

## ***LTR\_retriever on HPC***

### **What is LTR\_retriever?**

LTR\_retriever is a tool for identifying Long Terminal Repeat retrotransposons (LTR-RTs) in genomic sequences. LTR-RTs are a type of transposable element, which are mobile genetic elements that can move around within the genome of an organism. They are composed of two identical copies of a long terminal repeat (LTR) sequence flanking a central region that contains the coding sequences for the enzymes required for their own transposition. LTR-RTs are often found in large numbers in eukaryotic genomes, and they can have significant impacts on genome structure and function. LTR\_retriever is designed to identify LTR-RTs in genomic sequences by processing the output of several other tools that are commonly used to identify LTR-RTs, including LTRharvest, LTR\_FINDER, MGEScan 3.0.0, LTR\_STRUC, and LtrDetector. It then generates a non-redundant library of LTR-RTs for use in genome annotation.

Links:

[Official Website](#)

[Manual](#)

### **Versions Available:**

The following versions are available on the cluster:

- LTR\_retriever v2.9.0

### **How to load LTR\_RETRIEVER?**

To load LTR\_RETRIEVER, use the following commands:

```
#Load the LTR_RETRIEVER module
module load bio/LTR_retriever
```

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

```
#Show all the modules loaded
module list
```

This should list all the LTR\_RETRIEVER dependencies that are loaded – miniconda in this case.

## How to use LTR\_RETRIEVER?

Here are all the command line arguments to,

```
# See all command line args
LTR_retriever -h
```

Users need to specify path to several dependency programs if it automatically doesn't. Please edit /share/apps/LTR\_retriever/paths file to specify dependencies.

A sample slurm script to run LTR\_retriever is given below,

```
#!/bin/bash
#SBATCH --job-name=ltr_retriever
#SBATCH --output=ltr_retriever.out
#SBATCH --error=ltr_retriever.err
#SBATCH -p main
#SBATCH --qos main
#SBATCH --nodes=1
#SBATCH --ntasks 1
#SBATCH --cpus-per-task=12 # Specify no to threads needed
#SBATCH --time=24:00:00
#SBATCH --mem=4GB

# load necessary modules
module load bio/LTR_retriever
# run LTR_retriever
```

```
ltr_retriever --genome=input.fa --output=output.fa --  
threads=$SLURM_CPUS_PER_TASK
```

### ***Where to find help?***

If you are confused or need help at any point, please contact OIT at the following address.

<https://ua-app01.ua.edu/researchComputingPortal/public/oitHelp>

