

Sequence Bioinformatics

Assignment 2

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4 Comparison of run time and space requirement

The Needleman-Wunsch algorithm is an algorithm that tries to maximize $m * n$ elements out of three cases of the matrix.

The run time in quadratic space is $O(m * n)$ the memory of the matrix is also $O(mn)$. The computation of the provided FastA files resulted in 1ms(short), 4ms(medium) and 32ms for the long sequence.

The Needleman-Wunsch with linear space tries to implement the divide-and-conquer method. Basically the dynamic-programming problem is divided into n smaller problems that are solved individually and then concatenated again to obtain the final result. As each sub problem is solved individually we can assume that this method requires linear space. However the algorithm is twice as slow as the quadratic-space one $O(2mn)$. The computation of the provided FastA files resulted in 7ms(short), 12ms(medium) and 114ms for the long sequence.

The Needleman-Wunsch algorithm in task 3 is performed without a table but recursive implementation therefore the run time is exponentially higher than the other NW implementations. Assumably $O(3^n)$ for the run time, 3 for the amount of cases to process and n for the length of the sequence and $O(n^2)$ memory.

As the recursive algorithm has an exponential computation time we only used the short.fasta file and the first 10 or 15 characters respectively. The run time for the 10 characters took 29 milliseconds, for the 15 characters the run time grew exponentially resulting in approximately 101132 milliseconds. Therefore, the major drawback of the algorithm without a table is the run time.