Velvet on HPC cluster:

What is Velvet?

The Velvet *de novo* assembler can be used to quickly build long continuous sequences, or *contigs*, as well as gapped assemblies of contigs, or *scaffolds*, out of short-read datasets as produced by next-generation sequencing technologies. This function is useful when studying data from a new organism for which a reference genome has not been assembled yet, or when trying to determine the origin of unmapped reads.

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

Documentation

GitHub

Manual

Versions Available:

- Velvet –v1.2.10

How to load a version of Velvet?

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

```
module load bio/velvet
```

Verify by using this command:

```
module list
```

Since this is standalone software, no dependencies will be shown- only the software itself.

How to use Velvet on the cluster?

There are two methods to run Velvet 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/Velvet

# Start your commands here
velveth  --help
#Follow with commands to execute

#This method is ideal for a short job run which produces runtime
#output and to debug the codes.
```

Note:

Two important binaries for this module are:

velveth

velvetg

See docs for more information.

The Script (Preferred):

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

```
#Copy the input files to the test directory

cp /share/apps/velvet/1.2.10/tests/read* .

#This will copy all the required files to run Velvet

#Make a script
touch script.sbatch
```

Use the following script as a template,

```
#!/bin/bash
#SBATCH -J test
#SBATCH -n 1
#SBATCH –mem=16G
#SBATCH -p main
#SBATCH --qos main
#SBATCH -o vel-%J.txt
#SBATCH -e vel-%J.txt
#SBATCH -t 30

module load bio/velvet       # load the module


cd $SLURM_SUBMIT_DIR       # Moving to the test directory


#Run Velvet command line tools on the cluster
velveth Assem 29 -short -fasta *.fa -fastq *.fq
#ALL Output file will be under Assem directory
```

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