

## **Assignment 2 Report**

This report discusses the time analysis and Python implementation of a gene sequence alignment algorithm. With a time complexity of  $O(mn)$ , where  $n$  and  $m$  are sequence lengths, the algorithm efficiently aligns sequences using dynamic programming. The Python code emphasizes simplicity, initializing a matrix, filling it through nested loops, and reconstructing optimal alignment via traceback. Aligned sequences are crafted during this process. With  $O(mn)$  efficiency, this implementation holds promise for various bioinformatics applications, with potential for future optimization and adaptation.