/\*Commands used for MrMC-MinH population genome binning program

\* http://cs.gmu.edu/~mlbio/MrMC-MinH/

\*/

/\*Command that team corrected from MrMC-MinH page\*/

\*from within pig -X local

\*still errors

\*/

$ run -param INPUT=Data/Ecoli.10k.fa -param OUTPUT=Mr\_Out -param P=5 -param KMER=7 -param NUMHASH=15 -param DIV=3 -param CUTOFF=0.8 ScriptMrMCMinH/MrMCMinHGreedy.pig

//also tried this command

$ run -param INPUT=/home/ajm\_bigdata/hmpdata/stool/SRS052697/assembled/SRS052697.scaffolds.fa -param OUTPUT=/home/ajm\_bigdata/outputs/ -param P=5 -param KMER=7 -param NUMHASH=15 -param DIV=151717 -param CUTOFF=0.8 /home/biotools/MrMC-MinH/MrMCMinHGreedy.pig

/\* Developers' original command that team corrected:

pig -param INPUT=<fasta file> -param OUTPUT=<output dir> -param P=5 -param KMER=7 -param NUMHASH=15 -param DIV=<prime number> -param CUTOFF=0.8 -param MrMCMinHGreedy

\*uses 'pig' instead of 'run'

\*has -param in front of pig script

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