Phylogenetic Trees: UPGMA

Building on our example from last time, the table below shows the number of pairwise differences between samples in $\mathcal{X} = \{A, B, C, D, E\}$. We call this function δ a *dissimilarity map* since:

1. $\delta(x, x) = 0$

2. $\delta(x, y) = \delta(y, x)$

δ	A	B	C	D	E
A	0	1	3	6	6
B		0	2	5	5
C			0	5	5
D				0	2
E					0

| | A | B | C | D | E |

Use the tables below to run UPGMA, gradually building up the tree (use the space above) as you go.

Δ	AB	C	D	E
AB				
C				
D				
E				

Δ

Δ

Tree Metrics and Ultrametrics

1. You are given the dissimilarity map δ below for the samples $\mathcal{X} = \{A, B, C, D\}$. Is δ an ultrametric? Why or why not?

δ	A	B	C	D
A	0	3	4	4
B		0	5	5
C			0	2
D				0

2. Is δ a tree metric? If yes, demonstrate the tree metric by constructing a topology and edge weights that match δ. If not, explain why not.

3. Verify that the dissimilarity map d below is an ultrametric. Then confirm that when UPGMA is applied to this matrix, the induced tree metric is equal to the original.

d	P	Q	R	S
P	0	8	12	4
Q		0	12	8
R			0	12
S				0