# 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** 

<u>GitHub</u>

<u>Manual</u>

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:

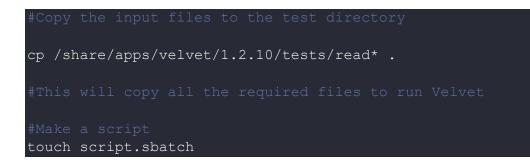
velveth

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,



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