

Humboldt-Universität Zu Berlin

Institute for Informatics and Theoretical Biology (ITB)



Silke Trißl

Email: trissl@informatik.hu-berlin.de

Lectures on Bioinformatics: Assignment 4

More information about the exercises can be found at http://zope.informatik.hu-berlin.de/forschung/gebiete/wbi/teaching/archive/sose09/vl_biophysik

Exercise 1: Modify your program from last assignment such that it can perform the following tasks:

- a) Comparing protein sequences (instead of only DNA)
- b) Reading a substitution table from a file (additionally to the sequences to be compared) and using this table during the alignment.

Exercise 2: BLOSUM Matrices

Download the matrices BLOSUM50, BLOSUM80 and BLOSUM100 from the BLOCKS FTP server (ftp://ftp.ncbi.nih.gov/repository/blocks/unix/blosum/BLOSUM). Format these matrices in such way that your program can read them. Calculate the similarity between two protein sequences using:

- a) An identity matrix (InsDelRep = -1, Match = +1)
- b) With all three BLOSUM matrices.
- c) Compare the results from both types of matrices qualitatively.

Protein sequences are available on the web site.

Exercise 3: Database Search and Sequence Alignment tool BLASTX

PHENYLKETONURIA is a relatively frequent hereditary disease, which must/can be treated on newborn children.

- a) Find out in the OMIM database which protein is responsible for this illness. On which chromosome is the corresponding gene located?
- b) Search the DNA sequence of this gene in the NCBI Genbank database. Describe its length, name and accession number.
- c) Search similar proteins using BLASTX
 - i. Give the accession number of homologous DNA sequences for the following organisms (in each case the first occurrence for the species in the hit list)
 - Homo Sapiens
 - Mus Musculus
 - Bos Taurus
 - Rattus Novegicus
 - Gallus gallus
 - Xenopus tropicalis
 - Drosophila Melanogaster
 - Danio rerio
- d) Write a program which compares the similarity between all pairs of those sequences (global alignment, INS/DEL/REP=-1, Match=+1). Which are the closest pair, which species have the longest distance from each other?

Note: Results of all exercises and the code should be zipped into one file including a README file describing the commands for running your code. Your code must be able to perform all task asked above.