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# Create environment in coda
conda create -n genomeanalysis -c bioconda -c conda-forge abyss quast
dfast fastani spades=4.1.0

# Activate the environment
conda activate genomeanalysis

# Assemble genome using SPAdes v4 1.0
spades.py -1 SRR5961529_1.fastq.gz -2 SRR5961529_2.fastq.gz -o
spadesout

# Assemble genome using AbySS v2 3.7
abyss-pe name=assembly k=96 B=2G in='SRR5961529_1.fastq.gz
SRR5961529_2.fastq.gz'

# Quality Assessment of assembly using Quast v5 3.0
quast.py spadesout/scaffolds.fasta -o quastspades

quast.py abyssout/assembly-scaffolds.fa -o quastabyss

# Barnap version 0.9 to get the 16S rRNA sequence
barrnap --kingdom bac spadesout/scaffolds.fasta > rRNAsequences.gff

# Use bedtools v2.31.1 to pull fasta sequences
bedtools getfasta -fi spadesout/scaffolds.fasta -bed rRNAsequences.gff
-fo rRNAsequences.fasta

# dfast 1.3.6 for protein annotation
dfast --genome spadesout/scaffolds.fasta --out dfast_output

# average nucleotide identity with fastANI 1.34
fastANI -q spadesout/scaffolds.fasta --rl neighbors.txt -o
Chromatiumneighbors.txt

# Protein annotation with RAST
Domain Bacteria, Genus Chromatium, Sp okenii, Genetic Code 11, RAST
annotation is RASTtk

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