

Mass spectrometry-based proteomics

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Biological information flow

There are three main biological entities that respectively store information, act as data intermediates, and the functional units, and the figure below show how information flows between these three levels.

DNA, that lives in the nucleus of cells, is the central information storage mechanism, and encodes the blueprint of the functional units as genes. DNA is **transcribed** into **messenger RNA (mRNA)**, that re-localises outside the nucleus and is further processed into its mature *exon-only* form after removal of the non-coding *introns* sequences. Finally, the mRNA is translated by the ribosomal machinery into **proteins** directly into the endoplasmic reticulum (ER) where they are then redirected to their final destination.

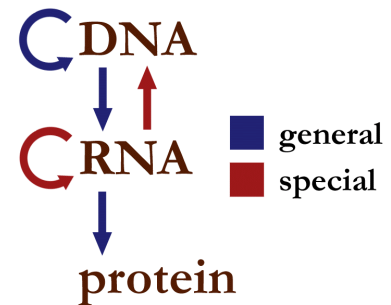


Figure 1: Information flow in biological systems (Source *Central dogma of biology* on Wikipedia).

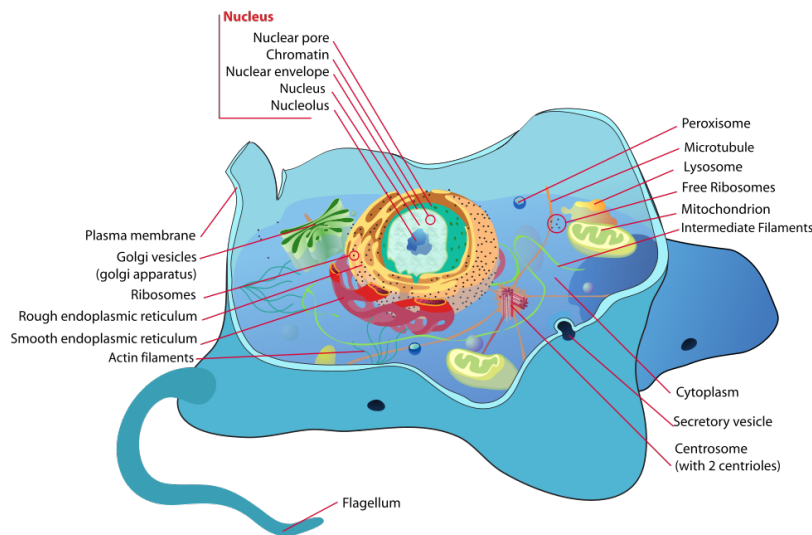


Figure 2: Sub-cellular structure of an animal cell (Source *Cell biology* on Wikipedia).

In addition to the standard information workflow where DNA is transcribed into RNA that itself is translated into proteins, information flow, there is also reverse transcription, that generates (comple-

mentary) DNA from and RNA molecule, as well as replication of DNA (during cell division) and RNA molecules.

Why studying proteins

Proteins as the functional units in all living organisms, and they are highly dynamic. The caterpillar and the resulting butterfly have the same genome. The complement of all the expressed proteins, termed the proteome is however very different.



Figure 3: The metamorphosis from a caterpillar to a monarch butterfly. (Image from Phys.prg)

There are different modalities of the proteome that are of interest. In addition to the presence or amount of protein in a biological samples, it is also important to study the interactions between proteins forming protein-protein complexes, the presence of post-transcriptional modification (such as, for example, phosphorylations), the rate at which proteins are produced and degraded, or where the proteins reside inside a cell.

The technique of choice to study proteins in a high throughput way is *mass spectrometry*.

Setup

We are going to use the Bioconductor (Huber et al. 2015) MSnbase package (L. Gatto and Lilley 2012), which can be install with the BiocManager package, available from CRAN. If BiocManager isn't available on your computer, install it with:

```
install.packages("BiocManager")
```

Now, install MSnbase and its dependencies with

```
BiocManager::install("MSnbase")
```

For additional information on how to analyse mass spectrometry-based proteomics data, refer to (Gatto and Christoforou 2014) and (L. Gatto 2019), or explore the the proteomics- and mass spectrometry-related packages on the Bioconductor page



Figure 4: The 'MSnbase' package.

How does mass spectrometry work?

Mass spectrometry (MS) is a technology that *separates* charged molecules (ions) based on their mass to charge ratio (M/Z). It is often coupled to chromatography (liquid LC, but can also be gas-based GC). The time an analyte takes to elute from the chromatography column is the *retention time*.

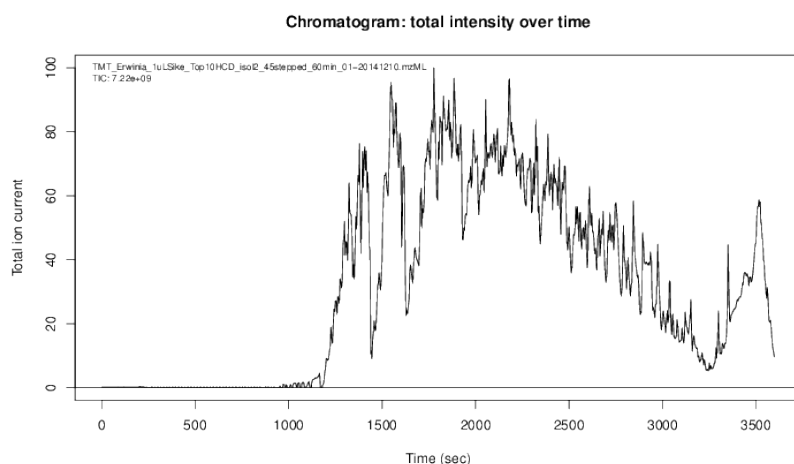


Figure 5: A chromatogram, illustrating the total amount of analytes over the retention time.

An mass spectrometer is composed of three components:

1. The *source*, that ionises the molecules: examples are Matrix-assisted laser desorption/ionisation (MALDI) or electrospray ionisation. (ESI)
2. The *analyser*, that separates the ions: Time of flight (TOF) or Orbitrap.
3. The *detector* that quantifies the ions.

When using mass spectrometry for proteomics, the proteins are first digested with a protease such as trypsin. In mass shotgun proteomics, the analytes assayed in the mass spectrometer are peptides.

Often, ions are subjected to more than a single MS round. After a first round of separation, the peaks in the spectra, called MS₁ spectra, represent peptides. At this stage, the only information we possess about these peptides are their retention time and their mass-to-charge (we can also infer their charge by inspecting their isotopic envelope, i.e. the peaks of the individual isotopes, see below), which is not enough to infer their identity (i.e. their sequence).

In MSMS (or MS₂), the settings of the mass spectrometer are set automatically to select a certain number of MS₁ peaks (for example 20). Once a narrow M/Z range has been selected (corresponding to

one high-intensity peak, a peptide, and some background noise), it is fragmented (using for example collision-induced dissociation (CID), higher energy collisional dissociation (HCD) or electron-transfer dissociation (ETD)). The fragment ions are then themselves separated in the analyser to produce a MS2 spectrum. The unique fragment ion pattern can then be used to infer the peptide sequence using de novo sequencing (when the spectrum is of high enough quality) or using a search engine such as, for example Mascot, MSGF+, ..., that will match the observed, experimental spectrum to theoretical spectra (see details below).

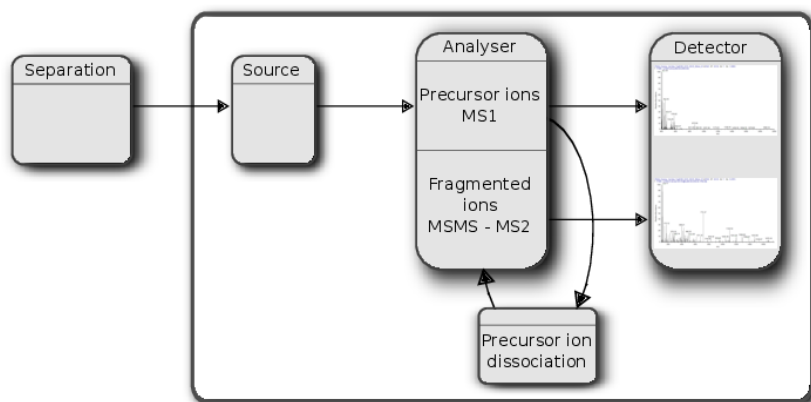


Figure 6: Schematics of a mass spectrometer and two rounds of MS.

The animation below show how 25 ions different ions (i.e. having different M/Z values) are separated throughout the MS analysis and are eventually detected (i.e. quantified). The final frame shows the hypothetical spectrum.

The figures below illustrate the two rounds of MS. The spectrum on the left is an MS1 spectrum acquired after 21 minutes and 3 seconds of elution. 10 peaks, highlighted by dotted vertical lines, were selected for MS2 analysis. The peak at M/Z 460.79 (488.8) is highlighted by a red (orange) vertical line on the MS1 spectrum and the fragment spectra are shown on the MS2 spectrum on the top (bottom) right figure.

The figures below represent the 3 dimensions of MS data: a set of spectra (M/Z and intensity) of retention time, as well as the interleaved nature of MS1 and MS2 (and there could be more levels) data.

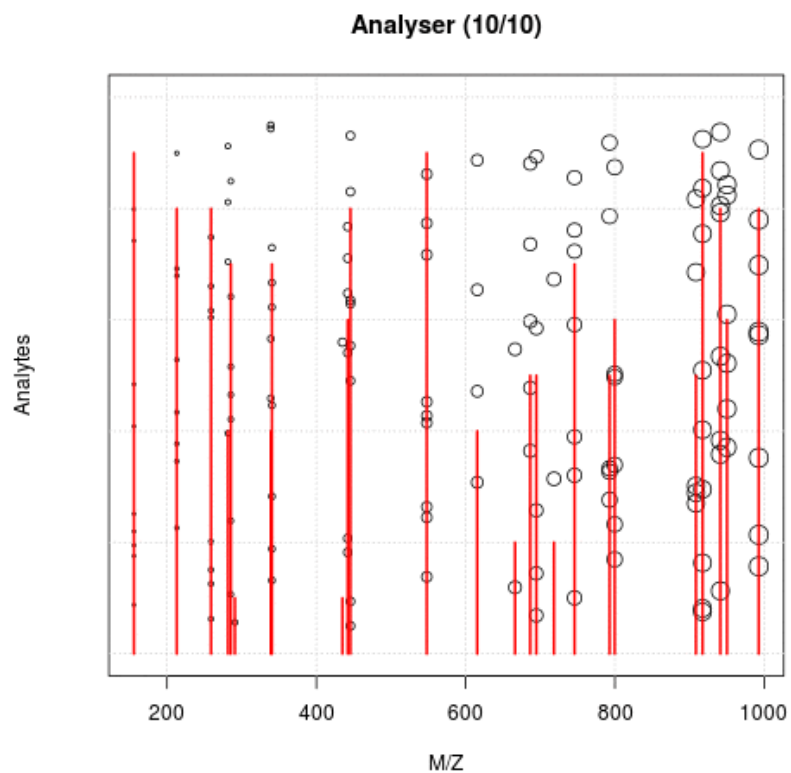


Figure 7: Separation and detection of ions in a mass spectrometer.

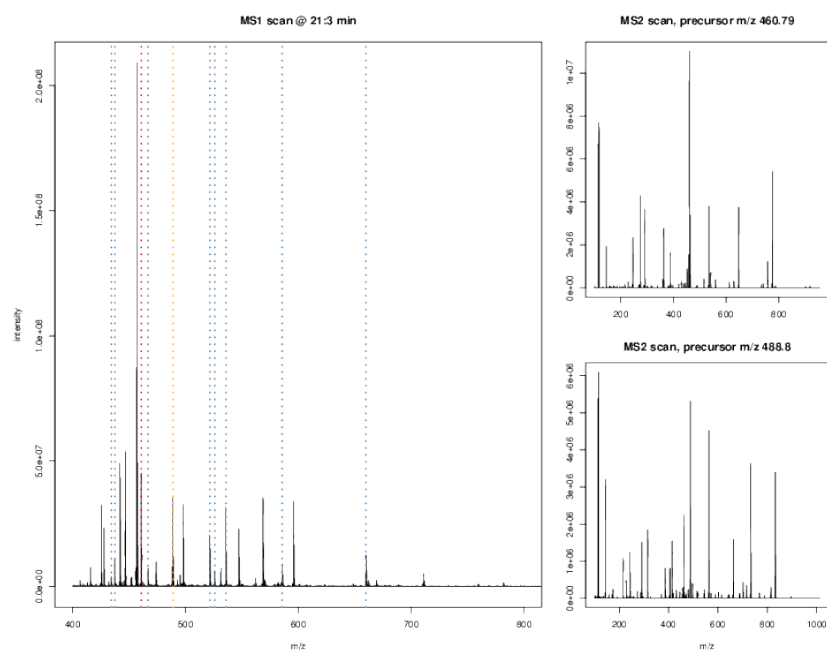


Figure 8: Parent ions in the MS1 spectrum (left) and two sected fragment ions MS2 spectra (right).

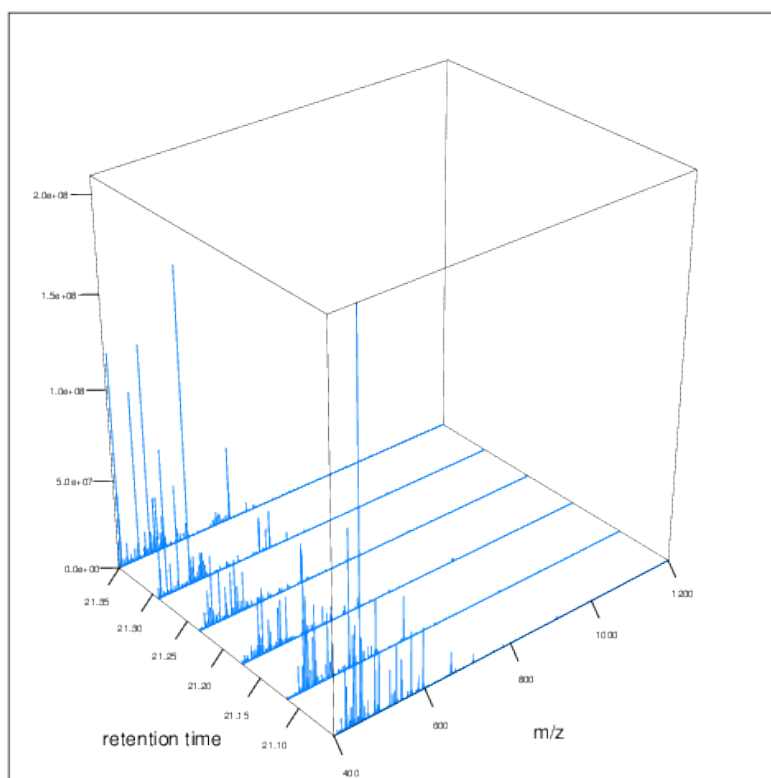


Figure 9: MS1 spectra over retention time.

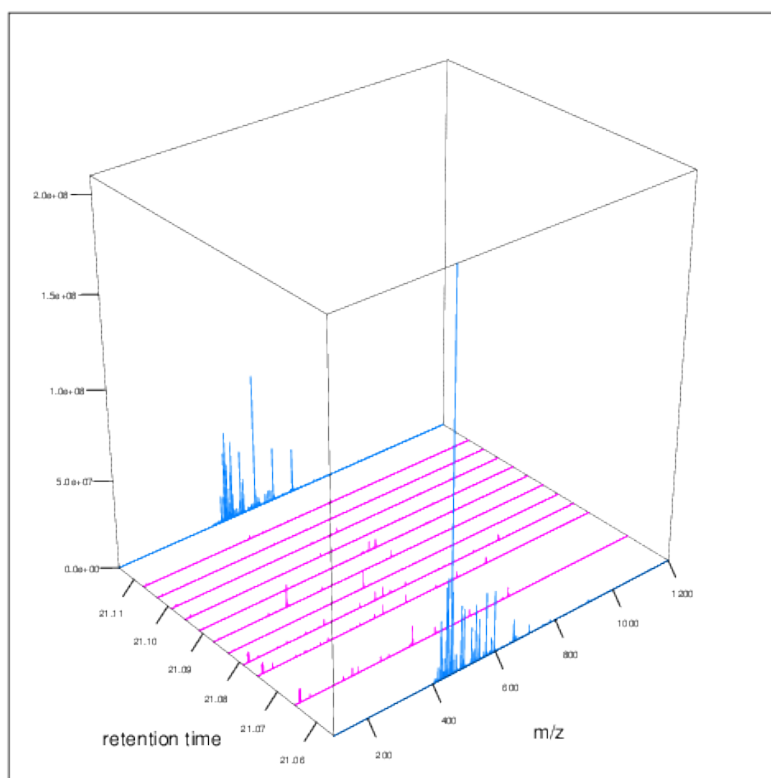


Figure 10: MS2 spectra interleaved between two MS1 spectra.

Practical: reading and accessing MS data

Let's read a very small raw MS data file into R using the `readMSData` from the `MSnbase` package. The file that we are going to load is also available in the package.

1. Load the `MSnbase` package

```
library("MSnbase")
```

2. Get the path to the `dummyiTRAQ.mzXML` file

```
rawf <- dir(system.file(package = "MSnbase", dir = "extdata"),
  full.name = TRUE, pattern = "mzXML$")
basename(rawf)
```

```
## [1] "dummyiTRAQ.mzXML"
```

3. Read it in using the `readMSData` function.

```
x <- readMSData(rawf)
x

## MSn experiment data ("MSnExp")
## Object size in memory: 0.18 Mb
## - - - Spectra data - - -
## MS level(s): 2
## Number of spectra: 5
## MSn retention times: 25:1 - 25:2 minutes
## - - - Processing information - - -
## Data loaded: Sun Mar 24 19:25:23 2019
## MSnbase version: 2.9.3
## - - - Meta data - - -
## phenoData
##   rowNames: dummyiTRAQ.mzXML
##   varLabels: sampleNames
##   varMetadata: labelDescription
## Loaded from:
##   dummyiTRAQ.mzXML
## protocolData: none
## featureData
##   featureNames: F1.S1 F1.S2 ... F1.S5
##   (5 total)
##   fvarLabels: spectrum
##   fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
```


The object that is returned by `readMSData` is of class `MSnExp`, that can store, access and manipulate raw MS data. Note that here we are focusing on MS-based proteomics data, but this also applied to MS-based metabolomics data.

```
class(x)
```

```
## [1] "MSnExp"
## attr(,"package")
## [1] "MSnbase"
```

4. We can find out how many spectra are available in that data using the function `length`. Full MS acquisitions would contain hundreds of thousands spectra.

```
length(x)
```

```
## [1] 5
```

5. We can use various accessor function to get the MS level of these spectra, their retention time, or the M/Z and intensity of the precursor peaks of the ion corresponding to the MS2 spectra.

```
msLevel(x)
```

```
## F1.S1 F1.S2 F1.S3 F1.S4 F1.S5
##      2      2      2      2      2
```

```
rtime(x)
```

```
## F1.S1 F1.S2 F1.S3 F1.S4 F1.S5
## 1501.35 1501.59 1501.85 1502.07 1502.31
```

```
precursorMz(x)
```

```
## F1.S1 F1.S2 F1.S3 F1.S4 F1.S5
## 645.3741 546.9586 645.3741 716.3405 437.8040
```

```
precursorIntensity(x)
```

```
## F1.S1 F1.S2 F1.S3 F1.S4 F1.S5
## 47659400 26356100 23432400 24854800 7052960
```

6. We can also extract individual spectra using `[]` and plot them.

```
x[[3]]
```

```
## Object of class "Spectrum2"
## Precursor: 645.3741
## Retention time: 25:2
## Charge: 2
## MSn level: 2
## Peaks count: 2125
## Total ion count: 150838188
```

```
plot(x[[3]])
```

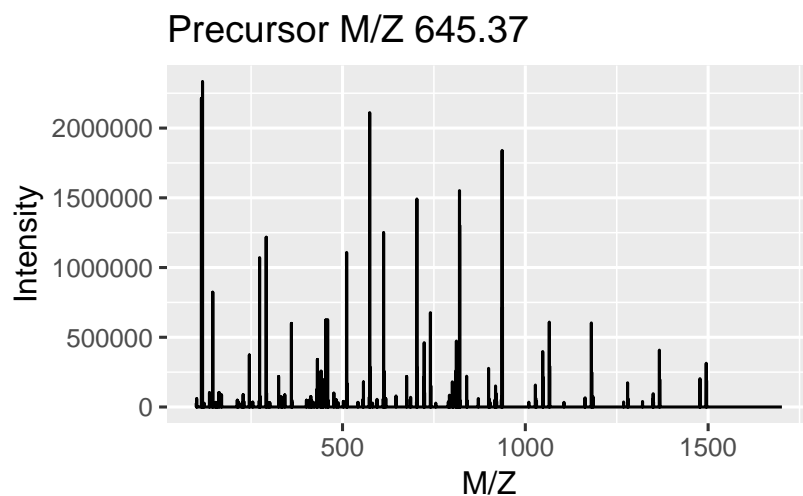


Figure 11: Visualisation of the 3rd MS spectrum in our small test data set.

Exercise

For the rest of this tutorial, we will be using a slightly larger dataset (still tiny compared to full acquisitions) that is distributed with the MSnbase package. Load it as shown below and compute the number of spectra available in that dataset, their MS level, and the retention time range over which these spectra have been acquired.

```
data(itraqdata)

length(itraqdata)

## [1] 55

unique(msLevel(itraqdata))

## [1] 2

formatRt(range(rtime(itraqdata)))

## [1] "19:9" "50:18"
```

This object also contains additional metadata for each spectrum, that can be accessed, as a `data.frame`, with `fData`.

Identification

The raw data is still a long way of obtaining biologically relevant proteomics data. The first step to obtain proteomics data is to identify the peptides that have been acquired in the MS. Peptide identification work by comparing expected and observed spectra. As shown below, when a precursor peptide ion is fragmented in a CID cell, it breaks at specific bonds, producing sets of peaks (*a*, *b*, *c* and *x*, *y*, *z*) that can be predicted.

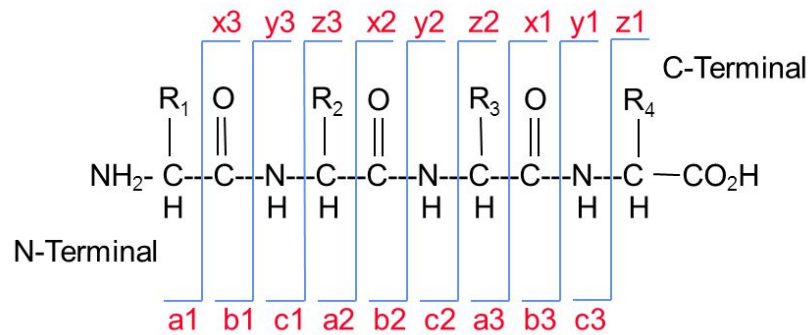


Figure 12: Peptide fragmentation.

Biemann, K *Methods Enzymol* (1990) **193** 886-887

It is thus possible to calculate the expected set of fragment peaks for a given peptide, such as *SIGFEGDSIGR* below.

`calculateFragments("SIGFEGDSIGR")`

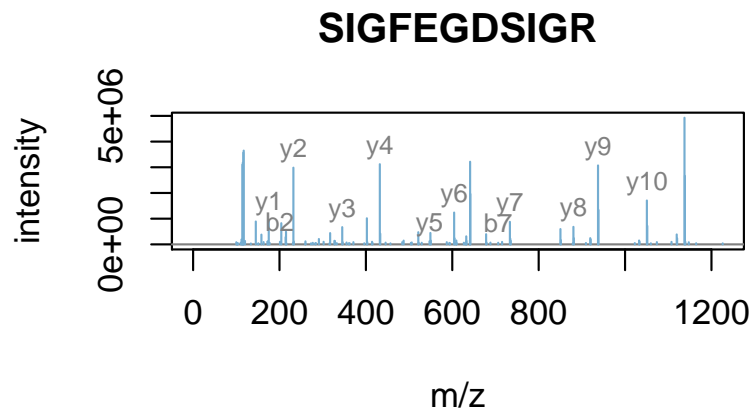
##	mz	ion	type	pos	z	seq
## 1	88.03931	b1	b	1	1	S
## 2	201.12337	b2	b	2	1	SI
## 3	258.14483	b3	b	3	1	SIG
## 4	405.21324	b4	b	4	1	SIGF
## 5	534.25583	b5	b	5	1	SIGFE
## 6	591.27729	b6	b	6	1	SIGFEG
## 7	706.30423	b7	b	7	1	SIGFEGD
## 8	793.33626	b8	b	8	1	SIGFEGDS
## 9	906.42032	b9	b	9	1	SIGFEGDSI
## 10	963.44178	b10	b	10	1	SIGFEGDSIG
## 11	175.11895	y1	y	1	1	R
## 12	232.14041	y2	y	2	1	GR
## 13	345.22447	y3	y	3	1	IGR
## 14	432.25650	y4	y	4	1	SIGR

```
## 15 547.28344 y5 y 5 1 DSIGR
## 16 604.30490 y6 y 6 1 GDSIGR
## 17 733.34749 y7 y 7 1 EGDSIGR
## 18 880.41590 y8 y 8 1 FEGDSIGR
## 19 937.43736 y9 y 9 1 GFEGDSIGR
## 20 1050.52142 y10 y 10 1 IGFEFDSIGR
## 21 873.42266 b9_ b_ 9 1 SIGFEFDSI
## 22 930.44412 b10_ b_ 10 1 SIGFEFDSIG
## 23 514.28579 y5_ y_ 5 1 DSIGR
## 24 571.30725 y6_ y_ 6 1 GDSIGR
## 25 700.34984 y7_ y_ 7 1 EGDSIGR
## 26 847.41825 y8_ y_ 8 1 FEGDSIGR
## 27 904.43971 y9_ y_ 9 1 GFEGDSIGR
## 28 1017.52377 y10_ y_ 10 1 IGFEFDSIGR
## 29 142.12130 y1_ y_ 1 1 R
## 30 199.14276 y2_ y_ 2 1 GR
## 31 312.22682 y3_ y_ 3 1 IGR
## 32 399.25885 y4_ y_ 4 1 SIGR
```

The last step is to compare observed and expected peaks. If there is a good match, the MS2 spectrum is assigned the peptide sequence.

```
itraqdata2 <- pickPeaks(itraqdata, verbose = FALSE)
s <- "SIGFEFDSIGR"
plot(itraqdata2[[14]], s, main = s)
```

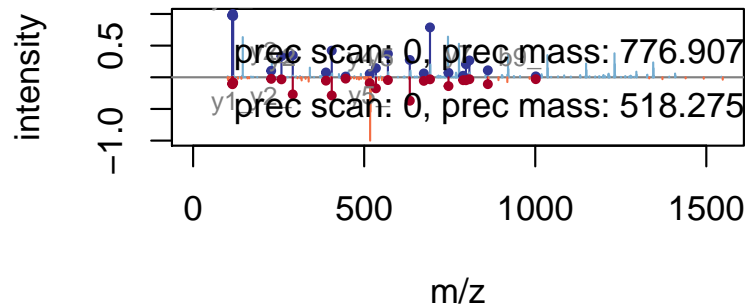
Figure 13: Matching observed and expected peaks.



It is also possible to plot 2 spectra to compare them directly.

```
plot(itraqdata2[[25]], itraqdata2[[28]], sequences = rep("IMIDLDGTENK",
2))
```

Figure 14: Direct comparison of 2 MS2 spectra.



In a full experiment, all possible peptides from the known (or relevant) proteome of interest (such as databases that can be downloaded from the UniProt site¹) are compared to the millions of observed spectra.

From the list of identified peptides, it is then necessary to infer the most probable proteins that were present in the biological sample.

¹ The Universal Protein Resource (UniProt) is a freely and accessible comprehensive resource for protein sequence and annotation data.

Exercise

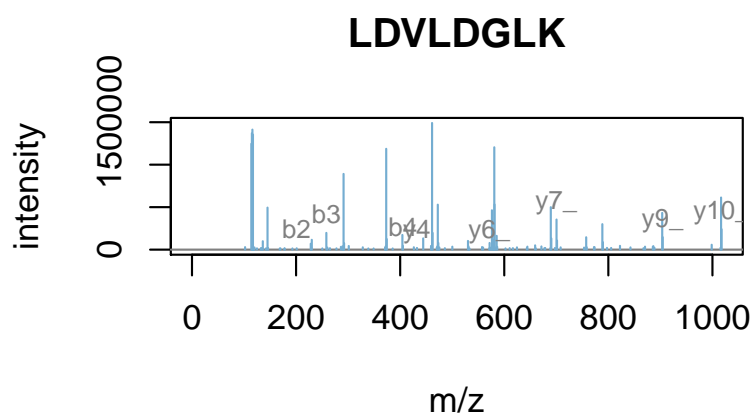
Plot the 44th spectrum of the `itraqdata2` experiment. The sequence can be accessed in the feature metadata with

```
fData(itraqdata2)$PeptideSequence[[44]]
```

```
## [1] LDVLDGLK
```

```
## 47 Levels: AADALLLK ... VVVVEGSK
```

```
plot(itraqdata2[[44]], s, main = fData(itraqdata2)$PeptideSequence[[44]])
```



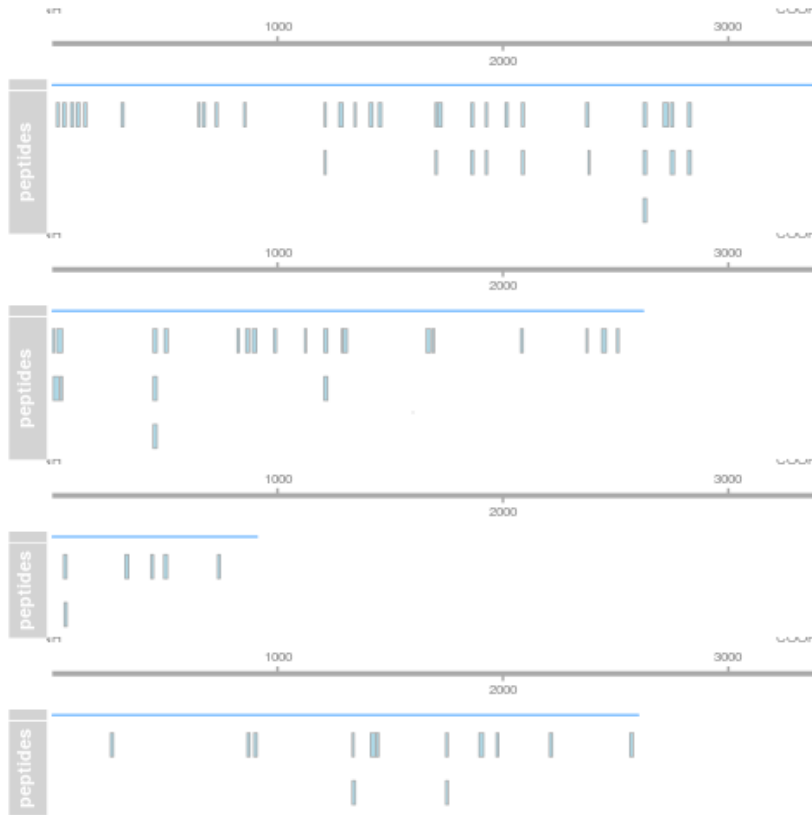
Quantitation

The last step of MS data processing is to quantify peptide abundances in the biological samples. The table below summarises the different possibilities depending whether the proteins or peptides are labelled, and whether the quantitation is performed in MS₁ or MS₂.

	Label-free	Labelled
MS ₁	XIC	SILAC, ¹⁵ N
MS ₂	Counting	iTRAQ, TMT

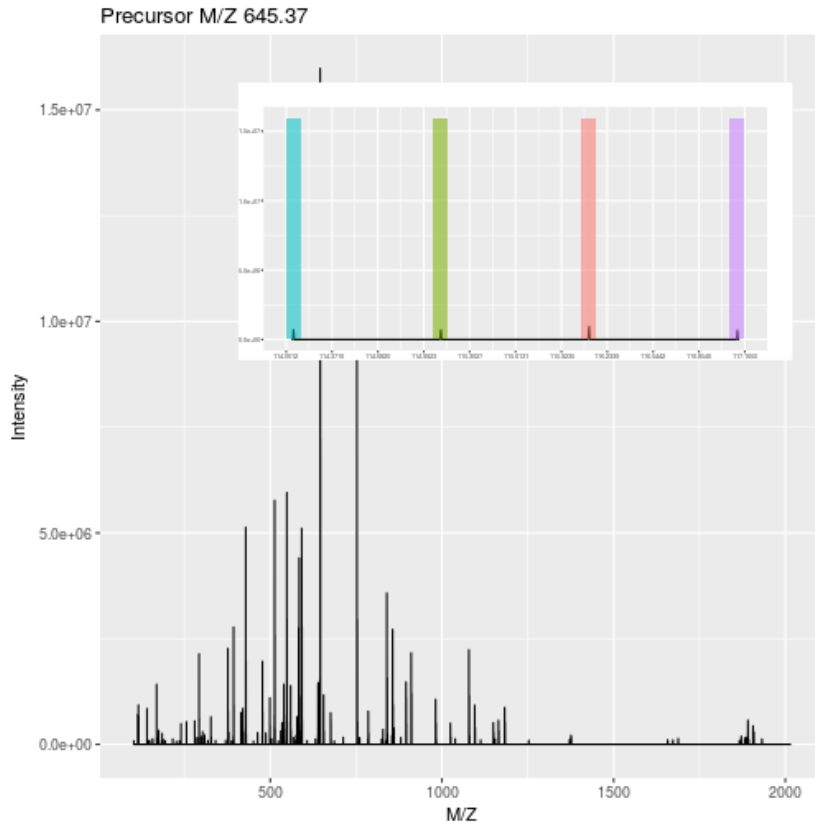
Label-free MS₂: Spectral counting

In spectral counting, one simply counts the number of quantified peptides that are assigned to a protein.



Labelled MS2: Isobaric tagging

Isobaric tagging refers to the labelling using isobaric tags, i.e. chemical tags that have the same mass and hence can't be distinguished by the spectrometer. The peptides of different samples (4, 6, 10 or 11) are labelled with different tags and combined prior to mass spectrometry acquisition. Given that they are isobaric, all identical peptides, irrespective of the tag and this the sample of origin, are co-analysed, up to fragmentation prior to MS2 analysis. During fragmentation, the isobaric tags fall off, fragment themselves, and result in a set of sample specific peaks. These specific peaks can be used to infer sample-specific quantitation, while the rest of the MS2 spectrum is used for identification.



Label-free MS1: extracted ion chromatograms

In label-free quantitation, the precursor peaks that match an identified peptide are integrated of retention time and the area under that *extracted ion chromatogram* is used to quantify that peptide in that sample.

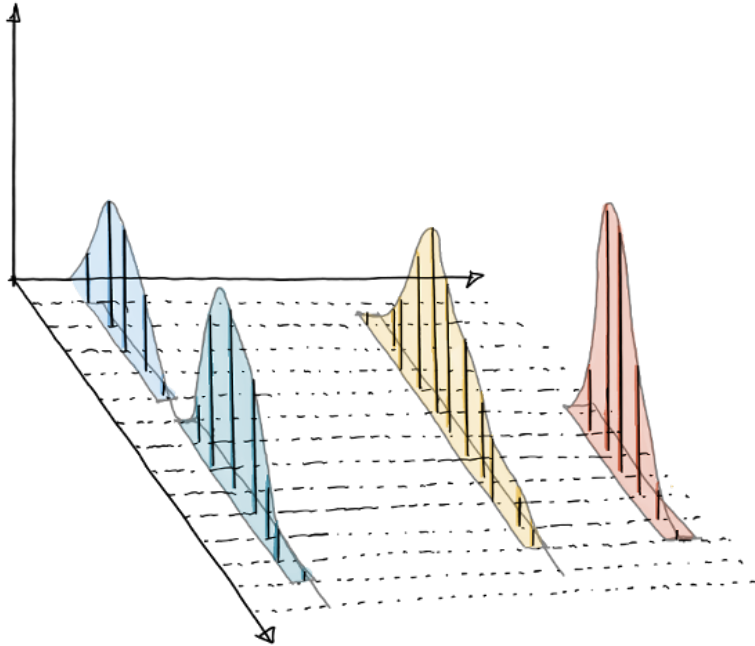


Figure: credit Johannes Rainer.

Labelled MS1: SILAC

In SILAC quantitation, samples are grown in a medium that contains heavy amino acids (typically arginine and lysine). All proteins grown in this *heavy* growth medium contain the heavy form of these amino acids. Two samples, one grown in heavy medium, and one grown in normal (light) medium are then combined and analysed together. The heavy peptide precursor peaks are systematically shifted compared to the light ones, and the ratio between the height of a heavy and light peaks can be used to calculate peptide and protein fold-changes.

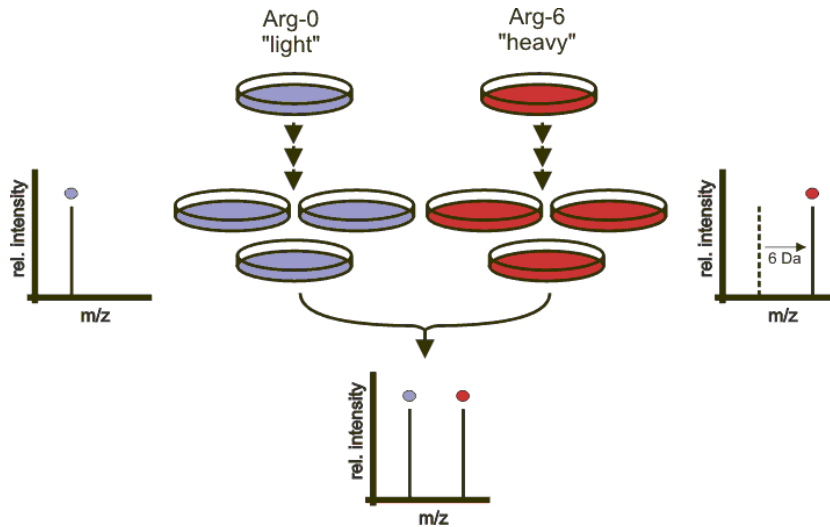


Figure: credit Wikimedia Commons.

Exercise

As its name implies, the `itraqdata` is an iTRAQ-based isobar quantitation experiment. We can visualise the reporter peaks as follows:

```
plot(itraqdata[[14]], reporters = iTRAQ4, full = TRUE)
```

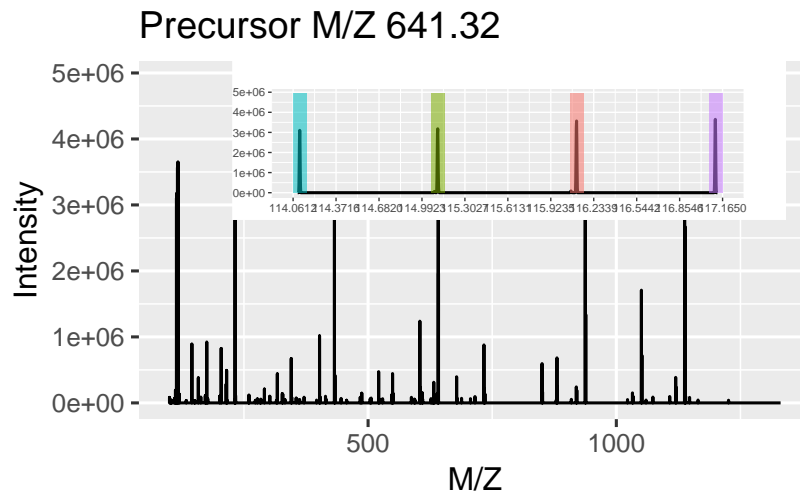


Figure 15: Visualisation of the iTRAQ reporter peaks.

We can quantify these four peaks with the `quantify` method, to produce an object of class `MSnSet` containing quantitation data. The quantitation values can be accessed with `exprs`.

```
msnset <- quantify(itraqdata, method = "trap",
```

```

    reporters = iTRAQ4)
msnset

## MSnSet (storageMode: lockedEnvironment)
## assayData: 55 features, 4 samples
##   element names: exprs
## protocolData: none
## phenoData
##   sampleNames: iTRAQ4.114 iTRAQ4.115
##               iTRAQ4.116 iTRAQ4.117
##   varLabels: mz reporters
##   varMetadata: labelDescription
## featureData
##   featureNames: X1 X10 ... X9 (55
##               total)
##   fvarLabels: spectrum ProteinAccession
##               ... collision.energy (15 total)
##   fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
## Annotation: No annotation
## - - - Processing information - - -
## Data loaded: Wed May 11 18:54:39 2011
## Updated from version 0.3.0 to 0.3.1 [Fri Jul  8 20:23:25 2016]
## iTRAQ4 quantification by trapezoidation: Sun Mar 24 19:25:25 2019
## MSnbase version: 1.1.22

head(exprs(msnset))

##   iTRAQ4.114 iTRAQ4.115 iTRAQ4.116
## X1   1347.6158  2247.3097  3927.6931
## X10   739.9861   799.3501   712.5983
## X11  27638.3582 33394.0252 32104.2879
## X12  31892.8928 33634.6980 37674.7272
## X13  26143.7542 29677.4781 29089.0593
## X14   6448.0829  6234.1957  6902.8903
##   iTRAQ4.117
## X1    7661.1463
## X10   940.6793
## X11  26628.7278
## X12  37227.7119
## X13  27902.5608
## X14   6437.2303

```

*Quantitative data processing**Applications in statistical learning*

- hypothesis testing
- classification
- clustering

Session information

```
## R version 3.5.3 Patched (2019-03-11 r76221)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 18.04.2 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/libf77blas.so.3.10.3
## LAPACK: /usr/lib/x86_64-linux-gnu/atlas/liblapack.so.3.10.3
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8
##  [2] LC_NUMERIC=C
##  [3] LC_TIME=fr_FR.UTF-8
##  [4] LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=fr_FR.UTF-8
##  [6] LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=fr_FR.UTF-8
##  [8] LC_NAME=C
##  [9] LC_ADDRESS=C
## [10] LC_TELEPHONE=C
## [11] LC_MEASUREMENT=fr_FR.UTF-8
## [12] LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats4      parallel  stats      graphics
## [5] grDevices  utils     datasets  methods
## [9] base
##
## other attached packages:
## [1] MSnbase_2.9.3      ProtGenerics_1.14.0
## [3] S4Vectors_0.20.1   mzR_2.16.2
## [5] Rcpp_1.0.1         Biobase_2.42.0
## [7] BiocGenerics_0.28.0
##
## loaded via a namespace (and not attached):
```

```
## [1] tidyselect_0.2.5
## [2] xfun_0.5
## [3] purrr_0.3.2
## [4] lattice_0.20-38
## [5] rhdf5_2.26.2
## [6] colorspace_1.4-1
## [7] htmltools_0.3.6
## [8] yaml_2.2.0
## [9] vsn_3.50.0
## [10] XML_3.98-1.19
## [11] rlang_0.3.2
## [12] pillar_1.3.1
## [13] glue_1.3.1
## [14] BiocParallel_1.16.6
## [15] affy_1.60.0
## [16] foreach_1.4.4
## [17] affyio_1.52.0
## [18] plyr_1.8.4
## [19] mzID_1.20.1
## [20] stringr_1.4.0
## [21] zlibbioc_1.28.0
## [22] munsell_0.5.0
## [23] pcaMethods_1.74.0
## [24] gtable_0.2.0
## [25] codetools_0.2-16
## [26] evaluate_0.13
## [27] labeling_0.3
## [28] knitr_1.22
## [29] IRanges_2.16.0
## [30] doParallel_1.0.14
## [31] preprocessCore_1.44.0
## [32] tufte_0.4
## [33] scales_1.0.0
## [34] formatR_1.6
## [35] BiocManager_1.30.4
## [36] limma_3.38.3
## [37] impute_1.56.0
## [38] ggplot2_3.1.0
## [39] digest_0.6.18
## [40] stringi_1.4.3
## [41] dplyr_0.8.0.1
## [42] ncd4_1.16.1
## [43] grid_3.5.3
## [44] tools_3.5.3
```

```
## [45] magrittr_1.5
## [46] lazyeval_0.2.2
## [47] tibble_2.1.1
## [48] crayon_1.3.4
## [49] pkgconfig_2.0.2
## [50] MASS_7.3-51.1
## [51] iterators_1.0.10
## [52] assertthat_0.2.1
## [53] rmarkdown_1.12
## [54] Rhdf5lib_1.4.2
## [55] R6_2.4.0
## [56] MALDIquant_1.19.2
## [57] compiler_3.5.3
```

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