Package ‘SLGI’

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**Title**  Synthetic Lethal Genetic Interaction

**Version**  1.34.0

**Author**  Nolwenn LeMeur, Zhen Jiang, Ting-Yuan Liu, Jess Mar and Robert Gentleman

**Description**  A variety of data files and functions for the analysis of genetic interactions

**Depends**  R (>= 2.10), ScISI, lattice

**Imports**  AnnotationDbi, Biobase, GO.db, ScISI, graphics, lattice, methods, stats, BiocGenerics

**Suggests**  GO.db, org.Sc.sgd.db

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**License**  Artistic-2.0

**biocViews**  GraphAndNetwork, Proteomics, Genetics, Network

**NeedsCompilation**  no

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Atong

Systematic genetic analysis with ordered arrays of yeast deletion Tong et. al. (2004).

Description

Data from Tong et. al. (2004) buffering experiments using ordered arrays of yeast deletion design by Tong et. al. (2001).

Usage

data(Atong)
data(tong2004raw)

Format

tong2004Raw is dataframe extracted from Table S1 of Tong et al. (2004) online supporting material. We added an extra column, queryGene.sysName, which is the systematic names of the query genes.

queryGene.geneName Column indicates the gene used as query in the synthetic genetic array screen (SGA).

Int.geneName Column indicates the gene identified as an interactor with a particular query.

Int.sysName Column indicates the systematic name of the open reading frame (ORF) that corresponds to the interactor gene.

Score An interaction scored three times in the three runs by visual inspection received a scored of 3. An interaction scored twice in the three runs by visual inspection received a scored of 2. An interaction scored by the computer-based image analysis but not visual inspection received a scored of 1. For interactions that scored once in the three runs by visual inspection confirmation was attempted only for those genes pairs related functions. Such confirmed interactions received a score of 0.
**RSA** Column identifies an interaction that was confirmed by random spore analysis.

**Tetrad** Column identifies an interaction confirmed by tetrad analysis.

**SS** Refers to synthetic sick interaction.

**SL** Refers to synthetic lethal interaction.

**Functional.Role** Column indicates the assigned GO functional annotation from their defined subset of annotations. All the interactions are identified in this study unless otherwise stated.

**References** Genetic Interactions that have been previously described.

**queryGene.sysName** Column indicates the systematic (ORF) name of the gene used as query in a SGA screen.

Atong is a 132 by 1008 adjacency matrix of the systematic genetic interactions identified between 132 query genes and the deletion gene set (Tong et al. 2001; see SGA for more details). The row names correspond to the systematic (ORF) names for the 132 query genes. The column names correspond to the systematic (ORF) names of the 1011 reporter genes, which showed a synthetic lethal or synthetic sick interaction with at least one query genes. Values are 0 or 1, with a 1 indicating the occurrence of the genetic interaction between the gene pairs.

**Source**


**References**


[http://www.sciencemag.org/cgi/data/303/5659/808/DC1/1](http://www.sciencemag.org/cgi/data/303/5659/808/DC1/1)

**See Also**

SGA

**Examples**

```r
data(Atong)
dim(Atong)
```

---

**AtongFnDomain**

The functional domains shared by the tested pairs in Tong et al experiment.

**Description**

Data developed from Tong et. al. buffering experiments.

**Usage**

```r
data(AtongFnDomain)
```
**AtongPair**

**Format**
A list containing 3 items.
- **pairs** Dataframe of all the gene pairs and their synthetic lethality status.
- **SharedPfam** List of the Pfam domains shared by each pair. The order of this list is the same as the order of the pairs.
- **SharedSMART** List of the SMART domains shared by each pair. The order of this list is also the same as the order of the pairs.

**Author(s)**
Z. Jiang

**Source**
Created from the association matrix reported by Tong et al. and the Pfam (Protein family database [http://pfam.janelia.org/](http://pfam.janelia.org/)) and SMART database of yeast.

**References**

**Examples**
```r
data(AtongFnDomain)
names(AtongFnDomain)
```

---

**AtongPair** Data frame the pair of yeast gene tested in Tong et al. 2004.

**Description**
Data from Tong et. al. buffering experiments (2004) using synthetic genetic arrays (SGA) (Tong et al. 2001).

**Usage**
```r
data(AtongPair)
```

**Format**
A data frame with 3 columns and 607881 rows.

**Details**
- **AtongPair** stores the yeast gene names for each tested pairs in Tong buffering experiment. Each row represents one pair.
- **query** Query gene name
- **array** Array gene name
- **interact** Logical indicating the synthetic lethal status, if TRUE the genetic interaction is lethal.
Author(s)

N. LeMeur

Source

Created from the association matrix reported by Tong et al (2004) and the genes from the SGA array developed by Tong et al. (2001).

References


Examples

data(AtongPair)
dim(AtongPair)

---

**Boeke**

*Incidence matrix of Synthetic Lethal interaction from the Boeke Lab*

Description

Data from Pan et al. experiments on DNA integrity Network in the Yeast S. cerevisiae.

Usage

data(Boeke2006raw)
data(Boeke2006)

Format

**Boeke2006raw** is a data frame with 5775 observations on the following 6 variables.

- **Query.ORF**: ORF associated with the query gene.
- **Query.Gene**: Common name of the query gene.
- **Target.ORF**: ORF for the array gene.
- **Target.Gene**: Common name of the array gene.
- **RSA**: Random spore analysis
- **Tetrad**: Tetrad dissection

**Boeke2006** is an incidence matrix is a 74 by 843 adjacency matrix of the systematic genetic interactions identified between 74 query genes and the deletion gene set in Pan et al.(2004). The row names correspond to the systematic (ORF) names for the 74 query genes. The column names correspond to the systematic (ORF) names of the 843 reporter genes, which showed a synthetic lethal or synthetic sick interaction with at least one query genes. Values are 0 or 1, with a 1 indicating the occurrence of the genetic interaction between the gene pairs.
Details

In Pan et al (2006), the authors provide this note. Note: SL - synthetically lethal; SF/SL-very severe synthetic fitness defects; SF-obvious but modest synthetic fitness defects; SF (slight) - slight synthetic fitness defect. Approximately 10% of the positive interactions presented here were not scored as positive in the dSLAM screens. These were individually tested because we wanted to make sure that they were indeed false negatives in the dSLAM screens. We also note that there is a small chance that the interactions scored as positive in RSA (random spore analysis) might not reflect direct growth defects of the double mutants but rather, the double mutants are defective in expressing the MFA1pr-HIS3 reporter.

Source

The data were extracted from Pan et al (2004) and Table S1 of Pan et al. (2006).

References


See Also

dSLAM.GPL1444, and dSLAM

| byComplex | Evaluate protein co-membership within cellular organizational units |

Description

Count the protein co-members of one (or more) cellular organizational units such as complex(es). This co-membership can be characterized by a synthetic lethal interaction if bpL is the list of observed synthetic lethal interactions or it can be characterized by the number of all the expected interactions within that complexes if bpL is all the interactions tested.

Usage

byComplex(bpL, interactome)

Arguments

bpL List of tested genes (or reported as synthetic lethal) per bait.
interactome Adjacency matrix where the rows are the genes and the columns represent the cellular organizational units, e.g., ScISI

Value

Vector of the number of genes(proteins) co-member in one or more biological complexes or pathways.
**comemberIn**

**Author(s)**

N. LeMeur and R. Gentleman

**See Also**

`withinComplex`

**Examples**

```r
data(ScISIC)
data(AtongPair)
pairSL <- AtongPair[, AtongPair[,3],]
SLlist <- split(as.character(pairSL[,2]),as.character(pairSL[,1]))
##Number of synthetic lethal pairs within the same complexe
bySL <- byComplex(SLlist, ScISIC)
```

---

**Description**

Retrieve the biological complexes within which two proteins are comembers.

**Usage**

```r
comemberIn(iMat, interactome)
```

**Arguments**

- `iMat`: Comembership matrix of genes (proteins) that linked to other genes (proteins) by any biological experiment.
- `interactome`: Adjacency matrix composed of genes (rows) and biological complexes (columns).

**Value**

Dataframe of pairs of genes (proteins) and their common biological complexes.

**Author(s)**

N. LeMeur

**See Also**

`withinComplex`

**Examples**

```r
data(Atong)
data(ScISIC)
coMember <- withinComplex(Atong, ScISIC)
SLpairWithinComplex <- comemberIn(coMember, ScISIC)
```
**compare**

Compare observed data to expected in permutation models

**Description**

This method summarizes the result of the `modelSLGI` function.

**Usage**

```r
## S4 method for signature 'siResult'
compare(x)
```

**Arguments**

- `x` a `siResult` object to summarize

**Details**

This compares the number of observed interactions to the number of expected interactions in each permutation model. It counts how many times the number of observed interactions is greater than the number of expected interactions (from the permutations) and divides by the number of permutations applied.

**Value**

Numerical vector

**Author(s)**

N. LeMeur

**See Also**

`modelSLGI`

**Examples**

```r
data(ScISIC)
data(Atong)
data(SGA)
model <- modelSLGI(Atong, universe= SGA, interactome=ScISIC, type="intM", perm=2)
ans <- compare(model)
```
congruence

Calculate congruence score between pairs of genes sharing pattern of synthetic genetic interactions (Ye et al. (2005)).

Description

The congruence score represents the number of common synthetic genetic interacting partners between two genes. The higher is the score the more overlap there is between the synthetic genetic partners of those genes.

Usage

congruence(iMat, sharedInt, mode="query", universe, padjust=FALSE)

Arguments

iMat       Adjacency matrix reporting genetic Interactions. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.
sharedInt  numeric vector representing the number of common genetic interactions between a pair of query or target genes. See getSharedInteraction for more details
mode       character vector of value "query" or "target"
universe   total number of genes tested
padjust    adjust by the number of genes tested that show at least one synthetic genetic interaction.

Value

A numeric vector of the congruence score values.

Author(s)

N. LeMeur

References


See Also

getSharedInteraction

Examples

```r
intM <- matrix(c(0,1,0,1,1,0,1,1,0,1,1,1,0,1,1),
nrow=4, ncol=4,
dimnames=list(c("p1", "p2", "p3", "p4"), c("p1", "p3", "p5", "p7"))
sharedInt <- getSharedInteraction(intM)
score <- congruence(intM, sharedInt, mode="query", universe=15, padjust=FALSE)
```
**createSquareMatrix**  
Create a square matrix

**Description**
Create a square matrix based on row and column names. The new matrix is created so that the row and column names are a perfect match and the added values are zero. In the case of genetic interactions, for example it could be useful that the matrix of all the interactions tested and not tested.

**Usage**
`createSquareMatrix(data)`

**Arguments**
- **data**  
  Matrix

**Value**
matrix.

**Author(s)**
N. LeMeur

**Examples**
```r
data(Atong)  
dim(Atong)  
Tong<- createSquareMatrix(Atong)  
dim(Tong)
```

---

**domainDist**  
Finds the number of gene sets for each shared domain

**Description**
`domainDist` takes a list of shared domains, and compute for each distinct domain how many gene sets share it.

**Usage**
`domainDist(domainL)`

**Arguments**
- **domainL**  
  Each element of the list is a vector of functional domains.
Details
For each domain that appears in the domain list, domainDist counts the number of elements that have this domain.

Value
Returns a frequency table with descending order.

Author(s)
Z. Jiang

See Also
getSharedDomains, sharedBy

Examples
data(AtongFnDomain)
domainDist(AtongFnDomain$SharedPfam[1:20])

---

dSLAM.GPL1444  dSLAM platform used for Synthetic Lethal screens in the Boeke Lab

Description
These data are the 21,991 probes spotted on the dSLAM array (heterozygote diploid-based synthetic lethality analyzed by microarray) used to test synthetic lethal interactions by Pan et al (2006).

Usage
data(dSLAM.GPL1444)
data(dSLAM)

Format
dSLAM.GPL1444 is a data frame with 21,991 observations on the following 10 variables.

ID  Serial identifier for probe.
ROW  Row number in the array as scanned with GenePix scanner.
COLUMN  Column number in the array as scanned with GenePix scanner.
TAGTYPE  Code for whether tag is 5’ (Up) or 3’ (Dn) relative to the open reading frame (ORF).
PROBE  Code for singleton probes arrayed in ORF order (ArrA, ArrB), five-fold replicate probes arrayed in randomized order (Rpts), systematic mutations arrayed across the center of the array (Muts), negative controls (NegT), or probes peripheral to the array as specified by the manufacturer (Edge).
GENE  Standard gene name (SGD) (or ORF if not available)
SEQUENCE  DNA sequence of probe (includes custom-designed sequences for 193 YA* and YM*
ORFs missing DnTags)

SGDID Unique ORF identifier from SGD; 'S000000000' denotes missing value

SPOT_ID  spot identifier; ('YQL' ORFs denote custom-designed sequences; 'NegA', 'NegB', 'PosA',
'PosB' denote proprietary sequences specified by the manufacturer)

dSLAM is a character vector of length 5641 that contains the unique and valid systematic ORF
names.

Details

The dSLAM.GPL1444 were directly obtain from parsing the GPL1444\_family.soft.gz available at

dSLAM is a vector of length 5641, extracted from the dSLAM.GPL1444 ORF, and that contains
the unique and valid systematic ORF names. This vector was built in three steps. First the ORFs
with SGDID equals to S000000000 in the dSLAM.GPL1444 data frame were removed as some
correspond to custom sequences and other were dubious ORFs that have been deleted from SGD
or merged with other ORFs. Secondly, the duplicated names were removed. Then, the systematic
ORF names were verified against the org.Sc.sgd.db data package.

Source

The data were extracted from the Gene Expression Omnibus (GEO) website: http://www.ncbi.
mlm.nih.gov/projects/geo/query/acc.cgi?acc=GPL1444

References

Pan X, Ye P, Yuan DS, Wang X, Bader JS, Boeke JD. A DNA integrity network in the yeast Sac-
charomyces cerevisiae. Cell. 2006 Mar 10;124(5):1069-81

See Also

Boeke2006raw, and Boeke2006

---

**essglist**

*The list of yeast essential genes*

**Description**

List of systematic names and common names of the yeast essential genes.

**Usage**

data(essglist)

**Format**

essglist is a list with 1103 elements (last download 03/17/2006). The name of each element is the
systematic gene name. The value of each element is its corresponding common (standard) name.
**getInteraction**

Details

The aliases of the yeast gene names can be retrieved with the `org.Sc.sgdALIAS` environment of the `org.Sc.sgd.db` package.

Source


References

Saccharomyces Genome Database [http://www.yeastgenome.org/](http://www.yeastgenome.org/)

Examples

data(essglist)
essglist[[1]]
names(essglist)

---

**getInteraction**  
*Count genetic interactions within and between cellular organizational units*

Description

Count the number of genetic interactions within and between the elements of the interactome.

Usage

genericInteraction(mat, universe, interactome)

Arguments

- **mat**  
  Interaction matrix. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.

- **universe**  
  Character vector of gene names, e.g., array genes used in synthetic genetic array experiments (SGA)

- **interactome**  
  Adjacency matrix where row are gene names and columns are cellular organizational units.

Value

The returned value is a list of 2 matrices:

- **bwMat**  
  A interaction matrix that corresponds to the cellular organizational units interaction matrix where row and columns a organizational units names and the value inside the matrix are the number of genetic interactions they share.

- **CDs**  
  Subset of the input interactome that shares interactions.

Author(s)

N. LeMeur
Examples

```r
##Create the genetic interaction matrix
gInt <- sample(c(0, 1), 25, TRUE)
iMat <- matrix(gInt, nrow=5, ncol=5, dimnames=list(letters[1:5],letters[4:8]))

##Create the interactome
cInt <- sample(c(0,1),30, TRUE)
interactome <- matrix(cInt, nrow=6, ncol=5,dimnames=list(letters[2:7],LETTERS[1:5]))

## Reduce the genetic interaction matrix to match the gene present in
## the interactome
reducediMat <- gi2Interactome(iMat, interactome)

## Get the interaction
prey <- letters[1:20]
myInteraction <- getInteraction(reducediMat, prey, interactome)
```

getSharedDomains

Find domains shared by a given list of gene names.

Description

getSharedDomains finds domains in the provided environment that are shared by a list of genes.

Usage

getSharedDomains(geneNameV, env)

Arguments

geneNameV Character vector of gene names.

env R object that provides mappings between an entrez gene identifier and the associated Pfam identifiers.

Value

getSharedDomains returns a vector of the names of the shared domains.

Author(s)

Z. Jiang

See Also

domainDist, sharedBy

Examples

```r
library("org.Sc.sgd.db")
getSharedDomains(c("YEL003W","YLR200W"), org.Sc.sgdPFAM)
```
getSharedInteraction

Calculate the number of shared synthetic genetic interactions between pairs of genes.

Description

The number of common synthetic genetic interacting partners between two genes.

Usage

getSharedInteraction(iMat, mode="query")

Arguments

iMat Adjacency matrix reporting genetic Interactions. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.

mode Character vector of value "query" or "target"

Value

A numeric vector of the number of common genetic interactions between a pair of query or target genes.

Author(s)

N. LeMeur

See Also

congruence

Examples

intM <- matrix(c(0,1,0,0,1,1,0,1,0,1,0,1,1,0,1,0),
               nrow=4, ncol=4,
               dimnames=list(c("p1","p2","p3","p4"),
                             c("p1","p3","p5","p7")))

sharedInt <- getSharedInteraction(intM)
getTestedPairs  

Find interacting and non-interacting tested pairs from an genetic interaction matrix.

Description

ggetTestedPairs find all the pairs from an interaction matrix and a list of tested genes.

Usage

ggetTestedPairs(iMat, respV)

Arguments

iMat  
Adjacency matrix reporting genetic Interactions. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.

respV  
Character vector of all gene names that were tested (found to interact or not)

Value

A data.frame with 4 columns:

query  
gene names of the query genes

array  
gene names og the tested genes (e.g., array genes)

interact  
numeric vector of the number of observed interactions (0: no interaction; 1: one interaction; 2: two interactions when the query genes were also on the array)

recip  
logical to indicate whether the reported genes were both query and array genes (TRUE: both genes were query and array genes)

Author(s)

N. LeMeur

See Also

ggetSharedDomains  
ggetUniquePairs

Examples

intM <- c(0,1,0,0,1,0,0,0,1,0,0,1,0,1,0,1)
dim(intM) <- c(4,4)
dimnames(intM) <- list(c("p1","p2","p3","p4"),c("p1","p3","p5","p7") )  
respV <- c("p6","p8")  
intM  
ggetTestedPairs(intM,respV)
getUniquePairs

Find unique pairs from an genetic interaction matrix.

**Description**

getUniquePairs can find all the unique pairs from an interaction matrix and supplementary array genes, or finds only the unique pairs that shows positive interaction.

**Usage**

getUniquePairs(iMat, respV = character(0), only = FALSE)

**Arguments**

- **iMat**: Adjacency matrix reporting genetic Interactions. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.
- **respV**: Character vector of all gene names that were tested (found to interact or not)
- **only**: has default value FALSE, if TRUE, then only reports the positively interacted pairs.

**Value**

A data.frame with two or three columns. The first two columns are the query gene name and the array gene name, respectively. If `only` is TRUE, the third column shows the interaction status.

**Author(s)**

Z. Jiang

**See Also**

getSharedDomains

**Examples**

```r
intM <- c(0,1,0,0,1,0,0,1,0,0,1,0,1,0,1,0)
dim(intM) <- c(4,4)
dimnames(intM) <- list(c("p1","p2","p3","p4"),c("p1","p3","p5","p7") )
respV <- c("p6","p8")
intM
getUniquePairs(intM,respV,only=FALSE)
ge...
**gi2005 Genetic Interaction Data (EMAP) from the yeast early secretory pathway**

**Description**

The data are in the form of a 424 by 424 array which contains the scores from using the EMAP procedure on yeast strains which are ideally double mutants, each strain with a different pair of genes knocked out. For each row, the gene named in the row label is knocked out in all pairs, and the same holds true for each column.

**Usage**

```r
data(gi2005)
data(gi2005.metadata)
```

**Format**

`gi2005` is a 424 by 424 array of real values. `gi2005.metadata` is a vector of length 424 which contains the common names for the genes that were knocked out. The row and column names of `gi2005` are standard names.

**Details**

NA values in `gi2005` are interactions that were not scored.

**Source**

Data were obtained as supplementary material from the publication listed below.

**References**


**Examples**

```r
data(gi2005)
data(gi2005.metadata)
```
gi2007

*Synthetic Genetic Interaction data from Collins et al*

**Description**

The data gi2007 are a 754 by 754 set of genetic interactions that were tested pairwise by either deletion or decreased abundance messenger RNA perturbation.

**Usage**

```r
data(gi2007)
data(gi2007.metadata)
```

**Format**

The gi2007 data are a 754 by 754 matrix where values indicate a score for a synthetic genetic interaction. An NA indicates that the genetic interaction was not measured.

gi2007.metadata is a data.frame of dimensions 754 rows and two columns. The columns are the systematic names and the mutation (which is typically either DAMP, DELETION or the name of the alternate allele that was tested. In 11 cases an alternative allele was tested.

**References**


**Examples**

```r
data(gi2007)
data(gi2007.metadata)
```

---

**gi2Interactome**

*Reduce genetic interactions matrix*

**Description**

Reduce genetic interactions matrix to the pairs that genetically interact and that are present in the interactome of interest.

**Usage**

```r
gi2Interactome(iMat, interactome, threshold=0)
```

**Arguments**

- **iMat**
  
  Genetic interaction matrix. Each entry has usually a value of 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.

- **interactome**
  
  Interactome matrix, e.g. ScISIC.

- **threshold**
  
  Integer
Value

The returned value is the genetic interaction matrix reduced to the row and column (genes) names that are present in the interactome and where the row and column sums are higher than the specified threshold.

Author(s)

N. LeMeur

Examples

```r
##Create the genetic interaction matrix
gInt <- sample(c(0, 1), 25, TRUE)
iMat <- matrix(gInt, nrow=5, ncol=5, dimnames=list(letters[1:5],letters[4:8]))

##Create the interactome
cInt <- sample(c(0,1),30, TRUE)
interactome <- matrix(cInt, nrow=6, ncol=5,dimnames=list(letters[2:7],LETTERS[1:5]))

## Reduce the genetic interaction matrix to match the gene present in
## the interactome
reducediMat <- gi2Interactome(iMat, interactome)
```

###Description

A hypergeometric test for genetic interaction data.

####Usage

`hyperG(data, nbTested, universe)`

####Arguments

- `data`: Matrix with 2 columns the first one corresponds to the number of interactions per pair of interacting complexes and the second one to number of tested interactions. This could be the first two columns resulting from a call to the `test2Interact` function.
- `nbTested`: Number of interacting pairs
- `universe`: Total Number of tested pairs

###Author(s)

N. LeMeur

###See Also

`phyper`
Examples

## Create matrix interaction x tested matrix
interact <- c(1, 3, 2, 2, 6, 5, 2, 4, 1, 3)
tested <- c(3, 3, 5, 4, 8, 5, 3, 4, 2, 3)
mat <- cbind(interact, tested)

## Perform test
res <- hyperG(mat, 1000, 10000)
summary(res$P)

---

**iSummary**  
*Summarize cellular organizational units sharing genetic interaction*

**Description**
Summarize the cellular organizational units sharing genetic interactions and display their GO annotation if available.

**Usage**

```r
iSummary(iMat, n=10, reverse=FALSE)
```

**Arguments**

- **iMat**: Comembership matrix of genes(proteins) that linked to other genes(proteins) by any biological experiment, e.g., output of the `getInteraction` function.
- **n**: Numeric threshold indicating the minimum number of genetic interactions that a pair of cellular organizational unit must share.
- **reverse**: Logical, by default the function return a list of pair of cellular organizational units where the name of each element is the number of genetic interactions they share. If reverse is TRUE, the output is a vector where the values are the number of interactions and the names are the combination of the 2 cellular organizational units.

**Value**

The function print the result in the standard output but can also save it in variable.

If reverse is FALSE the output is a list of pairs of cellular organizational units where the name of each element is the number of genetic interactions they share.

If reverse is TRUE the output is a vector where the values are the number of interactions and the names are the combination of the 2 cellular organizational units.

**Author(s)**

N. LeMeur
Examples

data(Atong)
data(ScISIC)
data(SGA)
SLa2 <- gi2Interactome(Atong, ScISIC)
## Search for synthetic lethal interaction
compM <- getInteraction(SLa2, SGA, ScISIC)
## Display the tightly interacting pairs
largInt <- iSummary(compM$bwMat, n=15)

modelSLGI

Permutation model for assessing synthetic genetic interactions in cellular organizational units.

Description

Permutation model for assessing synthetic genetic interactions within and between cellular organizational units such as multi-protein complexes.

Usage

modelSLGI(iMat, universe, interactome, type="intM", perm=50)

Arguments

iMat

Adjacency matrix reporting genetic interactions. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column.

universe

character vector of the names of the tested genes, e.g., names of the genes on the synthetic genetic array (SGA) used by Tong et al.

interactome

Adjacency matrix where row are genes and columns are cellular organizational units. Each entry has value 0 or 1, for absence or presence of a gene in a complex.

type

Character vector of value "intM" (Default) or "interactome" to either perform the test based on the genetic interaction matrix or the interactome, respectively.

perm

Number of permutations to apply. Default is 50.

Value

Interaction matrix between cellular organizational units.

Author(s)

N. LeMeur

See Also

gi2Interactome
normInteraction

Examples

```r
data(ScISIC)
data(Atong)
data(SGA)
model <- modelSLGI(Atong, universe= SGA, interactome=ScISIC,
type="intM", perm=2)
```

normInteraction Normalize a matrix of biological interactions

Description

Normalize a square matrix of biological interactions according to the number of possible interactions between each biological complex.

Usage

```r
normInteraction(data, genename, interactome)
```

Arguments

- `data` Square Matrix of biological complexes that shares one or more genes(proteins)
- `genename` Character vector of the gene names that possibly create interactions between complexes
- `interactome` Adjacency matrix where row are genes and columns are cellular organizational units. Each entry has value 0 or 1, for absence or presence of a gene in a complex, e.g., `ScISI`

Value

Square matrix of biological complexes linked by one or more interacting proteins and normalized by the possible number of interactions between each complex.

Author(s)

N. LeMeur

See Also

`getInteraction`

Examples

```r
data(Atong)
data(ScISIC)
data(SGA)
SLa2 <- gi2Interactome(Atong, ScISIC)
## Search for synthetic lethal interaction
compM <- getInteraction(SLa2, SGA, ScISIC)
## Normalize
normIntComplex<- normInteraction(compM$bwMat, SGA, ScISIC)
```
plot

Graphical method to represent the result of the modelSLGI.

Description

a plot method for siResult.

Usage

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

Arguments

- `x`: the `siResult` object to plot.
- `...`: general commands to be sent to plot.

Details

The plot generated from a `siResult` object is a dotplot with the observed and expected data average of interaction represented in 2 different colors.

Author(s)

N. LeMeur

See Also

`ScISI`

Examples

```r
data(ScISIC)
data(Atong)
data(SGA)
model <- modelSLGI(Atong, universe= SGA, interactome=ScISIC, type="intM", perm=2)
plot(model)
```

SDL

The Association matrix for the synthetic dosage lethal screens in Yeast.

Description

The data reported in Table 6 of the supplementary data of Measday et. al.

Usage

```r
data(SDL)
data(SLchr)
```
**Format**

SDL is a matrix with 141 rows and 9 columns. The columns represent 3 genes at each of 3 temperatures (16, 25, 37 Celsius). The gene names and temperatures are combined in the column names. The row names are yeast standard names. The values are NA, no effect, SDS for synthetic dosage sick, SL for synthetic lethal and SDL for synthetic dosage lethal.

SLchr is a matrix with 84 rows and 14 columns. Each column represents a query strain which was tested against the genome wide set of deletion strains. The entries can be NA for no effect, SL for synthetic lethal and SS for synthetic sick.

**Source**

Supplementary Table 6 of the reference given below.

**References**


**Examples**

```r
data(SDL)
table(SDL)
```

**Description**

seqMatcherAlign matches two sequences using the EMBOSS matcher program.

getAlignStats extract the statistics from the alignment result data.

**Usage**

```r
seqMatcherAlign(pairNameV,BankIDV,seqBank)
getAlignStats(alignRes)
```

**Arguments**

- `pairNameV` - a vector of gene pair names
- `BankIDV` - a vector of the sequence IDs in the sequence Bank.
- `seqBank` - a database of all the sequences
- `alignRes` - object returned by seqMatcherAlign

**Details**

seqMatcherAlign matches the gene pair names with the sequence bank IDs and export the two sequences in to two files: seq1.new and seq2.new. Then uses system calls to run EMBOSS matcher program to align the two sequences. The result from matcher is store in file "out.matcher". seqMatcherAlign read in this file and create a R object summarize the alignment results.

getAlignStats takes the alignment result data and extract the statistics of the result in to data.frame.
Value
names contains the names of the gene pair
results contains the alignment statistics: the aligned total length, the number of identical
match, the number of similar match, the number of gaps, and the alignment score
seq displays the aligned sequences

Note
pairMatcherAlign use system calls to run EMBUSS matcher program. You must have EMBUSS
matcher installed on your computer.

Author(s)
Z. Jiang

References
EMBOSS: The European Molecular Biology Open Software Suite (2000) Rice, P. Longden, I. and
Bleasby, A. Trends in Genetics 16, (6) pp276–277

Examples

seq1 <- "RPHEDEKEIADEAKMKVPGENEDESKEEEKSQEELEAIDSKEKSTDAROEQDEGONEENNEENENENENHTAPALVMPSPIEMEQRMM"
seq2 <- "OKYLLKDAIRNFSEYPFYAQNLQHIQ1QTILITEEKSQEELEKIIKKKKEEHLKKNLKHDYFQKLYKEKCEILTKSLLENLRKEK"
seq3 <- "IHQQ1TILITKIKKKEEHLKVPGENEDKKLKHLDYFQKLYKEKCEILTKSLLENLRKEEIENKRKEHELEQKRREEGIEEKSLRHPSSS"
seqBank <- list(seq1=list(seq=seq1), seq2=list(seq=seq2), seq3=list(seq=seq3))
bid <- names(seqBank)
pnames <- c("seq1", "seq3")
## Not run:
ar <- seqMatcherAlign(pnames, bid, seqBank)
ar
getAlignStats(ar)
## End(Not run)

SGA Systematic genetic analysis with ordered arrays of yeast deletion.

Description
Listed of yeast deletion genes used as array probes in the Systematic Genetic Analysis (SGA) of
yeast deletion Tong et. al. (2001).

Usage
data(SGAr raw)
data(SGA)
Details

SGArw is a character vector of length 4672, corresponding to the original yeast deletion genes set on the array. Note that some of those genes correspond to ORFs that have subsequently been rejected.

SGA is a character vector of length 4655, corresponding to the updated yeast deletion genes set on the array. The gene names have been updated from common gene name or alias to systematic names (last update Feb. 2006).

Source

Table S1 from Tong et al. (2001) online supporting material. http://www.sciencemag.org/cgi/content/full/294/5550/2364/DC1

References


Examples

```r
data(SGAraw)
length(SGAraw)
```

Description

The Saccharomyces Genome Database (SGD) provides, for download a table listing all known interactions in yeast. This table was downloaded on Jan 25, 2007 and three subsets were extracted. The synthetic lethal interactions, SGD.SL, the synthetic grow defect interactions, SGD.SynGrowthDefect and the synthetic rescue interactions, SGD.SynRescue. No other processing has been done.

Usage

```r
data(SGD.SL)
data(SGD.SynRescue)
data(SGD.SynGrowthDefect)
```

Format

Each data set is a data frame with the following 7 variables.

V1 Factor, indicating the type of data.
V2 Factor describing the interaction, in particular naming bait and prey and interactors.
V3 Factor indicating whether the cells were viable.
V4 Factor which is always NA for these data.
V5 Factor naming the reference for the interaction.
V6 Factor with levels indicating the PubMed ID for the publication in V5.
V7 Factor with level BioGRID, probably indicating the source.
Details

SGD says this about the file:

Contains interaction data. Tab-separated columns are:
1) interaction_type (mandatory)
2) genes involved and their mutation type, in the format: ORF (mutation_type, action), with multiples separated by a |
3) phenotype (optional, multiples separated by |)
4) description (optional)
5) citation (multiples separated by |)
6) PubMed ID (optional, multiples separated by |)

This file is updated weekly.

Author(s)

Z. Jiang

Source

The file can be downloaded from, ftp://genome-ftp.stanford.edu/pub/yeast/literature_curation.

Examples

data(SGD.SL)

sharedBy Find the gene pairs that share a domain.

Description

sharedBy finds whether the given domain is in each of the elements of the domain list.

Usage

sharedBy(domainL)

Arguments

domainL is a list, each element of the list is a vector of domains.

Details

sharedBy first remove all the elements with length 0 or have value 'NA'. Then apply the reverseSplit on the remaining list.

Value

A list with each element represent a domain, and the values of the element are the pairs that share this domain.
sharedInt

Author(s)
Z. Jiang

See Also
reverseSplit, domainDist, getSharedDomains

Examples

```r
## Load PFAM and SMART domains shared between Tong's Synthetic lethal data
data(AtongFnDomain)
## Find pair that share identical domain
sharedBy(AtongFnDomain$SharedPfam[1:20])
```

## List shared genetic interactions between genes

Description

List shared interactions and cellular organizational units names between genes.

Usage

```r
sharedInt(pairL, interactome, threshold=0)
```

Arguments

- **pairL**: Dataframe with 3 columns. The first columns are the pair of genes tested i.e., the query and array genes. The third columns in a logical: TRUE when the 2 genes genetically interact and FALSE when they do not.(see AtongPair dataset as example)
- **interactome**: Adjacency matrix where row are gene names and columns are cellular organizational units names. Each entry has value 0 or 1, for absence or presence of a gene in the complex.
- **threshold**: Numeric. Indicate the minimum number of interactions that 2 genes must share

Value

The return value is a list. Each element of the list has for name 2 genes that genetically interact. Each element of the list corresponds to the list of cellular organizational units where the interacting genes are found (independently or together).

Author(s)
N. LeMeur
## Synthetic genetic interactions

dat <- data.frame("query" = LETTERS[1:5], "array" = LETTERS[2:6], "interact" = as.logical(sample(c(TRUE, FALSE), 5, TRUE))
## interactome
interA <- matrix(sample(c(0, 1), 30, TRUE), nrow=6, ncol=5, dimnames = list(LETTERS[1:6], letters[1:5]))

sharedInt(dat, interA, threshold=1)

### Examples

```r
## apply a permutation model
data(ScISIC)
data(Atong)
data(SGA)
model <- modelSLGI(Atong, universe= SGA, interactome=ScISIC, type="intM", perm=2)
```

---

**siResult-class**

A class for representing the result of the SLGI graph permutation model.

### Description

A class for representing the result of the `modelSLGI` function.

### Slots

- **Observed**: Return a "numeric" vector: the observed number of synthetic genetic interactions between components of one or two cellular organizational units
- **Expected**: Return a matrix: the expected number of synthetic genetic interactions between components of one or two cellular organizational units

### Methods

- **plot**: Graphical representation of the permutation model result
- **compare**: Summarizes the result of the `modelSLGI` function

### Author(s)

N. LeMeur

### See Also

`modelSLGI`, `plot`

### Examples

```r
## apply a permutation model
data(ScISIC)
data(Atong)
data(SGA)
model <- modelSLGI(Atong, universe= SGA, interactome=ScISIC, type="intM", perm=2)
```

model
**test2Interact**

**Summarize genetic interactions within or between cellular organizational units**

**Description**

Summarize the genetic interactions within one cellular organizational unit or between 2 cellular organizational units.

**Usage**

```
test2Interact(iMat, tMat, interactome)
```

**Arguments**

- **iMat**  
  Genetic interaction matrix. Each entry has value 0 or 1, representing positive or negative interaction of corresponding pairs of row and column, respectively.

- **tMat**  
  Adjacency matrix of tested object. Each entry has value 0 or 1, representing the fact that the corresponding pairs of row and column have been tested for interaction or not.

- **interactome**  
  Adjacency matrix where row are gene names and columns are cellular organizational units names. Each entry has value 0 or 1, for absence or presence of a gene in the complex.

**Value**

The return value is a data.frame with 6 columns.

- **unit1, unit2**  
  Cellular organizational units tested and interacting

- **tested**  
  Number of interactions tested between unit1 and unit2

- **interact**  
  Number of interactions found between unit1 and unit2

- **sizeC1, sizeC2**  
  Number of genes in unit1 and unit2

**Author(s)**

N. LeMeur

**Examples**

```r
set.seed(123)
##Create the interactome
cInt <- sample(c(0,1),30, TRUE)
interactome <- matrix(cInt, nrow=6, ncol=5,dimnames=list(letters[2:7],LETTERS[1:5]))

## Create cellular organizational units interaction matrix
gInt <- sample(c(1:8), 25, TRUE)
gInt <- matrix(gInt, nrow=5, ncol=5, dimnames=list(LETTERS[1:5],LETTERS[1:5]))

## All interactome tested
gTest <- matrix(sample(c(0:3), 25, TRUE), nrow=5, ncol=5)
gTested <- gInt+gTest
val <- test2Interact(iMat=gInt, tMat=gTested, interactome=interactome)
```
Description

The data are from Lee et al., the rows of the matrix represent genes in S. cerevisiae, the columns known transcription factor. The value in each entry represents the p-value, as reported by Lee et al., for the transcription factor (TF) binding upstream of the gene.

Usage

data(TFmat)

Format

TFmat is a matrix, rows represent genes, columns transcription factors and the elements are p-values representing some notion of the likelihood that the transcription factor binds upstream of the gene.

Author(s)

Z. Jiang

Source

Supplementary material from http://web.wi.mit.edu/young/regulator_network/

References


Examples

data(TFmat)

topInteraction Extract interacting biological complexes

Description

Extract the top X interacting biological complexes.

Usage

topInteraction(data,top=10)

Arguments

data Square matrix of biological complexes that shares one or more genes(proteins)
top Interger that represents the percentage of interacting complexe
twoWayTable

Value
Data frame of biological complexes that interact. The first two columns are the cellular organizational units names and the third column indicates the number of interactions.

Author(s)
N. LeMeur

Examples

data(Atong)
data(ScISIC)
data(SGA)
SLa2 <- gi2Interactome(Atong, ScISIC)
## Search for synthetic lethal interaction
compM <- getInteraction(SLa2, SGA, ScISIC)
top10Interaction<- topInteraction(compM$bwMat,top=10)

twoWayTable
Generate two-way table for genetic interaction data

description
Generate two-way table from a vector of genetic interaction status and a vector of the pairs that share a functional domain.

Usage
twoWayTable(var1, var2idx)

Arguments

var1 Vector of the status of the first property.
var2idx Vector of the index in var1 that have the second property.

details
Calculates the count numbers from the given vectors. Then put them into a matrix format.

Value
A two-way contingency table of genetic interaction and whether sharing a functional domain.

Author(s)
Z. Jiang

See Also

sharedBy, getUniquePairs
withinComplex

Examples

```r
var1 <- c(0,1,1,0,0,0,1,0,1,1)
var2idx <- c(3,5,7)
twoWayTable(var1, var2idx)

data("AtongFnDomain")
pf <- Biobase::reverseSplit(AtongFnDomain$SharedPfam)
idx <- which(rownames(AtongFnDomain$pairs) %in% pf$PF00478)
twoWayTable(AtongFnDomain$pairs[, "interact"], idx)
```

**withinComplex**

*Search for protein co-membership within complexes.*

**Description**

Search for protein co-membership within one (or more) complex(es).

**Usage**

```r
withinComplex(data, interactome)
```

**Arguments**

- `data`  
  Binary matrix of genes (proteins) linked to other genes (protein) by any biological experiment

- `interactome`  
  Binary matrix composed of genes (rows) and biological complexes (columns)

**Value**

Matrix of genes (proteins) co-member of one or more biological complexes.

**Author(s)**

N. LeMeur

**See Also**

- `byComplex`

**Examples**

```r
data(Atong)
data(ScISIC)
coMember <- withinComplex(Atong, ScISIC)
table(coMember)
```
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