c) What is out-group sequence in phylogenetic tree and why it is so important in phylogenetic analysis ? Define the phylogenetic tree constriction methods that directly based on sequences. 5+2+3

Ex/MSBT-2/3/2019

M.Sc. (Biotechnology) Part - II Examination, 2019

Computer and Bioinformatics

Paper - 2/3

Time : Four hours Full Marks : 100

PART - I

Answer ***Q1*** and ***any two*** from rest

1. Answer ***any five*** questions : 5×4

   a) What do you mean by algorithm ? What are its properties?

   b) Differentiate between while and do while loop structure in C programming language.

   c) Perform the following using BCD arithmetic :

      i) 27 + 79 ii) 97 – 54

   d) Represent $(-123{\cdot}25)_{10}$ using IEEE 32-bit notation.

   e) Differentiate between i++ and ++i in C programming language.

   f) What are the differences between compiler and interpreter ?

2. a) Write an algorithm to check a given integer is prime or not.

b) Draw a flowchart to find maximum between three numbers.

c) What are the function of strlen( ), strcat( ) and gets( ) in C language. 5+5+5

3\. a) Write a C program to find maximum from a set of N numbers. N should be read from user.

b) Write an algorithm to calculate

$$1 + 1/X + 1/X^2 + ... + 1/X^N.$$

c) What are the different methods to represent a signed number in binary number system ? Represent $(-45)_{10}$ using these methods with 16 bits. 6+5+4

4\. a) Write a C program to convert a temperature from Celsius to Fahrenheit.

b) Write a C program that accept a string and find number of vowels present in the string.

c) Do you think that "1's complement is better than 2's complement" ? Give reason to support your opinion. 5+6+4

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c) What do you mean by similarity matrix ? Explain with example.

d) Define the Total Score, Max Score, Query coverage and E-value, Identity in the context of sequence alignment.

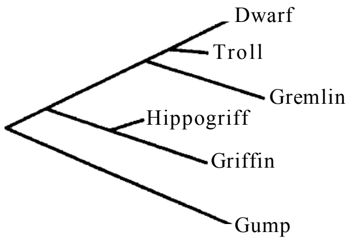
e) What's the three major databases with their respective operative countries. Name the two structure databases. 3+2

f) What are the differences between PAM and BLOSUM matrix. 5

8\. Answer ***any one*** of the following : 10×1=10

a) What are Databanks in the context of Bioinformatics ? How do you classify various types of databanks pertaining to bioinformatics. 5+5=10

b) Answer the following questions about this tree :



i) Which are the two most closely related species ?

ii) Which of these is probably the outgroup ?

iii) Which is most distantly related to the Gremlin other than the outgroup species ?

iv) Write down the few basic character of outgroup.

PART - II

Answer ***all the*** questions.

The figures in the margins indicate full marks.

5. Answer the following questions : 1×10=10

   a) What is primary and secondary database ?

   b) What makes BLAST more useful then FASTA for database search ?

   c) What are the basic structure of a GenBank and an EMBL entry ?

   d) Write the name of scoring model used to build similarity between nucleotide sequences ?

   e) For what purpose BLOSUM matrices are used ?

   f) What is FASTA format ?

   g) Which one is used for search all NCBI associated databases ?

      i) BLAST ii) CLUSAL W

      iii) ENTREZ iv) PDB

   h) If you want to BLAST the non-redundant database using a new protein sequences as query, which is the BEST search program to use ?

      i) blastp ii) blastn iii) tblastx iv) blastx

   i) Submission to GenBank include

      i) Sequin and Banklt ii) Sequin

      iii) Banklt iv) Banktl and sequeen

   j) Name two different methods used in pair wise sequence alignment.

6. Answer ***any five*** of the following : 2×5=10

   a) Write the two most commonly used scoring matrix.

   b) Why the alignment between two sequences is performed?

   c) Write name of two web based tools used for restriction mapping.

   d) What do you mean by Express Sequence Tags (EST) database ?

   e) What is bioinformatics ?

   f) What do you mean by local and global alignment ?

   g) What do you mean by identity and similarity between two protein sequences ?

7. Answer ***any four*** of the following : 5×4=20

   a) What is DNA sequencing chromatogram ? Explain how to interpret it ? 3+2

   b) What is Homologs, Paralogs, Orthologs. Explains them with examples. 3+2