

Project 4 Report

1. Time and Space complexity

Unrestricted Algorithm Pseudocode

Width = length of string1 or align length	decrement i and j
Height = length of string2 or align length	Time = 1 Space = $m \cdot n$
Table[width][height]	Time = 1 Space = $m \cdot n$
prevTable[width][height]	
Table[0][0] = 0	Time = n
Table[i][0] = table[i-1][0] + INDEL for all i	Time = m
Table[0][j] = table[0][j-1] + INDEL for all j	N repetitions
For i in width:	M repetitions
For j in height:	Constant time
Diagonal = MATCH if $\text{str1}[i] == \text{str2}[j]$, else SUB	""
Table[i][j] = min(top + INDEL, left + INDEL, diagonal)	""
prevTable = 'u' if top, 'l' if left, or 'm' if diagonal	
i = width	Getting alignment
j = height	Repeats at worst $n + m$ times
while i or j are greater than 0:	Constant time
if prevTable[i][j] = 'u':	
alignA = "-" + alignA	
alignB = B[j] + alignB	
j -= 1	
same but opposite for 'l'	
if prevTable[i][j] = 'm':	
alignA and alignB plus the letter at i and j	

Total time complexity is $N \cdot M$ for filling out the table. While loop for extracting the alignment is at worst case $N + M$ time so is dominated by filling out the table. Total time complexity is $O(nm)$

Storing the strings and alignments are not significant as they are just n or m in length. Space Complexity is dominated by the two tables for the score values and the previous pointers which are both $N \cdot M$ tables so total space complexity is $O(nm)$.

Banded Algorithm Pseudocode

If absolute value(length of str1 – length str2) > 100: skip and return nothing	Time = 1
Width = 1 + MAXINDEL*2	width = $3 \cdot 2 + 1 = 7$ (this is k)
Height = length of string2	
Table[width][height]	Space = kn
prevTable[width][height]	Space = kn
Table[0][j] = table[0][j-1] + INDEL for all j, prevTable = 'u'	
for j in width:	k repeats
for i in height:	n repeats
if i > MAXINDEL:	Calculate table value (constant time)
upper = table[i-1][j+1] + INDEL	
left = table[i][j-1] + INDEL	

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    diagonal = table[i-1][j] + MATCH if same or SUB if different
    table[i][j] = min(upper, left, diagonal)
    set prevPointer
else l <= MAXINDEL:
    do same as unrestricted for first 3 rows
i = length of string1
j = length of string2
while l or j are greater than 0:                                worst case n + m time and space
    adjust = j - i + MAXINDEL
    same as for restricted but use
        adjust instead of j in accessing
    the tables.

```

Total time complexity is $N \cdot k$ for filling out the table. While loop for extracting the alignment is at worst case $N + M$ time so is dominated by filling out the table. Total time complexity is $O(nk)$

Storing the strings and alignments are not significant as they are just n or m in length. Space Complexity is dominated by the two tables for the score values and the previous pointers which are both $N \cdot k$ tables so total space complexity is $O(nk)$.

2. Alignment Extraction Algorithm

I implemented the back trace algorithm using a previous pointer table that saved for each index, a letter signifying which direction that number was calculated from. For example, 'l' meant that the number at that index was based on the number to the left plus the value of an INDEL. 'm' signified a match or substitution.

Once the table was filled, I extracted the alignment strings by starting at the final goal index and checking the previous pointer. A previous pointer of 'u' for upper or 'l' for left meant and INDEL was used to reach that value so I added the character from one string to it's alignment and a '-' to the other string. I then decremented the i (or j) value to represent the upper or left cell. A previous pointer of 'm' signified a match or substitution so I added both strings characters at that index to both alignments and decremented both i and j .

The alignment strings were constructed thus in reverse direction from the left to the right. Each character was appended to the beginning of the current alignment string until the index $[0, 0]$ was reached. Since this was the start index, nothing is added and both alignments are returned.

3. Results

Unrestricted with align length = 1000



Restricted with Align length = 3000 and MAXINDEL = 3



Unrestricted Alignment for Seq #3 and Seq #10

```
gattgcgagcgatttgcgtgcgtgcacccgcttc-actg--at-ctcttgtagatcttttcataatctaaactttataaaaaacatccactccctgta-  
-ataa-gagtgattggcggtccgtacgtaccctttctactctcaaaactcttgtagtttaaatac-taatctaaactttataaa--cggc-acttctctgtg
```

Restricted Alignment for Seq #3 and Seq #10

```
ga-ttgcgagcgatttgcgtgcgtgcacccgcttc-actg--at-ctcttgtagatcttttcataatctaaactttataaaaaacatccactccctgta  
--ataa-gagtgattggcggtccgtacgtaccctttctactctcaaaactcttgtagtttaaatac-taatctaaactttataaa--cggc-acttctctgtg
```

Appendix: Commented Source Code

```
#!/usr/bin/python3  
  
from PyQt6.QtCore import QLineF, QPointF  
  
# Used to compute the bandwidth for banded version  
MAXINDELS = 3  
  
# Used to implement Needleman-Wunsch scoring  
MATCH = -3  
INDEL = 5  
SUB = 1  
  
class GeneSequencing:  
  
    def __init__(self):  
        self.banded = None  
  
    # This is the method called by the GUI. _seq1_ and _seq2_ are two sequences to be  
    aligned, _banded_ is a boolean that tells  
    # you whether you should compute a banded alignment or full alignment, and  
    _align_length_ tells you  
    # how many base pairs to use in computing the alignment  
  
    def align(self, seq1, seq2, banded, align_length):  
        self.banded = banded  
        self.MaxCharactersToAlign = align_length  
  
        seq1 = "-" + seq1 # Add a blank symbol to the beginning of each string so that  
        beginning is always a match  
        seq2 = "-" + seq2  
  
        AlignmentA = ""  
        AlignmentB = ""  
  
        ## Unrestricted  
        if not banded:  
            width = min(align_length + 1, len(seq1))  
            height = min(align_length + 1, len(seq2))  
            table = [[float('inf') for i in range(height)] for j in range(width)] #  
Initialize tables  
            prevTable = [[0 for i in range(height)] for j in range(width)]  
  
            table[0][0] = 0 # Set start point values  
            prevTable[0][0] = 'stop'  
            for i in range(1, width): # Set base cases  
                table[i][0] = table[i - 1][0] + INDEL
```

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    prevTable[i][0] = 'l'
    for j in range(1, height):
        table[0][j] = table[0][j - 1] + INDEL
        prevTable[0][j] = 'u'

    for i in range(1, width): # Fill in entire table from top left
        for j in range(1, height):
            left = table[i - 1][j] + INDEL
            top = table[i][j - 1] + INDEL
            if seq1[i] == seq2[j]: # If the letters match then set value to
MATCH, else SUB
                diag = table[i - 1][j - 1] + MATCH
            else:
                diag = table[i - 1][j - 1] + SUB
            minimum = min(left, top, diag)
            table[i][j] = minimum
            if minimum == left: # Determine which input was used and store in
previous pointer
                prevTable[i][j] = 'l'
            elif minimum == top:
                prevTable[i][j] = 'u'
            elif minimum == diag:
                prevTable[i][j] = 'm'

    score = table[-1][-1]

    # Get Alignment not Banded
    A = seq1
    B = seq2
    i = min(len(A) - 1, align_length) # Set the start point
    j = min(len(B) - 1, align_length) # Set the start point
    while i > 0 or j > 0: # While i and j are both above 0 meaning we have not
reached the beginning
        if j > 0 and prevTable[i][j] == 'u': # If previous was u then continue
trace in upper
            AlignmentA = "-" + AlignmentA
            AlignmentB = B[j] + AlignmentB
            j -= 1
        elif i > 0 and prevTable[i][j] == 'l': # If previous was l then continue
in left
            AlignmentA = A[i] + AlignmentA
            AlignmentB = "-" + AlignmentB
            i -= 1
        elif i > 0 and j > 0 and prevTable[i][j] == 'm': # If previous was m then
continue on diagonal
            AlignmentA = A[i] + AlignmentA
            AlignmentB = B[j] + AlignmentB
            i -= 1
            j -= 1
        else:
            print("Backtrace Failed") # If none matched then the trace was lost
(should never happen)
            exit(-111)

    # Restricted
    if banded:
        width = min(align_length + 1, len(seq1))
        height = min(align_length + 1, len(seq2))

        if abs(width - height) > 100: # Significant difference in length, return not
calculable
            print("No alignment possible as sequence differ in length significantly")
            score = float('inf')

```

```

        alignment1 = "No Alignment Possible"
        alignment2 = "No Alignment Possible"
        return {'align_cost': score, 'seq1_first100': alignment1,
'seqj_first100': alignment2}

width = 1 + MAXINDELS * 2 # Initialize tables
table = [[float('inf') for i in range(7)] for j in range(height)]
prevTable = [[0 for i in range(7)] for j in range(height)]

table[0][0] = 0 # Set start values
prevTable[0][0] = 'stop'
for i in range(1, 4): # Set base cases
    table[0][i] = table[0][i - 1] + INDEL
    prevTable[0][i] = 'u'
for i in range(1, height): # Fill table from top left
    for j in range(width):
        if i > MAXINDELS: # Use these comparisons once values are being
shifted in table
            if j + 1 > width - 1: # Get north value
                north = float('inf')
            else:
                north = table[i - 1][j + 1] + INDEL
            if j - 1 < 0: # Get west value
                west = float('inf')
            else:
                west = table[i][j - 1] + INDEL
            adjust = min(MAXINDELS - i, 0)
            if j - adjust < len(seq1) and seq1[j - adjust] == seq2[i]: #
Check for match
                nw = table[i - 1][j] + MATCH
            else:
                nw = table[i - 1][j] + SUB
            minimum = min(north, west, nw)
            table[i][j] = minimum

            if minimum == north: # Determine which value was previous
                prevTable[i][j] = 'u'
            elif minimum == west:
                prevTable[i][j] = 'l'
            else:
                prevTable[i][j] = 'm'

            else: # For the first 3 rows that don't need adjustment, run like
unbanded
                north = table[i - 1][j] + INDEL
                west = table[i][j - 1] + INDEL
                if seq1[i] == seq2[j]:
                    diag = table[i - 1][j - 1] + MATCH
                else:
                    diag = table[i - 1][j - 1] + SUB
                minimum = min(north, west, diag)
                table[i][j] = minimum
                if minimum == north:
                    prevTable[i][j] = 'u'
                elif minimum == west:
                    prevTable[i][j] = 'l'
                else:
                    prevTable[i][j] = 'm'

# Get Alignment Banded
A = seq2
B = seq1
i = min(len(A) - 1, align_length)

```

```

j = min(len(B) - 1, align_length)
while i > 0 or j > 0:
    if i > MAXINDELS: # For when table is shifted, use these comparisons
        adjust = j - i + MAXINDELS
        if i > 0 and j > 0 and prevTable[i][adjust] == 'l': # Check left
            AlignmentA = "-" + AlignmentA
            AlignmentB = B[j] + AlignmentB
            j -= 1
        elif i > 0 and prevTable[i][adjust] == 'u': # Check top
            AlignmentA = A[i] + AlignmentA
            AlignmentB = "-" + AlignmentB
            i -= 1
        elif j > 0 and prevTable[i][adjust] == 'm': # Check diag
            AlignmentA = A[i] + AlignmentA
            AlignmentB = B[j] + AlignmentB
            i -= 1
            j -= 1
        else:
            print("Backtrace Failed")
            exit(-111)
    else: # When table is not shifted (first 3 rows)
        if i > 0 and prevTable[i][j] == 'l':
            AlignmentA = A[i] + AlignmentA
            AlignmentB = "-" + AlignmentB
            i -= 1
        elif j > 0 and prevTable[i][j] == 'u':
            AlignmentA = "-" + AlignmentA
            AlignmentB = B[j] + AlignmentB
            j -= 1
        elif i > 0 and j > 0 and prevTable[i][j] == 'm':
            AlignmentA = A[i] + AlignmentA
            AlignmentB = B[j] + AlignmentB
            i -= 1
            j -= 1
        else:
            print("Backtrace Failed")
            exit(-111)

    # This is easier than changing the above code to switch the strings
    sub = AlignmentA
    AlignmentA = AlignmentB
    AlignmentB = sub

    i = min(len(A) - 1, align_length) # Get the length of str1
    j = min(len(B) - 1, align_length) # Get length of str2
    score = table[i][-abs(j-i)+MAXINDELS] # Get location of final score (Will
depend on offset between i and j)

    alignment1 = AlignmentA[:100]
    alignment2 = AlignmentB[:100]

#####

    return {'align_cost': score, 'seqi_first100': alignment1, 'seqj_first100':
alignment2}

```