\* ssh [tamarams@hpc-class.its.iastate.edu](mailto:tamarams@hpc-class.its.iastate.edu)

\* ls

\* cd eoob563

\* cd EEOB563-Spring2018

\* module load mafft

\* mafft ( for both 13speciescol1a1nt(2).txt and 13speciescol1a2nt.txt)

Output format?

1. Clustal format / Sorted

2. Clustal format / Input order

3. Fasta format / Sorted

4. Fasta format / Input order

5. Phylip format / Sorted

6. Phylip format / Input order

@ 4

OK. arguments = --inputorder

Strategy?

1. --auto

2. FFT-NS-1 (fast)

3. FFT-NS-2 (default)

4. G-INS-i (accurate)

5. L-INS-i (accurate)

6. E-INS-i (accurate)

@ 1

OK. arguments = --auto –inputorder

Additional arguments? (--ep #, --op #, --kappa #, etc)

@

\* paup

\* ToN fromFile=col1a1.aln toFile=col1a1.nxs dataType=nucleotide format=FASTA

\* ToN fromFile=col1a2.aln toFile=col1a2.nxs dataType=nucleotide format=FASTA

\* exe col1a1.nxs

\* log file=paup\_mpsearch.log

\* hsearch start=stepwise addseq=random nreps=100 swap=TBR

\* log file=paup\_bootstrap.log;

\* bootstrap nreps=200 treefile=boot.tre search=heuristic

\* gettrees file=boot.tre StoreTreeWts=yes mode=3;

Do you want to increase 'Maxtrees'? (Y/n)y

Enter new value for 'Maxtrees' (200):200

Action if limit is hit:

(1) Prompt for new value

(2) Automatically increase by 100 (= AUTOINC)

(3) Leave unchanged, and don't prompt

(1)>2

\* contree all/strict=no majrule=yes usetreewts=yes treefile=bootMajRule.tre;

\* mafft (for both files again)

\* Input file? (fasta format)

@ 13speciescol1A1nt(2).txt

OK. infile = 13speciescol1A1nt(2).txt

Output file?

@ col1a1.phy

OK. outfile = col1a1.phy

Output format?

1. Clustal format / Sorted

2. Clustal format / Input order

3. Fasta format / Sorted

4. Fasta format / Input order

5. Phylip format / Sorted

6. Phylip format / Input order

@ 6

OK. arguments = --phylipout --inputorder

Strategy?

1. --auto

2. FFT-NS-1 (fast)

3. FFT-NS-2 (default)

4. G-INS-i (accurate)

5. L-INS-i (accurate)

6. E-INS-i (accurate)

@ 1

OK. arguments = --auto --phylipout –inputorder

\* module load raxml (do for both)

\* alias raxmlHPC='raxmlHPC-PTHREADS-SSE3 -T2'

\* raxmlHPC -m GTRGAMMA -p 12345 -s col1a1.phy -# 20 -n T1

\* raxmlHPC -m GTRGAMMA -p 12345 -# 40 -s col1a1.phy -n T3

\* raxmlHPC -m GTRGAMMA -p 12345 -x 12345 -# 200 -s col1a1.phy -n T4

\* raxmlHPC -m GTRCAT -J MR -z RAxML\_bootstrap.T4 -n T5

\* module load newick\_utils

\* nw\_display RAxML\_MajorityRuleConsensusTree.T5