

Orthofinder on HPC

What is Orthofinder?

OrthoFinder is a fast, accurate and comprehensive platform for comparative genomics. It finds orthogroups and orthologs, infers rooted gene trees for all orthogroups and identifies all the gene duplication events in those gene trees. It also infers a rooted species tree for the species being analysed and maps the gene duplication events from the gene trees to branches in the species tree. OrthoFinder also provides comprehensive statistics for comparative genomic analyses. OrthoFinder is simple to use and all you need to run it is a set of protein sequence files (one per species) in FASTA format.

More info on orthofinder:

[Orthofinder- GitHub](#)

Versions Available:

The following versions are available on the cluster:

- Orthofinder-v1.110
- Orthofinder-v2.3.14

How to load Orthofinder?

To list all available version of Orthofinder on the HPC, use the following commands:

```
module avail bio/orthofinder
```

To load a specific version, use the following,

```
module load bio/orthofinder/2.3.14
```

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

```
module list
```

This should list all the software and dependencies that are loaded.

How to use Orthofinder?

There are two ways to use most of the software on the cluster.

The Interactive Way:

To run the Orthofinder in an interactive session, jump into a base terminal of a compute node using the following command:

```
srun -p main --qos main -n 1 -c 16 --mem 12G --pty bash
```

Now, load the Orthofinder module and start your job interactively on the terminal.

```
#Use this to see the full syntax and options available
orthofinder --help
#You can run commands here!
```

Note: This is preferred usage in case of short runtime jobs and debugging. After you exit the terminal session, your job will be terminated unlike batch method.

The Script method:

To use this method, the user will need to write a batch script and submit it to a slurm.

To copy the test files, use the following command,

```
#Make a test dir on home
mkdir ~/orth-test && cd ~/orth-test

#Get test file
cp -r /share/apps/orthofinder/OrthoFinder-2.3.14/ExampleData/ .

#make a sbatch script
touch script.sbatch
```

The sbatch script should be formatted like

```
#!/bin/bash
#SBATCH -J orth-test
#SBATCH -n 1
#SBATCH -c 12
#SBATCH --mem=16G
#SBATCH -p main
```

```
#SBATCH --qos main
#SBATCH -e err.err
#SBATCH -o out.out

module load bio/orthofinder/

# Move to test data directory
cd $SLURM_SUBMIT_DIR

#Run the Orthofinder command here
orthofinder -f ExampleData
```

To run the script, submit it using:

```
sbatch script.sbatch
```

All the output files will be under the ExampleData/Orthofinder/ 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>