Ashlee Gardiner

Bioinformatics for Biologists

Assignment 5

**Number 3-**

**(fasta file)** raxmlHPC-HYBRID-AVX -T 4 -s infile -N autoMRE -n result -f a -p 12345 -x 12345 -m PROTCATDAYHOFF

**(newick file)** muscle -in infile.fasta -seqtype protein -maxiters 16 -maxmb 30000000 -hydro 5 -hydrofactor 1.2 -log logfile.txt -weight1 clustalw -distance1 kmer6\_6 -cluster1 upgmb -sueff 0.1 -root1 pseudo -maxtrees 1 -weight2 clustalw -distance2 pctidkimura -cluster2 upgmb -sueff 0.1 -root2 pseudo -objscore sp -noanchors -out output.fasta

**Number 4-**

Syconycteris\_australis\_ace2

Dobsonia\_viridis\_ace2

Cynopterus\_sphinx\_ace2

Rousettus\_leschenaultii\_ace2

Epomophorus\_wahlbergi\_ace2

**Number 5-**

Phylogeny enriches our understanding of how organisms are related and gives us insight into events that occurred during evolution.