GRiD on HPC

What is GRiD?

Growth Rate Index (GRiD) measures bacterial growth rate from reference genomes (including draft quality genomes) and metagenomic bins at ultra-low sequencing coverage (> 0.2x). GRiD is described in Emiola and Oh (2018) "High throughput in situ metagenomic measurement of bacterial replication at ultra-low sequencing coverage."

GRiD algorithm consists of two modules:

- < single > which is applicable for growth analysis involving a single reference genome
- < multiplex > for the high-throughput growth analysis of all identified bacteria in a sample. Prior knowledge of microbial composition is not required. To use this module, you must either download the GRiD database or create your custom GRiD database.

Links:

<u>GitHub</u>

Versions Available:

The following versions are available on the cluster:

• grid v1.3

How to load GRiD?

To load GRID, use the following commands:

module load bio/GRiD

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



This should list all dependencies that are loaded. In this case, only grid will be loaded. The python environment will change after loading the module.

How to use GRiD?

To demonstrate the usage of GRiD, download the following test files in a test directory in home folder:

```
# Download test files
wget https://github.com/ohlab/GRiD/archive/1.3.tar.gz
#Unzip
tar xvf 1.3.tar.gz
# Move to the unzipped directory
cd GRiD-1.3/test
```

To use the Grid on this input files, use the following commands

```
# Use grid in input files
grid single -r . -g S_epidermidis.LRKNS118.fna -o output_single
# Run grid with 16 threads
grid multiplex -r . -d . -p -c 0.2 -o output multiplex -n 16
```

If you are using slurm scheduler, use a threaded sbatch script for this program for optimal efficiency.

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