VERSION 1

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Assign taxonomy to gene calls using Centrifuge V.1

James E Thornton Jr¹

¹Hurwitz Lab

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James E Thornton Jr
Hurwitz Lab

ABSTRACT

Uses a custom Centrifuge pipeline to assign taxonomy to gene calls.

OPEN ACCESS

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Protocol status: Working

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PROTOCOL integer ID:
8647

1 Log into the HPC

Command

```
$ ssh hpc  
$ ocelote
```

- 2 Move into your class directory.

Command

```
$ cd /rsgroups/bh_class/username
```

- 3 Clone the Centrifuge github repository.

Command

```
$ git clone git@github.com:jetjr/Centrifuge.git
```

- 4 Move into the Centrifuge directory.

Command

```
$ cd Centrifuge
```

Dependencies

- 5 This program uses R packages that must be installed prior to launching the job. Load the R module.

Command

```
$ module load unsupported  
$ module load markb/R/3.1.1
```

6 Launch R.

Command

```
$ R
```

7 Get the "optparse" package.

8 Get ggplot2 and plyr packages. You may be prompted to select a mirror. Any US server will work.

Command

```
> install.packages(

```

Note

If you receive an error when installing the dependencies, continue with the protocol.

9 Quit the R session. Do not save workspace image.

Command

```
> q()  
> Save workspace image? [y/n/c]: n
```

- 10** Edit the config.sh file to include the correct variable declarations. The following steps will detail how the config.sh file should be edited.

Command

```
$ nano  
config.sh
```

CENT_DB

- 11** `export CENT_DB="/rsgprs/bh_class/b_compressed+h+v/b_compressed+h+v"`

FASTA_DIR

- 12** `export FASTA_DIR="/rsgprs/bh_class/username/prodigal"`

Note

FASTA_DIR should point to the directory containing your nucleotides.fna file generated from step 2 and transferred to the anvio-genes directory.

TYPE

- 13** `export TYPE="single"`

FILE_EXT

14 `export FILE_EXT="fna"`

REPORT_DIR

15 `export REPORT_DIR="/rsgrps/bh_class/username/taxonomy"`

Note

The program will create this directory for you. Make sure to replace username.

PLOT_OUT

16 `export PLOT_OUT='/rsgrps/bh_class/username/taxonomy/'`

Note

Same as REPORT_DIR but make sure to include the trailing / as stated in the config.sh file.

PLOT_FILE and PLOT_TITLE

17 These should be named according to what sample your working with. For example, ocean data may name these:

```
export PLOT_FILE='ocean_depth'  
export PLOT_TITLE='ocean_depth'
```

Note

PLOT FILE will be the file name of the bubble plot that is generated.

PLOT TITLE will be the title found on the actual plot.

FILE_TYPE

18 `export FILE_TYPE="f"`

Note

The nucleotides.fna file is in FASTA format.

EXCLUDE

19 The exclude parameter can be left blank.

`export EXCLUDE=""`

20 Save and quit config.sh

21 Submit the job using the submit script found in the Centrifuge directory.

Command

```
$ ./submit.sh
```

22 Status of the job can be determined by the following command:

Command

```
$ stat -u username
```