

Exercise 4 help file: A portion of output for 3 models: M0, M3, and M8. The output is annotated with information that will help you to complete exercise 4. Note that the example output is for a different dataset than the one you will use in exercise 4.

Annotated portion of the results for codon model **M0**:

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.
.
TREE # 1: (((((3, 4), 1), 2), 5); MP score: 154
This is a rooted tree. Please check!
lnL(ntime: 8 np: 10): -1055.334638 ← This is the log likelihood
    6..7    7..8    8..9    9..3    9..4 score (lnL) computed for a
    0.600255 0.085489 0.209403 0.355149 0.79494 dataset of 5 sequences. 0.94 1.801114 0.079244

Note: Branch length is defined as number of nucleotide substitutions per codon (not per nucleotide
site).

tree length = 3.10091

((((3: 0.355149, 4: 0.794944): 0.209403, 1: 0.249128): 0.085489, 2: 0.231447): 0.600255, 5: 0.575094);

((((rabbit: 0.355149, rat: 0.794944): 0.209403, human: 0.249128): 0.085489, goat-cow: 0.231447):
0.600255, marsupial: 0.575094);

Detailed output identifying parameters
kappa (ts/tv) = 1.80111 ← This is the ML estimate of
                        kappa under model M0.
omega (dN/dS) = 0.07924 ← This is the ML estimate of
                        omega under model M0
.
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.
```

Annotated portion of the results for codon model **M3** with $k=3$ site classes:

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Model 3: discrete (3 categories)

TREE # 1: (((((3, 4), 1), 2), 5); MP score
This is a rooted tree. Please check!
lnL(ntime: 8 np: 14): -1045.839986
  6..7    7..8    8..9    9..3    9..4    8..1    7..2    6..5
0.695909 0.078848 0.194592 0.373577 0.883911 0.285355 0.219268 0.631211 1.823190 0.464043 0.514623
0.008677 0.142536 1.344918

Note: Branch length is defined as number of nucleotide substitutions per codon (not per nucleotide
site).

tree length = 3.36267

((((3: 0.373577, 4: 0.883911): 0.194592, 1: 0.285355): 0.078848, 2: 0.219268): 0.695909, 5: 0.631211);

((((rabbit: 0.373577, rat: 0.883911): 0.194592, human: 0.285355): 0.078848, goat-cow: 0.219268):
0.695909, marsupial: 0.631211);

Detailed output identifying parameters
kappa ( ) =  $p_0$  319  $p_1$   $p_2$ 
          ↓ ↓ ↓
dN/dS for site classes (K=3)
p: 0.46404 0.51462 0.02133
w: 0.00868 0.14254 1.34492
.
.
.
          ↑ ↑ ↑
           $\omega_0$   $\omega_1$   $\omega_2$ 

```

This is the log likelihood score (lnL) computed for the same dataset under M3

ML estimates of **proportions** for site classes 1, 2 & 3

ML estimates of **omega** for site classes 1, 2 & 3

Annotated portion of the results for codon model **M8**:

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Model 8: beta&w>1 (11 categories)

TREE # 1: (((((3, 4), 1), 2), 5); MP score
 This is a rooted tree. Please check!
 lnL(ntime: 8 np: 13): -1046.003808
 6..7 7..8 8..9 9..3 9..4 8..1 7..2 6..5
 0.694589 0.081476 0.198355 0.369476 0.877899 0.279892 0.219450 0.635145 1.831201 0.984555 0.693123
 7.401686 1.438893

This is the log likelihood score (lnL) computed for the same dataset under M8

Note: Branch length is defined as number of nucleotide substitutions per codon (not per nucleotide site).

tree length = 3.35628

((((3: 0.369476, 4: 0.877899): 0.198355, 1: 0.279892): 0.081476, 2: 0.219450): 0.694589, 5: 0.635145);

((((rabbit: 0.369476, rat: 0.877899): 0.198355, human: 0.279892): 0.081476, goat-cow: 0.219450): 0.694589, marsupial: 0.635145);

Detailed p_0 at ident Beta parameter p s

kappa (ts/tv) = 1.83120

Parameters in M8 (beta&w>1):

p0= 0.98456 p= 0.69312 q= 7.40169
 (p1= 0.01544) w= 1.43889

Beta parameter q

p_1

$\omega > 1$

NOTES:

p and q are shape parameters for the Beta distribution

p_0 is the **proportion** of beta-distributed sites

p_1 is the **proportion** of sites having $\omega > 1$

an ω is constrained > 1