

INTERNAL ASSIGNMENT QUESTIONS
Advanced Diploma in Bio Informatics Semester - II

2026



PROF. G. RAM REDDY CENTRE FOR DISTANCE EDUCATION

(RECOGNISED BY THE DISTANCE EDUCATION BUREAU, UGC, NEW DELHI)

OSMANIA UNIVERSITY

(A University with Potential for Excellence and Re-Accredited by NAAC with "A" + Grade)

DIRECTOR

Prof. N.Ch.Bhadracharyulu
Hyderabad – 7 Telangana State

**PROF.G.RAM REDDY CENTRE FOR DISTANCE EDUCATION
OSMANIA UNIVERSITY, HYDERABAD – 500 007**

Dear Students,

Each student has to write the answers to the Assignment questions with neat own handwriting using **BLUE PEN** (Black Ink not allowed) for each paper. Assignments have to submit after the payment of Rs.500/- by showing the receipt of the same. If the Assignment is not submitted within stipulated time i.e. before the theory exams / last date is treated as absent.

Methodology for writing the Assignments (Instructions) :

1. First read the subject matter in the course material that is supplied to you.
2. If possible read the subject matter in the books suggested for further reading.
3. You are welcome to use the PGRRCDE Library on all working days for collecting information on the topic of your assignments. (10.30 am to 5.00 pm).
4. Give a final reading to the answer you have written and see whether you can delete unimportant or repetitive words.
5. The cover page of the each theory assignments must have information as given in FORMAT below.

FORMAT

1. NAME OF THE STUDENT :
 2. ENROLLMENT NUMBER :
 3. NAME OF THE COURSE :
 4. SEMESTER (I, II, III & IV) :
 5. TITLE OF THE PAPER :
 6. DATE OF SUBMISSION :
6. Write the above said details clearly on every subject assignments paper, otherwise your paper will not be valued.
 7. Tag all the assignments paper wise and submit them in the concerned counter.
 8. Submit the assignments on or before **20th June, 2026** at the concerned counter at PGRRCDE, OU on any working day and obtain receipt.

DIRECTOR

COURSE : ADVANCED DIPLOMA IN BIOINFORMATICS – II SEMESTER

Paper : I _____ Subject: COMPUTATIONAL APPROACHES TO MODERN BIOLOGY

Note: Answer all the Questions. Each Question carries three marks Q10x3M=30M

1. How can missing values be identified and replaced using tidy and dplyr?
2. How can you make a ggplot2 plot interactive using ggplotly?
3. How do the default options for significance testing in R's t.test() and Python's scipy.stats.ttest_ind differ?
4. What are the structural and functional characteristics of FASTA, GenBank and PDB file formats?
5. Give an example of how genomics is applied in medicine?
6. Explain the process of merging datasets from different sources using tidyverse functions?
7. Discuss the working principle of Sanger sequencing?
8. Discuss the role of metagenomics in understanding microbial communities and their impact on human health?
9. Evaluate the importance of biostrings in motif detection and sequence alignment tasks?
10. Discuss the benefits of automating throughput sequencing tasks with bash?

Course : ADVANCED DIPLOMA IN BIOINFORMATICS – II Semester

Paper: II Subject: COMPUTER AIDED DRUG DESIGN AND DEVELOPMENT

Note: Answer all the Questions. Each Question carries three marks Q10x3M=30M

1. What are protein–protein interactions, and how can computational methods be used to predict and analyze interaction networks in biological systems?
2. Explain the principles of protein structure prediction
3. What are molecular dynamics simulations, and how are they used to study the dynamics of biomolecules?
4. Describe the process of protein–ligand docking and explain how docking is used to identify potential drug candidates.
5. How can protein structure prediction, protein–protein interaction analysis, molecular dynamics simulations, and protein–ligand docking be integrated into a computational drug discovery pipeline?
6. What is virtual screening? Explain its significance in modern drug discovery
7. Describe the concept of molecular modeling and discuss its applications in studying biomolecular structures and drug–target interactions.
8. Explain ligand-based drug design and discuss the techniques used when the three-dimensional structure of the target protein is unavailable.
9. What is molecular docking? Describe the steps involved in a docking study and explain how binding affinity and docking scores are evaluated.
10. Outline the major stages of the drug discovery and development process, highlighting the role of bioinformatics.

COURSE: Advanced Diploma in Bioinformatics

Paper: III Subject: ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING FOR BIOINFORMATICS

Note: Answer all the Questions. Each Question carries three marks

Q10x3M=30M

1. What is AI? How does AI aid in gene prediction in bioinformatics?
2. What techniques are used for analyzing drug interactions using AI?
3. What AI tools are commonly used for protein analysis?
4. How does the k-means algorithm work in partitioning data?
5. How does AI handle large gene expression datasets?
6. Discuss the impact of AI in visualizing protein interactions for drug discovery?
7. Explain the role of deep learning techniques like alphaFold in predicting protein structures?
8. Explain the architecture of CNN and their components used in bioinformatics applications?
9. How does PCA contribute to the interpretation of gene expression patterns in multi-omics studies?
10. Explain key methods for feature extraction from genomic data including sequence analysis and structural variant identification?