Uva Wellassa University of Sri Lanka
Faculty of Science and Technology
Department of Computer Science and Technology
1st Semester Examination – March/April 2013
CST 451-3 Bioinformatics

Uva Wellassa University

Allocated Time: Three (03) hours
Total 05 Questions
Answer all questions.

1. a. Briefly explain what Biotechnology and Bioinformatics is? (4 mark)

   b. What is the complementary DNA sequence to the following string of nucleotides? Remember to label the 5′ and 3′ ends of the sequence. (1 mark)

   5′ -C – G – A – T – T- G – C – C- A- C- G- A- T- G- C- 3′

   c. Explain the "Central Dogma" of molecular biology using clearly labeled diagram. Indicate the enzymes involved in each of the steps. (5 mark)

   d. Cloning and Polymerase Chain Reaction (PCR) are two different techniques used in DNA amplification.

      i. Explain major steps of amplifying DNA by cloning (3 mark)

      ii. List down the main PCR components (3 mark)

      iii. Explain major steps of amplifying DNA by PCR (3 mark)

      iv. What is "Mispriming" (1 mark)

2. a. What is "Inheritance"? (2 mark)

b. List down the patterns of inheritance? (2 mark)

c. Briefly explain the terms "Genotype" and "Phenotype" (4 mark)

d. Suppose a woman who is both a homozygous tongue-roller and a non-PTC-taster marries a man who is a heterozygous tongue-roller and is a PTC taster, and they have three children:

A homozygous tongue-roller who is also a PTC taster,
A heterozygous tongue-roller who is also a taster,
and a heterozygous tongue-roller who is a non-taster.

i. Identify the parents' genotype. (2 mark)

ii. Identify the first Childs' genotype. (2 marks)

iii. If the first child (the homozygous tongue-roller who is also a PTC taster) marries someone who is heterozygous for both traits draw the Punnett square that predicts what their children will be. (4 mark)

iv. Identify the Genotype and Phenotype ratios appropriately. (4 mark)

Note: **R** represent tongue-rolling, **r** represent a non-roller, **T** represent ability to taste PTC, and **t** represent non-tasting

3. a. What is the biological motivation behind "Sequence Alignment"? (3 mark)

b. List down the types of Alignments available in bioinformatics. (3 mark)

c. Using Pair-Wise alignment method identifies the better alignment. (4 mark)

Scoring Matrix: $S(x,y) = \begin{cases} +5 & if\ x = y \\ -3 & if\ x \neq y \end{cases}$ g= -4 (Liner gap Penalty)

Alignments:

1. A – C – G G A C T
   A T C G G A T C T

2. A – C G G – A C T
   A T C G G A T C T

d. Using the **Smith and Waterman** dynamic programing method, construct the partial alignment score table for the following two sequences, using following scoring parameters: match score = +1, mismatch = -1 , gap penalty= -2 . Write down the **local alignment** of these two sequences. (5 mark)

M A T C H E S

T H A T C H E R

e. Using the **Needleman and Wunsch** dynamic programing method, construct the partial alignment score table for the following two sequences, using following scoring parameters: match score = +1, mismatch = -1 , gap penalty= -2 . Write down the **Global alignment** of these two sequences. (5 mark)

A C A G T A G

A C T C G

4. a. What does it mean by a "Phylogenetic tree"? (2 mark)

b. Name two types of Phylogenetic trees. Identify the difference between these trees and kind of information that can be extracted from each type. (4 mark)

c. List down the phylogenetic tree approaches available. (3 mark)

d. Construct a phylogenetic tree to explain the genetic relationship among taxa A, B, C, D, and E, using UPGMA method. (8 mark)

Taxa	A	B	C	D	E
A	0				
B	9	0			
C	8	11			
D	12	15	10	0	
E	15	18	13	5	0

e. Compute the quality of the above Phylogenetic Tree. (3 mark)

5. a. What is the meaning of the term "Mutation" in genome study? (2 mark)

b. Explain how mutation causes genetic diseases/disorders. List down 4 genetic diseases that you are familiar with. (4 mark)

c. Name three databases/tools available at the National Center for Biotechnology Information (NCBI). (2 mark)

d. Briefly explain **Jukes – Cantor** Model and **Kimur** Model. (5 mark)

e. Describe the following topics. (7 mark)

i. DNA Micro Array Technology

ii. Production of Recombinant Proteins