

Instructions for 6-P weighting methods:

The reference that describes this method in detail is

Stanger-Hall, K., and C. W. Cunningham. 1998. Support for a monophyletic Lemuriformes: Overcoming incongruence between data partitions. *Mol. Biol. Evol.* 15:1572-1577.

You may also want to cite

Cunningham. 1997. Is congruence between data partitions a reliable predictor of phylogenetic accuracy? Empirically testing an iterative procedure for choosing among phylogenetic methods. *Syst. Biol.* 46:464-478.

and definitely cite

Williams, P. L., and W. M. Fitch. 1990. Phylogeny determination using the dynamically weighted parsimony method. *Methods Enzymol.* 183:615-626.

- 1) With PAUP\* 4.0, find either the most parsimonious tree, or the most likely tree under some simple model of evolution. The starting tree makes little difference in the end.
- 2) Under the "Analysis Menu" Choose "Likelihood"
- 3) Under the "Analysis Menu" choose "Likelihood settings".
- 4) For Substitution model (the first window you see) choose "General Time Reversible Model", and choose "estimate".

If you want, you can also go to the "among-site variation menu" and choose one of those options. This is not necessary, but may be good to try.

- 5) Under "tree menu" choose "describe tree". This may take a few minutes, but is usually pretty fast. Two matrices will be shown, the R-matrix and the Q-matrix. You want the R-matrix.

- 6) To copy this over, you go to the "Edit" menu, choose "Edit Display Buffer". This will allow you to manipulate the text of the R-matrix. Eliminate all the spaces to the left of the matrix, so the matrix is flush left.

Then, replace all of the spaces between the numbers with tabs (this is so excel can read the matrix).

- 7) FINALLY! You can paste this matrix into the excel spreadsheet I am sending. You can then paste the resulting matrix (along with the text beginning "Usertype" and ending with the semicolon" into your PAUP file anywhere after the first "end".

- 8) For different partitions, it is a great idea to do independent 6-P matrices for each of them. Here is a sample data file which defines character partitions, and has different partitions for each taxon.

[Matrix here]

;

END;

charpartition all5 = C1:1-1506,C2:1507-2154,C3:2155-2940,CY:2941-4035,A6:4036-4638;

BEGIN ASSUMPTIONS;

CHARSET CO1 = 1-1506;

CHARSET CO2 = 1507-2154;

CHARSET CO3 = 2155-2940;

CHARSET CYTB = 2941-4035;

CHARSET ATP6 = 4036-4638;

USERTYPE ATP6ln STEPMATRIX= 4

A C G T  
[A] . 1 2 1  
[C] 1 . 3 1  
[G] 2 3 . 3  
[T] 1 1 3 .

;

USERTYPE CO1ln STEPMATRIX= 4

A C G T  
[A] . 1 2 2  
[C] 1 . 3 1  
[G] 2 3 . 3  
[T] 2 1 3 .

;

USERTYPE CO2ln STEPMATRIX= 4

A C G T  
[A] . 1 2 2  
[C] 1 . 3 1  
[G] 2 3 . 3  
[T] 2 1 3 .

;

USERTYPE CO3ln STEPMATRIX= 4

A C G T  
[A] . 1 2 2  
[C] 1 . 3 1  
[G] 2 3 . 4  
[T] 2 1 4 .

;

USERTYPE CYTBln STEPMATRIX= 4

A C G T  
[A] . 1 2 2  
[C] 1 . 3 1  
[G] 2 3 . 4  
[T] 2 1 4 .

;

end

typeset \* 6P = ATP6ln:ATP6, CO1ln:CO1, CO2ln:CO2, CO3ln:CO3, CYTBln:CYTB;