USC Department Of Translational Genomics
Keck Medicine of USC

TRGN 599: Applied Data Science and Bioinformatics

UNIT I. Introduction and Basic Data Science

Week 3 – Assignment 3

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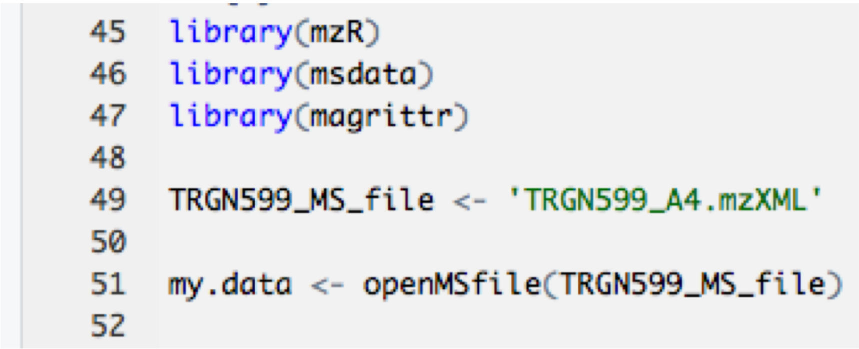
Assignment 4

- Instructions: Please answer the following questions, first 14 questions worth 7 points and last 2 questions worth 1 point (Total: 100 points).
- Load the file “TRGN599_A4.mzXML” in your R-Studio.
  - For example, using the following code:



```
library(mzR)
library(msdata)
library(magrittr)

TRGN599_MS_file <- 'TRGN599_A4.mzXML'

my.data <- openMSfile(TRGN599_MS_file)

```

- In order to answer the following questions you should
- 1) create an R markdown file as explained during the last class,
- 2) copy/paste & run with the new data file (TRGN599_A4.mzXML) the first 129 lines of code of the case study 1 Rmarkdown file (proteomics analysis) that you can find in Blackboard/Lecture 4:
  - File name: Rmarkdown_TRGN_599_Week_4_Proteomics_Analysis.Rmd.

Assignment 4

- Question 1
  - Which of the following R commands gives you access to the measurement-metadata?
    - A) [✓ runInfo(my.data)]
    - B) openMSfile(my.data)
    - C) boxplot(my.data)
    - D) plot(my.data)

- Question 2
  - Which is the number of actual spectra in the set by using the *“runInfo(my.data)$scanCount”* function?
    - A) 10
    - B) 5
    - C) 2
    - [✓ D) 7]

Assignment 4

- Question 3
  - Which is the ion source for the experiment by using the *“instrumentInfo(my.data)$ionisation”* function?
    - A) hybridization ionization
    - B) fluorescence ionization
    - C) electrophoresis ionization
    - D) electrospray ionization
- Question 4
  - How many columns you have in your data when use the header(my.data) function?
    - A) 50
    - B) 26
    - C) 31
    - D) 33

Assignment 4

- Question 5
  - When you plot the spectrum using the “*plot(pl, type=“h”)*” function how many peaks you observe greater than 4e+07?
    - A) 20
    - B) 10
    - [✓ C) 3]
    - D) 9

- Question 6
  - When you pick up the 15 strongest peaks using the function
    - “topnum <- 15
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]”
  - Which of the following is the highest peak?
    - A) 464.8184
    - [✓ B) 924.7365]
    - C) 395.8215
    - D) 789.7467

Assignment 4

- Question 7
  - When you pick up the 15 strongest peaks using the function
    - “topnum <- 15
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]”
  - Which of the following is the lowest peak?
    - A) 464.8184
    - B) 924.7365
    - [✓ C) 395.8215]
    - D) 789.7467

- Question 8
  - When you pick up the 20 strongest peaks using the function
    - “topnum <- 20
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]”
  - Which of the following is the highest peak?
    - A) 333.6765
    - [✓ B) 924.7365]
    - C) 395.8215
    - D) 789.7467

Assignment 4

- Question 9
  - When you pick up the 20 strongest peaks using the function:
    - “topnum <- 20
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]”
  - Which of the following is the lowest peak?
    - A) 333.6765
    - B) 924.7365
    - C) 395.8215
    - D) 789.7467

- Question 10
  - When you plot the peak differences using the function:
    - peakdiff <- outer(pl.top, pl.top, '-')
    - plot(density(abs(peakdiff)))
  - Which of the following is the probability function of the graph:
    - A) Probability density function (PDF)
    - B) Probability mass function (PMF)
    - C) Poisson distribution
    - D) Random distribution

Assignment 4

- Question 11
  - When you plot the peak differences using the function:
    - peakdiff <- outer(pl.top, pl.top, '-')
    - plot(density(abs(peakdiff)))
  - Which of the following would be the most suitable description of the observed curve distributions:
    - A) One can observe that the curve is a composition of two wide distributions.
    - B) One can observe that the curve is a composition of three wide distributions.
    - C) One can observe that the curve is a composition of one wide distributions.
    - D) One can observe that the curve is a composition of five wide distributions.

- Question 12
  - When you plot the peak differences using the function:
    - peakdiff <- outer(pl.top, pl.top, '-')
    - plot(density(abs(peakdiff)))
  - And previously used the 20 strongest peaks using the functions:
    - topnum <- 20
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]
    - pl.top
  - Which of the following would be the most suitable description of the peakdiff matrix:
    - A) It is by itself a 20x20 matrix containing the differences among the elements of the pl.top vector
    - B) It is by itself a 60x60 matrix containing the differences among the elements of the pl.top vector
    - C) It is by itself a 10x10 matrix containing the differences among the elements of the pl.top vector
    - D) It is by itself a 15x15 matrix containing the differences among the elements of the pl.top vector

Assignment 4

- Question 13
  - When you plot the peak differences using the function:
    - peakdiff <- outer(pl.top, pl.top, '-')
    - plot(density(abs(peakdiff)))
  - And previously used the 20 strongest peaks using the functions:
    - topnum <- 20
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]
    - pl.top
  - Which of the following numbers is the sample size of the plot?
    - A) N = 200
    - B) N = 300
    - C) N = 500
    - D) N = 400

Assignment 4

- Question 14
  - When you plot the peak differences using the function:
    - peakdiff <- outer(pl.top, pl.top, '-')
    - plot(density(abs(peakdiff)))
  - And previously used the 20 strongest peaks using the functions:
    - topnum <- 20
    - pl.top <- pl[pl[,2] %in% head(sort(pl[,2],decreasing=T),topnum),1]
    - pl.top
  - Which of the following numbers is the bandwidth of your plot?
    - A) Bandwidth = 32.53
    - B) Bandwidth = 53.52
    - C) Bandwidth = 22.53
    - [✓ D) Bandwidth = 52.53]

Assignment 4

- Question 15
  - Which of the following is an analytic technique that produces mass-to-charge ratio spectra of peptide fragment in samples:
    - A) Microarrays
    - [✓ B) Mass spectrometry (MS)]
    - C) Messenger RNA (mRNA)
    - D) Proteomics

- Question 16
  - Regarding the different file formats for MS data, which file format you are using in your proteomic analysis when uploading data through the mzR package from Bioconductor?
    - A) mzML
    - B) netCDF
    - [✓ C) mzXML]
    - D) mzCDF