

M. Sc. DEGREE EXAMINATION, APRIL 2023
BIOINFORMATICS
FOURTH SEMESTER

COURSE : CORE
PAPER : ADVANCES IN BIOINFORMATICS
TIME : 3 HOURS

MAX. MARKS: 100

SECTION – A

ANSWER ALL QUESTIONS

(20 x 1=20)

1. Write down the uses of following commands (a) mkdir; (b) echo
2. List out the applications of NGS.
3. Define SAM.
4. List out tools used for genomics analysis.
5. Define metagenome.
6. List out sources of metagenomic data.
7. What is microbiome beta-diversity?
8. How do you analyze metagenomics data?
9. Define SnRNA.
10. What is transcriptomics?
11. How do you identify differentially expressed genes?
12. Classify types of RNA.
13. Define motif.
14. What is dynamic structure of chromatin?
15. What is the interaction of transcription factors?
16. Define Chromatin.
17. How does Cas9 recognize its target sequence?
18. Define Targeted mutagenesis.
19. What does sgRNA do in CRISPR?
20. What is therapeutic genome editing?

SECTION – B

ANSWER ANY FOUR QUESTIONS. EACH ANSWER SHOULD NOT EXCEED 500 WORDS. ALL QUESTIONS CARRY EQUAL MARKS.

(4 x 10 = 40)

21. Summarize about different file formats in NGS.
22. Discuss about any 10 linux commands and its utilization.
23. Compare between Alpha and beta diversity metagenomics data.
24. Elaborate on steps in analysing RNA-seq data.
25. Explain about transcriptomics analysis with a case study?
26. Elaborate on gene regulatory dynamics.
27. Briefly describe about mechanisms, advances and prospects of genome editing technology in the targeted therapy of human diseases.

SECTION – C

ANSWER ANY TWO QUESTIONS. EACH ANSWER SHOULD NOT EXCEED 1200 WORDS. ALL QUESTIONS CARRY EQUAL MARKS. (2 x 20 = 40)

28. Explain the steps in NGS technology and its applications?
29. List out the logical steps for metagenome analysis.
30. Elaborate about types of epigenetics modifications.
31. Discuss about Genome engineering using the CRISPR-Cas9 system.
