Lab Worksheet 14

Problem 1. Draw out the trees corresponding to these Newick strings:
    ((A, B), (C, (D, E)), F)
    (A, B, C, D, E)

Problem 2. Which two of these three tree strings represent the same topology?
    (A, ((B, C), D))
    ((A, (B, C)), D)
    ((A, D), (B, C))

Problem 3. The file "cxcr4_aa.fasta" contains amino-acid sequences for mammalian chemokine receptor 4, a receptor that plays a fundamental role in the immune system. (You may have heard that HIV uses CXCR4 to infect cells.) Make two phylogenetic trees for these sequences, both with bootstrap values, one using the neighbor-joining (NJ) method and one using maximum likelihood (RAxML). Then discuss how the two trees compare, using the bootstrap values in your argument.

Follow these steps:
1. Make an alignment. Use this web service:
http://www.ebi.ac.uk/Tools/msa/clustalo/

2. Convert the output into phylip format. Use this web service:
http://www.ebi.ac.uk/Tools/sfc/readseq/

3. Make your trees. Use this web service:
http://www.trex.uqam.ca/
When the calculation is completed, click on "view tree" to visualize the tree.