

```

def align(
    seq1: str, seq2: str, match_award=-3, indel_penalty=5, sub_penalty=1, banded_width=-1,
    gap='-')
) -> tuple[float, str | None, str | None]:
    m, n = len(seq1), len(seq2)

    # Initialize the DP table with default value of float('inf')
    dp = {}

    # Initialize the first row and column
    dp[(0, 0)] = 0
    for i in range(1, m + 1):
        dp[(i, 0)] = i * indel_penalty
    for j in range(1, n + 1):
        dp[(0, j)] = j * indel_penalty

    # Fill in the DP table with either full or banded alignment
    if banded_width == -1:
        # Fill in the DP table with full alignment
        for i in range(1, m + 1):
            for j in range(1, n + 1):
                match = dp.get((i - 1, j - 1), float('inf')) + (match_award if seq1[i - 1] ==
seq2[j - 1] else sub_penalty)
                delete = dp.get((i - 1, j), float('inf')) + indel_penalty
                insert = dp.get((i, j - 1), float('inf')) + indel_penalty
                dp[(i, j)] = min(match, insert, delete)
    else:
        # Fill in the DP table with banded alignment
        for i in range(1, m + 1):
            for j in range(max(1, i - banded_width), min(n + 1, i + banded_width + 1)):
                match = dp.get((i - 1, j - 1), float('inf')) + (match_award if seq1[i - 1] ==
seq2[j - 1] else sub_penalty)
                delete = dp.get((i - 1, j), float('inf')) + indel_penalty
                insert = dp.get((i, j - 1), float('inf')) + indel_penalty
                dp[(i, j)] = min(match, insert, delete)

    # Backtracking to reconstruct the optimal alignment
    alignment_seq1, alignment_seq2 = [], []
    i, j = m, n

    while i > 0 or j > 0:
        current_cost = dp.get((i, j), float('inf'))

        if i > 0 and j > 0 and (seq1[i - 1] == seq2[j - 1] or current_cost == dp.get((i - 1, j
- 1), float('inf')) + sub_penalty):

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        alignment_seq1.append(seq1[i - 1])
        alignment_seq2.append(seq2[j - 1])
        i -= 1
        j -= 1
    elif i > 0 and current_cost == dp.get((i, j - 1), float('inf')) + indel_penalty:
        alignment_seq1.append(gap)
        alignment_seq2.append(seq2[j - 1])
        j -= 1
    else:
        alignment_seq1.append(seq1[i - 1])
        alignment_seq2.append(gap)
        i -= 1

    # Reverse the alignments to get the correct order
    alignment_seq1.reverse()
    alignment_seq2.reverse()

    alignment_cost = dp.get((m, n), float('inf'))

    return alignment_cost, ''.join(alignment_seq1), ''.join(alignment_seq2)

```

initialization of the DP

```

dp {}

for i in range(1, m + 1): # O(m)
    dp[(i, 0)] = i * indel_penalty
for j in range(1, n + 1): # O(n)
    dp[(0, j)] = j * indel_penalty

```

The first row and column are initialized in $O(m+n)$ times where m = length of seq1 and n = length of seq2.

A dictionary is used to store the dp values. In the case of unrestricted alignment, the dp requires a space complexity of $O(m*n)$ since it's a 2d structure of size $(m+1)*(n+1)$ and one entry is needed for each cell.

Filling the DP table

```

if banded_width == -1:
    for i in range(1, m + 1): # O(m)
        for j in range(1, n + 1): # O(n)

```

the unrestricted alignment ($\text{banded_width} = -1$), the loops iterate through all the cells of the table which leads to $O(m*n)$

The rest of the line of code after “for j in range(1, n + 1):” take a constant time of $O(1)$

The inner loop of the banded alignment is constrained by the banded width. So for each 'i', the 'j' index stretches for a limited range. If the banded width is k then the complexity of the alignment then becomes $O(m * k)$.

The band_width is used to constrain the matrix size. As the band for each row is being calculated the space complexity is $O(k*n)$

```
for i in range(1, m + 1): #  $O(m)$ 
    for j in range(max(1, i - banded_width), min(n + 1, i + banded_width + 1)): #  $O(k)$ 
```

Backtracking

```
while i > 0 or j > 0:
```

the backtracking runs back the alignment by iterating through the sequence which takes $O(m + n)$ times in both cases.

The operations within the loop is $O(1)$

Therefore, for **unrestricted alignment**:

Time complexity

Initialization: $O(m + n)$

Filling the Table: $O(m * n)$

Backtracking: $O(m + n)$

■ Total time complexity: $O(m * n)$

Space Complexity

Space complexity: $O(m*n)$

And for **banded alignment**:

Time complexity

Initialization: $O(m + n)$

Filling the Table: $O(m * k)$

Backtracking: $O(m + n)$

■ Total time complexity: $O(m * k)$

Space complexity

Space complexity: $O(k*n)$

Dependency Pointers

In the banded algorithm, the dependency pointers are modified to make sure that the cells within the band are accessible. The algorithm considers cells of $(i-1, j-1)$, $(i-1, j)$, and $(i, j-1)$ if they are within the band. This is to make sure the band doesn't access cells outside of the band.