

# Assignment 1:Abstract and Introduction summary

- Sequence alignment is one of the most extensively discussed bioinformatics topics, which have been the core skill for experimental biologists and professional bioinformaticians alike.
- Sequence alignment algorithms can be divided into pairwise alignment algorithms and multisequence alignment algorithms.
- We can use dynamic programming to solve the problem of pairwise sequence alignment. The feasible solution is to introduce gaps into the strings, so as to equalize the lengths. the addition of extra gaps after equalizing the lengths will only lead to increment of penalty.
- Dynamic Programming: break problems into a simpler subproblems. Problem can be divided into many smaller parts. Needleman and Wunsch were the first to propose this method.
- This paper will work on the algorithm development and program generation under PAR framework.
- analysis of the field of multiple sequence alignment algorithms, based on the component library of the DPPSAA domain, some algorithm components have been improved and added, and a component library of multiple cost of manual selection algorithms for sequence similarity analysis, improving the efficiency of algorithm execution, and even assembling a more efficient new sequence alignment algorithm based on dynamic programming.