

M.Sc Sem-3 Examination

501

Bioinformatics

November-2024

[Max. Marks : 70]

Time : 2-30 Hours]

Qu1 : Answer the following :

- Briefly explain the various operators in Python using examples. (7 Marks)
Include the in and not in operators.
- Briefly explain the loops in Python using examples. (7 Marks)
Write a program to input a DNA string and print the GC%

OR

Qu1 : Answer the following :

- Briefly explain the data types in Python. Explain strings and atleast 4 string functions with examples (7 Marks)
- Write a Python script to input a DNA string and print all the duplets of the sequence and the frequency of the duplet AT (7 Marks)

Qu2 : Answer the following :

- Briefly explain sets in Python using examples. Explain the union, difference, intersection and symmetric difference functions. (7 Marks)
- Briefly explain lists and splicing in lists using examples and what is list comprehension using atleast 2 examples. (7 Marks)

OR

Qu2 : Answer the following :

- Briefly explain how files are accessed in Python using examples (7 Marks)
- Write a Python script to read a fasta file with a nucleotide sequence print the header, the sequence and the sequence length. (7 Marks)

Qu3 : Answer the following :

- Briefly explain try ... except in Python using examples. Explain the difference between the else block and finally block. (7 Marks)
- Write a Python script to input 2 numbers and print its division. Use atleast two except blocks and the else block. (7 Marks)

OR

Qu3 : Answer the following :

- Briefly explain how metacharacters are used in Python and the match functions In Regular Expressions. (7 Marks)
- Briefly explain functions in Python. How parameters are passed.
Write a Python script to create a function that takes a string as a parameter and returns a list of characters in the string. (7 Marks)

Qu4 : Answer the following :

- Briefly explain the Biopython package using appropriate examples (7 Marks)
- Briefly explain the Numpy and Pandas package using examples (7 Marks)

OR

Qu4 : Answer the following :

- Write a Python script to create a class Protein (7 Marks)
Data Member : Sequence
Methods :
ShowSequence :
Displays the protein sequence
GetCount
Prints the length of the sequence

(P.T.O)

- b. Explain briefly inheritance is implemented in Python using examples. (7 Marks)

Qu5 : Attempt any 7 :

(14 Marks)

1. Given the list `genes = ['BRCA1', 'TP53', 'EGFR', 'BRCA2', 'MYC']`, write a Python code to find the index of the gene 'EGFR'

2. How would you extract the three nucleotide sequences from the second element in the list `sequences = ['ATGC', 'CGTA', 'GCTA', 'TACG', 'ATCG', 'CGAT']`

3. You have a dictionary `gene_info = {'BRCA1': 'Breast cancer', 'TP53': 'Tumor suppressor', 'EGFR': 'Lung cancer'}`. Write a Python code to add 'MYC': 'Oncogene' to this dictionary.
4. Given two sets of genes `set1 = {'BRCA1', 'TP53', 'EGFR'}` and `set2 = {'TP53', 'EGFR', 'MYC'}`, write a Python code to find the common genes in both sets
5. How do you check if a key 'key1' exists in a dictionary `d = {'key1': 'value1', 'key2': 'value2'}`
6. How would you remove all occurrences of the value 3 from the list `L = [1, 2, 3, 3, 4, 3, 5]`?
7. Write Python code to open a FASTA file named `sequences.fasta` in read mode and read all the lines in a list
8. Write Python code to handle the `FileNotFoundError` exception when trying to open a file named `genome.txt` in read mode.
9. Write a function that takes a positional parameter a `DNAStrng` and an optional parameter `size`. Assume `size` is 0. The function should print the entire string if `size` is 0. The function should print upto `size` characters if `size` is not zero
10. Write a lambda function that takes 2 numbers as argument and returns its square
11. Write the regular expression to find all occurrences of a digit sequence in the string `'Gene123TP53EGFR567'`
12. Write the pandas command to read `data.csv` in a dataframe
