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# Testing your FreeSurfer installation

## tkmedit

There is a sample subject, called 'bert', found in the freesurfer/subjects directory, which contains pre-processed data stored in .mgz files (not in COR formatted files, which is a deprecated format).

To view a volume, type:

```
tkmedit bert orig.mgz
```

To view the subcortical segmentation results, type:

```
tkmedit bert norm.mgz -segmentation aseg.mgz  
$FREESURFER_HOME/FreeSurferColorLUT.txt
```

Note: you may need to include 'mri/' in the aseg.mgz path shown above on older versions of tkmedit.

As you move the mouse over areas of the brain, the label info is found in the 'Sgmtn label' box.

## tksurfer

To view a surface, type:

```
tksurfer bert rh pial
```

To increase brightness on that surface, in tksurfer:

View->Configure->Lighting->Brightness

To view cortical parcellation labels, in tksurfer:

File->Label->Import Annotation Browse to file rh.aparc.annot and select OK Redraw  
View icon is the one with the up/down arrows

## qdec

To start the qdec application, type:

```
qdec
```

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There is no sample data with which to test it, so you should just confirm that the application starts without displaying any error messages.

## recon-all -help

The Freesurfer command:

```
recon-all --help | less
```

will print text on the overall functionality of Freesurfer.

## recon-all -all

To re-create all volume and surface files, on the command-line type:

```
recon-all -s bert -all
```

Note that this operation may take 24 hours to complete. Consult `recon-all --help` for instructions on how to conduct multi-stage processing (eg. `-autorecon1`, `-autorecon2` and `-autorecon3`). The `-autorecon1` stage completes in less than a half an hour, and is worth running to test your installation, as it exercises most of the libraries. To run, type:

```
recon-all -s bert -autorecon1
```

## Getting started with your own data

Given a subject having two sets of DICOMS (two runs of structural scans), do the following to setup a subject, where `<subjid>` is replaced with whatever name or id you want to give to that subject and `SUBJECTS_DIR` is set to the directory where you want to keep your subjects:

```
recon-all -s <subjid> \  
  -i <path_to_dicoms>/95555-2-1.dcm  
  -i <path_to_dicoms>/95555-3-1.dcm
```

Now you will have two files in `$SUBJECTS_DIR/<subjid>/mri/orig`, named `001.mgz` and `002.mgz`. The `recon-all -i` command has taken your two structural scans and converted them to `.mgz` format. Note that in your own case, the name of the dicom files will be different (in this example, `95555-2-1.dcm` is the first of a collection of 128 files). This import command is only issued **once**, i.e. once your data has been successfully imported, do not use the `-i` flags again. With the two structural scans now imported into a freesurfer subject directory, you can begin processing the subject:

```
recon-all -s <subjid> -all
```

# Questions?

Send email to: [freesurfer AT nmr DOT mgh DOT harvard DOT edu](mailto:freesurfer@nmr.mgh.harvard.edu)

Bug reports: [analysis-bugs AT nmr DOT mgh DOT harvard DOT edu](mailto:analysis-bugs@nmr.mgh.harvard.edu)

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