

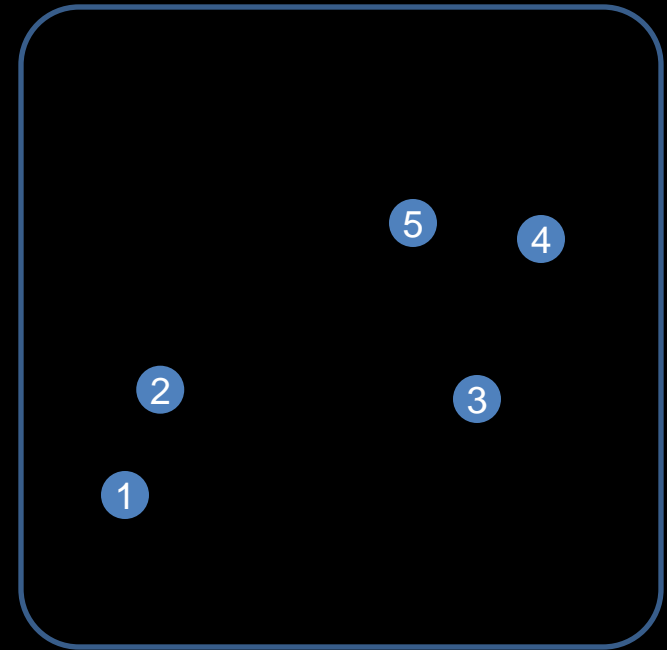
Building Phylogenetic Trees 2

Change in Implementation Project

- Before: “Identify a phylogenetic tree with parsimony superior to that of a UPGMA tree.”
- Now: “Compute a UPGMA tree and a Neighbor joining tree for any multiple sequence alignment”
- Why?
 - Slippery grading slope
 - If you work really hard to do a good job finding a parsimonious tree (and you can work really hard on this), depending on testing input, I might never notice that you did – and not give you credit

The UPGMA process

Input: A distance matrix



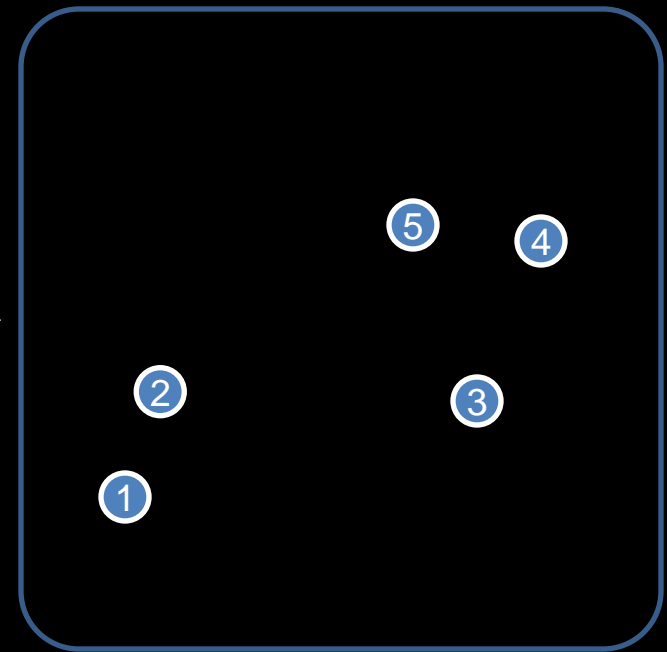
Sequences represented
by points in space.

Distances between points
represent sequence
similarity, specified with
the distance matrix

The UPGMA process

Input: A distance matrix

Step 1) make each sequence a member of its own group



1

2

3

4

5

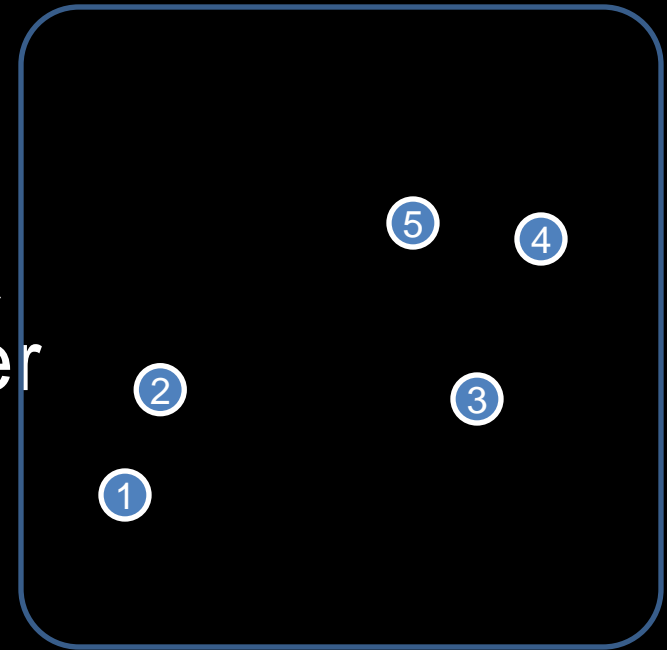
The UPGMA process

Input: A distance matrix

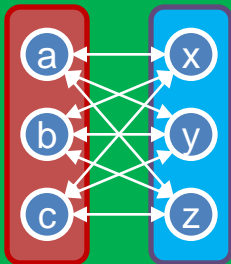
Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Step 2) Find the **closest pair** of clusters



The distance between two clusters is the average of the pairwise distances



Distance((abc), (xyz))
is the average of
 $d(a,x)$, $d(a,y)$, $d(a,z)$,
 $d(b,x)$, $d(b,y)$, $d(b,z)$,
 $d(c,x)$, $d(c,y)$, $d(c,z)$

1

2

3

4

5

The UPGMA process

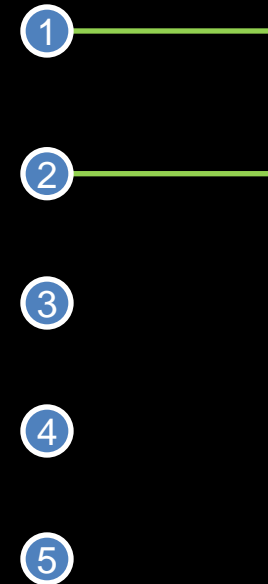
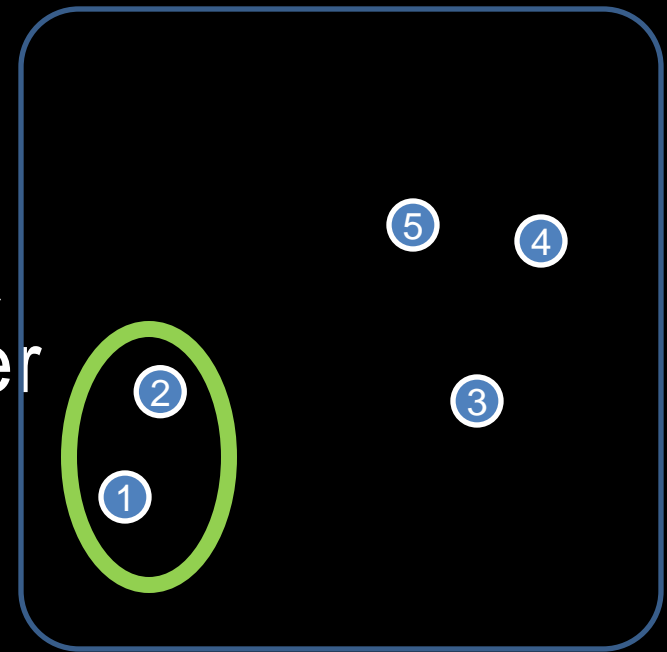
Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Step 2) Find the **closest pair** of among the active clusters (1,2)

Step 3) Group the closest pair in a new cluster



The UPGMA process

Input: A distance matrix

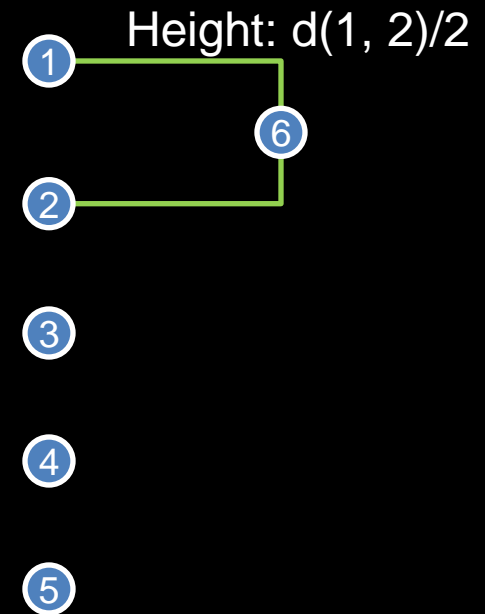
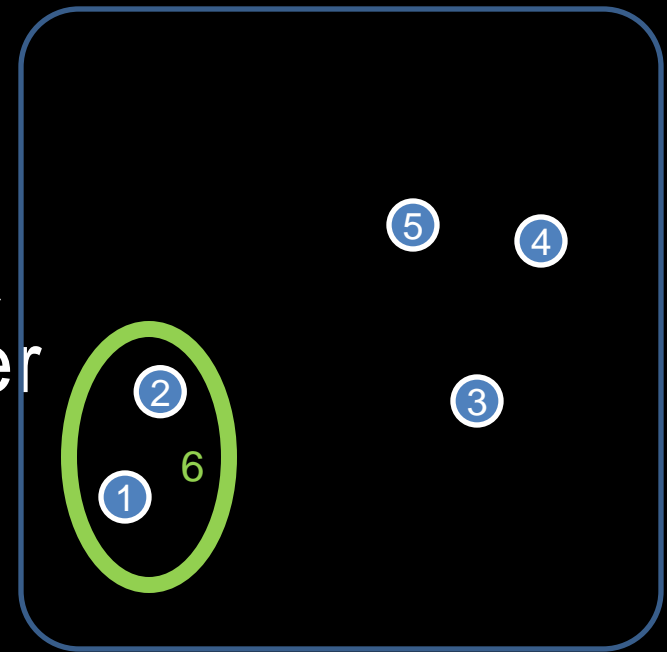
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While (num active clusters > 1)

Step 2) Find the **closest pair** of among the active clusters (1,2)

Step 3) Group the closest pair in a new cluster

Step 4) Set height of hypothetical shared ancestor at $d(1,2)/2$



The UPGMA process

Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

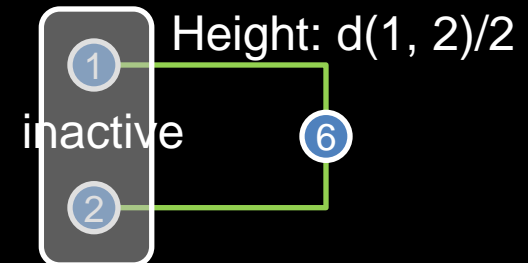
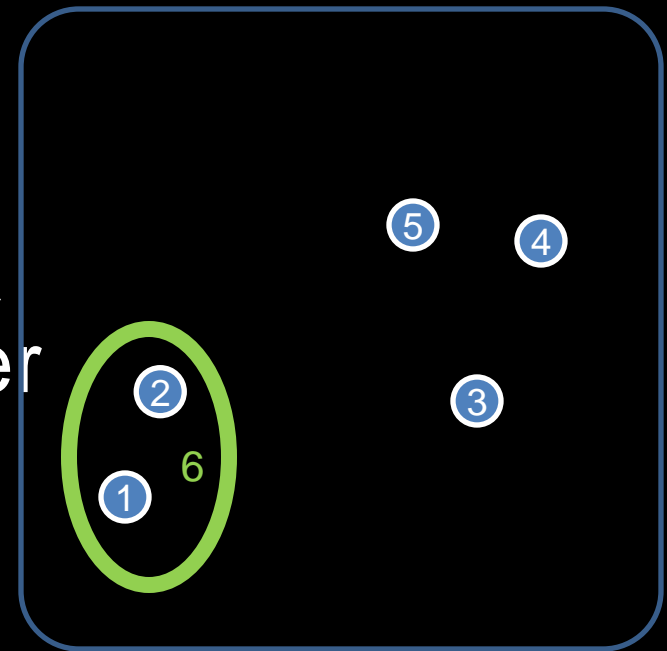
While (num active clusters > 1)

Step 2) Find the **closest pair** of among the active clusters (1,2)

Step 3) Group the closest pair in a new cluster

Step 4) Set height of hypothetical shared ancestor at $d(1,2)/2$

Step 5) Remove the old clusters 1,2, add the new one (6) to list of active clusters



3

4

5

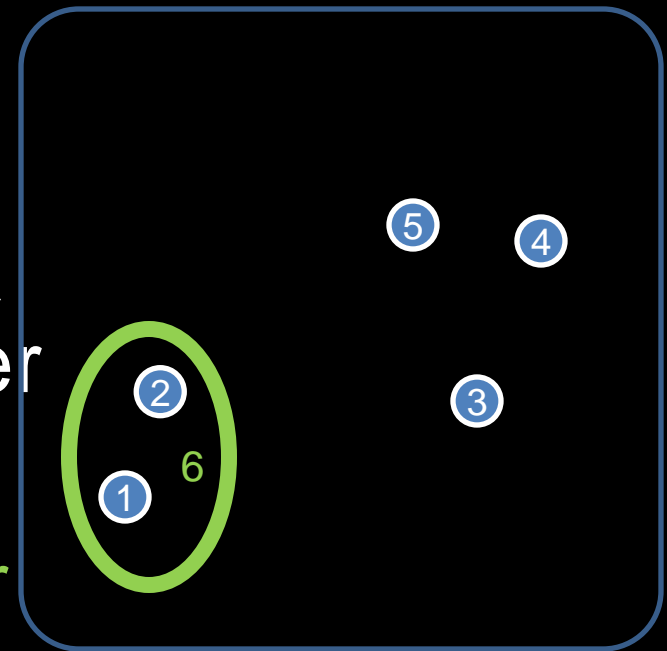
The UPGMA process

Input: A distance matrix

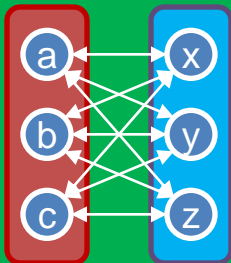
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While (num active clusters > 1)

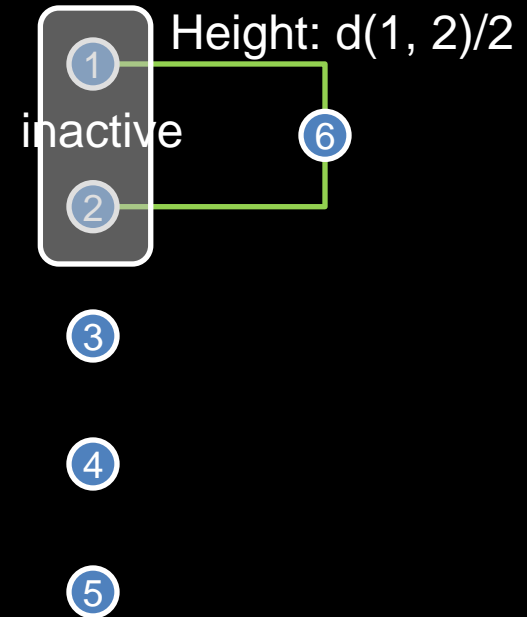
Step 2) Find the new **closest pair** among the active clusters (4,5)



The distance between two clusters is the average of the pairwise distances



Distance((abc), (xyz))
is the average of
 $d(a,x)$, $d(a,y)$, $d(a,z)$,
 $d(b,x)$, $d(b,y)$, $d(b,z)$,
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The UPGMA process

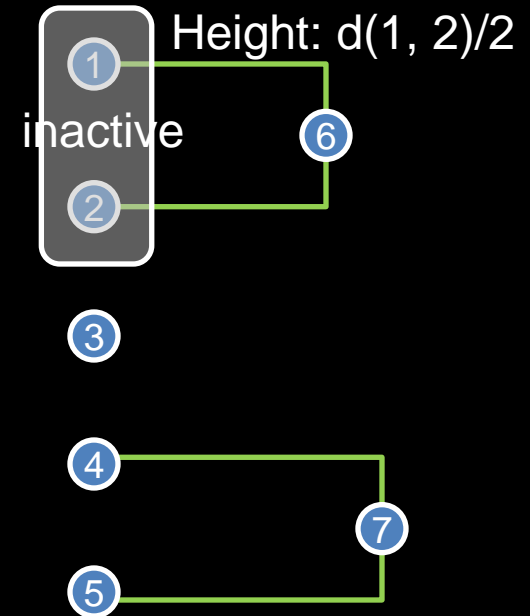
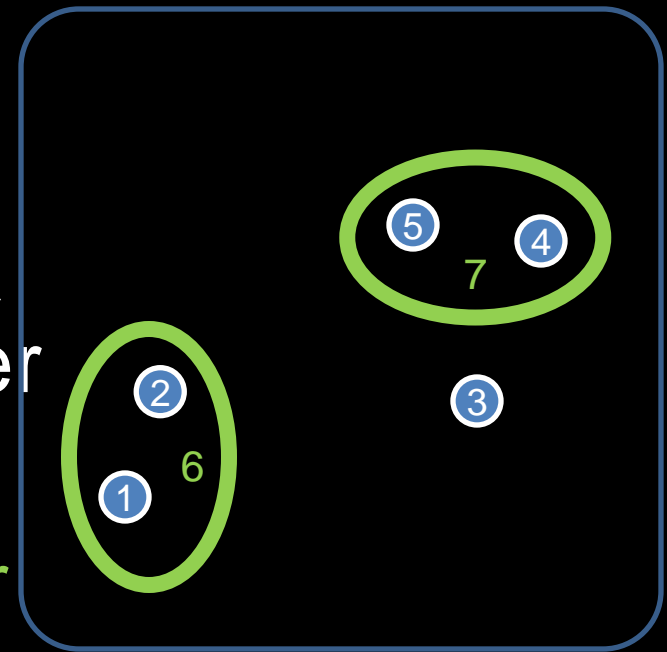
Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Step 2) Find the new **closest pair** among the active clusters (4,5)

Step 3) Group the closest pair in a new cluster



The UPGMA process

Input: A distance matrix

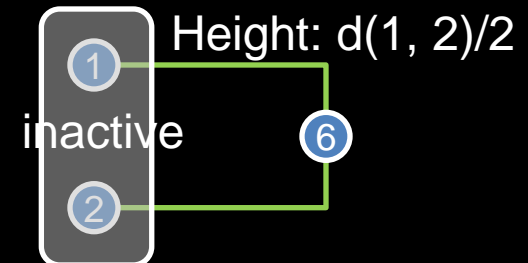
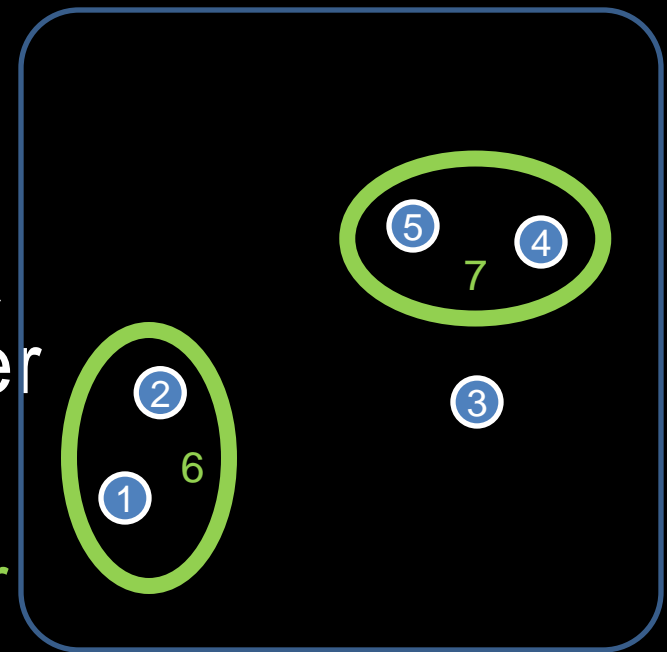
Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Step 2) Find the new **closest pair** among the active clusters (4,5)

Step 3) Group the closest pair in a new cluster

Step 4) Set height of hypothetical shared ancestor at $d(4,5)/2$



3



Height: $d(4,5)/2$

The UPGMA process

Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

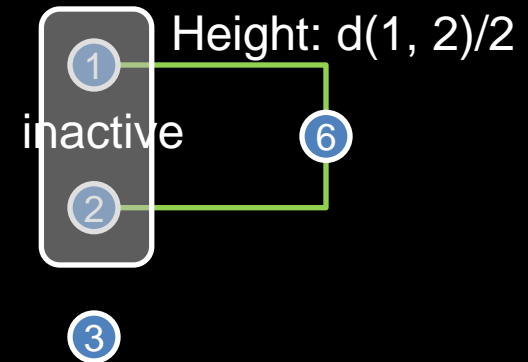
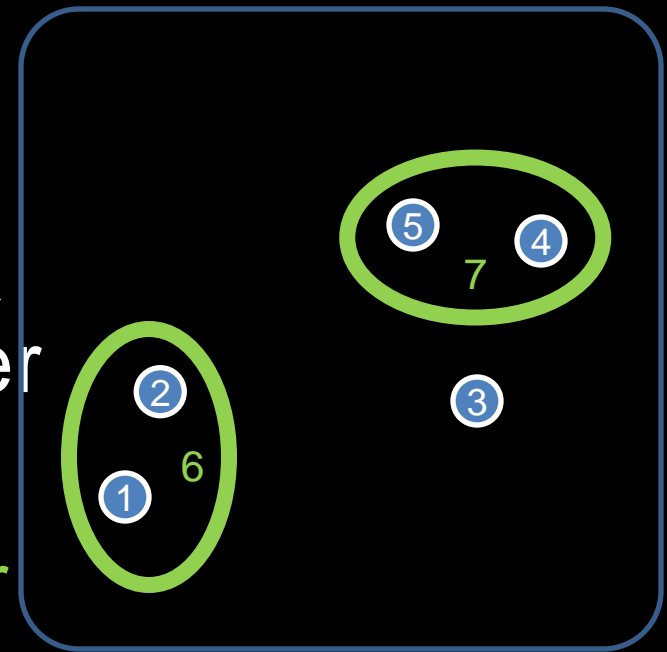
While (num active clusters > 1)

Step 2) Find the new **closest pair** among the active clusters (4,5)

Step 3) Group the closest pair in a new cluster

Step 4) Set height of hypothetical shared ancestor at $d(4,5)/2$

Step 5) Remove the old clusters 4,5, add the new one (6) to list of active clusters



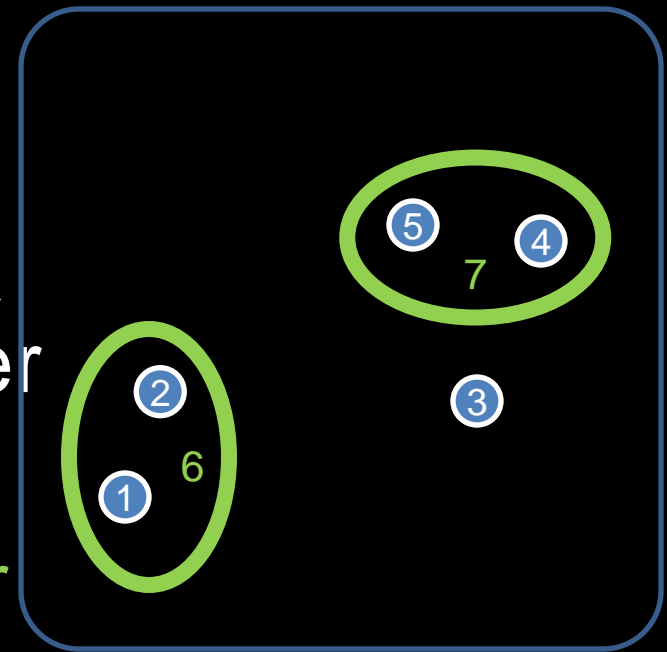
The UPGMA process

Input: A distance matrix

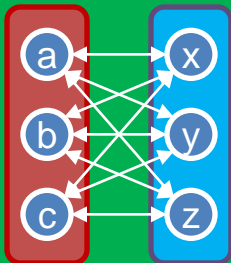
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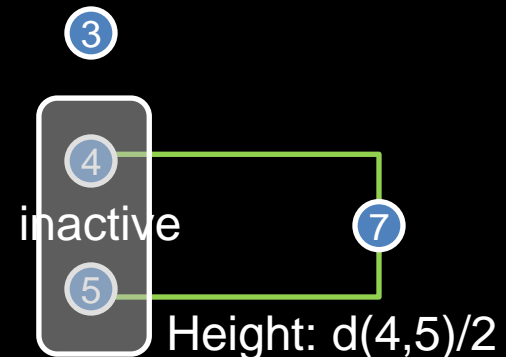
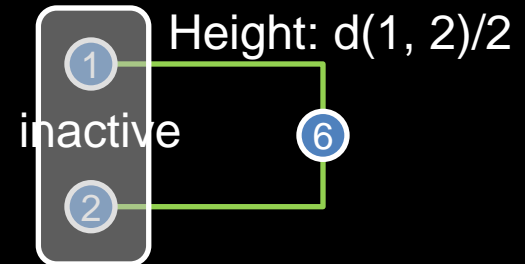
Step 2) Find the new **closest pair** among the active clusters (3,7)



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The UPGMA process

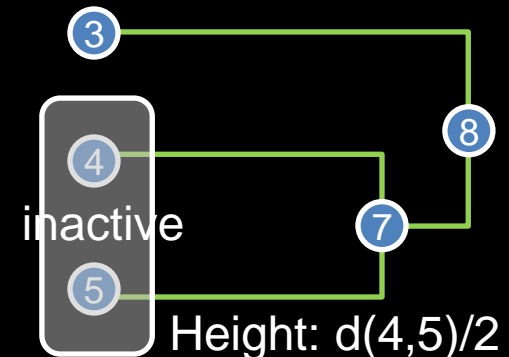
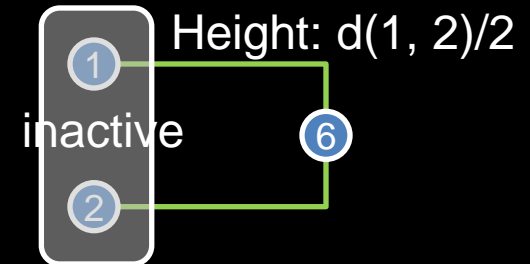
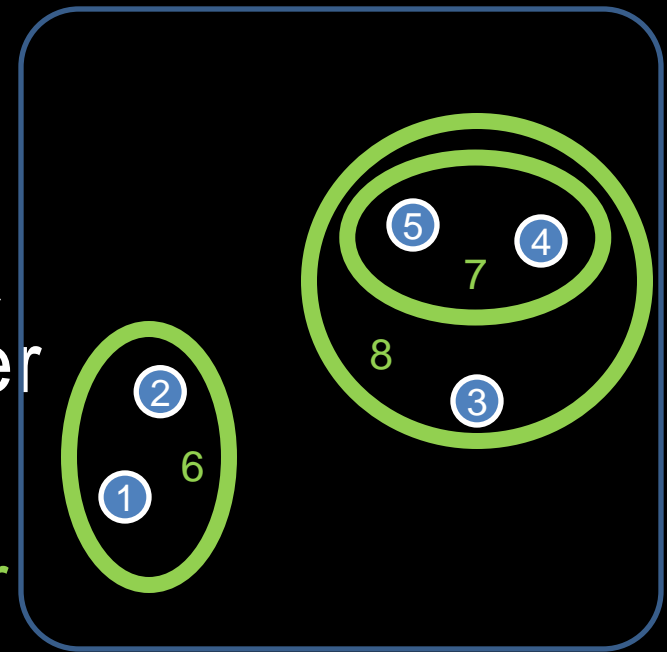
Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Step 2) Find the new **closest pair** among the active clusters (3,7)

Step 3) Group the closest pair in a new cluster (8)



The UPGMA process

Input: A distance matrix

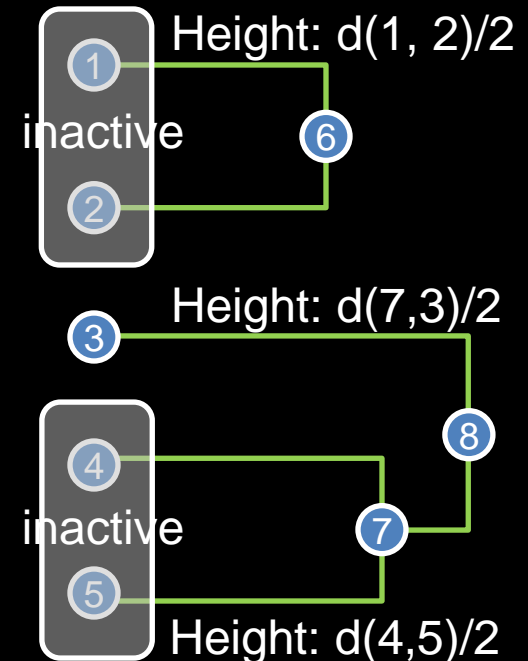
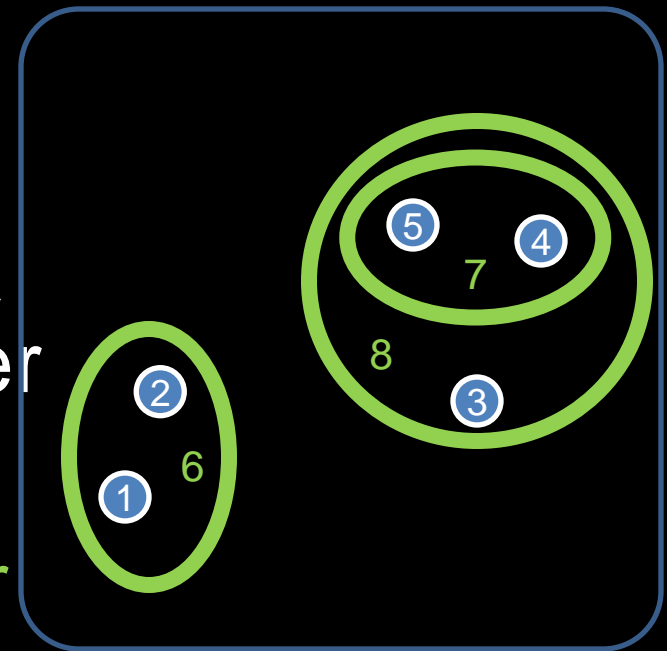
Step 1) make each sequence a member of its own active cluster

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Step 2) Find the new **closest pair** among the active clusters (3,7)

Step 3) Group the closest pair in a new cluster (8)

Step 4) Set height of hypothetical shared ancestor at $d(3,7)/2$



The UPGMA process

Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

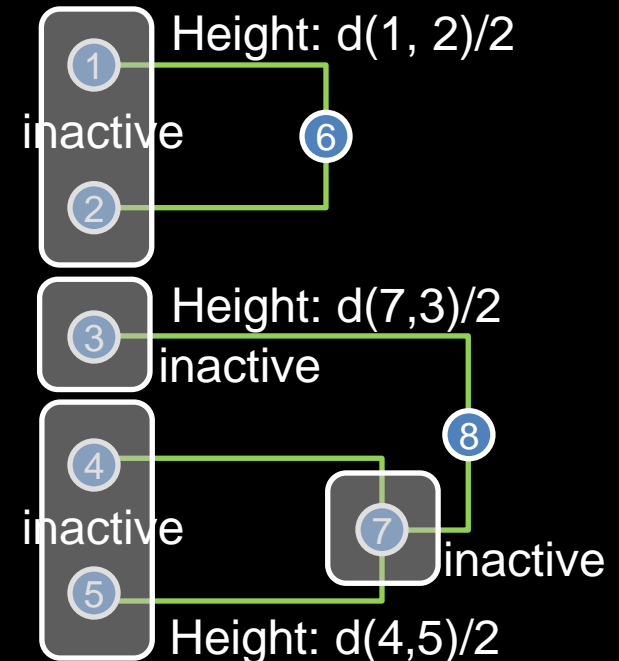
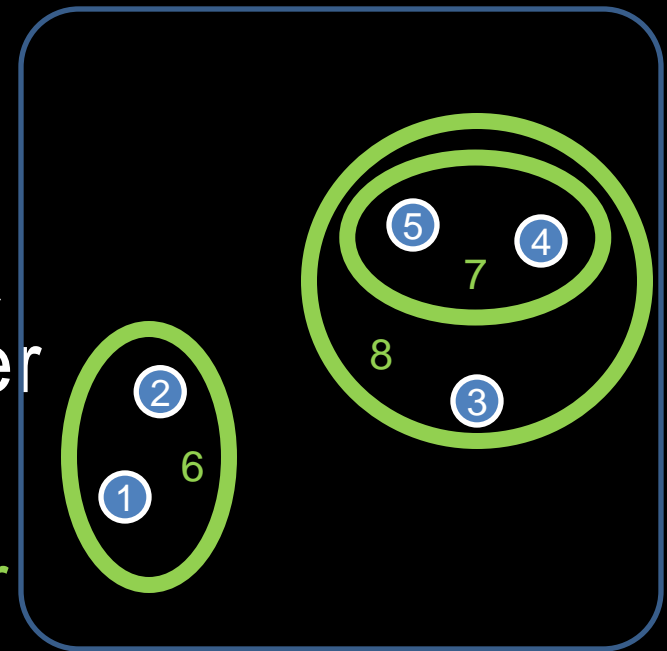
While (num active clusters > 1)

Step 2) Find the new **closest pair** among the active clusters (3,7)

Step 3) Group the closest pair in a new cluster (8)

Step 4) Set height of hypothetical shared ancestor at $d(3,7)/2$

Step 5) Remove the old clusters 3,7, add the new one (8) to list of active clusters



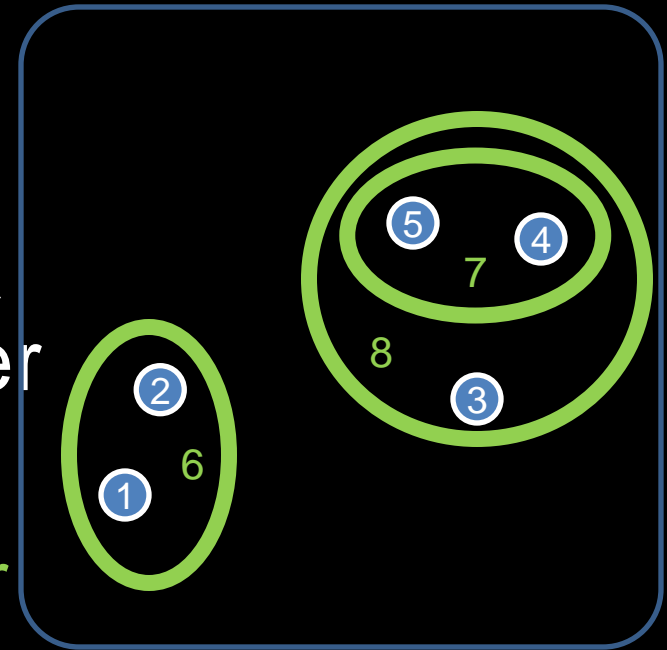
The UPGMA process

Input: A distance matrix

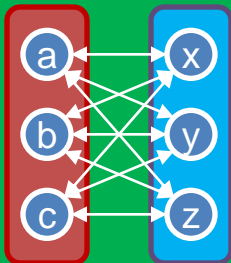
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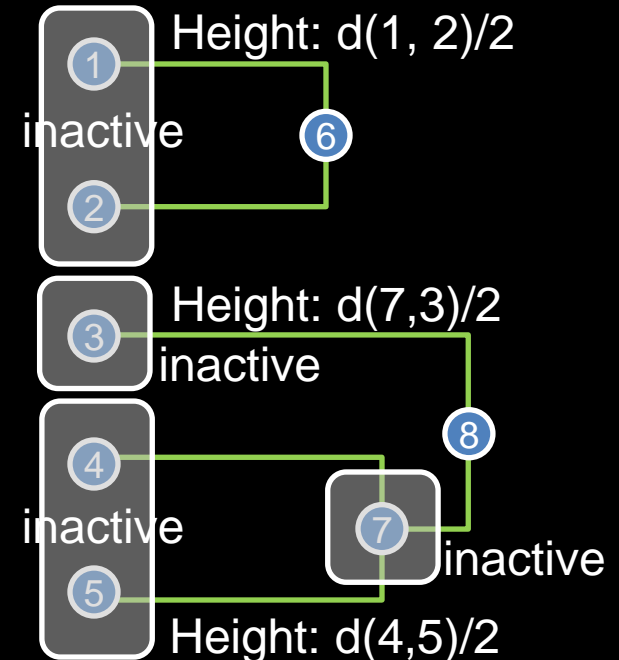
Step 2) Find the new **closest pair** among the active clusters (6,8)



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The UPGMA process

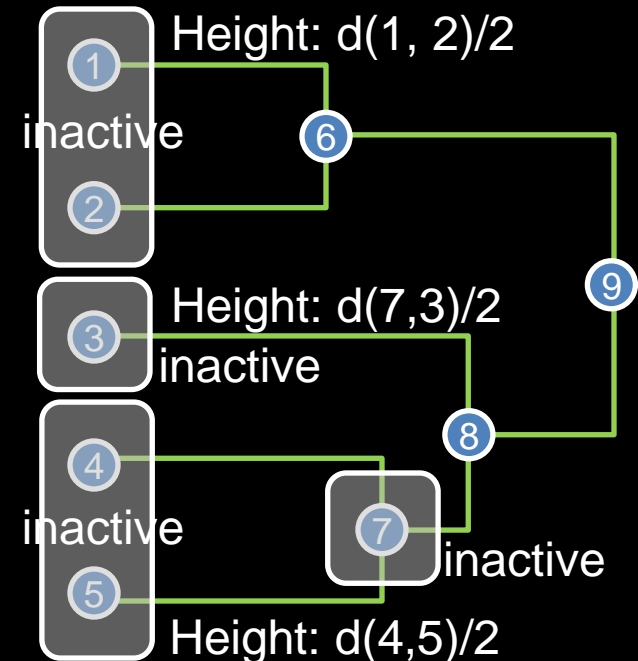
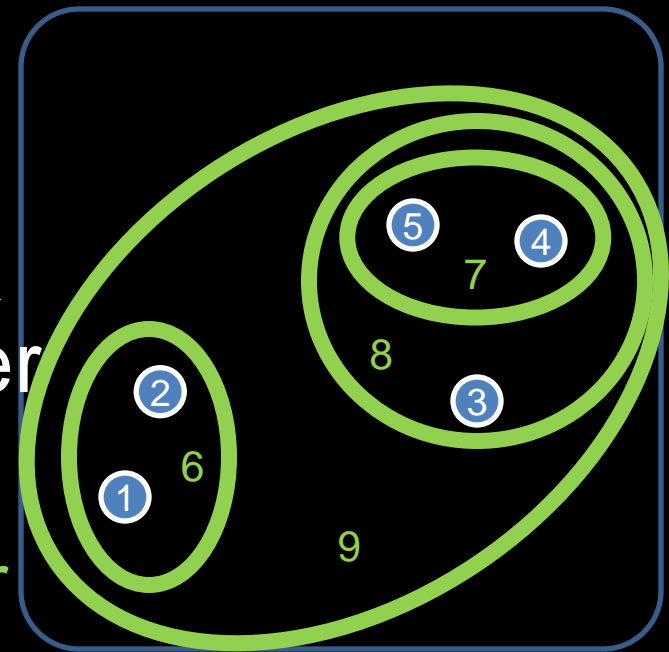
Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Step 2) Find the new **closest pair** among the active clusters (6,8)

Step 3) Group the closest pair in a new cluster (9)



The UPGMA process

Input: A distance matrix

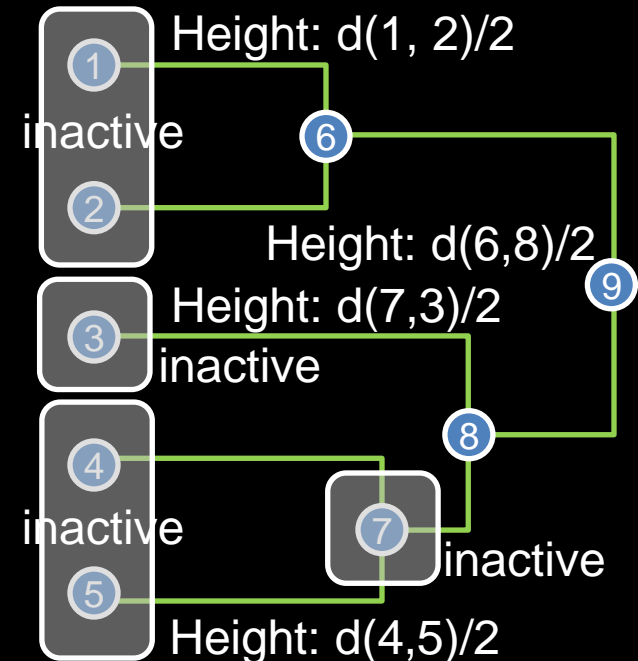
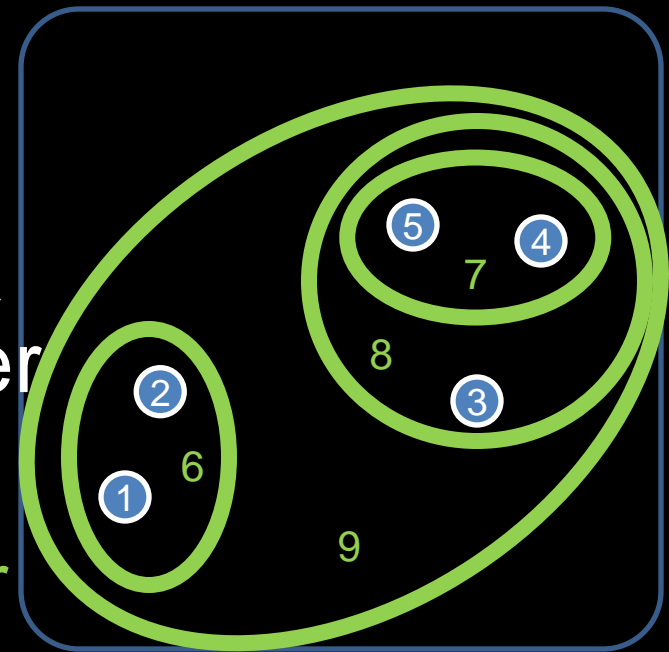
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Step 3) Group the closest pair in a new cluster (9)

Step 4) Set height of hypothetical shared ancestor at $d(6,8)/2$



The UPGMA process

Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

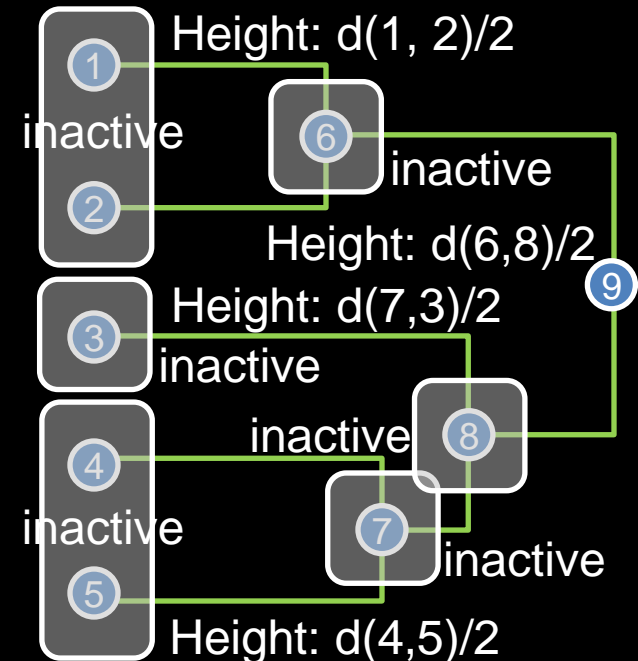
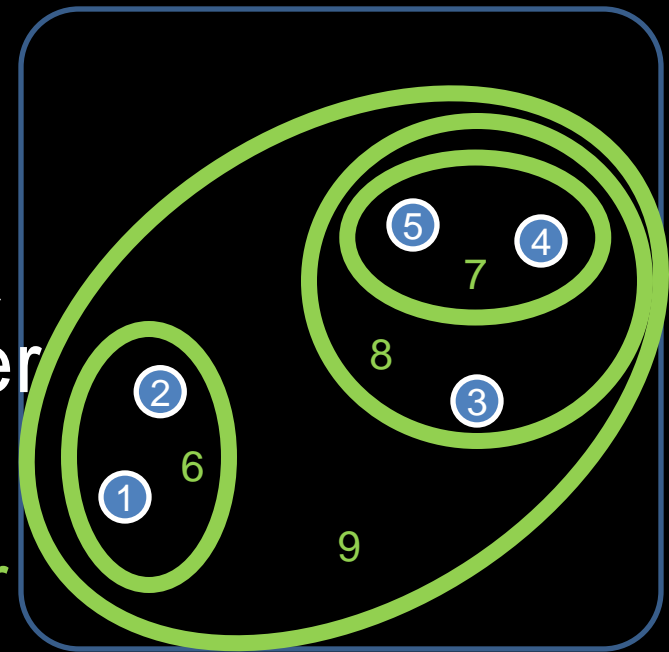
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Step 3) Group the closest pair in a new cluster (9)

Step 4) Set height of hypothetical shared ancestor at $d(6,8)/2$

Step 5) Remove the old clusters 6,8, add the new one (9) to list of active clusters



The UPGMA process

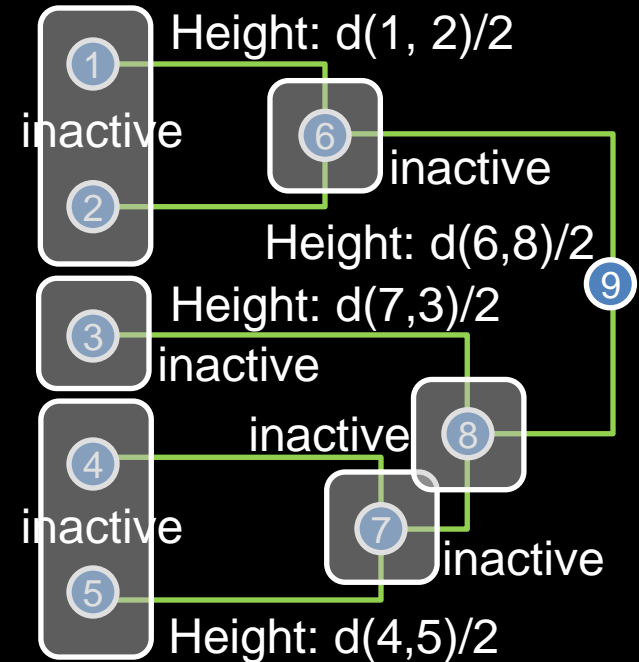
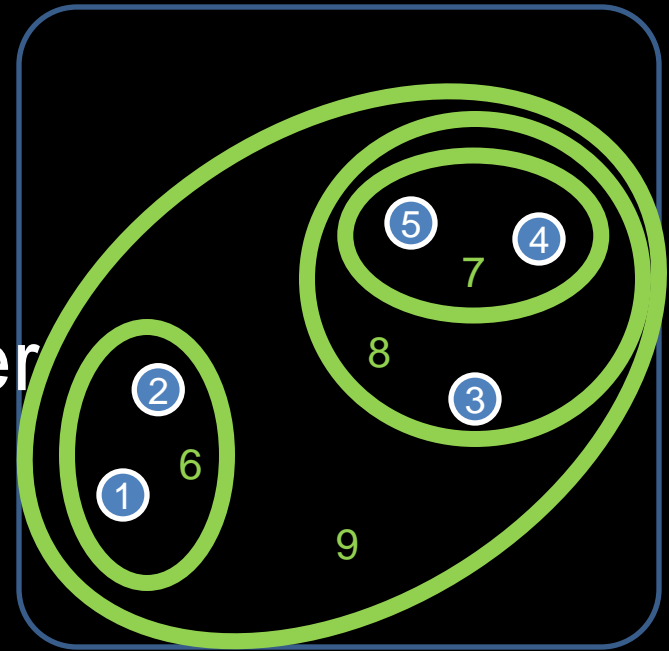
Input: A distance matrix

Step 1) make each sequence a member of its own active cluster

While (num active clusters > 1)

Num active clusters = 1

Done.



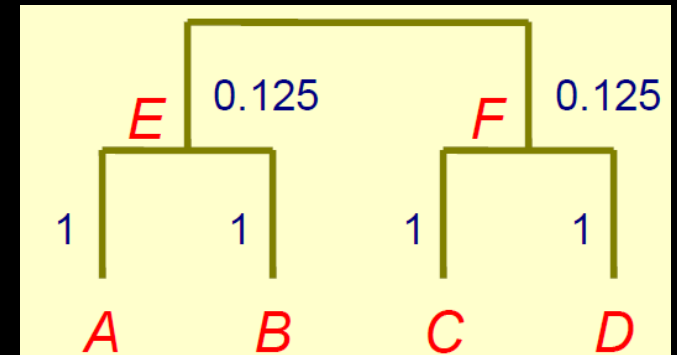
Suboptimality of UPGMA

- Recall that not every distance matrix is additive
 - Non-additive matrices cannot be converted into a tree such that the total edge weight between any two nodes is the same as distance in the matrix
- UPGMA attempts to remedy this by generating a similar tree
 - But it's not the same

	A	B	C	D
A	0	2	2	2
B	2	0	3	2
C	2	3	0	2
D	2	2	2	0

Original Distance Matrix

UPGMA tree



Matrix computed with UPGMA tree

	A	B	C	D
A	0	2	2.25	2.25
B	2	0	2.25	2.25
C	2.25	2.25	0	2
D	2.25	2.25	2	0

Rules for a better tree

- A better tree should have lower total edge weight

Why: Occam's Razor

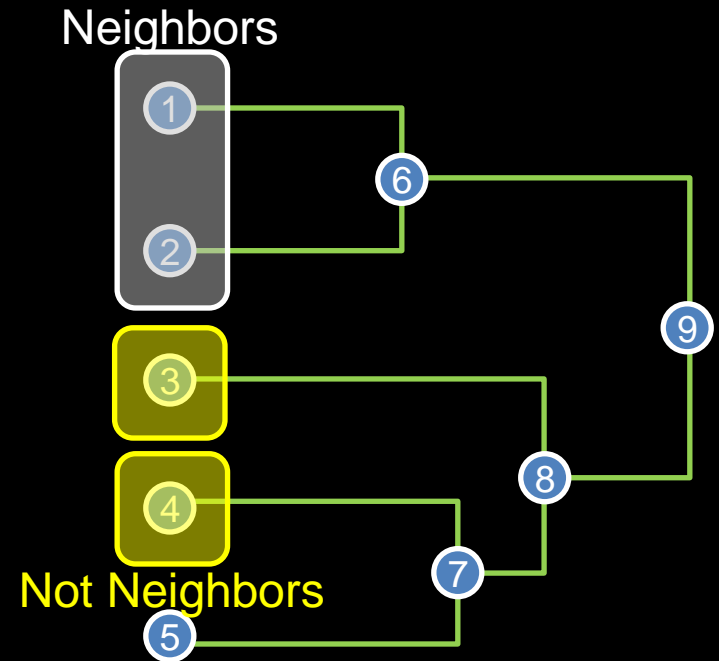
- Given two trees with different edgeweights, the lighter tree requires less random substitution to occur
 - It is more plausible that less random substitution occurs than more random substitution
- Thus, all tree generation methods seek to reduce the total edge weight of a tree.

Overview of Neighbor Joining

- Neighbor Joining tracks total tree weight in order to keep it minimal

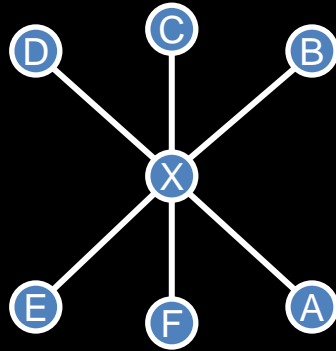
Definition: *Neighbor*

- Nodes x and y are said to be neighbors if they are separated in the tree by exactly one node



Edgeweights in Neighbor Joining

Initial “Star”
tree. Nodes
correspond to
sequences.
N total nodes.
X is extra.



Distance
Matrix D,
values
called D_{ij}

	A	B	C	D	E	F
A	0					
B	5	0				
C	4	7	0			
D	7	10	7	0		
E	6	9	6	5	0	
F	8	11	8	9	8	0

- Neighbor joining regards the initial state of the tree as a “star”
- The sum S_0 of the edge weights is written:

$$S_0 = \sum_{i=1}^N L_{iX} = \frac{1}{N-1} \sum_{i < j} D_{ij},$$

- Each weight D_{ij} corresponds to two legs of the star, since the path from i to j passes through X
- Hence, the sum of all D_{ij} adds each leg $N-1$ times.
- Use this equation to get the weight of an individual edge, L_{iX}

Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Distance
Matrix
N=6

	A	B	C	D	E	F
A	0					
B	5	0				
C	4	7	0			
D	7	10	7	0		
E	6	9	6	5	0	
F	8	11	8	9	8	0

$$L_{AU} = (5+4+7+6+8)/4 = 7.5$$

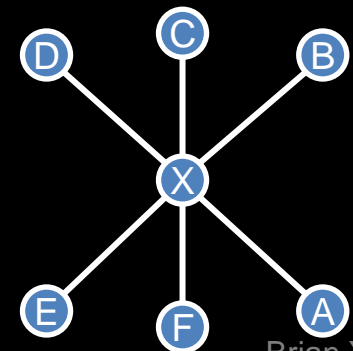
$$L_{BU} = (5+7+10+9+11)/4 = 10.5$$

$$L_{CU} = (4+7+7+6+8)/4 = 8$$

$$L_{DU} = (7+10+7+5+9)/4 = 9.5$$

$$L_{EU} = (6+9+6+5+8)/4 = 8.5$$

$$L_{FU} = (8+11+8+9+8)/4 = 11$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

This finds the closest pair of neighbors.
Since any pair of nodes that touches the center node, U, can be neighbors, you must check all pairs of nodes adjacent to U.

Resolve Ties arbitrarily.
Here we pick M_{AB}

Distance
Matrix
N=6

	A	B	C	D	E	F
A	0					
B	5	0				
C	4	7	0			
D	7	10	7	0		
E	6	9	6	5	0	
F	8	11	8	9	8	0

$$L_{AU} = (5+4+7+6+8)/4 = 7.5$$

$$L_{BU} = (5+7+10+9+11)/4 = 10.5$$

$$L_{CU} = (4+7+7+6+8)/4 = 8$$

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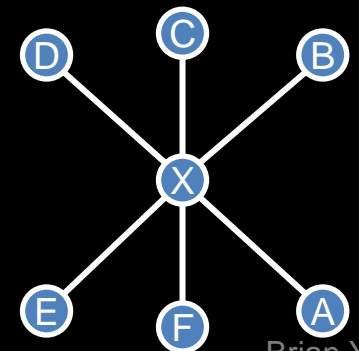
$$L_{EU} = (6+9+6+5+8)/4 = 8.5$$

$$L_{FU} = (8+11+8+9+8)/4 = 11$$

Smallest M_{ij} : (We pick M_{AB})

$$M_{AB} = 5 - 7.5 - 10.5 = -13$$

$$M_{DE} = 5 - 9.5 - 8.5 = -13$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U1 so that

$$L_{iU1} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

Note: weight (U,U1) does not need to be explicitly assigned

In this case:

$$L_{AU1} = D_{AB}/2 + (L_{AU} - L_{BU})/2 = 1$$

$$L_{BU1} = D_{BA}/2 + (L_{BU} - L_{AU})/2 = 4$$

Distance
Matrix
N=6

	A	B	C	D	E	F
A	0					
B	5	0				
C	4	7	0			
D	7	10	7	0		
E	6	9	6	5	0	
F	8	11	8	9	8	0

$$L_{AU} = (5+4+7+6+8)/4 = 7.5$$

$$L_{BU} = (5+7+10+9+11)/4 = 10.5$$

$$L_{CU} = (4+7+7+6+8)/4 = 8$$

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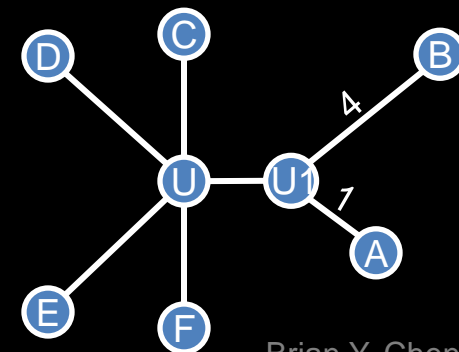
$$L_{EU} = (6+9+6+5+8)/4 = 8.5$$

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Smallest M_{ij} : (We pick M_{AB})

$$M_{AB} = 5 - 7.5 - 10.5 = -13$$

$$M_{DE} = 5 - 9.5 - 8.5 = -13$$



Neighbor Joining

Input: distance matrix, star graph

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$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U1 so that

$$L_{iU1} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

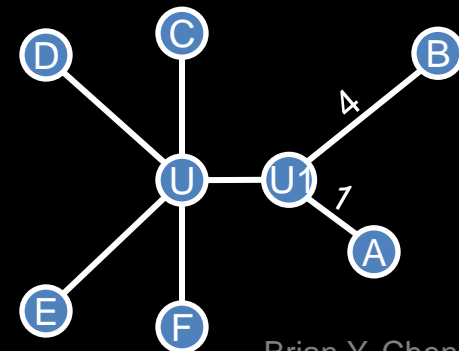
Step 4) Recalculate the distance matrix for all taxa x to U1, where

$$D_{xU1} = (D_{ix} + D_{jx} - D_{ij})/2$$

and i and j are the pair selected above

Distance
Matrix
N=5

	U1	C	D	E	F
U1	0				
C	3	0			
D	6	7	0		
E	5	6	5	0	
F	7	8	9	8	0



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Distance
Matrix
N=5

	U1	C	D	E	F
U1	0				
C	3	0			
D	6	7	0		
E	5	6	5	0	
F	7	8	9	8	0

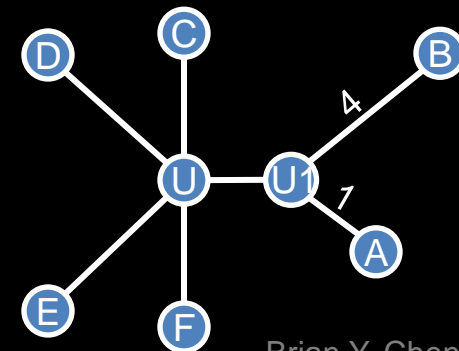
$$L_{U1U} = (3+6+5+7)/3 = 7$$

$$L_{CU} = (3+7+6+8)/3 = 8$$

$$L_{DU} = (6+7+5+9)/3 = 9$$

$$L_{EU} = (5+6+5+8)/3 = 8$$

$$L_{FU} = (6+8+9+8)/3 = 10.6$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

This finds the closest pair of neighbors.
Since any pair of nodes that touches the center node, U, can be neighbors, you must check all pairs of nodes adjacent to U.

Resolve Ties arbitrarily.
Here we pick M_{DE}

Distance
Matrix
N=5

	U1	C	D	E	F
U1	0				
C	3	0			
D	6	7	0		
E	5	6	5	0	
F	7	8	9	8	0

$$L_{U1U} = (3+6+5+7)/3 = 7$$

$$L_{CU} = (3+7+6+8)/3 = 8$$

$$L_{DU} = (6+7+5+9)/3 = 9$$

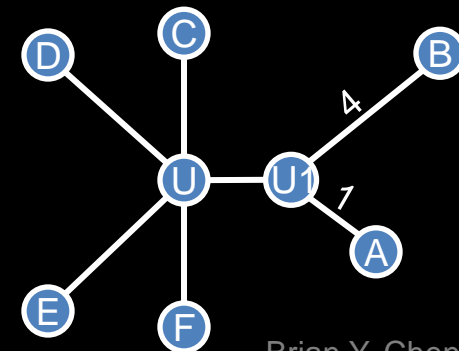
$$L_{EU} = (5+6+5+8)/3 = 8$$

$$L_{FU} = (6+8+9+8)/3 = 10.6$$

Smallest M_{ij} : (We pick M_{DE})

$$M_{CU1} = 3 - 7 - 8 = -12$$

$$M_{DE} = 5 - 9 - 8 = -12$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U2 so that

$$L_{iU2} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

Note: weight (U,U2) does not need to be explicitly assigned

In this case:

$$L_{DU2} = D_{DE}/2 + (L_{DU} - L_{EU})/2 = 3$$

$$L_{EU2} = D_{DE}/2 + (L_{EU} - L_{DU})/2 = 2$$

Distance
Matrix
N=5

	U1	C	D	E	F
U1	0				
C	3	0			
D	6	7	0		
E	5	6	5	0	
F	7	8	9	8	0

$$L_{U1U} = (3+6+5+7)/3 = 7$$

$$L_{CU} = (3+7+6+8)/3 = 8$$

$$L_{DU} = (6+7+5+9)/3 = 9$$

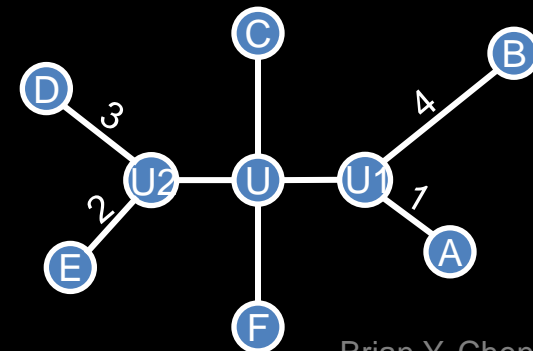
$$L_{EU} = (5+6+5+8)/3 = 8$$

$$L_{FU} = (6+8+9+8)/3 = 10.6$$

Smallest M_{ij} : (We pick M_{DE})

$$M_{CU1} = 3 - 7 - 8 = -12$$

$$M_{DE} = 5 - 9 - 8 = -12$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U2 so that

$$L_{iU2} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

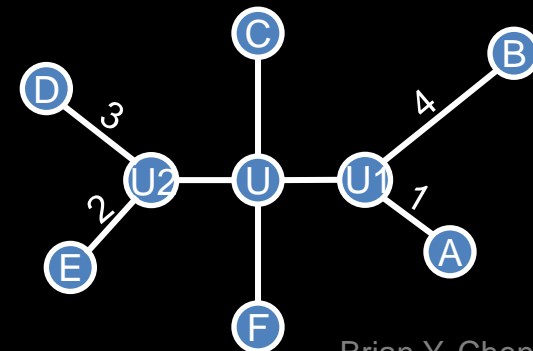
Step 4) Recalculate the distance matrix for all taxa x to U2, where

$$D_{xU1} = (D_{ix} + D_{jx} - D_{ij})/2$$

and i and j are the pair selected above

Distance
Matrix
N=4

	U1	C	U2	F
U1	0			
C	3	0		
U2	3	4	0	
F	7	8	6	0



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Distance
Matrix
N=4

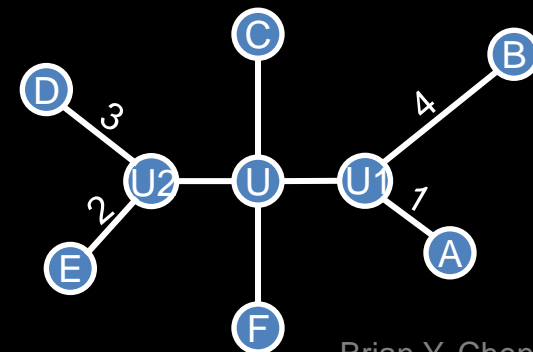
	U1	C	U2	F
U1	0			
C	3	0		
U2	3	4	0	
F	7	8	6	0

$$L_{U1U} = (3+3+7)/2 = 6.5$$

$$L_{CU} = (3+4+8)/2 = 7.5$$

$$L_{U2U} = (3+4+6)/2 = 6.5$$

$$L_{FU} = (7+8+6)/2 = 10.5$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

This finds the closest pair of neighbors.
Since any pair of nodes that touches the center node, U, can be neighbors, you must check all pairs of nodes adjacent to U.

Resolve Ties arbitrarily.
No ties this time

Distance
Matrix
N=4

	U1	C	U2	F
U1	0			
C	3	0		
U2	3	4	0	
F	7	8	6	0

$$L_{U1U} = (3+3+7)/2 = 6.5$$

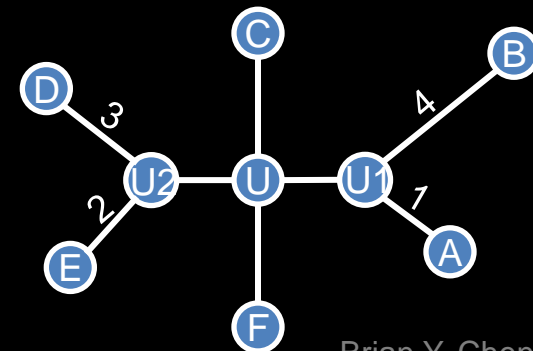
$$L_{CU} = (3+4+8)/2 = 7.5$$

$$L_{U2U} = (3+4+6)/2 = 6.5$$

$$L_{FU} = (7+8+6)/2 = 10.5$$

Smallest M_{ij} : (No tie this time)

$$M_{CU1} = 3 - 6.5 - 7.5 = -11$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U3 so that

$$L_{iU3} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

Note: weight (U,U3) does not need to be explicitly assigned

Distance
Matrix
N=4

	U1	C	U2	F
U1	0			
C	3	0		
U2	3	4	0	
F	7	8	6	0

$$L_{U1U} = (3+3+7)/2 = 6.5$$

$$L_{CU} = (3+4+8)/2 = 7.5$$

$$L_{U2U} = (3+4+6)/2 = 6.5$$

$$L_{FU} = (7+8+6)/2 = 10.5$$

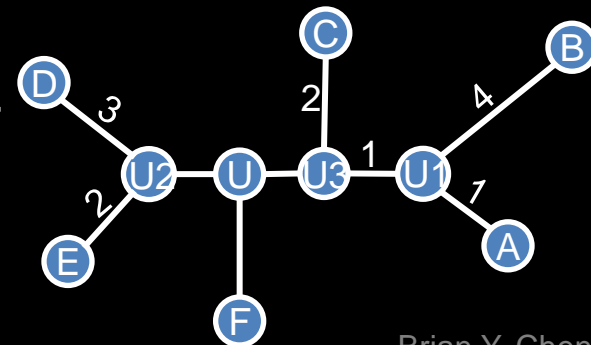
Smallest M_{ij} : (No tie this time)

$$M_{CU1} = 3 - 6.5 - 7.5 = -11$$

In this case:

$$L_{CU3} = D_{CU1}/2 + (L_{CU} - L_{U1U})/2 = 2$$

$$L_{U1U3} = D_{CU1}/2 + (L_{U1U} - L_{CU})/2 = 1$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U3 so that

$$L_{iU3} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

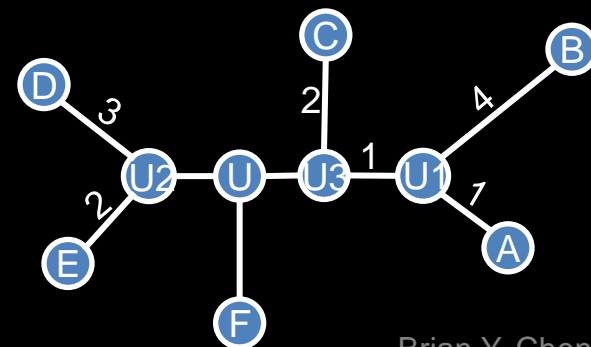
Step 4) Recalculate the distance matrix for all taxa x to U3, where

$$D_{xU1} = (D_{ix} + D_{jx} - D_{ij})/2$$

and i and j are the pair selected above

Distance
Matrix
N=3

	U3	U2	F
U3	0		
U2	2	0	
F	6	6	0



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

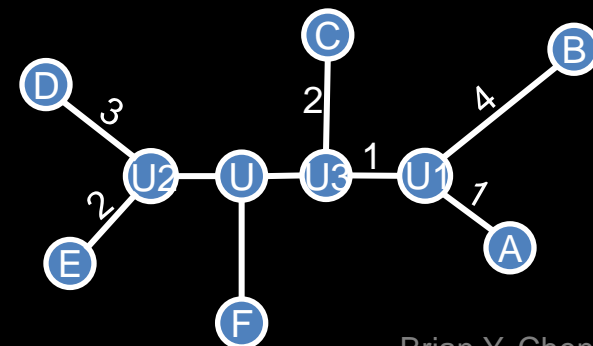
Distance
Matrix
N=3

	U3	U2	F
U3	0		
U2	2	0	
F	6	6	0

$$L_{U2U} = (2+6)/1 = 8$$

$$L_{U3U} = (2+6)/1 = 8$$

$$L_{FU} = (6+6)/1 = 12$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

This finds the closest pair of neighbors.
Since any pair of nodes that touches the center node, U, can be neighbors, you must check all pairs of nodes adjacent to U.

Resolve Ties arbitrarily.
We choose $M_{U_2U_3}$

Distance
Matrix
N=3

	U3	U2	F
U3	0		
U2	2	0	
F	6	6	0

$$L_{U_2U} = (2+6)/1 = 8$$

$$L_{U_3U} = (2+6)/1 = 8$$

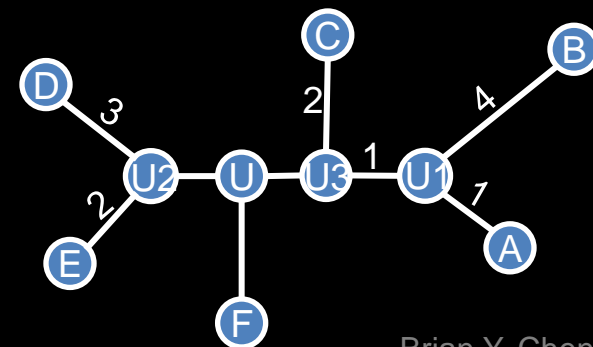
$$L_{FU} = (6+6)/1 = 12$$

Smallest M_{ij} : (We pick $M_{U_2U_3}$)

$$M_{U_2F} = 6 - 8 - 12 = -14$$

$$M_{U_3F} = 6 - 7 - 12 = -14$$

$$M_{U_2U_3} = 2 - 8 - 8 = -14$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U4 so that

$$L_{iU4} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

Note: weight (U,U4) does not need to be explicitly assigned

Distance
Matrix
N=3

	U3	U2	F
U3	0		
U2	2	0	
F	6	6	0

$$L_{U2U} = (2+6)/1 = 8$$

$$L_{U3U} = (2+6)/1 = 8$$

$$L_{FU} = (6+6)/1 = 12$$

Smallest M_{ij} : (We pick M_{U2U3})

$$M_{U2F} = 6 - 8 - 12 = -14$$

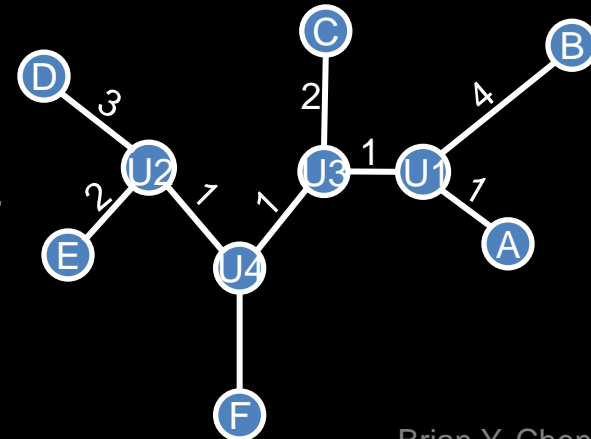
$$M_{U3F} = 6 - 7 - 12 = -14$$

$$M_{U2U3} = 2 - 8 - 8 = -14$$

In this case:

$$L_{U2U4} = D_{U2U3}/2 + (L_{U2U} - L_{U3U})/2 = 1$$

$$L_{U3U4} = D_{U2U3}/2 + (L_{U3U} - L_{U2U})/2 = 1$$



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U4 so that

$$L_{iU4} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$

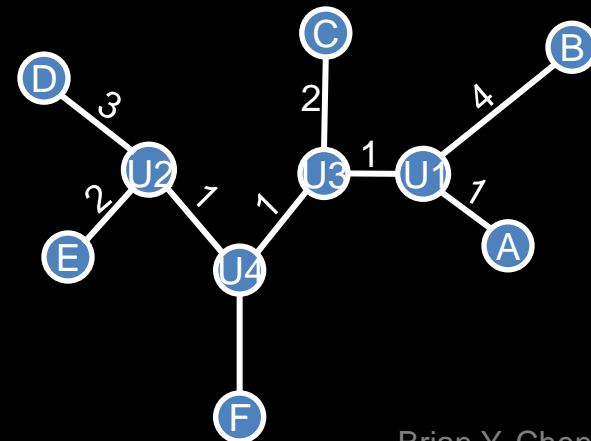
Step 4) Recalculate the distance matrix for all taxa x to U3, where

$$D_{xU1} = (D_{ix} + D_{jx} - D_{ij})/2$$

and i and j are the pair selected above

Distance
Matrix
N=2

	U4	F
U4	0	
F	5	0



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

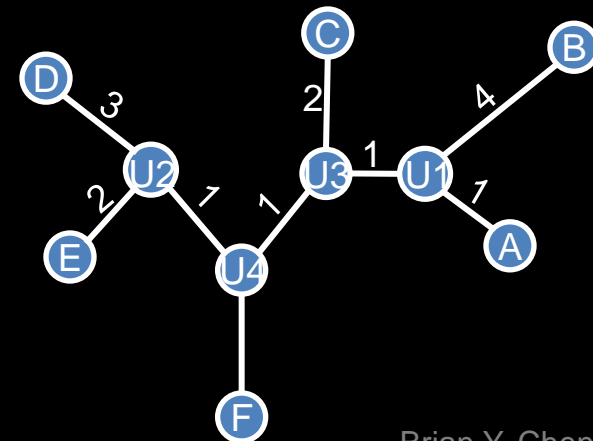
$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

This time computing this value is not possible, because $N-2 = 0$

Detecting this indicates the end of the algorithm

Distance
Matrix
N=2

	U4	F
U4	0	
F	5	0



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

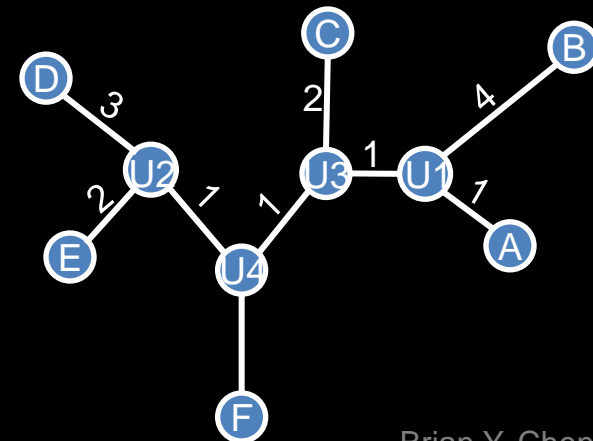
Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Again, not possible. There is only one possibility for i or j.
Also, L_{iU} is undefined for any i and j

Distance
Matrix
N=2

	U4	F
U4	0	
F	5	0



Neighbor Joining

Input: distance matrix, star graph

Step 1) estimate Star leg weights L_{iU}

$$L_{iU} = (\text{Sum of all } D_{ij}) / (N-2)$$

Step 2) Find pair (i, j) with smallest M_{ij} ,

$$M_{ij} = D_{ij} - L_{iU} - L_{jU}$$

Step 3) Separate the pair (i,j) and create a new node U4 so that

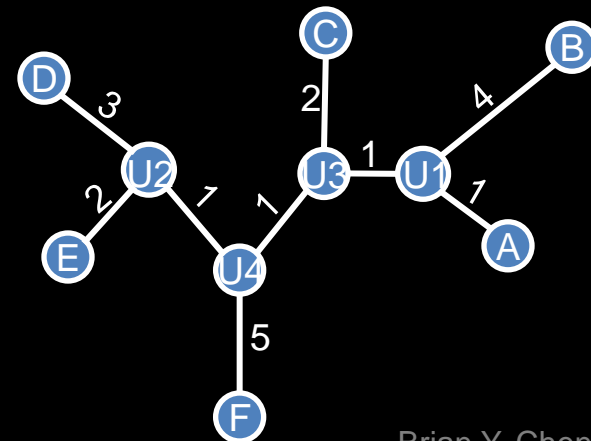
~~$$L_{iU4} = D_{ij}/2 + (L_{iU} - L_{jU})/2$$~~

$$L_{iU4} = D_{FU4}$$

There is no pair (i,j) to consider, so we do not need to worry about how the tree will be split: so we just use the Distance Matrix, D_{FU4}

Distance
Matrix
N=2

	U4	F
U4	0	
F	5	0



Neighbor Joining

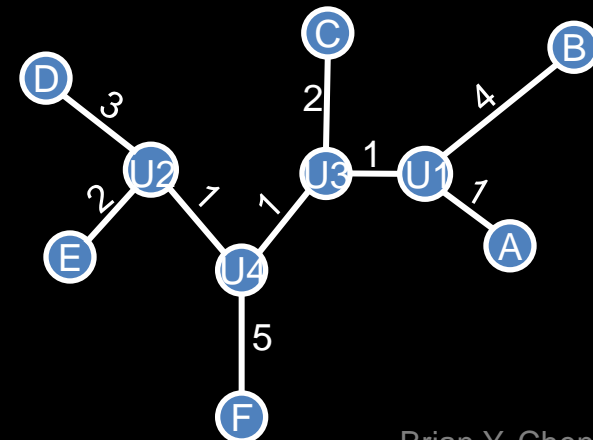
Input: distance matrix, star graph

Output:

Tree topology and Edge Weights

Distance
Matrix
N=2

	U4	F
U4	0	
F	5	0



Questions