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:

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

and definitely cite


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;
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;