

Quality control report generated with **qcmetrics**

lgatto

November 26, 2020

1 Metadata

data PXD000001

instrument LTQ Orbitrap Velos

source nanoelectrospray

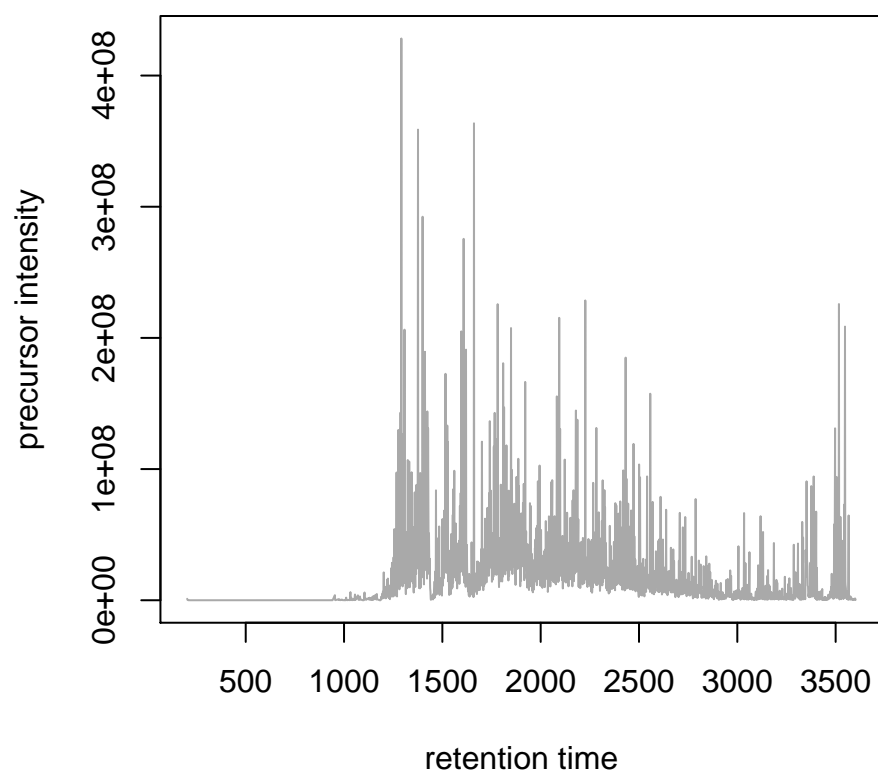
analyser orbitrap

detector inductive detector

manufacurer Thermo Scientific

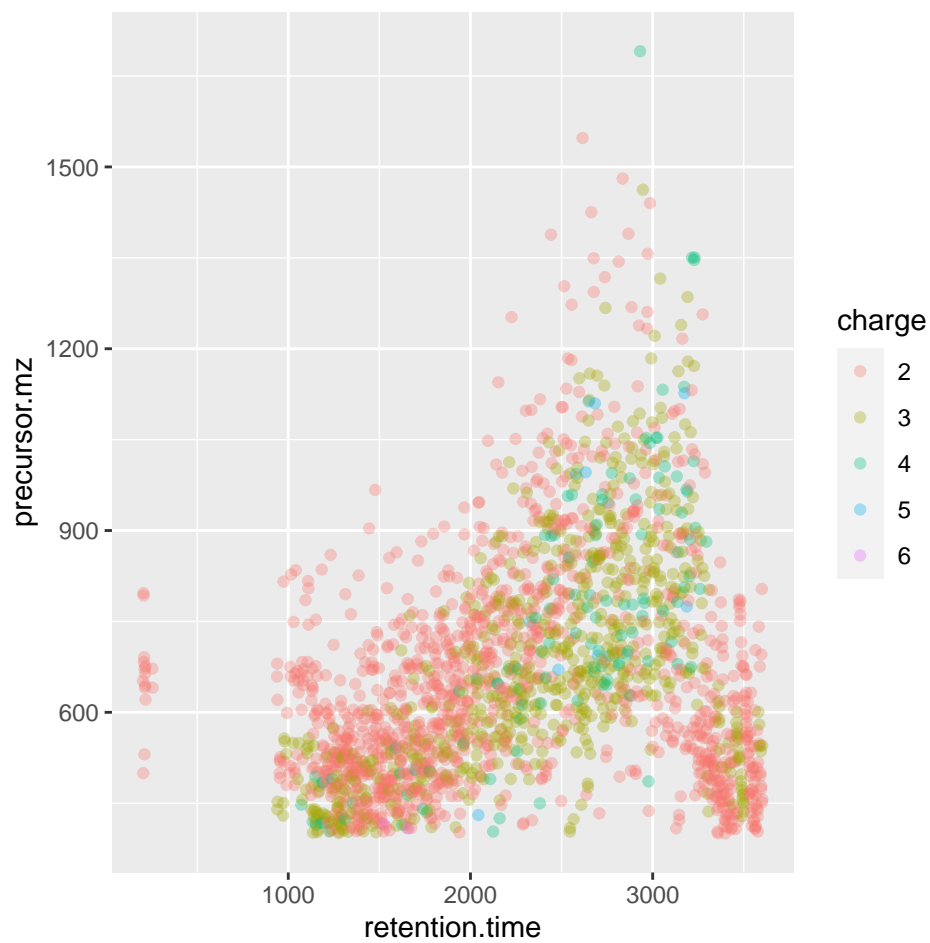
2 Chromatogram

```
## Object of class "QcMetric"  
## Name: Chromatogram  
## Status: NA  
## Data: x y
```



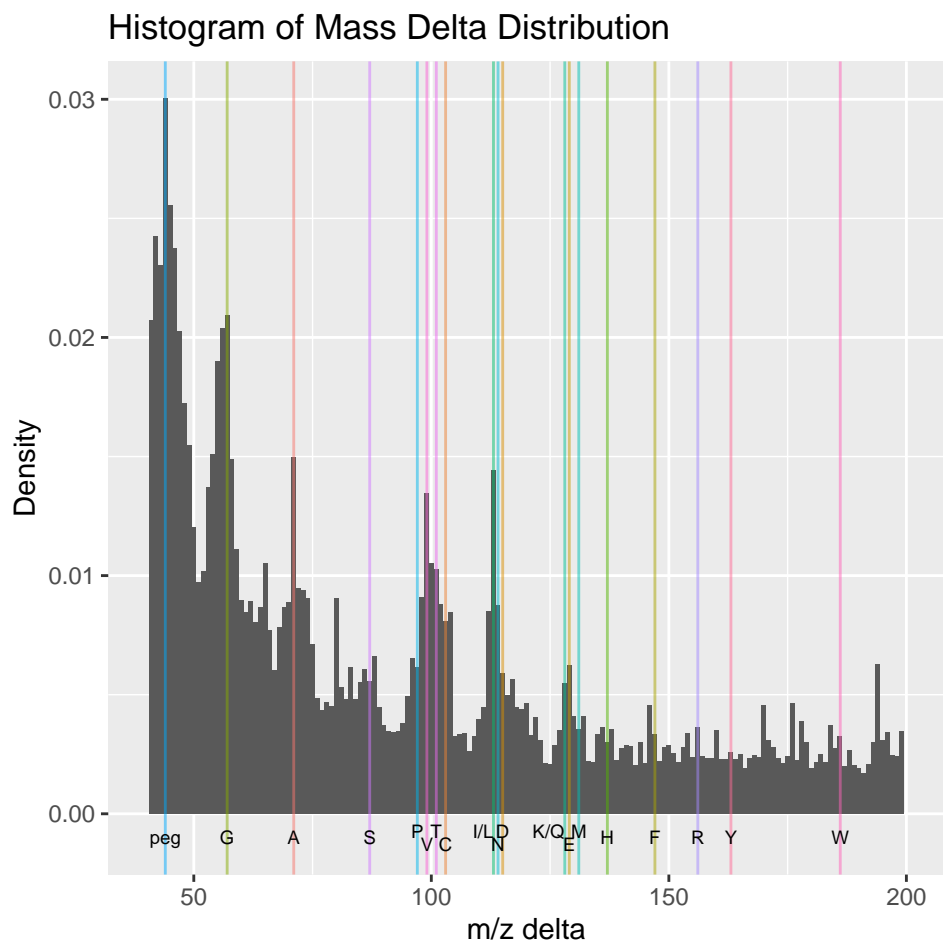
3 MS space

```
## Object of class "QcMetric"  
## Name: MS space  
## Status: NA  
## Data: p2d
```



4 m/z delta plot

```
## Object of class "QcMetric"  
## Name: m/z delta plot  
## Status: NA  
## Data: pmz
```



5 QC summary

	name	status
1	Chromatogram	
2	MS space	
3	m/z delta plot	

6 Session information

- R version 4.0.0 (2020-04-24), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=fr_FR.UTF-8, LC_COLLATE=en_US.UTF-8, LC_MONETARY=fr_FR.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=fr_FR.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=fr_FR.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 18.04.5 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
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, stats4, utils
- Other packages: affy 1.68.0, Biobase 2.50.0, BiocGenerics 0.36.0, gcrma 2.62.0, genefilter 1.72.0, ggplot2 3.3.2, MSnbase 2.16.0, mzR 2.24.1, ProtGenerics 1.23.1, qcmetrics 1.28.0, Rcpp 1.0.5, S4Vectors 0.28.0, simpleaffy 2.66.0, xtable 1.8-4, yaqcaffy 1.50.0
- Loaded via a namespace (and not attached): affyio 1.60.0, annotate 1.68.0, AnnotationDbi 1.52.0, BiocManager 1.30.10, BiocParallel 1.24.1, Biostrings 2.58.0, bit 4.0.4, bit64 4.0.5, blob 1.2.1, codetools 0.2-16, colorspace 2.0-0, compiler 4.0.0, crayon 1.3.4, DBI 1.1.0, digest 0.6.27, doParallel 1.0.16, dplyr 1.0.2, ellipsis 0.3.1, evaluate 0.14, farver 2.0.3, foreach 1.5.1, generics 0.1.0, glue 1.4.2, grid 4.0.0, gtable 0.3.0, highr 0.8, httr 1.4.2, impute 1.64.0, IRanges 2.24.0, iterators 1.0.13, knitr 1.30, labeling 0.4.2, lattice 0.20-41, lifecycle 0.2.0, limma 3.46.0, magrittr 2.0.1, MALDIquant 1.19.3, MASS 7.3-53, Matrix 1.2-18, memoise 1.1.0, munsell 0.5.0, mzID 1.28.0, ncd4 1.17, Nozzle.R1 1.1-1, pander 0.6.3, pcaMethods 1.82.0, pillar 1.4.7, pkgconfig 2.0.3, plyr 1.8.6, preprocessCore 1.52.0, purrr 0.3.4, R6 2.5.0, rlang 0.4.8, RSQLite 2.2.1, scales 1.1.1, splines 4.0.0, stringi 1.5.3, stringr 1.4.0, survival 3.2-7, tibble 3.0.4, tidyselect 1.1.0, tools 4.0.0, vctrs 0.3.5, vsn 3.58.0, withr 2.3.0, xfun 0.19, XML 3.99-0.5, XVector 0.30.0, zlibbioc 1.36.0