

Question 1. Below is part of the nuc44 scoring matrix for aligning nucleotides

	A	C	G	T	R
A	5	-4	-4	-4	1
C	-4	5	-4	-4	-4
G	-4	-4	5	-4	1
T	-4	-4	-4	5	-4
R	1	-4	1	-4	-1

The gaps are scored by linear gap penalty, with cost 10.

Construct the optimal alignment of sequences ARCR and AGG using Needleman-Wunsch –algorithm.

Question 2. Give detailed description of **either** of the following tests

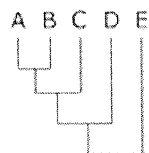
- TDT-test (Transmission-Disequilibrium Test)
- ASP-test (Affected sib pair)

Question 3.

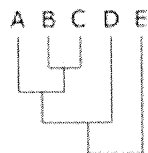
- Explain how mutual information can be used to check whether a Boolean (0/1) data stream A determines another Boolean data stream B.
- Explain briefly the main principle (no algorithm required) of constructing phylogenetic trees with distance based methods, maximum parsimony methods and maximum likelihood methods.

Question 4.

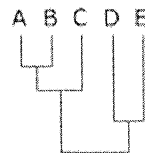
- Explain how bootstrapping can be used to estimate the confidence of the result in search of a phylogenetic tree or Bayesian network structure.
- Draw the strict consensus tree for the following cladograms



Tree 1



Tree 2



Tree 3