MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 211 BIOMATHEMATICS & STATISTICS

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. If U = {1,2,3,…9}, A= {1,2,3,4,5} and E={2,4,6,8}, Find $(A \backslash E)^c$

2. If U={1,2,3…9}, A={1,2,5,6}, B={2,5,7}, Verify De-Morgan's laws.

3. Let R and S be the following relations on A={1,2,3}

    R= { (1,1),(1,2),(2,3),(3,1),(3,3)}

    S={(1,2),(1,3),(2,1),(3,3)}. Find (a) R $\cap$ S, RUS , R^c

    (b). R_0S

    (c) $S^2 = S_0S$

4. Define the logical operations conjunction and disjunction.

5. What are tautologies and contradiction?

6. Define predicate and give example for it.

7. Explain isomorphism of graphs.

8. What is an Euler graph?

9. What are the difference between bipartite graph and complete graphs?

10. Define correlation.

11. Give the formula for finding the arithmetic mean of a weighted data.

12. What are interpolation and extrapolation?

                                                                    (10 x2=20)

Section B
Answer any five questions. Each carries seven marks

13. Prove the following identities

    (i)   (AUB) $\cap$ (AUB ^{c}) =A

    (ii)   (AUB)\ (A$\cap$B)=(A\B) U (B\A)

14. Let R be the following equivalence relation on the

    Set A = { 1,2,3,4,5,6}

R= {(1,1),(1,5),(2,2),(2,3),(2,6),(3,2),(3,3),(3,6),(4,4),(5,1),(5,5),(6,2)

(6,3),(6,6)} Find the partition of A induced by R.

15. Construct the truth table for the proposition

$[p \rightarrow q) \land (q \rightarrow r)] \vdash (p \rightarrow r)$

16. What are the types of quantifiers? Explain.

17. Let G be a connected planar graph with p vertices and q edged. Where $p \geq 3$. Then prove that $q \geq 3p-6$.

18. Calculate the mode in the following series.

Size	0-10	10-20	20-30	30-40	40-50	50-60	60-70
Frequency	5	7	19	18	16	10	5

19. To calculate the inverse of the following matrix

3   0   2
2   0   -2
0   1   1

(5 x 7=35)

Section C

Answer any two questions. Each carries ten Marks

20. (i).Examine whether the following argument is valid or not.

$p \rightarrow \neg q, \ r \rightarrow q, \ r \vdash \neg p$

(ii).If 7 is less than 4, then 7 is not a prime number.

7 is not less than 4

----

7 is a prime number

21. (i). Prove that the sum of degrees of the vertices of a graph G is equal to twice the number of edges in G.

(ii). Prove that the sum of degrees of the regions of a map is equal to twice the number of edges.

22. Calculate the coefficient of correlation for the following data.

    Series X: 2   3   4   5   6   7   8

    Series Y: 4   5   6   12   9   5   4

(2 x 10 =20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI212 INTRODUCTION TO BIOINFORMATICS AND DATABASES

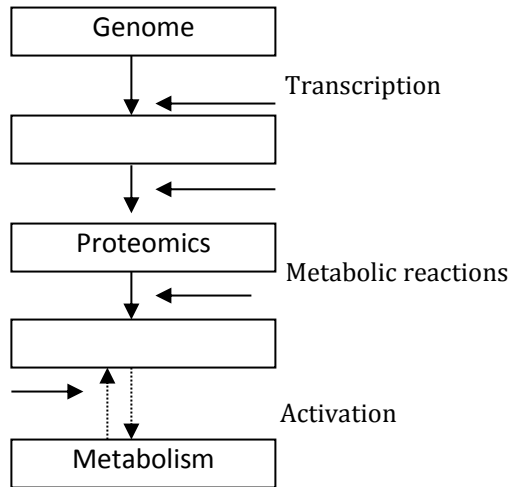Time: 3 Hrs.   Max. Marks: 75

Section A

Answer any ten questions. Each carries two marks

1. State the difference between global & local alignment.

2. Complete table of genetic information from the genome to phenotype of organism.

```
        ┌─────────────────┐
        │     Genome      │
        └─────────────────┘
                │    ←──────── Transcription
                ▼
        ┌─────────────────┐
        │                 │
        └─────────────────┘
                │    ←────────
                ▼
        ┌─────────────────┐
        │   Proteomics    │
        └─────────────────┘
                │    ←──────── Metabolic reactions
                ▼
        ┌─────────────────┐
        │                 │
        └─────────────────┘
          ──→   ↑  ┆       Activation
        ┌─────────────────┐
        │   Metabolism    │
        └─────────────────┘
```

3. List any two protein databases.

4. Write the salient features of standard genetic code.

5. What do you understand by sensitivity and specificity in BLAST?

6. What is the difference between structural & functional genomics?

7. What are primary databases?

8. What is meant by structural database?

9. Write expansion

   (a) EMBL

   (b) DDBJ

10. What is e-value of alignment scores?

11. What is OMIM?

12. What is the purpose of data compression?

13. Name two tools used in phylogenetic analysis.

(10 x 2= 20)

Section B
Answer any five questions. Each carries seven marks

13. What is meant by Affine Gap penalty?

14. Compare PAM & BLOSOM matrices.

15. Describe PHI-BLAST.

16. Discuss the importance of biological databases in bioinformatics.
17. Explain the working of BLAST based on your knowledge of sequence alignment.

18. Explain the concept of scoring matrices for aligning amino acid sequences. Briefly explain how PAM is derived?

19. What is meant by secondary database? What are the major secondary databases?

20. Illustrate Global alignment with suitable example.

(5 x 7 =35)

Section C

Answer any two questions. Each carries ten marks

21. If you get a particular protein named 'Keratin'. How will you retrieve its

    (a) Nucleic acid sequence

    (b) Protein sequence

    (c) Carbohydrate binding site, if present.

    (d) Protein chains

    (e) Amino acid frequency etc? Describe briefly?

22. It is noted that major sequence alignments differ in approach computational complexity and accuracy. Do you agree with this? Explain with suitable examples.

23. Let S1= AATTCGCGTA & S2 = TATCGCTACA

    (a) Build the complete dynamic programming table for these strings

    (b) What is the edit distance between S1 & S2

    (c) List all optimal global alignment between S1 & S2.

(2x10=10)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 213 BIODIVERSITY, ECOLOGY AND EVOLUTION

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. What is Red Data Book?

2. Differentiate Fundamental Niche and realized Niche?

3. Differentiate between *insitu* and *ex-situ* conservation?

4. Describe alpha, Beta and Gamma diversity?

5. Define Competitive exclusion principles?

6. Proteins are the macromolecules which evolved first. Justify the statement?

7. What is stereo chemical fitting?

8. What is 'C- value paradox'?

9. What is molecular clock hypothesis?

10. Comment on Biological time scale and its importance in evolution?

11. What are Biosensors?

12. What is the importance of Wild life Protection Act 1972?

(10 x 2=20)

Section B
Answer any five questions. Each carries seven marks

13. What are conserved sequences? How it is evolutionarily significant?

14. How ATP is evolved in the evolutionary time? Which is the source used at that time for the evolution of complex molecules?

15. Earth summit. A Global strategy. Comment on it?

16. How nature balances in intra specific and interspecific competition?

17. Describe the significance of Lotka & Voltera hypothesis in the population Dynamics?

18. What are protected areas? What is its importance in ecosystem conservation?

19. Describe about Hardy Weinberg equilibrium.

20. Briefly explain population growth curve.

(5 x 7=35)

Section C
Answer any two questions. Each carries ten marks

21. What is the importance of biodiversity conservation in present and future? Explain briefly?

22. Describe energy flow? Geographical efficiency of ecosystem?

23. What is molecular evolution and explain the evolution of   DNA & RNA, Amino acids, Codon, Protein?

(2 x 10 =20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 214 INTRODUCTION TO INFORMATION TECHNOLOGY AND C PROGRAMMING

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. Explain multi-tasking.

2. What are point and draw device?

3. What is machine language? Why is it required?

4. What is an interpreter? How does it differ from a compiler?

5. Explain posting.

6. Hardware is normally one time expense, whereas software is a continuing expense. Elaborate?

7. What is the purpose of ASCII?

8. How many times will the following program print "good". Give reasons

```
#include<stdio.h>

main()

  {

      printf ("good");

      main();

  }
```

9. What is the output of the following program?

```
#include<stdio.h>

main()

  {

      int a[10];

      printf("%d", *a+10- *a+5);
```

```
            }

10. What is the output of the following program?

            #include<stdio.h>

            main()

                {

                        int x;

                        x=~!printf;

                        printf("%d", x);

                }

11. Explain the concept of pointers in C?

    main()

    {

    int i=3,  *j, k;

            j=&i;

            k=*j;

            *j=4;

            printf("i=%d, *j=%d, k=%d\n", i , *j , k);

            }
```

12. Write the differences between entry controlled loops and exit controlled loops.

(10 x2=20)

Section B
Answer any five questions. Each carries seven marks

13. Write a program to read a number. If the number is odd multiply by 3 and add 1. If the number is even divide by 2. Continually apply the above operations to the intermediate results until the number reaches one.

14. Write a C functions to copy the contents of one file to other and to count the number of words in a file.

15. Name any four popular operating systems. Describe its main features.

16. Differentiate between the ways data are organized on a magnetic disk and an optical disk. Which data organization leads to faster random access time and why?

17. A programmer eliminates all language processor errors from his/her program, and then runs it to get printed results. The programmer therefore, concludes that the program is complete. Comment.

18. What are the limitations of an image scanner when it is used for inputting text documents? How does an OCR device overcome these limitations?

19. Briefly explain the control structures in C programming.

$$(5 \times 7 = 35)$$

Section C
Answer any two questions. Each carries ten marks

20. Name any four popular operating systems. Describe its main features.

21. A programmer eliminates all language processor errors from his/her program, and then runs it to get printed results. The programmer therefore, concludes that the program is complete. Comment.

22. Write a program to evaluate the following investment equation $V = P(1+r)^n$. And print the tables which would give the value of V for various combination of the following values of P, R and N.

   P: 1000, 2000, 3000, ……… 10,000

   R: 0.10, 0.11, 0.12, ……… 0.20

   N: 1,2,3,……10

   P is the principal amount and V is the value of money at the end of n years. This equation can be recursively written as

   $$V = P(1+r)$$

   $$P = V$$

That is, the value of money at the end of first year becomes the principal amount for the next year and so on.

(2 x 10 =20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 221 INTRODUCTION TO MOLECULAR BIOLOGY, CELL BIOLOGY & GENOMICS

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. What are motor proteins? Briefly discuss about the 3 types of motor proteins.

2. Briefly explain the role of MPF in cell cycle.

3. Explain the role of mobile genetic elements in evolution.

4. Explain the role of origin recognition complex in replication.

5. What are liposomes? Discuss the applications of liposomes in medicine and pharmacology.

6. What is Base calling? Name a software used for base calling.

7. State Chargaff's rule.

8. Write a short note on ESTs and their uses. Name a EST database.

9. How similarity & identity is inferred from Blast results?

10. Discuss the steps that have to be followed, to retrieve the fasta sequence of c- Myc gene from NCBI.

11. How do you interpret your BLAST result by using e-value and bit score?

12. Discuss 'Maximum Parsimony method'.

(10 x 2=20)

Section B

Answer any five questions. Each carries seven marks

13. Compare the structure of fully assembled microtubule, actin filament and intermediate element.

14. Explain the role of protein kinase I in cell division.

15. Explain RNA editing.

16. Discuss two major elements of the integral and peripheral proteins of the erythrocyte membrane.

17. What are the basic concepts of Phylogenetics? How will you determine the evolutionary distance from a tree?

18. To build a phylogenetic tree for a set of related sequences, what are the basic steps to be carried out? Explain with a suitable example.

19. Discuss the Clone contig approach of genome annotation.

20. Briefly explain UPGMA method for tree construction with Example.

(5 x 7 =35)

Section C
Answer any two questions. Each carry ten marks

21. Explain mechanism of splicing.

22. Discuss the role of G protein coupling receptors I in cell signaling?

23. How do you analyze the gene prediction results from Genscan, Genmark, Frame D and EST search?

(2 x 10 =20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 222 INTRODUCTION TO WEB PROGRAMMING

Time:3 Hrs.   Max.Marks:75

Section A

Answer any ten questions. Each carries two marks

1. Define Internet.

2. Differentiate between the HTTP methods GET and POST.

3. Define CSS.

4. Differentiate between javasript and jquery.

5. Differentiate between JSP and servlets.

6. Write short note on PHP and PHP life cycle.

7. Write a short note on XML and HTML.

8. Differentiate between web browsers and search engines.

9. How can u include an image in a HTML page.

10. Explain functions of a web server.

11. Write a short note on Web System architecture.

12. Importance of APACHE Server in web programming.

(10 x 2 =20)

Section B
Answer any five questions. Each carries seven marks

13. Explain briefly Java remote method invocations.

14. Write note on XML,XML attributes,elements and xsl.

15. Explain steps in Java database connectivity.

16. Write a short note on JSP and JSP objects.

17. Write short note on Servlet life cycle.

18. Briefly explain the server side programming PHP.

19. Write note on Java control structures.

<div align="right">(5 x 7 = 35)</div>

Section C

Answer any two questions. Each carries ten marks.

13. Write in detail about the client & server side programming Languages.

14. Define JDBC API and explain JDBC drivers in detail.

15. Illustrate servlet life cycle and its methods in detail.

<div align="right">(2 x 10 = 20)</div>

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 223 GENETICS & GENETIC ENGINEERING

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. State the unaltered law of Mendel?

2. What are the characters studied by Mendel and in which plant?

3. Explain the factors leading to the success of Mendel?

4. Differentiate between multiple allele and multiple gene inheritance?

5. Explain the principles behind the inheritance of flower color in Sweet Pea?

6. What is a vector? What are the essential features of a vector?

7. What are restriction enzymes? Explain neochizomers and isoschizomers?

8. What is iDNA? Explain how Agrobacterium is useful in plant transformation?

9. How antisense RNA and inference RNA differ?

10. Briefly explain gene Knockout with example?

11. What is gene therapy? Give one example for success in gene therapy?

12. Briefly describe the steps behind the production of flavoursavr tomato?

(10 x 2=20)

Section B

Answer any five questions. Each carries seven marks

13. Explain classical genetics?

14. Explain the inheritance of a multiple allelic character you have studied?

15. Explain the phenotypic ratio of the inheritance of skin color in human?

16. What do you understand by gene silencing? Illustrate with an example.

17. Write down the steps involved in gene cloning?

18. Explain PCR with a neat sketch on different steps?

19. Briefly explain DNA finger printing techniques.

(5 x 7=35)

Section C
Answer any two questions. Each carries ten marks

20. Explain non-allelic gene interaction. Justify your answer with the concept complimentary gene interaction.

21. All the Mendelian principles are universally applicable- do you agree with it? If not explain the reasons for it?

22. Write down the different gene transfer methods both physical and chemical?

(2 x 10 =20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI224 PROTEOMICS & COMPUTER AIDED DRUG DESIGN

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. What are the major features of Uniprot?

2. What is the rationale behind protein structure prediction?

3. Chaperonins play an important role in protein folding. How?

4. Outline the significance of hydrogen bonds in protein structure.

5. What is a molecular mechanics force field?

6. Define pharmacophore.

7. What do you mean by a search algorithm?

8. What are the major strategies for target identification?

9. Name any five docking programs.

10. What do you mean by double blind approach in CASP?

11. Differentiate between allosteric inhibition & allosteric activation.

12. Define binding mode.

13. What is high throughput screening?

14. Name the four classification systems in CATH.

(10 x 2= 20)

Section B
Answer any five questions. Each carries seven marks

15. What is virtual screening? How does it differ from high throughput screening?

16. Discuss the various structure based drug design approaches.

17. What are the major interatomic forces that determine protein structure?

18. Discuss the major features of Protein Data Bank.

19. Explain the Chou-Fasman method for protein secondary structure prediction.

20. Describe the term ADMET in the context of drug discovery process.

21. Discuss the major components of molecular mechanics.

22. Outline the levels of organization of protein structure.

(5 x 7 =35)

Section C
Answer any two questions. Each carries ten marks

23. What is the rationale behind homology modeling? Discuss the various steps involved in the same.

24. Discuss the X-ray crystallographic technique with the help of an appropriate diagram.

25. Discuss any two widely used search algorithms in molecular docking.

(2x10=20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 231 ADVANCED BIOINFORMATICS

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. State the difference between a "profile" and a "motif"?

2. Write short notes on:

    a. HMM

    b. Markov chain

3. Write down the significance of multiple sequence alignment in biological data analysis.

4. Discuss the key pros and cons of using higher order markov model?

5. Write short note on pairwise sequence similarity and its significance in function profiling of proteins.

6. Define the terms

    A) Genome b) chromosome

7. If you are working with protein dataset which homology search you would prefer. Justify the reason.

8. Explain the common bioinformatics pipeline in identifying the homologues gene regions in the sequence data of an unknown prokaryotic organism.

9. List down any two biological sequence formats with suitable examples.

10. Discuss the application of BLAST in sequence homology search.

11. What is the significance of E value in a BLAST result and how it is different from that of the score?

12. If a nucleotide sequence is given, how will you distinguish ORFs and why ORFs are important in sequence annotation?

(10 x 2 = 20)

Section B
Answer any five questions. Each carries seven marks

13. What are scoring matrices? Write short note on PAM and BLOSUM scoring matrices.

14. Briefly explain the differences between PSI-BLAST and PHI-BLAST.

15. Discuss the possible applications of Markov models in biological problems.

16. As a Bioinformatician what would be your primary analytical strategies if you are provided with a raw sequence and structure data?

17. Discuss the difference between local and global alignment with suitable examples.

18. Discuss progressive alignment method employed in multiple sequence alignment problems.

19. How can Hidden markov model framework be applied for gene prediction problem?

(5 x 7= 35)

Section C

Answer any two questions. Each carries ten marks

20. Let S1 = AATTCGCGTA and

S2 = TATCGCTACA

Obtain the optimal global alignment using dynamic programming method. Use any Scoring scheme of your choice.

21. With a suitable example demonstrate Needleman-Wunch algorithm.

22. Explain how a simple prediction strategy can be developed using a first order Markov Chain model for discriminating a biologically important functional site.

(2 x 10 = 20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 232 BIOENERGETICS, BIOCHEMISTRY & APPLIED CHEMISTRY

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. Cite an example where the entropy of a system decreases and increases.

2. What is the importance of the second law of thermodynamics?

3. Differentiate between an anode and cathode.

4. Why do electron transfers result in a greater release of energy?

5. What types of integral proteins reside in the plasma membrane of an erythrocyte?

6. What are the applications of electrophoresis?

7. What is the role of actin filaments in muscle contractions?

8. Draw the structure of a keto-triose. How many stereoisomers does it form?

9. Why myoglobin is more effective in oxygen binding than hemoglobin?

10. Which structural feature gives the antioxidant nature to Tocopherol?

11. Why does β-carotene have a sparing function for Vitamin –A?

(10 x 2 =20)

Section B
Answer any five questions. Each carries seven marks

12. What are marker enzymes? Explain the diagnostic importance of amino transferases.

13. Explain the principle and working of pulse field gel electrophoresis.

14. ATP has evolved as the central molecule in energy metabolism. Can 1,3-triphosphoglycerate serve the same function? Explain.

15. Discuss the secondary and tertiary structures of proteins with appropriate diagrams.

16. Describe the importance of different photo systems in light reactions.

17. Explain: - (a) Molarity, (b) Molality, (c) Normality.

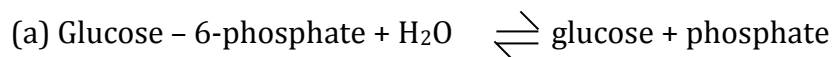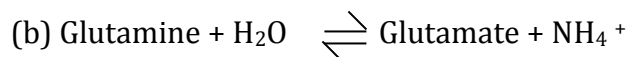18. Briefly explain electrophoresis and its application.

(5 x 7 =35)

Section C
Answer any two questions. Each carries ten marks

18. Calculate equilibrium constants for the following reactions at pH =7.0 &

    T=25^{0}C

    (a) Glucose – 6-phosphate + H$_2$O $\rightleftharpoons$ glucose + phosphate

    ΔG^0 = -3.3 Kcal/mol

    (b) Glutamine + H$_2$O $\rightleftharpoons$ Glutamate + NH$_4$$^+$

    ΔG^0 = -3.4 Kcal/mol

19. Which of the four classes of amino acids has side chains with greatest hydrogen bond forming potential? Which amino acid has the greatest potential to form ionic bonds and hydrophobic interactions? Explain with structures.

20. With a neat sketch explain the parts and principle of Transmission Electron Microscope.

(2 x10=20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 233 MICROBIOLOGY, IMMUNOLOGY AND ENZYMOLOGY

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. Write about general properties of antigens?

2. Role of substrate concentration in an enzyme catalyzed reaction?

3. Define Turn over number?

4. Comment on competitive inhibition with examples?

5. Industrial applications of enzymes?

6. Uses and application of immobilization of an enzyme?

7. How selective media is useful for microbial growth with Example?

8. Explain attenuation? What is the importance of attenuation in vaccine preparation?

9. Role of antigen presentation in immunity?

10. What is Lancefield grouping of *Streptococcus haemolyticus?*

11. Differentiate false negative and false positive test?

12. Properties of MHC molecules?

(10 x 2=20)

Section B
Answer any five questions. Each carries seven marks

13. What are lymphoid organs? Explain role of Spleen in innate immunity?

14. Properties of antigen antibody reaction; Explain agglutination reaction?

15. Describe the methods for purification of enzymes?

16. Explain multi enzyme complex?

17. What is differential staining exemplified with Gram staining?

18. What are the different types of fermentation?

19. Compare and contrast active and passive immunity

(5 x 7=35)

Section C
Answer any two questions. Each carries ten marks

20. Give an account on innate immunity?

21. a) Describe the structure of a bacterial endospore with a labeled diagram

    b) Briefly describe endospore formation and germination

    c) What is the importance of endospore? What might account for its heat   resistance?

22. a) Explain the pathogenicity and host interaction of HIV?

    b) Name three confirmatory laboratory tests for the diagnosis of HIV?

    c) Viral proteins/antigens are utilized for the preparations of HIV vaccine?

23. Derive Michaelis-Menten equation? What are the factors influencing the rate of enzyme

    catalyzed reaction?

(2 x10=20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 234 PERL PROGRAMMING FOR BIOINFORMATICS

Time: 3 Hrs.   Max. Marks: 75

Section A

Answer any ten questions. Each carries two marks

1. List any two data types in perl with suitable examples.

2. What would be the output for the following perl snippet:
   a. @a=('ATG','TGC','GCA','CAT','CCG');
   b. print "\n@a"; print @a[2];

3. Write down the output of the following perl script:
   a. $str = "Perl Programming";
   b. $var = substr($str, 0, -3); print $var;

4. What would be the output of the following perl code:
   a. $str = "Bioinformatics"; $var = substr($str, 2, -3); print $var;

5. Write a perl program which allows the user to enter a string and to test whether it is a RNA or not.

6. Write down the output for the given perl script:
   a. $x = "cgtagtgtcgt"; $x =~ s/t/u/;
   b. print $x;

7. Write down a perl script to validate a DNA sequence.

8. What is the difference between hash and array? Demonstrate with a suitable example.

9. Write a perl program to read a DNA sequence and print it in reverse order.

10. Write a Bioperl program to read a protein sequence form a file.

11. Write one example each for string splitting and string joining using perl.

12. Write a perl script to count the number of occurrence of the nucleotide Adenine in a given DNA sequence.   (10 x 2 =20)

Section B
Answer any five questions. Each carries seven marks

13. Write a perl script to find the most occurring amino acid in a protein sequence.

14. Discuss the application of regular expressions in perl and list five regular expression modifiers and describe the effect each has on a pattern match.

15. Discuss the application of perl-CGI in bioinformatics. Explain GET method with a suitable example.

16. Write a bio-perl program to find the complement and reverse complement of the sequence "TTGCTCGT".

17. Write a perl program to find the dinucleotide composition of a given DNA sequence.

18. Write a perl script to sort given 5 numbers in both ascending and descending orders.

19. Write a subroutine to find whether the string given by the user is a palindrome or not using a perl script.

20. Write a perl program which creates a hash table containing country names as keys and their capitals as values and perform the following:

    i) Print all pair of values (country name and capital)

    ii) Accept country name and print the capital of it.

(5 x 7 = 35)

Section C
Answer any two questions. Each carries 10 marks

21. Write a perl program to detect the ORFs in the +1 reading frame of a given genomic   sequence and display the total numner of ORFs detected.

22. Write a perl script to open a fasta file which contains a single nucleotide sequence. Read the sequences from the file and append a new sequence to the file.

23. Write down a Bioperl script to translate a DNA sequence

(2 x 10=20)

MSc. BIOINFORMATICS
MODEL QUESTION PAPER
BI 241 RESEARCH METHODOLOGY

Time: 3 Hrs.   Max. Marks: 75

Section A
Answer any ten questions. Each carries two marks

1. "A researcher begins with an observation and a natural Question"- Give your comments?

2. Give two examples each of Fact and opinion.

3. During your research, your experiments help to form a new hypothesis. You search in the web with appropriate keywords and find that similar results were obtained by another researcher. How will you react to such a situation?

4. Compare invention with innovation.

5. List 4 good critical thinking traits.

6. What is an open access publication?

7. What is SWOT analysis?

8. List two examples of pure and applied Research.

9. What is meant by impact factor?

10. Give examples for dependent and independent variables in a given experiment.

11. Differentiate the abstract of a research paper from Introduction.

12. Give examples of two copy rightable IPs and 2 patentable IPs.

13. What is plagiarism?

(10 x 2=20)

Section B
Answer any five questions. Each carries seven marks

14. Oxfordshire, Uk is looking for a Bioinformatician and the job profile is as follows:

"A dynamic cancer therapeutics company located in Oxford is currently looking for a Bioinformatician to join their expanding team. Using their exclusive human protein database which includes extensive proteomic and genomic data, they are poised to develop their novel targets within the diagnostic/ therapeutic cancer market. They are currently collaborating with several global pioneers in antibody development so that it is an excellent time to be joining this exciting and innovative company. You will be responsible for data mining and summarizing a

variety of mass spec data as well as protein sequence analysis. Using both in house and public databases, you will be mining data from an array of proteomic experimental data." Prepare a letter to them to apply for the job. Justify your suitability (You may make any assumption.)

15. Discuss techniques for sharp research on internet.
16. What is crux of the patent amendment of 2005 in India?
17. Discuss open access publishing in science.
18. Explain the design of a scientific experiment with a suitable example, bringing out its salient features.
19. Explain how a multimedia presentation can be prepared for a PhD open defense.
20. Explain the patenting process with the help of a suitable example.
21. Explain publication process of a scientific paper.

(5x7 =35)

Section C
Answer any two questions. Each carries ten marks

22. Explain the IMRAD model of a Research Paper.
23. If you are a referee for an international scientific journal, list out the major principles you will follow and methods you will adopt while reviewing.
24. Discuss the TREZ methodology for innovation.

(2x10=20)