

Hifiasm on HPC

What is Hifiasm?

Hifiasm is a fast haplotype-resolved de novo assembler for PacBio HiFi reads. It can assemble a human genome in several hours and assemble a ~30Gb California redwood genome in a few days. Hifiasm emits partially phased assemblies of quality competitive with the best assemblers. Given parental short reads or Hi-C data, it produces arguably the best haplotype-resolved assemblies so far.

Links:

[Official Website](#)

[Documentation](#)

Versions Available:

The following versions are available on the cluster:

- Hifiasm -v0.13-r308

How to load Hifiasm?

To load Hifiasm, use the following commands:

```
#Load the Hifiasm module  
module load bio/hifiasm
```

To verify if the module and dependencies are loaded correctly, use the following command.

```
#Show all the modules loaded
module list
```

This should list all the Hifiasm and dependencies that are loaded, in this case gcc compiler and itself.

How to use Hifiasm?

To demonstrate the use of hifiasm, use the following input file

```
# Input file for HiFi-only Assembly
wget
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR151/003/SRR1518133/SRR1518133_1.
fastq.gz
```

See the program command line usage with,

```
hifiasm -h
```

Use the following as a sample sbatch script,

```
#!/bin/bash
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -c 16
#SBATCH -p threaded
#SBATCH -q threaded
#SBATCH --mem-per-cpu=2G

# Load the module
module load bio/hifiasm
# go to script submit directory
cd $SLURM_SUBMIT_DIR

# Run hifiasm with 16 threads
echo -e "Threades $SLURM_CPUS_PER_TASK"
```

```
hifiasm -o SRR1518133_1.asm -t $SLURM_CPUS_PER_TASK  
SRR1518133_1.fastq.gz
```

All output files should be written in script submission directory.

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>