

Phylobayes on HPC cluster:

What is Phylobayes ?

PhyloBayes is a Bayesian Markov chain Monte Carlo (MCMC) sampler for phylogenetic inference. The program will perform phylogenetic reconstruction using nucleotide, protein, or Condon sequence alignment. Compared to other phylogenetic MCMC samplers, the main distinguishing feature of phylobayes is the use of non-parametric methods for modeling among-site variations in nucleotide or amino-acid propensities.

The documentation for the Phylobayes is found in the following links:

[Documentation](#)

[GITHUB](#)

Versions Available:

- Phylobayes - 1.6-slurm

How to load a version of Phylobayes ?

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

```
module avail bio/phylobayes
```

The version will be listed. To use a version of software, use following command:

```
module load bio/phylobayes /1.6-slurm
```

Verify by using this command:

```
module list
```

The loaded software and dependencies, openmpi in this case, will be shown.

How to use Phylobayes on the cluster?

Since phylobayes uses openMPI, it is better to run it in batch method.

The Script:

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

```
#Download input files through this command
wget
https://github.com/bayesiancook/phylobayes/blob/master/data/brpo/brpo.
ali

wget
https://github.com/bayesiancook/phylobayes/blob/master/data/brpo/brpo.
tree

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

Use the following template for the script,

```
#!/bin/bash
#SBATCH -J Phylobayes -test
#SBATCH --n_tasks=24
#SBATCH -mem=16G
```

```
#SBATCH -p main
#SBATCH --qos main # Quality of service
#SBATCH -o Phylobayes_sim_out-%J.txt
#SBATCH -e Phylobayes_sim_out-%J.txt
#SBATCH -t 30

module load bio/phylobayes # load the module

cd $SLURM_SUBMIT_DIR # Moving to the test directory

#Run Phylobayes
mpirun pb_mpi -d brpo.ali -t brpo.tree -x 5 20 test
```

Schedule the job with the following sbatch command.

```
sbatch script.sbatch
```

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