

2056
B.Sc. (Hons.) Bio-Informatics (FYUP)
Fourth Semester
Bioinformatics
BIFM-405: Concepts of Shell Scripting
(Common with B.Sc. Bioinformatics 4th Semester FYUP)

Time allowed: 3 Hours

Max. Marks: 60

NOTE: Attempt five questions in all, including Question No. 1 which is compulsory and selecting one question from each Unit.

x-x-x

I. Answer the following:-

- a) Define Shell and Terminal.
- b) Differentiate between CLI and GUI shells.
- c) List any four Linux file management commands with purpose.
- d) What is a shebang (!) in shell scripting?
- e) Explain difference between local and global variables in bash.
- f) What are positional parameters?
- g) Define grep and its use.
- h) What is FASTA file format?
- i) Write syntax of 'if' statement in bash.
- j) What is 'awk' used for?
- k) Define BLAST.
- l) What is file permission in Linux?

(12x1)

UNIT – I

- II. a) Explain Linux file system structure with suitable diagram.
b) Describe basic shell commands (ls, cd, pwd, mkdir, rm) with examples. (6,6)
- III. a) Explain bash scripting environment setup and writing a basic script.
b) Write a shell script to check whether a number is prime or not. (6,6)
- IV. a) Explain decision-making statements (if, case) with examples.
b) Write a shell script to find factorial using loops. (6,6)

P.T.O.

(2)

UNIT – II

- V. a) Explain sequence data extraction using 'grep', 'awk', and 'sed'.
b) Write commands to extract headers from a FASTA file and count sequences. (6,6)
- VI. a) Explain sorting and filtering of sequence data using shell tools.
b) Write commands to filter sequences longer than a given length. (6,6)
- VII. a) Explain usage of BLAST and Clustal Omega.
b) Write a pipeline using shell commands to download sequence data using 'wget' and process it. (6,6)

x-x-x