

Brainnetome Atlas in Freesurfer and Workbench

The main files are `lh.BN_Atlas.gcs`, `rh.BN_Atlas.gcs`, and `BN_Atlas_subcortex.gca`, which are used to map parcellation (cortex) and segmentation (subcortex) labels to subjects. And The `BN_Atlas_246_LUT.txt` is the color table file.

There is a demo script, `mapping_to_subjects.sh`, to execute the following commands on a sample subject 100307. The resulting files are listed in directory `100307`.

We have also mapped the BN_Atlas cortex on *fsaverage* space, the resulting files are in listed in directory `fsaverage`.

Brainnetome Atlas in Freesurfer and Workbench

1. Run Freesurfer processing and check the results
2. Download *BN_Atlas_freesurfer.zip*
3. Map BN_Atlas to a subject
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1. Run Freesurfer processing and check the results

Details info please refer:

<https://surfer.nmr.mgh.harvard.edu/fswiki/FreeSurfer>

<https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all>

<https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/TroubleshootingData>

2. Download *BN_Atlas_freesurfer.zip*

Download link: <http://atlas.brainnetome.org/download.html>

Unzip *BN_atlas_freesurfer.zip* and copy the four files, `lh.BN_Atlas.gcs`, `rh.BN_Atlas.gcs`, `BN_Atlas_subcortex.gca`, and `BN_Atlas_246_LUT.txt`, to the Freesurfer SUBJECTS_DIR folder.

3. Map BN_Atlas to a subject

For example, "100307" is a subject name in your SUBJECTS_DIR, map left BN_Atlas to subject 100307:

```
mris_ca_label -l $SUBJECTS_DIR/100307/label/lh.cortex.label 100307 lh
$SUBJECTS_DIR/100307/surf/lh.sphere.reg $SUBJECTS_DIR/lh.BN_Atlas.gcs
$SUBJECTS_DIR/100307/label/lh.BN_Atlas.annot
```

Similarly, map right BN_Atlas to subject 100307:

```
mris_ca_label -l $SUBJECTS_DIR/100307/label/rh.cortex.label 100307 rh
$SUBJECTS_DIR/100307/surf/rh.sphere.reg $SUBJECTS_DIR/rh.BN_Atlas.gcs
$SUBJECTS_DIR/100307/label/rh.BN_Atlas.annot
```

Then, use another command `mri_ca_label` to map BN_Atlas subcortex:

```
mri_ca_label $SUBJECTS_DIR/100307/mri/brain.mgz
$SUBJECTS_DIR/100307/mri/transforms/talairach.m3z
$SUBJECTS_DIR/BN_Atlas_subcortex.gca
$SUBJECTS_DIR/100307/mri/BN_Atlas_subcotex.mgz
```

For more help, please refer:

https://surfer.nmr.mgh.harvard.edu/fswiki/mris_ca_label

4. show the mapping results in Freeview

```
freeview -f
$SUBJECTS_DIR/100307/surf/lh.pial:annot=$SUBJECTS_DIR/100307/label/lh.BN_Atlas.annot
freeview -f
$SUBJECTS_DIR/100307/surf/rh.pial:annot=$SUBJECTS_DIR/100307/label/rh.BN_Atlas.annot
```

5. Calculate parcellation statistics

Calculate the statistics for left hemisphere:

```
mris_anatomical_stats -mgz -cortex
$SUBJECTS_DIR/100307/label/lh.cortex.label -f
$SUBJECTS_DIR/100307/stats/lh.BN_Atlas.stats -b -a
$SUBJECTS_DIR/100307/label/lh.BN_Atlas.annot -c
$SUBJECTS_DIR/BN_Atlas_246_LUT.txt 100307 lh white
```

Convert a cortical stats file into a table indicating *measure* (such as area, volume, thickness, thicknessstd, meancurv, foldind, ...) in which each line is a subject and each column is the *measure* on parcels. Take *thickness measure* for example:

```
aparcstats2table --subjects 100307 --hemi lh --parc BN_Atlas --meas
thickness --tablefile $SUBJECTS_DIR/100307/stats/lh.thickness.txt
```

The processing steps for right hemisphere are similar.

For more help, please refer:

https://surfer.nmr.mgh.harvard.edu/fswiki/mris_anatomical_stats

<https://surfer.nmr.mgh.harvard.edu/fswiki/aparcstats2table>

6. Calculate segmentation statistics

Calculate the statistics for subcortex:

```
mri_segstats --seg $SUBJECTS_DIR/100307/mri/BN_Atlas_subcotex.mgz --ctab
$SUBJECTS_DIR/BN_Atlas_246_LUT.txt --excludeid 0 --sum
$SUBJECTS_DIR/100307/stats/BN_Atlas_subcotex.stats
```

For more help, please refer:

https://surfer.nmr.mgh.harvard.edu/fswiki/mri_segstats

7. Show in Connectome Workbench

```
### convert to CIFTI files
mkdir -p 100307/Native
mris_convert --annot ./100307/label/lh.BN_Atlas.annot
./100307/surf/lh.white ./100307/Native/100307.L.BN_Atlas.native.label.gii
wb_command -set-structure
./100307/Native/100307.L.BN_Atlas.native.label.gii CORTEX_LEFT
mris_convert --annot ./100307/label/rh.BN_Atlas.annot
./100307/surf/rh.white ./100307/Native/100307.R.BN_Atlas.native.label.gii
wb_command -set-structure
./100307/Native/100307.R.BN_Atlas.native.label.gii CORTEX_RIGHT

mris_convert ./100307/surf/lh.white
./100307/Native/100307.L.white.native.surf.gii
wb_command -set-structure ./100307/Native/100307.L.white.native.surf.gii
CORTEX_LEFT -surface-type ANATOMICAL -surface-secondary-type GRAY_WHITE
mris_convert ./100307/surf/rh.white
./100307/Native/100307.R.white.native.surf.gii
wb_command -set-structure ./100307/Native/100307.R.white.native.surf.gii
CORTEX_RIGHT -surface-type ANATOMICAL -surface-secondary-type GRAY_WHITE

mris_convert ./100307/surf/lh.pial
./100307/Native/100307.L.pial.native.surf.gii
wb_command -set-structure ./100307/Native/100307.L.pial.native.surf.gii
CORTEX_LEFT -surface-type ANATOMICAL -surface-secondary-type PIAL
```

```

mris_convert ./100307/surf/rh.pial
./100307/Native/100307.R.pial.native.surf.gii
wb_command -set-structure ./100307/Native/100307.R.pial.native.surf.gii
CORTEX_RIGHT -surface-type ANATOMICAL -surface-secondary-type PIAL

wb_command -surface-average
./100307/Native/100307.L.midthickness.native.surf.gii -surf
100307/Native/100307.L.white.native.surf.gii -surf
./100307/Native/100307.L.pial.native.surf.gii
wb_command -set-structure
./100307/Native/100307.L.midthickness.native.surf.gii CORTEX_LEFT -surface-
type ANATOMICAL -surface-secondary-type MIDTHICKNESS

wb_command -surface-average
./100307/Native/100307.R.midthickness.native.surf.gii -surf
100307/Native/100307.R.white.native.surf.gii -surf
./100307/Native/100307.R.pial.native.surf.gii
wb_command -set-structure
./100307/Native/100307.L.midthickness.native.surf.gii CORTEX_RIGHT -
surface-type ANATOMICAL -surface-secondary-type MIDTHICKNESS

# generate Workbench spec file
cd 100307/Native
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_LEFT
./100307.L.white.native.surf.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_LEFT
./100307.L.pial.native.surf.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_LEFT
./100307.L.midthickness.native.surf.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_LEFT
./100307.L.BN_Atlas.native.label.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_RIGHT
./100307.R.white.native.surf.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_RIGHT
./100307.R.pial.native.surf.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_RIGHT
./100307.R.midthickness.native.surf.gii
wb_command -add-to-spec-file ./100307.native.wb.spec CORTEX_RIGHT
./100307.R.BN_Atlas.native.label.gii

```

Open Connectome Workbench then load the spec file to show the results.