README file for the parsimony analysis using Tree Analysis using New Technology (TNT v.1.5)

Reading from C:\Users\Giuseppe\Desktop\Works in progress_ELASMOBRANCHS

BOLCA\Manuscripts\Arechia\Arechia_TNT.tnt

Matrix (102x33, 16 states). Memory required for data 0.16 Mbytes

0 trees in memory

Random seed is 1

Warning:

1000 reps. With 10 trees each exceeds available treespace (100)

Search may have to be interrupted if tree-buffer is filled

Repl. 1000

Algor. TBR

Tree 26 of 26

Score ------

Best score 215

Time 0:00:05

Rearrangs. 32,156,150

Completed 1000 random addition sequences.

Total rearrangements examined: 32,156,150.

Best score hit 396 times out of 1000.

Best score (TBR): 215. 1 trees retained.

Time 5.11 secs.

Data matrix has 33 taxa, 102 characters

Valid character-state symbols: 01234

Missing data identified by '?'

Gaps identified by '-'

Character types changed:

      Of 102 total characters:

            All characters are of type 'unordered'

            All characters have equal weight

Outgroup status:

      2 taxa transferred to outgroup

      Total number of taxa now in outgroup = 2

      Number of ingroup taxa = 31

Taxon-status summary:

      Original data matrix contains 33 taxa

      No taxa have been deleted

      Number of (nondeleted) outgroup taxa = 2

Character-status summary:

      Current optimality criterion = parsimony

      No characters are excluded

      Of 102 total characters:

            All characters are of type 'unordered'

            All characters have equal weight

            3 characters are constant (proportion = 0.0294118)

            10 variable characters are parsimony-uninformative

            Number of parsimony-informative characters = 89

Traditional search settings (branch-and-bound):

Starting trees:

      1 random seed

      1000 repls.

Swapping algorithm:

      tree bisection reconnection (TBR)

Trees to save per replication 10

Collapse trees after the search

Replace existing trees