FSL on HPC cluster:

What is FSL?

FSL is a comprehensive library of analysis tools for FMRI, MRI and DTI brain imaging data. It runs on Apple and PCs (both Linux, and Windows via a Virtual Machine), and is quite easy to install. Most of the tools can be run both from the command line and as GUIs ("point-and-click" graphical user interfaces).

The full documentation for the FSL is found in the following links:

[Official Website](#)

[Documentation](#)

[Lectures and Tranining](#)

Versions Available:

- FSL v. 6.0.3

How to load a version of FSL?

To load a version of FSL on the HPC, use the following command:

```
module avail bio/fsl
```

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

```
module load bio/fsl/
```

Verify by using this command:

```
module list
```

Since this is a standalone software, it does not have dependencies. So, only FSL will be seen listed.

Many tools are available on the FSL module, which are listed on the following website:

[Tools of FLS](#)

How to use FSL on the cluster?

There are two methods to run FSL on the cluster.

The GUI:

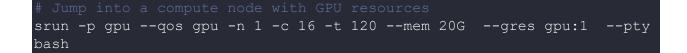To launch FSL on graphical interface, use the following command,

```
# Jump into a compute node
srun -p main --qos main -n 1 -c 12  -t 120 --mem 16G --pty bash

# Load the module and launch the GUI
fsl
```

Use the GUI to process data and launch different tools.

Note: Do not launch GUI in head node

Allocating GPU resources:

Some of the tools of the FSL module can utilize GPU for processing data. To allocate GPU resources, use the following command to jump into compute node:
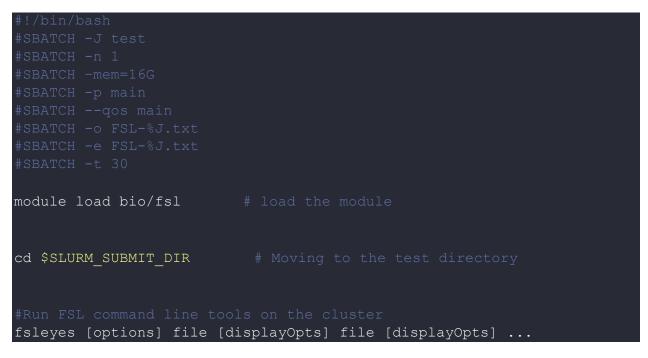
```
# Jump into a compute node with GPU resources
srun -p gpu --qos gpu -n 1 -c 16 -t 120 --mem 20G  --gres gpu:1  --pty
bash
```

GPU and CUDA version information can be found on the following link:

[FSl_GPU](FSl_GPU)

The Script:

Users can run Command Line tools available in FSL module in a batch script. Use the following template ,

Use the following template for the script,

```
#!/bin/bash
#SBATCH -J test
#SBATCH -n 1
#SBATCH -mem=16G
#SBATCH -p main
#SBATCH --qos main
#SBATCH -o FSL-%J.txt
#SBATCH -e FSL-%J.txt
#SBATCH -t 30


module load bio/fsl        # load the module



cd $SLURM_SUBMIT_DIR        # Moving to the test directory



#Run FSL command line tools on the cluster
fsleyes [options] file [displayOpts] file [displayOpts] ...
```

Schedule the job with the following sbatch command.

sbatch script.sbatch

All the processed files will be generated in the same directory as the sbatch script.

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