

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.ver. 0.1 Batch reconstruction interface
```

Options:

```
--version          show program's version number and exit
-h, --help        show this help message and exit
-g GENERATESUBSTRUCTURES, --generateSubstructures=GENERATESUBSTRUCTURES
                  maximum level of substructures (in the structure tree)
                  to be generated; defaults to 0
-d VOXELDIMENSIONS, --voxelDimensions=VOXELDIMENSIONS
                  voxel size [mm] (in coronal plane, along anterior-
                  posterior axis)
-e EXPORTDIR, --exportDir=EXPORTDIR
                  the path to a directory for reconstructions
-p PIPELINE, --usePipeline=PIPELINE
                  the path to a custom pipeline definition
-a CAMERAMOVEMENTANGLES, --cameraMovementAngles=CAMERAMOVEMENTANGLES
                  camera movement angles (azimuth, elevation, roll)
-b BACKGROUND, --background=BACKGROUND
                  RGB background colourcomponents (within 0.0-255.0
                  range)
--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 or thumbnail.
--ignoreBoundingBox
                  Overrides bounding box calculation - bounding
                  box will be always equal to hierarchy root element
                  bounding box. Volumes for all structures will always
                  have the same size and origin. This feature increases
                  memory usage and reconstruction time.
```

Output Format Options:

```
--exportToX3d      exports as X3D scene
--exportToVRML     exports as VRML scene
--exportToPOVRay  exports to POV-Ray
--exportToVTKPolydata
                  exports as VTKpolyMesh
--exportToVolume   exports as VTKstructGrid
--exportToNiftii   exports as Niftii 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 of requested structures generated with predefined voxel dimensions, pipeline and camera position 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 with commandline options.