

## ***Transposome on HPC***

### **What is Transposome?**

Transposome is a command line application to annotate transposable elements from paired-end whole genome shotgun data. There are many tools to estimate the mathematical nature of repeats from short sequence reads. There are also several tools for analyzing repeats directly from a genome assembly. This tool allows you to infer the abundance of repeat types in the genome without a reference genome sequence. The output files make it easy to quickly summarize genomic abundance by transposable element class, superfamily, family, or any other level of the repeat taxonomy.

More info on Transposome:

[Transposome- GitHub](#)

### **Versions Available:**

The following versions are available on the cluster:

- Transposome-v0.12.1

### **How to load Transposome?**

To load a specific version, use the following,

```
module load bio/transposome
```

To verify if the module and dependencies are loaded correctly, use the following command.

```
module list
```

This should list all the software and dependencies that are loaded.

### **How to use Transposome?**

There are two ways to use most of the software on the cluster.

*The Interactive Way:*

To run the Transposome in an interactive session, jump into a base terminal of a compute node using the following command:

```
srun -p main --qos main -n 1 -c 16 --mem 12G --pty bash
```

Now, load the Transposome module and start your job interactively on the terminal.

```
#Use this to see the full syntax and options available  
transposome --help
```

**Note:** This is preferred usage in case of short runtime jobs and debugging. After you exit the terminal session, your job will be terminated unlike batch method.

### The Script method:

To use this method, the user will need to write a batch script and submit it to a slurm.

To copy the test files, use the following command,

```
#Make a test dir on home  
mkdir ~/trs-test && cd ~/trs-test  
  
#Get a configuration file for transposome  
curl -sL https://git.io/bPVv > transposome_config.yml  
  
#get input files  
curl -o repeats.fas  
https://raw.githubusercontent.com/sestaton/Transposome/master/t/test_data/t_db.fas  
  
wget https://github.com/sestaton/Transposome/raw/master/t/test_data/t_reads.fas.gz  
&& gunzip *.gz  
  
#make a sbatch script  
touch script.sbatch
```

The sbatch script should be formatted like

```
#!/bin/bash
#SBATCH -J trs-test
#SBATCH -n 1
#SBATCH -c 12
#SBATCH --mem=16G
#SBATCH -p main
#SBATCH --qos main
#SBATCH -e err.err
#SBATCH -o out.out

module load bio/Transposome/

# Move to test data directory
cd $SLURM_SUBMIT_DIR

#Run the Transposome command here
transposome --config transposome_config.yml
```

All the output files will be transposome\_results\_out directory.

Input files and output directory can be changed by editing the configuration file. See further options on GitHub repository.

### ***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>

