

## FINAL EXAM – INTERMEDIATE PREVIEW 1

October 9, 2024

**Note:** This preview is approximately 25 percent the size of the actual final; thus you should need below 30 minutes.

Your name: \_\_\_\_\_

(1) Here is a small sequence: ACACA. Create the suffix tree.

[3 points]

(2) Explain how the posterior probability works in the context of Bayes' theorem. (*Steps: Write down Bayes' theorem. Indicate the posterior probability. Explain the conceptual difference to the likelihood.*)

[5 points]

- (3) Here is a short DNA sequence: ACTCGATACGTGCG. Compute the observed CpG / expected CPG ratio and explain each quantity.

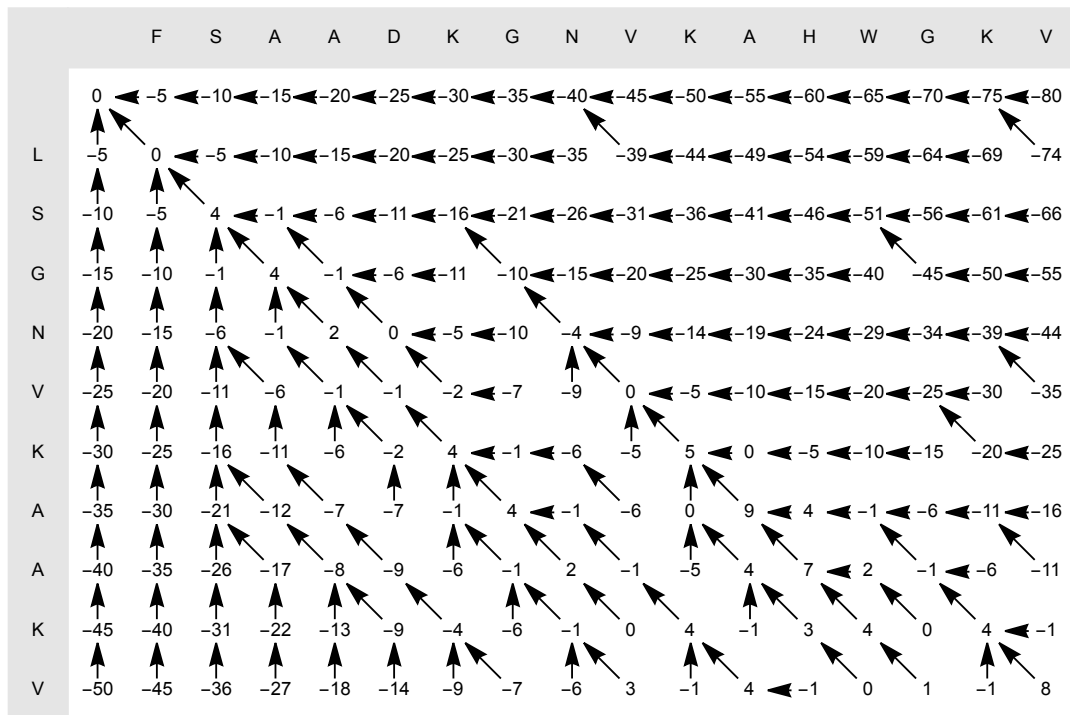
[3 points]

- (4) Think about our brief discussion of the PHYLIP tool for phylogenetic analyses. Which of the matrices below is a valid distance matrix and why?

$$M_1 = \begin{pmatrix} 0. & 0.6 & 0.7 \\ 0.2 & 0. & 0.7 \\ 0.5 & 1. & 0. \end{pmatrix}, M_2 = \begin{pmatrix} 0. & 1.6 & 1. \\ 1.6 & 0. & 0.7 \\ 1. & 0.7 & 0. \end{pmatrix}, M_3 = \begin{pmatrix} 1.6 & 1. & 1.6 \\ 0.6 & 0.1 & 1.6 \\ 1.1 & 0.8 & 1.5 \end{pmatrix}$$

[2 points]

- (5) Here is an F matrix for two sequences computed with one of the two alignment algorithms discussed:



- (a) Which algorithm has been used (Needleman-Wunsch or Smith-Waterman)? How do you see this?
- (b) Extract the corresponding optimal alignment.

[5 points]