Package ‘LINC’

November 20, 2016

Type Package
Title co-expression of lincRNAs and protein-coding genes
Version 1.2.0
Date 2016-10-13
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Depends R (>= 3.3.1), methods, stats
Description This package provides methods to compute co-expression networks of lincRNAs and protein-coding genes. Biological terms associated with the sets of protein-coding genes predict the biological contexts of lincRNAs according to the 'Guilty by Association' approach.
biocViews Software, BiologicalQuestion, GeneRegulation, GeneExpression
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LinkingTo Rcpp
Imports Rcpp (>= 0.11.0), DOSE, ggtree, gridExtra, ape, grid, png, Biobase, sva, reshape2, utils, grDevices, org.Hs.eg.db, clusterProfiler, ggplot2, ReactomePA
VignetteBuilder knitr
Suggests RUnit, BiocGenerics, knitr, biomaRt
NeedsCompilation yes

R topics documented:

Arith-methods .................................................. 2
assignment-methods ........................................... 2
BRAIN_EXPR .................................................... 3
changeOrgDb .................................................... 4
clusterlinc-methods .......................................... 5
correlation-methods ......................................... 7
express-methods .............................................. 8
feature ......................................................... 9
getbio-methods ................................................. 10
getcoexpr ...................................................... 11
getlinc-methods .............................................. 12
history-methods .............................................. 13
plotlinc is the generic function that creates plots based on objects of the LINC class.

Methods

signature(e1 = "LINCbio", e2 = "LINCfeature") (see feature())
signature(e1 = "LINCcluster", e2 = "LINCfeature") (see feature())
signature(input = "LINCmatrix", showCor = "LINCfeature") (see feature())

Examples

```r
data(BRAIN_EXPR)
# add a custom name
crbl_cluster_feat <- crbl_cluster + feature(customID = "CEREBELLUM")
plotlinc(crbl_cluster_feat)
```

assignment-methods

Methods for the Getter Function assignment in Package LINC

Description

Access the slot assignment of an object of class LINC

Arguments

x: a 'LINC' object, for instance LINCMatrix
Value

the respective substructure or information

Methods

signature(x = "LINCbio") assignment slot
signature(x = "LINCcluster") assignment slot
signature(x = "LINCMatrix") assignment slot
signature(x = "LINCsing1e") assignment slot

Author(s)

Manuel Goepferich

Examples

data(BRAIN_EXPR)

assignment(crbl_cluster)

BRAIN_EXPR | mRNA Expression Of Normal BRAIN From GTEX And TCGA

Description

These datasets represent sample mRNA expression matrices of brain tissue with normal tissue from the Genotype-Tissue Expression (GTEx) platform (ctx = Cortex, crbl = Cerebellum, phc = Hippocampus) and cancer tissue from The Cancer Genome Atlas (TCGA) platform (gbm = Glioblastoma).

Usage

data(BRAIN_EXPR)

Format

Gene expression matrices and objects of the LINC class.

Value

Rows represent genes and columns samples. Gene names are given as Entrez identifiers. For the normal tissue from GTEx, expression levels are in units of [FPKM], for cancer tissue from TCGA, the unit [RESM] is used to represent expression levels.

Source

http://www.gtexportal.org Genotype-Tissue Expression (GTEx)
https://tcga-data.nci.nih.gov/docs The Cancer Genome Atlas (TCGA)
changeOrgDb

References


Examples

data(BRAIN_EXPR)

changeOrgDb                     Change the Gene Annotation / Model Organism

Description

The standard gene annotation in LINC is "org.Hs.eg.db". This function is only relevant in case the input gene expression matrix is from another organism than Homo Sapiens.

Usage

changeOrgDb(object, OrgDb)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an instance of the LINC class</td>
</tr>
<tr>
<td>OrgDb</td>
<td>has to be one of: c(&quot;org.Ag.eg.db&quot;, &quot;org.At.tair.db&quot;,</td>
</tr>
</tbody>
</table>

Value

object with changed gene annotation hook

Note

Please, also consider the documentation of clusterProfiler and ReactomePA.

Author(s)

Manuel Goepferich

Examples

data(BRAIN_EXPR)

# change the used gene annotation, here from "human" to "mouse"
murine_matrix <- changeOrgDb(crbl_matrix, OrgDb = 'org.Mm.eg.db')
Description

The function clusterlinc will give an overview of ncRNAs in a dataset. An input LINCmatrix will be converted to a LINCcluster. The following steps are conducted (I) computation of a correlation test, (II) setup of a distance matrix, (III) calculation of a dendrogram and (IV) selection of co-expressed genes for each query. The result is a cluster of ncRNAs and their associated protein-coding genes.

Usage

```r
clusterlinc(linc,
  distMethod = "dicedist",
  clustMethod = "average",
  pvalCutOff = 0.05,
  padjust = "none",
  coExprCut = NULL,
  cddCutOff = 0.05,
  verbose = TRUE)
```

Arguments

- `linc`: an object of the class LINCmatrix
- `distMethod`: a method to compute the distance between ncRNAs; has to be one of c("correlation", "pvalue", "dicedist")
- `clustMethod`: an algorithm to compute the dendrogram, has to be one of c("ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid")
- `pvalCutOff`: a threshold for the selection of co-expressed genes. Only protein-coding genes showing a significance in the correlation test lower than pvalCutOff will assigned to queried ncRNAs as interaction partner.
- `padjust`: one of c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none")
- `coExprCut`: a single integer indicating the number of co-expressed genes to select. If this argument is used for each ncRNA the coExprCut = n protein-coding genes with the lowest p-value in the correlation test will be assigned to queries, respectively.
- `cddCutOff`: a threshold that is only relevant for distMethod = "dicedist". In this method cddCutOff defines whether a ncRNA and a protein-coding gene can be considered as interaction partners. This influences the distance matrix and the clustering process.
- `verbose`: whether to give messages about the progression of the function TRUE or not FALSE

Details

As a first step clusterlinc conducts the correlation test (stats::cor.test) using the correlation method and handling of missing values inherited from the input LINCmatrix. Resulting p-values indicate the statistical robustness of correlations instead of absolute correlation values. Co-expression of ncRNAs to protein-coding genes is assumed if the p-value from the cor.test is lower than the given pvalCutOff. An alternative way to select co-expressed genes is provided by coExprCut. This argument has priority over pvalCutOff and can be used to pick the n genes with
the lowest p-value for each ncRNA. In contrast to \texttt{pvalCutOff}, this will result in an equal number of assigned co-expressed genes. The argument \texttt{padjust} can be used for multiple testing correction. In most cases this is not compatible with \texttt{distMethod = "dicedist"}.

For the computation of the distance matrix of ncRNA genes three methods can be applied. The first method \textquote{correlation} uses $1 - \text{correlation}$ as distance measure. In contrast, \textquote{pvalue} considers not the absolute correlation values, but p-values from the correlation test. A third method is termed \textquote{dicedist} and takes the Czekanowski dice distance \cite{1} as distance measure. Here, the number of shared interaction partners between ncRNAs determines their relation to each other. The argument \texttt{cddCutOff} is an option to decide which p-values in the correlation matrix can be considered as interaction. A low threshold, for instance, will consider only interactions of ncRNAs and protein-coding genes supported by a p-value lower than the supplied threshold and therefore a robust correlation of these two genes. Based on the distance matrix a cluster of the ncRNAs will be computed by \texttt{stats::hclust}. Argument \texttt{clustMethod} defines which clustering method should be applied.

A \texttt{LINCcluster} can be recalculated with the command \texttt{clusterlinc(LINCcluster, \ldots))} in order to change further arguments. \texttt{plotlinc(LINCcluster, \ldots))} will plot a figure that shows the cluster of ncRNAs (dendrogram) and the number of co-expressed genes with respect to different thresholds. \texttt{getbio(LINCcluster, \ldots))} will derive the biological terms associated with the co-expressed genes. Due to the correlation test longer calculation times can occur. A faster alternative to this function is \texttt{singlelinc()}. User-defined correlation test functions are supported for \texttt{singlelinc()} but not for \texttt{clusterlinc()}.

Value

an object of the class \textquote{LINCmatrix} (S4) with 6 Slots

results a list containing an object of the class \textquote{phylo} with the additional entry \texttt{neighbours}, a list of queries and co-expressed genes

assignment a character vector of protein-coding genes

correlation a list of \texttt{cormatrix}, the correlation of non-coding to protein-coding genes, \texttt{lnctolnc}, the correlation of non-coding to non-coding genes and \texttt{cortest}, p-values of the correlation test of non-coding to protein-coding genes

expression the original expression matrix

history a storage environment of important methods, objects and parameters used to create the object

\texttt{linCenvir} a storage environment ensuring the compatibility to other objects of the LINC class

Methods

\texttt{signature(linc = "LINCcluster") (see details)}

\texttt{signature(linc = "LINCmatrix") (see details)}

Compatibility

\texttt{plotlinc(LINCcluster, \ldots)} \texttt{, getbio(LINCcluster, \ldots), \ldots}

Author(s)

Manuel Goepferich
correlation-methods

References


See Also

linc; singlelinc

Examples

data(BRAIN_EXPR)
class(crbl_matrix)

# call 'clusterlinc' with no further arguments
crbl_cluster <- clusterlinc(crbl_matrix)

# apply the distance method "correlation instead of "dicedist"
crbl_cluster_cor <- clusterlinc(crbl_matrix, distMethod = "correlation")
# do the same as recursive call using the 'LINcluster' object
# crbl_cluster_cor <- clusterlinc(crbl_cluster, distMethod = "correlation")

# select 25 genes with lowest p-values for each query
crbl_cluster_25 <- clusterlinc(crbl_matrix, coExprCut = 25)

# select only those with a p-value < 5e-5
crbl_cluster_5e5 <- clusterlinc(crbl_matrix, pvalCutOff = 5e-5)

# adjust for multiple testing
crbl_cluster_hochberg <- clusterlinc(crbl_matrix, distMethod = "correlation",
                                    padjust = "hochberg", pvalCutOff = 0.05)

# comparing two distance methods
plotlinc(crbl_cluster)
plotlinc(crbl_cluster_cor)

Description

Access the slot correlation of an object of class LINC

Arguments

x a ‘LINC’ object, for instance LINCmatrix

Value

the respective substructure or information
Methods

signature(x = "LINCbio") correlation slot
signature(x = "LINCcluster") correlation slot
signature(x = "LINCmatrix") correlation slot
signature(x = "LINCsingle") correlation slot

Author(s)

Manuel Goepferich

Examples

data(BRAIN_EXPR)
correlation(crbl_cluster)

Description

Access the slot expression of an object of class LINC

Arguments

x a 'LINC' object, for instance LINCmatrix

Value

the respective substructure or information

Methods

signature(x = "LINCbio") expression slot
signature(x = "LINCcluster") expression slot
signature(x = "LINCmatrix") expression slot
signature(x = "LINCsingle") expression slot

Author(s)

Manuel Goepferich

Examples

data(BRAIN_EXPR)
express(crbl_cluster)
**feature**

*Manipulate Objects Of The 'LINC' class*

**Description**

*feature* provides useful options intended to be used with 'LINC' objects.

**Usage**

```r
feature(setLevel = NULL,
         customID = NULL,
         customCol = "black",
         showLevels = FALSE)
```

**Arguments**

- `setLevel`: a character string of the class the object should be converted into
- `customID`: a character string of a name for the object
- `customCol`: a character string of a valid colour for the object
- `showLevels`: whether to show the inherited classes of the object TRUE or not FALSE

**Details**

Custom ids and colours enable the identification of a particular object in plots created by `plotlinc` and `querycluster`. With `setLevel` it is possible to change the class of an object.

*feature* works in combination with the plus operator: `object + feature(customID = ..., customCol = ...)`

**Value**

an object of the class 'LINCfeature' (S4) with 5 Slots (not shown)

**Author(s)**

Manuel Goepferich

**See Also**

`querycluster`; `strlinc`

**Examples**

```r
data(BRAIN_EXPR)

# add a custom name
crbl_cluster_feat <- crbl_cluster + feature(customID = "CEREBELLUM")
plotlinc(crbl_cluster_feat)
```
getbio-methods  

Find Enriched Biological Terms For A Cluster

Description

The function provides an interface to the clusterProfiler package. For each query in a cluster it seeks the biological terms that can be associated with the co-expressed genes, respectively. The input for getbio is of the class 'LINCcluster'.

Usage

getbio(cluster, enrichFun = 'enrichGO', ont = "BP", ...)

Arguments

cluster  
a 'LINCcluster'. The number of co-expressed genes has to be sufficient.
enrichFun  
a function given as character string which will derive significant biological terms based on the set of co-expressed genes from a gene annotation resource. Supported functions are: c("enrichGO", "enrichPathway", "enrichDO")
ton  
a subontology, only used for enrichFun = 'enrichGO'. This has to be one of "MF", "BP", "CC".
...  
further arguments, mainly for functions from clusterProfiler

Details

In contrast to the function singlelinc here, a group of queries, those present in the input cluster, will be analyzed for enriched biological terms. The annotation function can be one of c("enrichGO", "enrichPathway")

[1] The gene system of the input object has to be translated for the enrichment function in case genes are not given as Entrez ids. The function clusterProfiler:bitr [2] will be used in order to translate gene ids.

Value

an object of the class 'LINCmatrix' (S4) with 6 Slots

results  
a list containing the identified enriched biological terms plus their respective p-values
assignment  
a character vector of protein-coding genes
correlation  
a list of cormatrix, the correlation of non-coding to protein-coding genes and lnctolnc, the correlation of non-coding to non-coding genes
expression  
the original expression matrix
history  
a storage environment of important methods, objects and parameters used to create the object
linCenvir  
a storage environment ensuring the compatibility to other objects of the LINC class
Methods
signature(cluster = "LINCcluster") (see details)

Author(s)
Manuel Goepferich

References

See Also
cclusterlinc; singlelinc;

Examples

data(BRAIN_EXPR)
## Find the enriched cellular components for each query in the cluster
crbl_cc <- getbio(crbl_cluster, ont = "CC")
plotlinc(crbl_cc)

getcoexpg

Get IDs For Co-Expressed Genes from The 'LINC' Class

Description
getcoexpg provides access to co-expressed genes of a query in 'LINC' objects.

Usage
getcoexpg(input,
query = NULL,
keyType = NULL)

Arguments
input a 'LINCcluster' or 'LINCsingl e' object
query for a 'LINCcluster' the name of the query gene
keyType The 'keyType' (gene system) for the output.

Value
a vector containing the co-expressed genes for a query

Author(s)
Manuel Goepferich
Examples

```r
data(BRAIN_EXPR)
# Get the co-expressed genes for the query gene '55384' alias MEG3
getcoexpr(crbl_cluster, query = "55384")

# The co-expressed genes can also be returned as gene symbols.
getcoexpr(crbl_cluster, query = "55384", keyType = "SYMBOL")
```

### Description

`getlinc` is a function to derive substructures from LINC objects.

### Usage

```r
getlinc(input, subject = "queries")
```

### Arguments

- `input`: a `LINC` object, for instance `LINCmatrix`
- `subject`: has to be one of c("queries", "geneSystem", "results", "history", "customID")

### Value

the respective substructure or information

### Methods

signature(input = "ANY", subject = "character") (see details)

### Author(s)

Manuel Goepferich

### See Also

`linc`

### Examples

```r
data(BRAIN_EXPR)

# getlinc() is used to access information
getlinc(crbl_cluster, subject = "geneSystem")
getlinc(crbl_cluster, subject = "queries")
getlinc(crbl_cluster, subject = "customID")
```
Methods for the Getter Function history in Package LINC

Description
Access the slot history of an object of class LINC

Arguments
x  a 'LINC' object, for instance LINCmatrix

Value
the respective substructure or information

Methods
signature(x = "LINCbio") history slot
signature(x = "LINCcluster") history slot
signature(x = "LINCmatrix") history slot
signature(x = "LINCsingle") history slot

Author(s)
Manuel Goepferich

Examples
data(BRAIN_EXPR)
history(crbl_cluster)

Co-Expression Analysis Of ncRNA Genes In One Step

Description
justlinc is a wrapper that uses different functions of the LINC package. It applies fixed thresholds for gene selection and requires only an (unprocessed) expression matrix as input. This enables a fast co-expression analysis with or without a list candidates.

Usage
justlinc(object,  
targetGenes = "lincRNA",  
rmPC = TRUE)
Arguments

- **object**
a gene expression matrix with Ensembl gene ids (rows correspond to genes)

- **targetGenes**
the gene biotype like "lincRNA" or a vector of query(s) - one or multiple genes ids

- **rmPC**
remove 30 percent of the variance in the data by PCA TRUE or not FALSE.

Details

This function was built for expression matrices which uses the Ensembl gene system with gene expression values for over 50,000 genes. The input will be matched with a static gene annotation. Genes will be selected for median expression and variance. The final correlation matrix of protein-coding genes versus the target genes (lincRNAs) considers 5000 protein-coding genes and 500 target genes. Enriched pathways will be computed for the co-expressed genes showing the highest Spearman’s rank correlation. In case targetGenes = "lincRNA", then the function will search for the 10 best lincRNAs. Supplying a vector of gene ids the method will determine the best co-expressed genes for the given queries. Importantly, this function is only a wrapper. Thresholds can be changed using linc and related functions.

Value

depending on the input in targetGenes one or two plots and the result of the co-expression analysis

Methods

signature(object = "matrix") (see details)

Author(s)

Manuel Goepferich

See Also

linc

Examples

# NOT RUN:

# large gene expression matrix not avaliable in this version

# data(LIVER_EXPR)
# a gene expression matrix with > 50,000 genes
# str(GTEX_LIVER_CRUDE)

# 'justlinc' will search for the 10 best candidates
try(justlinc(GTEX_LIVER_CRUDE), silent = TRUE)

# 'justlinc' called with queries
my_lincRNAs <- c("ENSG00000224153", "ENSG00000197813", "ENSG00000179136", "ENSG0000008259439", "ENSG00000267462")

try(justlinc(GTEX_LIVER_CRUDE, targetGenes = my_lincRNAs), silent = TRUE)
**linc-methods**

**Compute A Correlation Matrix of Co-expressed Coding And Non-Coding Genes**

**Description**

The function `linc` can be considered as the main function of this package. It converts a given input object into a LINCmatrix. This process includes (I) statistical analysis and (II) correction of the input, (III) separation of coding and non-coding genes and (IV) computation of a correlation matrix. The input could be for instance a gene expression matrix. Rows correspond to genes; columns represent samples. Besides a suitable object a vector identifying the protein-coding genes is required.

**Usage**

```r
linc(object, codingGenes, corMethod = "spearman", batchGroups, nsv = 1, rmPC, outlier, userFun, verbose = TRUE)
```

**Arguments**

- **object** a matrix, data.frame or ExpressionSet with genes corresponding to rows, preferentially the high-variance genes in a given set
- **codingGenes** a logical vector with the same length of the supplied genes in object. TRUE indicates that the gene is a protein-coding one. Alternatively, codingGenes can be a vector of gene biotypes.
- **corMethod** a method for the correlation function; has to be one of c("pearson", "kendall", "spearman", "user")
- **batchGroups** a vector naming the batch conditions. The length of this vector has to match the number of samples supplied in object. There has to be at least two different batch conditions for the method to work.
- **nsv** a single integer indicating the number of hidden surrogate variables. This argument is only relevant in case batchGroups is used.
- **rmPC** a vector of principle components (PCs) which should be removed. PCs are counted staring from 1 up to the maximal count of samples.
- **outlier** a method for the genewise removal of single outliers; has to be one of c("esd", "zscore")
- **userFun** a function or its name that should be used to calculate the correlation between coding and non-coding genes. This argument has to be used in combination with corMethod = "user"
- **verbose** whether to give messages about the progression of the function TRUE or not FALSE
Details

object can be a matrix, a data.frame or an ExpressionSet with rows corresponding to genes and columns to samples, the assumed co-expression conditions. Genes with duplicated names, genes having 0 variance plus genes with to many missing or infinite values will be removed from the input. For inputs showing a high inter-sample variance (ANOVA) in combination with many single outliers a warning message will appear. By default Spearman’s rank correlation will be computed between protein-coding to non-coding genes. For this method a time-efficient C++ implementation will be called. Longer computation times occur for genes > 5000 and samples > 100. Missing values are handled in a manner that only pairwise complete observations will be compared. A customized correlation function can be applied supplying the function in userFun and requires the formal arguments x and x. This has priority over corMethod.

A number of statistical methods are available in order to remove effects from a given input expression matrix which depend on the used platform or technology and may hide relevant biology. The argument batchGroups works as a rapper of the SVA package calling sva::svaseq. The number of hidden surrogate variables is set to nsv = 1 by default; it can be estimated utilizing the function sva::num.sv. For this model to work the description of at least two different batches are required in batchGroups. Principle Component Analysis (PCA) can be performed by rmPC = c(...) where ... represents a vector of principle components. The command rmPC = c(2:ncol(object)) will remove the first PC from the input. This method can be used to determine whether observations are due to the main variance in the dataset i.e. main groups or subtypes. Outliers are handled genewise. The extreme Studentized deviate (ESD) test by Rosner, Bernard (1983) will detect one up to four outliers in a gene and replace them by NA values. The alternative zscore will perform a robust zscore test suggested by Boris Iglewicz and David Hoaglin (1993) and detect a single outlier in a gene if |Z| > 3.5.

A LINCmatrix can be recalculated with the command linc(LINCmatrix, ...) in order to change further arguments. plotlinc(LINCmatrix, ...) will plot a figure depicting the statistical analysis and correlation values. As for most objects of the LINC class manipulation of the last slot linCenvir will likely result in unexpected errors.

Value

an object of the class ‘LINCmatrix’ (S4) with 6 Slots

results a list containing the original input expression matrix or a transformed matrix if rmPC, batchGroups or outlier was applied
assignment a character vector of protein-coding genes
correlation a list of $cormatrix, the correlation of non-coding to protein-coding genes and $lnctolnc, the correlation of non-coding to non-coding genes
expression the original expression matrix
history a storage environment of important methods, objects and parameters used to create the object
linCenvir a storage environment ensuring the compatibility to other objects of the LINC class

Methods

signature(object = "data.frame", codingGenes = "ANY") (see details)
signature(object = "ExpressionSet", codingGenes = "ANY") (see details)
signature(object = "LINCmatrix", codingGenes = "missing") (see details)
signature(object = "matrix", codingGenes = "ANY") (see details)
Compatibility

plotlinc(LINCmatrix, ...), clusterlinc(LINCmatrix, ...), singlelinc(LINCmatrix, ...), ...

Author(s)

Manuel Goepferich

References


See Also

justlinc; clusterlinc; singlelinc

Examples

data(BRAIN_EXPR)

# call 'linc' with no further arguments
crbl_matrix <- linc(cerebellum, codingGenes = pcgenes_crbl)

# remove first seven principle components
crbl_matrix_pc <- linc(cerebellum, codingGenes = pcgenes_crbl, rmPC = c(1:7))

# negative correlation by using 'userFun'
crbl_matrix_ncor <- linc(cerebellum, codingGenes = pcgenes_crbl,
 userFun = function(x,y){ -cor(x,y) })

# remove outliers using the ESD method
crbl_matrix_esd <- linc(cerebellum, codingGenes = pcgenes_crbl, outlier = "esd")

# plot this object
plotlinc(crbl_matrix_esd)
Slots

results: Object of class "list" ~
assignment: Object of class "vector" ~
correlation: Object of class "list" ~
expression: Object of class "matrix" ~
history: Object of class "environment" ~
linCenvir: Object of class "environment" ~

Extends

Class "LINCmatrix", directly.

Methods

+ signature(e1 = "LINCbio", e2 = "LINCfeature"): ...
linctable signature(file_name = "character", input = "LINCbio"): ...
overlaylinc signature(input1 = "LINCbio", input2 = "LINCbio"): ...
plotlinc signature(input = "LINCbio", showCor = "character"): ...
plotlinc signature(input = "LINCbio", showCor = "missing"): ...

Examples

showClass("LINCbio")

LINCcluster-class  Class "LINCcluster"

Description

code"LINCcluster"

Objects from the Class

Objects can be created by calls of the form new("LINCcluster", ...).

Slots

results: Object of class "list" ~
assignment: Object of class "vector" ~
correlation: Object of class "list" ~
expression: Object of class "matrix" ~
history: Object of class "environment" ~
linCenvir: Object of class "environment" ~

Extends

Class "LINCmatrix", directly.
Methods

signature(e1 = "LINCcluster", e2 = "LINCfeature"): ...

clusterlinc signature(linc = "LINCcluster"): ...

getbio signature(cluster = "LINCcluster"): ...

linctable signature(file_name = "character", input = "LINCcluster"): ...

plotlinc signature(input = "LINCcluster", showCor = "character"): ...

plotlinc signature(input = "LINCcluster", showCor = "missing"): ...

Examples

showClass("LINCcluster")

Description

Access the slot linCenvir of an object of class LINC

Arguments

x a 'LINC' object, for instance LINCmatrix

Value

the respective substructure or information

Methods

signature(x = "LINCbio") linCenvir slot
signature(x = "LINCcluster") linCenvir slot
signature(x = "LINCmatrix") linCenvir slot
signature(x = "LINCsingel") linCenvir slot

Author(s)

Manuel Goepferich

Examples

data(BRAIN_EXPR)

linCenvir(crbl_cluster)
LINCfeature-class  
Class "LINCfeature"

**Description**

"LINCfeature"

**Objects from the Class**

Objects can be created by calls of the form `new("LINCfeature", ...)`. 

**Slots**

- `customID`: Object of class "character"
- `customCol`: Object of class "character"
- `setLevel`: Object of class "character"
- `showLevels`: Object of class "logical"

**Methods**

- signature(e1 = "LINCbio", e2 = "LINCfeature"): ...
- signature(e1 = "LINCcluster", e2 = "LINCfeature"): ...
- signature(e1 = "LINCmatrix", e2 = "LINCfeature"): ...

**Examples**

`showClass("LINCfeature")`

LINCmatrix-class  
Class "LINCmatrix"

**Description**

an object of the class 'LINCmatrix' (S4) with 6 Slots

**Objects from the Class**

Objects can be created by calls of the form `new("LINCmatrix", ...)`. 

**Slots**

- `results`: Object of class "list"
- `assignment`: Object of class "vector"
- `correlation`: Object of class "list"
- `expression`: Object of class "matrix"
- `history`: Object of class "environment"
- `linCenvir`: Object of class "environment"
Methods

+ signature(e1 = "LINCmatrix", e2 = "LINCfeature"): ...
  
  clusterlinc signature(linc = "LINCmatrix"): ...
  
  linc signature(object = "LINCmatrix", codingGenes = "missing"): ...
  
  plotlinc signature(input = "LINCmatrix", showCor = "character"): ...
  
  plotlinc signature(input = "LINCmatrix", showCor = "missing"): ...
  
  singlelinc signature(input = "LINCmatrix"): ...

Examples

showClass("LINCmatrix")
Write To Table LINC

Description
Write and save a table in LINC

Methods
signature(file_name = "character", input = "LINCcluster") Table of co-expressed genes.

Examples
```r
# NOT RUN:
# write to a table
# linctable(file_name = "crbl_co_expr", input = crbl_cluster)
```

Plot Objects Of The 'LINC' class

Description
plotlinc is the generic function that creates plots based on objects of the LINC class.

Usage
```r
plotlinc(input,
          showCor,
          returnDat = FALSE)
```

Arguments
- **input**: usually a LINCmatrix, LINCcluster, LINCbio or LINCsingle object
- **showCor**: a vector of gene names; length 2 up to 6 elements; the first entry is the subject (see example)
- **returnDat**: whether to return the data used to create the plot TRUE or not FALSE

Details
A plot will be created based on the information found in the slots: history and linCenvir of a LINCmatrix, LINCcluster, LINCbio or LINCsingle object. Using the argument showCor = ... will output scatterplots for one query, the first entry in ... , and up to five subjects (see example). This can be used to manually check the correlation of genes. Individual or modified plots can be generated by returning the plotting data with returnDat Unexpected extreme values may corrupt plots.

Value
an object of the class 'gtable' containing multiple 'grobs' or a 'list' if returnDat = TRUE
querycluster

Methods
signature(input = "LINCbio", showCor = "character") (see details)
signature(input = "LINCbio", showCor = "missing") (see details)
signature(input = "LINCcluster", showCor = "character") (see details)
signature(input = "LINCcluster", showCor = "missing") (see details)
signature(input = "LINCmatrix", showCor = "character") (see details)
signature(input = "LINCmatrix", showCor = "missing") (see details)
signature(input = "LINCsingle", showCor = "character") (see details)
signature(input = "LINCsingle", showCor = "missing") (see details)

Compatibility
plotlinc(LINCmatrix, ...).plotlinc(LINCcluster, ...).plotlinc(LINCbio, ...).plotlinc(LINCsingle, ...

Author(s)
Manuel Goepferich

See Also
querycluster; feature

Examples
data(BRAIN_EXPR)
plotlinc(crbl_matrix)
plotlinc(crbl_cluster)

# show correlations and expression; "647979" as query plus 4 subjects
plotlinc(crbl_cluster, showCor = c("647979", "6726", "3337", "3304", "3320"))

querycluster

Cluster One ncRNA Gene Based On Its Co-Expression in Multiple Datasets

Description
querycluster takes a set of 'LINCcluster' objects, extracts the respective co-expressed protein-coding genes and plots a dendrogram with the distance matrix attached. This function is intended to be applied in a case where a particular ncRNA occurs in datasets which represent different tissues, batches, statistical corrections, reduced gene sets, controls and so on. The output will show the clustering of the groups and therefore the information under which condition is the co-expression to the query most similar.
Usage

querycluster(query = NULL,
queryTitle = NULL,
traits = NULL,
method = "spearman",
returnDat = FALSE,
mo_promise,
...)

Arguments

query the query name, i.e. the gene id of a ncRNA present in the supplied input
queryTitle a character string used as the title of the plot
traits NULL or a single integer. For NULL all co-expressed genes will be used. A number instead will be considered as maximal number of traits.
method a character string, has to be one of c("spearman", "dicedist")
returnDat whether to return the data used to create the plot TRUE or not FALSE
mo_promise mo_promise = 'list', a list of 'LINCcluster' objects (see example)
... the 'LINCcluster' objects itself, but not a combination of both, mo_promise = 'list' and supplying the objects itself (see example)

Details

This function will search for co-expressed protein-coding genes which belong to a the defined query. Based on the co-expression in the input 'LINCcluster' objects a distance matrix is computed. The method "spearman" finds the union of all interaction partners for the query and calculates the correlation between the 'LINCcluster' objects. For this method the distance measure is \((1 - \text{correlation})\). Alternatively, method = "dicedist" takes the Czekanovski dice distance \([1]\) as distance measure of the traits = n genes. This method, however, will not work with traits = NULL. Choosing a low number for n will limit the number of different values in the distance matrix.

Apart from queryTitle the command 'LINCcluster' + feature(customID = ..., customCol = ...) enables a customized plot as output. For this to work the supplied 'LINCcluster' objects in ... have to be modified by the function feature(....) in advance.

Value

an object of the class 'gg' or a 'list' if returnDat = TRUE

Author(s)

Manuel Goepferich

References


See Also

feature; clusterlinc
Examples

data(BRAIN_EXPR)

# add custom names and colors
gbm_cluster <- gbm_cluster + feature(customID = "CANCER_GBM", customCol = "red")
ctx_cluster <- ctx_cluster + feature(customID = "HEALTHY_CTX", customCol = "blue")
hpc_cluster <- hpc_cluster + feature(customID = "HEALTHY_HPC", customCol = "blue")
crbl_cluster <- crbl_cluster + feature(customID = "HEALTHY_CRBL", customCol = "blue")

# plot the dendrogram
querycluster('647979', queryTitle = 'NORAD',
            gbm_cluster, # Glioblastoma
            ctx_cluster, # Cortex
            hpc_cluster, # Hippocampus
            crbl_cluster) # Cerebellum

# objects can also be supplied as a list
query_list <- list(gbm_cluster,
                    ctx_cluster,
                    hpc_cluster,
                    crbl_cluster)

# mo_promise is the (informal) argument for multiple objects
querycluster(query = '647979', queryTitle = 'NORAD', mo_promise = query_list)

# used the Czekanovski dice distance based on the 25 best
# interaction partners in each tissue
querycluster(query = '647979', method = "dicedist", traits = 25, mo_promise = query_list)

# NOT RUN:
# querycluster(query = '647979', method = "dicedist", mo_promise = query_list)

---

results-methods

Methods for the Getter Function results in Package LINC

Description

Access the slot results of an object of class LINC

Arguments

- x: a 'LINC' object, for instance LINCmatrix

Value

the respective substructure or information

Methods

signature(x = "LINCbio") results slot
signature(x = "LINCcluster") results slot
signature(x = "LINCmatrix") results slot
signature(x = "LINCsingle") results slot
Author(s)
Manuel Goepferich

Examples
data(BRAIN_EXPR)
results(crbl_cluster)

Description
The function `singlelinc` performs co-expression analysis for a single query. An input LINCmatrix will be converted to a LINCsingle object. As a first step (I) a set of co-expressed protein-coding genes of a query is determined. Secondly, (II) biological terms related to these genes are derived. The result will show the co-expression for the query.

Usage
```r
singlelinc(input, 
    query = NULL, 
    onlycor = FALSE, 
    testFun = cor.test, 
    alternative = "greater", 
    threshold = 0.05, 
    underth = FALSE, 
    coExprCut = NULL, 
    enrichFun = 'enrichGO', 
    ont = "BP", 
    verbose = TRUE, 
    ...)
```

Arguments
- **input**: an object of the class LINCmatrix
- **query**: the name of the (ncRNA) gene to be evaluated; has to be present in input
- **onlycor**: if TRUE co-expression will be decided based on absolute correlation values from the input LINCmatrix object. If FALSE co-expressed genes will be selected based on p-values from the correlation test.
- **testFun**: a function to test the robustness of correlations. User-defined functions are allowed. The expected output is a p-value.
- **alternative**: one of c("two.sided", "less", "greater"). This argument indicates the alternative in the correlation test. "less" instead of "greater" can be used for negative correlations.
- **threshold**: a single number representing the threshold for selecting co-expressed genes
singlelinc-methods

underth

if TRUE values lower than the threshold will be considered (intended for p-values). If FALSE values higher than the threshold will be considered (intended for absolute correlations)

coExprCut

a single integer indicating the maximal number of co-expressed genes to select. In case too many genes fulfill the supplied threshold criterion their number can be reduced by this argument.

enrichFun

a function given as character string which will derive significant biological terms based on the set of co-expressed genes from a gene annotation resource. Supported functions are: c("enrichGO", "enrichPathway", "enrichDO")

ont

a subontology, only used for enrichFun = 'enrichGO'. This has to be one of "MF", "BP", "CC".

verbose

whether to give messages about the progression of the function TRUE or not FALSE

... further arguments, mainly for cor.test and functions from clusterProfiler

Details

In comparison to the function clusterlinc this function will provide more flexibility in terms of the selection of co-expressed genes. The option onlycor = TRUE in combination with a suitable threshold can be used to choose co-expressed protein-coding genes based on the correlation values inherited from the input LINCmatrix object. For this to work it is required to set underth = FALSE because then, values higher than the threshold will be picked. By default, co-expression depends on the p-values from the correlation test (stats::cor.test) which demonstrate the robustness of a given correlation between two genes. A user-defined test function supplied in testFun requires the formal arguments x, y, method and use. Moreover, the p-values of the output should be accessible by $pvalue. The number of co-expressed genes can be restricted not only by threshold, but also by coExprCut. The value n for coExprCut = n will be ignored in case the number of genes which fulfill the threshold criterion is smaller than n. Options for enrichFun are for example: ReactomePA::enrichPathway() or clusterProfiler::enrichGO. Further arguments (…) are intended to be passed to the called enrichFun function. enrichFun = 'enrichGO', ont = "CC" will call the subontology "Cellular Component" from GO. In case genes are not given as Entrez ids they will be translated. For more details see the documentation of clusterProfiler.

Value

an object of the class 'LINCmatrix' (S4) with 6 Slots

results a list of four entries: $query, the queried gene, $bio, a list of biological terms and their p-values, $cor, absolute correlations of co-expressed genes, $pval, p-values from the correlation test of co-expressed genes

assignment a character vector of protein-coding genes

correlation a list of $single, the correlation of the query to protein-coding genes

expression the original expression matrix

history a storage environment of important methods, objects and parameters used to create the object

linCenvir a storage environment ensuring the compatibility to other objects of the LINC class

Methods

signature(input = "LINCmatrix") (see details)
Compatibility

plotlinc(LINCs, ...)

Author(s)

Manuel Goepferich

See Also

linc; singlelinc

Examples

data(BRAIN_EXPR)

# selection based on absolute correlation
meg3 <- singlelinc(crbl_matrix, query = "55384", onlycor = TRUE, underth = FALSE, threshold = 0.5)
plotlinc(meg3)

# using the 'cor.test' in combination with 'underth = TRUE'
meg3 <- singlelinc(crbl_matrix, query = "55384", underth = TRUE, threshold = 0.0005, ont = 'BP')
plotlinc(meg3)
Index

*Topic index

∗ other possible keyword(s)

plotlinc-methods, 22

∗ Topic assignment
assignment-methods, 2

∗ Topic changeOrgDb
changeOrgDb, 4

∗ Topic clusterlinc
clusterlinc-methods, 5

∗ Topic correlation
expression-methods, 8

∗ Topic express
expression-methods, 8

∗ Topic feature
linc-methods, 15

∗ Topic linCenvir
linCenvir-methods, 19

∗ Topic linctable
linctable-methods, 22

∗ Topic plotlinc
plotlinc-methods, 22

∗ Topic querycluster
querycluster, 23

∗ Topic results
results-methods, 25

∗ Topic singlelinc
singlelinc-methods, 26

∗ Topic classes
LINCbio-class, 17
LINCcluster-class, 18
LINCfeature-class, 20
LINCmatrix-class, 20

∗ Topic datasets
BRAIN_EXPR, 3

∗ Topic linc
linc-methods, 15

∗ Topic methods
Arith-methods, 2
assignment-methods, 2
clusterlinc-methods, 5
correlation-methods, 7
express-methods, 8
getbio-methods, 10
getlinc-methods, 12
history-methods, 13
justlinc-methods, 13
linc-methods, 15
linCenvir-methods, 19
linctable-methods, 22
plotlinc-methods, 22
results-methods, 25
singlelinc-methods, 26
+(Arith-methods), 2
+,LINCbio,LINCfeature-method
(Arith-methods), 2
+,LINCcluster,LINCfeature-method
(Arith-methods), 2
+,LINCmatrix,LINCfeature-method
(Arith-methods), 2
+-methods (Arith-methods), 2

Arith (Arith-methods), 2
Arith-methods, 2
assignment (assignment-methods, 2
assignment,LINCbio-method
(Assignment-methods), 2
assignment,LINCcluster-method
(Assignment-methods), 2
assignment,LINCmatrix-method
(Assignment-methods), 2
assignment,LINCsingle-method
(Assignment-methods), 2
assignment-methods, 2
BRAIN_EXPR, 3
cerebellum (BRAIN_EXPR), 3
cchangeOrgDb, 4
clusterlinc (clusterlinc-methods), 5
clusterlinc, LINClnccluster-method (clusterlinc-methods), 5
clusterlinc, LINClncmatrix-method (clusterlinc-methods), 5
clusterlinc-methods, 5
correlation (correlation-methods), 7
correlation, LINClncbio-method (correlation-methods), 7
correlation, LINClnccluster-method (correlation-methods), 7
correlation, LINClncmatrix-method (correlation-methods), 7
correlation, LINClncsingle-method (correlation-methods), 7
correlation-methods, 7
cortex (BRAIN_EXPR), 3
crbl_cc (BRAIN_EXPR), 3
crbl_cluster (BRAIN_EXPR), 3
crbl_matrix (BRAIN_EXPR), 3
ctx_cc (BRAIN_EXPR), 3
cctx_cluster (BRAIN_EXPR), 3
cexpr (express-methods), 8
express, LINClncbio-method (express-methods), 8
express, LINClnccluster-method (express-methods), 8
express, LINClncmatrix-method (express-methods), 8
express, LINClncsingle-method (express-methods), 8
express-methods, 8
feature, 9
gbm_cluster (BRAIN_EXPR), 3
getbio (getbio-methods), 10
getbio, LINClnccluster-method (getbio-methods), 10
getbio-methods, 10
gtcoexpr, 11
getlinc (getlinc-methods), 12
getlinc, ANY, character-method (getlinc-methods), 12
getlinc-methods, 12
glioblastoma (BRAIN_EXPR), 3
hippocampus (BRAIN_EXPR), 3
history (history-methods), 13
history, LINClncbio-method (history-methods), 13
history, LINClnccluster-method (history-methods), 13
history, LINClncmatrix-method (history-methods), 13
history, LINClncsingle-method (history-methods), 13
history-methods, 13
hpc_cluster (BRAIN_EXPR), 3
justlinc (justlinc-methods), 13
justlinc, matrix-method (justlinc-methods), 13
justlinc-methods, 13
linc (linc-methods), 15
linc, data.frame, ANY-method (linc-methods), 15
linc, ExpressionSet, ANY-method (linc-methods), 15
linc, LINClncmatrix, missing-method (linc-methods), 15
linc, matrix, ANY-method (linc-methods), 15
linc-methods, 15
LINClncbio-class, 17
LINClnccluster-class, 18
linCenvir (linCenvir-methods), 19
linCenvir, LINClncbio-method (linCenvir-methods), 19
linCenvir, LINClnccluster-method (linCenvir-methods), 19
linCenvir, LINClncmatrix-method (linCenvir-methods), 19
linCenvir, LINClncsingle-method (linCenvir-methods), 19
linCenvir-methods, 19
linCenvir-methods, 19
LINClncfeature-class, 20
LINClncmatrix, 18, 21
LINClncmatrix-class, 20
LINClncsingle-class, 21
linctable (linctable-methods), 22
linctable, character, LINClnccluster-method (linctable-methods), 22
linctable-methods, 22
pcgenes_crbl (BRAIN_EXPR), 3
pcgenes_ctx (BRAIN_EXPR), 3
pcgenes_gbm (BRAIN_EXPR), 3
pcgenes_hpc (BRAIN_EXPR), 3
plotlinc (plotlinc-methods), 22
plotlinc, LINClncbio, character-method (plotlinc-methods), 22
plotlinc\text{,} LINCbio\text{,} missing-method
(plotlinc-methods), 22
plotlinc\text{,} LINCcluster\text{,} character-method
(plotlinc-methods), 22
plotlinc\text{,} LINCcluster\text{,} missing-method
(plotlinc-methods), 22
plotlinc\text{,} LINCmatrix\text{,} character-method
(plotlinc-methods), 22
plotlinc\text{,} LINCmatrix\text{,} missing-method
(plotlinc-methods), 22
plotlinc\text{,} LINCsingle\text{,} character-method
(plotlinc-methods), 22
plotlinc\text{,} LINCsingle\text{,} missing-method
(plotlinc-methods), 22
plotlinc-methods, 22
querycluster, 23
results (results-methods), 25
results\text{,} LINCbio-method
(results-methods), 25
results\text{,} LINCcluster-method
(results-methods), 25
results\text{,} LINCmatrix-method
(results-methods), 25
results\text{,} LINCsingle-method
(results-methods), 25
results-methods, 25
singlelinc (singlelinc-methods), 26
singlelinc\text{,} LINCmatrix-method
(singlelinc-methods), 26
singlelinc-methods, 26