

Maximum Parsimony: Compute Nodes

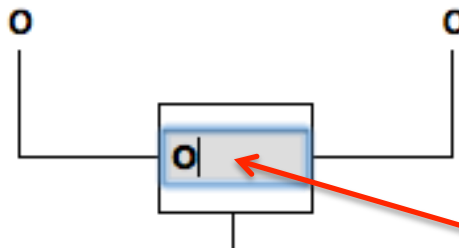
This tutorial explains how to use the Quiz Mode for the Maximum Parsimony algorithm. The point of the algorithm is to determine *which phylogenetic tree has fewer overall “steps” or mutations* over the whole data set. This so-called “shortest tree” is the Most Parsimonious tree for the data set. (See Background and Concept Mode.)

The first step in finding the Most Parsimonious Tree is compute the internal nodes. This reduces the number of possibilities. In this exercise, the data set is a protein sequence alignment with 5 sequences (S1-S5). Using Set Theory, determine which character or characters should be placed at each node. In this case, the characters are the Amino Acids at each position of the alignment.

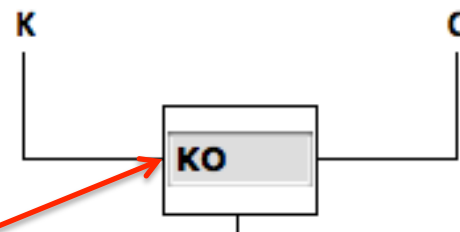
Set Theory Node Calculation:

- (1) Find the Union of the characters (amino acids) in the higher nodes.
- (2) If the Union is the NULL SET (no overlap), keep all characters.

In the case below, the Union of the two higher node is O because they are both O:



In this case, the Union of the two higher is NULL (an empty set) since they do not share anything. So keep both K and O:



Maximum Parsimony: Compute Nodes

Step 1: Position 1

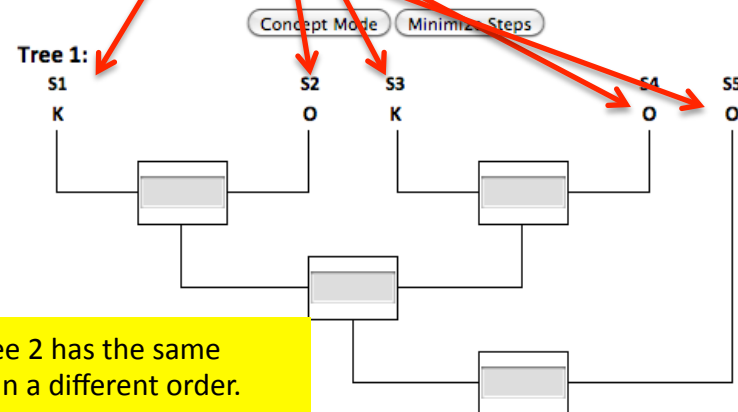
For each position of the alignment, determine the character or suite of characters that should be entered at every node.

We start with position 1, highlighted in green.

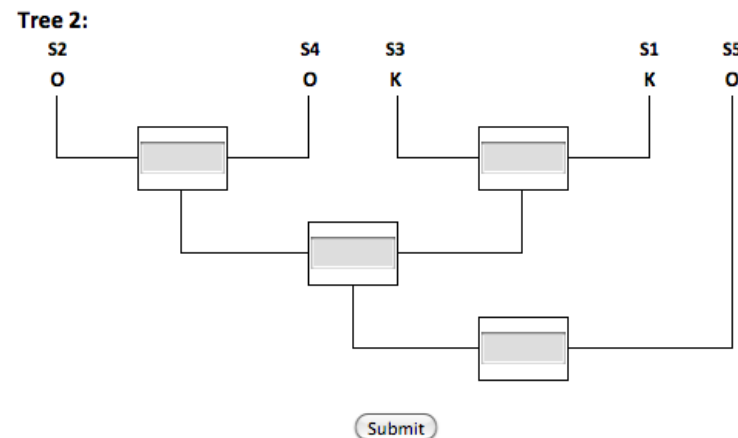
You must fill in the nodes at the top before you can do the lower nodes of the tree.

	1	2	3	4	5	6	7	8	9	10
S1	K	L	G	Q	N	K	E	Y	F	S
S2	O	L	A	T	N	K	A	Y	P	S
S3	K	L	G	Q	U	K				
S4	O	L	A	T	U	K				
S5	O	L	G	U	U					

At the tips of the tree, you see the amino acids for each sequence in position 1.



Notice how tree 2 has the same sequence but in a different order.

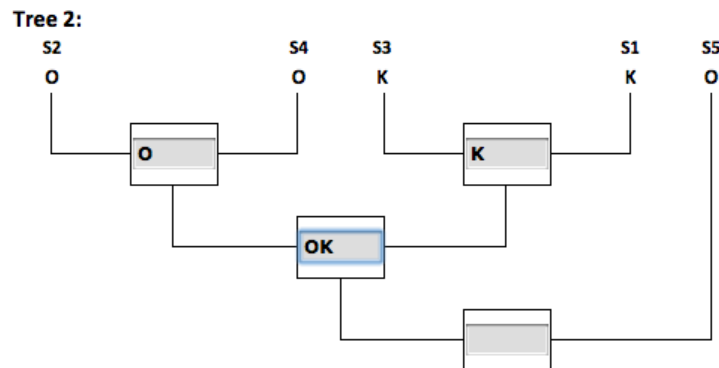
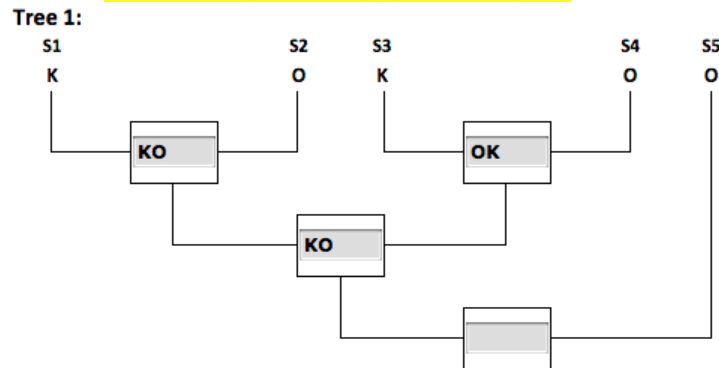


Maximum Parsimony: Compute Nodes

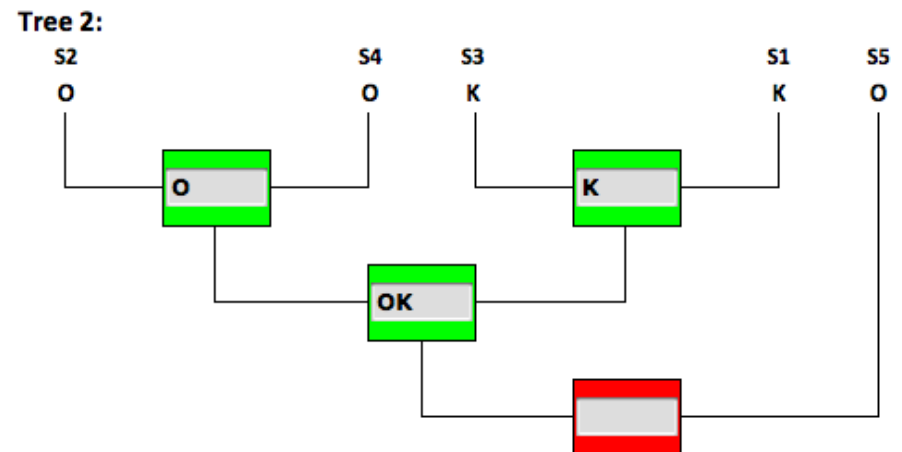
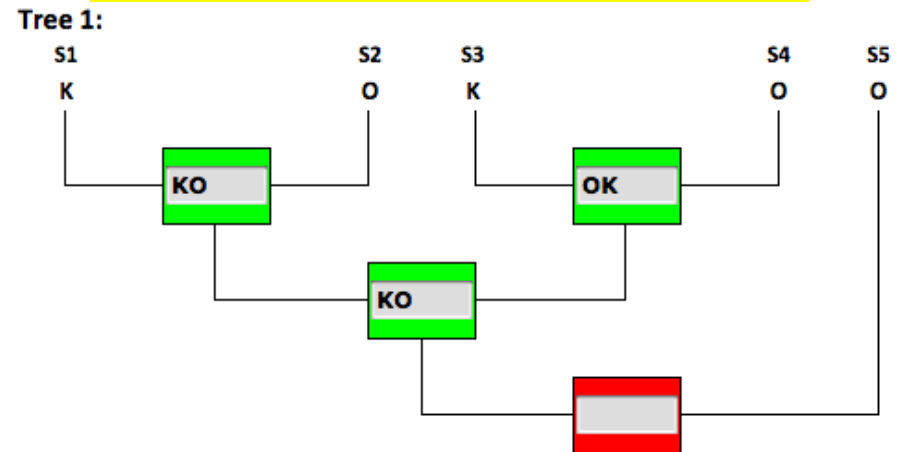
Step 2: Fill in the Nodes

Using set theory rules, fill in the nodes. (Also, see Concept Mode.)

Fill in Nodes, starting at the top.



Click Submit button at the bottom to check answers.
Green=Correct; Red=Incorrect (or empty).

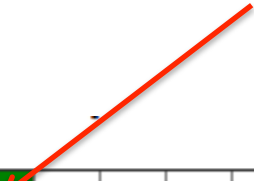


→ Submit

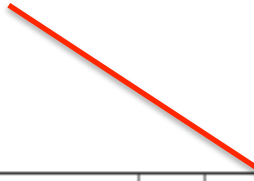
Maximum Parsimony: Compute Nodes

Step 3: Fill in for the other positions

Click on the next positions and fill in the nodes for each tree.



	<u>1</u>	<u>2</u>	<u>3</u>	<u>4</u>	<u>5</u>	<u>6</u>	<u>7</u>	<u>8</u>	<u>9</u>	<u>10</u>
S1	P	W	A	R	Q	A	C	E	Y	A
S2	D	K	A	R	Q	A	C	H	I	R
S3	D	W	T	P	D	A	C	E	Y	A
S4	D	K	T	P	D	A	D	H	I	R
S5	D	G	L	P	D	A	C	E	Y	A



	<u>1</u>	<u>2</u>	<u>3</u>	<u>4</u>	<u>5</u>	<u>6</u>	<u>7</u>	<u>8</u>	<u>9</u>	<u>10</u>
S1	P	W	A	R	Q	A	C	E	Y	A
S2	D	K	A	R	Q	A	C	H	I	R
S3	D	W	T	P	D	A	C	E	Y	A
S4	D	K	T	P	D	A	D	H	I	R
S5	D	G	L	P	D	A	C	E	Y	A

Maximum Parsimony: Minimize Steps

After computing the nodes, thereby reducing the set of possibilities, the next phase is to determine the **MINIMAL NUMBER OF CHANGES** needed to explain the data on the tree.

In other words, given the possibilities at all the nodes, can you select the characters at each node that result in the fewest transitions? In this exercise, the internal nodes have been pre-computed.

Step 1: Click Minimize Steps button

This will take you to the Quiz page.

QUIZ page.

Minimize Steps

	1	2	3	4	5	6	7	8	9	10
S1	K	P	R	H	T	L	N	M	H	A
S2	I	K	A	H	U	L	N	O	H	S
S3	K	P	R	V	T	E	D	M	H	A
S4	I	K	A	V	U	L	D	O	H	A
S5	I	U	A	L	T	L	D	M	H	A
Tree 1:										
Tree 2:										

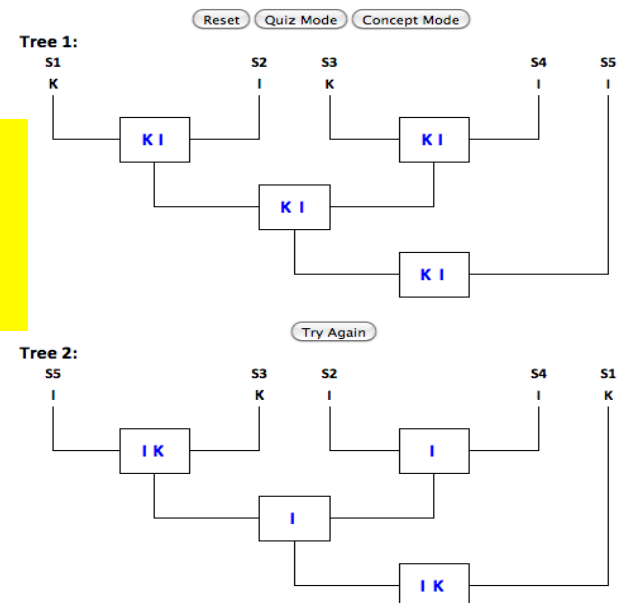
Concept Mode
Compute Nodes

	1	2	3	4	5	6	7	8	9	10
S1	Q	I	R	H	S	D	H	C	P	W
S2	N	I	R	H	O	D	I	N	V	K
S3	Q	F	L	L	S	D	I	C	P	W
S4	N	I	L	L	O	D	I	N	V	K
S5	Q	I	C	L	O	D	I	K	P	W

Reset Quiz Mode Minimize Steps

NOTICE: All the internal nodes are already computed for both trees for Position 1.

Click Here.

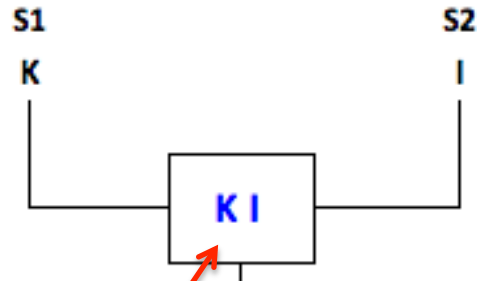


Maximum Parsimony: Minimize Steps

Step 2: Select internal nodes

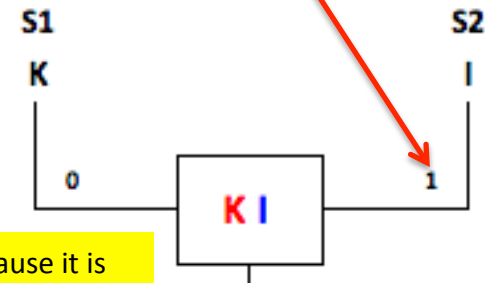
Start at top left and click on individual characters (amino acids) to try and minimize the number of changes over the whole tree for that position.

Tree 1:



Click either K or I in this example.

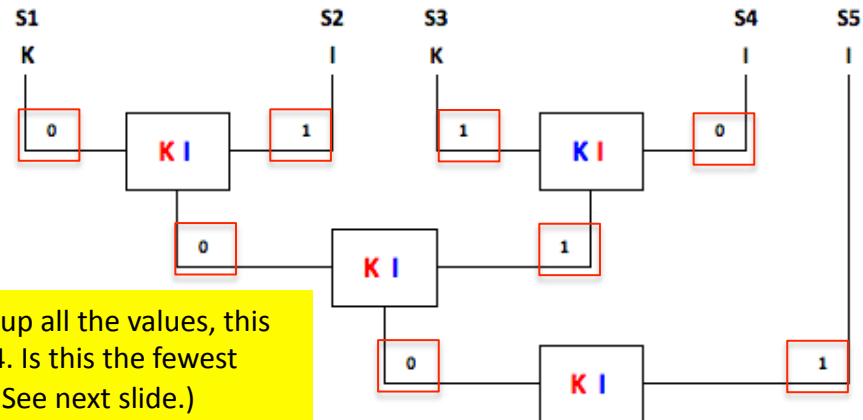
Tree 1:



K to K is Zero because it is the same.

Click through the rest of the Nodes, trying to get the fewest changes overall:

Tree 1:

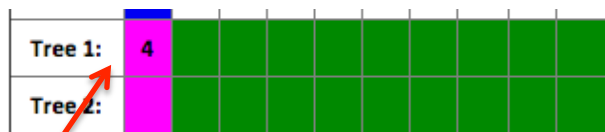


If you add up all the values, this comes to 4. Is this the fewest possible? (See next slide.)

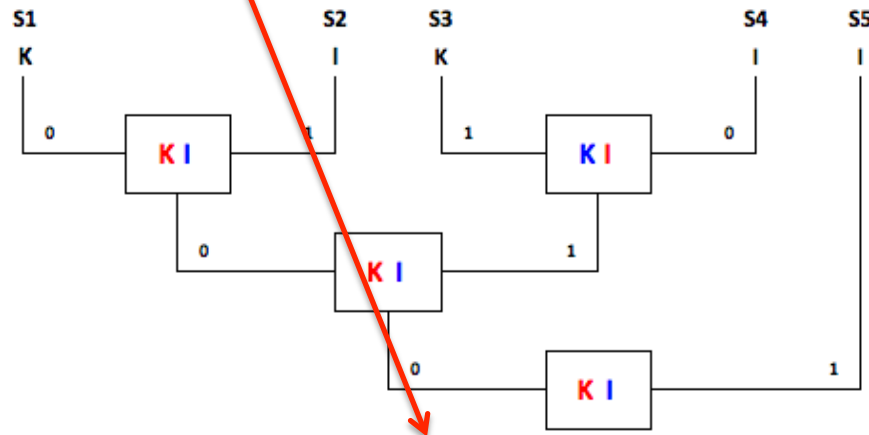
Maximum Parsimony: Minimize Steps

Step 2 (cont.): Select internal nodes

If not minimal, Try Again!

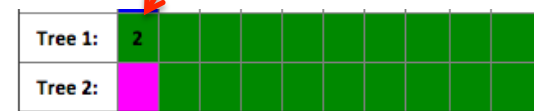


Oops! 4 Steps is not the minimal number. We can do better. Click Try Again.



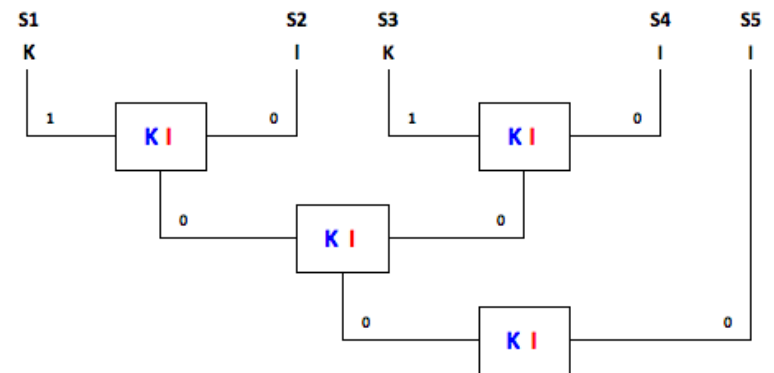
Try Again

Much better! In fact it is 2 Steps shorter!



Reset Quiz Mode Concept Mode

Tree 1:



Maximum Parsimony: Minimize Steps

Step 3: Complete for all Positions

Finish the analysis for all the positions of the alignment.

The better of the two trees is the one with the lowest overall score (total) over all positions of the sequence alignment.

In this case, Tree 2 is more parsimonious than Tree 1 so is preferred by the Maximum Parsimony criterion.

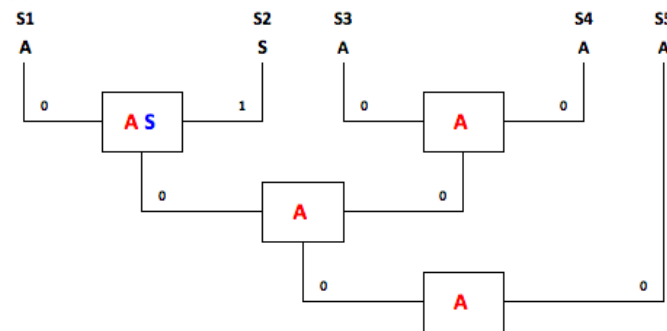
Minimize Steps

	1	2	3	4	5	6	7	8	9	10
S1	K	P	R	H	T	L	N	M	H	A
S2	I	K	A	H	U	L	N	O	H	S
S3	K	P	R	V	T	E	D	M	H	A
S4	I	K	A	V	U	L	D	O	H	A
S5	I	U	A	L	T	L	D	M	H	A
Tree 1:	2	3	2	2	2	1	1	2	0	1
Tree 2:	2	2	2	3	1	1	2	1	0	1

Sum of all steps for Tree 2 is one less than Tree 1.

Reset Quiz Mode Concept Mode

Tree 1:



Try Again

Tree 2:

