

Problem 1. Dynamic Programming (10 points).

With the following scoring function: *MATCH: 5 MISMATCH: -10 GAP: -5*
Consider the task of finding the optimal global alignment of the following two sequences: ATC and ATATCTC. Construct the dynamic programming table.

Answer:

Problem 2. Amino acid sequence (10 points).

Translate the following sequence to the sequence of amino acids.
AUG-AAG-CCG-AGU-GUA-UGA

Answer:

Problem 3. UniProt database (10 points).

UniProt database (<https://www.uniprot.org/>) is where you can find the sequence of a specific gene. Please use the UniProt database to find the amino acid sequence of the gene **KMT2A_HUMAN** and the gene **KMT2A_MOUSE**.

Write down the first 50 amino acids of **KMT2A_HUMAN (5 points)** and the first 50 amino acids of **KMT2A_MOUSE (5 points)** here.

Answer: