

- iv) What are the differences between PAM and BLOSUM matrix ? 5
- v) What are Accession number and Identifiers in GenBank sequence format ? Identify their differences with examples. 2+3
9. Answer **any one** of the following : 10×1=10
- i) Calculate the dynamic programming matrix and an optimal alignment for the DNA sequences GAATTC and GATTA, scoring +2 for a match, -1 for a mismatch, and -2 for a gap (i.e. 2 is the gap penalty), but without a separate gap creation and extension penalty.
- What is dotplot matrix in pairwise sequences alignments ? When and why it is less efficient than dynamic programming in pairwise sequences alignments. 6+2+2
- ii) What is out-group sequence in phylogenetic tree and why it is so important in phylogenetic analysis ? Define the phylogenetic tree construction methods that directly based on sequences. 5+2+3
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M. SC. BIO-TECHNOLOGY PART II EXAMINATION, 2018**COMPUTER & BIOINFORMATICS****PAPER - 2/3**

Time : Four hours

Full Marks : 100

(50 marks for each Group)

Use a separate Answer-Script for each Group

GROUP - AAnswer **Q.1** and **any three** from rest.

1. Answer **any five** questions : 4×5=20
- a) Perform the following BCD arithmetic :
- i) 52 + 64
- ii) 95 - 27
- b) What do you mean by operating system ? What are the responsibilities of an operating system ?
- c) What do you mean by algorithm ? What are its properties ?
- d) Differentiate between i ++ and ++ i in C language.
- e) Assume 8-bits are used to store an integer. Perform the following using 2's complement representation.
- i) $(-25)_{10} + (+30)_{10}$
- ii) $(-25)_{10} - (+30)_{10}$

[Turn over

- f) Describe the basic block diagram of a computer.
2. a) Draw a flowchart to add the odd numbers from 1 to 500.
- b) Write an algorithm to find the sum

$$1 + \frac{1}{2^2} + \frac{1}{3^2} + \dots + \frac{1}{N^2} \quad 5+5$$

3. a) Write a program in C that find the maximum of n integers stored in an array.
- b) Explain use of FOR loop and WHILE loop in C language with suitable example. 5+5
4. a) The marks obtained by a student in 4 different subjects are input through keyboard. The students gets division as per following rules :

Percentage above or equal to 60 - First division

Percentage between 50 and 59 - Second division

Percentage between 40 and 49 - Third division

Percentage less than 40 - Fail.

Write a program in C to calculate the division obtained by a student.

- j) Name two different methods used in pair wise sequence alignment.
7. Answer **any five** of the following : 2×5=10
- What are **Init1** and Initn score in FASTA sequences search algorithms ?
 - Why the alignment between two sequences is performed ?
 - What are primary and secondary database in bioinformatics? Explain with examples.
 - What are Cladogram and Phylogram in phylogenetic analysis ? Explain with schematic diagrams.
 - What do you mean by local and global alignment ?
 - What do you mean by identity and similarity between two protein sequences ?
8. Answer **any four** of the following : 5×4=20
- What is DNA sequencing chromatogram ? Explain how to interpret it ? 3+2
 - What is Homologs, Paralogs, Orthologs. Explains them with examples. 3+2
 - Define the Total Score, Max Score, Query coverage and E-value, Identity in the context of sequence alignment. 5

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GROUP - B

Answer *all the* questions.

The figures in the margins indicate full marks.

6. Answer the following questions : 1×10=10
- a) What are the three major databases with their respective operative countries ?
 - b) Why BLAST is more popular than FASTA for database search ?
 - c) Why Entrez in NCBI is so important ?
 - d) For what purpose BLOSUM matrices are used ?
 - e) What is FASTA format ?
 - f) What is LOCUS in GenBank sequences format ?
 - g) What are root and un-rooted phylogenetic tree ? Which one carries more information ?
 - h) If you want to BLAST the non-redundant database using a new protein sequence as query, which is the BEST search program to use ?
i) blastp ii) blastn iii) tblastx iv) blastx
 - i) Name two methods for database search in bioinformatics. Identify their differences.

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- b) Describe the operation performed by the following functions :

i) Strlen () ii) Strcat () iii) gets ()

5+(1+2+2)

5. a) Write a program in C that takes an integer in Base 10 and convert it into binary.
- b) Write a program in C that accept a string and a character from user. The program will show the positions of occurrences of the character in the string. Consider, upper case and lower case of the character as equivalent.

5+5

[Turn over