#!/bin/bash

#SBATCH -c 4

#SBATCH --mail-user=laura.woods@monash.edu

#SBATCH --time=4:00:00

# Requires abricate

# Note that when results aren’t found, slurm says job failed

conda\_source="/monfs00/scratch/lwoo0007/WoodsL/miniconda/bin/activate"

conda\_env="/monfs00/scratch/lwoo0007/WoodsL/miniconda/conda/envs/abricate\_env"

inp\_dir="../../MAGs/"

op\_dir="./Mackay\_MAGs/"

ext=".fa"

db="ncbi"

minid=70

mincov=80

# Abricate database versions (abricate --list)

#DATABASE SEQUENCES DBTYPE DATE

#argannot 2223 nucl 2022-May-18

#plasmidfinder 460 nucl 2022-May-18

#farmeDB\_filtered\_Woods2022 11234 nucl 2022-May-18

#megares 6635 nucl 2022-May-18

#vfdb 2597 nucl 2022-May-18

#card 2631 nucl 2022-May-18

#ecoli\_vf 2701 nucl 2022-May-18

#ecoh 597 nucl 2022-May-18

#resfinder 3077 nucl 2022-May-18

#ncbi 5386 nucl 2022-May-18

source $conda\_source base

conda activate $conda\_env

# Get version

echo abricate --version

# Check output directory

if [ ! -d $op\_dir ]

then

mkdir $op\_dir

fi

# Abricate all MAGs together

# Can be performed for each MAG--see abricate github

abricate ${inp\_dir}/\*${ext} --minid $minid --mincov $mincov --db $db >> ${op\_dir}/abricate\_${db}\_combined\_minid-${minid}\_mincov-${mincov}.tsv

# Get abricate summary file for easy heatmaps

abricate --summary ${op\_dir}/abricate\_${db}\_combined.tsv > ${op\_dir}/abricate\_${db}\_combined\_minid-${minid}\_mincov-${mincov}\_summary.tsv