

## **For likelihood computations, the command file should include:**

### 1- The name of the sequence files.

Each sequence file is preceded by the instruction seqfileN (N indicates the number of the sequence file).

For example in the case of the mitochondrial data set:

```
seqfile1 ND1.ali  
seqfile2 ND2.ali  
seqfile3 COX1.ali  
seqfile4 COX2.ali  
seqfile5 ATP8.ali  
seqfile6 ATP6.ali  
seqfile7 COX3.ali  
seqfile8 ND3.ali  
seqfile9 ND4L.ali  
seqfile10 ND4.ali  
seqfile11 ND5.ali  
seqfile12 CYTB.ali
```

### 2- The format of the sequence files.

For each sequence file, the file format should be indicated. fasta, phylip, clustal, and mase formats can be recognized by the program. Each file format is preceded by the instruction formatN (N indicates the number of the sequence file).

For example in the case of the mitochondrial data set:

```
format1 fasta  
format2 fasta  
format3 fasta  
format4 fasta  
format5 fasta  
format6 fasta  
format7 fasta  
format8 fasta  
format9 fasta  
format10 fasta  
format11 fasta  
format12 fasta
```

### 3- The model of sequence of the sequence.

For each sequence file, the model of sequence evolution should be indicated. JTT , dayoff (“DAY”), and REV models can be recognized by the program. Each model of sequence evolution is preceded by the instruction modelN (N indicate the number of the sequence file).

For example in the case of the mitochondrial data set:

```
model1 rev  
model2 rev  
model3 rev  
model4 rev  
model5 rev  
model6 rev  
model7 rev  
model8 rev  
model9 rev  
model10 rev  
model11 rev  
model12 rev
```

4- The size of the alphabet of the model of sequence of the sequence.

The program is, currently, only able to consider protein sequences so the size of the alphabet should be 20 for each sequence file.

For example in the case of the mitochondrial data set:

```
alphabet1 20  
alphabet2 20  
alphabet3 20  
alphabet4 20  
alphabet5 20  
alphabet6 20  
alphabet7 20  
alphabet8 20  
alphabet9 20  
alphabet10 20  
alphabet11 20  
alphabet12 20
```

For nucleotide sequences, a beta version is available upon request.

5- The name of the tree file.

The tree file should be in NEWICK/PHYLIP format and unrooted. It may include branch lengths or not (but no negative branch lengths...). If branch lengths are indicated, they will be used as a first guess for the reconstruction of the best tree (it can save computation time). The name of the tree file should be preceded by the instruction treefile.

For example:

```
treefile tree.tre
```

6- The name of the output file.

The name of the tree file should be preceded by the instruction logfile.

For example:  
logfile outfile.txt

### 7- Gamma

The word gamma should be added if among site rate variation is to be taken into account. Otherwise, the homogenous model is considered.

### 8- Log level

loglvl indicated the level of the details included in the output file. Currently it is better to use "loglvl 10"

In order to shorten the computation time it is possible to indicate a first guess for the alpha parameters of each tree and for the rates of each gene. The second case should only be applied when the proportional model is used.

For example:

For the N-GAM models:

```
gamma  
alpha1 0.49  
alpha2 0.52  
alpha3 0.68  
...  
alphaN 0.35
```

For the 1-GAM models:

```
gamma  
alpha 0.49
```

(no index should be added to the instruction alpha)

For the proportional models:

```
rate1 0.49  
rate2 1.58  
rate3 2.86  
...  
rateN 0.34
```

## **For Kishino-Hasegawa test computations, the two command files MUST include**

All the information included above all (point 1-8), as well as all the information concerning the alpha parameters of each tree and the rates of each gene (for the proportional model). The tree files considered must also include branch lengths. In the case of the separate model, the N trees should be given in one file one after the other.

For example in the case of a data set including 3 genes the tree file format should be:

```
((spA:0.6,spB:0.56), spC:0.04,spD:1.06);  
((spA:0.3,spB:0.79), spC:0.43,spD:0.007);  
((spA:0.2,spB:0.1), spC:0.783,spD:0.12345);
```