Extract of thesis
Alignments in bioinformatics in principle and in practice

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The main ami of the thesis is to summaryze and show the pairwise, multiple alignment in theory and in practice used in bioinformatics. Morover to give an impression about the widespread algorithm which are used in practice and some alternative solution for computationally hard problems.

In the first part of the thesis we introduce the basic biological problems and after that we define the problem of the alignment in details the three main types of it: global, local and the semi global alignment. The problem of the global alignment will be shown in the sight of graph theory.

The existing solutions of theory we can see that in real usage differs many times. The programm BLAST and FASTA will be shown which are use to align and search for DNA strings or amino acids. During the requering process we need to use the algorithm of alignment from theory. Here we highlight how the practice and the theory are joining. We show the most important steps of these programs and describe why they are useful.

The BLAST and FASTA use the so called PAM matrix durnig the caluclations, so we mention how this matrix works, and how we can construct in principle.

The next topic is the multiple alignment. We show that this problem is computationally hard, and probably there are no polinomial algorithm which could solve it unless P=NP. To show the hardness of the multiple alignment we describe another problem which can be reduce to the original problem, this is the problem of superstirng which proof will be discussed. Similarly, to the pairwise alignment, we show a solution to this problem used in practice, the compatible pairwise alignment. This alignment won't return the best multiple alignment but thanks for it's running time it semms to be useful in bioinformatics.

The aim of this thesis is to show the problems mentionned above, in the part of mathematics and in the part of practice.

Meanwhile we work up the results of different scope of the mathematics and bioinformatics.

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