

Paper: BI-522 & 526 Programming in PERL for Bioinformatics

CO1 Students will know the importance and effectiveness of PERL in handling biological data as compared to other programming languages

A1 Write comparison of PERL with other popular languages such as C++, JAVA, C etc.

A2 Write features of the PERL Language make it effective for handling biological data

| Marks | Roll No | Assignment1 | Assignment2 | Total marks of attempted | | Percentage | Score (3,2,1) | Target >= 60% (Y/N) | |
|-------|----------------|-------------|-------------|--------------------------|-------|------------|---------------|---------------------|--|
| | | | | questions | Marks | | | | |
| | | 5 | 5 | 10 | 10 | | | | |
| | 25101 | 4 | 4 | 8 | 10 | 80 | 3 Y | | |
| | 25103 | 5 | 5 | 10 | 10 | 100 | 3 Y | | |
| | 25104 | 4 | 4 | 8 | 10 | 80 | 3 Y | | |
| | 25105 | 4 | 4 | 8 | 10 | 80 | 3 Y | | |
| | 25106 | 5 | 5 | 10 | 10 | 100 | 3 Y | | |
| | Average | | | | | | | 3 | |

| %age | score |
|---------|-------|
| >=60 | 3 |
| 50-59.9 | 2 |
| 40-49.0 | 1 |

CO2 Students will be able to retrieve a specific data from a large text files of different formats

GD1 Group discussion on File Handling

CA2 Retrieve a genome sequence from NCBI in fasta format and read it using the File hadling feature of PERL

| Marks | Roll No | GD1 | CA2 | Total marks of attempted | | Percentage | Score (3,2,1) | Target | |
|-------|----------------|-----|-----|--------------------------|-------|------------|---------------|----------|--|
| | | | | questions | Marks | | | | |
| | | 10 | 10 | 20 | 20 | | | | |
| | 25101 | 9 | 8 | 17 | 20 | 85 | 3 Y | | |
| | 25103 | 8 | 8 | 16 | 20 | 80 | 3 Y | | |
| | 25104 | 9 | 8 | 17 | 20 | 85 | 3 Y | | |
| | 25105 | 8 | 8 | 16 | 20 | 80 | 3 Y | | |
| | 25106 | 9 | 9 | 18 | 20 | 90 | 3 Y | | |
| | Average | | | | | | | 3 | |

CO3 Students will be able to select, install and use various BIOPERL Libraries for analysis of biological data

A1 Write a short note on Bioperl and its applications

CA2 Install BIOPERL, show reading of sequence files in Genbank format using Bioperl and Do local BLAST using it

| Marks | Roll No | Assignment1 | Class Activity 1 | Total marks of attempted | | Percentage | Score (3,2,1) | Target |
|-------|---------|-------------|------------------|--------------------------|-------|------------|---------------|--------|
| | | | | questions | Marks | | | |
| | | 10 | 10 | | 20 | | | |

| | | | | | | |
|-------|---|----|----|----|----|-----|
| 25101 | 9 | 9 | 18 | 20 | 90 | 3 Y |
| 25103 | 8 | 9 | 17 | 20 | 85 | 3 Y |
| 25104 | 8 | 8 | 16 | 20 | 80 | 3 Y |
| 25105 | 8 | 8 | 16 | 20 | 80 | 3 Y |
| 25106 | 9 | 10 | 19 | 20 | 95 | 3 Y |

| | |
|----------------|----------|
| Average | 3 |
|----------------|----------|

- CO4** Students will be able to write programs to analyze biological data
Write a program to count Number of Positively charged, negatively charged, hydrophobic and polar amino acids in a given sequence download from Swissprot
- T1**
- T2** Write a program to read atoms information from PDB file

| | Roll No | Test1 | Assignment1 | Total marks of attempted questions | Total Marks | Percentage | Score (3,2,1) | Target |
|--------------|---------|-------|-------------|------------------------------------|-------------|------------|---------------|--------|
| Marks | | | 10 | 10 | | 20 | | |
| | 25101 | | 10 | 8 | 18 | 20 | 90 | 3 Y |
| | 25103 | | 7 | 8 | 15 | 20 | 75 | 3 N |
| | 25104 | | 8 | 8 | 16 | 20 | 80 | 3 Y |
| | 25105 | | 6 | 5 | 11 | 20 | 55 | 2 N |
| | 25106 | | 10 | 10 | 20 | 20 | 100 | 3 Y |

| | |
|----------------|------------|
| Average | 2.8 |
|----------------|------------|