Package ‘PCpheno’

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Type Package
Title Phenotypes and cellular organizational units
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Author Nolwenn Le Meur and Robert Gentleman
Description Tools to integrate, annotate, and link phenotypes to cellular organizational units such as protein complexes and pathways.
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Suggests KEGG.db, GO.db, org.Sc.sgd.db
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R topics documented:

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Description

Tools to integrate, annotate and search for associations between phenotypes, protein complexes, and pathways.

Details

- **Package**: PCpheno
- **Type**: Package
- **Version**: 1.3.1
- **Date**: 2006-03-09
- **License**: The Artistic License, Version 2.0

Author(s)

N. LeMeur and R. Gentleman

Maintainer: N. LeMeur <nlemeur@fhcrc.org>

References


**buildFDMat**

See Also

ScISI, SLGI

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### Description

Function to build a fitness defect contingency matrix where rows correspond to tested genes and columns to experimental conditions.

### Usage

```r
buildFDMat(data, genenames, condition)
```

### Arguments

- `data` List of "significant" fitness defect scores and the associated genes at different experimental conditions.
- `condition` Character vector of the different experimental conditions tested
- `genenames` Character vector of all the tested genes for fitness defect.

### Value

Contingency matrix of genes that present significant fitness defect in different experimental conditions.

### Author(s)

N. LeMeur

### Examples

```r
data(GiaeverPheno)
data(GiaeverExpCdt)
data(GiaeverGene)
fitnessData <- getFDgene(GiaeverPheno, condition=GiaeverExpCdt, cutoff=c(20, 100, 100), mode="generation", subset=c(5, 15, 20))
GiaeverPhenoM <- buildFDMat(data=fitnessData, genenames=GiaeverGene, condition=GiaeverExpCdt[, 3])
```
categoryToEntrezBuilder

Return a list mapping multi-protein complexes IDs to YEAST ids

Description

Return a list mapping multi-protein complexes (category) IDs to the YEAST ids annotated at the category id.

Usage

```r
## S4 method for signature 'CoHyperGParams'
categoryToEntrezBuilder(p)
```

Arguments

- `p`: A subclass of `HyperGParams-class`

Details

End users **should not** call this directly. This method gets called from `hyperGTest`. To add support for a new category, a new method for this generic must be defined. Its signature should match a subclass of `HyperGParams-class` appropriate for the new category.

Value

A list mapping category IDs to YEAST identifiers.

Author(s)

S. Falcon and N. LeMeur

See Also

`hyperGTest` `CoHyperGParams-class`

Examples

```r
data(ScISIC)
data(essglist)
essential <- names(essglist)

params <- new("CoHyperGParams",
geneIds=essential,
universeGeneIds=rownames(ScISIC),
annotation="org.Sc.sgd.db",
categoryName="ScISIC",
pvalueCutoff=0.01,
testDirection="over")

categoryToEntrezBuilder(params)[1:2]
```

Class "CoHyperGParams"

Description
A parameter class for representing all parameters needed for running the hyperGTest method with multiprotein complexes.

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

Slots
- `geneIds`: Object of class "ANY": A vector of gene identifiers. Numeric and character vectors are probably the only things that make sense. These are the gene ids for the selected gene set.
- `universeGeneIds`: Object of class "ANY": A vector of gene ids in the same format as `geneIds` defining a subset of the gene ids on the chip that will be used as the universe for the hypergeometric calculation. If this is `NULL` or has length zero, then all gene ids on the chip will be used.
- `annotation`: A string giving the name of the annotation data package for the chip used to generate the data.
- `categorySubsetIds`: Object of class "ANY": If the test method supports it, can be used to specify a subset of category ids to include in the test instead of all possible category ids.
- `categoryName`: A string describing the category. Usually set automatically by subclasses. For example "ScISI".
- `pvalueCutoff`: The p-value to use as a cutoff for significance for testing methods that require it. This value will also be passed on to the result instance and used for display and counting of significant results. The default is 0.01.
- `testDirection`: A string indicating whether the test should be for overrepresentation ("over") or underrepresentation ("under").

Methods
- `hyperGTest signature(p = "HyperGParams")`: Perform hypergeometric tests to assess over-representation of category ids in the gene set. See the documentation for the generic function for details. This method must be called with a proper subclass of `HyperGParams`.
- `geneIds(r), geneIds(r) <- value` Accessors for the gene identifiers that will be used as the selected gene list.
- `codeannotation(object)` Accessor for annotation
- `ontology(r)` Accessor for GO ontology.
- `pvalueCutoff(r), pvalueCutoff(r) <- value` Accessor for the p-value cutoff. When setting, value should be a numeric value between zero and one.
- `testDirection` Accessor for the test direction. When setting, value must be either "over" or "under".
- `universeGeneIds(r)` accessor for vector of gene identifiers.
- `isConditional(r)` Returns TRUE if the instance has its conditional flag set
CoHyperGResult-class

Author(s)

S. Falcon and N. LeMeur

See Also

HyperGResult-class CoHyperGResult-class hyperGTest

---

Description

This class represents the results of a test for over-representation of genes in a selected gene set based among protein complexes upon the Hypergeometric distribution.

Objects from the Class

Objects is created by calls to the function hyperGTest.

Slots

- pvalues: "numeric" vector: the ordered p-values for each category term tested.
- oddsRatios: Object of class "numeric" Odds ratio for each category term tested
- expectedCounts: Object of class "numeric" The expected number of genes for each gene term tested
- geneCounts: "integer" vector: for each category term tested, the number of genes from the gene set that are annotated at the term.
- universeCounts: "integer" vector: for each category term tested, the number of genes from the gene universe that are annotated at the term.
- catToGeneId: Object of class "list". The names of the list are category IDs. Each element is a vector of gene IDs annotated at the given category ID and in the specified gene universe.

Extends

Class "HyperGResultBase", directly.

Methods

- **geneCounts** signature(r = "CoHyperGResult"): return an "numeric" vector: for each category term tested, the number of genes from the gene set that are annotated at the term.
- **pvalues** signature(r = "HyperGResult"): return a "numeric" vector: the ordered p-values for each category term tested.
- **oddsRatios** signature(r = "HyperGResult"): return a "numeric" vector: the odds ratio for each category term tested.
- **expectedCounts** signature(r = "HyperGResult"): return a "numeric" vector: the expected number of genes for each GO term tested.
Complex status

**universeCounts** signature(r = "HyperGResult"): return an "numeric" vector: for each category term tested, the number of genes from the gene universe that are annotated at the term.

**geneIdUniverse** signature(r = "CoHyperGResult"): return a list named by the protein Complexes. Each element of the list is a vector of gene identifiers (from the gene universe) annotated at the corresponding protein complex.

**summary** signature(r = "CoHyperGResult"): Returns a data.frame summarizing the test result. Optional arguments pvalue and categorySize allow specification of minimum p-value and categorySize, respectively. Optional argument htmlLinks is a logical value indicating whether to add HTML links (useful in conjunction with xtables print method with type set to "html").

**Author(s)**

S. Falcon and N. LeMeur

**See Also**

HyperGResultBase-class

**Examples**

data(DudleyPhenoM)
data(ScISIC)

```r
## Select genes sensitive to paraquat
DudleyPhenoL <- apply(DudleyPhenoM,2,function(x) names(which(x==1)))
paraquat <- DudleyPhenoL["Paraq"]

## Apply a hypergeometric test
params <- new("CoHyperGParams",
  geneIds=paraquat,
  universeGeneIds=rownames(ScISIC),
  annotation="org.Sc.sgd.db",
  categoryName="ScISIC",
  pvalueCutoff=0.01,
  testDirection="over")

paraquat.complex <- hyperGTest(params)

## access the p-values
pvalues(paraquat.complex)[1:5]

## Display a summary of the results
summary(paraquat.complex)[,1:4]
```

complexStatus

<table>
<thead>
<tr>
<th>Complex Status</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Description</strong></td>
</tr>
</tbody>
</table>

Categorize the complex whether or not a complex is composed of a significant number of genes involved in a particular phenotype than expected by chance.
complexStatus

Usage

complexStatus(data, phenotype, interactome, threshold=0.05)

Arguments

data Output from CoHyperG test
phenotype List of gene names inducing an observed phenotype, e.g., list of essential gene names (see package SLGI)
interactome A binary matrix composed of genes (rows) and biological complexes (columns) (see package ScISI)
threshold p-value threshold (default 0.05)

Details

We form four distinct categories from A to D to characterize how a complex might be involved in a particular phenotype (according to the number of genes it contains and that are involved in a particular phenotype - see also hyperGTest function)

Value

The returned value is a list with components:

A "interesting" complexes, complexes with a significant number of interesting genes, i.e., genes that participate to a particular phenotype (at a given p-values threshold)
B complexes with a NON significant number of interesting genes BUT that SHARE genes with complexes from the A status
C complexes with a NON significant number of interesting genes AND that DON’T SHARE interesting genes with complexes from cat A
D complexes WITHOUT interesting genes, i.e. the one involved in the studied phenotype

Author(s)

N. LeMeur

Examples

data(ScISI)
data(essglist)
essential <- names(essglist)

CoparamsESS <- new("CoHyperGParams",
geneIds=essential,
universeGeneIds=rownames(ScISI),
anotation="org.Sc.sgd.db",
categoryName="ScISI",
pvalueCutoff=0.01,
testDirection="over")

sign<- hyperGTest(CoparamsESS)
test05 <- complexStatus(data=sign, phenotype=essential, interactome=ScISI, threshold=0.05)
**densityEstimate**

**Observed versus Expected Ratios**

**Description**

Function to calculate the ratio of genes that characterize a phenotype (observed) among the genes that characterize a biological complex versus the ratio of a set of randomly sampled genes (expected) among the genes that characterize a biological complex.

**Usage**

```
densityEstimate(genename, interactome, perm)
```

**Arguments**

- `genename`: Character vector of the gene names that characterize a specific phenotype.
- `interactome`: Contingency matrix of genes (rows) and biological complexes (columns) (see package `ScISI`).
- `perm`: Numeric vector indicating the number of simulations to run to compute the expected ratios.

**Value**

List of observed and simulated ratios.

**Author(s)**

N. LeMeur

**Examples**

```r
data(ScISI)
data(essglist)
esential <- names(essglist)
ScISI <- as.matrix(ScISI)
ratio<- densityEstimate(genename=essential, interactome=ScISI, perm=50)
```

**deResult-class**

A class for representing the result of a densityEstimate test.

**Description**

A class for representing the result of a densityEstimate test.

**Slots**

- `Size`: Object of class "numeric" representing the size of the cellular organizational unit tested
- `Observed`: Return a "numeric" vector: the observed number of interactions between genes inducing a specific phenotype and each cellular organizational units
- `Expected`: Return a matrix: the expected number of interactions between genes inducing a specific phenotype and each cellular organizational units
DudleyPheno

Extends

Class "testResult", directly.

Methods

plot Graphical representation of the test result

Author(s)

N. LeMeur

See Also

testResult, gtResult, densityEstimate, plot

Examples

## apply a densityEstimate test
data(DudleyPhenoM)
data(ScISIC)

DudleyPhenoL <- apply(DudleyPhenoM,2,function(x) names(which(x==1)))

pH3 <- DudleyPhenoL["pH3"]

perm <- 20

pH3Density <- densityEstimate(genename=pH3, interactome=ScISIC, perm=perm)

## access results

pH3Density@Observed[1:5]

## use of the plot method

plot(pH3Density)

DudleyPheno

List of fitness defect score generated from Dudley et al 2005

Description

Dudley et al (2005) create a collection of gene-deletion mutants to determine genes that contribute to a particular phenotype in specific environmental conditions. This list is generated from a fitness analysis under 21 different experimental conditions.

Usage

data(DudleyGenelist)
data(DudleyPhenoFull)
data(DudleyPhenoM)
data(DudleySign)
Format

DudleyGenelist is a character vector of length 814 genes. DudleyPhenoFull is a dataframe of 814 genes by 23 elements. The column contains the yeast gene name. The 22 remaining columns are the experimental conditions (see details). The values obtained in the different condition are the fitness defect scores for the 814 genes sensitive to the experimental condition, as defined by Dudley et al (2005). DudleyPhenoM is a 814 by 22 incidence matrix with rownames corresponding to the genes names and columns to an experimental condition. This matrix contains a 1 in the (i,j) position if the i-th gene is sensitive to the experimental condition of the j-th column; it contains a 0 otherwise.

Yname  Yeast systematic gene name
benomyl  15ug/ml benomyl, microtubule function
CaCl2  0.7M calcium chloride, divalent cation
CAD  55uM Cadmium, heavy metal
Caff  2mg/ml Caffeine
cyclohex  0.18ug/ml cycloheximide, protein synthesis
DTT  unknown
EtOH  YPD + 6% Ethanol
FeLim  iron limited, nutrient limited condition
HU  11.4mg/ml Hydroxyurea, DNA replication and repair
HygroB  50ug/ml hygromycin B, aminoglycosides
lowPO4  Low phosphate, nutrient limited condition
MPA  20ug/ml mycophenolic acid, transcriptional elongation
NaCl  1.2M sodium chloride, general stress condition
Paraq  1mM paraquat, oxidative stress
pH3  Low pH, general stress condition
rap  0.1ug/ml rapamycin, protein synthesis
Sorb  1.2M sorbitol, general stress condition
UV  100J/m2 ultra-violet, DNA replication and repair
YPGal  2% galactose, carbon source
YPGly  3% glycerol, carbon source
YPLac  2% lactate, carbon source
YPRaff  2% raffinose, carbon source

DudleySign is a list of dataframe that summaryzes in which complexes the gene related to the phenotype are found, the size of the complexes and the associated p-value. This is the result of applying a Hypergeometric test (see CoHyperGParams-class for more details) and the complexStatus function.

Dudleyresult is a data.frame that summaryzes the number of sensitive genes per condition, how many of those genes are present in the ScISI interactome and the associated p-value. This is the result of applying a Hypergeometric test (see CoHyperGParams-class for more details) and the complexStatus function.

Author(s)

N. LeMeur
getDescr

Source

Dudley et al (2005), supplementary information: http://arep.med.harvard.edu/pheno/default.htm

References


Examples

data(DudleyPhenoFull)
data(DudleyPhenoM)

getDescr(x, database="GO.db")

Arguments

x Vector of multi-protein complexes or pathways IDs to be described
database Source of annotation. The database currently available are MIPS, GO.db and KEGG.db

Author(s)

N. LeMeur

Examples

xx <- getDescr(c("MIPS-220","MIPS-260.20","04111"),c("MIPS","KEGG.db"))
getFDgene

Get fitness defect genes

Description

Function to select genes that present a significant growth defect according to the condition (media) or generation time.

Usage

getFDgene(data, condition, cutoff, mode="generation", subset)

Arguments

data List of fitness defect scores for genes tested at different experimental conditions.
condition Dataframe of experimental conditions

cutoff Numerical vector of length one or more, defining the threshold of 'significance' for the fitness defect score

mode Character string defining the base of the selection either 'condition' (media) or 'generation' time, Default=generation.

subset Numerical vector or list to which apply the different cutoffs.

Value

Reduced list of gene fitness scores per experimental condition according to the experimental condition or the generation time.

Author(s)

N. LeMeur

References


Examples

data(GiaeverPheno)
data(GiaeverExpCdt)

# Select all the genes, in the different experimental conditions, that present a fitness score above 20, 100 fitnessGen <- getFDgene(GiaeverPheno, condition=GiaeverExpCdt, cutoff=c(20,100,100), mode="generation", subset=c(5,15,20))

# Select all the genes, that present a fitness score above 15 and 100
#in the condition set A and B respectively, independently of the generation time

fitnessCondt <- getFDgene(GiaeverPheno, condition=GiaeverExpCdt, cutoff=c(100,15), mode="condition", subset=list(a=c(1:23,27,30,31),b=c(24:26,28,29)))
GiaeverPheno

List of fitness defect score generated from Giaever et al 2002

Description

Giaever et al (2002) create a collection of gene-deletion mutants to determine genes that contribute to a particular phenotype in specific environmental conditions. This list is generated from a fitness analysis under six different experimental conditions.

Usage

data(GiaeverPheno)
data(GiaeverGene)
data(GiaeverExpCdt)

Format

GiaeverPheno is a list with 31 elements. The name of each element is a experimental condition (see details). The value of each element are the fitness defect scores for the genes sensitive to the experimental condition, as defined by Giaever et al (2002).

GiaeverGene Vector of the systematic gene names of the 5898 tested genes. Note that some updates have been made for the list to be consistent with Saccharomyces Genome Database.

GiaeverExpCdt is a 3 columns dataframe with fileID from which the data were extracted, the generation time (growth time) and the condition (media).

gen. generations
rep. replicate
ypg5a,ypg5b yeast/peptone/galactose 5 gen. rep. a and b ==> carbone source
ypg15a ypg15b yeast/peptone/galactose 15 gen. rep. a and b ==> carbone source
sorbitol5a sorbitol5b 1.5M Sorbitol 5 gen. rep. a and b ==> sugar, osmotic stress
sorbitol20a sorbitol15b 1.5M Sorbitol 20 and 15 gen. rep. a and b respectively ==> sugar, osmotic stress
NaCl5a NaCl5b 1M NaCl 5 gen. rep. a and b ==> salt, osmotic stress
NaCl15a NaCl15b 1M NaCl 15 gen. rep. a and b ==> salt, osmotic stress
lysM5a lysM5b lysine minus 5 gen. rep. a and b ==> lack of required AA
thM5a threonine minus 5 gen. rep. a ==> lack of required AA
trpM5a trpM5b tritophanee minus 5 gen. rep. a ==> lack of required AA
minimalPlus5a minimalPlus5b minimal + histidine/leuvine/uracile 5 gen. rep. a and b
minimalPlus15a minimalPlus15b minimal + histidine/leuvine/uracile 15 gen. rep. a and b
minimalC5a minimalC5b minimal complete 5 gen. rep. a and b
nystatin5a nystatin5b Nystatin 5 gen. rep. a and b ==> antifungal drug
nystatin15a nystatin15b Nystatin 5 gen. rep. a and b ==> antifungal drug
pH8g5a pH8g5b pH 8.5 gen. rep. a and b ==> alkali stress
pH8g15a pH8g20b pH 8.5 and 20 gen. rep. a and b respectively ==> alkali stress
graphTheory

Note: in their study they confound the 15 and 20 generations.

GiaeverResult is a data.frame that summarizes the number of sensitive genes per condition, how many of those genes are present in the ScISI interactome and the associated p-value. This is the result of applying a Hypergeometric test (see CoHyperGParams-class for more details) and the complexStatus function.

Author(s)

N. LeMeur

Source


References


Examples

data(GiaeverPheno)
data(GiaeverExpCdt)
data(GiaeverGene)

```r
graphTheory
```

Description

Graph theory approach associated with a permutation test to evaluate whether the number of associations is unexpectedly large.

Usage

```r
graphTheory(genename, interactome, perm)
```

Arguments

- `genename`: A vector a gene names that are associated with a particular phenotype
- `interactome`: A binary matrix composed of genes (rows) and biological complexes (columns) (see package ScISI)
- `perm`: Numeric, number of permutation run

Details

We form two distinct graphs where the set of nodes are the proteins (genes) in the organism. In one graph we create edges between genes if the two genes are members of one, or more, protein complexes. In the second graph we create an edge between all genes that are associated to a particular phenotype. We then construct a third graph on the same node set, but where there is an edge in this graph only if there is an edge in both of the first to graphs. We count the number of edges in the third and test by permutation whether the number of edges is unexpectedly large.
Value

The returned value is a list with components:

- **edgeCount**: Number of associations observed between the genes that are linked to a particular phenotype and the given interactome.
- **edgeSimul**: Number of associations if the genes that are linked to a particular phenotype are randomly distributed across the given interactome.
- **p.value**: Returned p.value

Author(s)

R. Gentleman and N. LeMeur

References


Examples

data(ScISI)
data(essglist)
ans <- graphTheory(names(essglist), ScISI, perm=3)

gtResult-class

* A class for representing the result of a graphTheory test.

Description

A class for representing the result of a graphTheory test.

Slots

- **Pvalue**: Object of class "numeric"
- **Observed**: Return a "numeric" vector: the observed number of interactions between genes inducing a specific phenotype and each cellular organizational units
- **Expected**: Return a matrix: the expected number of interactions between genes inducing a specific phenotype and each cellular organizational units

Extends

Class "testResult", directly.

Methods

- **plot** Graphical representation of the test result

Author(s)

N. LeMeur
HI

See Also
deResult.plot

testResult

Examples

```r
## apply a densityEstimate test
data(DudleyPhenoM)
data(ScISIC)

DudleyPhenoL <- apply(DudleyPhenoM,2,function(x) names(which(x==1)))
NaCl <- DudleyPhenoL["NaCl"]
perm <- 20
NaClGraph <- graphTheory(genename=NaCl, interactome=ScISIC, perm=perm)

## access results
slotNames(NaClGraph)
NaClGraph@Pvalue[1:5]

## use of the plot method
plot(NaClGraph)
```

HI

Data from Deutshbauer et al. (2005)

Description

Mechanisms of Haploinsufficiency revealed by Genome-Wide Profiling in Yeast (Deutshbauer et al., 2005)

Usage

data(HI)

Details

HI stands for haploinsufficient. The dataframe is composed of:

- **orf**: Yeast ORF, systematic name
- **gene**: Yeast common gene name of the corresponding ORF
- **go**: GO terms

Source

http://www.sciencemag.org/cgi/data/303/5659/808/DC1/1

References

Examples

data(HI)

KastenmayerRaw  Data from Kastenmayer et al. 2006

Description

Kastenmayer et al. (2006) undertook the first functional studies of small open reading frames (sORFs) in any system, using the model eukaryote Saccharomyces cerevisiae. Phenotypic analyses of the new gene-deletion strains identified 22 sORFs required for haploid growth, growth at high temperature, growth in the presence of a non-fermentable carbon source, or growth in the presence of DNA damage and replication-arrest agents.

Usage

data(KastenmayerRaw)

Format

Kastenmayer is a 5 columns dataframe.

SYSTEMATIC  Systematic name of the sORF.
COMMUN  Commun name of the sORF.
Length  Length of the small ORF sequence in number of amino acids.
Evidence  Experimental source of the data
refHomology  Bibliographical evidence of reported homology.
Kocollection  Bibliographical evidence of reported homology.
ESSENTIAL  Indicates if the sORF knockout is essential. A blank in this column indicates that the knockout is not-essential, if available.
GFPTAP  "GFP" or "TAP" signifies that sORF was detected by the indicated technique. "both" indicates that sORF was detected both as a TAP-tagged and GFP-tagged protein. "None" indicates that sORF was not detected by either method. Empty field indicates that sORF was not tested.
UPTAG  Sequence of the upstream primer.
DOWNTAG  Sequence of the downstream primer.

Author(s)

N. LeMeur

Source

References
Boeke JD, Snyder MA, Basrai MA. (2006) Functional genomics of genes with small open reading
frames (sORFs) in S. cerevisiae. Genome Res. 16(3):365-73. PMID: 16510898

Examples
data(KastenmayerRaw)
str(KastenmayerRaw)

KEGG2SCISI  Mapping between KEGG and ScISI

Description
Count the number of genes shared between a KEGG pathway and a protein complex from the ScISI
interactome.

Usage
KEGG2SCISI(pw, pc, pcMat, pwMat)

Arguments
pw  list of pathway names
pc  list of complex names
pwMat  pathway incidence matrix
pcMat  complex incidence matrix

Value
matrix

Author(s)
N. LeMeur

See Also
ScISI KEGG

Examples
data(ScISIC)
## Mapping from Yeast genes to KEGG pathways.
KeggMat <- PWAmat("org.Sc.sgd")
KEGG2SCISI(pw = colnames(KeggMat)[1:5], pc = colnames(ScISIC)[1:5], pwMat =
KeggMat, pcMat =ScISIC)

Description

Lesage et al. (2005) assembled a network of 316 interactions among 163 genes using deletion mutants in CHS1, CHS3, CHS4, CHS5, CHS6, CHS7 and BNI4 in a synthetic genetic array analysis.

Usage

data(LesageRaw)

Format

LesageRaw is a 5 column dataframe.

**SYSTEMATIC** Systematic gene names. NOTE: All mutants are isogenic to BY4741 (MATa his3Δ0394 leu2Δ0394 met15Δ0394 ura3Δ0394) except anp1Δ0394 and mnn9Δ0394 that are isogenic to BY4742 (MATα his3Δ0394 leu2Δ0394 lys2Δ0394 ura3Δ0394).

**COMMUN** Commun gene names.

**CFW** Mutants showing increased, decreased or wild type sensitivity to Calcofluor white are scored s, r, or wt, respectively.

**ChitinLevel** Chitin level (nmole GlcNAc/mg dry weight). Values are an average of at least three independent determinations. Values statistically higher and lower than wild type (p < 0.01) are highlighted in red and green, respectively.

**ChitinLevel.SD** Standard deviation of the average of at least three independent determinations of Chitin level.

Author(s)

N. LeMeur

Source


References


Examples

data(LesageRaw)
str(LesageRaw)
Description

Osterberg et al. (2006) report growth phenotypes in yeast for a strain collection over-expression ~600 C-terminal tagged integral membrane proteins growth both under normal and three different stress conditions.

Usage

data(OsterbergRaw)

Format

OsterbergRaw is a 17 columns dataframe.

- **SYSTEMATIC**  Systematic gene names of the studied membrane protein
- **COMMUN**  Commun gene names of the studied membrane protein
- **TMHMM.C**  The topology predicted by TMHMM (TransMembrane prediction using Hidden Markov Models) using the experimentally assigned C-terminal location for the protein as a constraint. The topology is represented in the format Location of N-terminus TMhelices Location of C-terminus (i and o stand for in and out respectively)
- **WesternBlot**  Protein expression levels (arbitrary units), estimated from the band intensity and normalized to the internal standard on each Western blot.
- **Bands**  Proteins detected as two distinct bands with different molecular mass on the Western blot analysis. category 1 indicates that both bands were insensitive to Endo H digestion, 2 indicates the higher molecular mass was shifted down upon Endo H digestion on SDS/PAGE and one band was predominant compared to the other, and 3 indicates that a higher molecular mass band shifted down upon Endo H digestion on SDS/PAGE and both bands were equal intensity on Western blot.
- **Toxicity**  Toxicity index from Spoko et al. (2006). The index varies between 1 and 5, where 1 means the strain is dead, and 5 indicates no difference in growth rate compared with the wild type strain.
- **sign.norm**  Over-expression strains that show a significant (P<0.001) growth rate phenotype (LSCrate) in synthetic defined medium conditions (Warringer et al., 2003). An average of two replicates is given. Strains that do not show a significant difference in doubling time compared with the wild-type strain are indicated by 0.
- **all.norm**  Phenotypes (significant or not) of over-expression strains (LSCrate) in synthetic defined medium conditions (Warringer et al., 2003). An average of two replicates is given.
- **sign.NaCl**  Over-expression strains that show a significant (P<0.001) growth rate phenotype (LPI-rate) in NaCl. An average of two replicates is given. Strains that do not show a significant difference in doubling time compared with the wild-type strain under NaCl stress are indicated by 0.
- **all.NaCl.LSC**  Phenotypes (significant or not) of over-expression strains (LSCrate) in NaCl (Warringer et al., 2003). An average of two replicates is given.
- **all.NaCL.LPI**  Phenotypes (significant or not) of over-expression strains (LPIrate) in NaCl (Warringer et al., 2003). An average of two replicates is given.
sign.caff Over-expression strains that show a significant (P<0.001) growth rate phenotype (LPI-rate) in caffeine. An average of two replicates is given. Strains that do not show a significant difference in doubling time compared with the wild-type strain under caffeine stress are indicated by 0.

all.caff.LSC Phenotypes (significant or not) of over-expression strains (LSCrate) in caffeine (Warringer et al., 2003). An average of two replicates is given

all.caff.LPI Phenotypes (significant or not) of over-expression strains (LPIrate) in caffeine (Warringer et al., 2003). An average of two replicates is given.

sign.paraq Over-expression strains that show a significant (P<0.001) growth rate phenotype (LPI-rate) in paraquat. An average of two replicates is given. Strains that do not show a significant difference in doubling time compared with the wild-type strain under paraquat stress are indicated by 0.

all.paraq.LSC Phenotypes (significant or not) of overexpression strains (LSCrate) in paraquat (Warringer et al., 2003). An average of two replicates is given.

all.paraq.LPI Phenotypes (significant or not) of overexpression strains (LPIrate) in paraquat (Warringer et al., 2003). An average of two replicates is given.

Author(s)
N. LeMeur

Source
Osterberg et al (2006), supplementary information: http://www.pnas.org/content/vol0/issue2006/images/data/0604078103/DC1/04078Table1.xls or ftp://genome-ftp.stanford.edu/pub/yeast/systematic_results/phenotypes

References

Examples
data(OsterbergRaw)
str(OsterbergRaw)

overlap Count the number of proteins shared by protein complexes

Description
Count the number of proteins shared by protein complexes

Usage
overlap(interactome)
Arguments

**interactome**  Binary matrix composed of genes (rows) and biological complexes (columns)  (see package *ScISI*)

Value

The returned value is a data frame with components:

- **C1**  Name of the first biological complex
- **C2**  Name of the second biological complex
- **nbSharedProt**  Number of proteins in common

Author(s)

N. LeMeur

See Also

*ScISI*

Examples

```r
xx = cbind("a"=c(0,1,1,1),"b"=c(1,1,0,1))
overlap(xx)
```

---

**plot**  
*Graphical method to represent the result of the density or graph test.*

Description

a plot method for deResult and gtResult objects.

Usage

```r
## S4 method for signature 'deResult'
plot(x,...)
## S4 method for signature 'gtResult'
plot(x,...)
```

Arguments

- **x**  the deResult or gtResult object to plot.
- **...**  general commands to be sent to plot.

Details

The plot generated from a deResult object is a set of density plots.  
The plot generated from a gtResult object is a histogram.

Author(s)

N. LeMeur
ppiInteract

Test the association between AP-MS data and phenotype

Description

Test the association between AP-MS data and phenotype data via a graph and permutation model.

Usage

ppiInteract(genename, expGraph, bait, prey, perm=10)

Arguments

genename          Genes associated to a phenotype
expGraph          A graphNEL object (a direct graph instance of classgraph). The nodes are the
                  union of viable baits (VB) and viable prey (VP) of the experiment (see package
                  ScISI)
bait              Proteins which was sampled as a bait in the binary relationship
prey              Proteins which was sampled as a prey in the binary relationship
perm              Number of permutation

Value

The returned value is a list:

  Observed          Observed values
  Expected          Expected values after each permutation

Author(s)

R. Gentleman and N. LeMeur

See Also

ScISI
**reduceM**

**Examples**

```r
data(ScISI)
data(essglist)
s1 <- ppiInteract(names(essglist), Gavin2002BPGraph, viableBaits[[8]],
                  viablePrey[[8]], perm=10)
```

---

**reduceM**  
*Resize a matrix*

**Description**

Resize a matrix to the number of rows common to a vector.

**Usage**

```
reduceM(x, mat, threshold=0)
```

**Arguments**

- `x` Character or numeric vector.
- `mat` Matrix sharing rownames with the supplied vector `x`.
- `threshold` Threshold upon column. Only the columns with a `colSums` above the threshold are kept.

**Value**

Resized matrix.

**Author(s)**

N. LeMeur

**Examples**

```r
mat <- matrix(c(1:25), nrow = 5, ncol = 5, dimnames = list(c(LETTERS[1:5]), c(1:5)))
xx <- LETTERS[c(2, 4, 5)]
reduceM(xx, mat)
```
SGDphenoL  Saccharomyces Genome Database list of phenotypic data

Description
Saccharomyces Genome Database list of phenotypes and associated genes from several published experiments (last update 2006).

Usage
`data(SGDphenoL)`

Format
`SGDphenoL` is a list of phenotypes. Under each phenotype is listed the genes that potentially induce that phenotype. A binary matrix can be built from that list using the `list2Matrix` function from the `Rintact` package.

Author(s)
N. LeMeur

Source
SGD, supplementary information: [http://www.yeastgenome.org/](http://www.yeastgenome.org/)

Examples
`data(SGDphenoL)`

testResult-class  A virtual class for representing the result of a test.

Description
The `testResult` class is the virtual base class for all result objects of the densityEstimate and graphTheory tests proposed in `PCpheno`.

Objects from the Class
A virtual Class: No objects may be created from it.

Slots
- `Observed`: Return a "numeric" vector: the observed number of genes or interactions within each cellular organizational units
- `Expected`: Return a numeric or a matrix: the expected number of genes or interactions within each cellular organizational units
Methods

No methods defined with class "testResult" in the signature.

Author(s)

N. LeMeur

See Also

gtResult, deResult

---

| truncName | Truncate character strings |

Description

Truncate character strings

Usage

truncName(x, n)

Arguments

x    Character string
n    Maximum length (in characters)

Value

Character string

Author(s)

N. LeMeur

Examples

xx <- "Anticonstitutionnelement is a family name"
truncName(xx, 5)
**YEASTOHNOLOG**

List of ohnolog gene pairs from Byrne, K.P and Wolfe, K.H (2005)

**Description**

List of 551 paralogous *Saccharomyces cerevisiae* gene pairs formed by Whole Genome Duplication (WGD) or ohnolog pairs.

**Usage**

data(YEASTOHNOLOG)

**Format**

YEASTOHNOLOG is a dataframe of 551 paired genes. The first two columns are the ohnolog gene pairs (systematic gene names). The third column is an index (numeric) of the rate of sequence evolution. The last two columns define the chromosome location.

**Details**

- **Gene1 Gene2** Systematic gene names of the ohnolog pairs
- **Ka** Coefficient that represents the extent of non-synonymous sequence divergence between each ohnolog pairs (Yang and Nielsen, 2000). The highest is the coefficient the fastest the 2 elements of a pair have diverged.
- **ChrG1 ChrG2** Chromosome location of the each element of a pair. Note that repeat of the same chromosome locations shared by a set of pairs define a block of duplication.

**Author(s)**

N. LeMeur

**Source**

Byrne, KP and Wolfe KH (2005), Table2 of supplementary information and Scerevisiae\_genome.tab file, chromosome location, from YGOB [http://wolfe.gen.tcd.ie/ygob/](http://wolfe.gen.tcd.ie/ygob/) (last update 03/20/06)

**References**


**Examples**

data(YEASTOHNOLOG)

str(YEASTOHNOLOG)
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