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.