

Gene Alignment Algorithm Analysis

The algorithm uses a dynamic programming approach to save the sums of each subsequence. To calculate the value of a cell representing a subsequence, the maximum of three routes is taken:

1. Find the value of the current match + the value of the top left diagonal cell
2. Find the value of the current nucleotide of the first sequence only + the value of the top cell
3. Find the value of the current nucleotide of the second sequence only + the value of the left cell

Once the maximum of the three calculations is determined the cell is populated, the chosen calculation's type is also saved for reference when printing the alignment solution. The rest of the table of dimension **(n+1) x (m+1)** is filled accordingly, where n is the length of the first sequence and m is the length of the second sequence. This has a time complexity of $O(nm)$.

The solution is printed with reference to the traceback matrix. This has a time complexity of $O(nm)$ as well.

Finally, the sum of the alignment values is calculated, which has a time complexity of $O(2n)$ or $O(2m)$, depending on the larger sequence.

The overall time complexity is $O(nm)$.