

Last on HPC cluster:

What is Last?

Last is a Genome-Scale Sequence Comparison tool. Last finds similar regions between sequences and aligns them. It is usually used for comparing large datasets to each other (e.g., vertebrate genomes and/or considerable number of DNA reads).

Some of the features of the last are:

- Indicate the (un)ambiguity of each column in an alignment.
- Use sequence quality data in a rigorous fashion.
- Align DNA to proteins with frameshifts.
- Compare PSSMs to sequences.
- Calculate the likelihood of chance similarities between random sequences.

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

[GitHub](#)

[Docs](#)

Versions Available:

- Last v921

How to load a version of Last?

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

```
module load bio/last/921
```

Verify by using this command:

```
module list
```

Above command should list Gcc compiler and last itself since it is a standalone software.

Note:

```
The executable can be found in the following directory:  
/share/apps/last/bin/lastdb
```

How to use Last on the cluster?

The Script:

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

```
#Get the example input files  
  
svn checkout  
https://github.com/UCSantaCruzComputationalGenomicsLab/last/trunk/exam  
ples
```

Here is the link to additional tutorials.

[Tutorials](#)

Use the following template for the script,

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

# Load the module
module load bio/last/921

#Compare the human and fugu mitochondrial genomes
lastdb -c humdb $SLURM_SUBMIT_DIR/examples/humanMito.fa

#Aligns similar regions between the two genomes | out file is
myalns.maf
lastal humdb $SLURM_SUBMIT_DIR/examples/fuguMito.fa > myalns.maf

# remove temp files
rm humdb*
```

Schedule the job with the following sbatch command.

```
sbatch script.sbatch
```

The result file named myalns.maf should be available in the same directory.

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>