

PAC1.R

Toni

2024-10-24

```
# Comprovem si el paquet "BiocManager" està disponible al sistema
# La funció requireNamespace() retorna TRUE si el paquet està instal·lat, i FALSE si no ho està
# El paràmetre 'quietly = TRUE' evita mostrar missatges durant la comprovació
if (!requireNamespace("BiocManager", quietly = TRUE)) {
  # Si el paquet "BiocManager" no està instal·lat, el descarreguem i instal·lem des de CRAN
  install.packages("BiocManager")
}

# Un cop tenim "BiocManager" instal·lat, utilitzem la seva funció per instal·lar el paquet "SummarizedExperiment"
# "SummarizedExperiment" és un paquet del repositori Bioconductor, que s'utilitza per treballar amb dades
BiocManager::install("SummarizedExperiment")
```

```
## Bioconductor version 3.19 (BiocManager 1.30.25), R 4.4.1 (2024-06-14 ucrt)
```

```
## Warning: package(s) not installed when version(s) same as or greater than current; use
## `force = TRUE` to re-install: 'SummarizedExperiment'
```

```
## Installation paths not writeable, unable to update packages
## path: C:/Program Files/R/R-4.4.1/library
## packages:
## boot, foreign, MASS, Matrix, nlme, survival
```

```
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, 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
```

```
# Carregar les dades des d'un fitxer CSV
data <- read.csv("C:/Users/tonim/Documents/PAC1/human_cachexia.csv", row.names = 1)

# Matriu de dades (valors de metabòlits)
# Excloem les primeres dues columnes, que són identificadors i informació clínica
assay_data <- as.matrix(data[, -c(1,2)])

# Metadades de les files (informació sobre els pacients)
row_metadata <- data.frame(
  Muscle_loss = data$Muscle.loss, # Indicació de pèrdua de massa muscular
  row.names = rownames(data) # Assignem les files del dataframe a les metadades
)

# Metadades de les columnes (nom dels metabòlits)
col_metadata <- data.frame(
  Metabolite = colnames(assay_data) # Assignem els noms dels metabòlits com a metadades de les columnes
)

# Crear l'objecte SummarizedExperiment
se <- SummarizedExperiment(
  assays = list(counts = assay_data), # Dades d'expressió o valors dels metabòlits
  rowData = row_metadata, # Metadades dels pacients
  colData = col_metadata # Metadades dels metabòlits
)

se # Mostrar l'objecte creat
```

```
## class: SummarizedExperiment
## dim: 77 62
## metadata(0):
## assays(1): counts
## rownames(77): PIF_178 PIF_087 ... NETL_003_V1 NETL_003_V2
## rowData names(1): Muscle_loss
## colnames(62): X1.Methylnicotinamide X2.Aminobutyrate ...
##      pi.Methylhistidine tau.Methylhistidine
## colData names(1): Metabolite
```

```
# 1. Resum estadístic de les dades numèriques
```

```
summary(data[, -c(1,2)]) # Excloem les columnes 'Patient ID' i 'Muscle loss' per fer el resum
```

```
## X1.Methylnicotinamide X2.Aminobutyrate X2.Hydroxyisobutyrate X2.Oxoglutarate
## Min. : 6.42 Min. : 1.28 Min. : 4.85 Min. : 5.53
## 1st Qu.: 15.80 1st Qu.: 5.26 1st Qu.:15.80 1st Qu.: 22.42
## Median : 36.60 Median : 10.49 Median :32.46 Median : 55.15
## Mean : 71.57 Mean : 18.16 Mean :37.25 Mean : 145.09
## 3rd Qu.: 73.70 3rd Qu.: 19.49 3rd Qu.:54.60 3rd Qu.: 92.76
## Max. :1032.77 Max. :172.43 Max. :93.69 Max. :2465.13
## X3.Aminoisobutyrate X3.Hydroxybutyrate X3.Hydroxyisovalerate X3.Indoxylsulfate
## Min. : 2.61 Min. : 1.70 Min. : 0.92 Min. : 27.66
## 1st Qu.: 11.70 1st Qu.: 5.99 1st Qu.: 5.26 1st Qu.: 82.27
## Median : 22.65 Median : 11.70 Median : 12.55 Median : 144.03
## Mean : 76.76 Mean : 21.72 Mean : 21.65 Mean : 218.88
## 3rd Qu.: 56.26 3rd Qu.: 29.96 3rd Qu.: 30.27 3rd Qu.: 333.62
## Max. :1480.30 Max. :175.91 Max. :164.02 Max. :1043.15
## X4.Hydroxyphenylacetate Acetate Acetone Adipate
## Min. : 15.49 Min. : 3.49 Min. : 2.29 Min. : 1.55
## 1st Qu.: 41.68 1st Qu.: 16.28 1st Qu.: 4.95 1st Qu.: 6.11
## Median : 70.11 Median : 39.65 Median : 7.10 Median : 10.18
## Mean :112.02 Mean : 66.14 Mean : 11.43 Mean : 24.76
## 3rd Qu.:145.47 3rd Qu.: 86.49 3rd Qu.: 10.49 3rd Qu.: 19.11
## Max. :796.32 Max. :411.58 Max. :206.44 Max. :327.01
## Alanine Asparagine Betaine Carnitine
## Min. : 16.78 Min. : 6.69 Min. : 2.29 Min. : 2.18
## 1st Qu.: 78.26 1st Qu.: 20.49 1st Qu.: 28.79 1st Qu.: 14.44
## Median : 194.42 Median : 42.10 Median : 64.72 Median : 23.81
## Mean : 273.56 Mean : 62.28 Mean : 90.32 Mean : 52.09
## 3rd Qu.: 399.41 3rd Qu.: 89.12 3rd Qu.:127.74 3rd Qu.: 60.95
## Max. :1312.91 Max. :273.14 Max. :391.51 Max. :487.85
## Citrate Creatine Creatinine Dimethylamine
## Min. : 59.74 Min. : 2.75 Min. : 1002 Min. : 41.26
## 1st Qu.: 788.40 1st Qu.: 17.64 1st Qu.: 3498 1st Qu.: 142.59
## Median : 1790.05 Median : 44.26 Median : 7631 Median : 304.90
## Mean : 2235.35 Mean : 126.83 Mean : 8734 Mean : 358.17
## 3rd Qu.: 3071.74 3rd Qu.: 117.92 3rd Qu.:12333 3rd Qu.: 454.86
## Max. :13629.61 Max. :1863.11 Max. :33860 Max. :1556.20
## Ethanolamine Formate Fucose Fumarate
## Min. : 16.12 Min. : 6.42 Min. : 5.70 Min. : 0.79
## 1st Qu.: 86.49 1st Qu.: 53.52 1st Qu.: 29.37 1st Qu.: 2.23
## Median : 204.38 Median : 95.58 Median : 61.56 Median : 4.10
## Mean : 276.26 Mean : 147.40 Mean : 88.67 Mean : 8.44
## 3rd Qu.: 407.48 3rd Qu.: 167.34 3rd Qu.:123.97 3rd Qu.: 7.85
```

##	Max. :1436.55	Max. :1480.30	Max. :407.48	Max. :96.54
##	Glucose	Glutamine	Glycine	Glycolate
##	Min. : 26.84	Min. : 23.34	Min. : 38.09	Min. : 5.42
##	1st Qu.: 80.64	1st Qu.: 113.30	1st Qu.: 262.43	1st Qu.: 50.91
##	Median : 210.61	Median : 225.88	Median : 528.48	Median :130.32
##	Mean : 559.85	Mean : 306.87	Mean : 880.72	Mean :187.99
##	3rd Qu.: 407.48	3rd Qu.: 445.86	3rd Qu.:1096.63	3rd Qu.:267.74
##	Max. :8690.62	Max. :1685.81	Max. :5064.45	Max. :720.54
##	Guanidoacetate	Hippurate	Histidine	Hypoxanthine
##	Min. : 7.03	Min. : 92.76	Min. : 14.15	Min. : 3.78
##	1st Qu.: 33.78	1st Qu.: 492.75	1st Qu.: 66.69	1st Qu.: 20.70
##	Median : 64.72	Median : 1224.15	Median : 174.16	Median : 40.04
##	Mean : 86.37	Mean : 2286.84	Mean : 292.64	Mean : 61.10
##	3rd Qu.:108.85	3rd Qu.: 2921.93	3rd Qu.: 419.89	3rd Qu.: 83.93
##	Max. :561.16	Max. :19341.34	Max. :1863.11	Max. :265.07
##	Isoleucine	Lactate	Leucine	Lysine
##	Min. : 1.790	Min. : 7.32	Min. : 2.51	Min. : 10.49
##	1st Qu.: 3.900	1st Qu.: 35.52	1st Qu.: 9.12	1st Qu.: 30.27
##	Median : 7.170	Median : 81.45	Median : 19.11	Median : 69.41
##	Mean : 8.709	Mean : 158.46	Mean : 24.36	Mean :108.79
##	3rd Qu.:11.250	3rd Qu.: 139.77	3rd Qu.: 31.19	3rd Qu.:121.51
##	Max. :40.040	Max. :3640.95	Max. :103.54	Max. :788.40
##	Methylamine	Methylguanidine	N.N.Dimethylglycine	O.Acetylcarnitine
##	Min. : 1.51	Min. : 1.70	Min. : 0.79	Min. : 1.23
##	1st Qu.: 5.26	1st Qu.: 4.26	1st Qu.: 7.03	1st Qu.: 3.94
##	Median :14.73	Median : 7.85	Median : 21.98	Median : 11.47
##	Mean :17.38	Mean : 15.32	Mean : 26.35	Mean : 19.73
##	3rd Qu.:24.05	3rd Qu.: 19.30	3rd Qu.: 40.04	3rd Qu.: 20.91
##	Max. :52.46	Max. :141.17	Max. :120.30	Max. :254.68
##	Pantothenate	Pyroglutamate	Pyruvate	Quinolinate
##	Min. : 2.59	Min. : 21.33	Min. : 0.90	Min. : 5.21
##	1st Qu.: 11.13	1st Qu.: 68.72	1st Qu.: 4.85	1st Qu.: 26.58
##	Median : 22.65	Median : 157.59	Median : 13.46	Median : 51.42
##	Mean : 44.88	Mean : 211.45	Mean : 21.29	Mean : 66.44
##	3rd Qu.: 41.26	3rd Qu.: 301.87	3rd Qu.: 29.08	3rd Qu.: 87.36
##	Max. :692.29	Max. :1064.22	Max. :184.93	Max. :259.82
##	Serine	Succinate	Sucrose	Tartrate
##	Min. : 16.12	Min. : 1.72	Min. : 6.49	Min. : 2.20
##	1st Qu.: 83.10	1st Qu.: 8.58	1st Qu.: 19.30	1st Qu.: 6.89
##	Median : 142.59	Median : 30.88	Median : 40.85	Median : 12.94
##	Mean : 197.69	Mean : 60.23	Mean : 113.23	Mean : 40.00
##	3rd Qu.: 270.43	3rd Qu.: 74.44	3rd Qu.: 94.63	3rd Qu.: 25.79
##	Max. :1248.88	Max. :589.93	Max. :2079.74	Max. :837.15
##	Taurine	Threonine	Trigonelline	Trimethylamine.N.oxide
##	Min. : 17.81	Min. : 8.25	Min. : 10.07	Min. : 55.7
##	1st Qu.: 99.48	1st Qu.: 31.82	1st Qu.: 53.52	1st Qu.: 175.9
##	Median : 249.64	Median : 64.07	Median : 114.43	Median : 383.8
##	Mean : 525.12	Mean : 95.36	Mean : 270.44	Mean : 652.2
##	3rd Qu.: 665.14	3rd Qu.:137.00	3rd Qu.: 340.36	3rd Qu.: 735.1
##	Max. :4272.69	Max. :450.34	Max. :2252.96	Max. :5486.2
##	Tryptophan	Tyrosine	Uracil	Valine
##	Min. : 8.67	Min. : 4.22	Min. : 3.10	Min. : 4.10
##	1st Qu.: 21.33	1st Qu.: 23.57	1st Qu.: 11.94	1st Qu.: 12.18
##	Median : 46.99	Median : 60.34	Median : 27.39	Median : 33.12

```
## Mean : 66.24 Mean : 81.76 Mean : 35.56 Mean : 35.67
## 3rd Qu.: 96.54 3rd Qu.:113.30 3rd Qu.: 44.26 3rd Qu.: 50.40
## Max. :259.82 Max. :539.15 Max. :179.47 Max. :160.77
## Xylose cis.Aconitate myo.Inositol trans.Aconitate
## Min. : 10.07 Min. : 12.94 Min. : 11.59 Min. : 4.90
## 1st Qu.: 29.96 1st Qu.: 36.23 1st Qu.: 30.27 1st Qu.: 12.43
## Median : 50.40 Median : 129.02 Median : 78.26 Median : 26.84
## Mean : 100.93 Mean : 204.22 Mean :135.40 Mean : 40.63
## 3rd Qu.: 89.12 3rd Qu.: 254.68 3rd Qu.:167.34 3rd Qu.: 57.40
## Max. :2164.62 Max. :1863.11 Max. :854.06 Max. :217.02
## pi.Methylhistidine tau.Methylhistidine
## Min. : 11.36 Min. : 8.00
## 1st Qu.: 67.36 1st Qu.: 27.39
## Median : 162.39 Median : 68.72
## Mean : 370.29 Mean : 89.69
## 3rd Qu.: 387.61 3rd Qu.:130.32
## Max. :2697.28 Max. :317.35
```

2. Comprovació de valors mancats

```
missing_values <- sum(is.na(data)) # Comptar el nombre de valors mancats en tot el conjunt de dades
print(paste("Total de valors mancats:", missing_values))
```

```
## [1] "Total de valors mancats: 0"
```

Proporció de valors mancats per cada metabòlit

```
missing_proportions <- colSums(is.na(data)) / nrow(data) # Proporció de NA's en cada columna
print("Proporció de valors mancats per metabòlit:")
```

```
## [1] "Proporció de valors mancats per metabòlit:"
```

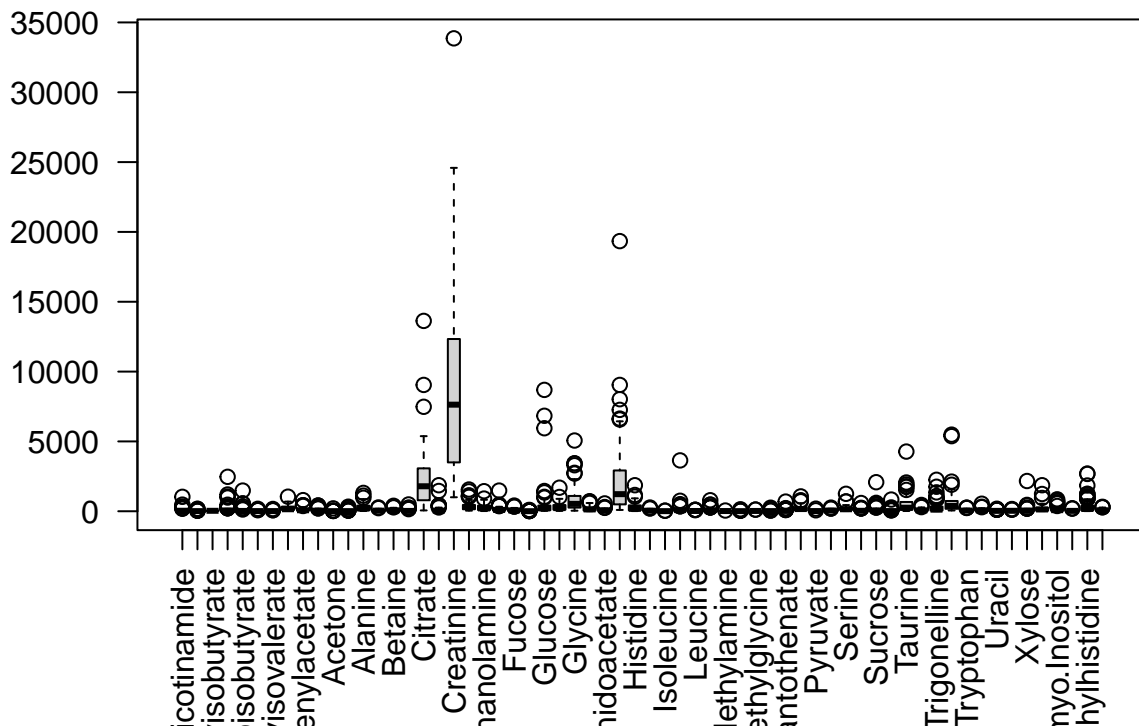
```
print(missing_proportions)
```

```
## Muscle.loss X1.6.Anhydro.beta.D.glucose
## 0 0
## X1.Methylnicotinamide X2.Aminobutyrate
## 0 0
## X2.Hydroxyisobutyrate X2.Oxoglutarate
## 0 0
## X3.Aminoisobutyrate X3.Hydroxybutyrate
## 0 0
## X3.Hydroxyisovalerate X3.Indoxylsulfate
## 0 0
## X4.Hydroxyphenylacetate Acetate
## 0 0
## Acetone Adipate
## 0 0
## Alanine Asparagine
## 0 0
## Betaine Carnitine
## 0 0
## Citrate Creatine
## 0 0
```

##	Creatinine	Dimethylamine
##	0	0
##	Ethanolamine	Formate
##	0	0
##	Fucose	Fumarate
##	0	0
##	Glucose	Glutamine
##	0	0
##	Glycine	Glycolate
##	0	0
##	Guanidoacetate	Hippurate
##	0	0
##	Histidine	Hypoxanthine
##	0	0
##	Isoleucine	Lactate
##	0	0
##	Leucine	Lysine
##	0	0
##	Methylamine	Methylguanidine
##	0	0
##	N.N.Dimethylglycine	O.Acetylcarnitine
##	0	0
##	Pantothenate	Pyroglutamate
##	0	0
##	Pyruvate	Quinolate
##	0	0
##	Serine	Succinate
##	0	0
##	Sucrose	Tartrate
##	0	0
##	Taurine	Threonine
##	0	0
##	Trigonelline	Trimethylamine.N.oxide
##	0	0
##	Tryptophan	Tyrosine
##	0	0
##	Uracil	Valine
##	0	0
##	Xylose	cis.Aconitate
##	0	0
##	myo.Inositol	trans.Aconitate
##	0	0
##	pi.Methylhistidine	tau.Methylhistidine
##	0	0

```
# 3. Visualització de la distribució dels metabòlits (Boxplot)
# Crear un boxplot per veure la distribució dels valors dels metabòlits
boxplot(data[, -c(1,2)], main = "Distribució dels metabòlits", las = 2)
```

Distribució dels metabòlits



```
# 4. Comparació entre pacients cachectics i no cachectics
# Separen els pacients segons la seva condició de pèrdua de massa muscular (cachexia)
cachectic <- data[data$Muscle.loss == "cachexic", -c(1,2)] # Dades de pacients cachectics
non_cachectic <- data[data$Muscle.loss != "cachexic", -c(1,2)] # Dades de pacients no cachectics

# Calcular la mitjana dels metabòlits per a cada grup
cachectic_mean <- colMeans(cachectic, na.rm = TRUE)
non_cachectic_mean <- colMeans(non_cachectic, na.rm = TRUE)

# Crear un dataframe per comparar les mitjanes
comparison <- data.frame(Cachectic = cachectic_mean, Non_cachectic = non_cachectic_mean)
print("Comparació entre pacients cachectics i no cachectics:")
```

```
## [1] "Comparació entre pacients cachectics i no cachectics:"
```

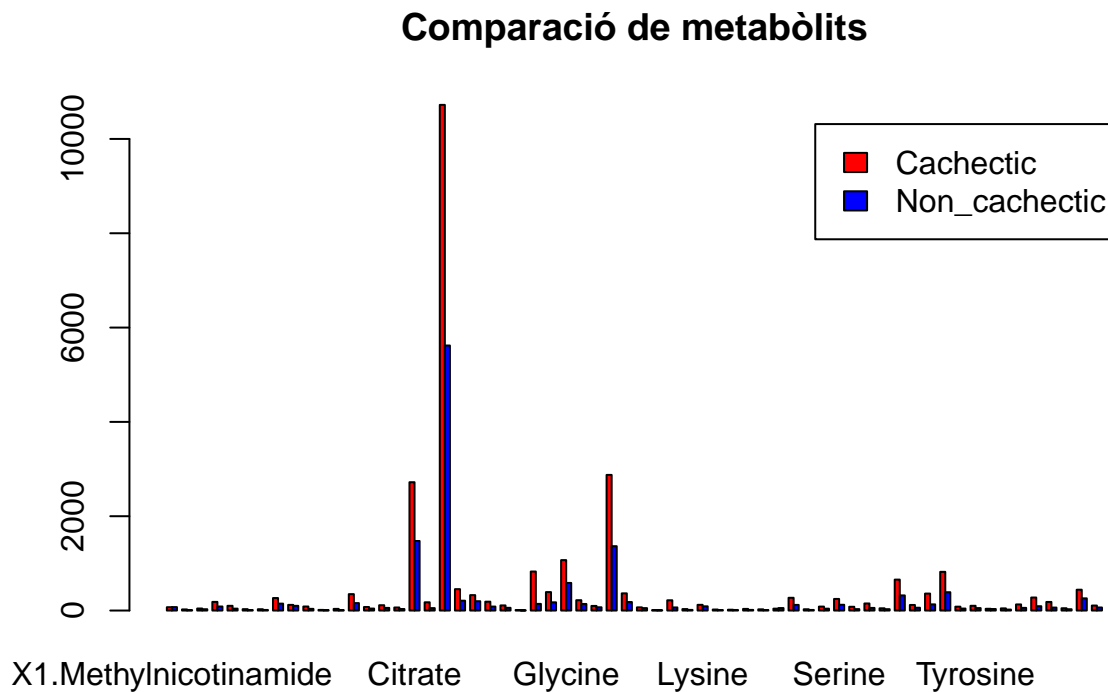
```
print(comparison)
```

##	Cachectic	Non_cachectic
## X1.Methylnicotinamide	70.564255	73.155000
## X2.Aminobutyrate	23.669149	9.528333
## X2.Hydroxyisobutyrate	43.237660	27.871000
## X2.Oxoglutarate	183.110426	85.517333
## X3.Aminoisobutyrate	100.274681	39.911000
## X3.Hydroxybutyrate	29.260638	9.898667
## X3.Hydroxyisovalerate	27.606383	12.312667

## X3.Indoxylsulfate	265.157660	146.376333
## X4.Hydroxyphenylacetate	119.822553	99.798667
## Acetate	85.632979	35.604667
## Acetone	13.346383	8.420000
## Adipate	34.817872	8.993333
## Alanine	347.591064	157.584000
## Asparagine	75.390851	41.749000
## Betaine	112.252979	55.970333
## Carnitine	64.622128	32.443667
## Citrate	2720.852766	1474.718667
## Creatine	174.913404	51.504333
## Creatinine	10722.140213	5619.174667
## Dimethylamine	453.580638	208.683333
## Ethanolamine	326.772128	197.125333
## Formate	187.564468	84.483333
## Fucose	108.599149	57.444667
## Fumarate	10.921915	4.552000
## Glucose	827.218936	140.958000
## Glutamine	391.410426	174.427333
## Glycine	1069.377872	585.149333
## Glycolate	219.269574	138.983667
## Guanidoacetate	97.624255	68.739667
## Hippurate	2875.729574	1364.240333
## Histidine	364.232340	180.472333
## Hypoxanthine	67.087021	51.714333
## Isoleucine	9.660851	7.218000
## Lactate	217.631915	65.748333
## Leucine	31.261702	13.556667
## Lysine	121.282340	89.229333
## Methylamine	21.216383	11.360000
## Methylguanidine	17.364681	12.128333
## N.N.Dimethylglycine	34.489787	13.596667
## O.Acetylcarnitine	25.564468	10.598000
## Pantothenate	39.944043	52.622667
## Pyroglutamate	270.292340	119.258000
## Pyruvate	26.865532	12.566333
## Quinolate	83.747234	39.324000
## Serine	245.829787	122.263000
## Succinate	79.628936	29.836000
## Sucrose	150.024468	55.579667
## Tartrate	47.234681	28.676000
## Taurine	655.720000	320.522333
## Threonine	118.233191	59.518667
## Trigonelline	359.637660	130.687000
## Trimethylamine.N.oxide	820.340638	388.669000
## Tryptophan	81.824043	41.833000
## Tyrosine	100.742340	52.014000
## Uracil	37.513617	32.493333
## Valine	45.582553	20.132667
## Xylose	129.289149	56.509333
## cis.Aconitate	276.025532	91.724000
## myo.Inositol	181.837660	62.641333
## trans.Aconitate	48.814043	27.809333
## pi.Methylhistidine	441.553191	258.640000

```
## tau.Methylhistidine      105.667660      64.650333
```

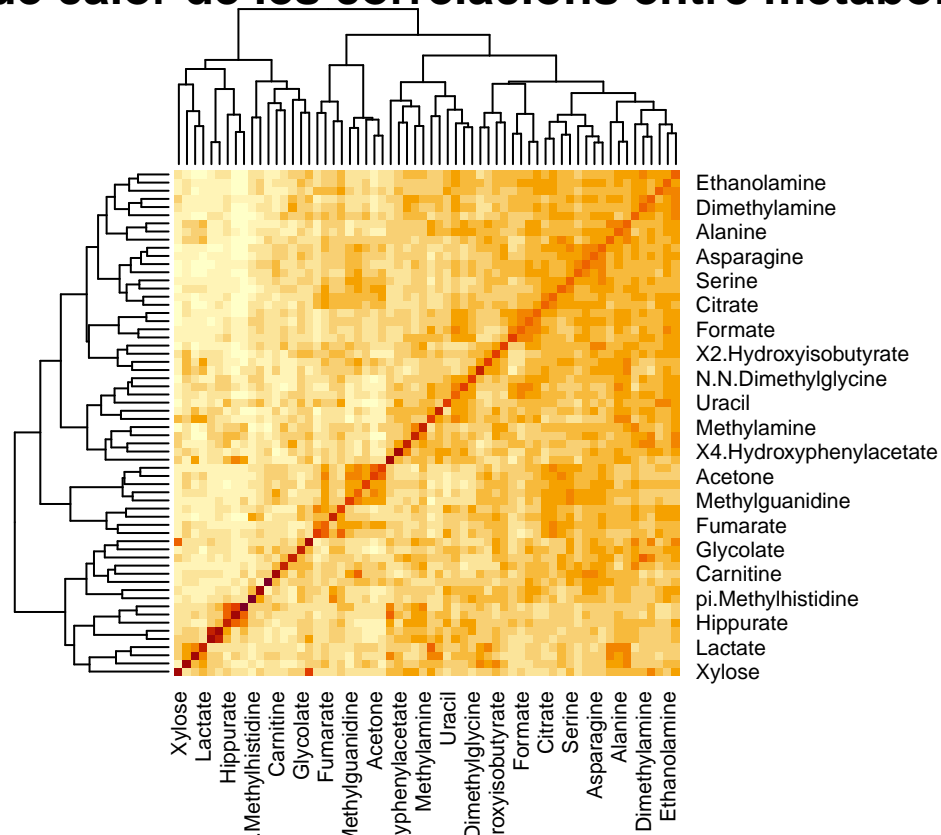
```
# Gràfic de barres per a la comparació de les mitjanes dels metabòlits
barplot(t(as.matrix(comparison)), beside = TRUE, col = c("red", "blue"),
        legend = TRUE, main = "Comparació de metabòlits")
```



```
# 5. Correlacions entre metabòlits
# Calcular la matriu de correlacions entre els diferents metabòlits
correlations <- cor(data[, -c(1,2)], use = "complete.obs")

# Crear un mapa de calor per visualitzar les correlacions
heatmap(correlations, main = "Mapa de calor de les correlacions entre metabòlits")
```

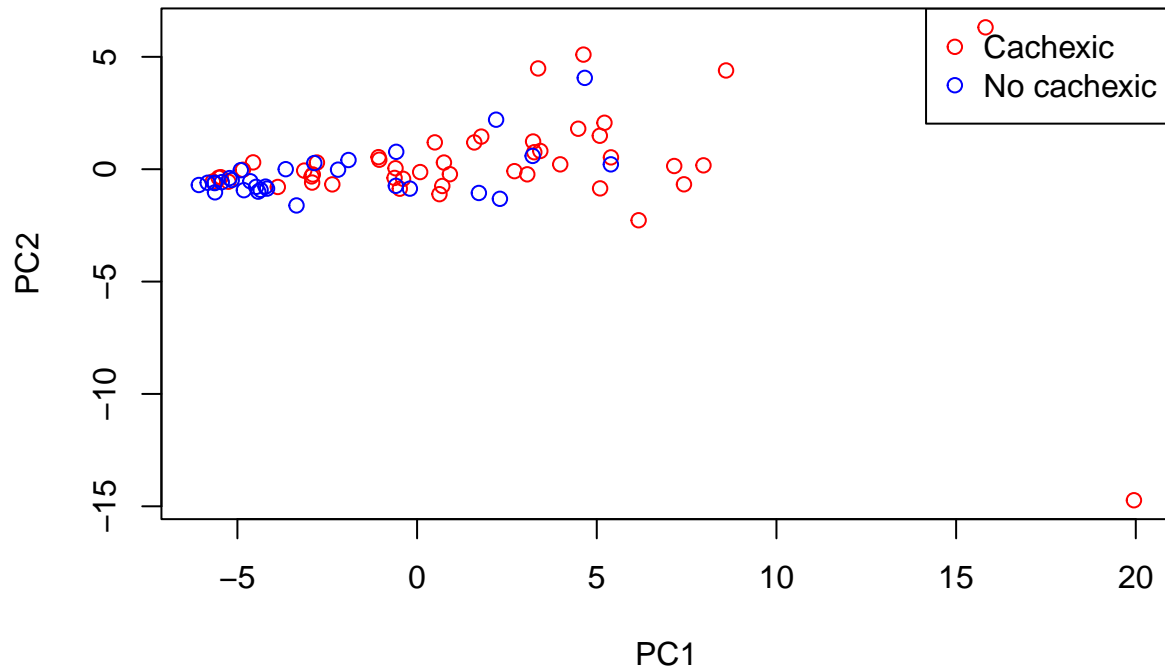
Mapa de calor de les correlacions entre metabòlits



```
# 6. Anàlisi de components principals (PCA)
# Aplicar PCA a les dades dels metabòlits
pca <- prcomp(data[, -c(1,2)], scale. = TRUE)

# Gràfic dels primers dos components principals
plot(pca$x[, 1:2], col = ifelse(data$Muscle.loss == "cachexic", "red", "blue"),
     main = "PCA dels pacients", xlab = "PC1", ylab = "PC2")
legend("topright", legend = c("Cachexic", "No cachexic"), col = c("red", "blue"), pch = 1)
```

PCA dels pacients



```
# 7. Diferències estadístiques (t-test)
# Aplicar un t-test per a cada metabòlit per comparar els grups cachectics i no cachectics
t_tests <- apply(data[, -c(1,2)], 2, function(metabolite) t.test(metabolite ~ data$Muscle.loss)$p.value)

# Identificar els metabòlits amb diferències significatives (p-valor < 0.05)
significant_metabolites <- which(t_tests < 0.05)
print("Metabòlits significatius:")
```

```
## [1] "Metabòlits significatius:"
```

```
print(names(significant_metabolites))
```

```
## [1] "X2.Aminobutyrate"      "X2.Hydroxyisobutyrate" "X3.Hydroxybutyrate"
## [4] "X3.Hydroxyisovalerate" "X3.Indoxylsulfate"     "Acetate"
## [7] "Adipate"              "Alanine"               "Asparagine"
## [10] "Betaine"              "Carnitine"             "Citrate"
## [13] "Creatine"             "Creatinine"            "Dimethylamine"
## [16] "Ethanolamine"         "Formate"               "Fucose"
## [19] "Fumarate"             "Glucose"               "Glutamine"
## [22] "Glycine"              "Glycolate"             "Hippurate"
## [25] "Histidine"            "Leucine"               "Methylamine"
## [28] "N.N.Dimethylglycine"  "O.Acetylcarnitine"     "Pyroglutamate"
## [31] "Pyruvate"             "Quinolate"             "Serine"
## [34] "Succinate"            "Taurine"               "Threonine"
```

## [37]	"Trigonelline"	"Trimethylamine.N.oxide"	"Tryptophan"
## [40]	"Tyrosine"	"Valine"	"cis.Aconitate"
## [43]	"myo.Inositol"	"trans.Aconitate"	"tau.Methylhistidine"