

# Package ‘coRNAi’

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**Type** Package

**Title** Analysis of co-knock-down RNAi data

**Version** 1.24.0

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**Description** Analysis of combinatorial cell-based RNAi screens

**License** Artistic-2.0

**Depends** R (>= 2.10), cellHTS2, limma, locfit

**Imports** MASS, gplots, lattice, grDevices, graphics, stats

**SystemRequirements** Graphviz

**biocViews** CellBasedAssays

**NeedsCompilation** no

## R topics documented:

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---

|               |   |
|---------------|---|
| BoxPlotShorth | <i>Boxplot with horizontal bars at the midpoint of the shorth</i> |
|---------------|---|

---

## Description

Produces a boxplot, but instead of horizontal bars at the median, the bars are at the midpoint of the shorth.

## Usage

```
BoxPlotShorth(formula, data = NULL, ...)
```

## Arguments

|         |   |
|---------|---|
| formula | formula for how the boxplot should be drawn.      |
| data    | the data to be used                               |
| ...     | other arguments to be passed to the plot function |

## Value

a boxplot object

## Author(s)

Elin Axelsson

## See Also

See Also [boxplot.formula](#)

## Examples

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral= "Fluc")
BoxPlotShorth(value~replicate,df)
```

---

|            |   |
|------------|---|
| cellHTS2df | <i>converts cellHTS objects to dataframes</i> |
|------------|---|

---

**Description**

converts a cellHTS2 object into a data.frame object and check that all mandatory meta data is included. Adds Directions, replicates and Pair columns.

**Usage**

```
cellHTS2df(x, neutral)
```

**Arguments**

|         |   |
|---------|---|
| x       | a cellHTS object with correct annotations               |
| neutral | string stating which RNAi is neutral (negative control) |

**Value**

data.frame, with the data from the cellHTS object in column "value". Meta data from annotation file and the new columns; Directions, Replicate and Pair

**Author(s)**

Elin Axelsson

**See Also**

[cellHTS](#)

**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw, neutral="Fluc")
head(df)
```

---

|                 |   |
|-----------------|---|
| cortestmatrices | <i>Function to extract correlations and corresponding p-values from interaction matrix.</i> |
|-----------------|---|

---

**Description**

This is a wrapper function for `cor.test`, given a matrix of interaction values, correlations and corresponding p-values for the genewise interaction profiles are calculated.

**Usage**

```
cortestmatrices(mat, method = c("pearson", "kendall", "spearman"))
```

**Arguments**

|        |  |
|--------|--|
| mat    | mat interaction matrix                                     |
| method | character deciding which correlation method should be used |

**Value**

List of two matrices

|            |                          |
|------------|--------------------------|
| cor.matrix | matrix with correlations |
| p.matrix   | matrix with p-values     |

**Author(s)**

Elin Axelsson

**See Also**

[cor.test](#)

**Examples**

```
## simulate data with 2 genes with similar profiles

mat = matrix(rnorm(100*100,0,1),100,100)
pr = sample(2:10,100,replace=TRUE)
mat[1:2,] = mat[1:2,] + matrix(pr,ncol=100,nrow=2,byrow=TRUE)
mat = mat+t(mat)
diag(mat) = NA
dimnames(mat)=list(1:100,1:100)
res = cortestmatrices(mat,method="spearman")
cors= res[[1]]
ps = res[[2]]
print(which(ps==min(ps,na.rm=TRUE),arr.ind=TRUE))
```

---

data2graph

*Function to create .dot files for graph representation of data*

---

**Description**

From a interaction table or list of data matrices a .dot file is created for visualisation of the interaction/correlation network

**Usage**

```
data2graph(indata, sizethres=0, thres, thresBy = "P.Value", cols = c("blue", "white", "red"), gamm
```

**Arguments**

|             |  |
|-------------|--|
| indata      |  |
| sizethres   | numerical, lower treshold on the absolute effect size for edges  |
| thres       | threshold that should be used for interactions/correlations to be included in graph  |
| thresBy     | what data should the the threshold by used at. By default the p value from the moderated t test is used but one could also use e.g. the ordinary t or the size |
| cols        | colors to be used in the plot, should be a character vector with the colors for low, neutral and hig values  |
| gamma.col   | Factor used to scale the colors  |
| scaleFactor | Scale factor to adjust the distances beteen nodes in the graph   |
| nodecolor   | character or character vector, which color(s) should the nodes have. Should either be of lenth 1 (all nodes same color) or same length as the number of nodes. |
| writedot    | logical, should a .dot file be created.  |
| filename    | charcter string with name of .dot file   |
| width       | width of the nodes   |
| penwidth    | width of the lines in the plot   |
| shape       | shape of the nodes in the plot   |
| fixedsize   | should all nodes have the same size  |
| fontsize    | size of the font in the plot   |

**Value**

a .dot file is written if writefile argument is TRUE

|       |   |
|-------|---|
| ninf  | Dataframe with information about the nodes in the network |
| einfo | Dataframe with information about the edges in the network |

**Author(s)**

Greg Pau, Elin Axelsson

**See Also**

Also see Graphviz documantation <http://www.graphviz.org/>

**Examples**

#see vignette

---

|          |  |
|----------|--|
| df2array | <i>function to do go from data frame to an array with values</i> |
|----------|--|

---

**Description**

The function transforms a float column in a data frame (from cHTS2df) to an array.

**Usage**

```
df2array(df, what)
```

**Arguments**

|      |  |
|------|--|
| df   | Data frame (from cellHTS2df) with additional column weights. |
| what | which column contains the data, eg. value or residuals       |

**Value**

An array with the data from the data frame.

**Author(s)**

Elin Axelsson

**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw, neutral = "Fluc")
df$weights = as.numeric(df$type=="comb")

aa = df2array(df, what="value")

## see head for first replicate

head(aa[, ,1])
```

---

|              |  |
|--------------|--|
| df2fitmatrix | <i>matrix for lmFit from dataframe</i> |
|--------------|--|

---

**Description**

converts a dataframe into the right format for lmFit function

**Usage**

```
df2fitmatrix(df)
```

**Arguments**

df                      dataframe from cellHTS2df function

**Value**

A matrix with the genepairs as rows and the replicates as columns. This matrix is in the right format for the lmFit.

**Author(s)**

Elin Axelsson

**See Also**

[df2lmFit](#)

**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
df = weightDf(df)
lmm = lmmain(df)
df = updateDf(df,lmm)
mfit = df2fitmatrix(df)
head(mfit)
```

---

df2lmFit

*lmFit from dataframe*

---

**Description**

converts a dataframe into the right format for lmFit function, calls the lmFit from limma and returns the result.

**Usage**

```
df2lmFit(df)
```

**Arguments**

df                      dataframe from cellHTS2df function

**Value**

Object of class 'MArrayLM'

**Author(s)**

Elin Axelsson

**See Also**[lmFit](#)**Examples**

```

data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
df = weightDf(df)
lmm = lmmain(df)
df = updateDf(df,lmm)
mfit = df2lmFit(df)
str(mfit)

```

---

estmodel

---

*Function to do estimate the main effects from data using median, mean or shorth.*


---

**Description**

The function estimates the main effect  $i$  from all data with the RNI $i$  against  $i$ . It can be done by median, mean or shorth.

**Usage**

```
estmodel(df, estimate = c("median", "mean", "shorth"), per = NULL)
```

**Arguments**

|          |  |
|----------|--|
| df       | df data frame from cellHTS2df function with extra column weight (see weightDf)       |
| estimate | estimate median, mean or shorth, decides how the main effects will be estimated.     |
| per      | per for which factor should the analysis be done separately, eg. batch or replicate. |

**Value**

for per =NULL, a list with

|             |  |
|-------------|--|
| coefficient | the estimated main effects   |
| residuals   | the residual after the main effects have been subtracted from the observations |

for other per, a list of lists like the once described above, one for each level of the factor per.

**Author(s)**

Elin Axelsson



**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
df$weight = as.numeric(df$type=="comb")
main = estmodel(df,estimate="median")
str(main)
```

---

|              |                      |
|--------------|----------------------|
| faultyscreen | <i>faulty screen</i> |
|--------------|----------------------|

---

**Description**

A screen with both systematic errors and sporadic contaminations.

**Usage**

```
data(faultyscreen)
```

**Format**

The format is: chr "cellHTS"

**Examples**

```
data(faultyscreen)
## maybe str(faultyscreen) ; plot(faultyscreen) ...
```

---

|               |   |
|---------------|---|
| InteractGraph | <i>functions to visualize interactions as a graph</i> |
|---------------|---|

---

**Description**

visualizes significant interactions as a graph

**Usage**

```
InteractGraph(toptable, thresh, sizecutoff=0, by, key=FALSE, file="interactions", colors = list(neg="b
```

**Arguments**

|            |   |
|------------|---|
| toptable   | toptable table from function topTable   |
| thresh     | thresh numeric, threshold for significance  |
| sizecutoff | sizecutoff a minimal absolute size of a interaction for it to be included in the graph as an edge.              |
| by         | by column in topTable that thresh should be applied to  |
| key        | key optional, data frame with groupings of the genes in the toptable  |
| file       | file name of the file the results will be outputed to.  |
| colors     | colors list with colors to be used for pos interactions, neg interactions, key (nodes in key) and normal nodes. |

**Value**

pdf file with graph

**Author(s)**

Elin Axelsson

**See Also**

[levelplot](#)

**Examples**

```
#see vignette
```

---

|                  |   |
|------------------|---|
| interactiontable | <i>Returns a list of interactions with associated statistics.</i> |
|------------------|---|

---

**Description**

This is an extended wrapper around the topTable function from the limma package, as an option the ordinary t statistics can be calculated as well.

**Usage**

```
interactiontable(ebfit, sort = "none", ord.t = FALSE, correction = "BH")
```

**Arguments**

|            |   |
|------------|---|
| ebfit      | ebfit a MArrayLM object produced by the eBayes function   |
| sort       | character string specifying which statistic to rank genes by, possible arguments are none, ID,size, t,B,adj.P.val,P.Value, and if ord.t = TRUE: ord.t, ord.p and ord.p.adj. |
| ord.t      | Logical, should ordinary t statistics be calculated? Default is FALSE.  |
| correction | method used to adjust the p-values for multiple testing. Default is BH. See p.adjust for the complete list of options.  |

**Value**

Returns a dataframe where the rows are the interaction pairs and the columns the statistics:

ID: Interaction pair id

size: the average interaction size

t: the moderated t statistics

P.Value: p-value for the moderated t statistics

adj.P.Val: adjusted p-value

B: the b statistics

if the ord.t=TRUE, the ordinary t statistics (ord.t), with corresponding p-values (ord.p) and adjusted p-values (ord.p.adj)

**Warning**

usage of the ordinary t statistics is not recommended for data sets with few replicates.

**Author(s)**

Elin Axelsson

**See Also**

[p.adjust](#), [topTable](#)

**Examples**

```
## simulated data
y <- matrix(rnorm(50*4,sd=1),50,4)
rownames(y) <- paste("Pair",1:50)

# fit and eBayes
fit <- lmFit(y)
fit <- eBayes(fit)
tt = interactiontable(fit,sort="size")
head(tt)
```

---

InteractLevelPlot      *function to visualize interactions as a levelplot*

---

**Description**

visualizes significant interactions as a levelplot

**Usage**

```
InteractLevelPlot(toptable, thresh = 0.001, by = "P.Value", key = FALSE, col.regions = colorRampPa
```

**Arguments**

|             |  |
|-------------|--|
| toptable    | toptable table from function topTable                                |
| thresh      | thresh numeric, threshold for significance                           |
| by          | by column in topTable that thresh should be applied to               |
| key         | key optional, data frame with groupings of the genes in the toptable |
| col.regions | col.regions colors to be used  |
| zerolimit   | zerolimit threshold below which interactions should be colored as 0. |

**Value**

a levelplot, pdf files with graphs

**Author(s)**

Elin Axelsson

**See Also**[levelplot](#)**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw, neutral="Fluc")
tt = data.frame("size"=runif(length(unique(df$Pair[df$Type=="comb"])), -2, 2), stringsAsFactors=FALSE)
rownames(tt) = unique(df$Pair[df$Type=="comb"])
InteractLevelPlot(tt, thres=0, by="size")
```

---

|     |  |
|-----|--|
| key | <i>A key to data set screen1, contains (additional) information about the genes in the screen.</i> |
|-----|--|

---

**Description**

Contains information about which of the 16 genes in screen1 are cell cycle related. This is used in interaction graphs/plots.

**Usage**

```
data(key)
```

**Format**

A data frame with 16 observations on the following 2 variables.

GeneID a factor with levels AnnIX CG12785 CG16935 CG3165 CG7889 CG8108 CSN3 CSN4 CSN5 fwd  
pbl Rbf Rho1 sos trb1 zip

cellCycle a numeric vector

**Examples**

```
data(key)
table(key$cellCycle)
```

---

|         |                               |
|---------|-------------------------------|
| LS main | <i>main effect estimation</i> |
|---------|-------------------------------|

---

**Description**

for rlmmain the main effects are estimated using rlm function from MASS package, with lmmmain the OLS is used.

**Usage**

```
rlmmain(df, per=NULL)
lmmmain(df, per=NULL)
```

**Arguments**

df                   df dataframe created by function cellHTS2df  
 per                   string argument for which factor the analysis should be done separately, eg. replicate or batch

**Value**

lm,rlm

**Author(s)**

Elin Axelsson

**See Also**

[rlm,lm](#)

**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
df = weightDf(df,exclude=c("controlP1","controlP2","controlN1","controlN2","controlP1N1","double"))
mains = rlmmain(df)
hist(coef(mains))
```

---

MainFitPlot

*Diagnostic plot*

---

**Description**

Plots residuals vs fitted values after fitting of main effects.

**Usage**

```
MainFitPlot(fit, xlab = "Fitted values", ylab = "Residuals", sd.fit = TRUE, main = "Residuals vs Fitted values")
```

**Arguments**

fit                   a fit from lmmmain, rlmmain or similar  
 xlab                   label for x-axis  
 ylab                   label for y-axis  
 sd.fit                logical, should the local estimator of the standard deviation be plotted  
 main                   main title for the plot  
 ...                   arguments to be passed on to the plot function

**Value**

a plot

**Author(s)**

Elin Axelsson

**See Also**[locfit](#)**Examples**

```
## simulated data

fitted.value = rnorm(100,2,1)
residuals = rnorm(100,0,1)
fit = list(fitted.value=fitted.value, residuals = residuals)
class(fit) = "lm"
MainFitPlot(fit)
```

---

PlotHeatmap

*Plot a heatmap of interactions*


---

**Description**

Plots a heatmap of the mean residuals for each interaction pair.

**Usage**

```
PlotHeatmap(toptable, colpal = colorRampPalette(c("blue", "white", "yellow")),
key=FALSE, margins=c(7,7), na.color="grey", breaks=seq(-1,1,by=0.01),...)
```

**Arguments**

|          |  |
|----------|--|
| toptable | a data frame created by with the interaction estimates as "logFC" and pair id as "ID". Usually created by topTable function in limma |
| colpal   | color palette to be used in the plot   |
| key      | logical should a color key be included   |
| margins  | margins for plot   |
| na.color | color for NA values  |
| breaks   | mapping data to colors in colpal   |
| ...      | additional arguments to be passed to heatmap.2 call  |

**Value**

a plot

**Author(s)**

Elin Axelsson

**See Also**[heatmap.2](#)**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
tt = data.frame("size"=runif(length(unique(df$Pair[df$Type=="comb"])),-2,2),stringsAsFactors=FALSE)
rownames(tt) = unique(df$Pair[df$Type=="comb"])
PlotHeatmap(tt)
```

---

**Pplot***Function to plot cumulative p-values*

---

**Description**

Given a vector of p-values a cumulative p-value plot is produced

**Usage**

```
Pplot(x, col = "darkblue", maintitle="", nrpoints = 100, ...)
```

**Arguments**

|           |  |
|-----------|--|
| x         | vector with p-values                       |
| col       | color to be used                           |
| maintitle | character, main plot title                 |
| nrpoints  | numeric, how many points should be plotted |
| ...       | additional arguments passed on to the plot |

**Value**

a plot

**Author(s)**

Wolfgang Huber

**Examples**

```
x = runif(1000,0,1)
Pplot(x,col="red",maintitle="uniform dist.", nrpoints=200)
```

---

replots

*reproducibility plots*

---

## Description

plots reproducibility of replicates within/between screens

## Usage

```
BetweenScreenPlot(df, what="value",names,smooth=TRUE)
```

```
WithinScreenPlot(df, what="value",main="within-screen replicates",ylab ="technical replicate 2",x
```

## Arguments

df df dataframe created by the cellHTS2df function

names names optional, character vector with names of the different screens.

what what what should be plotted, eg value or residuals

main main title

ylab ylab label for y-axis

xlab xlab label for x-axis

smooth smooth should the smoothScatter function be called. Default is TRUE.

... further argument to be passed to the plot function

## Value

pairs plot

## Author(s)

Elin Axelsson

## See Also

[pairs,plot](#)

## Examples

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
BetweenScreenPlot(df)
WithinScreenPlot(df)
```



---

|             |                         |
|-------------|-------------------------|
| screen1_raw | <i>screen1 raw data</i> |
|-------------|-------------------------|

---

**Description**

cellHTS2 object containing the raw data from screen1 (cellcycle related)

**Usage**

```
data(screen1_raw)
```

**Format**

The format is: chr "cellHTS"

**Examples**

```
data(screen1_raw)  
state(screen1_raw)
```

---

|             |                         |
|-------------|-------------------------|
| screen2_raw | <i>screen2 raw data</i> |
|-------------|-------------------------|

---

**Description**

cellHTS2 object containing the raw data from screen2 (phospatases)

**Usage**

```
data(screen2_raw)
```

**Format**

The format is: chr "cellHTS"

**Examples**

```
data(screen2_raw)  
state(screen2_raw)
```

---

signalplots

*plot variation vs signal intensity*

---

### Description

plots the variation of replicates vs the mean intensity either by within screen replicate separately or over all screen replicates.

### Usage

```
SDplot(df, xlab="intensity mean",ylab="sd",add=FALSE,main,...)
MAplot(df, main,rank=FALSE)
```

### Arguments

|      |   |
|------|---|
| df   | df dataframe created by cellHTS2df function                   |
| main | main character string to be used as main title                |
| xlab | xlab label for x-axis   |
| ylab | ylab label for y-axis   |
| add  | add logical, should result be added to existing plot          |
| rank | rank if TRUE the rank of the average intensities will be used |
| ...  | ... further arguments to be passed to the plot function.      |

### Value

plot

### Author(s)

Elin Axelsson

### See Also

[plot](#)

### Examples

```
data(screen1_raw)
df=cellHTS2df(screen1_raw,neutral="Fluc")
MAplot(df,main="raw data")
SDplot(df,main="raw data")
```

---

tt2matrix

*Extracting data from a toptable and format it to matrix*


---

**Description**

Given an dataframe with data, typically from the interactiontable, the gene pair data is converted to a symmetric matrix.

**Usage**

```
tt2matrix(toptable, what)
```

**Arguments**

|          |  |
|----------|--|
| toptable | a dataframe with data for the pairwise interactions. Typically from the interactiontable function. |
| what     | character indicating which of the columns in the dataframe should be used in the matrix.           |

**Value**

a symmetric matrix with the selected data for gene pair i,j in matrix[i,j] and matrix[j,i]

**Author(s)**

Elin Axelsson

**Examples**

```
## simulated data
mytoptable = data.frame("ID" = c("A B", "A C", "B C"), "size"=c(1:3), stringsAsFactors=FALSE)
rownames(mytoptable) = mytoptable$ID
mat = tt2matrix(mytoptable, what="size")
```

---

updateDf

*updates dataframe after fitting of main estimates*


---

**Description**

adds residuals (value-main effects) to a dataframe

**Usage**

```
updateDf(df, lm, per=NULL)
```

**Arguments**

|     |  |
|-----|--|
| df  | df dataframe created by cellHTS2df function  |
| lm  | lm lm objects, residuals from fitting main effects to data                             |
| per | per string argument, for which factor the analysis was done separately, eg. replicate. |

**Value**

data frame with a new column "residuals"

**Author(s)**

Elin Axelsson

**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw, neutral="Fluc")
df = weightDf(df, exclude=c("double", "controlP1", "controlP2", "controlN1", "controlN2", "controlP1N1"))
lmain = lmain(df)
df = updateDf(df, lmain)
hist(df$residuals)
```

---

|          |   |
|----------|---|
| weightDf | <i>Function to indicate which data points should be involved in down stream analysis.</i> |
|----------|---|

---

**Description**

Function to do add weights to the data points in a data frame. At the time being 0 means excluded and everything >0 means included.

**Usage**

```
weightDf(df, exclude = c("double", "controlN2", "controlP2", "controlP1N1", "controlN1"))
```

**Arguments**

|         |  |
|---------|--|
| df      | data frame from cellHTS2df                           |
| exclude | which type of data should be excluded from analysis. |

**Details**

See also vignette for information about different "Type" types.

**Value**

A data frame with an added column 'weight'

**Author(s)**

Elin Axelsson

**Examples**

```
data(screen1_raw)
df = cellHTS2df(screen1_raw,neutral="Fluc")
##stupid example
df = weightDf(df,exclude="controlN2")
head(df)
```

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