

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 --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.