# Package: uem915 (via r-universe)

October 24, 2026

**Title** Omic Analysis uem915

**Version** 1.0.2

**Description** Omic Analysis uem915.

**License** GPL-3

**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)

**RoxygenNote** 7.3.2

**Config/pak/sysreqs** cmake libfontconfig1-dev libfreetype6-dev make libicu-dev

**Repository** https://fdumbioinfo.r-universe.dev

**Date/Publication** 2026-06-26 20:49:06 UTC

**RemoteUrl** https://github.com/fdumbioinfo/uem915

**RemoteRef** HEAD

**RemoteSha** 57fe964eb0ce9b1e8aa94dc050c657900f95de87

## Contents


acp . . . . . 2
annot . . . . . 3
boxplot . . . . . 4
boxplot1 . . . . . 5
ena . . . . . 6
env . . . . . 7

hc . . . . . 7
heatmap . . . . . 8
input . . . . . 9
norm . . . . . 10
omic . . . . . 11
output . . . . . 14
qc . . . . . 15
replacegroupmed . . . . . 16
venn . . . . . 17

**Index** **19**

---

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
```

# Index

acp, 2
annot, 3

boxplot, 4
boxplot1, 5

ena, 6
env, 7

hc, 7
heatmap, 8

input, 9

norm, 10

omic, 11
output, 14

qc, 15

replacegroupmed, 16

venn, 17