Uva Wellassa University, Sri Lanka
End Semester Examination – January 2010
CST411-3 Bioinformatics

Time: Three (03) hours

Total 05 Questions.
Answer ALL questions.

Question 1.

(a) What are macromolecules? (01 marks)

(b) In DNA replication, DNA replicates in *semi-conservative* manner. What does it mean by *semi-conservative* gene replication? (02 marks)

(c) Explain the *Central Dogma of Molecular Biology.* (03 marks)

(d) In human body, new cells required for development and bodily functions are produced by a process called cell division. According to genetic material transfer from parent cell to offspring, this cell division can be categorized into two categories. Explain these two categories. (04 marks)

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

i. Explain the major steps of amplifying DNA by cloning. (04 marks)

ii. What are the key ingredients of PCR? (02 marks)

(f) Mice, ability to run normally is considered as a dominant trait. Mice with this trait are called running mice (RR). The recessive trait causes mice to run in circles only. Mice with this trait are called waltzing mice (rr). Hair color is also inherited in mice. Black hair (BB) is dominant over brown hair (bb).

Assume a homozygous running heterozygous black male mouse mates with a female waltzing brown mouse,

i. Construct a Punnett Square to show the expected genetic makeup of their offspring. (03 marks)

ii. State the ratios of offspring bearing the possible combination of phenotype. (01 marks)

Question 2.

(a) What is Sequence Alignment? (01 marks)

(b) Briefly explain the biological motivations behind "*Sequence Alignment*" (03 marks)

(c) What are the issues in Sequence Alignment? (03 marks)

(d) What are the pros and cons of heuristic methods and dynamic methods when searching similar sequences in bioinformatics databases? (03 marks)

(e) Using the Needleman and Wunsch Dinamic 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.

ACGGACT
ATCGGATCT

Write down the global alignment of these two sequences. (05 marks)

(f) 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.

TATCCGCTATA
GCTCTCGCATA

Write down the local alignment of these two sequences. (05 marks)

Question 3.

(a) What does it mean by a "*phylogenetic tree*"? (01 marks)

(b) Explain different kinds of phylogenetic trees. (02 marks)

(c) "*Genetically humans and chimpanzees are more closely related to each other than either is to the gorilla*" Explain the above statement. Construct a phylogenetic tree to show the above relationship. (03 marks)

(d) Briefly describe the different approaches that can be employed in constructing phylogenetic trees. (03 marks)

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

	A	B	C	D	E
A	0	22	39	39	41
B		0	41	41	43
C			0	18	20
D				0	10
E					0

(09 marks)

(f) Compute the quality of the above phylogenetic tree. (02 marks)

Question 4.

(a) What is the meaning of the term '*mutation*' in genome study? (02 marks)

(b) Explain how mutations cause genetic diseases/disorders. (03 marks)

(c) Give the names of ***four*** genetic diseases/disorders.

Note: It is sufficient to give the commonly used term for the disease/disorder. The scientific name is not necessary. (02 marks)

(d) Name three databases/tools available at the **National Center for Biotechnology Information** (NCBI) Website for analyzing genome data and disseminating biomedical information. (03 marks)

(e) By taking two databases/tools you mentioned in answer to question (d),

Explain what type of information you can retrieve from those databases.

Or

Explain what type of data you can analyze using those tools. (04 marks)

(f) Briefly explain the importance of the following primer design programs.

i. Oligo

ii. Primer3

(06 marks)

Question 5.

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

(a) Gene expression. (05 marks)

(b) DNA Microarray Technology. (05 marks)

(c) DNA Finger Printing. (05 marks)

(d) Genetically Modified Crops. (05 marks)