

# ***GMAP on HPC***

## **What is GMAP?**

The programs GMAP and GSNAP, for aligning RNA-Seq and DNA-Seq datasets to genomes, have evolved along with advances in biological methodology to handle longer reads, larger volumes of data, and new types of biological assays. The genomic representation has been improved to include linear genomes that can compare sequences using single-instruction multiple-data (SIMD) instructions, compressed genomic hash tables with fast access using SIMD instructions, handling of large genomes with more than four billion bp, and enhanced suffix arrays (ESAs) with novel data structures for fast access. [\[Source\]](#)

Links:

[Website](#)

## **Versions Available:**

The following versions are available on the cluster:

- GMAP version 2017-11-15

## **How to load GMAP?**

To load GMAP, use the following commands:

```
#Load the GMAP module  
module load bio/gmap
```

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

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

This is a standalone software hence has no dependency.

## **How to use GMAP?**

The default genome directory is /home/ltian6/gmap/share. However, user can pass "-D" or "-d" to change the database or request access to the directory.

The usage of the gmap executable is found in the following link,

[Gmap Command Line Arguments](#)

[Gmap HPC](#)

The documentation of the usage of the binaries are found in,

[ReadMe](#)

## ***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>

