The Sequence Alignment Problem

In this problem, we utilize dynamic programming to find the highest-scoring alignment between two gene sequences. Given two strings, x[1...n] and y[1...m], and a scoring matrix, the algorithm calculates the optimal alignment. The time complexity of this algorithm is O(mn), where m and n are the lengths of the two sequences.

The implementation was tested using given sequences and a specified scoring matrix. The results demonstrate the algorithm's effectiveness in determining the highest-scoring alignment efficiently. The running time aligns with the theoretical time complexity of O(mn), showcasing dynamic programming's capability in solving complex sequence alignment problems.

The dynamic programming approach for sequence alignment proves to be efficient and effective, particularly for longer sequences. Its polynomial time complexity makes it suitable for practical applications in bioinformatics, such as comparing genetic sequences.