Diyabc on HPC

What is Diyabc?

DIYABC is a set of tools implementing *Approximate Bayesian Computation* (ABC) combined with supervised machine learning based on *Random Forests* (RF), for **model choice** and **parameter inference** in the context of **population genetics** analysis.[source]

Documentation

GitHub

Versions Available:

The following versions are available on the cluster:

- diyabc-RF-linux-v1.1.24

How to load Diyabc?

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

```
#Load the diyabc module
module load bio/diyabc
```

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 software and dependencies that are loaded. In this case, only diyabc will be loaded since this is a standalone software.

How to use Diyabc?

For this tutorial, download the test files from the following link,

```
# Download test files | should download human directory with all input
files
svn checkout
https://github.com/diyabc/diyabc/trunk/tests/datasets/human
```

To use diyabc on this input file, use the following script,

```
#!/bin/bash
#SBATCH -J test
#SBATCH -p main
#SBATCH -q main
#SBATCH --nodes 1
#SBATCH --ntasks-per-node 8

#Load the module
module load bio/diyabc

# Go to job submission directory
cd $SLURM_SUBMIT_DIR

# Run diyabc with 8 threads
diyabc-RF-linux-v1.1.24 -p human/ -R ALL -r 12000 -g 50 -m -t
$SLURM_NTASKS
```

The results should be 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