

Hisat2 on HPC cluster:

What is Hisat2?

HISAT2 is a fast and sensitive alignment program for mapping next-generation sequencing reads (whole-genome, transcriptome, and exome sequencing data) to a population of human genomes (as well as to a single reference genome).

The full documentation for Hisat2 is found in the following links:

[GitHub](#)

[Full Documentation](#)

Versions Available:

- Hisat2-v 2.0.5

How to load a version of Hisat2?

To load a version of Hisat2 on the HPC, use the following command:

```
module load bio/hisat2
```

Verify by using this command:

```
module list
```

The loaded software and runtime dependencies, python 2.7, GDAL2 and Perl in this case, will be shown.

How to use Hisat2 on the cluster?

There are two methods to run Hisat2 on the cluster.

The Interactive Way:

To run the program interactively, follow the steps:

```
#Open a bash session on compute node
srun -p main --qos main -n 1 -c 12 --mem 10G --pty bash

#Load the module
module load bio/hisat2

# Start your commands here
hisat2 --help

#Follow with commands to execute
```

This method is used for short job runs and debugging since the job terminates after the user exits the current terminal session.

The Script (Preferred):

To run a slurm job, the user must prepare input files. For this example, get input files with,

```
#Copy the input files to the test directory
cp /share/apps/hisat/hisat2-2.0.5/example/reads/reads_1.fa ~/test/
cp /share/apps/hisat/hisat2-2.0.5/example/reference/* ~/test/
```

```
#Make a script
touch script.sbatch
```

Use the following script as a template,

```
#!/bin/bash
#SBATCH -J hisat-test
#SBATCH -n 1
#SBATCH -mem=16G
#SBATCH -p main
#SBATCH --qos main
#SBATCH -o Miniiasm_sim_out-%J.txt
#SBATCH -e Miniiasm_sim_out-%J.txt
#SBATCH -t 30
#Load the module
module load bio/hisat

#Go to the test directory
cd $SLURM_SUBMIT_DIR

#Run hisat
#Index a reference genome
hisat2-build 22_20-21M.fa --snp 22_20-21M.snp 22_20-21M_snp

#Align example read
hisat2 -f -x 22_20-21M_snp -U reads_1.fa -S eg1.sam
```

Schedule the job with the following sbatch command.

```
sbatch script.sbatch
```

All the processed files will be generated in the same directory as the 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>