

## Bowtie on HPC cluster:

### *What is Bowtie?*

Bowtie, a super-fast memory efficient, short read aligner is made for quickly aligning large set of short DNA sequences to large genome. Bowtie uses Burrows-Wheeler index to keep memory usage relatively low: for human genome, the index is typically 2.2 GB (unpaired alignment) or 2.9 (for pair end alignment). Multiple processors can be used to achieve super-fast alignment speeds. It is also a basis for other software like: Top Hat, Bowtie, Myrna etc.

More about Bowtie:

[Bowtie Manual](#)

[Bowtie Official Website](#)

### Versions Available:

Bowtie – 1.1.2

Bowtie – 2. 2.5

Bowtie – 2. 3

### *How to load a version of Bowtie?*

To load a version of Bowtie on the HPC on current terminal session, use the following command:

`module avail bio/bowtie`

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

```
module load bio/bowtie/2.3
```

Verify by using this command:

```
module list
```

The loaded software and dependencies will be shown.

### *How to use Bowtie on the cluster?*

Here is one example of how to use the Bowtie on the cluster. To get a test file to process through Bowtie, use the following commands

```
cd ~ && mkdir Bowtie_test && cd Bowtie_test      # Make a test directory on home folder
der

#Go to example directory folder
cd /share/apps/bowtie/bowtie2-2.3.4.1-linux-x86_64/

#Copy test data to test folder
cp example/reads/reds2.fq ~/Bowtie_test
cp example/reference/lambda_virus.fa ~/Bowtie_test

# Now after you loaded your module and copied test files, we can make a script to run
Bowtie
```

### The Script:

```
#!/bin/bash
$SBATCH -J Jobname # Jobname
#SBATCH -n 1      # Nodes per task
#SBATCH -mem=5G   # Must need to allocate memory to run Bowtie - at least 4G
#SBATCH -p main   # Partition
```

```
#SBATCH --qos main # Quality of service
#SBATCH -o Bowtie_sim_out-%J.txt # STDOUT Out file
#SBATCH -e Bowtie_sim_out-%J.txt # Error file
#SBATCH -t 25 # Time in minutes

module load bio/Bowtie/2.3 # load the module

cd $SLURM_SUBMIT_DIR # Moving to the test directory

#Now run the test job. This generates index files
bowtie2-build lambda_virus.fa lambda_virus

#This aligns file with the reference sequences
bowtie2 -x lambda_virus -U reads_1.fq -S out.sam
```

Schedule the job with the following sbatch command.

```
sbatch myscript.sh
```

All the processed files will be generated in the same directory as the script. The results will be in test.out file.

**Interactive Mode:**

**To run it interactively, go** to a bash session in a compute node and load the module.

```
# Run a bash session on the compute node
srun -p main --qos main -n 1 --mem 6G --pty bash
```

```
# load the module  
module load bio/bowtie/2.3
```

**Note: Do not do computations on the head node**

## ***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>

Resources:

[BowTie Usuag](#)