# Trinity on HPC cluster:

## *What is Trinity?*

Developed at the Broad Institute and the Hebrew University of Jerusalem, Trinity is a novel method for the efficient and robust de novo reconstruction of transcriptomes for RNA-seq data. Trinity combines three independent software modules: Inchworm, Chrysalis, and Butterfly, applied sequentially to process large volumes of RNA-seq reads

The documentation for the Trinity is found in:

[Home · trinityrnaseq/trinityrnaseq Wiki · GitHub](#)

[Trinity Screencast | Broad Institute](#)

## Versions Available:

Trinity – 2.10.0

Trinity – 2. 8 .4

Trinity – 2. 2. 0

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

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

module avail bio/trinity

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

module load bio/trinity/2.10.0

Verify by using this command:

module list

The loaded software and dependencies will be shown.

## How to use Trinity on the cluster?

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

```
cd ~ && mkdir Trinity_test && cd Trinity_test     # Make a test directory on home #fo
lder


#Location of test data on server

test_data=/share/apps/trinity/trinityrnaseq-v2.10.0/sample_data/test_Trinity_Assembly


# Copy the test files from trinity folder

cp $test_data/reads* ~/Trinity_test && gunzip reads*


# Now after you load your module and copied test files, we can make a script to run T
rinity
```

The Script:

```
#!/bin/bash

$SBATCH -J Jobname # Jobname

#SBATCH -n 1        # Nodes per task

#SBATCH –mem=20G     # Must need to allocate memory to run Trinity – at least 4G

#SBATCH -p main     # Partition

#SBATCH --qos main  # Quality of service

#SBATCH -o Trinity_sim_out-%J.txt  # STDOUT Out file

#SBATCH -e Trinity_sim_out-%J.txt  # Error file

#SBATCH -t 120                     # time in minuets
```

```
module load bio/trinity/2.10.0          # load the module


cd $SLURM_SUBMIT_DIR               # Moving to the test directory


#Now run the the test job. (Note --no_bowtie flag is needed)
Trinity --seqType fa --left reads.left.fa --right reads.right.fa --CPU 8 --max_memory
20G --no_bowtie
```

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.

## *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:

Home · trinityrnaseq/trinityrnaseq Wiki · GitHub