

CHAPTER V

CONCLUSION

DIALIGN is a quite successful sequence alignment algorithm, which does not use a gap penalty. This is an attractive algorithm since it finds good alignments without using a gap penalty, which is always arbitrary and difficult to determine. However, its success depends on the ability to calculate accurately the probability with which a diagonal between two unrelated sequences will attain a certain score.

According to simulation of the program, can be concluded that DIALIGN algorithm is able to produce optimal sequence alignment from a pair of sequence accurately. The program is simulated on short sequences only and it performs well. From seven sequence samples taken at random with length of a sequence not more than 100, running time of the program is fast (in hundreds of seconds). From the simulation can be seen that the number of optimal alignment depends on the content of sequences.