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.