PEC1_SummarizedExperiment

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Lo primero de todo cargamos nuestro dataset que estudia la caquexia humana y lo exploramos.

```
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.4.3
```

```
human_cachexia <- read_excel("C:/Users/celch/OneDrive/Desktop/UOC/Datos omicos/Bloque 1 - las omicas/PEC
head (human_cachexia)
```

```
## # A tibble: 6 x 65
##   'Patient ID' 'Muscle loss' '1,6-Anhydro-beta-D-glucose' '1-Methylnicotinamide'
##   <chr>        <chr>         <chr>                        <chr>
## 1 PIF_178      cachexic      40.85                        65.37
## 2 PIF_087      cachexic      62.18                        340.36
## 3 PIF_090      cachexic      270.43                       64.72
## 4 NETL_005_V1  cachexic      154.47                       52.98
## 5 PIF_115      cachexic      22.2                         73.7
## 6 PIF_110      cachexic      212.72                       31.82
## # i 61 more variables: '2-Aminobutyrate' <chr>, '2-Hydroxyisobutyrate' <chr>,
## #   '2-Oxoglutarate' <chr>, '3-Aminoisobutyrate' <chr>,
## #   '3-Hydroxybutyrate' <chr>, '3-Hydroxyisovalerate' <chr>,
## #   '3-Indoxylsulfate' <chr>, '4-Hydroxyphenylacetate' <chr>, Acetate <chr>,
## #   Acetone <chr>, Adipate <chr>, Alanine <chr>, Asparagine <chr>,
## #   Betaine <chr>, Carnitine <chr>, Citrate <chr>, Creatine <chr>,
## #   Creatinine <chr>, Dimethylamine <chr>, Ethanolamine <chr>, ...
```

```
str(human_cachexia)
```

```
## tibble [77 x 65] (S3: tbl_df/tbl/data.frame)
##  $ Patient ID              : chr [1:77] "PIF_178" "PIF_087" "PIF_090" "NETL_005_V1" ...
##  $ Muscle loss             : chr [1:77] "cachexic" "cachexic" "cachexic" "cachexic" ...
##  $ 1,6-Anhydro-beta-D-glucose: chr [1:77] "40.85" "62.18" "270.43" "154.47" ...
##  $ 1-Methylnicotinamide    : chr [1:77] "65.37" "340.36" "64.72" "52.98" ...
##  $ 2-Aminobutyrate         : chr [1:77] "18.73" "24.29" "12.18" "172.43" ...
##  $ 2-Hydroxyisobutyrate    : chr [1:77] "26.05" "41.68" "65.37" "74.44" ...
##  $ 2-Oxoglutarate          : chr [1:77] "71.52" "67.36" "23.81" "1199.91" ...
##  $ 3-Aminoisobutyrate      : chr [1:77] "1480.3" "116.75" "14.3" "555.57" ...
##  $ 3-Hydroxybutyrate       : chr [1:77] "56.83" "43.82" "5.64" "175.91" ...
##  $ 3-Hydroxyisovalerate    : chr [1:77] "10.07" "79.84" "23.34" "25.03" ...
##  $ 3-Indoxylsulfate        : chr [1:77] "566.8" "368.71" "665.14" "411.58" ...
```

```
##  $ 4-Hydroxyphenylacetate  : chr [1:77] "120.3" "432.68" "292.95" "214.86" ...
##  $ Acetate                 : chr [1:77] "126.47" "212.72" "314.19" "37.34" ...
##  $ Acetone                 : chr [1:77] "9.49" "11.82" "4.44" "206.44" ...
##  $ Adipate                 : chr [1:77] "38.09" "327.01" "131.63" "144.03" ...
##  $ Alanine                 : chr [1:77] "314.19" "871.31" "464.05" "589.93" ...
##  $ Asparagine              : chr [1:77] "159.17" "157.59" "89.12" "273.14" ...
##  $ Betaine                 : chr [1:77] "109.95" "244.69" "116.75" "278.66" ...
##  $ Carnitine               : chr [1:77] "265.07" "120.3" "25.03" "200.34" ...
##  $ Citrate                 : chr [1:77] "3714.5" "2617.57" "862.64" "13629.61" ...
##  $ Creatine                : chr [1:77] "196.37" "212.72" "221.41" "85.63" ...
##  $ Creatinine              : chr [1:77] "16481.6" "15835.35" "24587.66" "20952.22" ...
##  $ Dimethylamine           : chr [1:77] "632.7" "607.89" "735.1" "1064.22" ...
##  $ Ethanolamine            : chr [1:77] "645.48" "487.85" "407.48" "820.57" ...
##  $ Formate                 : chr [1:77] "441.42" "252.14" "249.64" "468.72" ...
##  $ Fucose                  : chr [1:77] "336.97" "198.34" "186.79" "407.48" ...
##  $ Fumarate                : chr [1:77] "7.69" "18.92" "7.1" "96.54" ...
##  $ Glucose                 : chr [1:77] "395.44" "8690.62" "1352.89" "862.64" ...
##  $ Glutamine               : chr [1:77] "871.31" "601.85" "301.87" "1685.81" ...
##  $ Glycine                 : chr [1:77] "2038.56" "1107.65" "620.17" "5064.45" ...
##  $ Glycolate               : chr [1:77] "685.4" "651.97" "141.17" "70.81" ...
##  $ Guanidoacetate          : chr [1:77] "154.47" "109.95" "183.09" "102.51" ...
##  $ Hippurate               : chr [1:77] "4582.5" "1737.15" "4315.64" "757.48" ...
##  $ Histidine               : chr [1:77] "925.19" "845.56" "284.29" "1043.15" ...
##  $ Hypoxanthine            : chr [1:77] "97.51" "82.27" "114.43" "223.63" ...
##  $ Isoleucine              : chr [1:77] "5.58" "8.17" "9.3" "37.71" ...
##  $ Lactate                 : chr [1:77] "106.7" "368.71" "749.95" "368.71" ...
##  $ Leucine                 : chr [1:77] "42.1" "77.48" "31.5" "103.54" ...
##  $ Lysine                  : chr [1:77] "146.94" "284.29" "97.51" "290.03" ...
##  $ Methylamine             : chr [1:77] "52.46" "23.57" "18.73" "48.91" ...
##  $ Methylguanidine         : chr [1:77] "9.97" "7.69" "4.66" "141.17" ...
##  $ N,N-Dimethylglycine     : chr [1:77] "23.34" "87.36" "24.53" "40.04" ...
##  $ O-Acetylcarnitine       : chr [1:77] "52.98" "50.4" "5.58" "254.68" ...
##  $ Pantothenate            : chr [1:77] "25.79" "186.79" "145.47" "42.52" ...
##  $ Pyroglutamate           : chr [1:77] "437.03" "437.03" "713.37" "566.8" ...
##  $ Pyruvate                : chr [1:77] "21.12" "36.97" "29.37" "64.07" ...
##  $ Quinolinate             : chr [1:77] "165.67" "72.97" "192.48" "86.49" ...
##  $ Serine                  : chr [1:77] "284.29" "391.51" "295.89" "1248.88" ...
##  $ Succinate               : chr [1:77] "154.47" "244.69" "142.59" "144.03" ...
##  $ Sucrose                 : chr [1:77] "45.15" "459.44" "160.77" "111.05" ...
##  $ Tartrate                : chr [1:77] "97.51" "32.79" "16.28" "837.15" ...
##  $ Taurine                 : chr [1:77] "1919.85" "1261.43" "4272.69" "1525.38" ...
##  $ Threonine               : chr [1:77] "184.93" "198.34" "109.95" "376.15" ...
##  $ Trigonelline            : chr [1:77] "943.88" "208.51" "192.48" "992.27" ...
##  $ Trimethylamine N-oxide  : chr [1:77] "2121.76" "639.06" "1152.86" "1450.99" ...
##  $ Tryptophan              : chr [1:77] "259.82" "83.1" "82.27" "235.1" ...
##  $ Tyrosine                : chr [1:77] "290.03" "167.34" "60.34" "323.76" ...
##  $ Uracil                  : chr [1:77] "111.05" "46.99" "31.5" "30.57" ...
##  $ Valine                  : chr [1:77] "86.49" "109.95" "59.15" "102.51" ...
##  $ Xylose                  : chr [1:77] "72.24" "192.48" "2164.62" "125.21" ...
##  $ cis-Aconitate           : chr [1:77] "237.46" "333.62" "330.3" "1863.11" ...
##  $ myo-Inositol            : chr [1:77] "135.64" "376.15" "86.49" "247.15" ...
##  $ trans-Aconitate         : chr [1:77] "51.94" "217.02" "58.56" "75.94" ...
##  $ pi-Methylhistidine      : chr [1:77] "157.59" "307.97" "145.47" "249.64" ...
##  $ tau-Methylhistidine     : chr [1:77] "160.77" "130.32" "83.93" "254.68" ...
```

Como hemos visto, en vez de números los valores son una cadena de caracteries entonces tenemos que cambiarlo a valores numéricos. Aprovecharemos y tambien cambiamos Muscle Loss a tipo factor.

```r
human_cachexia$`Muscle loss`<-as.factor(human_cachexia$`Muscle loss`)
# Para cada columna desde la tercera en el dataset cambiaremos el string a numérico
for (i in 3:ncol(human_cachexia)) {
  human_cachexia[, i] <- as.numeric(human_cachexia[[i]])}
str(human_cachexia)
```

```
## tibble [77 x 65] (S3: tbl_df/tbl/data.frame)
##  $ Patient ID               : chr [1:77] "PIF_178" "PIF_087" "PIF_090" "NETL_005_V1" ...
##  $ Muscle loss              : Factor w/ 2 levels "cachexic","control": 1 1 1 1 1 1 1 1 1 1 ...
##  $ 1,6-Anhydro-beta-D-glucose: num [1:77] 40.9 62.2 270.4 154.5 22.2 ...
##  $ 1-Methylnicotinamide     : num [1:77] 65.4 340.4 64.7 53 73.7 ...
##  $ 2-Aminobutyrate          : num [1:77] 18.7 24.3 12.2 172.4 15.6 ...
##  $ 2-Hydroxyisobutyrate     : num [1:77] 26.1 41.7 65.4 74.4 83.9 ...
##  $ 2-Oxoglutarate           : num [1:77] 71.5 67.4 23.8 1199.9 33.1 ...
##  $ 3-Aminoisobutyrate       : num [1:77] 1480.3 116.8 14.3 555.6 29.7 ...
##  $ 3-Hydroxybutyrate        : num [1:77] 56.83 43.82 5.64 175.91 76.71 ...
##  $ 3-Hydroxyisovalerate     : num [1:77] 10.1 79.8 23.3 25 69.4 ...
##  $ 3-Indoxylsulfate         : num [1:77] 567 369 665 412 166 ...
##  $ 4-Hydroxyphenylacetate   : num [1:77] 120.3 432.7 292.9 214.9 97.5 ...
##  $ Acetate                  : num [1:77] 126.5 212.7 314.2 37.3 407.5 ...
##  $ Acetone                  : num [1:77] 9.49 11.82 4.44 206.44 44.26 ...
##  $ Adipate                  : num [1:77] 38.1 327 131.6 144 15 ...
##  $ Alanine                  : num [1:77] 314 871 464 590 1119 ...
##  $ Asparagine               : num [1:77] 159.2 157.6 89.1 273.1 42.5 ...
##  $ Betaine                  : num [1:77] 110 245 117 279 392 ...
##  $ Carnitine                : num [1:77] 265.1 120.3 25 200.3 84.8 ...
##  $ Citrate                  : num [1:77] 3714 2618 863 13630 854 ...
##  $ Creatine                 : num [1:77] 196.4 212.7 221.4 85.6 105.6 ...
##  $ Creatinine               : num [1:77] 16482 15835 24588 20952 6768 ...
##  $ Dimethylamine            : num [1:77] 633 608 735 1064 242 ...
##  $ Ethanolamine             : num [1:77] 645 488 407 821 365 ...
##  $ Formate                  : num [1:77] 441 252 250 469 114 ...
##  $ Fucose                   : num [1:77] 337 198.3 186.8 407.5 26.1 ...
##  $ Fumarate                 : num [1:77] 7.69 18.92 7.1 96.54 19.69 ...
##  $ Glucose                  : num [1:77] 395 8691 1353 863 6836 ...
##  $ Glutamine                : num [1:77] 871 602 302 1686 433 ...
##  $ Glycine                  : num [1:77] 2039 1108 620 5064 395 ...
##  $ Glycolate                : num [1:77] 685.4 652 141.2 70.8 26.6 ...
##  $ Guanidoacetate           : num [1:77] 154 110 183 103 53 ...
##  $ Hippurate                : num [1:77] 4582 1737 4316 757 1153 ...
##  $ Histidine                : num [1:77] 925 846 284 1043 327 ...
##  $ Hypoxanthine             : num [1:77] 97.5 82.3 114.4 223.6 66.7 ...
##  $ Isoleucine               : num [1:77] 5.58 8.17 9.3 37.71 40.04 ...
##  $ Lactate                  : num [1:77] 107 369 750 369 3641 ...
##  $ Leucine                  : num [1:77] 42.1 77.5 31.5 103.5 101.5 ...
##  $ Lysine                   : num [1:77] 146.9 284.3 97.5 290 122.7 ...
##  $ Methylamine              : num [1:77] 52.5 23.6 18.7 48.9 27.9 ...
##  $ Methylguanidine          : num [1:77] 9.97 7.69 4.66 141.17 5.31 ...
##  $ N,N-Dimethylglycine      : num [1:77] 23.3 87.4 24.5 40 46.1 ...
##  $ O-Acetylcarnitine        : num [1:77] 52.98 50.4 5.58 254.68 45.6 ...
##  $ Pantothenate             : num [1:77] 25.8 186.8 145.5 42.5 74.4 ...
```

```
##  $ Pyroglutamate          : num [1:77] 437 437 713 567 185 ...
##  $ Pyruvate               : num [1:77] 21.1 37 29.4 64.1 12.3 ...
##  $ Quinolinate            : num [1:77] 165.7 73 192.5 86.5 38.1 ...
##  $ Serine                 : num [1:77] 284 392 296 1249 206 ...
##  $ Succinate              : num [1:77] 154.5 244.7 142.6 144 68.7 ...
##  $ Sucrose                : num [1:77] 45.1 459.4 160.8 111 75.2 ...
##  $ Tartrate               : num [1:77] 97.51 32.79 16.28 837.15 4.53 ...
##  $ Taurine                : num [1:77] 1920 1261 4273 1525 469 ...
##  $ Threonine              : num [1:77] 184.9 198.3 110 376.1 64.1 ...
##  $ Trigonelline           : num [1:77] 943.9 208.5 192.5 992.3 86.5 ...
##  $ Trimethylamine N-oxide : num [1:77] 2122 639 1153 1451 172 ...
##  $ Tryptophan             : num [1:77] 259.8 83.1 82.3 235.1 103.5 ...
##  $ Tyrosine               : num [1:77] 290 167.3 60.3 323.8 142.6 ...
##  $ Uracil                 : num [1:77] 111 47 31.5 30.6 44.3 ...
##  $ Valine                 : num [1:77] 86.5 110 59.1 102.5 160.8 ...
##  $ Xylose                 : num [1:77] 72.2 192.5 2164.6 125.2 186.8 ...
##  $ cis-Aconitate          : num [1:77] 237 334 330 1863 101 ...
##  $ myo-Inositol           : num [1:77] 135.6 376.1 86.5 247.2 750 ...
##  $ trans-Aconitate        : num [1:77] 51.9 217 58.6 75.9 98.5 ...
##  $ pi-Methylhistidine     : num [1:77] 157.6 308 145.5 249.6 84.8 ...
##  $ tau-Methylhistidine    : num [1:77] 160.8 130.3 83.9 254.7 79.8 ...
```

Estudiamos el dataset seleccionado.

```
class(human_cachexia)
```

```
## [1] "tbl_df"     "tbl"          "data.frame"
```

```
colnames(human_cachexia)
```

```
##  [1] "Patient ID"                "Muscle loss"
##  [3] "1,6-Anhydro-beta-D-glucose" "1-Methylnicotinamide"
##  [5] "2-Aminobutyrate"           "2-Hydroxyisobutyrate"
##  [7] "2-Oxoglutarate"            "3-Aminoisobutyrate"
##  [9] "3-Hydroxybutyrate"         "3-Hydroxyisovalerate"
## [11] "3-Indoxylsulfate"          "4-Hydroxyphenylacetate"
## [13] "Acetate"                   "Acetone"
## [15] "Adipate"                   "Alanine"
## [17] "Asparagine"                "Betaine"
## [19] "Carnitine"                 "Citrate"
## [21] "Creatine"                  "Creatinine"
## [23] "Dimethylamine"             "Ethanolamine"
## [25] "Formate"                   "Fucose"
## [27] "Fumarate"                  "Glucose"
## [29] "Glutamine"                 "Glycine"
## [31] "Glycolate"                 "Guanidoacetate"
## [33] "Hippurate"                 "Histidine"
## [35] "Hypoxanthine"              "Isoleucine"
## [37] "Lactate"                   "Leucine"
## [39] "Lysine"                    "Methylamine"
## [41] "Methylguanidine"           "N,N-Dimethylglycine"
## [43] "O-Acetylcarnitine"         "Pantothenate"
## [45] "Pyroglutamate"             "Pyruvate"
```

```
## [47] "Quinolinate"               "Serine"
## [49] "Succinate"                 "Sucrose"
## [51] "Tartrate"                  "Taurine"
## [53] "Threonine"                 "Trigonelline"
## [55] "Trimethylamine N-oxide"    "Tryptophan"
## [57] "Tyrosine"                  "Uracil"
## [59] "Valine"                    "Xylose"
## [61] "cis-Aconitate"             "myo-Inositol"
## [63] "trans-Aconitate"           "pi-Methylhistidine"
## [65] "tau-Methylhistidine"
```

```r
dim(human_cachexia)
```

```
## [1] 77 65
```

Encontramos que nuestro dataset es un dataframe con 77 muestras y presenta 65 columnas siendo la primera columna el ID de la muestra del paciente y la segunda si ha habido pérdida de masa muscular y grasa (caquexia) o no (control), el resto de columna se corresponden con diversos metabolitos.

Para tener más información acerca de nuestro estudio determinamos el número de pacientes que presenta caquexia y los pacientes control.

```r
summary(human_cachexia$`Muscle loss`)
```

```
## cachexic  control
##       47       30
```

De los 77 pacientes tenemos 30 control y 47 con caquexia.

A continuación, procedemos a crear el SummarizedExperiment

```r
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install(version = "3.20")
```

```
## Bioconductor version 3.20 (BiocManager 1.30.25), R 4.4.2 (2024-10-31 ucrt)
```

```
## Installation paths not writeable, unable to update packages
##   path: C:/Program Files/R/R-4.4.2/library
##   packages:
##     class, cluster, foreign, KernSmooth, lattice, MASS, Matrix, mgcv, nlme,
##     nnet, rpart, spatial, survival
```

```r
library(SummarizedExperiment)
```

```
## Cargando paquete requerido: MatrixGenerics
```

```
## Cargando paquete requerido: matrixStats
```

```
##
## Adjuntando el paquete: 'MatrixGenerics'
```

```
## The following objects are masked from 'package:matrixStats':
##
##      colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse,
##      colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
##      colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
##      colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
##      colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
##      colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
##      colWeightedMeans, colWeightedMedians, colWeightedSds,
##      colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,
##      rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
##      rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
##      rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
##      rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
##      rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
##      rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
##      rowWeightedSds, rowWeightedVars


## Cargando paquete requerido: GenomicRanges


## Cargando paquete requerido: stats4


## Cargando paquete requerido: BiocGenerics


##
## Adjuntando el paquete: 'BiocGenerics'


## The following objects are masked from 'package:stats':
##
##      IQR, mad, sd, var, xtabs


## The following objects are masked from 'package:base':
##
##      anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##      colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##      get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
##      match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##      Position, rank, rbind, Reduce, rownames, sapply, saveRDS, setdiff,
##      table, tapply, union, unique, unsplit, which.max, which.min


## Cargando paquete requerido: S4Vectors


##
## Adjuntando el paquete: 'S4Vectors'


## The following object is masked from 'package:utils':
##
##      findMatches


## The following objects are masked from 'package:base':
##
##      expand.grid, I, unname
```

```
## Cargando paquete requerido: IRanges


##
## Adjuntando el paquete: 'IRanges'


## The following object is masked from 'package:grDevices':
##
##     windows


## Cargando paquete requerido: GenomeInfoDb


## Cargando paquete requerido: Biobase


## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.


##
## Adjuntando el paquete: 'Biobase'


## The following object is masked from 'package:MatrixGenerics':
##
##     rowMedians


## The following objects are masked from 'package:matrixStats':
##
##     anyMissing, rowMedians
```

A continuación tenemos que crear dos matrices, la de datos y la de metadatos.

```r
# Para crear la matriz de datos solo incluimos los datos de las concentraciones de metabolitos
matriz_caquexia<-as.matrix(human_cachexia[, 3:ncol(human_cachexia)])

# ID de los sujetos como nombre de fila
rownames(matriz_caquexia)<-human_cachexia$`Patient ID`
# Nombre de los metabolitos
metabolitos<-colnames(matriz_caquexia)

# Ahora creamos los metadatos de columnas y filas,

metadatos_columnas <-DataFrame(
  metabolitos = metabolitos,
  Dataset = rep ("Human_cachexia.csv", ncol(matriz_caquexia)),
  row.names = metabolitos)

  metadatos_filas <-DataFrame(
    Perdida_muscular = human_cachexia$`Muscle loss`,
    Dataset = rep ("Human_cachexia.csv", nrow(human_cachexia)),
    row.names = human_cachexia$`Patient ID`)
```

Una vez ya hemos creado las matrices me dispongo a crear el objeto SummarizedExperiment, al que luego agregaremos información acerca de los experimentos en los metadatos.

```
SE <-SummarizedExperiment(assays = list(counts = matriz_caquexia),
                          rowData = metadatos_filas,
                          colData = metadatos_columnas)
SE
```

```
## class: SummarizedExperiment
## dim: 77 63
## metadata(0):
## assays(1): counts
## rownames(77): PIF_178 PIF_087 ... NETL_003_V1 NETL_003_V2
## rowData names(2): Perdida_muscular Dataset
## colnames(63): 1,6-Anhydro-beta-D-glucose 1-Methylnicotinamide ...
##   pi-Methylhistidine tau-Methylhistidine
## colData names(2): metabolitos Dataset
```

```
# Anadimos la información obtenida de GitHub en los metadatos
# Como se trata de una lista podemos añadir toda la información que queramos, alguna de ella me la inves

metadata(SE) <- list(
  Descripción =  "Cachexia is a complex metabolic syndrome associated with an underlying illness (such a
  Dataset= "Human_cachexia.csv",
  Informacion_muestras ="77 muestras urinarias de 47 pacientes con caquexia y 30 controles",
  Tecnica = "RMN unidimensional",
  Projecto= "Estudio de la metabolomica urinaria para mejorar la detección de caquexia",
  IP = "Celia Martínez Saz")

SE
```

```
## class: SummarizedExperiment
## dim: 77 63
## metadata(6): Descripción Dataset ... Projecto IP
## assays(1): counts
## rownames(77): PIF_178 PIF_087 ... NETL_003_V1 NETL_003_V2
## rowData names(2): Perdida_muscular Dataset
## colnames(63): 1,6-Anhydro-beta-D-glucose 1-Methylnicotinamide ...
##   pi-Methylhistidine tau-Methylhistidine
## colData names(2): metabolitos Dataset
```

Ahora podríamos probar algunas operzaciones comunes en esta clase de objetos como por ejemplo subconjuntos:

```
SE[1:5,1:3] #Mostramos las 5 primeras muestras de los 3 primeros metabolitos
```

```
## class: SummarizedExperiment
## dim: 5 3
## metadata(6): Descripción Dataset ... Projecto IP
## assays(1): counts
## rownames(5): PIF_178 PIF_087 PIF_090 NETL_005_V1 PIF_115
## rowData names(2): Perdida_muscular Dataset
```

```
## colnames(3): 1,6-Anhydro-beta-D-glucose 1-Methylnicotinamide
##   2-Aminobutyrate
## colData names(2): metabolitos Dataset
```

```r
control <-SE[rowData(SE)$Perdida_muscular == "control,"] # Solo mostramos los individuos control
assay(SE)[1:5,1:3]
```

```
##               1,6-Anhydro-beta-D-glucose 1-Methylnicotinamide 2-Aminobutyrate
## PIF_178                            40.85               65.37           18.73
## PIF_087                            62.18              340.36           24.29
## PIF_090                           270.43               64.72           12.18
## NETL_005_V1                       154.47               52.98          172.43
## PIF_115                            22.20               73.70           15.64
```

Finalmente guardamos nuestro objeto SummarizedExperiment para poder subirlo a GitHub.

```r
save(SE, file = "SummarizedExperiment_PEC1.Rda")
```