BIOINFORMATICS In Focus

Class 6 Quiz

Each question is worth 1 point. You can get maximum of 10 points for this quiz. Good luck! :)

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* Indicates required question

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What are the main elements of each function? *   1 point

- [x] Argument(s)
- [x] Function's name
- [x] Function's body
- [ ] Annotation for each calculation step

Which is the correct way to write a function? *   1 point

- ( ) Function_name<-function[x]{function's body}
- ( ) Function_name<-function(x)(function's body)
- ( ) Function_name<-function[x][function's body]
- (•) Function_name<-function(x){function's body}

○ Function_name<-function{x}(function's body)

Imagine you have a vector "V". You want to check   * 1 point
how many "NA" elements are contained in this
vector. Choose the right option to do that

◉ sum(is.na(V))

○ which(is.na(V))

○ which.min(V)

○ mean(which.min(V))

○ is.na(V)

Imagine you have a vector M and you know that   * 1 point
this vector has "NA" values in it. How would you
calculate the average value of all elements in this
vector

☑ mean(M, na.rm=TRUE)

☑ mean(na.omit(M))

☐ mean(M)

☐ mean(is.na(M))

☐ mean(na.omit[M])

Which functions would you use to find the number * 1 point
of rows, columns, or both rows & columns in a
data frame?

☑ ncol()

☐ numbcol()

☐ numbrow()

☑ nrow()

☑ dim()

Which command would you use to install new * 1 point
CRAN package on your computer?

🔘 install.packages("package_name")

⚪ install.packages(package_name)

⚪ library(package_name)

⚪ library("package_name")

Which package would you use to make high quality * 1 point
plots?

○ bio3d

◉ ggplot2

○ readr

○ dplyr

○ tidyr

○ Other: _____

Which command(s) would you use to get some * 1 point
documentation about a function you want to use?
Imagine, you are working with mean() function

☑ ?mean

☑ help(mean)

☐ mean?

☐ mean()?

☐ help(mean())

Imagine you want to install one of the Bioconductor packages. What would be your first step?

- ● BiocManager::install()
- ○ biocLite()
- ○ install.packages("Bioconductor")
- ○ library("Bioconductor")

Which package would you use to analyze protein structure, sequence and trajectory data?

- ○ ggplot2
- ○ stats
- ● bio3d
- ○ shiny
- ○ tidyverse

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