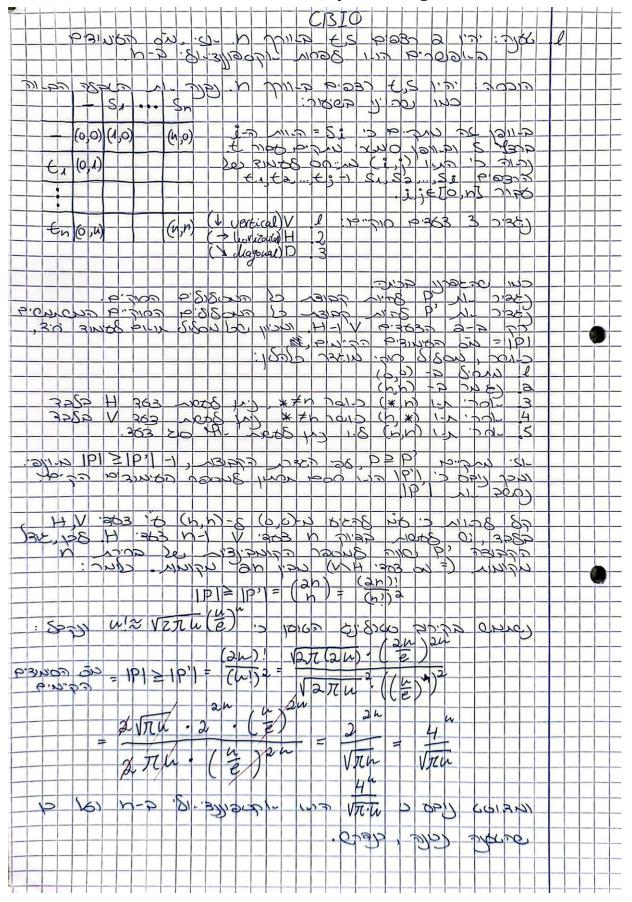
Course: 76558: Algorithms in Computational Biology

Students: Inbar Neuwirth (214775264), Yishai Ben Zvi (208307843)

Exercise: 1

Part 1: theoretical lower bound on number of possible alignments:



Part 2: segmentation program:

Complexity Analysis of Our Algorithm

Setup:

The setup phase has a time complexity of **O(n)**. In this step, we precompute the cumulative sums and the sum of squares for the input data. This precomputation allows us to later find the cost of any given segment in constant time, **O(1)**. (see below):

Loop Analysis:

Our algorithm consists of nested loops:

- The **outer loop** runs **O(n)** times.
- Within each iteration of the outer loop, there is an inner loop that runs O(q) times.
- The operations inside the inner loop are completed in constant time, **O(1)**.

Extract Segments:

This final step has a time complexity of O(k), where k is the number of segments and is less than or equal to $n (k \le n)$.

Overall Complexity

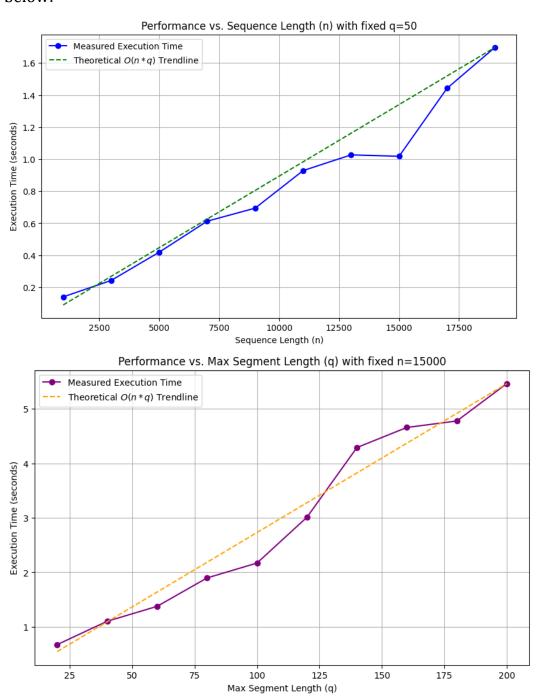
Considering the nested loop structure as the dominant part of the algorithm, the overall time complexity is O(n * q).

Reference code for efficient segment cost:

```
s = np.zeros(n + 1)
s2 = np.zeros(n + 1)
np.cumsum(x, out=s[1:])
np.cumsum(x**2, out=s2[1:])
def quick_seg_cost(j, i):
  length = i - j
  # sum of values in x[j:i]
  sum_val = s[i] - s[j]
  # sum of squared values in x[j:i]
```

$$sum_sq_val = s2[i] - s2[j]$$
Cost = $sum(x^2) - (sum(x))^2 / N$
return $sum_sq_val - (sum_val^{**}2) / length$

Complexity Visualized: for reference see the plot_complexity function, and plots below:



Appendix: AI usage:

After developing a DP program based on the recursive problem:

We used google gemini 2.5 via google ai studio to generate code for the pseudo code structure.