Lab 04
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Question 1

Use the commands above to explore the dataset.

paup> cstatus

```
    Character-status summary:
        Current optimality criterion = parsimony
        No characters are excluded
        Of 898 total characters:
            All characters are of type 'unord'
            All characters have equal weight
            377 characters are constant (proportion = 0.419822)
            154 variable characters are parsimony-uninformative
            Number of parsimony-informative characters = 367
```

paup> showdist

```
    Uncorrected ("p") distance matrix
        898 characters are included
        All characters have equal weight
```

	1	2	3	4	5	6	7	8	9	10	11	12
1 Lemur catta	–											
2 Homo sapiens	0.30794	–										
3 Pan	0.30906	0.08929	–									
4 Gorilla	0.29341	0.10379	0.10603	–								
5 Pongo	0.29265	0.16087	0.17093	0.16645	–							
6 Hylobates	0.29559	0.18192	0.18862	0.18862	0.18768	–						
7 Macaca fuscata	0.28215	0.23214	0.24330	0.23661	0.24467	0.24665	–					
8 M. mulatta	0.28878	0.23326	0.25112	0.23549	0.24703	0.23884	0.03571	–				
9 M. fascicularis	0.29782	0.24888	0.26786	0.26228	0.26155	0.25670	0.08371	0.09263	–			
10 M. sylvanus	0.28656	0.25558	0.24888	0.24442	0.24144	0.24219	0.12388	0.11942	0.12277	–		
11 Saimiri sciureus	0.28529	0.27337	0.28455	0.27100	0.28380	0.26879	0.28893	0.29341	0.28669	0.28673	–	
12 Tarsius syrichta	0.25186	0.32200	0.32090	0.31419	0.30335	0.30856	0.31432	0.31641	0.31096	0.31865	0.31978	–

paup> showmatrix

```
    Input data matrix: (first part only)
                    1         2         3         4         5         6         7         8         9         0         1         2         3         4  4
    Taxon           1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345
    -----------------------------------------------------------------------------------------------------------------------------------------------------------
    Lemur catta     AAGCTTCATAGGAGCAACCATTCTAATAATCGCACATGGCCTTACATCATCCATATTATTCTGTCTAGCCAACTCTAACTACGAACGAATCCATAGCCGTACAATACTACTAGCACGAGGGATCCAAACCATTCTCCCTCTTATA
    Homo sapiens    AAGCTTCACCGGCGCAGTCATTCTCATAATCGCCCACGGGCTTACATCCTCATTACTATTCTGCCTAGCAACCTCAAACTACGAACGCACTCACAGTCGCATCATAATCCTCTCTCAAGGACTTCAAACTCTACTCCCACTAATA
    Pan             AAGCTTCACCGGCGCAATTATCCTCATAATCGCCCACGGACTTACATCCTCATTATTATTCTGCCTAGCAAACTCAAATTATGAACGCACCCACAGTCGCATCATAATTCTCTCCCAAGGACTTCAAACTCTACTCCCACTAATA
    Gorilla         AAGCTTCACCGGCGCAGTTGTTCTTATAATTGCCCACGGACTTACATCATCATTATTATTCTGCCTAGCAAACTCAAACTACGAACGAACCCACAGCCGCATCATAATTCTCTCTCAAGGACTCCAAACCCTACTCCCACTAATA
    Pongo           AAGCTTCACCGGCGCAACCACCCTCATGATTGCCCACGGACTCACATCCTCCCTACTGTTCTGCCTAGCAAACTCAGCACTACGAACGCCACCCACAGCCGCATCATAATCCTCTCTCAAGGCCTTCAAACTCTACTCCCCCTAATA
    Hylobates       AAGCTTTACAGGTGCAACCGTCCTCATAATCGCCCACGGACTAACCTCTTCCCTGCTATTCTGCCTTGCAAACTCAAACTACGAACGAACTCACAGCCGCATCATAATCCTATCTCGAGGGCTCCAAGCCTTACTCCCACTGATA
    Macaca fuscata  AAGCTTTTCCGGCGCAACCATCCTTATGATCGCTCACGGACTCACCTCTTCCATATATATTCTGCCTAGCCAATTCAAACTATGAACGCACTCACAACCGTACCATACTACTGTCCCGAGGACTTCAAATCCTCCTTCCACTAACA
    M. mulatta      AAGCTTTTCTGGCGCAACCATCCTCATGATTGCTCACGGACTCACCTCTTCCATATATTTCTGCCTAGCCAATTCAAACTATGAACGCACTCACAACCGTACCATACTACTGTCCCGGGGACTTCAAATCCTCCTTCCACTAACA
    M. fascicularis AAGCTTCTCCGGCGCAACCACCCTTATAATCGCCCACGGGCTCACCTCTTCCATGTATTTCTGCTTGGCCAATTCAAACTATGAGCGCACTCATAACCGTACCATACTACTATCCCGAGGACTCCAAATCTTACTTCCATTGACA
    M. sylvanus     AAGCTTCTCCGGTGCAACTATCCTTATAGTTGCCCATGGACTCACCTCTTCCATATACTTCTGCTTGGCCAACTCAAACTACGAACGCACCCACAGCCGCATCATACTACTATCCCGAGGACTCCAAATCCTACTCCCACTAACA
    Saimiri sciureus AAGCTTCACCGGCGCAATGATCCTAATAATCGCTCACGGGTTTACTTCGTCTATGCTATTCTGCCTAGCAAACTCAAATTACGAACGCACTCACAGTCGCATCATAATCCTCTCTCAAGGGCTCCAAACACTATTCCCGCTTATA
    Tarsius syrichta AAGTTTCATTGGAGCCACCACTCTTATAATTGCCCATGGCCTCACCTCCTCCCTATTATTTTGCCTAGCAAATACAAACTACGAACGAGTCCACAGTCGAACAATAGCACTAGCCCGTGGCCTTCAAACCCTATTACCTCTTGCA
```

paup> tstatus

```
    Taxon-status summary:
        Original data matrix contains 12 taxa
        No taxa have been deleted
        No taxa have been assigned to the outgroup: outgroup
    defaults to first taxon (Lemur catta)
```

Question 1(continued)

What is the optimality criterion currently set to?

The optimality criterion currently is set to **parsimony**

Are these characters ordered or unordered?

All characters are of type 'unord', which means **unordered**.

What is the distance between chimpanzees and humans?

The distance between chimpanzees and humans is **0.08929** (marked yellow in last page).

Question 2

What is the total branch length sum for your UPGMA tree? For your NJ tree? [HINT: Scroll back up through your PAUP window to find this information]

The total branch length sum for my UPGMA tree is **1.09123**.

The total branch length sum for my UPGMA tree is **1.08944**.

Question 3

Examine your parsimony, UPGMA, and NJ trees in FigTree. Do the tarsiers fall out in the same place in all your trees?

Tarsius_syrichta and Lemur_catta are both relatively distant from other taxon. Both of these two taxon are more primitive. Yet, the exact places that tarsiers fall out is a bit different in these three trees.

Question 4

Figure out a way to show your tree with bootstrap support in FigTree. Note: The program can be a bit glitchy for some reason so you may need to open the program first and then go to File - Open to select your file. Highlight the weakly supported Pan clade and take a screenshot.

Show the bootstrap support value:
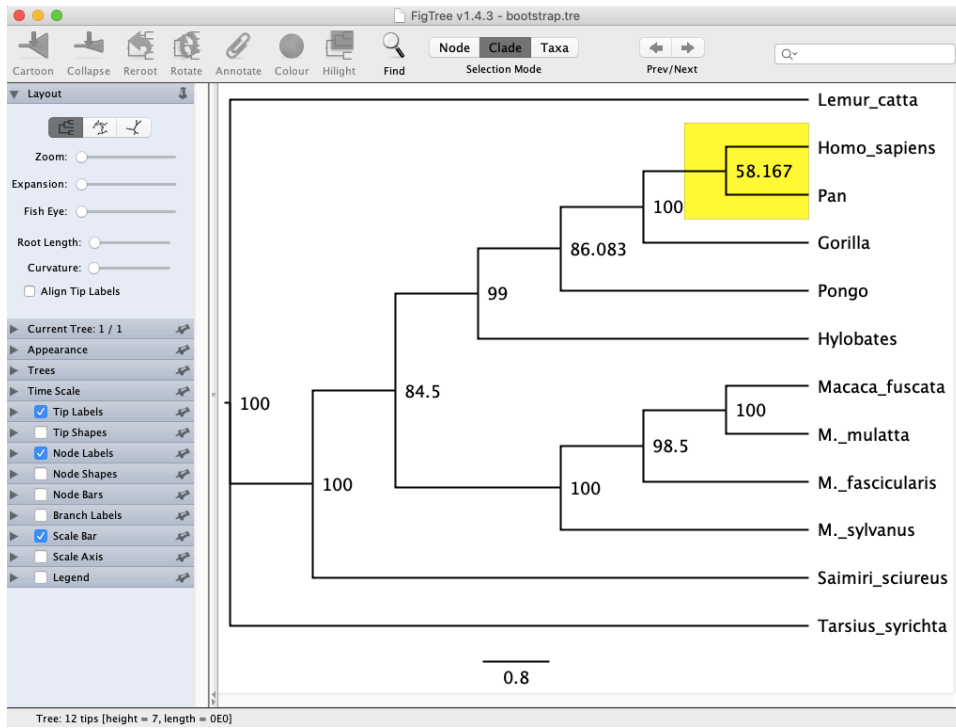
Left side [Node Labels]

[Display] select [label]
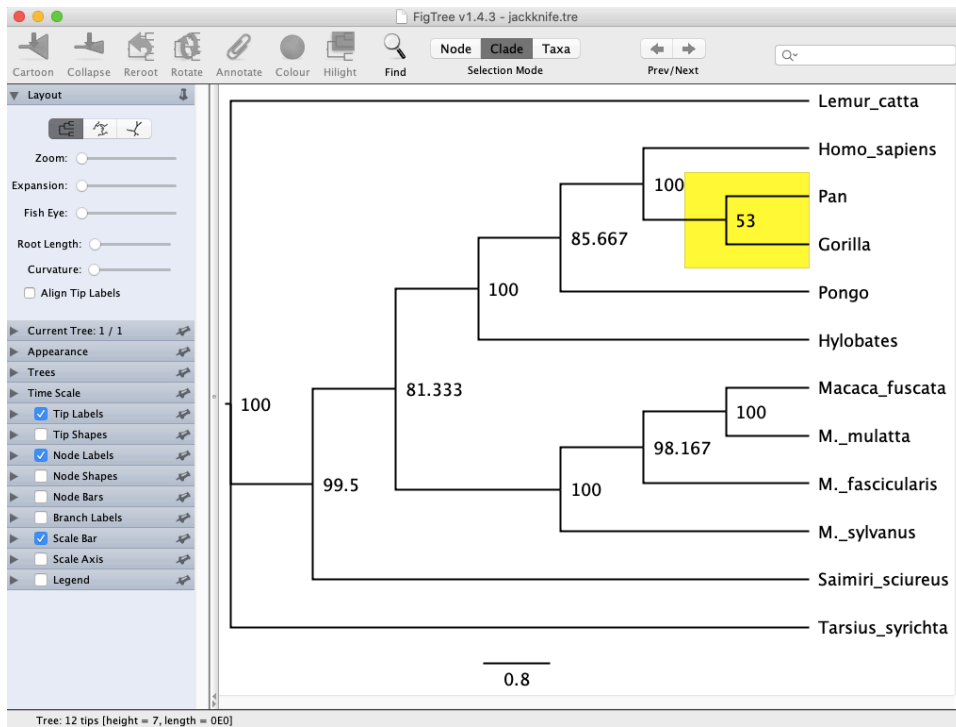
Highlight the weakly supported Pan clade:

Middle-top [Clade]

Top [Highlight]

Question 4 (continued)

Question 5

Bonus

1. Your code for concatenating and aligning the sequences

      Concatenate:

            (direct to the directory where there is a folder called "sequence_folder".
            The "sequence_folder" contains the 10 separated sequence files.)

          awk '{print}' sequences_folder/*.fasta > sequences.fasta

      Align:

            mafft --auto sequences.fasta > aligned.fasta

      Convert:

            I used this website to convert fasta format to nexus format.
             (http://phylogeny.lirmm.fr/phylo_cgi/data_converter.cgi)

      PAUP*

            execute aligned.nex
            set criterion=parsimony
            hs
            savetrees file=parstree_BONUS.tre

2. Your treefile

      File [parstree_BONUS.tre]

3. A screenshot of your tree

      File [BONUS]