Cufflinks on HPC cluster:

What is Cufflinks?

Cufflinks assembles transcripts, estimates their abundances, and tests for differential expression and regulation in RNA-Seq samples. It accepts aligned RNA-Seq reads and assembles the alignments into a parsimonious set of transcripts. Cufflinks then estimates the relative abundances of these transcripts based on how many reads support each one, considering biases in library preparation protocols.[source]

The official documentation can be found on:

GitHub- Cufflinks

Documentation

Versions Available:

- cufflinks v2.2.1

How to load a version of Cufflinks?

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

```
module load bio/cufflinks/
```

Verify by using this command:

```
module list
```

It is standalone software so only cufflink should be loaded.

How to use Cufflinks on the cluster?

For this demonstration, download the test file from the following link,

```
wget http://cole-trapnell-
lab.github.io/cufflinks/assets/downloads/test_data.sam
```

Use the following sbatch script for using cufflinks,

```bash
#!/bin/bash
#SBATCH -J cufflinks-test
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=12
#SBATCH -p main
#SBATCH --qos main
#SBATCH --output=output.%j.cufflinks-test
#SBATCH --time=00:10:00


#Load Module
module purge
module load bio/cufflinks

# Run cufflinks with 12 threads
cufflinks --quiet --num-threads $SLURM_NTASKS --output-dir
$SLURM_SUBMIT_DIR $SLURM_SUBMIT_DIR/test_data.sam
```

The output should be in the job submission directory along with the log file.

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