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#navigating into genome folder
cd /Users/gracemrodrigues/Desktop/genome-final

#activating spades 410
conda activate spades410

#running spades with my files
spades.py -1 DRR568552_1.fastq.gz -2 DRR568552_2.fastq.gz -o spadesoutput

#activating environment
conda activate genomeanalysis

#running ABySS with my files 2.3.7
abyss-pe name=assembly k=96 B=2G in='DRR568552_1.fastq.gz
DRR568552_2.fastq.gz'

#cleaning up ABySS files
mkdir abyssout
mv assembly* abyssout/

#using QUAST on the spades assembly v5.3.0
quast.py spadesoutput/scaffolds.fasta -o quastspades

#using QUAST on ABySS assembly v5.3.0
quast.py abyssout/assembly-scaffolds.fa -o quastabyss

#annotating files with dfast 1.3.6
dfast --genome spadesoutput/scaffolds.fasta --out dfast_output

#protein annotation with Prokka Galaxy Version 1.14.6+ galaxy1

#installing barrnap
barrnap --kingdom bac spadesoutput/scaffolds.fasta > rRNAsequences.gff

#creating a file with the rRNA sequences
bedtools getfasta -fi spadesoutput/scaffolds.fasta -bed rRNAsequences.gff -fo
rRNAsequences.fasta

#combining into two new files
mkdir rRNAinfo
mv rRNAs* rRNAinfo/

#copying 16S rRNA sequence from fasta and pasting it into blastn using default settings
Closest match is clostridium tetani KHSU-144316-041 DNA, complete genome

#downloaded two closest relatives to clostridium tetani which are clostridium
cochlearium and clostridium perfringens
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#saved fasta files into new folder called neighbors

#creating a new file called neighbors.txt

Pico neighbors.txt

neighbors/clostridium-c.fasta

neighbors/clostridium-p.fasta

#using fastANI v.1.34 to determine average nucleotide identity

fastANI -q spadesoutput/scaffolds.fasta --rl neighbors.txt -o clostridium.neighbors.txt

Clostridium p less than 70 percent did not output a result