

3d Brain Atlas Reconstructor on-line service

queryReconstruction

Return AJAX data describing reconstructions in the service matching the criteria.

syntax

```
queryReconstruction?cafDatasetName=<dataset identifier>  
                    ;structureList=<structure name>  
                    ;outputFormats=<output format list>  
                    [;resolution=<resolution>]  
                    [;pipeline=<pipeline name>]  
                    [;switches=<switches list>]
```

Required arguments

cafDatasetName

The service identifier of the selected CAF dataset.

structureName

Name of structure from hierarchy tree. In practice nearly all names should be fine. Formally name has to point to a root node of a subtree containing at least one node with representation among paths in CAF slides.

outputFormats

Nonempty coma-separated list of reconstruction file format descriptors. Allowed format descriptors are:

- ◇ 'exportToVRML': VRML files,
- ◇ 'exportToX3d': X3D files,
- ◇ 'exportToPOVRay': POV-Ray files,
- ◇ 'exportToNiftii': NIFTI files
- ◇ 'exportToVTKPolydata': vtk polydata files,
- ◇ 'exportToNumpy': NumPy? array files,
- ◇ 'exportToVolume': vtk structured grid files,
- ◇ 'exportScreenshot': PNG images,
- ◇ 'exportThumbnail': PNG thumbnails.

Optional arguments

resolution

Coronal and anterior-posterior voxel size separated with a coma.

pipeline

Service identifier of the pipeline the reconstructions has been generated with.

switches

Nonempty coma-separated list of switches:

- ◇ brainoutline

match only structures containing the outline of hierarchy tree root structure; forces 'composite' switch,

- ◇ composite

only scene format descriptors ('exportToVRML', 'exportToX3d', 'exportToPOVRay', 'exportScreenshot', 'exportThumbnail') are allowed in the *outputFormats* list.

AJAX data type

```
[{
  String: String,
  String: [Number, Number, String],
  String: String,
  String: Boolean,
  String: String,
  String: Number,
  String: Number | null,
  String: String,
  String: String
},
...]
```

AJAX data description

The data is provided in format:

```
[{
  'groups': <groups>,
  'quality': [<xyres>, <zres>, <pipeline>],
  'format': <format>,
  'compressed': <compressed>,
  'status': <status>,
  'cacheID': <id>,
  'size': <size>,
  'groupsID': <groups id>,
  'CAFSlideUnits': <unit>
},
...]
```

where:

<groups>

is a string describing structures included in the reconstruction,

<xyres>

is the coronal voxel size used in the reconstruction process,

<zres>

is the anterior-posterior voxel size used in the reconstruction process,

<pipeline>

is the service identifier of the pipeline used in the reconstruction process,

<format>

is a string describing the format of reconstruction file,

<compressed>

indicates if the reconstruction file has been compressed as a zip archive,

<status>

is a string describing the status of the reconstruction; possible values are:

◇ 'None',

◇ 'Scheduled',

◇ 'Pending',

Optional arguments

- ◇ 'In progress',
- ◇ 'Completed',
- ◇ 'Finished',
- ◇ 'Failed',
- ◇ 'Removed',

<id>

is the service identifier of the reconstruction,

<size>

is the reconstruction file size (in bytes),

<groups id>

is a string composed of reconstructed groups names separated with '_' character; if an outline is present in the reconstruction, its name precedes others and is separated with double '_' character,

<unit>

is the voxel size unit.

Examples

- http://service.3dbar.org/queryReconstruction?cafDatasetName=sba_DB08:structureList=Br:outputFormats=exportT
- http://service.3dbar.org/queryReconstruction?cafDatasetName=whs_0.6.1:structureList=Brain:outputFormats=exportT
- http://service.3dbar.org/queryReconstruction?cafDatasetName=sba_DB08:structureList=Amg:switches=brainoutline