Using R and Bioconductor for Proteomics Data Analysis.

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April 9, 2013

Abstract

This vignette shows and executes the code presented in the manuscript *Using R for proteomics data analysis*. It also aims at being a general overview useful for new users who wish to explore the R environment and programming language for the analysis of proteomics data.

Keywords: bioinformatics, proteomics, mass spectrometry, tutorial.

Contents

1 Introduction

This document illustrates some existing R infrastructure for the analysis of proteomics data. It presents the code for the use cases taken from [7].

There are however numerous additional R resources distributed by the Bioconductor[1] and CRAN[2] repositories, as well as packages hosted on personal websites. Section 7 on page 35 tries to provide a wider picture of available packages, without going into details.

1.1 General R resources

The reader is expected to have basic R knowledge to find the document helpful. There are numerous R introductions freely available, some of which are listed below.

From the R project web-page:

- **An Introduction to R** is based on the former *Notes on R*, gives an introduction to the language and how to use R for doing statistical analysis and graphics. [browse HTML | download PDF]
- Several introductory tutorials in the contributed documentation section.

Relevant background on the R software and its application to computational biology in general and proteomics in particular can also be found in [7]. For details about the Bioconductor project, the reader is referred to [9].

1.2 Getting help

All R packages come with ample documentation. Every command (function, class or method) a user is susceptible to use is documented. The documentation can be accessed by preceding the command by a ? in the R console. For example, to obtain help about the `library` function, that will be used in the next section, one would type `?library`. In addition, all Bioconductor packages come with at least one vignette (this document is the vignette that comes with the **RforProteomics** package), a document that combines text and R code that is executed before the pdf is assembled. To look up all vignettes that come with a package, say **RforProteomics** and then open the vignette of interest, one uses the `vignette` function as illustrated below. More details can be found in `?vignette`.

```
> ## list all the vignettes in the RforProteomics
> ## package
> vignette(package = "RforProteomics")
> ## Open the vignette called RforProteomics
> vignette("RforProteomics", package = "RforProteomics")
> ## or just
> vignette("RforProteomics")
```

[1] http://www.bioconductor.org
[2] http://cran.r-project.org/web/packages/

R has several mailing lists[3]. The most relevant here being the main R-help list, *for discussion about problem and solutions using R* . This one is for general R content and is not suitable for bioinformatics or proteomics questions.

Bioconductor also offers several mailing lists[4] dedicated to bioinformatics matters and Bioconductor packages. The main Bioconductor list is the most relevant one. It is possible to post[5] questions without subscribing to the list.

It is important to read and comply to the posting guides (here and here) to maximise the chances to obtain good responses. It is important to specify the software versions using the sessionInfo() functions (see an example output at the end of this document, on page 38). It the question involves some code, make sure to isolate the relevant portion and report it with your question, trying to make your code/example reproducible[6].

All lists have browsable archives.

1.3 Installation

The package should be installed using as described below:

```
> ## only first time you install Bioconductor
> ## packages
> source("http://www.bioconductor.org/biocLite.R")
> ## else
> library("BiocInstaller")
> biocLite("RforProteomics")
```

To install all dependencies (78 packages) and reproduce the code in the vignette, replace the last line in the code chunk above with:)

```
> biocLite("RforProteomics", dependencies = TRUE)
```

Finally, the package can be loaded with

```
> library("RforProteomics")

This is the 'RforProteomics' version 1.0.0.
Run 'RforProteomics()' in R or visit
'http://lgatto.github.com/RforProteomics/' to get started.
```

1.4 External dependencies

Some packages used in the document depend on external libraries that need to be installed prior to the R packages:

[3] http://www.r-project.org/mail.html
[4] http://bioconductor.org/help/mailing-list/
[5] http://bioconductor.org/help/mailing-list/mailform/
[6] https://github.com/hadley/devtools/wiki/Reproducibility

mzR depends on the Common Data Format[7] (CDF) to CDF-based raw mass-spectrometry data. On linux, the `libcdf` libraries are required. On debian-based systems, for instance, you will need to install `netCDFlibnetcdf-dev`, `netcdf-dev` and `netcdf-bin`.

IPPD (and others) depend on the **XML** package which requires the `libxml2` infrastructure on linux. On debian-based systems, you will need to install `libxml2-dev`.

biomaRt performs on-line requests using the `curl`[8] infrastructure. On debian-based systems, you will need to install `libcurl-dev` or `libcurl4-openssl-dev`.

1.5 Obtaining the code

The code in this document describes all the examples presented in [7] and can be copy, pasted and executed. It is however more convenient to have it in a separate text file for better interaction with R (using ESS[9] for emacs or RStudio[10] for instance) to easily modify and explore it. This can be achieved with the `Stangle` function. One needs the Sweave source of this document (a document combining the narration and the R code) and the `Stangle` then specifically extracts the code chunks and produces a clean R source file. If the package is installed, the following code chunk will create a `RforProteomics.R` file in your working directory containing all the annotated source code contained in this document.

```
> ## gets the vignette source
> rnwfile <- dir(system.file(package = "RforProteomics",
+                            dir = "doc/vigsrc"),
+                full.name = TRUE,
+                pattern = "RforProteomics.Rnw")
> ## produces the R file in the working directory
> Stangle(rnwfile)

Writing to file RforProteomics.R
```

Alternatively, you can obtain the `Rnw` file on the github page https://github.com/lgatto/RforProteomics/blob/master/inst/doc/vigsrc/RforProteomics.Rnw.

1.6 Prepare the working environment

The packages that we will depend on to execute the examples will be loaded in the respective sections. Here, we pre-load packages that provide general functionality used throughout the document.

```
> library("RColorBrewer")  ## Color palettes
> library("ggplot2")  ## Convenient and nice plotting
> library("reshape2")  ## Flexibly reshape data
```

[7] http://cdf.gsfc.nasa.gov/
[8] http://curl.haxx.se/
[9] http://ess.r-project.org/
[10] http://rstudio.org/

2 Data standards and input/output

2.1 The mzR package

The **mzR** package [3] provides a unified interface to various mass spectrometry open formats. This code chunk, taken mainly from the `openMSfile` documentation illustrated how to open a connection to an raw data file. The example `mzML` data is taken from the **msdata** data package. The code below would also be applicable to an `mzXML`, `mzData` or `netCDF` file.

```
> ## load the required packages
> library("mzR")  ## the software package
> library("msdata")  ## the data package
> ## below, we extract the releavant example file
> ## from the local 'msdata' installation
> filepath <- system.file("microtofq", package = "msdata")
> file <- list.files(filepath, pattern = "MM14.mzML",
+     full.names = TRUE, recursive = TRUE)
> ## creates a commection to the mzML file
> mz <- openMSfile(file)
> ## demonstraction of data access
> basename(fileName(mz))

[1] "MM14.mzML"

> isInitialized(mz)

[1] TRUE

> runInfo(mz)

$scanCount
[1] 112

$lowMz
[1] 0

$highMz
[1] 0

$dStartTime
[1] 270.3

$dEndTime
[1] 307.7

$msLevels
[1] 1

> instrumentInfo(mz)
```

```
$manufacturer
[1] "Unknown"

$model
[1] "instrument model"

$ionisation
[1] "electrospray ionization"

$analyzer
[1] "mass analyzer type"

$detector
[1] "detector type"

> ## once finished, it is good to explicitely close
> ## the connection
> close(mz)
```

mzR is used by other packages, like **MSnbase** [8], **TargetSearch** [5] and **xcms** [11, 1, 12], that provide a higher level abstraction to the data.

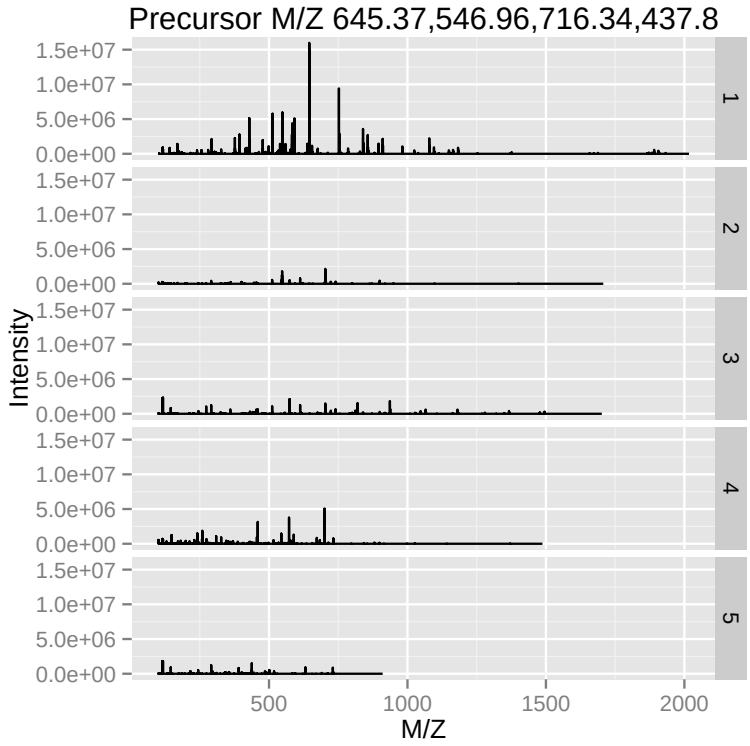
3 Raw data abstraction with MSnExp objects

MSnbase [8] provides base functions and classes for MS-based proteomics that allow facile data and meta-data processing, manipulation and plotting (see for instance figure 1 on page 9).

```
> library("MSnbase")
> ## uses a simple dummy test included in the
> ## package
> mzXML <- dir(system.file(package = "MSnbase", dir = "extdata"),
+     full.name = TRUE, pattern = "mzXML$")
> basename(mzXML)

[1] "dummyiTRAQ.mzXML"

> ## reads the raw data into and MSnExp instance
> raw <- readMSData(mzXML, verbose = FALSE)
> raw

Object of class "MSnExp"
 Object size in memory: 0.2 Mb
- - - Spectra data - - -
 MS level(s): 2
 Number of MS1 acquisitions: 1
 Number of MSn scans: 5
 Number of precursor ions: 5
```

```
 4 unique MZs
 Precursor MZ's: 437.8 - 716.34
 MSn M/Z range: 100 2017
 MSn retention times: 25:1 - 25:2 minutes
- - - Processing information - - -
Data loaded: Tue Apr  9 23:05:14 2013
 MSnbase version: 1.8.0
- - - Meta data  - - -
phenoData
  rowNames: 1
  varLabels: sampleNames fileNumbers
  varMetadata: labelDescription
Loaded from:
  dummyiTRAQ.mzXML
protocolData: none
featureData
  featureNames: X1.1 X2.1 ... X5.1 (5 total)
  fvarLabels: spectrum
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'

> ## Extract a single spectrum
> raw[[3]]

Object of class "Spectrum2"
 Precursor: 645.4
 Retention time: 25:2
 Charge: 2
 MSn level: 2
 Peaks count: 2125
 Total ion count: 150838188
```

```
> plot(raw, full = TRUE)
```




```
> plot(raw[[3]], full = TRUE, reporters = iTRAQ4)
```

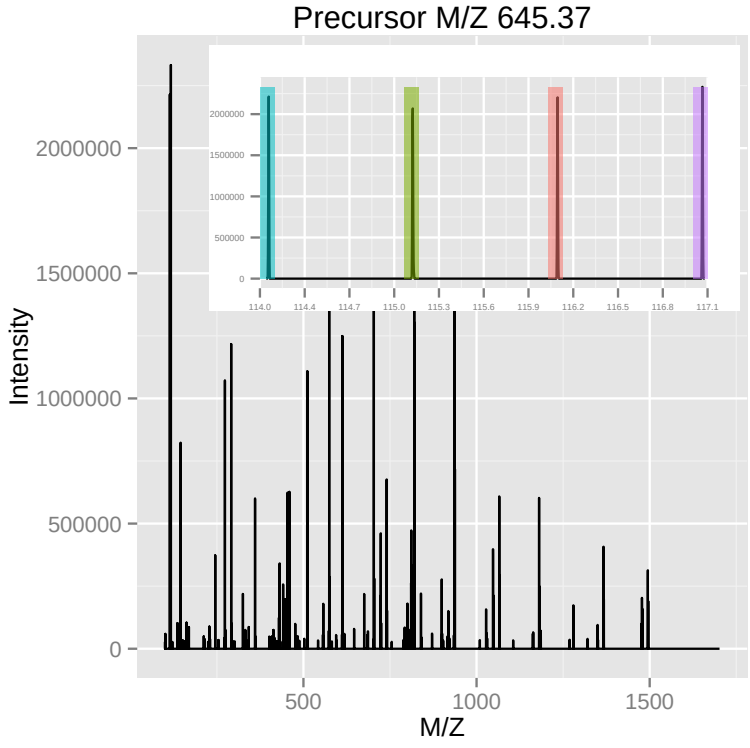


Figure 1: The `plot` method can be used on experiments, i.e. spectrum collections (left), or individual spectra (right).

3.1 mgf read/write support

Read and write support for data in the mgf[11] and mzTab[12] formats are available via the readMgfData/writeMgfData and readMzTabData/writeMzTabData functions, respectively. An example for the latter is shown in the next section.

4 Quantitative proteomics

As an running example throughout this document, we will use a TMT 6-plex data set, PXD000001 to illustrate quantitative data processing. The code chunk below first downloads this data file from the ProteomeXchange server using the getPXD000001mzTab function from the **RforProteomics** package.

4.1 The mzTab format

The first code chunk downloads the data, reads it into R and generates an MSnSet instance and then calculates protein intensities by summing the peptide quantitation data. Figure 2 illustrates the intensities for 5 proteins.

```
> ## Downloads the experiment
> mztab <- getPXD000001mzTab()
> mztab ## the mzTab file name

[1] "./F063721.dat-mztab.txt"

> ## Load mzTab peptide data
> qnt <- readMzTabData(mztab, what = "PEP")

Detected a metadata section
Detected a peptide section

> sampleNames(qnt) <- reporterNames(TMT6)
> head(exprs(qnt))

  TMT6.126 TMT6.127 TMT6.128 TMT6.129 TMT6.130 TMT6.131
1 10630132 11238708 12424917 10997763  9928972 10398534
2 11105690 12403253 13160903 12229367 11061660 10131218
3  1183431  1322371  1599088  1243715  1306602  1159064
4  5384958  5508454  6883086  6136023  5626680  5213771
5 18033537 17926487 21052620 19810368 17381162 17268329
6  9873585 10299931 11142071 10258214  9664315  9518271

> ## combine into proteins
> ## - using the 'accession' feature meta data
> ## - sum the peptide intensities
> protqnt <- combineFeatures(qnt,
+                            groupBy = fData(qnt)$accession,
+                            fun = sum)

Combined 1528 features into 404 using user-defined function
```

[11] http://www.matrixscience.com/help/data_file_help.html#GEN
[12] https://code.google.com/p/mztab/

```
> cls <- brewer.pal(5, "Set1")
> matplot(t(tail(exprs(protqnt), n = 5)), type = "b",
+         lty = 1, col = cls,
+         ylab = "Protein intensity (summed peptides)",
+         xlab = "TMT reporters")
> legend("topright", tail(featureNames(protqnt), n=5),
+        lty = 1, bty = "n", cex = .8, col = cls)
```

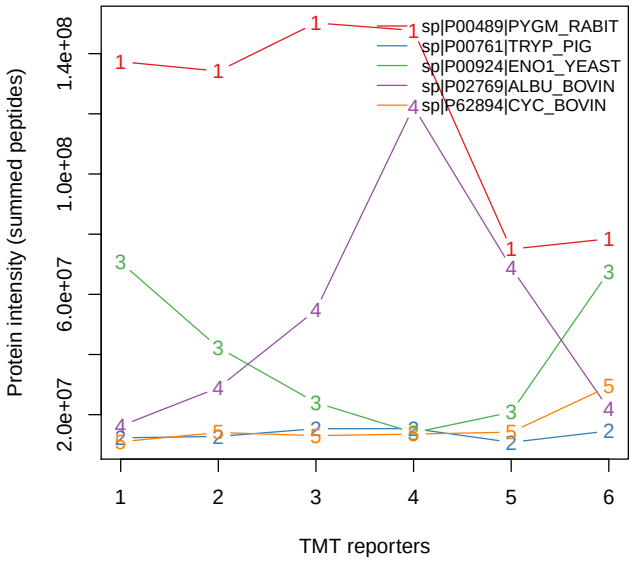


Figure 2: Protein quantitation data.

```
> qntS <- normalise(qnt, "sum")
> qntV <- normalise(qntS, "vsn")
> qntV2 <- normalise(qnt, "vsn")
>
> acc <- c("P00489", "P00924", "P02769", "P62894", "ECA")
>
> idx <- sapply(acc, grep, fData(qnt)$accession)
> idx2 <- sapply(idx, head, 3)
> small <- qntS[unlist(idx2), ]
>
> idx3 <- sapply(idx, head, 10)
> medium <- qntV[unlist(idx3), ]
>
> m <- exprs(medium)
> colnames(m) <- c("126", "127", "128", "129", "130",
+     "131")
> rownames(m) <- fData(medium)$accession
> rownames(m)[grep("CYC", rownames(m))] <- "CYT"
> rownames(m)[grep("ENO", rownames(m))] <- "ENO"
```

```
> rownames(m)[grep("ALB", rownames(m))] <- "BSA"
> rownames(m)[grep("PYGM", rownames(m))] <- "PHO"
> rownames(m)[grep("ECA", rownames(m))] <- "Background"
>
> cls <- c(brewer.pal(length(unique(rownames(m))) - 1,
+     "Set1"), "grey")
> names(cls) <- unique(rownames(m))
> wbcol <- colorRampPalette(c("white", "darkblue"))(256)
```

```
> heatmap(m, col = wbcol, RowSideColors = cls[rownames(m)])
```

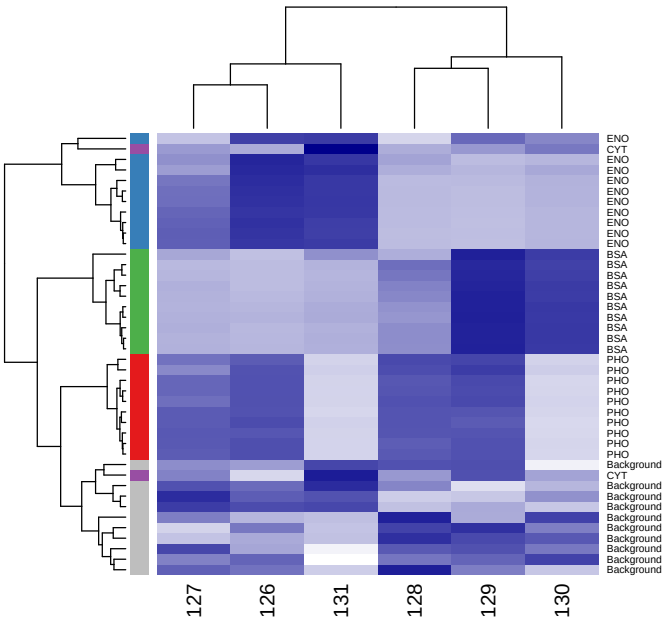


Figure 3: A heatmap.

```
> dfr <- data.frame(exprs(small),
+                   Protein = as.character(fData(small)$accession),
+                   Feature = featureNames(small),
+                   stringsAsFactors = FALSE)
> colnames(dfr) <- c("126", "127", "128", "129", "130", "131",
+                    "Protein", "Feature")
> dfr$Protein[dfr$Protein == "sp|P00924|ENO1_YEAST"] <- "ENO"
> dfr$Protein[dfr$Protein == "sp|P62894|CYC_BOVIN"]  <- "CYT"
> dfr$Protein[dfr$Protein == "sp|P02769|ALBU_BOVIN"] <- "BSA"
> dfr$Protein[dfr$Protein == "sp|P00489|PYGM_RABIT"] <- "PHO"
> dfr$Protein[grep("ECA", dfr$Protein)] <- "Background"
> dfr2 <- melt(dfr)

Using Protein, Feature as id variables

> ggplot(aes(x = variable, y = value, colour = Protein),
+        data = dfr2) +
+   geom_point() +
+   geom_line(aes(group=as.factor(Feature)), alpha = 0.5) +
+   facet_grid(. ~ Protein) + theme(legend.position="none") +
+   labs(x = "Reporters", y = "Normalised intensity")
```

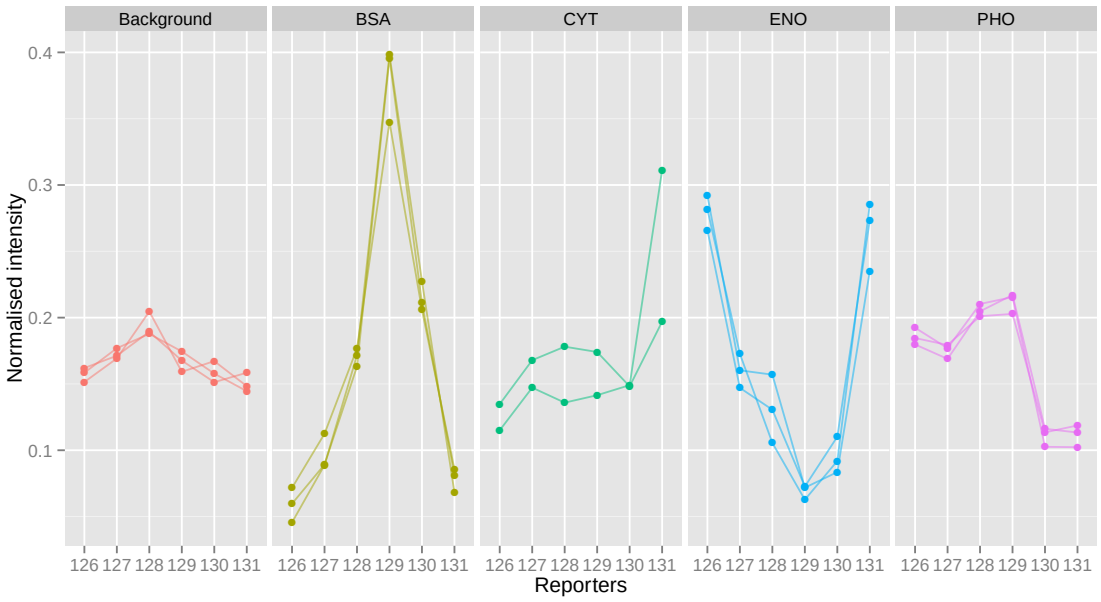


Figure 4: Spikes plot using **ggplot2**.

4.2 Working with raw data

```
> mzxml <- getPXD000001mzXML()
> rawms <- readMSData(mzxml, centroided = TRUE, verbose = FALSE)
> qntms <- quantify(rawms, reporters = TMT7, method = "max",
+     verbose = FALSE, parallel = FALSE)
>
> d <- data.frame(Signal = rowSums(exprs(qntms)[, 1:6]),
+     Incomplete = exprs(qntms)[, 7])
> d <- log(d)
> cls <- rep("#00000050", nrow(qnt))
> pch <- rep(1, nrow(qnt))
> cls[grep("P02769", fData(qnt)$accession)] <- "gold4"  ## BSA
> cls[grep("P00924", fData(qnt)$accession)] <- "dodgerblue"  ## ENO
> cls[grep("P62894", fData(qnt)$accession)] <- "springgreen4"  ## CYT
> cls[grep("P00489", fData(qnt)$accession)] <- "darkorchid2"  ## PHO
> pch[grep("P02769", fData(qnt)$accession)] <- 19
> pch[grep("P00924", fData(qnt)$accession)] <- 19
> pch[grep("P62894", fData(qnt)$accession)] <- 19
> pch[grep("P00489", fData(qnt)$accession)] <- 19
```

```
> mzp <- plotMzDelta(rawms, reporters = TMT6, verbose = FALSE) +
+     ggtitle("")

Scale for 'x' is already present. Adding another scale for 'x', which
will replace the existing scale.
```

```
> mzp
```

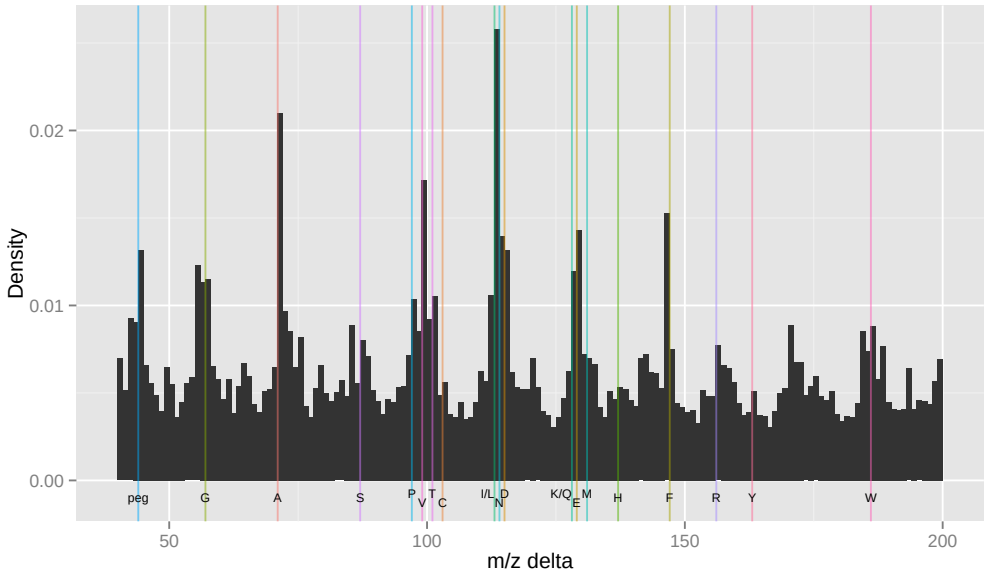


Figure 5: A m/z delta plot.

```
> plot(Signal ~ Incomplete, data = d,
+      xlab = expression(Incomplete~dissociation),
+      ylab = expression(Sum~of~reporters~intensities),
+      pch = 19,
+      col = "#4582B380")
> grid()
> abline(0, 1, lty = "dotted")
> abline(lm(Signal ~ Incomplete, data = d), col = "darkblue")
```

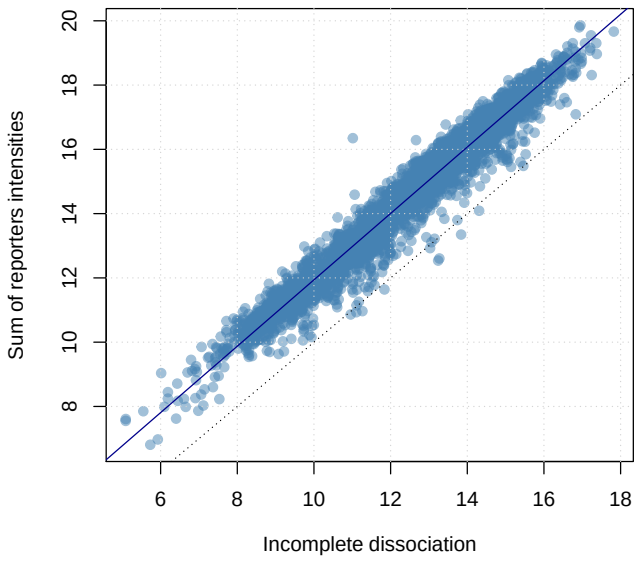


Figure 6: Incomplete dissociation.

```
> MAplot(qnt[, c(4, 2)], cex = 0.9, col = cls, pch = pch,
+     show.statistics = FALSE)
```

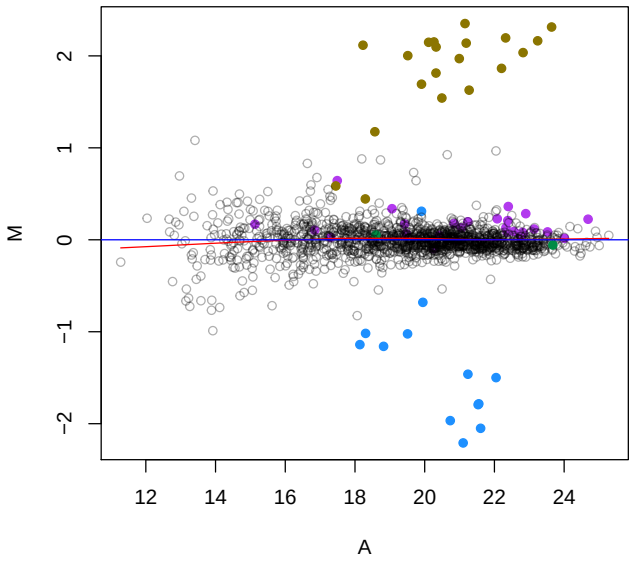


Figure 7: MAplot on an MSnSet instance.

4.3 The MALDIquant package

This section illustrates some of **MALDIquant**'s data processing capabilities [10]. The code is taken from the `processing-peaks.R` script downloaded from the package homepage[13].

Loading the data

```
> ## load packages
> library("MALDIquant")
> library("readBrukerFlexData")
> library("MALDIquantForeign")
> ## getting test data
> datapath <-
+   file.path(system.file("Examples",
+                         package = "readBrukerFlexData"),
+             "2010_05_19_Gibb_C8_A1")
> dir(datapath)

[1] "0_A1" "0_A2"

> sA1 <- importBrukerFlex(datapath)
> # in the following we use only the first spectrum
> s <- sA1[[1]]
>
> summary(mass(s))

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1000    2370    4330    4720    6870   10000

> summary(intensity(s))

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
      4     180    1560    2840    4660   32600

> head(as.matrix(s))

       mass intensity
[1,]  999.9     11278
[2,] 1000.1     11350
[3,] 1000.3     10879
[4,] 1000.5     10684
[5,] 1000.7     10740
[6,] 1000.9     10947
```

Preprocessing

[13] http://strimmerlab.org/software/maldiquant/

```
> plot(s)
```

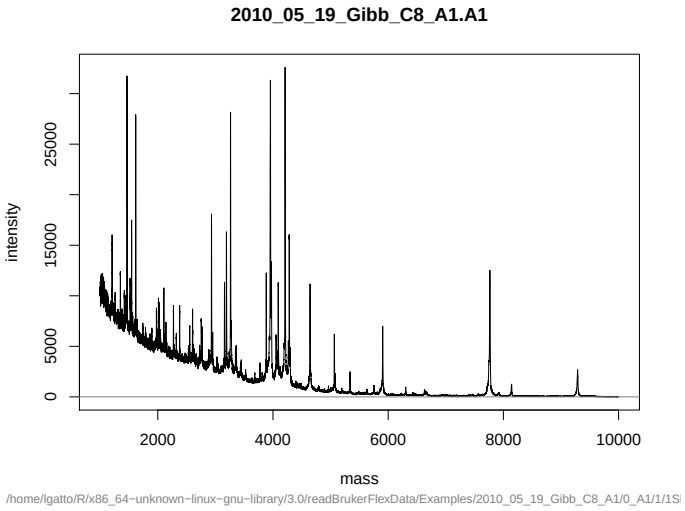


Figure 8: Spectrum plotting in **MALDIquant**.

```
> ## sqrt transform (for variance stabilization)
> s2 <- transformIntensity(s, fun = sqrt)
> s2

S4 class type            : MassSpectrum
Number of m/z values     : 22431
Range of m/z values      : 999.939 - 10001.925
Range of intensity values: 2e+00 - 1.805e+02
Name                     : 2010_05_19_Gibb_C8_A1.A1
File                     : /home/lgatto/R/x86_64-unknown-linux-gnu-library/3.0/read

>
> ## smoothing - 5 point moving average
> simpleSmooth <- function(y) {
+     return(filter(y, rep(1, 5)/5, sides = 2))
+ }
>
> s3 <- transformIntensity(s2, simpleSmooth)
> s3

S4 class type            : MassSpectrum
Number of m/z values     : 22427
Range of m/z values      : 1000.324 - 10000.705
Range of intensity values: 3.606e+00 - 1.792e+02
Name                     : 2010_05_19_Gibb_C8_A1.A1
File                     : /home/lgatto/R/x86_64-unknown-linux-gnu-library/3.0/read

> length(s2)  # 22431

[1] 22431
```

```
> length(s3)  # 22427 - at both ends data points have been removed

[1] 22427

>
> ## baseline subtraction
> s4 <- removeBaseline(s3, method = "SNIP")
> s4

S4 class type            : MassSpectrum
Number of m/z values     : 22427
Range of m/z values      : 1000.324 - 10000.705
Range of intensity values: 0e+00 - 1.414e+02
Name                     : 2010_05_19_Gibb_C8_A1.A1
File                     : /home/lgatto/R/x86_64-unknown-linux-gnu-library/3.0/read
```

Peak picking

```
> ## peak picking
> p <- detectPeaks(s4)
> length(p)  # 181

[1] 181

> peak.data <- as.matrix(p)  # extract peak information
```

```
> par(mfrow = c(2, 3))
> xl <- range(mass(s))
> # use same xlim on all plots for better
> # comparison
> plot(s, sub = "", main = "1: raw", xlim = xl)
> plot(s2, sub = "", main = "2: variance stabilisation",
+     xlim = xl)
> plot(s3, sub = "", main = "3: smoothing", xlim = xl)
> plot(s4, sub = "", main = "4: base line correction",
+     xlim = xl)
> plot(s4, sub = "", main = "5: peak detection", xlim = xl)
> points(p)
> top20 <- intensity(p) %in% sort(intensity(p), decreasing = TRUE)[1:20]
> labelPeaks(p, index = top20, underline = TRUE)
> plot(p, sub = "", main = "6: peak plot", xlim = xl)
> labelPeaks(p, index = top20, underline = TRUE)
```

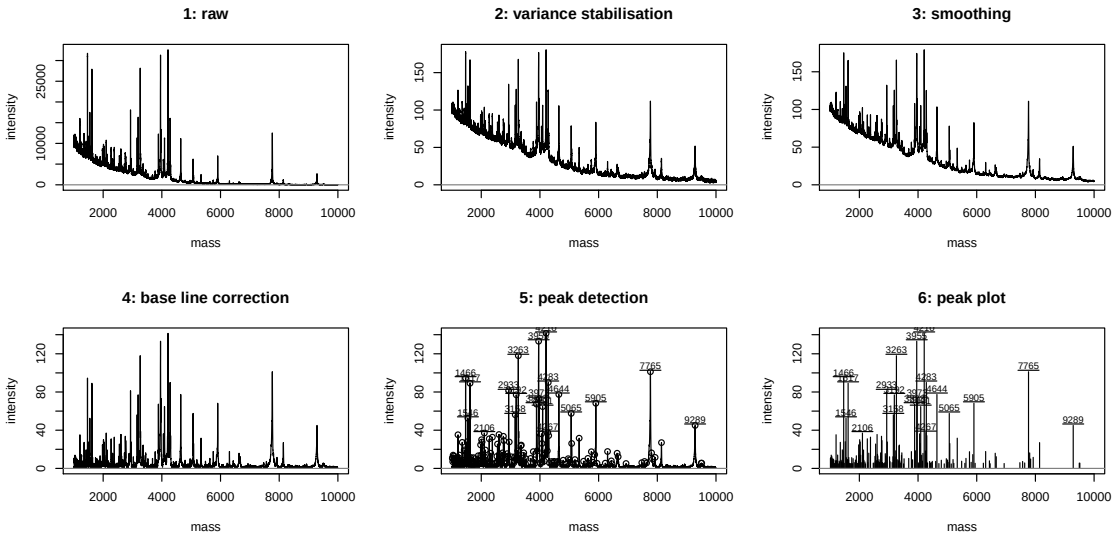


Figure 9: Spectrum plotting in **MALDIquant**.

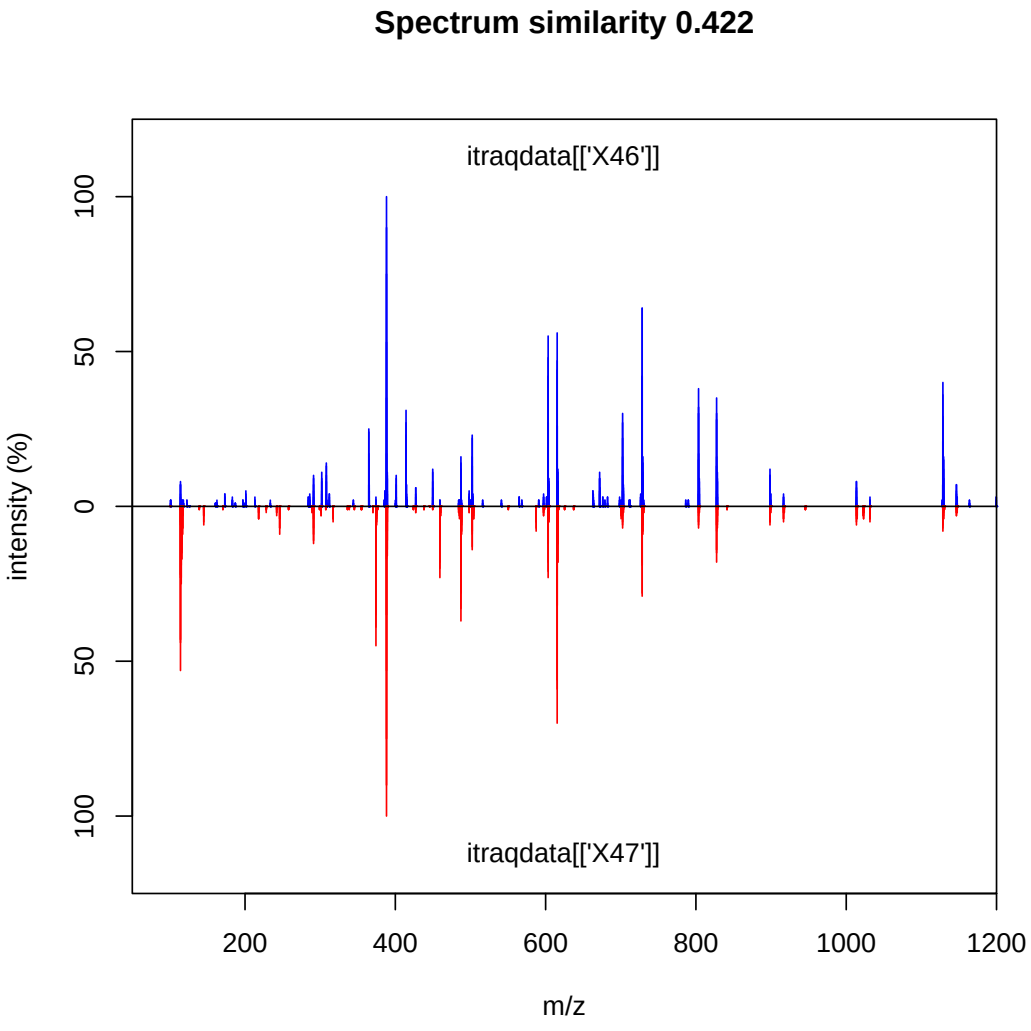
4.4 Working with peptide sequences

```
> library(IPPD)
> library(BRAIN)
> atoms <- getAtomsFromSeq("SIVPSGASTGVHEALEMR")
> unlist(atoms)

  C   H   N   O   S
 77 129  23  27   1

>
> library(Rdisop)
> pepmol <- getMolecule(paste0(names(atoms),
+                              unlist(atoms),
+                              collapse = ""))
> pepmol

$formula
[1] "C77H129N23O27S"

$score
[1] 1

$exactmass
[1] 1840

$charge
[1] 0

$parity
[1] "e"

$valid
[1] "Valid"

$DBE
[1] 25

$isotopes
$isotopes[[1]]
          [,1]      [,2]      [,3]      [,4]      [,5]
[1,] 1839.9149 1840.9177 1841.9197 1.843e+03 1.844e+03
[2,]    0.3427    0.3353    0.1961 8.474e-02 2.953e-02
          [,6]      [,7]      [,8]      [,9]     [,10]
[1,] 1.845e+03 1.846e+03 1.847e+03 1.848e+03 1.849e+03
[2,] 8.692e-03 2.226e-03 5.066e-04 1.040e-04 1.950e-05

>
```

```
> ##
> library(OrgMassSpecR)
> data(itraqdata)
>
> simplottest <-
+   itraqdata[featureNames(itraqdata) %in% paste0("X", 46:47)]
> sim <- SpectrumSimilarity(as(simplottest[[1]], "data.frame"),
+                           as(simplottest[[2]], "data.frame"),
+                           top.lab = "itraqdata[['X46']]",
+                           bottom.lab = "itraqdata[['X47']]",
+                           b = 25)
```

	mz	intensity.top	intensity.bottom
1	114.1	0	44
2	114.1	0	53
3	114.1	0	43
4	115.1	0	25
5	364.7	25	0
6	374.2	0	39
7	374.2	0	45
8	374.2	0	35
9	388.2	0	35
10	388.3	0	75
11	388.3	0	100
12	388.3	0	90
13	388.3	35	53
14	388.3	100	53
15	388.3	90	53
16	388.3	53	53
17	388.3	75	53
18	414.3	31	0
19	414.3	27	0
20	487.3	0	33
21	487.3	0	37
22	487.3	0	28
23	603.3	42	0
24	603.4	55	0
25	603.4	48	0
26	603.4	27	0
27	615.3	0	28
28	615.3	0	56
29	615.4	0	70
30	615.4	0	59
31	615.4	26	32
32	615.4	44	32
33	615.4	56	32
34	615.4	47	32
35	702.4	27	0

```
36  702.4             30                  0
37  728.4              0                 28
38  728.5             64                 29
39  728.5             64                 29
40  728.5             42                 29
41  728.5             42                 29
42  803.4             30                  0
43  803.5             38                  0
44  803.5             32                  0
45  827.5             28                  0
46  827.5             35                  0
47  827.5             30                  0
48 1128.6             36                  0
49 1128.6             40                  0
50 1128.7             29                  0

> title(main = paste("Spectrum similarity", round(sim, 3)))
```



```
>
> MonoisotopicMass(formula = list(C = 2, O = 1, H=6))

[1] 46.04

> molecule <- getMolecule("C2H5OH")
> molecule$exactmass

[1] 46.04

> ## x11()
> ## plot(t(.pepmol$isotopes[[1]]), type = "h")
>
> ## x <- IsotopicDistribution(formula = list(C = 2, O = 1, H=6))
> ## t(molecule$isotopes[[1]])
> ## par(mfrow = c(2,1))
> ## plot(t(molecule$isotopes[[1]]), type = "h")
> ## plot(x[, c(1,3)], type = "h")
>
> ## data(myo500)
> ## masses <- c(147.053, 148.056)
> ## intensities <- c(93, 5.8)
> ## molecules <- decomposeIsotopes(masses, intensities)
>
> ## experimental eno peptides
> exppep <-
+   as.character(fData(qnt[grep("ENO", fData(qnt)[, 2]), ])[, 1]) ## 13
> minlength <- min(nchar(exppep))
>
> eno <- download.file("http://www.uniprot.org/uniprot/P00924.fasta",
+                      destfile = "P00924.fasta")
> eno <- paste(readLines("P00924.fasta")[-1], collapse = "")
> enopep <- Digest(eno, missed = 1)
> nrow(enopep) ## 103

[1] 103

> sum(nchar(enopep$peptide) >= minlength) ## 68

[1] 68

> pepcnt <- enopep[enopep[, 1] %in% exppep, ]
> nrow(pepcnt) ## 13

[1] 13
```

```
> ## example code to generate an Texshade image to
> ## be included directly in a Latex document or R
```

```
> ## vignette
>
> ## seq1file <- 'seq1.tex'
> ## cat('\\begin{texshade}{Figures/P00924.fasta}
> ## \\setsize{numbering}{footnotesize}
> ## \\setsize{residues}{footnotesize}
> ## \\residuesperline*{70}
> ## \\shadingmode{functional} \\hideconsensus
> ## \\vsepspace{1mm} \\hidenames
> ## \\noblockskip\n', file = seq1file) tmp <-
> ## sapply(1:nrow(pepcnt), function(i) { col <-
> ## ifelse((i %% 2) == 0, 'Blue', 'RoyalBlue')
> ## cat('\\shaderegion{1}{', pepcnt$start[i],
> ## '..', pepcnt$stop[i], '}{White}{', col,
> ## '}\n', file = seq1file, append = TRUE) })
> ## cat('\\end{texshade} \\caption{Visualising
> ## observed peptides for the Yeast enolase
> ## protein. Peptides are shaded in blue and
> ## black. The last peptide is a mis-cleavage and
> ## overlaps with
> ## \\texttt{IEEELGDNAVFAGENFHHGDK}.}
> ## \\label{fig:seq} \\end{center}
> ## \\end{figure}\n\n', file = seq1file,
> ## append = TRUE)
```

^{15}N incorporation

```
> ## 15N example
> ## incorporation rates from 0, 0.1, ..., 0.9, 0.95, 1
> incrate <- c(seq(0, 0.9, 0.1), 0.95, 1)
> inc <- lapply(incrate, function(inc)
+               IsotopicDistributionN("YEVQGEVFTKPQLWP", inc))
> par(mfrow = c(4,3))
> for (i in 1:length(inc))
+   plot(inc[[i]][, c(1, 3)], xlim = c(1823, 1848),
+        type = "h",
+        main = paste0("15N incorporation at ", incrate[i]*100, "%"))
```

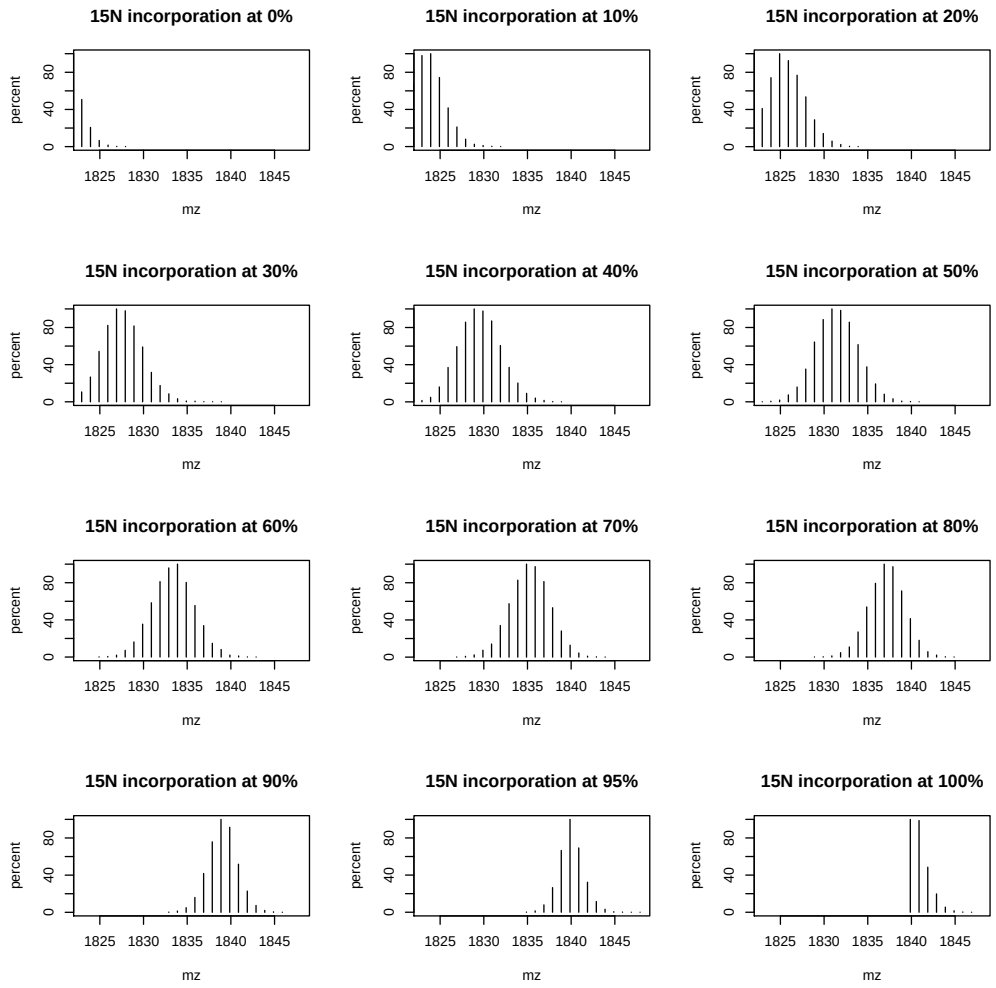


Figure 10: Isotopic envelope for the YEVQGEVFTKPQLWP peptide at different ^{15}N incorporation rates.

4.5 The isobar package

The **isobar** package [2] provides methods for the statistical analysis of isobarically tagged MS^2 experiments.

```
> library(isobar)
>
> ## Prepare the PXD000001 data for isobar analysis
> .ions <- exprs(qnt)
> .mass <- matrix(mz(TMT6), nrow(qnt), byrow=TRUE, ncol = 6)
> colnames(.ions) <- colnames(.mass) <-
+   reporterTagNames(new("TMT6plexSpectra"))
> rownames(.ions) <- rownames(.mass) <-
+   paste(fData(qnt)$accession, fData(qnt)$sequence, sep = ".")
> pgtbl <- data.frame(spectrum = rownames(.ions),
+                     peptide = fData(qnt)$sequence,
+                     modif = ":",
+                     start.pos = 1,
+                     protein = fData(qnt)$accession,
+                     accession = fData(qnt)$accession)
> x <- new("TMT6plexSpectra", pgtbl, .ions, .mass)
> featureData(x)$proteins <- as.character(fData(qnt)$accession)
>
> x <- correctIsotopeImpurities(x) ## using identity matrix here

LOG: isotopeImpurities.corrected:  TRUE

> x <- normalize(x, per.file = FALSE)

LOG: is.normalized:  TRUE
LOG: normalization.multiplicative.factor channel 126:  1.1229
LOG: normalization.multiplicative.factor channel 127:  1.0766
LOG: normalization.multiplicative.factor channel 128:  1
LOG: normalization.multiplicative.factor channel 129:  1.0537
LOG: normalization.multiplicative.factor channel 130:  1.1524
LOG: normalization.multiplicative.factor channel 131:  1.1154

> ## spikes
> spks <- c(protein.g(proteinGroup(x), "P00489"),
+           protein.g(proteinGroup(x), "P00924"),
+           protein.g(proteinGroup(x), "P02769"),
+           protein.g(proteinGroup(x), "P62894"))
>
> cls2 <- rep("#00000040", nrow(x))
> pch2 <- rep(1, nrow(x))
> cls2[grep("P02769", featureNames(x))] <- "gold4" ## BSA
> cls2[grep("P00924", featureNames(x))] <- "dodgerblue" ## ENO
> cls2[grep("P62894", featureNames(x))] <- "springgreen4" ## CYT
> cls2[grep("P00489", featureNames(x))] <- "darkorchid2" ## PHO
> pch2[grep("P02769", featureNames(x))] <- 19
```

```
> pch2[grep("P00924", featureNames(x))] <- 19
> pch2[grep("P62894", featureNames(x))] <- 19
> pch2[grep("P00489", featureNames(x))] <- 19
>
> nm <- NoiseModel(x)

[1]   0.07345 941.47896   2.82447

> ib.background <- subsetIBSpectra(x, protein=spks,
+                                  direction = "exclude")
> nm.background <- NoiseModel(ib.background)

[1] 0.01346 2.85121 0.84631

> ib.spks <- subsetIBSpectra(x, protein = spks,
+                            direction="include",
+                            specificity="reporter-specific")
> nm.spks <- NoiseModel(ib.spks, one.to.one=FALSE, pool=TRUE)

4 proteins with more than 10 spectra, taking top 50.
[1] 1.000e-10 5.829e+00 6.610e-01

>
> ratios <- 10^estimateRatio(x, nm,
+                            channel1="127", channel2="129",
+                            protein = spks,
+                            combine = FALSE)[, "lratio"]
>
> res <- estimateRatio(x, nm,
+                      channel1="127", channel2="129",
+                      protein = unique(fData(x)$proteins),
+                      combine = FALSE,
+                      sign.level = 0.01)[, c(1, 2, 6, 8)]
> res <- as.data.frame(res)
> res$lratio <- -(res$lratio)
>
> cls3 <- rep("#00000050", nrow(res))
> pch3 <- rep(1, nrow(res))
> cls3[grep("P02769", rownames(res))] <- "gold4" ## BSA
> cls3[grep("P00924", rownames(res))] <- "dodgerblue" ## ENO
> cls3[grep("P62894", rownames(res))] <- "springgreen4" ## CYT
> cls3[grep("P00489", rownames(res))] <- "darkorchid2" ## PHO
> pch3[grep("P02769", rownames(res))] <- 19
> pch3[grep("P00924", rownames(res))] <- 19
> pch3[grep("P62894", rownames(res))] <- 19
> pch3[grep("P00489", rownames(res))] <- 19
>
> rat.exp <- c(PHO = 2/2,
+              ENO = 5/1,
+              BSA = 2.5/10,
+              CYT = 1/1)
```

```
> par(mfrow = c(1, 2))
> maplot(x, noise.model = c(nm.background, nm.spks, nm),
+     channel1 = "127", channel2 = "129", pch = 19, col = cls2,
+     main = "Spectra MA plot")
> abline(h = 1, lty = "dashed", col = "grey")
> legend("topright", c("BSA", "ENO", "CYT", "PHO"), pch = 19,
+     col = c("gold4", "dodgerblue", "springgreen4",
+         "darkorchid2"), bty = "n", cex = 0.7)
> plot(res$lratio, -log10(res$p.value.rat), col = cls3,
+     pch = pch3, xlab = expression(log[10] ~ fold -
+         change), ylab = expression(-log[10] ~ p - value),
+     main = "Protein volcano plot", xlim = c(-0.7, 0.7))
> grid()
> abline(h = -log10(0.01), lty = "dotted")
> abline(v = log10(c(2, 0.5)), lty = "dotted")
> abline(v = -0.003, col = "springgreen4", lty = "dashed",
+     lwd = 2)
> abline(v = 0.003, col = "darkorchid2", lty = "dashed",
+     lwd = 2)
> abline(v = log10(5), col = "dodgerblue", lty = "dashed",
+     lwd = 2)
> abline(v = log10(0.25), col = "gold4", lty = "dashed",
+     lwd = 2)
> points(res[spks, "lratio"], -log10(res[spks, "p.value.rat"]),
+     col = c("darkorchid2", "dodgerblue", "gold4", "springgreen4"),
+     pch = 19)
```

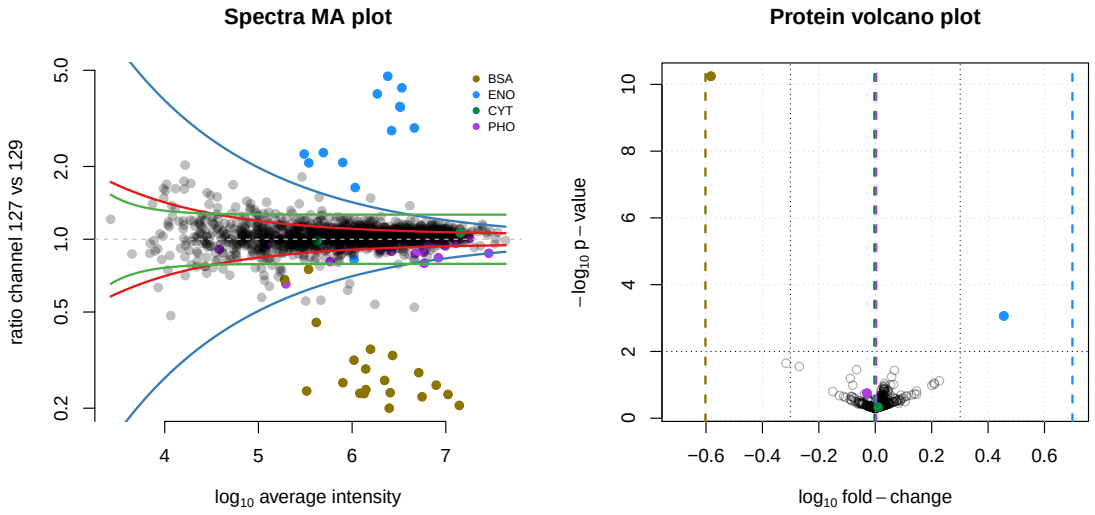


Figure 11: Result from the **isobar** pipeline.

4.6 The synapter package

The **synapter** package comes with a detailed vignette that describes how to prepare the MS^E data and then process it in R . Several interfaces are available provided the user with maximum control, easy batch processing capabilities or a graphical user interface. The conversion into MSnSet instances and filter and combination thereof as well as statistical analysis are also described.

```
> ## open the synapter vignette
> library("synapter")
> synapterGuide()
```

5 MS^2 spectra identification

A recent addition to Bioconductor 2.12 is the **rTANDEM** package, that provides a direct interface to the X!Tandem software [4]. A typical **rTANDEM** pipeline comprises

1. Prepare the input data.
2. Run the search.
3. Import the search results and extract the peptides and proteins

Using example code/data from the **rTANDEM** vignette/package, these steps are executed as described below.

5.1 Preparation of the input data

```
> library(rTANDEM)
> taxonomy <- rTTaxo(taxon = "yeast",
+                    format = "peptide",
+                    URL = system.file(
+                      "extdata/fasta/scd.fasta.pro",
+                      package="rTANDEM"))
> param <- rTParam()
> param <- setParamValue(param,
+                        'protein', 'taxon',
+                        value="yeast")
> param <- setParamValue(param, 'list path',
+                        'taxonomy information', taxonomy)
> param <- setParamValue(param,
+                        'list path', 'default parameters',
+                        value = system.file(
+                          "extdata/default_input.xml",
+                          package="rTANDEM"))
> param <- setParamValue(param, 'spectrum', 'path',
+                        value = system.file(
```

```
+                           "extdata/test_spectra.mgf",
+                           package="rTANDEM"))
> param <- setParamValue(param, 'output', 'xsl path',
+                         value = system.file(
+                           "extdata/tandem-input-style.xsl",
+                           package="rTANDEM"))
> param <- setParamValue(param, 'output', 'path',
+                         value = paste(getwd(),
+                           "output.xml", sep="/"))
```

5.2 Performing the search

The analysis is run using the tandem function (see also the rtandem function), which returns the results data file path (only the file name is displayed below).

```
> resultPath <- tandem(param)

Loading spectra
 (mgf). loaded.
Spectra matching criteria = 242
Starting threads . started.
Computing models:
testin sequences modelled = 5 ks
Model refinement:
partial cleavage ..... done.
unanticipated cleavage ..... done.
modified N-terminus ..... done.
finishing refinement ... done.
Creating report:
initial calculations  ..... done.
sorting  ..... done.
finding repeats ..... done.
evaluating results ..... done.
calculating expectations ..... done.
writing results ..... done.

Valid models = 31
Unique models = 30
Estimated false positives = 1 +/- 1

> basename(resultPath)

[1] "output.2013_04_09_23_06_03.t.xml"
```

5.3 Import and analyse results

```
> res <- GetResultsFromXML(resultPath)
> ## the inferred proteins
> proteins <- GetProteins(res, log.expect = -1.3, min.peptides = 2)
> proteins[, -(4:5), with = FALSE]

    uid expect.value   label description num.peptides
1:  576        -19.4 YCR012W     YCR012W            4
2: 2281        -14.0 YGR234W     YGR234W            3
3: 1811         -8.3 YFR053C     YFR053C            2
4:    4         -6.5 YAL005C     YAL005C            2
5: 3517         -6.5 YLL024C     YLL024C            2

> ## the identified peptides for YFR053C
> peptides <- GetPeptides(protein.uid = 1811, results = res,
+     expect = 0.05)
> peptides[, c(1:4, 9, 10:16), with = FALSE]

    pep.id prot.uid spectrum.id spectrum.mh tandem.score
1: 102.1.1     1811         102       942.5         31.9
2: 250.1.1     1811         250      1212.6         35.0
       mh   delta peak.count missed.cleavages
1:  942.5 -0.0220         NA                0
2: 1212.6  0.0079         NA                0
   start.position end.position    sequence
1:            166          173    INEGILQR
2:            437          447 DIYGWTGDASK
```

More details are provided in the vignette available with (vignette("rTANDEM")), for instance the extraction of degenerated peptides, i.e. peptides found in multiple proteins.

6 Annotation

In this section, we briefly present some Bioconductor annotation infrastructure.

We start with the **hpar** package, an interface to the *Human Protein Atlas* [13, 14], to retrieve subcellular localisation information for the ENSG00000002746 ensemble gene.

```
> id <- "ENSG00000002746"
> library("hpar")
> getHpa(id, "SubcellularLoc")

              Gene                      Main.location
24 ENSG00000002746 Nucleus but not nucleoli;Cytoplasm
   Other.location Expression.type Reliability
24                            APE        High
```

Below, we make use of the human annotation package **org.Hs.eg.db** and the Gene Ontology annotation package **GO.db** to retrieve the same information as above.

```
> library(org.Hs.eg.db)
> library(GO.db)
> ans <- select(org.Hs.eg.db, keys = id, cols = c("ENSEMBL",
+     "GO", "ONTOLOGY"), keytype = "ENSEMBL")
> ans <- ans[ans$ONTOLOGY == "CC", ]
> ans

          ENSEMBL         GO EVIDENCE ONTOLOGY
2 ENSG00000002746 GO:0005634      IDA       CC
3 ENSG00000002746 GO:0005737      IDA       CC

> sapply(as.list(GOTERM[ans$GO]), slot, "Term")

 GO:0005634  GO:0005737
  "nucleus" "cytoplasm"
```

Finally, this information can also be retrieved from on-line databases using the **biomaRt** package [6].

```
> library("biomaRt")
> ensembl <- useMart("ensembl", dataset = "hsapiens_gene_ensembl")
> efilter <- "ensembl_gene_id"
> eattr <- c("go_id", "name_1006", "namespace_1003")
> bmres <- getBM(attributes = eattr, filters = efilter,
+     values = id, mart = ensembl)
> bmres[bmres$namespace_1003 == "cellular_component",
+     "name_1006"]

[1] "nucleus"   "cytoplasm"
```

7 Other packages

7.1 Bioconductor packages

This section provides a complete list of packages available in the relevant Bioconductor version 2.13 (as of April 9, 2013) *biocView*[14] categories. Tables 1, 2 and 3 represent the packages for the `Proteomics` (35 packages), `MassSpectrometry` (21 packages) and `MassSpectrometryData` (6 experiment packages) categories.

Package	Title
ASEB	Predict Acetylated Lysine Sites
BRAIN	Baffling Recursive Algorithm for Isotope distributioN calculations
CellNOptR	Training of boolean logic models of signalling networks using prior knowledge networks and perturbation data.
ChemmineR	Cheminformatics of Drug-like Small Molecule Data
cisPath	Visualization of the Shortest Functional Paths between Proteins.
clippda	A package for the clinical proteomic profiling data analysis
CNORdt	Add-on to CellNOptR: Discretized time treatments
CNORfeeder	Integration of CellNOptR to add missing links
CNORode	ODE add-on to CellNOptR
deltaGseg	deltaGseg
eiR	Accelerated similarity searching of small molecules
fmcsR	Flexible Maximum Common Substructure (FMCS) Searching
GraphPAC	Identification of Mutational Clusters in Proteins via a Graph Theoretical Approach.
hpar	Human Protein Atlas in R
iPAC	Identification of Protein Amino acid Clustering
IPPD	Isotopic peak pattern deconvolution for Protein Mass Spectrometry by template matching
isobar	Analysis and quantitation of isobarically tagged MSMS proteomics data
LPEadj	A correction of the local pooled error (LPE) method to replace the asymptotic variance adjustment with an unbiased adjustment based on sample size.
MassSpecWavelet	Mass spectrum processing by wavelet-based algorithms
MSnbase	MSnbase: Base Functions and Classes for MS-based Proteomics
mzR	parser for netCDF, mzXML, mzData and mzML files (mass spectrometry data)
PAnnBuilder	Protein annotation data package builder
pathview	a tool set for pathway based data integration and visualization
PCpheno	Phenotypes and cellular organizational units
plgem	Detect differential expression in microarray and proteomics datasets with the Power Law Global Error Model (PLGEM)
PLPE	Local Pooled Error Test for Differential Expression with Paired High-throughput Data
ppiStats	Protein-Protein Interaction Statistical Package
PROcess	Ciphergen SELDI-TOF Processing
procoil	Prediction of Oligomerization of Coiled Coil Proteins
RCASPAR	A package for survival time prediction based on a piecewise baseline hazard Cox regression model.
RpsiXML	R interface to PSI-MI 2.5 files
rTANDEM	Encapsulate X!Tandem in R.
ScISI	In Silico Interactome
SLGI	Synthetic Lethal Genetic Interaction
synapter	Label-free data analysis pipeline for optimal identification and quantitation

Table 1: Packages available under the `Proteomics` *biocViews* category.

7.2 The Chemometrics and Computational Physics CRAN Task View

The CRAN task view on Chemometrics and Computational Physics[15] lists 67 packages, including a set of packages for mass spectrometry and proteomics, some of which are illustrated in this document. The most relevant (non Bioconductor) packages are summarised below.

[14] http://www.bioconductor.org/packages/devel/BiocViews.html
[15] http://cran.r-project.org/web/views/ChemPhys.html

Package	Title
apComplex	Estimate protein complex membership using AP-MS protein data
BRAIN	Baffling Recursive Algorithm for Isotope distributioN calculations
CAMERA	Collection of annotation related methods for mass spectrometry data
flagme	Analysis of Metabolomics GC/MS Data
gaga	GaGa hierarchical model for high-throughput data analysis
iontree	Data management and analysis of ion trees from ion-trap mass spectrometry
isobar	Analysis and quantitation of isobarically tagged MSMS proteomics data
MassArray	Analytical Tools for MassArray Data
MassSpecWavelet	Mass spectrum processing by wavelet-based algorithms
MSnbase	MSnbase: Base Functions and Classes for MS-based Proteomics
mzR	parser for netCDF, mzXML, mzData and mzML files (mass spectrometry data)
PAPi	Predict metabolic pathway activity based on metabolomics data
PROcess	Ciphergen SELDI-TOF Processing
Rdisop	Decomposition of Isotopic Patterns
Risa	Converting experimental metadata from ISA-tab into Bioconductor data structures
RMassBank	Workflow to process tandem MS files and build MassBank records
rols	An R interface to the Ontology Lookup Service
rTANDEM	Encapsulate X!Tandem in R.
synapter	Label-free data analysis pipeline for optimal identification and quantitation
TargetSearch	A package for the analysis of GC-MS metabolite profiling data.
xcms	LC/MS and GC/MS Data Analysis

Table 2: Packages available under the `MassSpectrometry` *biocViews* category.

Package	Title
faahKO	Saghatelian et al. (2004) FAAH knockout LC/MS data
gcspikelite	Spike-in data for GC/MS data and methods within flagme
msdata	Various Mass Spectrometry raw data example files
RforProteomics	Companion package to the 'Using R and Bioconductor for proteomics data analysis' publication
RMassBankData	Test dataset for RMassBank
synapterdata	Data accompanying the synapter package

Table 3: Experimental Packages available under the `MassSpectrometryData` *biocViews* category.

MALDIquant provides tools for quantitative analysis of MALDI-TOF mass spectrometry data, with support for baseline correction, peak detection and plotting of mass spectra (http://cran.r-project.org/web/packages/MALDIquant/index.html).

OrgMassSpecR is for organic/biological mass spectrometry, with a focus on graphical display, quantification using stable isotope dilution, and protein hydrogen/deuterium exchange experiments (http://cran.r-project.org/web/packages/OrgMassSpecR/index.html).

FTICRMS provides functions for Analyzing Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry Data (http://cran.r-project.org/web/packages/FTICRMS/index.html).

titan provides a GUI to analyze mass spectrometric data on the relative abundance of two substances from a titration series (http://cran.r-project.org/web/packages/titan/index.html).

7.3 Other CRAN packages

Finally, **digeR**[16], which is available on CRAN but not listed in the Chemometrics and Computational Physics Task View, provides a GUI interface for analysing 2D DIGE data.

[16] http://cran.r-project.org/web/packages/digeR/index.html

It allows to perform correlation analysis, score plot, classification, feature selection and power analysis for 2D DIGE experiment data.

Suggestions for additional R packages are welcome and will be added to the vignette. Please send suggestions and possibly a short description and/or a example utilisation with code to lg390@cam.ac.uk. The only requirement is that the package must be available on an official package channel (CRAN, Bioconductor, R-forge, Omegahat), i.e. not only available through a personal web page.

8 Session information

All software and respective versions used in this document, as returned by `sessionInfo()` are detailed below.

- R version 3.0.0 Patched (2013-04-05 r62500), `x86_64-unknown-linux-gnu`
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, utils
- Other packages: AnnotationDbi 1.22.1, Biobase 2.20.0, BiocGenerics 0.6.0, biomaRt 2.16.0, Biostrings 2.28.0, bitops 1.0-5, BRAIN 1.6.0, data.table 1.8.8, DBI 0.2-5, digest 0.6.3, ggplot2 0.9.3.1, GO.db 2.9.0, hpar 1.2.0, IPPD 1.8.0, IRanges 1.18.0, isobar 1.6.0, knitr 1.1, lattice 0.20-15, MALDIquant 1.6, MALDIquantForeign 0.3, MASS 7.3-26, Matrix 1.0-12, msdata 0.1.13, MSnbase 1.8.0, mzR 1.6.0, org.Hs.eg.db 2.9.0, OrgMassSpecR 0.3-12, plyr 1.8, PolynomF 0.94, RColorBrewer 1.0-5, Rcpp 0.10.3, RcppClassic 0.9.3, Rdisop 1.20.0, readBrukerFlexData 1.6.2, reshape2 1.2.2, RforProteomics 1.0.0, rols 1.2.0, RSQLite 0.11.2, rTANDEM 1.0.0, XML 3.96-1.1, xtable 1.7-1
- Loaded via a namespace (and not attached): affy 1.38.0, affyio 1.28.0, base64enc 0.1-1, BiocInstaller 1.10.0, codetools 0.2-8, colorspace 1.2-1, dichromat 2.0-0, distr 2.4, downloader 0.2.2, evaluate 0.4.3, formatR 0.7, grid 3.0.0, gtable 0.1.2, impute 1.34.0, labeling 0.1, limma 3.16.1, munsell 0.4, preprocessCore 1.22.0, proto 0.3-10, RCurl 1.95-4.1, readMzXmlData 2.6, R.methodsS3 1.4.2, R.oo 1.13.0, R.utils 1.23.2, scales 0.2.3, sfsmisc 1.0-23, SSOAP 0.8-0, startupmsg 0.8, stats4 3.0.0, stringr 0.6.2, tools 3.0.0, vsn 3.28.0, XMLSchema 0.7-2, zlibbioc 1.6.0

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