Dr. Jayashree Raman

Course Code: 13M11BT112   MAX. MARKS: 25

Course Name: Advanced Bioinformatics

Course Credits: 03   MAX. TIME: 1.5 Hr

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated in square brackets against each question

1. Explain how genomics-assisted breeding has revolutionized the field of crop improvement, citing examples of the application of bioinformatics tool at every step. (5)

2. Explain the different approaches used for homology modeling. (3)

3. Explain the different steps of homology modeling. (4)

4. Write the output of the following R statements. (1+1+2+1)

(a) seq.int (5, 11, 3)

(b) rep.int(1:5, 3)

(c) myfavorite_array <- array(
1:24,
dim = c(4,3,2),
dimnames= list(
c("one", "two", "three", "four"),
c("ein", "zwei", "drei"),
c("un", "deux")
)
))

(d) class(myfavorite_array)

5. Answer in the context of R: (4×2=8)

(a) Describe the different ways of indexing a vector or array or list.

(b) How will you convert a vector into list and vice-versa? Explain with example.

(c) Explain the difference between a list and dataframe, giving examples.

(d) What is the length of a 3-by-4-by-5 array? Explain.