Package: apComplex (via r-universe)

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Title Estimate protein complex membership using AP-MS protein data

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Description Functions to estimate a bipartite graph of protein complex membership using AP-MS data.

Depends R (>= 2.10), graph, RBGL

Imports Rgraphviz, stats, org.Sc.sgd.db

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Contents

AP-MS complexes . . . 2
apEX . . . 3
bhmaxSubgraph . . . 4
findComplexes . . . 5
gavinBP2006 . . . 7
HMSPCI . . . 7
HMSPCI complexes . . . 9
Krogan . . . 10
Krogan complexes . . . 11
kroganBPMat2006 . . . 12

LCjoin 12
mergeComplexes 13
plotComplex 15
sortComplexes 16
TAP 17
TAP complexes 18
yNameTAP complexes 20
yTAP 21

Index **22**

`AP-MS complexes` *AP-MS data complex estimates*

Description

List of complex estimates after filtering baits prone to systematic bias

Usage

```
data(gavin06FilteredEstimates)
data(krogan06FilteredEstimates)
```

Details

`gavin06FilteredEstimates` contains results from an analysis of the AP-MS data published by Gavin et al. (2006). These estimates were constructed using `findComplexes` with a sensitivity parameter of .70, specificity of .999, and commonFrac=0.5

`krogan06FilteredEstimates` contains results from an analysis of the AP-MS data published by Krogan et al. (2006). These estimates were constructed using `findComplexes` with a sensitivity parameter of .70, specificity of .999, and commonFrac=1/3.

Both sets of estimates are reported as lists of length three, corresponding to MBME, SBMH, and UnRBB complex estimate types (see Scholtens et al., 2005). Each of the three elements contains a list of character vectors of estimated complex members.

Source

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

References

Gavin, et al. (2006)

Krogan, et al. (2006)

See Also

gavinBP2006, kroganBPMat2006, findComplexes

Examples

```
data(gavin06FilteredEstimates)
lapply(gavin06FilteredEstimates,FUN=length)

data(krogan06FilteredEstimates)
lapply(krogan06FilteredEstimates,FUN=length)
```

---

apEX *Example data set for apComplex package*

Description

A matrix and corresponding graph of AP-MS purifications from a small hypothetical experiment.

Usage

```
data(apEX)
data(apEXG)
```

Details

apEX is a matrix of hypothetical AP-MS data. The 4 rows correspond to bait proteins and the 8 columns correspond to proteins found as hits in the hypothetical experiment and are named accordingly. The first 4 column names are the same as the 4 row names; bait proteins can also be found as hits by other baits, hence their inclusion as columns in apEX. An entry of "1" in the ith row and jth column of apEX indicates that bait protein i found protein j as a hit. All other entries are "0". There are a total of 9 "1" entries in the matrix, corresponding to 9 comemberships detected in the experiment.

apEXG is a graphNEL object in which 8 nodes represent proteins and 9 directed edges represent comemberships detected in the purification. Each directed edge originates at the bait and ends at the hit. Each edge in apEXG corresponds to an entry of "1" in the apEX matrix.

These data are used in the apComplex vignette.

Examples

```
data(apEX)
apEX

data(apEXG)
adj(apEXG,"P1")
```

bhmaxSubgraph *Find maximal BH-complete subgraph*

Description

Given an adjacency matrix of bait-hit AP-MS protein data, this function finds the maximal BH-complete subgraphs and reports them as an affiliation matrix.

Usage

```
bhmaxSubgraph(adjMat,VBs=NULL,VPs=NULL,unrecip=1)
```

Arguments

adjMat	adjMat is an N by (N+M) adjacency matrix with N equal to the number of bait proteins and M equal to the number of hit-only proteins. adjMat should have row and column names corresponding to the proteins in the experiment. An entry of "1" in the ith row and jth column of adjMat corresponds to bait protein i finding protein j as a hit. All other entries should be 0.
VBs	VBs is an optional vector of viable baits.
VPs	VPs is an optional vector of viable prey.
unrecip	By default set to 1 so that unreciprocated bait-bait edges are treated as present. If set to 0, unreciprocated bait-bait edges will be treated as absent.

Details

A BH-complete subgraph with n bait nodes and m hit-only nodes for AP-MS data is defined as a subgraph for which all n*(n-1)+nm directed edges exist. A maximal BH-complete subgraph is a BH-complete subgraph which is not contained in any other BH-complete subgraph.

If VBs and/or VPs are not specified, then by default VBs will be assigned the set of baits that detect at least one prey and VPs the set of prey that are detected by at least one bait.

By default, unreciprocated bait-bait observations will be treated as present. If unrecip is set to 0, they will be treated as absent. If the sensitivity of the AP-MS technology is believed to be less than the specificity, then it is suggested that unrecip=1.

This function calls maxCliques from the RBGL package.

Value

A list of length one named 'maxCliques' which is itself a list of character vectors containing the names of the elements in the cliques.

Author(s)

Denise Scholtens

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

mergeComplexes,findComplexes

Examples

```
data(apEX)
PCMG0 <- bhmaxSubgraph(apEX)
PCMG1 <- mergeComplexes(PCMG0,apEX,sensitivity=.7,specificity=.75)
```

`findComplexes` *Estimate a Protein Complex Membership Graph (PCMG) using protein complex comembership data from AP-MS technology*

Description

Performs all steps in the local modeling algorithm described by Scholtens and Gentleman (2004) and Scholtens, Vidal, and Gentleman (submitted), beginning with an adjacency matrix recording bait-hit AP-MS data.

Usage

```
findComplexes(adjMat,VBs=NULL,VPs=NULL,simMat=NULL,sensitivity=.75,specificity=.995,Beta=0,commonFr
= 2e7)
```

Arguments

`adjMat`	Adjacency matrix of bait-hit data from an AP-MS experiment. Rows correspond to baits and columns to hits.
`VBs`	`VBs` is an optional vector of viable baits.
`VPs`	`VPs` is an optional vector of viable prey.
`simMat`	An optional square matrix with entries between 0 and 1. Rows and columns correspond to the proteins in the experiment, and should be reported in the same order as the columns of `adjMat`. Higher values in this matrix are interpreted to mean higher similarity for protein pairs.
`sensitivity`	Believed sensitivity of AP-MS technology.
`specificity`	Believed specificity of AP-MS technology.
`Beta`	Optional additional parameter for the weight to give data in `simMat` in the logistic regression model.

commonFrac	This is the fraction of baits that need to be overlapping for a complex combination to be considered.
wsVal	A numeric. This is the value assigned as the work-space in the call to fisher.test

Details

findComplexes performs all steps in the complex estimation algorithm using the apComplex package functions bhmaxSubgraph, LCdelta, and mergeComplexes. These steps can also be performed separately by the user.

If VBs and/or VPs are not specified, then by default VBs will be assigned the set of baits that detect at least one prey and VPs the set of prey that are detected by at least one bait.

By default commonFrac is set relatively high at 2/3. This means that some potentially reasonable complex combinations could be missed. For smaller data sets, users may consider decreasing the fraction. For larger data sets, this may cause a large increase in computation time.

Value

A list of character vectors containing the names of the proteins in the estimated complexes.

Author(s)

Denise Scholtens

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

bhmaxSubgraph,mergeComplexes

Examples

```
data(apEX)
PCMG2 <- findComplexes(apEX,sensitivity=.7,specificity=.75)
```

gavinBP2006 *Tandem Affinity Purification (TAP) Data from Gavin et al. (2006)*

Description

TAP data published by Gavin, et al. (2006).

Usage

```
data(gavinBP2006)
```

Details

gavinBP2006 is a matrix of the TAP data published by Gavin, et al. (2006). The 1752 rows correspond to bait proteins and the 2551 columns correspond to proteins found as hits in the TAP experiment and are named accordingly. The first 1752 column names are the same as the 1752 row names; bait proteins can also be found as hits by other baits, hence their inclusion as columns in gavinBP2006. An entry of "1" in the ith row and jth column of gavinBP2006 indicates that bait protein i found protein j as a hit. All other entries are "0". There are a total of 19105 "1" entries in the matrix, corresponding to the 19105 comemberships detected in the experiment.

These data are available in the IntAct repository under Gavin et al - 2006.

Source

Gavin, et al. Functional Organization of the Yeast Proteome by Systematic Analysis of the Yeast Complex. Nature 440, 631-636 (2002).

See Also

yTAP,MBMEcTAP,SBMHcTAP,UnRBBcTAP,HMSPCI

Examples

```
data(gavinBP2006)
which(gavinBP2006[1,]==1)
```

HMSPCI *High-Throughput Mass Spectromic Protein Complex Identification (HMS-PCI) Data from Ho, et al. (2002)*

Description

HMS-PCI data published by Ho, et al. (2002).

Usage

```
data(HMSPCI)
data(HMSPCIgraph)
```

Details

HMSPCI is a matrix of the HMS-PCI data published by Ho, et al. (2002). The 493 rows correspond to bait proteins and the 1578 columns correspond to proteins found as hits in the HMSPCI experiment and are named accordingly. The first 493 column names are the same as the 493 row names; bait proteins can also be found as hits by other baits, hence their inclusion as columns in HMSPCI. An entry of "1" in the ith row and jth column of HMSPCI indicates that bait protein i found protein j as a hit. All other entries are "0". There are a total of 3687 "1" entries in the matrix, corresponding to the 3687 comemberships detected in the experiment.

HMSPCIgraph is a graphNEL object in which 1578 nodes represent proteins and 3687 directed edges represent comemberships detected in the purification. Each directed edge originates at the bait and ends at the hit. Each edge in HMSPCIgraph corresponds to an entry of "1" in the HMSPCI matrix.

These data are available at http://www.mdsp.com/yeast.

Source

Ho, et al. Systematic identification of protein complexes in Saccharomyces cerevisiae by mass spectrometry. Nature 415, 180-183 (2002).

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

MBMEcHMSPCI,SBMHcHMSPCI,UnRBBcHMSPCI,TAP

Examples

```
data(HMSPCI)
which(HMSPCI["YAL015C",]==1)

data(HMSPCIgraph)
adj(HMSPCIgraph,"YAL015C")
```

HMSPCI complexes *HMSPCI data complex estimates*

Description

Affiliation matrices with rows corresponding to proteins and columns corresponding to complexes.

Usage

```
data(MBMEcHMSPCI)
data(SBMHcHMSPCI)
data(UnRBBcHMSPCI)
```

Details

These are the results from an analysis of the HMS-PCI data (Ho et al., 2002) described by Scholtens and Gentleman (2004) and Scholtens, Vidal, and Gentleman (submitted). These estimates were constructed using `findComplexes` with a sensitivity parameter of .75, specificity of .99, and Beta=-0.2 for externally derived similarity measure based on Gene Ontology cellular component annotation (see Scholtens and Gentleman (2004)).

`MBMEcHMSPCI` contains 242 multi-bait-multi-edge complex estimates. `SBMHcHMSPCI` contains 437 single-bait-multi-hit complex estimates. `UnRBBcHMSPCI` contains 329 unreciprocated bait-bait complex estimates. These data are also available at http://www.bioconductor.org/Docs/Papers/2003/apComplex.

Source

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

References

Ho, et al. Systematic identification of protein complexes in Saccharomyces cerevisiae by mass spectrometry. Nature 415, 180-183 (2002).

See Also

`HMSPCI`,`HMSPCIgraph`,`findComplexes`

Examples

```
data(MBMEcHMSPCI)
MBMEcHMSPCI[1:4,1:4]
which(MBMEcHMSPCI[,"MBME1"]==1)
```

Krogan *High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes (2004)*

Description

AP-MS data published by Krogan et al. (2004)

Usage

```
data(Krogan)
```

Details

Krogan is a matrix of the AP-MS data published by Krogan et al (2004). The 153 rows correspond to bait proteins and the 485 columns correspond to proteins found as hits in the AP-MS experiment and are named accordingly. The first 153 column names are the same as the 153 row names; bait proteins can also be found as hits by other baits, hence their inclusion as columns in Krogan. An entry of "1" in the ith row and jth column of Krogan indicates that bait protein i found protein j as a hit. All other entries are "0". There are a total of 1132 "1" entries in the matrix, corresponding to the 1132 comemberships detected in the experiment.

These data are available at http://www.molecule.org/cgi/content/full/13/2/225/DC1/.

Source

Krogan, et al. High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes; Molecular Cell, Vol 13, 225-239, 30 January 2004.

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

MBMEcKrogan

Examples

```
data(Krogan)
```

Krogan complexes *Krogan data complex estimates*

Description

Affiliation matrices with rows corresponding to proteins and columns corresponding to complexes.

Usage

```
data(MBMEcKrogan)
```

Details

These are the results from an analysis of the AP-MS data (Krogan et al., 2004). These estimates were constructed using `findComplexes` with a sensitivity parameter of .75, specificity of .99, and Beta=-0.2 for externally derived similarity measure based on Gene Ontology cellular component annotation (see Scholtens and Gentleman (2004)).

`MBMEcHMSPCI` contains 82 multi-bait-multi-edge complex estimates.

Source

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

References

High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes; Molecular Cell, Vol 13, 225-239, 30 January 2004

Examples

```
data(MBMEcKrogan)
MBMEcKrogan[1:4,1:4]
```

kroganBPMat2006 *Tandem Affinity Purification (TAP) Data from Krogan et al. (2006)*

Description

TAP data published by Krogan, et al. (2006).

Usage

```
data(kroganBPMat2006)
```

Details

kroganBPMat2006 is a matrix of the TAP data published by Krogan, et al. (2006). The 2264 rows correspond to bait proteins and the 5361 columns correspond to proteins found as hits in the TAP experiment and are named accordingly. The first 2264 column names are the same as the 2264 row names; bait proteins can also be found as hits by other baits, hence their inclusion as columns in kroganBPMat2006. An entry of "1" in the ith row and jth column of kroganBPMat2006 indicates that bait protein i found protein j as a hit. All other entries are "0". There are a total of "1" entries in the matrix, corresponding to the 63360 comemberships detected in the experiment.

These data were obtained from the Primary Source -

Source

N Krogan et al. Global Landscape of Protein Complexes in the Yeast, S. Cerevisiae. Nature, 440:667-643, 2006.

See Also

yTAP,MBMEcTAP,SBMHcTAP,UnRBBcTAP,HMSPCI

Examples

```
data(kroganBPMat2006)
which(kroganBPMat2006[1,]==1)
```

LCjoin *Computes change in LxC measure*

Description

Computes the change in the P=LxC measure for AP-MS protein data when two protein complex estimates are combined into one complex.

Details

These functions are used to evaluate changes in the penalized likelihood when two complexes are combined. They are not meant to be directly used.

Value

The numeric value of the change in P=LxC when two complexes are combined.

Author(s)

Denise Scholtens

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

bhmaxSubgraph,mergeComplexes,findComplexes

Examples

```
data(apEX)
PCMG0 <- bhmaxSubgraph(apEX)
PCMG1 <- mergeComplexes(PCMG0,apEX,sensitivity=.7,specificity=.75)
```

---

mergeComplexes *Iteratively combine columns in initial PCMG estimate*

Description

Repeatedly applies the function LCdelta to make combinations of columns in the affiliation matrix representing the protein complex membership graph (PCMG) for AP-MS data.

Usage

```
mergeComplexes(bhmax,adjMat,VBs=NULL,VPs=NULL,simMat=NULL,sensitivity=.75,specificity=.995,Beta=0,c
```

Arguments

bhmax	Initial complex estimates coming from bhmaxSubgraph
adjMat	Adjacency matrix of bait-hit data from an AP-MS experiment. Rows correspond to baits and columns to hits.
VBs	VBs is an optional vector of viable baits.
VPs	VPs is an optional vector of viable prey.
simMat	An optional square matrix with entries between 0 and 1. Rows and columns correspond to the proteins in the experiment, and should be reported in the same order as the columns of adjMat. Higher values in this matrix are interpreted to mean higher similarity for protein pairs.
sensitivity	Believed sensitivity of AP-MS technology.
specificity	Believed specificity of AP-MS technology.
Beta	Optional additional parameter for the weight to give data in simMat in the logistic regression model.
commonFrac	This is the fraction of baits that need to be overlapping for a complex combination to be considered.
wsVal	A numeric. This is the value assigned to the work-space in the call to fisher.test.

Details

The local modeling algorithm for AP-MS data described by Scholtens and Gentleman (2004) and Scholtens, Vidal, and Gentleman (2005) uses a two-component measure of protein complex estimate quality, namely P=LxC. Columns in cMat represent individual complex estimates. The algorithm works by starting with a maximal BH-complete subgraph estimate of cMat, and then improves the estimate by combining complexes such that P=LxC increases.

By default commonFrac is set relatively high at 2/3. This means that some potentially reasonable complex combinations could be missed. For smaller data sets, users may consider decreasing the fraction. For larger data sets, this may cause a large increase in computation time.

Value

A list of character vectors containing the names of the proteins in the estimated complexes.

Author(s)

Denise Scholtens

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

bhmaxSubgraph,findComplexes

Examples

```
data(apEX)
PCMG0 <- bhmaxSubgraph(apEX)
PCMG1 <- mergeComplexes(PCMG0,apEX,sensitivity=.7,specificity=.75)
```

---

plotComplex *Render complex estimates*

Description

plotComplex renders complex estimates from the apComplex algorithm using Rgraphviz.

Usage

```
plotComplex(complexMembers,g,VBs,VPs,geneName=FALSE,baitColor="yellow",preyColor="white",recipLineC
```

Arguments

complexMembers	A character vector of proteins composing a complex estimate.
g	An object of class graph, the full bait-prey graph of AP-MS data used in analysis. complexMembers must be a subset of the node names of g.
VBs	A vector of viable baits used in the AP-MS experiment.
VPs	A vector of viable prey used in the AP-MS experiment.
geneName	A logical indicating whether or not nodes should be plotted with common gene names as labels rather than systematic names.
baitColor	Color of bait nodes.
preyColor	Color of prey nodes.
recipLineColor	Color of edges connecting baits which both detected each other as prey
.	
unrecipBBLineColor	Color of edges connecting baits in which one bait finds the other as prey but not vice versa.
unrecipBPLineColor	Color of edges extending from baits to proteins that were only used as prey, hence reciprocity is not possible.
y	Layout of plot

Details

This is a simple function for plotting complex estimates resulting from the apComplex algorithm. Giving the upcoming changes in Rgraphviz, it will likely be changed substantially.

Value

A plotted graph of the complex estimate subgraph.

Author(s)

Denise Scholtens

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

findComplexes

Examples

```
data(apEX)
data(apEXG)
PCMG2 <- findComplexes(apEX,sensitivity=.7,specificity=.75)
PCMG2sorted <- sortComplexes(PCMG2,apEX)

VBs <- rownames(apEX)
VPs <- setdiff(colnames(apEX),VBs)

plotComplex(PCMG2sorted$MBME[[1]],g=apEXG,VBs=VBs, VPs=VPs)
```

---

sortComplexes *Sort complex estimates*

Description

Sorts complexes recorded in PCMG list into three separate lists containing MBME, SBMH, and UnRBB complexes.

Usage

```
sortComplexes(PCMG, adjMat)
```

Arguments

PCMG	Current PCMG estimate
adjMat	Adjacency matrix of bait-hit data from an AP-MS experiment. Rows correspond to baits and columns to hits.

Details

MBME complexes contain multiple bait proteins and multiple edges. SBMH complexes contain one bait and a collection of hit-only proteins. UnRBB complexes contain only two baits (no hit-only proteins) that are connected by an unreciprocated edge.

Value

A list of lists representing the MBME, SBMH, and UnRBB complex estimates.

Author(s)

Denise Scholtens

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

findComplexes

Examples

```
data(apEX)
PCMG2 <- findComplexes(apEX,sensitivity=.7,specificity=.75)
sortComplexes(PCMG2,apEX)
```

TAP *Tandem Affinity Purification (TAP) Data from Gavin et al. (2002)*

Description

TAP data published by Gavin, et al. (2002).

Usage

```
data(TAP)
data(TAPgraph)
```

Details

TAP is a matrix of the TAP data published by Gavin, et al. (2002). The 455 rows correspond to bait proteins and the 1364 columns correspond to proteins found as hits in the TAP experiment and are named accordingly. The first 455 column names are the same as the 455 row names; bait proteins can also be found as hits by other baits, hence their inclusion as columns in TAP. An entry of "1" in the ith row and jth column of TAP indicates that bait protein i found protein j as a hit. All other entries are "0". There are a total of 3420 "1" entries in the matrix, corresponding to the 3420 comemberships detected in the experiment.

TAPgraph is a graphNEL object in which 1364 nodes represent proteins and 3420 directed edges represent comemberships detected in the purification. Each directed edge originates at the bait and ends at the hit. Each edge in TAPgraph corresponds to an entry of "1" in the TAP matrix.

These data are available in Supplementary Table S1 of Gavin et al. at http://www.nature.com.

Source

Gavin, et al. Functional organization of the yeast proteome by systematic analysis of protein complexes. Nature 415, 141-147 (2002).

References

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

See Also

yTAP,MBMEcTAP,SBMHcTAP,UnRBBcTAP,HMSPCI

Examples

```
data(TAP)
which(TAP["Abd1",]==1)

data(TAPgraph)
adj(TAPgraph,"Abd1")
```

TAP complexes *TAP data complex estimates*

Description

Affiliation matrices with rows corresponding to proteins and columns corresponding to complexes.

Usage

```
data(MBMEcTAP)
data(SBMHcTAP)
data(UnRBBcTAP)
```

Details

These are the results from an analysis of the TAP data (Gavin et al., 2002) by Scholtens and Gentleman (2004) and Scholtens, Vidal, and Gentleman (submitted). These estimates were constructed using `findComplexes` with a sensitivity parameter of .75, specificity of .995, and Beta=-0.2 for externally derived similarity measure based on Gene Ontology cellular component annotation (see Scholtens and Gentleman (2004)).

`MBMEcTAP` contains 260 multi-bait-multi-edge complex estimates. `SBMHcTAP` contains 325 single-bait-multi-hit complex estimates. `UnRBBcTAP` contains 123 unreciprocated bait-bait complex estimates. These data are also available at http://www.bioconductor.org/Docs/Papers/2003/apComplex.

Source

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

References

Gavin, et al. Functional organization of the yeast proteome by systematic analysis of protein complexes. Nature 415, 141-147 (2002).

See Also

`TAP`, `TAPgraph`, `yTAP`, `findComplexes`

Examples

```
data(MBMEcTAP)
MBMEcTAP[1:10,1:3]
which(MBMEcTAP[,"MBME1"]==1)
```

yNameTAP complexes *TAP data complex estimates using standard gene names*

Description

Affiliation matrices with rows corresponding to proteins and columns corresponding to complexes.

Usage

```
data(yNameTAP)
```

Details

These are the results from an analysis of the TAP data (Gavin et al., 2002) by Scholtens and Gentleman (2004) and Scholtens, Vidal, and Gentleman (submitted). These estimates were constructed using `findComplexes` with a sensitivity parameter of .75, specificity of .995, and Beta=-0.2 for externally derived similarity measure based on Gene Ontology cellular component annotation (see Scholtens and Gentleman (2004)).

`yNameTAP` contains 260 multi-bait-multi-edge complex estimates.

Source

Scholtens D and Gentleman R. Making sense of high-throughput protein-protein interaction data. Statistical Applications in Genetics and Molecular Biology 3, Article 39 (2004).

Scholtens D, Vidal M, and Gentleman R. Local modeling of global interactome networks. Bioinformatics 21, 3548-3557 (2005).

References

Gavin, et al. Functional organization of the yeast proteome by systematic analysis of protein complexes. Nature 415, 141-147 (2002).

See Also

`TAP`, `TAPgraph`, `yTAP`, `findComplexes`

Examples

```
data(yNameTAP)
yNameTAP[1:10,1:3]
```

yTAP *yTAP Complexes published Gavin, et al. (2002).*

Description

A list of the 232 'yTAP' complexes published by Gavin, et al. (2002) using their TAP data.

Usage

```
data(yTAP)
```

Details

Each element of the yTAP list contains a vector of the proteins reported as part of the complex, as well as the functional annotation category published by Gavin, et al. (2002).

These data are available in Supplementary Table S3 of Gavin, et al. (2002) at http://www.nature.com and at http://yeast.cellzome.com.

Source

Gavin, et al. Functional organization of the yeast proteome by systematic analysis of protein complexes. Nature 415, 141-147 (2002).

See Also

TAP,TAPgraph,MBMEcTAP,SBMHcTAP,UnRBBcTAP,HMSPCI

Examples

```
data(yTAP)
yTAP[1]
```

Index

∗ **array**
bhmaxSubgraph, 4
∗ **datasets**
AP-MS complexes, 2
apEX, 3
gavinBP2006, 7
HMSPCI, 7
HMSPCI complexes, 9
Krogan, 10
Krogan complexes, 11
kroganBPMat2006, 12
TAP, 17
TAP complexes, 18
yNameTAP complexes, 20
yTAP, 21
∗ **graphs**
findComplexes, 5
LCjoin, 12
mergeComplexes, 13
plotComplex, 15
sortComplexes, 16

adjBinFUN *(*LCjoin*)*, 12
AP-MS complexes, 2
apEX, 3
apEXG *(*apEX*)*, 3

bhmaxSubgraph, 4, *6*, *13*, *15*

findComplexes, 5, *5*, *13*, *15–17*
fisherFUN *(*LCjoin*)*, 12

gavin06FilteredEstimates *(*AP-MS complexes*)*, 2
gavinBP2006, *3*, 7
gavinBP2006graph *(*gavinBP2006*)*, 7

HMSPCI, 7, *7*, *9*, *12*, *18*, *21*
HMSPCI complexes, 9
HMSPCIgraph, *9*
HMSPCIgraph *(*HMSPCI*)*, 7

Krogan, 10
Krogan complexes, 11
krogan06FilteredEstimates *(*AP-MS complexes*)*, 2
kroganBPMat2006, *3*, 12

LCjoin, 12
LCjoinadjBin *(*LCjoin*)*, 12
LCjoinfisher *(*LCjoin*)*, 12
LCjoinLchange *(*LCjoin*)*, 12

MBMEcHMSPCI, *8*
MBMEcHMSPCI *(*HMSPCI complexes*)*, 9
MBMEcKrogan, *10*
MBMEcKrogan *(*Krogan complexes*)*, 11
MBMEcTAP, *7*, *12*, *18*, *21*
MBMEcTAP *(*TAP complexes*)*, 18
mergeComplexes, *5, 6*, 13, *13*

plotComplex, 15

SBMHcHMSPCI, *8*
SBMHcHMSPCI *(*HMSPCI complexes*)*, 9
SBMHcTAP, *7*, *12*, *18*, *21*
SBMHcTAP *(*TAP complexes*)*, 18
sortComplexes, 16

TAP, *8*, 17, *19–21*
TAP complexes, 18
TAPgraph, *19–21*
TAPgraph *(*TAP*)*, 17

UnRBBcHMSPCI, *8*
UnRBBcHMSPCI *(*HMSPCI complexes*)*, 9
UnRBBcTAP, *7*, *12*, *18*, *21*
UnRBBcTAP *(*TAP complexes*)*, 18

yNameTAP *(*yNameTAP complexes*)*, 20
yNameTAP complexes, 20
yTAP, *7*, *12*, *18–20*, 21