainly a slight update to 4.3, with limited improvements.

- Drop compatibility with python 2.5: 2.6 or higher must be installed on all systems ((/) done)

- Axon:
  - Pipelining infrastructure will be entirely redesigned ((!) not done)
  - Databasing will be redesigned ((!) not done)
    - Allow remote, multi-user databases, as well as local lightweight databases
    - Overcome concurrent access problems and limitations
    - Allow databases copies and easy data sharing (partially done)
  - More modularization: ((!) not done)
    - pipelining and databasing APIs will be available as independent library modules. "Axon" will just use several components
    - Processes will look more like standard python functions

- Morphologist:
  - More restructuring of the pipeline, allowing better parallelization (partially done in Morphologist 2013)
  - user-friendly interface: Connectomist-style with integrated Anatomist views ((!) not released)
  - Integrating the morphometric stats part ((!) not done)

- Anatomist:
  - ROI toolbox GUI refactoring ((!) not done)
  - New fibers rendering ((/) done for version 4.5)
  - Redesign the referentials/transformations system ((!) not done)
  - Integration of connectivity profiles visualizations (Pauline Roca) ((/) done in Constellation 4.5, but not released yet)
  - Various GUI improvements and visual interactive feedbacks (partly done)

Version 4.5

Target date: july 2015

New web site (currently brainvisa.fr)

- create an account brainvisa
- create 2 directories:

```
~/prod/www
~/testing/www
```

- create 2 directories for repositories and installers

```
~/prod/packages/<release>/<system>/brainvisa-installer
                                    packages
~/testing/packages/...
```

((/) done)
Test site: http://brainvisa.fr:8080

make bug_fix branches

bv_maker correspondance

bv_maker	svn
trunk	trunk

bug_fix	`branches/4.3`
	`         4.2`
	`         bug_fix (= future 4.4)`

tag	`tags/latest_release (= 4.3.1)` `     4.3.0`

The correspondance between bv_maker names and svn/git branches can be setup independently.
We will do so wile setting up the new svn branches bug_fix, so that developers will not be impacted.

make a new script: bv_release, for automatic version / branch change

it will replace bv_create_branch

- The script should deal with svn and git, with a priority for svn, first.
- 2 modes:
  - change trunk -> bug fix branch
  - tag a new release

both modes are similar with small differences.

For svn:

- bug_fix branch:

```
bv_release -i <project(s)>
```

  - move the bug_fix branch to a new numbered version: <tt>bug_fix -> 4.4</tt>
    if the numbered branch already exists ? delete it first ? display an error ? merge it ?
    if bug_fix doesn't exist yet: do nothing ?
  - copy the trunk branch to the (new) bug_fix one
  - increment the version number in trunk sources (project_info.cmake/info.py etc)

- tag a release:

```
bv_release -r <project(s)>
```

- move the latest_release branch/tag to a numbered version: <tt>latest_release -> 4.3.1</tt>
- copy the bug_fix branch to the (new) latest_release one
    (version is not changed) *** questionable ? maybe the version in bug_fix should be incremented (4.3.2) ?

((/) done for svn)

For git, the branch policy has to be defined first.

- git has a master branch, which is generally the "stable" one, corresponding to bug_fix (in svn or bv_maker). this "stable" branch should not include new features.
- we need a development one, equivalent to trunk, but which integrates new features: integration ?

- creating a new bug_fix branch will merge integration into master (and tag wit a number)
- creating a release will move the latest_release tag, and create a numbered tag

Distributions will use the Qt installer. ((/) done)

Features

web site

- complete images, especially for developing toolboxes demos
- link to CATI project ((/) done)
- validate things with Jeff

software

- soma-io: the OpenSlide plugin and lib has modifs for Zeis format, not integrated to the main Openslide project due to possible license issues.
- fix tests which do not pass at the moment
- fix Matplotlib on Windows which randomly fails to load some of its modules
- cleanup soma-base
    - clarify separation between Capsul and Soma-base libs (Controller GUI...) (ongoing)
    - move some things from soma-base to axon, remove obsolete things (ongoing)

To be further discussed and continued...