

Exercises before Quiz – Computational Biology

You are given 2 sequences to work with:

Sequence A is obtained from a.fasta

Sequence B is obtained from b.fasta

1. Sequence Manipulation:

- a. Find and display the total length of Sequence A and B.
- b. Find and display which index the first time codon (TAC) appears in both Sequence A and B.
- c. Take the first 10 nucleotides from Sequence A, and the last 15 nucleotides from Sequence B. Then combine the sequences and reverse it to a new sequence, Sequence C.

2. Sequence Analysis & Plotting:

- a. Determine and display the nucleotides base (A, C, G, T) frequency for Sequence A, B, and C with a chart using matplotlib library.
- b. Determine and display the GC & AT content percentage for Sequence A, B, and C.
- c. Determine and display the melting temperature for Sequence A, B, and C (using built-inWallace Method).
- d. Determine and display the molecular weight for Sequence A, B, and C.

3. DNA & mRNA Protein Synthesis:

- a. Transcribe and display the DNA Sequence A, B, and C into mRNA Sequences.
- b. Translate and display the mRNA Sequence A, B, and C into amino acids sequences.
(Clue: for translate, use the mRNA sequences that already transcribed on the first step)

4. Sequence Alignment & Similarities:

- a. Perform local alignment pairwise between Sequence A and Sequence “CGCTACTA GCATGCGCAT” and display the alignments’ score. (Clue: Use localxx)
- b. Perform global alignment pairwise between Sequence B and Sequence “CAGTGCG CTAGCAGCTACGTGTG” and display the alignments’ score. (Clue: Use globalxx)

- c. Find and display the Levenshtein distance between Sequence A and B