

## Freesurfer on HPC cluster:

### *What is Freesurfer?*

FreeSurfer is a software package for the analysis and visualization of structure and functional neuroimaging data from cross-sectional or longitudinal studies. It provides a full processing stream for structural MRI data.

The documentation for the Freesurfer is found in:

[Freesurfer](#)

[Freesurfer GitHub](#)

### Versions Available:

Freesurfer – 6.0.0

Freesurfer – 7.1.1

### *How to load a version of Freesurfer?*

To view available version of Freesurfer on the HPC, use the following command:

```
module avail bio/freesurfer
```

The version will be listed. To a version of software, use following command:

```
module load bio/freesurfer/7.1.1
```

Verify by using this command:

```
module list
```

The loaded software and dependencies will be shown.

## *How to use Freesurfer on the cluster?*

Here is one example of how to use Freesurfer on the cluster. To get a test file to process through Freesurfer, use the following commands

```
cd ~ && mkdir freesurfer_test && cd freesurfer_test # Make a test directory on home
folder

#Location of test data on server
wget https://github.com/Donders-Institute/hpc-wiki-v2/raw/master/docs/cluster_howto/exercise_f
reesurfer/FSdata.tgz

#Unpack
tar -xvf FSdata.tgz && FSdata

# Now after you load your module and copied test files, we can make a script to run F
reesurfer
```

## The Script:

```
#!/bin/bash
$SBATCH -J Jobname # Jobname
#SBATCH -n 1 # Nodes per task
#SBATCH --mem=10G # Must need to allocate memory to run Freesurfer - at least 4G
#SBATCH -p main # Partition
#SBATCH --qos main # Quality of service
#SBATCH -o Freesurfer_sim_out-%J.txt # STDOUT Out file
#SBATCH -e Freesurfer_sim_out-%J.txt # Error file
#SBATCH -t 120 # time in minuets
```

```
module load bio/freesurfer/7.1.1          # load the module

export SUBJECTS_DIR=$(pwd)                # Point to the output directory

export SUBJECTS_DIR=$(pwd)                # point freesurfer towards the working directory

#Now run the the test job.
recon-all -subjid TEST -i MP2RAGE.nii -all
```

Schedule the job with the following sbatch command.

```
sbatch myscript.sh
```

All the processed files will be generated in the same directory as the script. There will be a directory named TEST.

### ***Where to find help?***

If you are stuck on some part or need help at any point, please contact OIT at the following address.

<https://ua-app01.ua.edu/researchComputingPortal/public/oitHelp>

Resources:

[Freesurfer GitHub](#)