MG_HW6: Gene Calls with Prodigal Version 3

James Thornton

Abstract

This protocol provides the procedure to generate gene calls on your contigs using Prodigal.

Citation: James Thornton MG_HW6: Gene Calls with Prodigal. **protocols.io**
dx.doi.org/10.17504/protocols.io.f47bqzn
Published: 17 Oct 2016

Protocol

Step 1.

Login to the HPC and move into Cluster(ICE).

cmd COMMAND
```
$ ssh hpc
$ ice
```

NOTES
James Thornton Jr 17 Oct 2016

Option 3 if you have menu enabled.

Step 2.

Move into your class directory.

cmd COMMAND
```
$ cd /rsgrps/bh_class/username
```
Use YOUR username to be in the right directory

Step 3.

Copy the following into a new script called run-interactive.sh :

cmd COMMAND
```
#!/bin/bash

#PBS -W group_list=bh_class
#PBS -q windfall
#PBS -l jobtype=cluster_only
#PBS -l select=1:ncpus=2:mem=4gb
#PBS -l walltime=24:00:00
#PBS -l cput=24:00:00
#PBS -l place=pack:shared
#PBS -M netid@email.arizona.edu
```

```
#PBS -m bea
```
Replace netid

Step 4.

Submit run-interactive.sh interactively using qsub:

cmd COMMAND

```
qsub -I run-interactive.sh
```
The capital " I " indicates this will be an interactive job

EXPECTED RESULTS

Step 5.

Once the job is ready move back into your class directory.

cmd COMMAND

```
$ cd /rsgrps/bh_class/username
```
Use YOUR username

Step 6.

Make a directory named prodigal:

cmd COMMAND

```
$ mkdir prodigal
```

Step 7.

Move into your assembly directory which contains your contigs:

cmd COMMAND

```
$ cd /rsgrps/bh_class/username/assembly
```

NOTES

James Thornton Jr 17 Oct 2016

Note: Its possible your contigs are in another directory (megahit-out). Move to the directory where final_contigs.fa are located. Remember final_contigs.fa is the combined assemblies from your partner.

Step 8.

Load prodigal and run it on your fixed_contigs.fa to generate gene calls.

cmd COMMAND

```
$ module load prodigal/2.6.2
$ prodigal -i fixed_contigs.fa -o ../prodigal/gene_calls -a ../prodigal/proteins.faa -
```

```
d ../prodigal/nucleotides.fna
```

IMPORTANT: make sure to run prodigal on the fixed_contigs.fa file which was generated when simplifying the fasta header lines. The output will be placed in the prodigal directory that was created and the file name will be gene_calls in addition to a file containing the protein (proteins.faa) and nucleotide (nucleotide.faa) sequences for the genes.

NOTES

James Thornton Jr 17 Oct 2016

Since final_contigs.fa may be located somewhere other than the assembly directory, you can write out the full paths to make sure the output goes where its suppose to:

$ prodigal -i /path/to/final_contigs.fa -o /rsgrps/bh_class/username/prodigal/gene_calls -
a /rsgrps/bh_class/username/prodigal/proteins.faa -
d /rsgrps/bh_class/username/prodigal/nucleotides.fna

ANNOTATIONS

James Thornton Jr 17 Oct 2016

The prodigal command is executed in one line.

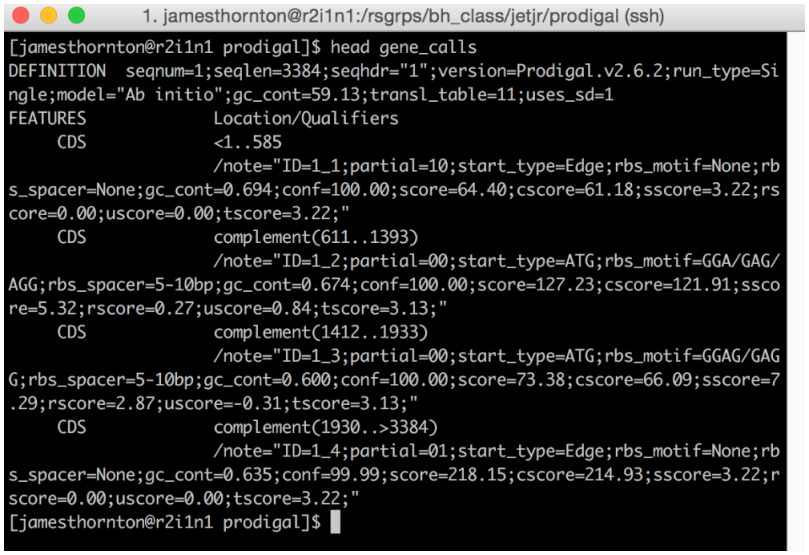
Step 9.

Move into your prodigal directory and make sure the gene calls were generated.

COMMAND

```
$ cd /rsgrps/bh_class/username/prodigal
$ head gene_calls
```

EXPECTED RESULTS



Step 10.

Use your scripting or unix skills to detect how many genes were detected on each of the assemblies. Create a table in google documents that shows the number of "ORFs" or open reading frames

detected on each assembly. We will add addiitonal data to this table later on # of genes with annotation, so the table should have a single column for #ORFs and the rows should be the name of each sample "SRR..."