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.