task5_0930

2025-09-30

```
options(help_type = "text")

data("CO2")     #open data CO2
dim(CO2)
```

```
## [1] 84  5
```

```
str(CO2)
```

```
## Classes 'nfnGroupedData', 'nfGroupedData', 'groupedData' and 'data.frame':   84 obs. of  5
variables:
##  $ Plant    : Ord.factor w/ 12 levels "Qn1"<"Qn2"<"Qn3"<..: 1 1 1 1 1 1 1 2 2 2 ...
##  $ Type     : Factor w/ 2 levels "Quebec","Mississippi": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Treatment: Factor w/ 2 levels "nonchilled","chilled": 1 1 1 1 1 1 1 1 1 1 ...
##  $ conc     : num  95 175 250 350 500 675 1000 95 175 250 ...
##  $ uptake   : num  16 30.4 34.8 37.2 35.3 39.2 39.7 13.6 27.3 37.1 ...
##  - attr(*, "formula")=Class 'formula'  language uptake ~ conc | Plant
##   .. ..- attr(*, ".Environment")=<environment: R_EmptyEnv>
##  - attr(*, "outer")=Class 'formula'  language ~Treatment * Type
##   .. ..- attr(*, ".Environment")=<environment: R_EmptyEnv>
##  - attr(*, "labels")=List of 2
##   ..$ x: chr "Ambient carbon dioxide concentration"
##   ..$ y: chr "CO2 uptake rate"
##  - attr(*, "units")=List of 2
##   ..$ x: chr "(uL/L)"
##   ..$ y: chr "(umol/m^2 s)"
```

```
help("CO2", package = "datasets")   # use help function
summary(CO2)
```

```
##      Plant             Type         Treatment       conc          uptake
##  Qn1    : 7   Quebec     :42   nonchilled:42   Min.   :  95   Min.   : 7.70
##  Qn2    : 7   Mississippi:42   chilled   :42   1st Qu.: 175   1st Qu.:17.90
##  Qn3    : 7                                     Median : 350   Median :28.30
##  Qc1    : 7                                     Mean   : 435   Mean   :27.21
##  Qc3    : 7                                     3rd Qu.: 675   3rd Qu.:37.12
##  Qc2    : 7                                     Max.   :1000   Max.   :45.50
##  (Other):42
```

```
#calculate the average and median CO2 uptake of the plants from Quebec and Mississippi
avg <- tapply(CO2$uptake, CO2$Type, mean,   na.rm = TRUE)
med <- tapply(CO2$uptake, CO2$Type, median, na.rm = TRUE)
avg; med
```

```
##      Quebec Mississippi
##    33.54286    20.88333
```

```
##      Quebec Mississippi
##       37.15       19.30
```

```
if (requireNamespace("airway", quietly = TRUE) &&
    requireNamespace("SummarizedExperiment", quietly = TRUE)) {

library(airway)
library(SummarizedExperiment)

data("airway")
cts <- assays(airway)[["counts"]]

#[Optional] In the “airway” example data from Bioconductor, how many genes are expressed in ea
ch sample? How many genes are not expressed in any sample?
expressed_per_sample <- colSums(cts > 0)
  expressed_tbl <- data.frame(
    sample = colnames(cts),
    expressed_genes = as.integer(expressed_per_sample),
    row.names = NULL
  )
  expressed_tbl

#not expressed in any sample
not_expressed_any <- sum(rowSums(cts > 0) == 0)
not_expressed_any

} else {
  cat("Skipped airway analysis: install 'airway' and 'SummarizedExperiment' in the console fir
st.\n")
}
```

```
## Loading required package: 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: stats4
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: generics
```

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

```
## The following objects are masked from 'package:base':
##
##     as.difftime, as.factor, as.ordered, intersect, is.element, setdiff,
##     setequal, union
```

```
##
## 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, is.unsorted, lapply, Map, mapply, match, mget,
##     order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##     rbind, Reduce, rownames, sapply, saveRDS, table, tapply, unique,
##     unsplit, which.max, which.min
```

```
## Loading required package: S4Vectors
```

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

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

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

```
## 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
```

```
## [1] 30208
```