HMMER on HPC

What is HMMER?

HMMER is used for searching sequence databases for sequence homologs, and for making sequence alignments. It implements methods using probabilistic models called profile hidden Markov models (profile HMMs).

HMMER is often used together with a profile database, such as Pfam or many of the databases that participate in Interpro. But HMMER can also work with query *sequences*, not just profiles, just like BLAST. For example, you can search a protein query sequence against a database with **phmmer**, or do an iterative search with **jackhmmer**. [Source]

Links:

[Official Website](#)

[Documentation](#)

Versions Available:

The following versions are available on the cluster:

- Hmmer 3.1b2

How to load HMMER?

To load HMMER, use the following commands:

```
#Load the HMMER module
module load bio/hmmer/3.1b2
```

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 HMMER and dependencies that are loaded. In this case, only hmmer will be loaded since it is a standalone software.

How to use HMMER?

To demonstrate the usage of HMMER, download the following test files,

```
#Download the test files
svn checkout https://github.com/EddyRivasLab/hmmer/trunk/tutorial
```

Useful program of this modules are listed,

hmmbuild	build profile from input multiple alignment
hmmalign	make multiple sequence alignment using a profile
hmmsearch	search profile against sequence database
hmmscan	search sequence against profile database
hmmpress	prepare profile database for hmmscan
phmmer	search single sequence against sequence database
jackhmmer	iteratively search single sequence against database
nhmmer	search DNA query against DNA sequence database
nhmmscan	search DNA sequence against a DNA profile database
hmmfetch	retrieve profile(s) from a profile file
hmmstat	show summary statistics for a profile file
hmmemit	generate (sample) sequences from a profile
hmmlogo	produce a conservation logo graphic from a profile
hmmconvert	convert between different profile file formats
hmmpgmd	search daemon for the hmmer.org website
hmmpgmd_shard	sharded search daemon for the hmmer.org website
makehmmerdb	prepare an nhmmer binary database
hmmsim	collect score distributions on random sequences
alimask	add column mask to a multiple sequence alignment

Use the following sbatch script – located in same directory as the test files- to submit job for the scheduler,

```bash
#!/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/hmmer/3.1b2

# go to script submit directory
```

```
cd $SLURM_SUBMIT_DIR

# build a database
hmmbuild --cpu $SLURM_CPUS_PER_TASK  fn3.hmm fn3.sto

#search the database
hmmsearch --cpu  $SLURM_CPUS_PER_TASK fn3.hmm 7LESS_DROME > fn3.out
```

The search output should be in fn3.out.

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