Practical Bioinformatics Assignment-1

Introduction to R

For Practice but will be considered as continuous evaluation

Time = 30 Jan 2022.

- 1. Write a R program to accept input from the user (say, name and user-ID) and display them. Also, print the version of the R installation.
- 2. Write an R program for the following task: -

2+2+3

- i) Create a sequence X having first 100 multiples of 3.
- ii) Find the mean and standard deviation of X.
- iii) Design a function to find the difference of two consecutive numbers in a series and apply it on X.
- 3. Write an R program for the following task:-

1+1+1+2+1+3+3

- i) Create a vector named norm_vec of length 100 having random normally distributed numbers with mean 0 and sd 1 and multiply the series with 100.
- ii) Create a vector named binom_vec of length 100 following random binomial distribution with p i.e. prob of success =0.55.
- iii) Create a vector named pois_vec of length 100 following random poission distribution with mean=0.02 and multiply the vec by 100.
- iv) Create a matrix using cbind command having columns norm_vec,binom_vec,pois_vec.
- v) Convert this matrix to dataframe and name as df.
- vi) Draw histogram, densityplot of each column.
- vii) Find all possible scatterplot of the given data.

##Note :- Use applot for plotting

- 4) Write a R program to create an 3 dimensional array of 24 elements using the 3 dim() function. (Note: The dim() is an inbuilt R function that either sets or returns the dimension of the matrix, array, or data frame)
- 5) Write R program for the following task:-

3+3+3+1

- i) Take input from user asking to print name of fruit, colour, amount to purchase, price.
- ii) Run this function for 10 times i.e.10 entries should be done.
- iii) Store each item i.e. name, colour, price, amount in separate vector and then create a list having these elements stored with their name as Name_fruit,Color_fruit,Price_fruit,Amount.
- iv) Convert this list into a dataframe.

##Additional Problem

Explore NCBI GEO Datasets website and find out possible ways to download data to R directly. Coming assignments will be based on downloading data from GEO dataset and finding differentially expressed genes.