

1. Calculate by hand to get the UPGMA and Neighbor-Joining (NJ) trees from the distance matrix showing below.

手算

$$\begin{pmatrix} 0 & 17 & 21 & 27 \\ 17 & 0 & 12 & 18 \\ 21 & 12 & 0 & 14 \\ 27 & 18 & 14 & 0 \end{pmatrix}$$

Confirm your result by R.

2. Given the tree and the characters of 5 species, you define the name of the internal nodes and the branches to express the **likelihood** in production of terms according to the **3<sup>rd</sup> character** only.

定義 node branch 名子

Table 1.1: A simple data set with 0/1 characters.

Species	Characters					
	1	2	3	4	5	6
Alpha	1	0	0	1	1	0
Beta	0	0	1	0	0	0
Gamma	1	1	0	0	0	0
Delta	1	1	0	1	1	1
Epsilon	0	0	1	1	1	0

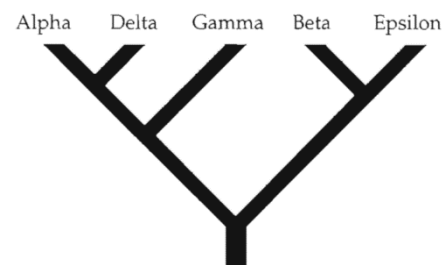


Figure 1.1: A phylogeny that we want to evaluate using parsimony.

3. Run the R code from the practice and show your neighbor-joining (NJ) network with branch reliabilities according to 500 times of bootstrapping.

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