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Gene calling with Prodigal V.1

Forked from [MG_HW6: Gene Calls with Prodigal](#)

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ABSTRACT

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

1 Login to the HPC and move into ocelote.

Command

```
$ ssh hpc  
$ ocelote
```

- 2 Move into your class directory.

Command

Use YOUR username to be in the right directory

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

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

Command

Replace netid

```
#!/bin/bash  
#PBS -W group_list=bh_class  
#PBS -q windfall  
#PBS -l select=1:ncpus=2:mem=4gb  
#PBS -l walltime=24:00:00  
#PBS -l cput=24:00:00  
#PBS -M netid@email.arizona.edu  
#PBS -m bea
```

- 4 Submit run-interactive.sh interactively using qsub:

Command

The capital

```
qsub -I run-interactive.sh
```

Expected result

A terminal window screenshot with a title bar showing three colored buttons (red, yellow, green) and the text '1. jamesthornton@r2i1n1'. The terminal content shows a user at a prompt '[jamesthornton@service2 jetjr]\$' typing 'qsub -I run-interactive.sh'. The output is 'qsub: waiting for job 655455.service2 to start' followed by 'qsub: job 655455.service2 ready'. The prompt then changes to '[jamesthornton@r2i1n1 ~]\$' with a cursor.

```
1. jamesthornton@r2i1n1  
[jamesthornton@service2 jetjr]$ qsub -I run-interactive.sh  
qsub: waiting for job 655455.service2 to start  
qsub: job 655455.service2 ready  
[jamesthornton@r2i1n1 ~]$
```

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

Command

Use YOUR username

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

- 6 Make a directory named prodigal:

Command

```
$ mkdir prodigal
```

7 Move into your assembly directory which contains your contigs:

Note

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.

Command

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

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

Note

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
```

Note

The prodigal command is executed in one line.

Command

IMPORTANT: make sure to run prodigal on the final_contigs.fa file which was generated when combining assemblies with your partner. 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.

```
$ prodigal -i final_contigs.fa -o ../prodigal/gene_calls -a ../prodigal/proteins.faa -d  
../prodigal/nucleotides.fna
```

- 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 result

```

1. jamesthornton@r2i1n1:/rsgrps/bh_clas
[jamesthornton@r2i1n1 prodigal]$ head gene_calls
DEFINITION  seqnum=1;seqlen=3384;seqhdr="1";versi
ngle;model="Ab initio";gc_cont=59.13;transl_table
FEATURES             Location/Qualifiers
     CDS             <1..585
                     /note="ID=1_1;partial=10;sta
s_spacer=None;gc_cont=0.694;conf=100.00;score=64.
core=0.00;uscore=0.00;tscore=3.22;"
     CDS             complement(611..1393)
                     /note="ID=1_2;partial=00;sta
AGG;rbs_spacer=5-10bp;gc_cont=0.674;conf=100.00;s
re=5.32;rscore=0.27;uscore=0.84;tscore=3.13;"
     CDS             complement(1412..1933)
                     /note="ID=1_3;partial=00;sta
G;rbs_spacer=5-10bp;gc_cont=0.600;conf=100.00;sco
.29;rscore=2.87;uscore=-0.31;tscore=3.13;"
     CDS             complement(1930..>3384)
                     /note="ID=1_4;partial=01;sta
s_spacer=None;gc_cont=0.635;conf=99.99;score=218.
score=0.00;uscore=0.00;tscore=3.22;"
[jamesthornton@r2i1n1 prodigal]$ █

```

- 10 Use your scripting or unix skills to detect how many genes were detected in your contigs file. Create a table that shows the number of 'ORFs' or open reading frames detected on the contigs.