

# PCpheno

February 8, 2012

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CoHyperGParams-class

*Class "CoHyperGParams"*

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## 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

**Author(s)**

S. Falcon and N. LeMeur

**See Also**

[HyperGResult-class](#) [CoHyperGResult-class](#) [hyperGTest](#)

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CoHyperGResult-class

*Class "CoHyperGResult"*

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**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.

**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)

## 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]

```

---

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 summarizes 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 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

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

### References

Aim'ee Marie Dudley, Daniel Maarten Janse, Amos Tanay, Ron Shamir and George McDonald Church. (2005).A global view of pleiotropy and phenotypically derived gene function in yeast. *Molecular Systems Biology* doi:10.1038/msb4100004

### Examples

```
data(DudleyPhenoFull)
data(DudleyPhenoM)
```

---

 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 15 and 20 gen. rep. a and b respectively ==> alkali stress

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

Giaever et al (2002), supplementary information: [http://genomics.lbl.gov/YeastFitnessData/websitefiles/cel\\_index.html](http://genomics.lbl.gov/YeastFitnessData/websitefiles/cel_index.html) Saccharomyces Genome Database (last update 03/17/06): <http://www.yeastgenome.org/>

#### References

Giaever G et al (2002) Functional profiling of the Saccharomyces cerevisiae genome. Nature. 418(6896):387-91. PMID: 12140549

#### Examples

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

---

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

Deutschbauer AM, Jaramillo DF, Proctor M, Kumm J, Hillenmeyer ME, Davis RW, Nislow C, Giaever G. (2005) Mechanisms of haploinsufficiency revealed by genome-wide profiling in yeast. *Genetics*. 169(4):1915-25.

## Examples

```
data(HI)
```

---

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)
```

---

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

Kastenmayer et al. (2006), supplementary information: <http://www.genomeresearch.org> or [ftp://genome-ftp.stanford.edu/pub/yeast/systematic\\_results/phenotypes](ftp://genome-ftp.stanford.edu/pub/yeast/systematic_results/phenotypes)

### References

Kastenmayer JP, Ni L, Chu A, Kitchen LE, Au WC, Yang H, Carter CD, Wheeler D, Davis RW, 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)
```

---

 LesageRaw

*Data from Lesage et al. 2005*


---

**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 his3\u0394 leu2\u0394 met15\u0394 ura3\u0394) except anp1\u0394 and mnn9\u0394 that are isogenic to BY4742 (MAT\u03b1 his3\u0394 leu2\u0394 lys2\u0394 ura3\u0394).

**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**

Lesage et al. (2005), supplementary information: <http://www.biomedcentral.com/1471-2156/6/8/suppl/S2> or [ftp://genome-ftp.stanford.edu/pub/yeast/systematic\\_results/phenotypes](ftp://genome-ftp.stanford.edu/pub/yeast/systematic_results/phenotypes)

**References**

Lesage G, Shapiro J, Specht CA, Sdicu AM, Menard P, Hussein S, Tong AH, Boone C, Bussey H. (2005) An interactional network of genes involved in chitin synthesis in *Saccharomyces cerevisiae*. *BMC Genet.*6(1):8. PMID: 15715908

**Examples**

```
data(LesageRaw)
str(LesageRaw)
```

---

OsterbergRaw

*Data from Osterberg et al. 2006*

---

## 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 (LPIrate) 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 (LPIrate) 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 (LPIrate) 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/vol10/issue2006/images/data/0604078103/DC1/04078Table1.xls> or [ftp://genome-ftp.stanford.edu/pub/yeast/systematic\\_results/phenotypes](ftp://genome-ftp.stanford.edu/pub/yeast/systematic_results/phenotypes)

#### References

Osterberg M, Kim H, Warringer J, Melen K, Blomberg A, von Heijne G. (2006) Phenotypic effects of membrane protein overexpression in *Saccharomyces cerevisiae*. PNAS. 103(30):11148-53. PMID: 16847257

#### Examples

```
data(OsterbergRaw)
str(OsterbergRaw)
```

---

PCpheno-package

*Linkage between Protein Complexes, Pathways, and Phenotypes*

---

#### 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**

Giaever G, et al.(2002) Functional profiling of the *Saccharomyces cerevisiae* genome. *Nature*. 418(6896):387-91. PMID: 12140549

Deutschbauer AM, Jaramillo DF, Proctor M, Kumm J, Hillenmeyer ME, Davis RW, Nislow C, Giaever G. (2005) Mechanisms of haploinsufficiency revealed by genome-wide profiling in yeast. *Genetics*. 169(4):1915-25.

Byrne KP, Wolfe KH. (2005) The Yeast Gene Order Browser: combining curated homology and syntenic context reveals gene fate in polyploid species. *Genome Res*. 15(10):1456-61. PMID: 16169922

**See Also**

ScISI,SLGI

---

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/>**Examples**

```
data(SGDphenoL)
```

---

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/> (last update 03/20/06)

## References

Byrne KP, Wolfe KH. (2005) The Yeast Gene Order Browser: combining curated homology and syntenic context reveals gene fate in polyploid species. *Genome Res.* 15(10):1456-61. PMID: 16169922

## Examples

```
data(YEASTOHNOLOG)
str(YEASTOHNOLOG)
```

---

buildFDMat	<i>Build fitness defect contingency matrix</i>
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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

```
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

```
data(GiaeverPheno)
data(GiaeverExpCdt)
data(GiaeverGene)
fitnessData <- getFDgene(GiaeverPheno, condition=GiaeverExpCdt, cutoff=c(20,100,100), mode=
GiaeverPhenoM <- buildFDMat(data=fitnessData, genenames=GiaeverGene, condition=GiaeverExpCdt)
```

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

```
## 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

```
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]
```

---

complexStatus	<i>Complex Status</i>
---------------	-----------------------

---

### Description

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.

### 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 <i>SLGI</i> )
interactome	A binary matrix composed of genes (rows) and biological complexes (columns) (see package <i>ScISI</i> )
threshold	pvalue 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),
  annotation="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)
```

---

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

## 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)
```

---

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 <i>ScISI</i> )
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**

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

---

getDescr *Get formatted annotation data*

---

### Description

Function to retrieve the annotation of multi-protein complexes or pathways via GO, MIPS or KEGG.

### Usage

```
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**

Giaever G. et al. (2002) Functional profiling of the *Saccharomyces cerevisiae* genome. *Nature*. 418(6896):387-91. PMID: 12140549

**Examples**

```
data(GiaeverPheno)
data(GiaeverExpCdt)
##Select all the genes, in the different experimental conditions, that present a fitness
fitnessGen <- getFDgene(GiaeverPheno,condition=GiaeverExpCdt,cutoff=c(20,100,100),mode="
##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="con
```

---

graphTheory

*Graph theory to test associations between two or more relationships*


---

**Description**

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

**Usage**

```
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 <i>ScISI</i> )
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**

Balasubramanian, R., LaFramboise, T., Scholtens, D., Gentleman, R. (2004) A graph-theoretic approach to testing associations between disparate sources of functional genomics data. *Bioinformatics*, 20(18), 3353-3362.

**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

**See Also**

[testResult](#), [deResult](#), [plot](#)

**Examples**

```
## 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)
```

---

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**

```
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**

```
## 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

**See Also***ScISI***Examples**

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

---

ppiInteract	<i>Test the association between AP-MS data and phenotype</i>
-------------	--

---

### 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 <i>ScISI</i> )
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*

### Examples

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

---

<code>reduceM</code>	<i>Resize a matrix</i>
----------------------	------------------------

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

Resized matrix.

**Author(s)**

N. LeMeur

**Examples**

```
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)
```

---

<code>testResult-class</code>	<i>A virtual class for representing the result of a test.</i>
-------------------------------	---

---

**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	<i>Truncate character strings</i>
-----------	-----------------------------------

---

**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)
```

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