

# PEC\_OMICAS

2024-11-07

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("SummarizedExperiment")

## Bioconductor version 3.16 (BiocManager 1.30.25), R 4.2.3 (2023-03-15)

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

## Old packages: 'KernSmooth', 'nlme'

if (!requireNamespace("S4Vectors", quietly = TRUE)) {
  install.packages("BiocManager")
  BiocManager::install("S4Vectors")
}

library(S4Vectors)

## Loading required package: stats4

## Loading required package: BiocGenerics

##
## Attaching package: '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, sort,
##   table, tapply, union, unique, unsplit, which.max, which.min

##
## Attaching package: 'S4Vectors'
```

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

```
library(readr)
DataInfo_S013 <- read_csv("DataInfo_S013.csv")
```

```
## New names:
## Rows: 695 Columns: 4
## -- Column specification
## ----- Delimiter: "," chr
## (4): ...1, VarName, varTpe, Description
## i Use 'spec()' to retrieve the full column specification for this data. i
## Specify the column types or set 'show_col_types = FALSE' to quiet this message.
## * ' -> '...1'
```

```
View(DataInfo_S013)
```

```
head(DataInfo_S013)
```

```
## # A tibble: 6 x 4
##   ...1      VarName varTpe      Description
##   <chr>    <chr>    <chr>    <chr>
## 1 SUBJECTS SUBJECTS integer dataDesc
## 2 SURGERY  SURGERY  character dataDesc
## 3 AGE      AGE      integer  dataDesc
## 4 GENDER   GENDER   character dataDesc
## 5 Group    Group    integer  dataDesc
## 6 MEDDM_TO MEDDM_TO integer  dataDesc
```

```
library(readr)
DataValues_S013 <- read_csv("DataValues_S013.csv")
```

```
## New names:
## Rows: 39 Columns: 696
## -- Column specification
## ----- Delimiter: "," chr
## (2): SURGERY, GENDER dbl (693): ...1, SUBJECTS, AGE, Group, MEDDM_TO,
## MEDCOL_TO, MEDINF_TO, MEDHT... lgl (1): X
## i Use 'spec()' to retrieve the full column specification for this data. i
## Specify the column types or set 'show_col_types = FALSE' to quiet this message.
## * ' -> '...1'
```

```
View(DataValues_S013)
```

```
head(DataValues_S013)
```

```
## # A tibble: 6 x 696
##   ...1 SUBJECTS SURGERY AGE GENDER Group MEDDM_TO MEDCOL_TO MEDINF_TO
##   <dbl>    <dbl> <chr>    <dbl> <chr> <dbl>    <dbl>    <dbl>    <dbl>
```

```
## 1      1      1 by pass    27 F      1      0      0      0
## 2      2      2 by pass    19 F      2      0      0      0
## 3      3      3 by pass    42 F      1      0      0      0
## 4      4      4 by pass    37 F      2      0      0      0
## 5      5      5 tubular    42 F      1      0      0      0
## 6      6      6 by pass    24 F      2      0      0      0
## # i 687 more variables: MEDHTA_TO <dbl>, GLU_TO <dbl>, INS_TO <dbl>,
## #   HOMA_TO <dbl>, HBA1C_TO <dbl>, HBA1C.mmol.mol_TO <dbl>, PESO_TO <dbl>,
## #   bmi_TO <dbl>, CC_TO <dbl>, CINT_TO <dbl>, CAD_TO <dbl>, TAD_TO <dbl>,
## #   TAS_TO <dbl>, TG_TO <dbl>, COL_TO <dbl>, LDL_TO <dbl>, HDL_TO <dbl>,
## #   VLDL_TO <dbl>, PCR_TO <dbl>, LEP_TO <dbl>, ADIPO_TO <dbl>, GOT_TO <dbl>,
## #   GPT_TO <dbl>, GGT_TO <dbl>, URICO_TO <dbl>, CREAT_TO <dbl>, UREA_TO <dbl>,
## #   HIERRQ_TO <dbl>, TRANSF_TO <dbl>, FERR_TO <dbl>, Ile_TO <dbl>, ...
```

```
data_matrix <- as.matrix(DataValues_S013[1:10, c("GLU_TO", "INS_TO", "HOMA_TO")])
colData <- DataFrame(
  Condition = c("GLU_TO", "INS_TO", "HOMA_TO"),
  row.names = colnames(data_matrix)
)
rowData <- DataFrame(
  Subject = DataValues_S013$SUBJECTS[1:10],
  Surgery = as.factor(DataValues_S013$SURGERY[1:10]),
  row.names = rownames(data_matrix)
)
library(SummarizedExperiment)
```

```
## Loading required package: MatrixGenerics
```

```
## Loading required package: matrixStats
```

```
##
```

```
## Attaching package: '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
```

```
## Loading required package: GenomicRanges
```

```
## Loading required package: IRanges
```

```
## Loading required package: GenomeInfoDb

## Loading required package: Biobase

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

##
## Attaching package: 'Biobase'

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

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

```
se <- SummarizedExperiment(
  assays = list(counts = data_matrix),
  colData = colData,
  rowData = rowData
)
print(se)
```

```
## class: SummarizedExperiment
## dim: 10 3
## metadata(0):
## assays(1): counts
## rownames: NULL
## rowData names(2): Subject Surgery
## colnames(3): GLU_TO INS_TO HOMA_TO
## colData names(1): Condition
```

```
assays(se)$counts
```

```
##      GLU_TO INS_TO HOMA_TO
## [1,]    85  11.40    2.40
## [2,]    78  12.10    2.32
## [3,]    75   8.41    1.56
## [4,]    71  12.80    2.25
## [5,]    82   6.01    1.22
## [6,]    71   9.88    1.73
## [7,]    80   9.20    1.82
## [8,]    90   3.40    0.76
## [9,]    92   5.43    1.23
## [10,]   84   6.98    1.45
```

```
colData(se)
```

```
## DataFrame with 3 rows and 1 column
##           Condition
##      <character>
## GLU_T0      GLU_T0
## INS_T0      INS_T0
## HOMA_T0     HOMA_T0
```

```
se[, se$dex == "trt"]
```

```
## class: SummarizedExperiment
## dim: 10 0
## metadata(0):
## assays(1): counts
## rownames: NULL
## rowData names(2): Subject Surgery
## colnames(0):
## colData names(1): Condition
```