Package: uem915 (via r-universe)

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Title Omic Analysis uem915

Version 1.0.2

Description Omic Analysis uem915.

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Depends R (>= 4.3)

Imports broom, dendextend, doParallel, dplyr, foreach, ggforce, ggplot2, ggpubr, gplots, graphics, grDevices, gridExtra, limma, magrittr, moalannotensg, moalannotensp, moalannotenst, moalannotgene, parallel, plyr, rlang, scales, stats, tidyselect, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

Roxygen list(markdown = TRUE)

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Contents

`acp` *Principal Component Analysis*

Description

Principal Component Analysis

Usage

```
acp(
  dat,
  factor = NULL,
  samplename = NULL,
  pc1 = 1,
  pc2 = 2,
  center = TRUE,
  scale = TRUE,
  title = "ACP",
  legendtitle = "TREATMENT"
)
```

Arguments

`dat`	matrix numeric
`factor`	factor
`samplename`	character
`pc1`	numeric
`pc2`	numeric
`center`	logical TRUE
`scale`	logical TRUE
`title`	character
`legendtitle`	character

Value

no values

Author(s)

Florent Dumont florent.dumont@univresite-paris-saclay.fr

Examples

```
# not run
# acp( mat1 , sif1 )
```

`annot` *Annotation*

Description

Annotate a list of symbols or IDs

Usage

```
annot(
  symbollist,
  species = NULL,
  ortholog = F,
  dboutput = "ncbi",
  idtype = NULL
)
```

Arguments

`symbollist`	character list of IDs or Symbols
`species`	character for species hs mm rn dr
`ortholog`	logical return homo sapiens ortholog of species
`dboutput`	character database used for Symbol annotation ncbi or ebi
`idtype`	character annotation database ID type among SYMBOL (by defaut) GENE, ENST, ENSG, ENSP, UNIPROT

Details

supported is : symbol, ncbi gene, ensembl gene , transcrit, protein, uniprot swissrot, uniprot trembl species : hs homo sapien , mm mus musculus , rn rattus norvegicus, dr danio rerio

Value

data.frame

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# annot(SymbolList)
```

`boxplot` *Boxplot*

Description

Boxplot

Usage

```
boxplot(
  dat,
  factor,
  outline = FALSE,
  title = "Boxplot",
  legendtitle = "TREATMENT",
  outlier = T,
  coefiqr = 1.5,
  ggplot = FALSE
)
```

Arguments

`dat`	matrix numeric
`factor`	factor
`outline`	logical display outliers FALSE by default
`title`	character
`legendtitle`	character
`outlier`	boolean
`coefiqr`	numeric
`ggplot`	logical use graphics library or ggplot FALSE by default

Details

To make boxplot from matrix.

Value

plot

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# mat1 %>% boxplot( factor = sif1$F3 )
```

`boxplot1` *boxplot for one var*

Description

boxplot for one var

Usage

```
boxplot1(dat, ylab = "y", xlab = "TREATMENT", log = T)
```

Arguments

`dat`	data.frame
`ylab`	character
`xlab`	character
`log`	logical if TRUE data are delog in base 2

Value

plot

Author(s)

Florent Dumont florent.dumont@univresite-paris-saclay.fr

Examples

```
# not run
```

---

ena *MSigDB enrichment analysis*

Description

MSigDB enrichment analysis

Usage

```
ena(
  SymbolList = NULL,
  geneannot = NULL,
  species = "hs",
  bg = 25000,
  filtergeneset = "all",
  overlapmin = 2,
  enaScoremin = 1,
  top = 80,
  labsize = 11,
  dpibarplot = "screen",
  path = ".",
  dirname = NULL
)
```

Arguments

`SymbolList`	character Symbol or NCBI gene ID
`geneannot`	data.frame
`species`	character hs mm rn dr ss
`bg`	numeric
`filtergeneset`	regexp to filter geneset database
`overlapmin`	numeric for minimum overlap between geneset and list
`enaScoremin`	numeric for minimum ratio ena
`top`	numeric top features to plot
`labsize`	numeric size of function in barplot
`dpibarplot`	character barplot resolution
`path`	character for relative path of output directory
`dirname`	character name for output

Value

file with enrichment analysis results

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# ena( Symbollist , filtergeneset = "reactome")
```

`env` *loading regular libraries*

Description

load magrittr, dplyr, gplots, ggplot2, foreach, parallel, doParallel

Usage

```
env()
```

`hc` *Hierarchical clustering classification*

Description

make a hierarchical clustering classification

Usage

```
hc(
  dat,
  factor = NULL,
  title = "Hierarchical Clustering",
  plot = TRUE,
  method = "complete",
  legendtitle = "TREATMENT",
  cexlabel = 0.6
)
```

Arguments

`dat`	matrix numeric
`factor`	factor
`title`	character
`plot`	logical
`method`	character to choose agglomerative method of clustering dendrogramm
`legendtitle`	character
`cexlabel`	numeric

Details

Possible agglomerative method are the same hclust fonction : "complete" method by default

Value

a dendrogram

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# hc(dat)
```

`heatmap` *Heatmap*

Description

To make a heatmap

Usage

```
heatmap(
  dat,
  factor,
  method = "complete",
  dendrogram = "both",
  k = NULL,
  labCol = "",
  cexCol = 0.85,
  labRow = "",
  cexRow = 0.35,
  cexlegend = 0.65,
  keysize = 0.9,
  keycolor = c("darkgreen", "orange", "darkred"),
  parmar = c(5, 4, 5, 6)
)
```

Arguments

`dat`	matrix numeric
`factor`	factor
`method`	character

`dendrogram`	character to display 'none', 'row', 'column' or 'both' (by default) dendrograms
`k`	numeric number of clusters to colorize for rows
`labCol`	character
`cexCol`	numeric
`labRow`	Character
`cexRow`	numeric
`cexlegend`	numeric
`keysize`	numeric
`keycolor`	character of 3 for low mid high value of the key
`parmar`	numeric 4 values for margin sizes

Details

To make a heatmap from a matrix or a data.frame

Value

no returned value

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# library(magrittr)
# data(sif1)
# data(mat1)
# mat1 %>% heatmap(sif1$F3)
```

`input` *import tab file in data.frame*

Description

import tab file in data.frame

Usage

```
input(filename, sep = "\t", quote = "")
```

Arguments

`filename`	character path to the file to read
`sep`	character for field separator
`quote`	character for field quote

Details

wrapper of read.table function for tabular separated files

Value

data.frame

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# input( "filename" ) -> dt
```

`norm` *Normalization*

Description

quantile normalization and log2

Usage

```
norm(dat, method = NULL, log = TRUE)
```

Arguments

`dat`	data.frame
`method`	character apply quantile normalization by default see details
`log`	logical apply log base 2

Details

for .method see limma normalizeBetweenArrays method

Value

data.frame

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# norm(dt)
```

`omic` *Omic bioanalysis workflow*

Description

Biostatistics analysis: QCs, ANOVA, threshold filtering, venn diagramm, cluster analysis for significant rows, pattern search

Graphics: volcanoplots, heatmaps, lineplots, boxplots (with Kruskal-Wallis test)

Functional analysis: MSigDB enrichment analysis, stringDB protein interaction network, topGO analysis (gene ontology)

See example section to test workflow with internal data.

Usage

```
omic(
  dat,
  sif,
  annot = NULL,
  species = "hs",
  model = NULL,
  paired = NULL,
  nested = NULL,
  batch = NULL,
  addfactor = NULL,
  qcs = TRUE,
  threshold = c(c(2, 6, 11), c(2, 6, 11) + 120),
  padj = "none",
  pattern = TRUE,
  venn = TRUE,
  cluster = TRUE,
  nc = c(2, 3, 6, 12),
  heatmap = TRUE,
  maxheatmap = NULL,
  volcanoplot = TRUE,
  lineplot = TRUE,
  boxplotrow = TRUE,
  ena = TRUE,
  enamin = 2,
  filtergeneset = "all",
  enaScoremin = 1.1,
  bg = 25000,
  sample = NULL,
  dopar = NULL,
  path = ".",
  dirname = NULL,
  zip = FALSE,
```

```
  remove = FALSE
)
```

Arguments

`dat`	data.frame normalize data table
`sif`	data.frame sample information file including model factors
`annot`	data.frame annotation with Symbol column for functional analysis
`species`	character available species: bt ce dr dm gg hs mm pt rn ss xt
`model`	character anova model factors (see details)
`paired`	character factor for paired design
`nested`	character factor for nested design
`batch`	character factor for batch effect design
`addfactor`	character additionnal factors
`qcs`	logical quality controls
`threshold`	numeric vector from 1 to 160 (see details)
`padj`	character fdr by defaut for Benjamini-Hochberg false discovery correction
`pattern`	logical search relevant pattern accross comparisons (see details)
`venn`	logical venn diagram
`cluster`	logical row hierarchical clustering using pearson correlation
`nc`	numeric number of clusters to cut in dendrogramm
`heatmap`	logical do heatmaps for all lists
`maxheatmap`	numeric max rows for heatmap
`volcanoplot`	logical make volcanoplot for each threshold
`lineplot`	logical do lineplot for significant features
`boxplotrow`	logical do boxplot for significant features with Kruskal
`ena`	logical msigdb enrichement analysis (over-representation analysis)
`enamin`	numeric min list size for functional analysis
`filtergeneset`	character regular expression to filter collection geneset (e.g. "reactomeltft")
`enaScoremin`	numeric for minimum ratio ena
`bg`	numeric background used for over-representation test
`sample`	numeric subset analysis
`dopar`	numeric core number
`path`	character results directory path
`dirname`	character results directory name
`zip`	logical compress results directory if TRUE
`remove`	logical remove uncompress results directory if TRUE

Details

Use uem915::env() to load required libraries before uem915::omic() (see example)

Accepted values for threshold param (1 to 150): see list -> uem915:::thresholdlist %>% lapply("[",c(1,2)) %>% unlist %>% matrix(ncol=2,byrow = T) %>% data.frame %>% setNames(c("pval","fc"))

Pattern: search relevant profiles among up and down comparison combinations

filtergeneset param: see geneset collections -> moalannotgene::genesetdb %>% lapply(names)

Experimental design examples:

- model = "TREAMTENT" for 1-way anova
- model = "TREATMENT+TIME+TREATMENT*TIME" for 3-ways anova with interaction
- model = "TREATMENT", paired = "CASE" for 2-ways paired anova
- model = "TREATMENT", batch = "BATCH" for 2-ways anova with remove batch effect (<=> paired anova)
- model = "TREATMENT+PHENOTYPE" for 2-ways anova
- model = "TREATMENT", addfactor = "PHENOTYPE" for 2-ways anova but venn, cluster and pattern are not applied to addfactor
- model = "TREATMENT", nested = "TREATMENTinCASE" for 2-ways nested design
- model = "TREATMENT", paired = "CASE", batch = "BATCH" for 3-ways paired anova with remove batch effect

Limitations:

- Complete block designs only
- Use dopar = 2 to decrease computing resources
- sample param will subsets random rows in dat and decrease analysis time.

Annotation updates: 05112023 for gene and ensembl, MSigDB 7.5.1, StringDB 12.0

Input format:

- Use uem915::input() to load external data from tsv files
- norm data table must contains IDs in first column
- norm data (in columns) and sample information (in rows) must have same order
- norm data and annotation rows must have same order
- use uem915::annot() function to annotate IDs (Symbols, ensembl and gene ids accepted)

Value

omic results directory

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# # test omic() with internal dataset GSE65055:
# # loading libraries
# library(uem915)
# uem915::env()
# # loading norm data
# moal:::GSE65055normdata -> normdata
# normdata %>% head
# # loading sample information file
# moal:::GSE65055sampledata -> sampledata
# sampledata %>% head
# # ordering factor levels
# sampledata$ANEUPLOIDY %>% ordered( c("Control","T13","T18","T21") ) -> sampledata$ANEUPLOIDY
# sampledata$TISSUE %>% as.factor -> sampledata$TISSUE
# # annotation
# normdata$rowID %>% moal::annot( species = "hs", idtype = "GENE" ) -> annotdata
# # omic analysis
# moal::omic(
#  dat = normdata, sif = sampledata, annot = annotdata, species = "hs",
#  model = "ANEUPLOIDY", batch = "TISSUE", threshold = c(6,126),
#  heatmap = T, lineplot = T, boxplotrow = T,
#  venn = F, cluster = F, pattern = F,
#  ena = T, network = F, topgo = F,
#  sample = NULL, dopar = NULL, zip = F,
#  dirname = "test", path = "." )
```

`output` *export data.frame in tab file*

Description

export data.frame in tab file

Usage

```
output(dt, filename)
```

Arguments

`dt`	data.frame
`filename`	character

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# output( dt )
```

---

qc *Quality Controls*

Description

do descriptive statistics : histogram, boxplot , hierarchical clustering and ACP for column

Usage

```
qc(
  dat,
  sif = NULL,
  inputdata = F,
  histo = TRUE,
  boxplot = TRUE,
  hc = TRUE,
  acp = TRUE,
  dirname = NULL,
  path = "."
)
```

Arguments

`dat`	matrix numeric
`sif`	data.frame
`inputdata`	logical to export input data or not
`histo`	logical do histogram if TRUE by defaut
`boxplot`	logical do boxplot if TRUE by defaut
`hc`	logical do hierarchical clustering if TRUE by defaut
`acp`	logical do principal component analysis if TRUE by defaut
`dirname`	character
`path`	character

Details

return pval for each factor of anova model function use doparalle

Value

data.frame

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# qc(dat, metadata)
```

`replacegroupmed` *replace value by group median*

Description

replace value by group median

Usage

```
replacegroupmed(dat, value = 0, factor)
```

Arguments

`dat`	character vector of mzxml file
`value`	numeric value to substitute
`factor`	character

Details

replace value by column median if group size is one and replace by row group median if group size > 1

Value

data.frame

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# replacegroupmed(dat)
```

---

venn *Venn diagramm*

Description

To make a Venn diagramm of 2, 3 or 4 lists

Usage

```
venn(
  list = NULL,
  listnames = NULL,
  returnlist = F,
  title = "Venn Diagram",
  plot = T,
  export = F,
  path = ".",
  dirname = "venn"
)
```

Arguments

`list`	list of 2 , 3 or 4 character vector or list of two data.frame to compare
`listnames`	character list names to display on graph
`returnlist`	logical
`title`	character title to display on graph
`plot`	logical to display the plot or not
`export`	logical export list in file
`path`	character
`dirname`	character name of the directory created when export = T

Details

until 4 list

Value

venn plot and new lists generated by venn.

Author(s)

Florent Dumont florent.dumont@universite-paris-saclay.fr

Examples

```
# not run
# library(magrittr)
# list(
#   c(letters[6:20] , letters[25] ) ,
#   letters[1:15] ,
#   c( letters[2:5] , letters[8:23] ) ) %>% venn
```

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