



CENTRAL UNIVERSITY OF SOUTH BIHAR

Department of Bioinformatics

School of Earth, Biological and Environmental Sciences

End -Term Examination

Session: 2020-22

Semesters: II

Programme: M.Sc. Bioinformatics
Course Code: MSBIS2003C04
Duration: 2 Hrs. 30 Min.

Course Title: Programming with Perl
Total points: **50**

Instructions:

1. Preferably write your answers on A4 size plain paper (non-ruled) sheets.
2. Write your required details on the first page in the same order as specified below:

Name: **Programme:**..... **Semester:**

Course Title: **Course Code:**

.....

Total No. of pages used:

Date: **Signature:**

.....

3. After completing the examination, write page number on the top right corner of each page in the format: 1/x, 2/x, ..., x/x where 'x' is the total number of pages used. If you have used total 6 pages then your page numbers will be 1/6, 2/6,.....6/6.

4. The students have to write the answers on both side of the sheet (A4 size plain paper non ruled sheet).

5. The questions asked here are basically designed to assess the interpretation and application of knowledge, comprehension skills, and critical thinking skills rather than only recalling capacity.

6. Total twelve short answer questions of **five points each** are given covering the entire course content.

7. Answer **any ten** questions in total in maximum **two and half hours**.

8. The maximum limit to answer a question is 200 -300 words.

9. At the start of the examination all the questions will be released through e-mail and/or WhatsApp.

10. The total time limit to attempt the question paper is **two and half hours**. Along with the two and half hours, extra 30 minutes will be given for IT related activities such as downloading questions, scanning of answer sheets and uploading/emailing them.

11. After completing the examination within the stipulated time (two and half hours, scan your answer sheets or click pictures and submit it electronically in **one single file** (preferably PDF) to the course instructor through e-mail (**kumaranil@cub.ac.in**) strictly within stipulated time limit for submission (Three hours). Before submitting, rename your file and keep your name and enrolment number as file name.

12. **Please note** that do not use these extra 30 minutes for writing answers. Rather, finish writing as soon as possible within two and half hours and immediately submit your answers in

*the prescribed way given below. **Due to any reason, if a student is unable to submit the answer sheet file within the time limit, the university will not consider this examination and conduct another examination in the conventional mode whenever the conditions return to normal and circumstances permit or the university deems suitable. No other option or reason shall be entertained.***

*13. In case you feel difficulty in submitting the answer sheet file through e-mail, then you are required to submit it to the concerned course instructor through WhatsApp **within the stipulated time only** and email it later on (within 48 hours) along with the screen shots of WhatsApp submission.*

.....

Question Paper (Answer any 10 questions)

(5 x 10 = 50 Points)

- Q1. Describe the advantages and disadvantages of using Perl scripting language.
- Q2. Sometimes information flows from RNA to DNA. Write a program to reverse transcribe RNA to DNA.
- Q3. Write a Perl script which asks the user to enter the number of DNA strings to be concatenated. After taking the input of DNA strings, it concatenates all of them and prints the final DNA string.
- Q4. Write a Perl script to take input of 10 protein names in an array from the user, and print the results.
- Q5. Differentiate between the **splice** and **substr** function with suitable examples.
- Q6. Write a Perl script to calculate the T_m value for a DNA sequence entered by the user.
(Formula: $T_m = 2 * (A+T) + 4 * (G+C)$ where A, T, G and C are the number of respective DNA bases)
- Q7. Discuss the differences between **chop** and **chomp** function with suitable examples.
- Q8. Discuss the advantages of using subroutines with suitable example.
- Q9. A researcher wishes to create point mutation in a DNA string at a specific position. Write a Perl script to do the same.
- Q10. Write a Perl script to generate a random DNA string of a length entered by the user.
- Q11. What is a Perl module? How can we create it? Discuss its uses with a suitable example.
- Q12. A researcher wish to display multiple DNA sequences from a FASTA file using Bioperl. Write a program which performs this task.
