1. **Build pangenome**
   1. **CheckM**

cd ../01\_genome\_assemblies

pwd

source /home/mrgao/scratch/miniconda3/bin/activate checkm

checkm taxonomy\_wf genus Cronobacter genomes\_0326/ output\_checkm/files\_out -t 8 -x fna -f output\_checkm/checkm\_result\_0326.txt

* 1. **Prokka**

cd ../01\_genome\_assemblies/genomes\_pass\_QC\_A || exit

pwd

ls \*.fna

source /home/mrgao/scratch/miniconda3/bin/activate prokka\_env

for F in \*.fna; do

N=$(basename $F .fna) ;

prokka --locustag $N --outdir $N --prefix $N $F ; gzip $N/\*;

done

* 1. **Panaroo**

cd ../01\_genome\_assemblies/gff\_genomes\_pass\_QC || exit

pwd

source /home/mrgao/scratch/miniconda3/bin/activate panaroo

panaroo -i \*.gff -o panaroo\_out\_merge\_paralog --clean-mode strict -t 18 --merge\_paralogs

1. **Features annotation**
   1. **Prodigal**

prodigal -i pan\_genome\_reference.fna -o pan\_genome\_reference -a pan\_genome\_reference.proteins.faa

* 1. **eggnog-mapper**

cd ../02\_features || exit

pwd

source /home/mrgao/scratch/miniconda3/bin/activate eggnog-mapper

emapper.py -i pan\_genome\_reference.proteins.faa -o emapper\_out2 --cpu 18 --target\_orthologs one2one

* 1. **VFDB**

cd ../02\_features || exit

pwd

module load blast-plus/2.9.0

blastp -query pan\_genome\_reference.proteins.faa -subject VFDB\_setA\_pro.fas -outfmt 6 -max\_target\_seqs 1 -out blast\_pan\_VFDB\_A\_out.txt

* 1. **CARD**

cd ../02\_features || exit

pwd

module load blast-plus/2.9.0

blastp -query pan\_genome\_reference.proteins.faa -subject protein\_fasta\_protein\_homolog\_model.fasta -outfmt 6 -max\_target\_seqs 1 -out blast\_pan\_card\_out.txt

1. **MLST tree**

cd ../genomes\_pass\_QC

pwd

source /home/mrgao/scratch/miniconda3/bin/activate mlst\_env

mlst --scheme cronobacter \*.fna

grapetree -p mlst.txt > mlst.nwk