# ModelTest-NG on HPC

## What is ModelTest-NG?

ModelTest-NG is a tool for estimating the evolutionary parameters of a DNA or protein sequence alignment using maximum likelihood. It is designed to be used with sequence alignments that have been generated using the FastTree or RAxML programs, and can be used to test a variety of different models of sequence evolution. ModelTest-NG is an updated version of the original ModelTest tool, which was developed by Paul J. P. Huelsenbeck and Fredrik Ronquist.

Links:

Official Website

Manual

## **Versions Available:**

The following versions are available on the cluster:

• ModelTest-NG 0.1.6

#### How to load MODELTEST-NG?

To load MODELTEST-NG, use the following commands:

module load bio/modeltest-ng/0.1.6

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 MODELTEST-NG dependencies that are loaded – openMPI and GCC.

#### How to use MODELTEST-NG?

To demonstrate the usage for modern-gl, download the test files from the following command,

#download test file
svn checkout https://github.com/ddarriba/modeltest/trunk/example-data

Use the following sampe slurm script to use modeltest-ng on input test data,



The output file should be in the same directory as the slurm script. The processed files will be in ./example-data/dna/ directory.

## Where to find help?

If you are confused or need help at any point, please contact OIT at the following address.

https://ua-app01.ua.edu/researchComputingPortal/public/oitHelp