Molly Hayward: **kgxj22**
Phylogenetic Tree

Step 1)

	a	b	c	d	e	f
a	0	17	21	31	23	45
b	17	0	30	34	21	29
c	21	30	0	28	39	29
d	31	34	28	0	43	37
e	23	21	39	43	0	31
f	45	29	29	37	31	0

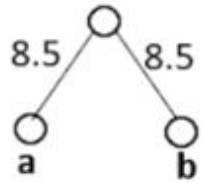
17 is the minimum score in the distance matrix therefore we group a and b by creating new species x

	a	x	b	c	d	e	f
a	0		17	21	31	23	45
x				25.5	32.5	22	37
b	17		0	30	34	21	29
c	21	25.5	30	0	28	39	29
d	31	32.5	34	28	0	43	37
e	23	22	21	39	43	0	31
f	45	37	29	29	37	31	0

Fill in x column and x row:
Average distance of **a** and **b** from:
c = (30+21)/2 = 25.5
d = (31+34)/2 = 32.5
e = (23+21)/2 = 22
f = (45+29)/2 = 37

	x	c	d	e	f
x	0	25.5	32.5	22	37
c	25.5	0	28	39	29
d	32.5	28	0	43	37
e	22	39	43	0	31
f	37	29	37	31	0

Remove a and b from the distance matrix



Step 2).

	x	c	d	e	f
x	0	25.5	32.5	22	37
c	25.5	0	28	39	29
d	32.5	28	0	43	37
e	22	39	43	0	31
f	37	29	37	31	0

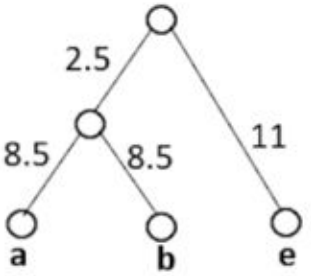
22 is the minimum score in the distance matrix therefore we group x and e by creating new species y

	x	y	c	d	e	f
x	0		25.5	32.5	22	37
y			32.25	37.75		34
c	25.5	32.25	0	28	39	29
d	32.5	37.75	28	0	43	37
e	22		39	43	0	31
f	37	34	29	37	31	0

Fill in y column and y row:
Average distance of **x** and **e** from:
c = (25.5+39)/2 = 32.25
d = (31+34)/2 = 32.5
f = (37+31)/2 = 34

	y	c	d	f
y	0	32.25	37.75	34
c	32.25	0	28	29
d	37.75	28	0	37
f	34	29	37	0

Remove x and e from the distance matrix



Molly Hayward: **kgxj22**
Phylogenetic Tree

Step 3).

	y	c	d	f
y	0	32.25	37.75	34
c	32.25	0	28	29
d	37.75	28	0	37
f	34	29	37	0

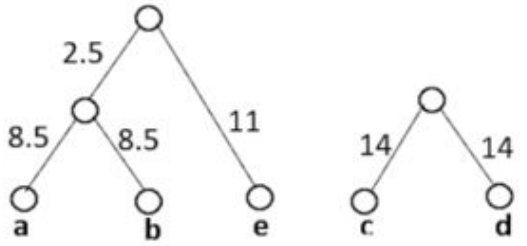
28 is the minimum score in the distance matrix therefore we group c and d by creating new species z

	y	c	z	d	f
y	0	32.25	35	37.75	34
c	32.25	0		28	29
z	35				33
d	37.75	28		0	37
f	34	29	33	37	0

Fill in z column and z row:
Average distance of **c** and **d** from:
z = (32.25+37.75)/2 = 35
f = (29+37)/2 = 33

	y	z	f
y	0	35	34
z	35	0	33
f	34	33	0

Remove c and d from the distance matrix



Step 4).

	y	z	f
y	0	35	34
z	35	0	33
f	34	33	0

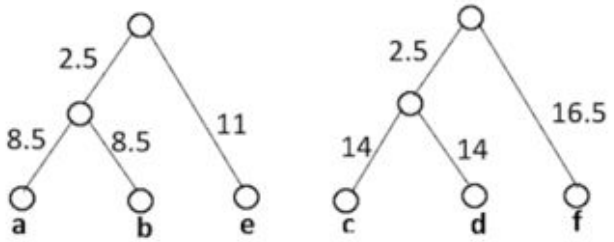
33 is the minimum score in the distance matrix therefore we group z and f by creating new species w

	y	z	w	f
y	0	35	34.5	34
z	35	0		33
w	34.5			
f	34	33		0

Fill in w column and w row:
Average distance of **z** and **f** from:
y = (35+34)/2 = 34.5

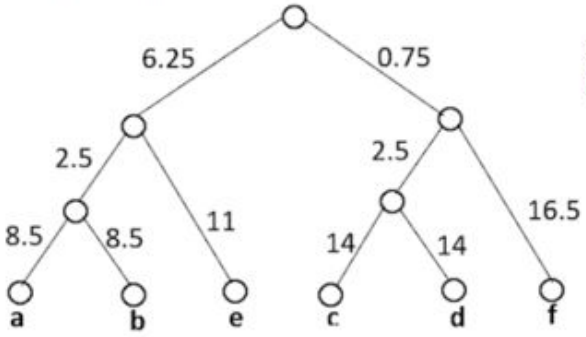
	y	w
y	0	34.5
w	34.5	0

Remove z and f from the distance matrix



Molly Hayward: **kgxj22**
Phylogenetic Tree

Final step).



34.5 is the minimum score in the distance matrix therefore we group y and w