Deadline: Start of class 11/26/18 on paper

Instructor: Dr. Spielman

Υc	Your Name: Names of Lab Group (one per line in the space below):		
Na			
1.	Draw your lab group's most parsimonious tree in the space below. Its treelength is:		
2.	Draw Mesquite's most parsimonious tree in the space below. Its treelength is:		
Αlα	ong the Mesquite tree for #2 above, draw the evolutionary steps for your assigned column.		
Als	so include the character at each tip and the character which you predict is the answer, based parsimony.		
	e tree length for your assigned column is		

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Analyze each column given below, using Mesquite's most parsimonious tree. Answer each question in 1-2 complete sentences.

Column 7		
1.	How many and which taxa have the sequence "T"?	
2.	Is the "T" a derived or ancestral character for this column?	
3.	Did taxa gain T due to homology (shared ancestry), homoplasy (convergent evolution), or some combination? <i>Be very specific</i> .	
4.	Do taxa with T form a monophyletic, paraphyletic, or polyphyletic group?	

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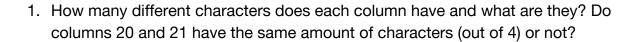
Column 8

1.	How many and which taxa have the sequence "T"?
2.	Is the "T" a derived or ancestral character for this column?
3.	Did taxa gain T due to homology (shared ancestry), homoplasy (convergent evolution), or some combination? <i>Be very specific</i> .
4.	Do taxa with T form a monophyletic, paraphyletic, or polyphyletic group?

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Compare columns 20 and 21



2. Which column do you think is evolving FASTER? Fast evolution is when there are more changes during some period of time, and slow evolution is when there are fewer changes during some period of time.

Column 49

1. This column has evolved to contain all 4 nucleotides in different species. It is therefore a very *variable* column in the character matrix. Determine the most parsimonious number of changes for the circumstance where the ancestor is each of the 4 nucleotides. In other words, first assume the ancestor is "A". How many changes would need to happen in the tree to produce the data we observe? Do the same for C, G, and T as the ancestor. You should use the space below to DRAW each option, i.e. draw the same tree 4 times and map changes for each one assuming a different ancestor. Label each tree clearly and CIRCLE YOUR FINAL ANSWER. Any answer uncircled will be ignored.

Mesquite Phylogenetics Lab SUBMISSION

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2. Now, assume that **C** is the ancestor for this column. Draw a new tree which would make all characters at column 49 *homologous*. In other words, draw one possible tree that represents evolution with NO convergence using the data for column 49. Make sure the tree is fully bifurcating, i.e. no polytomies.