Phylogenetic Trees: Neighbor Joining

You are given the dissimilarity map δ below for the samples $\mathcal{X} = \{A, B, C, D, E\}$. Fill in the steps below to create the Neighbor-Joining tree for \mathcal{X} . First, in the space to the right of δ , draw the initialization of the NJ tree and let (lowercase) c be the center node. Write out N_c and $|N_c|$. To start, we let $d = \delta$.

δ	A	В	С	D	Е
А	0	1	3	6	6
В		0	2	5	5
С			0	5	5
D				0	2
Е					0

1. (a) The tables below show S and Q for the first iteration. Verify that S_C and Q(D, E) are correct.

						(Q	В	С	D	Ε
i	А	В	С	D	E	Ā	A	-26	-22	-16	-16
	16	12	15	19	19	Η	В		-22	-16	-16
\mathcal{D}_i	10	10	10	10	10	(C			-18	-18
						Ι	D				-30

(b) Join D and E at internal vertex v and draw the new tree. Then calculate:

- d(D, v) =
- d(E, v) =

(c) Fill in the updated d matrix:

d	A	В	С	v
А	0	1	3	
В		0	2	
\mathbf{C}			0	
V				0

2. (a) Second iteration: verify S_v , Q(A, B), and Q(C, v).

					Q	B	С	v
i	A	В	С	V	A	-14	-12	-12
S_i	9	7	9	13	В		-12	-12
					С			-14

(b) We will arbitrarily choose A and B to join at vertex w. Draw the new tree and calculate:

- d(A, w) =
- d(B,w) =

(c) Fill in the updated d matrix:

d	w	С	V
W	0		
С		0	4
v			0

3. (a) Third iteration: fill in the tables below.



(b) We will arbitrarily choose w and C to combine, but we don't change the topology since they are already joined at center vertex c. We do need to fill in the remaining edge weights:

- d(w,c) =
- d(C,c) =

(c) To fill in the last edge weight we update the distance matrix d:

 $\begin{array}{c|c} d & c & v \\ \hline c & 0 & 3 \\ v & 0 \end{array}$