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8373

Read Recruitment Using Bowtie2 V.6

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ABSTRACT

This protocol details how to perform read recruitment to the contigs generated from the previous protocol using Bowtie2.

1 Log into the HPC.

Command

```
$ ssh hpc  
$ ocelote
```

PAIRED END CLEAN UP

2 For paired end only:

Move into your fasta directory. Ensure only 1 pair from each file is in the fasta directory. Keep the pair that is "_1.fasta". Move all "_2.fasta" files into the fastq directory.

Command

```
$ cd /rsgrps/bh_class/username/assembly/fastq  
$ mv *_2.fasta ../../fastq
```

Note

In the previous protocol we ended up only using 1 pair for assembly to simplify the process. In this protocol we only want to map the one pair that we used during assembly. Make sure the fasta directory only contains the _1.fasta of the pair.

3 Move into the assembly/megahit-out directory created from the previous protocol.

Command

```
$ cd /rsgrps/bh_class/username/assembly/megahit-out
```

4 Append your final.contigs.fa file with your partners final.contigs.fa file.

Command

```
$ cat final.contigs.fa /rsgrps/bh_class/partnerusername/assembly/megahit-out/final.contigs.fa >
</ProtocolCommand>
<ProtocolNote id=
```

- 5 Simplify the fasta headers of your combined-contigs.fa file using fasta_renamer from the Fastx toolkit.

Command

```
$ module load fastx
$ fastx_renamer -n COUNT -I combined-contigs.fa -o final-contigs.fa
```

Note

Important: If you get 'This looks like a multi-line FASTA file', try this alternative method to rename sequence headers:

```
awk '/^>/{print ">" ++i; next}{print}' < contigs_in.fa > contigs_out.fa
```

- 6 Move into your project directory. Then create a 'read_recruit' directory. Move into that directory.

Command

```
$ cd /rsgrps/bh_class/username
$ mkdir read_recruit
$ cd !$
```

- 7 Create a bam and bowtie2 index directory.

Command

```
$ mkdir bam bt2_index
```

- 8 Move into the contig indexing directory. And create the contig index.

Command

```
$ cd bt2_index  
$ module load bowtie2  
$ bowtie2-build -f /rsgrps/bh_class/username/assembly/megahit-out/final-contigs.fa  
contig_index
```

Note

This step could take awhile depending on the size of your contig file.

- 9 Move into your bam directory found at /rsgrps/bh_class/username/read_recruit/bam

Command

```
$ cd ../bam
```

- 10 Make directories for standard error and standard out.

Command

```
$ mkdir std-err std-out
```

- 11 Copy the following script named bt2_align.sh. Edit the username variables found in the script.

Note

Many of you actually had your fasta files located in:
/rsgroups/bh_class/username/assembly/fasta

Which is fine, just make sure the script points to the correct location.

Command

```
#!/bin/bash
#PBS -W group_list=bh_class
#PBS -q windfall
#PBS -l select=1:ncpus=4:mem=15gb
#PBS -l pvmem=14gb
#PBS -l walltime=24:00:00
#PBS -l cput=24:00:00
#PBS -M netid@email.arizona.edu
#PBS -m bea
echo "my job_id is: ${PBS_JOBID}"
#####change here #####
FASTA_DIR=
```

Note

Important: CONTIGS variable is the contigs that you combined with your partner.

12 Submit the job.

Command

```
$ qsub -e std-err/ -o std-out/ bt2_align.sh
```

13 Upon job completion navigate to your bam std-err directory.

Command

```
$ cd /rsgrps/bh_class/username/read_recruit/bam/std-err
```

- 14** Cat the standard error file to view the alignment rate for each file.

Command

Your file name will differ

```
$ cat 881767.head1.cm.cluster.ER
```