

Supplementary command 1: The site models command of PAML program.

```
seqfile = lysin.nuc
treefile = lysin.trees

outfile = mlc          * main result file name
  noisy = 9    * 0,1,2,3,9: how much rubbish on the screen
verbose = 1    * 1: detailed output, 0: concise output
runmode = 0    * 0: user tree; 1: semi-automatic; 2: automatic
               * 3: StepwiseAddition; (4,5):PerturbationNNI; -2: pairwise

seqtype = 1    * 1:codons; 2:AAs; 3:codons-->AAs
CodonFreq = 2  * 0:1/61 each, 1:FIX4, 2:F3X4, 3:codon table
  clock = 0    * 0: no clock, unrooted tree, 1: clock, rooted tree
  model = 0

               * models for codons:
               * 0:one, 1:b, 2:2 or more dN/dS ratios for branches

NSsites = 1 2 * 0:one w;1:neutral;2:positive; 3:discrete;4:freqs;
               * 5:gamma;6:2gamma;7:beta;8:beta&w;9:beta&gamma;
               * 10:beta&l+gamma; 11:beta&l>normal; 12:0&2normal; 13:3normal
icode = 0    * 0:standard genetic code; 1:mammalian mt; 2-10:see below

fix_kappa = 0  * 1: kappa fixed, 0: kappa to be estimated
  kappa = 1.6  * initial or fixed kappa
fix_omega = 0  * 1: omega or omega_1 fixed, 0: estimate
  omega = .8   * initial or fixed omega, for codons or codon-based AAs

ncatG = 10    * # of categories in dG of NSsites models

getSE = 0    * 0: don't want them, 1: want S.E.s of estimates
RateAncestor = 0 * (0,1,2): rates (alpha>0) or ancestral states (1 or 2)

Small_Diff = 3e-7
cleandata = 0 * remove sites with ambiguity data (1:yes, 0:no)?
  method = 0  * 0: simultaneous; 1: one branch at a time
```

Supplementary command 2: The Branch-site Null models command of PAML program.

```
seqfile = lysozymeLarge.nuc
treefile = lysozymeLarge.trees

outfile = mlc
noisy = 3
verbose = 0
runmode = 0

seqtype = 1 * 1:codons; 2:AAs; 3:codons-->AAs
CodonFreq = 2 * 0:1/61 each, 1:F1X4, 2:F3X4, 3:codon table
clock = 0 * 0:no clock, 1:global clock; 2:local clock; 3:TipDate
aaDist = 0 * 0:equal, +:geometric; -:linear, 1-6:G1974,Miyata,c,p,v,a
aaRatefile = ../wag.dat
model = 2
    * models for codons:
        * 0:one, 1:b, 2:2 or more dN/dS ratios for branches

NSsites = 2 * 0:one w;1:neutral;2:selection; 3:discrete;4:freqs;
            * 5:gamma;6:2gamma;7:beta;8:beta&w;9:beta&gamma;
            * 10:beta&gamma+1; 11:beta&normal>1; 12:0&2normal>1;
            * 13:3normal>0

icode = 0 * 0:universal code; 1:mammalian mt; 2-10:see below
fix_kappa = 0 * 1: kappa fixed, 0: kappa to be estimated
kappa = 3 * initial or fixed kappa
fix_omega = 1 * 1: omega or omega_1 fixed, 0: estimate
omega = 1 * initial or fixed omega, for codons or codon-based AAs

fix_alpha = 1 * 0: estimate gamma shape parameter; 1: fix it at alpha
alpha = 0 * initial or fixed alpha, 0:infinity (constant rate)
Malpha = 0 * different alphas for genes
ncatG = 10 * # of categories in dG of NSsites models

getSE = 0 * 0: don't want them, 1: want S.E.s of estimates
RateAncestor = 0 * (0,1,2): rates (alpha>0) or ancestral states (1 or 2)

Small_Diff = .5e-6
* cleandata = 1
* method = 1 * 0: simultaneous; 1: one branch at a time
```

Supplementary command 3: The Branch-site Alternative models command of PAML program.

```
seqfile = lysozymeLarge.nuc
treefile = lysozymeLarge.trees

outfile = mlc
noisy = 3
verbose = 0
runmode = 0

seqtype = 1 * 1:codons; 2:AAs; 3:codons-->AAs
CodonFreq = 2 * 0:1/61 each, 1:F1X4, 2:F3X4, 3:codon table
clock = 0 * 0:no clock, 1:global clock; 2:local clock; 3:TipDate
aaDist = 0 * 0:equal, +:geometric; -:linear, 1-6:G1974,Miyata,c,p,v,a
aaRatefile = ../wag.dat
model = 2
    * models for codons:
        * 0:one, 1:b, 2:2 or more dN/dS ratios for branches

NSsites = 2 * 0:one w;1:neutral;2:selection; 3:discrete;4:freqs;
            * 5:gamma;6:2gamma;7:beta;8:beta&w;9:beta&gamma;
            * 10:beta&gamma+1; 11:beta&normal>1; 12:0&2normal>1;
            * 13:3normal>0

icode = 0 * 0:universal code; 1:mammalian mt; 2-10:see below
fix_kappa = 0 * 1: kappa fixed, 0: kappa to be estimated
kappa = 3 * initial or fixed kappa
fix_omega = 0 * 1: omega or omega_1 fixed, 0: estimate
omega = 1.5 * initial or fixed omega, for codons or codon-based AAs

fix_alpha = 1 * 0: estimate gamma shape parameter; 1: fix it at alpha
alpha = 0 * initial or fixed alpha, 0:infinity (constant rate)
Malpha = 0 * different alphas for genes
ncatG = 10 * # of categories in dG of NSsites models

getSE = 0 * 0: don't want them, 1: want S.E.s of estimates
RateAncestor = 0 * (0,1,2): rates (alpha>0) or ancestral states (1 or 2)

Small_Diff = .5e-6
* cleandata = 1
* method = 1 * 0: simultaneous; 1: one branch at a time
```

