

Small Additive Distance Phylogeny Problem:

Given: An $n \times n$ additive distance matrix D and an unweighted Phylogenetic tree T
Find: Branch lengths such that $d_T(i, j) = D_{ij}$ for all $1 \leq i, j \leq n$.

In this example, the Four Point Condition was used to reconstruct the branch lengths for the given unweighted Phylogenetic tree T . Follow through this example and make sure you understand how to get the solution. Then try it yourself on the Practice Problem on Page 2.

D

	V	W	X	Y	Z
V	0	10	17	16	16
W	-	0	15	14	14
X	-	-	0	9	15
Y	-	-	-	0	14
Z	-	-	-	-	0

Find neighbors V and W. Label common parent A.

See work on right for how to get this equation.

- $d_{AX} = \frac{1}{2}(d_{VX} + d_{WX} - d_{VW}) = 11$
- $d_{AY} = \frac{1}{2}(d_{VY} + d_{WY} - d_{VW}) = 10$
- $d_{AZ} = \frac{1}{2}(d_{VZ} + d_{WZ} - d_{VW}) = 10$

	A	X	Y	Z
A	0	11	10	10
X	-	0	9	15
Y	-	-	0	14
Z	-	-	-	0

} removed w, v added A

Find neighbors X and Y. Label common parent B.

Since $d_{AB} = 4$, and $d_{AC} = 3$, then $d_{BC} = 3$

- $d_{AB} = \frac{1}{2}(d_{AX} + d_{AY} - d_{XY}) = 6$
- $d_{BZ} = \frac{1}{2}(d_{XZ} + d_{YZ} - d_{XY}) = 10$

	B	A	Z
B	0	6	10
A	-	0	10
Z	-	-	0

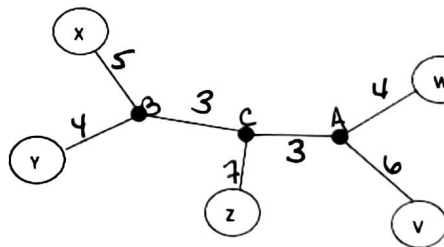
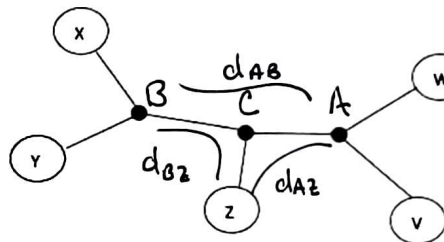
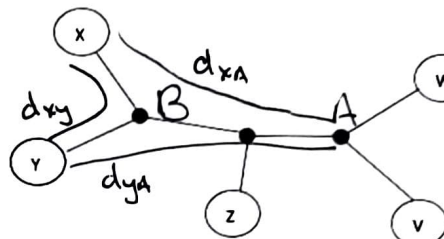
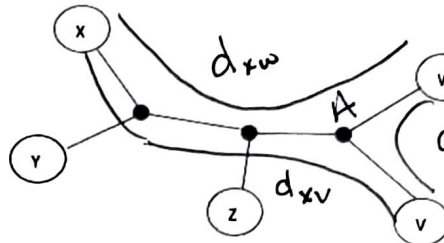
Find neighbors B and Z. Label common parent C.

- $d_{AC} = \frac{1}{2}(d_{AB} + d_{AZ} - d_{BZ}) = 3$

	C	A
C	0	3
A	-	0

Fill in distances going backwards.

start at d_{AC} , fill in.



Because D is additive

$$d_{AX} + d_{AW} = d_{XW}$$

$$d_{AX} + d_{AV} = d_{XV}$$

$$d_{AW} + d_{AV} = d_{WV}$$

Need to solve for unknowns. Add equations to eliminate

$$d_{AX} + d_{AW} = d_{XW}$$

$$+ d_{AX} + d_{AV} = d_{XV}$$

$$2d_{AX} + d_{AW} + d_{AV} = d_{XW} + d_{XV}$$

$$d_{AW} + d_{AV} = d_{WV}$$

$$2d_{AX} + d_{WV} = d_{XW} + d_{XV}$$

$$d_{AX} = \frac{1}{2}(d_{XW} + d_{XV} - d_{WV})$$

Practice problem. Add the appropriate weights to the given Phylogenetic tree T for the additive distance matrix D .

D

	A	B	C	D	E
A	0	11	10	9	15
B	-	0	3	12	18
C	-	-	0	11	17
D	-	-	-	0	8
E	-	-	-	-	0

