Species name can not have ‘-‘ character , ‘\_’ is ok

paste ref.3colum /home/Sunhh/WM\_Reseq/Final\_Raw/\*/\*.1col > temp-102-acc.table &

nohup snp-table-filter.2 temp-102-acc.table wm-102acc-snp.noMiss.table 0.999999 &

script-cut-1-colum (wwz server)

script-colum-2-fasta ### each column -> each fasta file

java -cp ~/bin/readseq.jar run -informat=8 -f 17 wm-102acc-snp.noMiss.faseq # fasta -> nexus format)

Near the top of the file find this "MISSING=-" and change it into "GAP=-".

Paup

* Near the top of the file find this "MISSING=-" and change it into "GAP=-".
* paup> execute wm-102acc-snp.noMiss.faseq.nexus

Processing of file "/data/home/linyong/linyong-under-fei-account/watermelon-reseq/pau/wm-102acc-snp.noMiss.faseq.nexus" begins...

Data read in DNA format

Data matrix has 103 taxa, 814730 characters

Valid character-state symbols: ACGT

Missing data identified by '-'

"Equate" macros in effect:

R,r ==> {AG}

Y,y ==> {CT}

M,m ==> {AC}

K,k ==> {GT}

S,s ==> {CG}

W,w ==> {AT}

H,h ==> {ACT}

B,b ==> {CGT}

V,v ==> {ACG}

D,d ==> {AGT}

N,n ==> {ACGT}

Processing of file "/data/home/linyong/linyong-under-fei-account/watermelon-reseq/pau/wm-102acc-snp.noMiss.faseq.nexus" completed.

paup> hsearch start=stepwise addseq=random nreps=100 rseed=98367 swap=TBR increase=auto

paup> savetrees file=temp-alltrees.nexus brlens=yes

1. exclude gapped, "exclude 1-29 560-577" makes PAUP\* ignore columns 1 through 29 as well as columns 560 through 577
2. outgroup olive\_baboon macaque yellow\_baboon
3. set root=outgroup outroot=monophyl
4. pscores [all] (This prints the length of the trees that are currently in memory.)
5. describetrees all/plot=cladogram Tree number 2 (rooted using default outgroup); Tree length = 403; Consistency index (CI) = 0.9603; Homoplasy index (HI) = 0.0397; CI excluding uninformative characters = 0.9252; HI excluding uninformative characters = 0.0748; Retention index (RI) = 0.9884; Rescaled consistency index (RC) = 0.9491. (plot=phylogram)
6. gettrees file=mhcalltrees.nexus mode=7 (append trees from the nexus file to the ones currently in memory)
7. treedist
8. cleartrees
9. delete 5-40 (delete taxa # 5 – 40)
10. set criterion=likelihood
11. lset nst=2 tratio=estimate basefreq=equal rates=gamma shape=estimate
12. bootstrap nreps=200 treefile=boot.tre search=heuristic/ start=stepwise addseq=random nreps=10 swap=TBR;
13. savetrees file=bootMajRule.tree.nexus from=1 to=1 savebootp=nodelabels;
14. mm

BEGIN SETS;

CHARSET beginning = 1-12;

CHARSET end = 895-898;

TAXSET outgroups = Lemur\_catta;

END;

begin paup;

1. log start replace=yes file=FILENAME\_log.txt;
2. set autoclose=yes criterion=parsimony root=outgroup storebrlens=yes increase=auto;
3. outgroup MyOutgroup;
4. hsearch addseq=random nreps=1000 swap=tbr hold=1;
5. savetrees file=mytrees.tre format=altnex brlens=yes;
6. log stop;

END;

begin paup;

1. log start replace=yes file=FILENAME\_log.txt;
2. set autoclose=yes criterion=parsimony root=outgroup storebrlens=yes increase=auto;
3. outgroup MyOutgroup;
4. bootstrap nreps=1000 search=heuristic/ addseq=random nreps=10 swap=tbr hold=1;
5. savetrees from=1 to=1 file=MyBootTree.tre format=altnex brlens=yes savebootp=NodeLabels MaxDecimals=0;
6. log stop;

END;