

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
  6..7    7..8    8..9    9..3    9..4
0.600255 0.085489 0.209403 0.355149 0.794944 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
omega (dN/dS) = 0.07924
.
.
.
```

This is the log likelihood score (lnL) computed for a dataset of 5 sequences.

This is the ML estimate of kappa under model M0.

This is the ML estimate of omega under model M0.

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  $p_0$  =  $p_1$  319  $p_2$ 

dN/dS for site classes (K=3)
p: 0.46404 0.51462 0.02133
w: 0.00868 0.14254 1.34492
.
.
.

```

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

ω_0 ω_1 ω_2

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

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 p0 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

```

p₀

Beta parameter p

Beta parameter q

p₁

$\omega > 1$

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

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