# BBmap on HPC cluster:

## What is BBmap?

BBMap is a short read aligners. It is written in pure Java, can run on any platform, and has no dependencies other than Java being installed (compiled for Java 6 and higher). All tools are efficient and multithreaded.

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

<u>GitHub</u>

Versions Available:

• BBmap-v 37.32

How to load a version of BBmap?

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

module load bio/bbmap

Verify by using this command:

module list

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

#### How to use BBmap on the cluster?

There are two methods to run BBmap on the cluster.

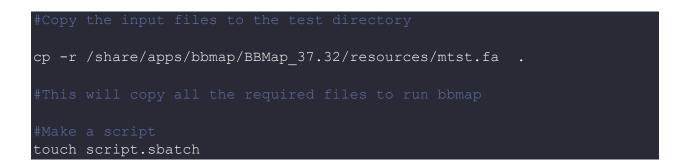
The Interactive Way:

To run the program interactively, follow the steps:

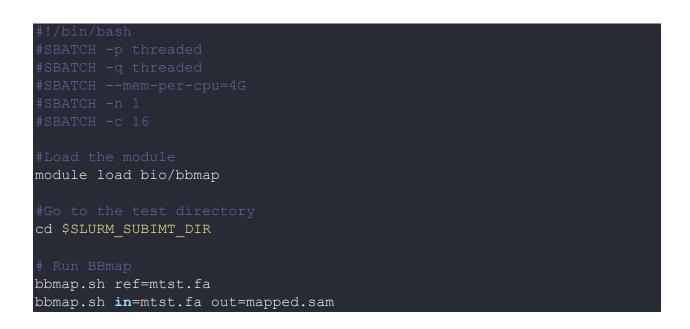
```
#Open a bash session on compute node
srun -p main --qos main -n 1 -c 12 --mem 10G --pty bash
#Load the module
module load bio/bbmap
# Start your commands here
bbmap.sh --help
#Follow with commands to execute
#This method is ideal for a short job run which produces runtime
#output and to debug the codes.
```

### The Script (Preferred):

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



Use the following script as a template,



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