Uva Wellassa University, Sri Lanka
First Semester Examination – February 2012
CST 411-3 Bioinformatics
CST 451-3 Bioinformatics

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

Question 1. **(20 marks)**

(a) Describe the detection and removal of environmental pollution using biotechnology.

(b) Prokaryotes and eukaryotes both carry out transcription (synthesis of mRNA) and translation (synthesis of protein). Describe the similarities and differences between prokaryotes and eukaryotes in the way they carry out these processes.

(c) **"In DNA replication, the leading strand is synthesized continuously while the lagging strand is synthesized discontinuously"** Explain the above statement.

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

I. Explain major steps of amplifying DNA by cloning.
II. What are the key parts of a vector?
III. Explain major steps of amplifying DNA by PCR.
IV. What are the key ingredients of PCR?

(e) In pea plants, yellow seeds are dominant to green seeds. Predict the genotypic ratio of offspring produced by crossing two parents heterozygous for this trait. Draw a Punnett square to illustrate your prediction.

Question 2. **(20 marks)**

(a) Briefly explain the biological motivations behind "**Sequence Alignment**".

(b) Using the **Smith and Waterman** dynamic programming method, construct the partial alignment score table for the following two sequences, using following scoring parameters: match score = +1, mismatch score = -1, gap penalty = -2.

MATCHES
THATCHER

Write down the local alignment of these two sequences.

(c) Using the **Needle and Wunsch** dynamic programming method, construct the partial alignment score table for the following two sequences, using following scoring parameters: match score = +1, mismatch score = -1, gap penalty = -2

ACAGTAG
ACTCG

Write down the global alignment of these two sequences.

(d) What is the importance of finding the similar sequence?

(e) What is "ClustalW"? What type of sequences can ClustalW align?

Question 3. **(20 marks)**

(a) What does it mean by a "**phylogenetic tree**"?

(b) Which are the **three** main methods for constructing phylogenetic trees?

(c) Briefly explain the parsimony based approach of developing phylogenetic trees.

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

	A	B	C	D	E	F
A	0	3	8	7	10	9
B		0	9	8	11	10
C			0	9	12	11
D				0	9	8
E					0	5
F						0

(e) Compute the quality of the above phylogenetic tree.

Question 4. **(20 marks)**

(a) Write down the characteristics of good primers.

(b) Primers can be designed to amplify multiple products. Such primers are called "universal primers". Write down the strategy of designing primers to amplify all HPV genes?

(c) Name three databases/tools available at the **National Center for Biotechnology Information (NCBI)** website for analyzing genome data and disseminating biomedical information.

(d) Select two databases/tools you mentioned in part (c) and explain,

What type of information you can retrieve from those databases.
Or
What type of data you can analyze using those tools.

(e) Briefly explain the importance of the following primer design programs.
I. **Oligo**
II. **Primer3**

Question 5. **(20 marks)**

Write short notes about the following topics. Use diagrams where appropriate.

a) Bioprocessing technology
b) Monoclonal antibody technology
c) Cell culture technology
d) Tissue engineering technology
e) Genetic engineering technology