

Alignment DNA issues are still actual in modern genetics. Known algorithms (for example, heuristic algorithm used by BLAST software, Needleman–Wunsch algorithm) are provide solution, but possible are not completely optimal by speed, computational resources or don't provide fullness search (needed accuracy) for solution finding. In this connection optimal algorithm developing is actual. Such algorithm must combine accomplishments of known algorithms and satisfy requirements for program for running into multithread environment.

In this paper a method that can ensure absolute accuracy, is presented. Methods for solve DNA longest common subsequence problem are present also. Known methods of alignments are discussed and demonstrated. Dynamic programming techniques (using memorization through tabular computation) are discussed. Requirements for algorithm, which optimized for using on modern hardware, are discussed. New method of alignments is presented and applied to the implementations.