Problem Set 3: Curricula vitae, careers and alignments

Answer the following questions related to performing the requested tasks and then include your answers in an electronic file, save as a pdf, and merge together as a single pdf. Upload your PDF file to the Blackboard Assignment page for Problem Set 3 by 5 pm on the due date.

Part 0

Develop a CV for yourself-if you already have one, take some time to refine it. Include the information we've talked about in class and anything else you think might be relevant. Be sure to format it is an attractive way so you win the hypothetical award/grant/job!!!

Part 1

Identify and list 5 internship/job opportunities in bioinformatics that might be of interest to you. Give the details of the opportunity and explain why these opportunities are of interest to you.

Part 2: Alignments

In class, you learned about alignments and substitution matrices. Use your knowledge, the textbook and online resources to complete the following:

1. Your friend, who is a non-science major, wants to learn more about how biologists study evolution. Describe to them what an "alignment" is in the context of biology/bioinformatics and why alignments matter in the study of evolution.

2. MAFFT is one software that scientists often use to generate multiple sequence alignments (MSAs). There is a tendency for people to use "default" settings because it requires less decision-making and knowledge on their part. Not making a decision, however, is sometimes the worst decision. You should know what the parameters of your software are and know how changing them will affect your results. Pick 5 parameters (aka settings) in the "Advanced Settings" of the above MAFFT webpage and explain what they are & how you expect they will affect your alignment using the MAFFT manual, what you've learned in class and your superb Internet research skills. MAFFT manual

3. Download both the amino acid and nucleotide FASTA files from the supplementary materials. Use MAFFT to generate two sets of multiple sequence alignments (MSA). List your parameters (settings). Attach your alignment output files (not zipped).

4. View your two alignments using an alignment viewer of your choice—there are both web-based and downloadable viewers. Which alignment do you think is more accurate and why?