

Practical R

BIOF339

---Final project

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Dec, 2018

Loading the raw data

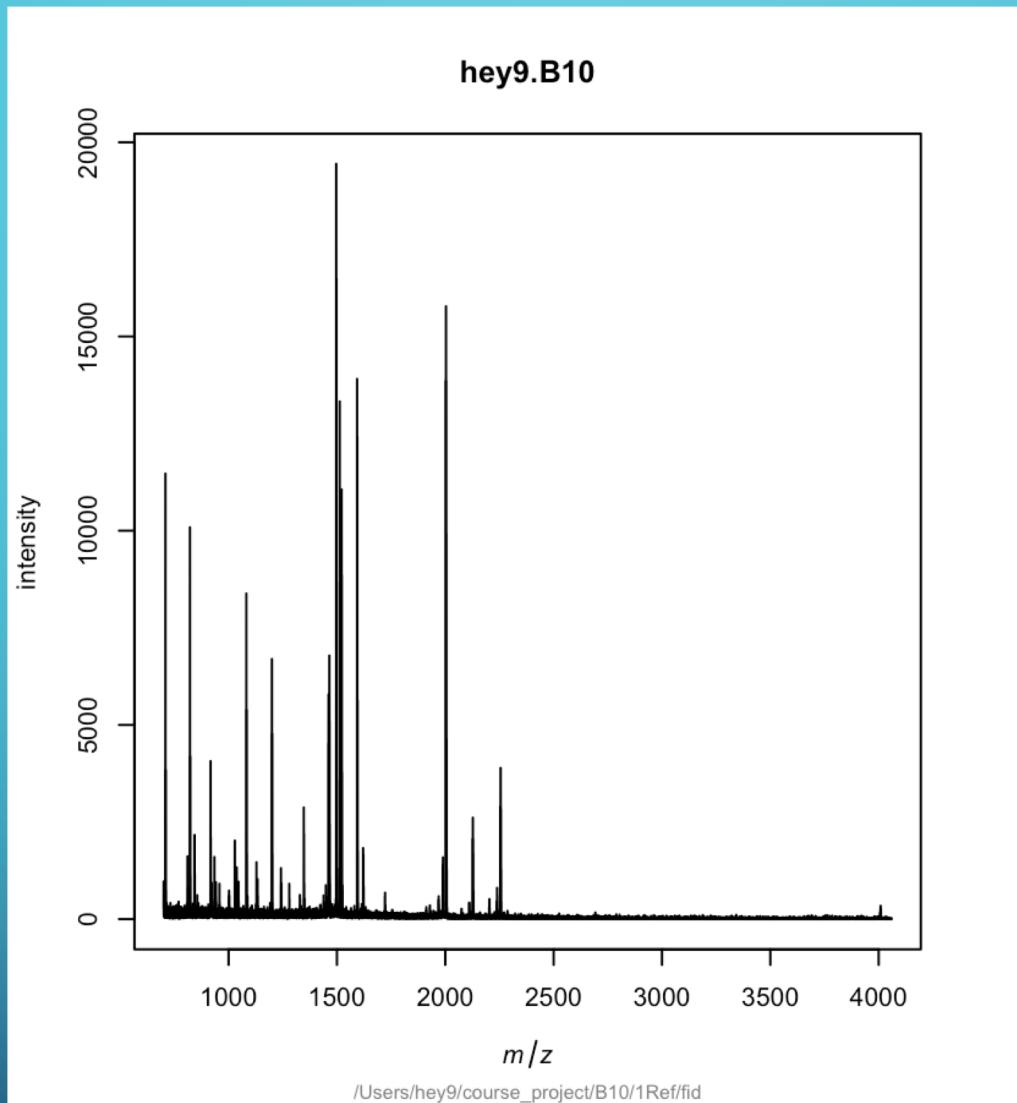
```
library("MALDIquant")
datapath <- "/Users/hey9/course_project/B10/1Ref/fid"

s <- importBrukerFlex(datapath, verbose=FALSE)
summary(mass(s))
> summary(mass(s))
   Min. 1st Qu. Median  Mean 3rd Qu.  Max.
    700    1280   2033   2149   2960   4060

summary(intensity(s))
> summary(intensity(s))
   Min. 1st Qu. Median  Mean 3rd Qu.  Max.
    0.00   10.00  48.00  93.76 109.00 19443.00

head(as.matrix(s))
> head(as.matrix(s))
      mass intensity
[1,] 699.9932     334
[2,] 700.0158     313
[3,] 700.0383     282
[4,] 700.0609     318
[5,] 700.0835     460
[6,] 700.1060     445

plot(s)
```



Transforming data

```
s2 <- transformIntensity(s, method="sqrt")
```

```
s2
> s2
[[1]]
S4 class type      : MassSpectrum
Number of m/z values : 87373
Range of m/z values  : 699.993 - 4060.017
Range of intensity values: 0e+00 - 1.394e+02
Memory usage        : 1.343 MiB
Name                : hey9.B10
File                : /Users/hey9/course_project/B10/1Ref/fid
```

```
s3 <- smoothIntensity(s2, method="MovingAverage",
halfWindowSize=2)
```

```
s3
> s3
[[1]]
S4 class type      : MassSpectrum
Number of m/z values : 87373
Range of m/z values  : 699.993 - 4060.017
Range of intensity values: 0e+00 - 1.267e+02
Memory usage        : 1.343 MiB
Name                : hey9.B10
File                : /Users/hey9/course_project/B10/1Ref/fid
```

plotting

```
s4 <- removeBaseline(s3, method="SNIP")
s4
> s4
[[1]]
S4 class type      : MassSpectrum
Number of m/z values : 87373
Range of m/z values  : 699.993 - 4060.017
Range of intensity values: 0e+00 - 1.179e+02
Memory usage        : 1.343 MiB
Name                : hey9.B10
File                : /Users/hey9/course_project/B10/1Ref/fid

p <- detectPeaks(s4)

peak.data <- as.matrix(p)
par(mfrow=c(2,3))
xl <- range(mass(s))

points(p)
top20 <- intensity(p) %in% sort(intensity(p), decreasing=TRUE)[1:20]
summary(top20)
> summary(top20)
  Mode  FALSE   TRUE
logical 1987    20

labelPeaks(p, index=top20, underline=TRUE)
plot(p, sub="", main="6: peak plot", xlim=xl)
labelPeaks(p, index=top20, underline=TRUE)
```

