

Description of GUI of the 3D model building tool

To facilitate reconstruction process a simple graphical user interface was prepared. Below, the 3dBAR reconstruction GUI with an exemplary CAF dataset loaded ([Johnson et. al., 2010](#)) is presented.

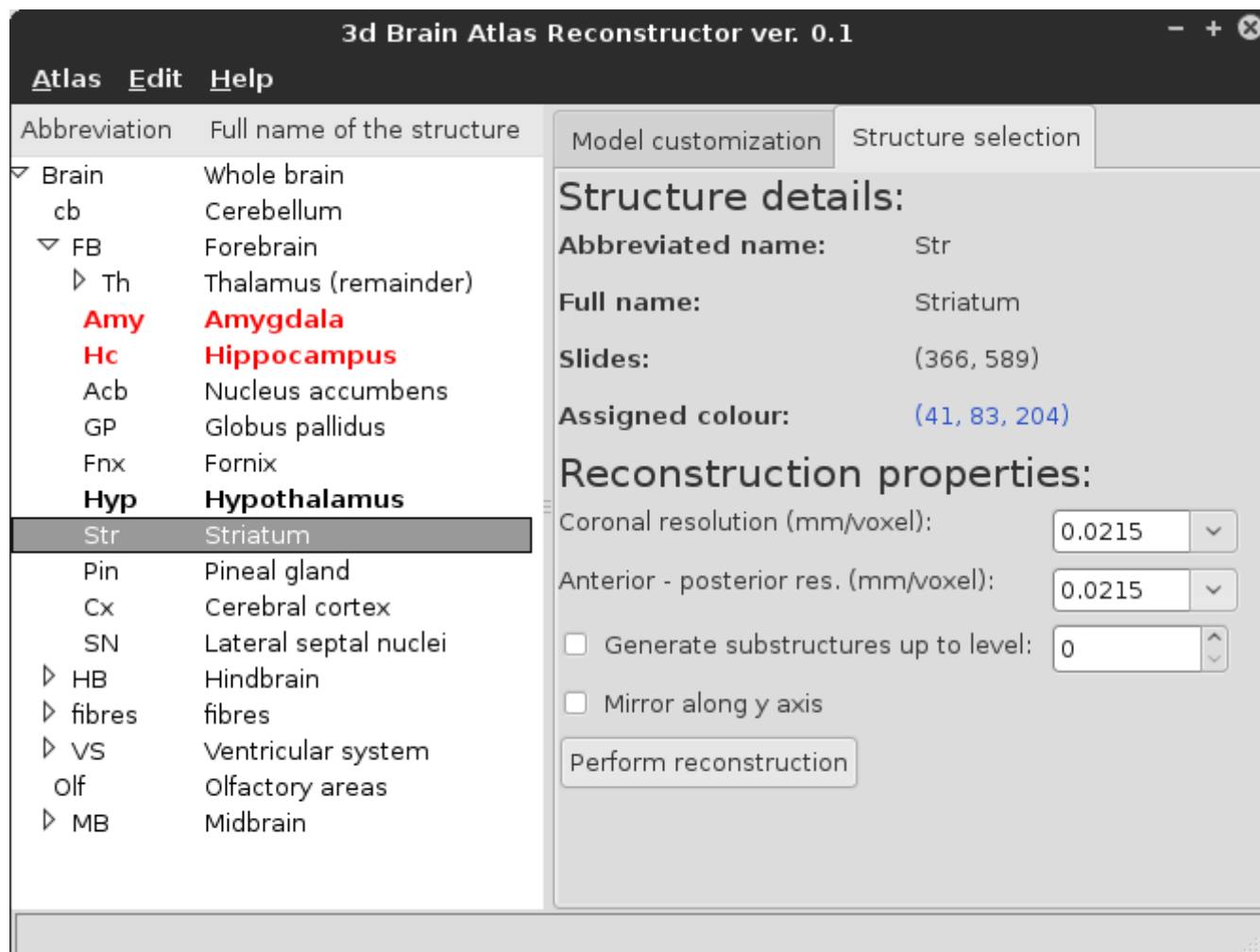


Figure 1: The *structure selection* tab. The *Striatum* selected for reconstruction (gray highlight); *Amygdala* and *Hippocampus* loaded as context models (red font). The reconstruction of *Hypothalamus* is cached and available for loading (bold font).

Selecting structures

The left panel contains *ontology tree* loaded from CAF index file. One can browse through structures, select them for reconstruction or load already reconstructed, cached models. The right panel contains two tabs. *Structure selection* tab displays detailed information about the currently selected structure for reconstruction. This includes abbreviated and full name of the structure, span of slides on which it is defined as well as color assigned to this structure. Here one can also set the resolution, the depth of decomposition of the structure into substructures according to ontology tree, and mirroring of brain hemisphere may be enabled if needed.

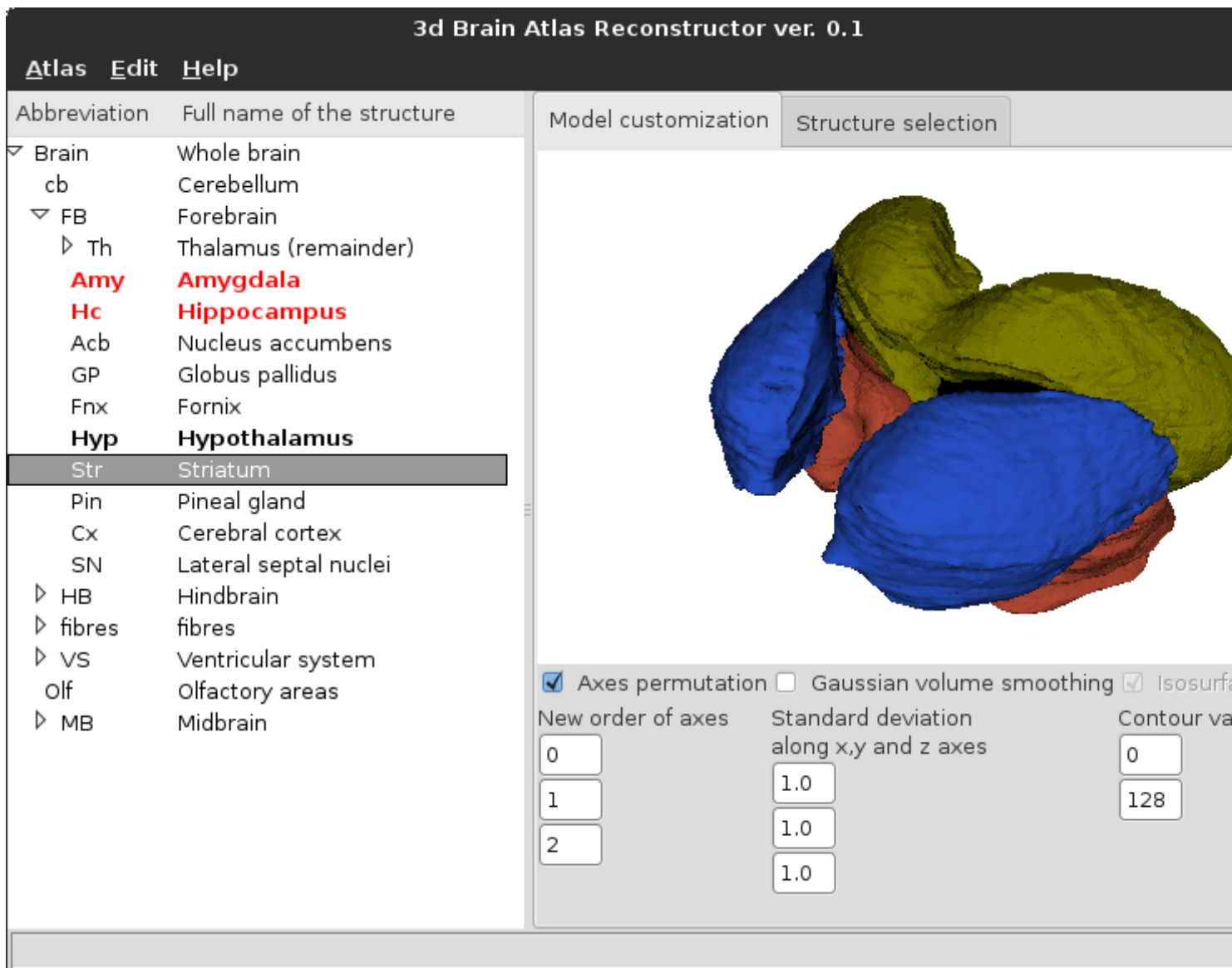


Figure 2: The *model customization tab*. Reconstructions of *Striatum*, *Amygdala* and *Hippocampus* are presented.

Viewing and customizing the reconstructions

Reconstructed models can be viewed in the *Model customization tab* (Fig. 2) which also provides access to parameters of VTK pipeline. The preview is displayed in the form of triangular mesh although the actual model is still stored in volumetric form. The model can be rotated by pressing and holding left mouse button, zoomed in or out by pressing and holding the right button. Pressing the middle button allows one to pan the model over the scene. One can switch between wireframe and surface representations of the model by pressing *w* or *s* keys.

After changing VTK pipeline parameters, mesh may be recalculated by pressing *Refresh* button and cached by pressing *Save model*. Models are cached in form of polygonal meshes (*vtkPolyData*). *Clear scene* button removes all models from preview window. When a model is cached, the corresponding element of the ontology tree is displayed with bold font. Cached models can be loaded in the preview window as *context models* alongside the model being presently reconstructed, however they cannot be modified. When a cached model is loaded into

context, the corresponding element in ontology tree is displayed in red.

Generating multiple reconstructions

Multiple reconstructions can be performed one by one as described above. However, this is convenient only when few models are required. To reconstruct multiple structures one can choose a parent structure containing desired substructures and reconstruct them down to a desired level of detail. All substructures are generated using the same set of reconstruction parameters provided in *Structure selection tab* and the same VTK pipeline. Models are generated one by one and automatically cached. When all the substructures are reconstructed they are loaded into preview window as context models.

Exporting the models

By default models are cached in the directory where CAF dataset is located. One may choose another export directory by selecting *Set cache directory* from *Edit* menu. When cache directory is changed, all currently loaded structures are removed from preview and ontology tree updates information about availability of cached models from the new directory.

3d Brain Atlas Reconstructor GUI offers three ways of exporting three dimensional models. Single reconstructions may be cached as polygonal data ([vtkPolyData](#)) or exported as volumetric datasets in the native VTK [vtkImageData](#) or [Nifti](#) (Neuroimaging Informatics Technology Initiative) formats. Complex scenes containing numerous context models may be exported into [VRML](#) (Virtual Reality Modelling Language) or [X3D](#) format.

3D Brain Atlas Reconstructor CLI reconstruction tool

Apart from GUI, 3D Brain Atlas Reconstructor comes with command line interface (or shorter: CLI) allowing the user to perform batch reconstructions without configured graphics environment. After invoking the batch interface, following information will appear:

```
./batchinterface.sh
```

```
Usage: ./batchinterface.sh [options] <CAF index> [<structure 1> [<structure 2> ...]]
3d Brain Atlas Reconstructor ver.0.1 Batch reconstruction interface
```

Options:

```
-h, --help                show this help message and exit
-g GENERATESUBSTRUCTURES, --generateSubstructures=GENERATESUBSTRUCTURES
                          maximum level of substructures (in the structure tree)
                          to be generated; default: 0
-d VOXELDIMENSIONS, --voxelDimensions=VOXELDIMENSIONS
                          voxel size (in units defined in given dataset) in slide plane
                          and in plane perpendicular to the slides, consecutively.
-e EXPORTDIR, --exportDir=EXPORTDIR
                          the path to a directory for reconstructions
-p PIPELINE, --usePipeline=PIPELINE
                          the path to a custom pipeline definition
-v CAMERA, --useViewport=CAMERA
                          the direction vector from the center of the scene to
                          the camera position
--exportToWindow, --show
                          the reconstruction is displayed to the user
--composite
                          perform a reconstruction of the structure as a scene
```

```
composed of the reconstructions of the basic
substructures in the hierarchy tree (up to the maximum
given level)
--includeBrainOutline
    Includes additional translucent brain outline to the
    reconstructions. Applies only when exporting to VRML,
    X3D, screenshot or thumbnail.
```

Output Format Options:

```
--exportToX3d      exports as X3D scene
--exportToVRML    exports as VRML scene
--exportToVTKPolydata
                    exports as vtkPolyData
--exportToVolume  exports as vtkStructuredPoints
--exportToNifti   exports as NIfTI file
--exportToNumpy   exports as NumPy array
--exportScreenshot saves screenshot as an PNG image
--exportThumbnail saves scaled screenshot as an PNG image
```

The `<CAF index>` is a location of the index file of the given CAF dataset while the `[<structure 1> [<structure 2> ...]]` is space-separated list of all structures to reconstruction contained in the CAF dataset.

The simplest usage of the CLI is to generate reconstruction of a single structure from provided CAF dataset using default settings. Assume that our CAF dataset is located in the `~/atlases/mouse/caf/` directory and we would like to reconstruct the *Thalamus* as save a nifti volume with the reconstruction:

```
./batchinterface.sh ~/atlases/mouse/caf/index.xml Thalamus --exportToNiftii
```

By default, the reconstructions generated using a predefined pipeline and stored in directory parallel to the CAF dataset directory (in this example it would be `~/atlases/mouse/reconstructions/`). However, this behavior can be customized using various switches.