

Dynamic Programming for DNA Sequence Alignment

Xinyu Cheng, Zhihao Wang, Xueni Tang, Jieni Tang

August 2025

Contents

1	Introduction	2
1.1	DNA Sequence Alignment	2
1.2	The Role of Dynamic Programming	2
1.3	Project Structure Overview	2

1 Introduction

1.1 DNA Sequence Alignment

abc

1.2 The Role of Dynamic Programming

abc

1.3 Project Structure Overview

Together, these components form a cohesive investigation into how dynamic programming enables efficient DNA sequence alignment and how theoretical models perform when applied to real data.

References

- [1] Needleman, Saul B., and Christian D. Wunsch. "A general method applicable to the search for similarities in the amino acid sequence of two proteins." *Journal of molecular biology* 48.3 (1970): 443-453.
- [2] Smith, Temple F., and Michael S. Waterman. "Identification of common molecular sub-sequences." *Journal of molecular biology* 147.1 (1981): 195-197.