

Solutions:

1. The likelihood has the expression

$$L(t) = \left(\frac{1}{4}\right)^n \left(\frac{1}{4} + \frac{3}{4}e^{-\frac{4}{3}t}\right)^{n_1} \left(\frac{1}{4} - \frac{1}{4}e^{-\frac{4}{3}t}\right)^{n_2}$$

where $n = n_1 + n_2$. We can simplify the analysis by using the transformation $a = e^{-\frac{4}{3}t}$ and working on the log scale. Notice that since $t \geq 0$, it follows that $0 < a \leq 1$ for finite t and that a maximum at $a = 0$ implies that $t = +\infty$. The log-likelihood is as follows.

$$\ell(a) = n \log\left(\frac{1}{4}\right) + n_1 \log\left(\frac{1}{4} + \frac{3}{4}a\right) + n_2 \log\left(\frac{1}{4} - \frac{1}{4}a\right)$$

Take the derivative with respect to a .

$$\begin{aligned} \ell'(a) &= n_1 \frac{3/4}{1/4 + 3a/4} - n_2 \frac{1/4}{1/4 - a/4} \\ &= \frac{3n_1}{1 + 3a} - \frac{n_2}{1 - a} \end{aligned}$$

Set the result to 0 and solve for a .

$$\begin{aligned} 3n_1(1 - a) &= (1 + 3a)n_2 \\ 3n_1 - n_2 &= 3n_1a + 3n_2a \\ a &= \frac{3n_1 - n_2}{3n} \end{aligned}$$

Notice that while this expression for a cannot exceed 1, it could be negative. So, if $3n_1 - n_2 \leq 0$, the mle for a is 0. Express in terms of t . The maximum likelihood estimate of t is

$$\hat{t} = \begin{cases} -\frac{3}{4} \log\left(\frac{3n_1 - n_2}{3n}\right) & \text{if } 3n_1 > n_2 \\ +\infty & \text{otherwise} \end{cases}$$

2. The matrix of pairwise differences is as follows.

	Dol	Hip	Cam	Cow	Gir
Dolphin	0	5	4	6	5
Hippopotamus	5	0	4	6	6
Camel	4	4	0	5	5
Cow	6	6	5	0	3
Giraffe	5	6	5	3	0

The matrix of Jukes-Cantor maximum likelihood distances is here.

	Dol	Hip	Cam	Cow	Gir
Dolphin	0.0000	0.1885	0.1468	0.2326	0.1885
Hippopotamus	0.1885	0.0000	0.1468	0.2326	0.2326
Camel	0.1468	0.1468	0.0000	0.1885	0.1885
Cow	0.2326	0.2326	0.1885	0.0000	0.1073
Giraffe	0.1885	0.2326	0.1885	0.1073	0.0000

The algorithm for finding the UPGMA tree produces this.

```
> upgma(jc)
[1] "Join 4 and 5"
[1] " len( 4 , 4:5 ) = 0.0536628163652525"
[1] " len( 5 , 4:5 ) = 0.0536628163652525"
[1] "Join 1 and 3"
[1] " len( 1 , 1:3 ) = 0.0734042164222857"
[1] " len( 3 , 1:3 ) = 0.0734042164222857"
[1] "Join 1:3 and 2"
[1] " len( 1:3 , 1:3:2 ) = 0.0104193470915270"
[1] " len( 2 , 1:3:2 ) = 0.0838235635138127"
[1] "Join 1:3:2 and 4:5"
[1] " len( 1:3:2 , 1:3:2:4:5 ) = 0.0214519408458271"
[1] " len( 4:5 , 1:3:2:4:5 ) = 0.0516126879943873"
```

The parenthetic representation is this.

```
((Dolphin:0.0734,Camel:0.0734):0.0104,Hippopotamus:0.0838):0.0214,(Cow:0.0537,Giraffe:0.0537):0.0516);
```

3. The neighbor-joining tree has cow with giraffe and camel with hippo. The UPGMA tree also has cow and giraffe together, but camel dolphin are closer than camel hippo.
4. Output from PHYLIP

UPGMA method

Negative branch lengths allowed

```

      +---Dolphin
     +-2
    +-3 +---Camel
     !!
--4 +----Hippopotam
     !
     ! +---Cow
     +--1
       +---Giraffe

```

From	To	Length	Height
4	3	0.02145	0.02145
3	2	0.01043	0.03188
2	Dolphin	0.07340	0.10528
2	Camel	0.07340	0.10528

3	Hippopotam	0.08383	0.10528
4	1	0.05163	0.05163
1	Cow	0.05365	0.10528
1	Giraffe	0.05365	0.10528

Neighbor-joining method

Negative branch lengths allowed

```

+----Hippopotam
+-2
! +--Camel
!
! +---Cow
3---1
! +--Giraffe
!
+----Dolphin
    
```

remember: this is an unrooted tree!

Between	And	Length
-----	---	-----
3	2	0.01043
2	Hippopotam	0.09485
2	Camel	0.05195
3	1	0.07308
1	Cow	0.06100
1	Giraffe	0.04630
3	Dolphin	0.08383