

# Command-line reconstruction interface

Apart from GUI, the 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 tree depth, see -g switch)
--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* and save a nifti volume with the reconstruction:

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

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.

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