Augustus on HPC

What is Augustus?

AUGUSTUS is a gene prediction program written or maintained by Mario Stanke, Oliver Keller, Stefanie König, Lizzy Gerischer, Katharina Hoff, Giovanna Migliorelli, Lars Gabriel, Anica Hoppe, Tonatiuh Peña Centeno, Henry Mehlan, Daniel Honsel and Steffen Herbold. It can be used as an ab initio program, which means it bases its prediction purely on the sequence. AUGUSTUS may also incorporate hints on the gene structure coming from extrinsic sources such as EST, MS/MS, protein alignments and syntenic genomic alignments. Since version 3.0 AUGUSTUS can also predict the genes simultaneously in several aligned genomes. AUGUSTUS has been trained for predicting genes of many common species.

More info on AUGUSTUS:

GitHub-About

References-GitHub

Versions Available:

The following versions are available on the cluster:

- Augustus–v3.3.2
- Augustus –v3.4.0

How to load Augustus?

To load Augustus on the HPC, use the following commands:

```
module avail bio/augustus
#This will show all the available versions of augustus
```

Use the following command to load the desired version.

```
module load bio/augustus/3.4.0
```

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 Augustus?

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

The Interactive Way:

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

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

Now, load the augustus module and start your operation on the terminal.

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 slrum.

To copy the example file, use the following command,

```
mkdir ~/ag-test && cd ~/ag-test
cp /share/apps/augustus/3.4.0/augustus-3.4.0/examples ~/ag-test
```

The example.fa sequence file will be transferred to ag-test directory. Now make a script using following format.

```
#!/bin/bash
#SBATCH --job-name=qe-test          # create a short name for your job
#SBATCH -n 1
#SBATCH -c 8                         # number of cores

#SBATCH --mem=16G                    # total memory per node
#SBATCH --time=00:15:00              # total run time limit (HH:MM:SS)
#SBATCH -p main
#SBATCH --qos main
#SBATCH -e err.err
#SBATCH -o out.out

module load bio/augustus/

cd $SLURM_SUBMIT_DIR
#Use Augustus commands here
srun augustus --species=human --UTR=on example.fa > output.txt
```

The output file will be written in the current directory in output.txt file.

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