Package ‘ProCoNA’

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Type Package

Title Protein co-expression network analysis (ProCoNA).

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Author David L Gibbs

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License GPL (>= 2)

LazyLoad yes

Depends R (>= 2.10), methods, WGCNA, MSnbase, flashClust

Imports BiocGenerics, GOstats

Suggests RUnit

biocViews GraphAndNetwork, Software, Proteomics

NeedsCompilation no

R topics documented:

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Peptide co-expression network construction.

Description

Peptide co-expression network construction, analysis, and visualization.

Details

Package: procona
Type: Package
Title: Peptide co-expression network construction.
Version: 0.13
Date: 2011-08-10
Author: David L Gibbs
Maintainer: David Gibbs <gibbsd@ohsu.edu>
License: GPLv3
LazyLoad: yes
Depends: WGCNA, GOstats, multicore

Author(s)

David L Gibbs
### Description

Accessor functions allow access to the object data.

### Methods

- **TOM**: The topological overlap matrix or TOM. "matrix"
- **adj**: The adjacency matrix. "matrix"
- **networkName**: A name describing the data or experiment used to build the network. "character"
- **samples**: The names of samples used in building the network. "character"
- **peptides**: The names of peptides used in the network, also the node names. "character"
- **pepTree**: The network dendrogram. "hclust"
- **dynamicColors**: The module labels on each node (or peptide). "numeric"
- **MEs**: The module eigenvectors (or eigen-peptides). "data.frame"
- **mergedMEs**: The module eigenvectors after merging similar modules. "data.frame"
- **mergedColors**: The module labels after merging similar modules. "numeric"
- **colorOrder**: Modules are ordered by size, these labels correspond to that order. "character"
- **power**: The soft thresholding power used in scaling the adjacency matrix. "numeric"
- **networkType**: Either a signed or unsigned network regarding the method used in computing the initial correlations between nodes. "character"
- **permtest**: The results of the permutation test on significance of topological overlap within modules. "matrix"
- **proconaVersion**: Returns the version number of the software that built the object. "character"

### Author(s)

David L Gibbs

### Examples

```r
data(ProCoNA_Data)
tomMatrix <- TOM(net1)
```
bootstrapProconaNetwork

Description

This function returns a peptide co-expression network object based on a bootstrapped correlation matrix.

Usage

```r
bootstrapProconaNetwork(networkName = "bootstrap procona", pepdat = NULL,
pow = NULL, powMax = 20, networkType = "signed", scaleFreeThreshold = 0.8,
deepSplit = 2, minModuleSize = 30, mergeThreshold = 0.1,
clusterType = "average", pamRespectsDendro = T, performTOPermtest = TRUE,
toPermTestPermutes = 100, bootstrapThreshold = 1e-04)
```

Arguments

- `networkName`: Name of this network
- `pepdat`: This variable is the data set with rows as samples and cols as peptides
- `pow`: The scaling power, NULL if unknown
- `powMax`: The maximum power to be searched.
- `networkType`: Whether the sign is considered in constructing adjacency and TOM
- `scaleFreeThreshold`: The threshold for fitting to scale-free topology. will use closest power.
- `deepSplit`: Course grain control of module size
- `minModuleSize`: The minimum module size allowed
- `mergeThreshold`: Below this threshold, modules are merged.
- `clusterType`: Clustering option
- `pamRespectsDendro`: When cutting the dendrogram, pay attention to branch membership.
- `performTOPermtest`: Performs permutation testing on modules
- `toPermTestPermutes`: Number of permutations to do.
- `bootstrapThreshold`: When to stop resampling...

Value

returns the procona network object

Author(s)

David L. Gibbs
Examples

```r
data(ProCoNA_Data)
net <- bootstrapProconaNetwork("peptide network", peptideData,
performTOPermtest=FALSE, bootstrapThreshold=0.1)
```

Description

This function returns a peptide co-expression network object.

Usage

```r
buildProconaNetwork(networkName = "ProCoNA", pepdat, pow=1,
powMax = 20, networkType = "signed", pearson = FALSE, scaleFreeThreshold = 0.8,
depthSplit = 2, minModuleSize = 30, mergeThreshold = 0.1,
clusterType = "average", pamRespectsDendro = TRUE, performTOPermtest = TRUE,
toPermTestPermutes = 100)
```

Arguments

- `networkName` Name of this network
- `pepdat` This variable is the data set with rows as samples and cols as peptides
- `pow` The scaling power, NULL if unknown
- `powMax` The maximum power to be searched.
- `networkType` Should the sign be considered in constructing adjacency and TOM ("signed" or "unsigned")
- `pearson` use Pearson’s cor or the robust bi-weight correlation
- `scaleFreeThreshold` The threshold for fitting to scale-free topology.. will use closest power.
- `depthSplit` Course grain control of module size
- `minModuleSize` The minimum module size allowed
- `mergeThreshold` Below this threshold, modules are merged.
- `clusterType` Clustering option
- `pamRespectsDendro` When cutting the dendrogram, pay attention to branch membership.
- `performTOPermtest` Performs permutation testing on modules
- `toPermTestPermutes` Number of permutations to do.

Details

The procona network object contains a number of slots which store information relevant to the construction of the network. Accessor functions provide direct access to the slots. See getSlots("proconaNet") for a complete list.
Value
returns the procona network object

Author(s)
David L Gibbs

Examples
data(ProCoNA_Data)
net <- buildProconaNetwork("peptide network", peptideData)

c2i

Description
coordinates to index

Usage
c2i(nrows, x, y)

Arguments

nrows number of rows in the matrix
x the row coordinate
y the col coordinate

Value
the index into the matrix

Author(s)
David L Gibbs
```

Description

Fisher’s exact test is used pairwise on modules to compare two networks. The arguments to Fisher’s exact test are given below.

\( n \) == number of entities in the network
\( m \) == number of entities in intersection of two modules
\( d_1 \) == number of entities in module A but not in module B
\( d_2 \) == number of entities in module B but not in module A
2x2 matrix for the test is then: \( m \ d_1 \ d_2 \ n-d_1-d_2-m \)

Usage

```
```
```

CompareNetworksWithFishersExactTest

Arguments

- `peps1`: Nodes in network 1, character vector
- `peps2`: Nodes in network 2, character vector
- `colors1`: Modules for net 1
- `colors2`: Modules for net 2
- `title`: Plot title
- `net1label`: X-label
- `net2label`: Y-label

Value

Returns fishers exact test -log pvalues and overlap matrix showing the number of shared members for each pair of modules.

Author(s)

David L. Gibbs

Examples

```
```
```
```
```
```
```
**compareNetworksWithFishersExactTestProcona**

**Description**
Convienence function for calling the `compareNetworksWithFishersExactTest` using only two procona objects.

**Usage**
```r
compareNetworksWithFishersExactTestProcona(net1, net2, title)
```

**Arguments**
- `net1`: procona object for network 1
- `net2`: procona object for network 2
- `title`: plot title

**Value**
Returns a list of fisher -log pvalues, and overlaps between modules.

**Author(s)**
David L. Gibbs

**Examples**
```r
## Not run:
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData)
#net2 <- buildProconaNetwork("peptide network", peptideData)
compareNetworksWithFishersExactTestProcona(net1, net2, "new comparison")
## End(Not run)
```

---

**corBootstrap**

**Description**
Boosts a correlation matrix. In order to bootstrap a large correlation matrix, several thousand samplings may be necessary. To avoid storing thousands of matrices, a running mean is kept for each pairwise correlation. In addition, a running standard deviation is computed so that for each pairwise correlation, we can estimate the distribution of values across resamplings. After each resampling, a new correlation matrix is computed. A difference is taken between this new matrix and the running mean. If all differences are less than the specified threshold, then the bootstrapped matrix has converged to a final state.
correlationWithPhenotypesHeatMap

Usage

corBootstrap(dataMatrix, networkType = "signed", threshold = 1e-04, tmpSaveFile = TRUE)

Arguments

dataMatrix: Matrix with samples in rows and peptides (or other data type) in columns.
networkType: Whether the sign is considered in constructing adjacency and TOM
threshold: Maximum difference allowed between running mean bootstrap correlation matrix, and new resampled cor matrix. Defines how soon we consider the bootstrap to have converged.
tmpSaveFile: Should temporary saves be done?

Value

Returns a list of the bootstrapped matrix, standard deviation matrix, and the number of resamplings done.

Author(s)

David L Gibbs

Examples

data(ProCoNA_Data)
x <- peptideData[,1:10]
y <- corBootstrap(dataMatrix=x, networkType="unsigned", threshold=0.1, tmpSaveFile=FALSE)

correlationWithPhenotypesHeatMap

correlationWithPhenotypesHeatMap

Description

Plots a heatmap showing the Pearson correlation of modules with phenotypes.

Usage

correlationWithPhenotypesHeatMap(net, phenotypes, modules, plotName, title, textSize)

Arguments

net: The ProCoNA network object.
phenotypes: Matrix of phenotypic traits, can include character strings (converted to factors).
modules: Vector of modules to plot. Default is all modules.
plotName: Name of the saved plot, NULL to show on screen.
title: Plot title.
textSize: The font size of the correlations shown in each module-phenotype pair.
Valu
the module eigenvector correlations

Author(s)
David L. Gibbs

Examples
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("pepnet", peptideData, pow=12)
n <- length(samples(net1))
phenotypes <- matrix(rnorm(10*n), nrow=60)
moduleCors <- correlationWithPhenotypesHeatMap(net1, phenotypes, modules = 1:7,
    plotName = "Phenotype Associations", title = "Module-trait relationships", textSize = 0.5)

getFisherMatrix

Description
Fisher's exact test pairwise on modules.

Usage
getFisherMatrix(peps1, peps2, colors1, colors2)

Arguments
peps1 Names of entities in the network (nodes of network 1)
peps2 Names of entities in the network (nodes of network 2)
colors1 the module assignments for network 1
colors2 the module assignments for network 2

Value
Returns the fisher test pvalues and count of overlapping peptides.

Author(s)
David L. Gibbs

Examples
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=12)
#net2 <- buildProconaNetwork("peptide network", peptideData + 0.3*rnorm(length(peptideData)), pow=12)
getFisherMatrix(peptides(net1), peptides(net2), mergedColors(net1), mergedColors(net2))
**getPeptideNAs**

**Description**
This function returns the number of NAs for each peptide.

**Usage**
```r
getPeptideNAs(pepdat)
```

**Arguments**
- `pepdat`  the peptide data.

**Value**
returns a list of counts of NAs for each peptide.

**Author(s)**
David L Gibbs

---

**goStatTest**

**Description**
Wrapper function to run the hyperGTest from package GOstats, after mapping each peptide to an entrez ID.

**Usage**
```r
goStatTest(pnet, module, pepinfo, pepColName, protColName, universe, onto, annot, pvalue, cond)
```

**Arguments**
- `pnet`  Procona network object.
- `module`  Module of interest (numeric)
- `pepinfo`  The mass tag info, mapping peptides to proteins.
- `pepColName`  Column name in mass tag info for peptides
- `protColName`  Column name in mass tag info for proteins
- `universe`  Table mapping protein IDs to entrez IDs
- `onto`  The ontology catagory (bp etc).
- `annot`  The annotation database to use
- `pvalue`  pvalue cutoff
- `cond`  conditional parameter, see GOstats.
Value

Returns the results of the hyper geometric test.

Author(s)

David L. Gibbs

Examples

```r
## Not run:
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=12)
goStatTest(net1, 1, masstagdb, "Mass_Tag_ID", "Reference", universe, "BP", "org.Mm.eg.db", 0.005, FALSE)
## End(Not run)
```

Description

From the OneHandClapping package. Thanks! Dummy class to permit object of S3 class `hclust` in S4 class definition of Screening

Objects from the Class

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

Slots

- `.Data`: Object of class "list" ~~

Extends

Class "list", from data part. Class "vector", by class "list", distance 2.

Methods

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

Warning

This class is just defined as a dummy class. No objects should be instantiated.

Note

This class is just defined as a dummy class. No objects should be instantiated.

Examples

```r
showClass("hclust")
```
**i2c**

**Description**
Index to coordinates

**Usage**
\[ \text{i2c}(\text{nrows}, \text{i}) \]

**Arguments**
- **nrows**: number of rows in the matrix
- **i**: the index into the matrix

**Value**
The row col coordinates into the matrix

**Author(s)**
David L. Gibbs

---

**i2col**

**Description**
index to column

**Usage**
\[ \text{i2col}(\text{nrows}, \text{i}) \]

**Arguments**
- **nrows**: number of rows in matrix
- **i**: the index

**Value**
returns the column of the matrix

**Author(s)**
David L. Gibbs
**MMvsPS**

Module members vs Peptide Significance

**Description**

Plots the module membership (correlation to eigenvector) against the peptide significance (correlation to phenotype) for a given trait and module.

**Usage**

`MMvsPS(pnet, pepdat, phenoVec, mod)`

**Arguments**

- `pnet`: The procona network.
- `pepdat`: The peptide data, with rows as samples and columns as peptides.
- `phenoVec`: The phenotypic trait, vector.
- `mod`: The module of interest.

**Value**

Returns a list of module memberships and peptide significances.

**Author(s)**

David L. Gibbs

**Examples**

```r
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=13)
MMvsPS(net1, peptideData, phenotypes[,5], 1)
```

**MMvsPSallModules**

Call MMvsPS, producing plots for all modules.

**Usage**

`MMvsPSallModules(net, peptable, phenoVec, prefixName)`

**Arguments**

- `net`: The procona network object.
- `peptable`: The peptide data.
- `phenoVec`: The phenotypic trait, as a numeric vector.
- `prefixName`: The plot files prefix name. Writes pdfs.
moduleMemberCorrelations

Value

nothing returned

Author(s)

David L. Gibbs

Examples

## Not run:
# This function outputs a set of pdfs.
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=13)
MMvsPSallModules(net1, peptideData, phenotypes[,5], 1)

## End(Not run)

Description

Computes the relation between peptides and eigenvector summaries and also peptides and phenotypes.

Usage

moduleMemberCorrelations(pnet, pepdat, phenotypes)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pnet</td>
<td>The peptide net object</td>
</tr>
<tr>
<td>pepdat</td>
<td>The peptide data matrix</td>
</tr>
<tr>
<td>phenotypes</td>
<td>The matrix of traits</td>
</tr>
</tbody>
</table>

Value

Matrix of Pearson correlations with peptides in rows.

Author(s)

David L. Gibbs
modulePhenotypeCorrelations

Examples

data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData)

n <- length(samples(net1))

phenotypes <- matrix(rnorm(10*n), nrow=60)

pepcor <- moduleMemberCorrelations(net1, peptideData, phenotypes)

# To plot the heatmap:
# moduleCors <- correlationWithPhenotypesHeatMap(net1, phenotypes, modules = 1:5,
#  plot = NULL, title = "Module-trait relationships", textSize = 0.5)

#########################################################################
# quick function to write out the tables for specific modules.
# moduleData <- function(pepnet, pepcors, module, pepinfo, fileprefix) {
#   moduleX <- pepnet@peptides[which(pepnet@mergedColors==module)]
#   moduleInfo <- pepinfo[which(pepinfo$Mass_Tag_ID %in% moduleX),]
#   moduleCors <- pepcors[which(pepcors$Module==module),]
#   corname <- paste(fileprefix, ",_correlations.csv", sep="")
#   write.table(moduleCors, file=corname, sep="", row.names=F)
#   infoname <- paste(fileprefix, ",_peptide_info.csv", sep="")
#   write.table(moduleInfo, file=infoname, sep="", row.names=F)
#
#}
# WRITE OUT A TABLE WITH THE BELOW FUNCTION CALL :)#
# moduleData(peptideNetwork, pepcor, 1, masstagdb, "Module_1")

modulePhenotypeCorrelations

modulePhenotypeCorrelations

Description

Computes the relation between the modules and the phenotypes.

Usage

modulePhenotypeCorrelations(pnet, phenotypes)

Arguments

pnet The peptide net object
phenotypes The matrix of traits

Value

returns a matrix of correlations between modules and phenotypes.

Author(s)

David L Gibbs
Examples

data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=13)
N <- length(samples(net1))
phenotypes <- matrix(rnorm(10*N), nrow=60)
m <- modulePhenotypeCorrelations(net1, phenotypes)

# To plot the heatmap:
# moduleCors <- correlationWithPhenotypesHeatMap(net1, phenotypes, modules = 1:5,
# plot = NULL, title = "Module-trait relationships", textSize = 0.5)

Description

Order the matrix by upper diag in a greedy fashion

Usage

orderMatrixIndex(mat)

Arguments

mat A matrix

Value

returns a matrix in order of greatest in upper diagonal direction.

Author(s)

David L Gibbs

peptideConnectivityTest

Description

This function will compare the connectivity between peptides mapped to a given protein, against a randomly drawn, similarly sized, selection of peptides. The hypothesis is that peptides from a given protein should be more connected than random.

Usage

peptideConnectivityTest(pnet, pepInfo, pepCol, protCol, repsPerProt)
peptideCorrelationTest

Arguments

- **pnet**: The peptide net object
- **pepInfo**: The peptide information table, mapping peptides to proteins
- **pepCol**: The string identifying the column in the pepInfo table with peptide ID
- **protCol**: String identifying column in pepInfo with Protein ID.
- **repsPerProt**: Number of repetitions for the null

Value

Returns a list of the connected peptides and the random samples.

Author(s)

David L Gibbs

Examples

data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=12)
p <- peptideConnectivityTest(net1, masstagdb, "Mass_Tag_ID", "Reference", 200)

peptideCorrelationTest

Description

Take the data, and a mapping of peptides to proteins, and compute the mean correlation between peptides linked to a given protein. Compare a similar number of random correlations.

Usage

peptideCorrelationTest(dat, pepinfo, pepCol, protCol)

Arguments

- **dat**: The data with samples as rows and peptides as columns
- **pepinfo**: The mapping of peptides to proteins as a data frame
- **pepCol**: The column name of peptide info table containing peptide IDs
- **protCol**: The column name of pepinfo info table containing protein IDs

Value

return a t-test comparing protein correlations to random correlations.

Author(s)

David L Gibbs
Examples

```r
data(ProCoNA_Data)
net1 <- buildProconaNetwork(“peptide network”, peptideData, pow=12)
peptideCorrelationTest(peptideData, masstagdb, “Mass_Tag_ID”, “Reference”)
```

Description

Plots the dendrogram and module colors. See ?plotDendroAndColors

Usage

```r
plotNet(object)
```

Arguments

- `object` The procona network object.

Value

None.

Author(s)

David L. Gibbs

Examples

```r
data(ProCoNA_Data)
#net1 <- buildProconaNetwork(“peptide network”, peptideData)
plotNet(net1)
```

ppiPermTest

Description

Performs a permutation test for enrichment of PPI edges given a database. Peptides are selected from each module and mapped to potential protein parents in the mass tag database. We check if these proteins are found in the PPI network, and record any edges between them. This is compared to edges found using randomly selected proteins (taken from the mass tag database). A p-value is computed as the number of times the randomly sampled proteins incurred more edges than the observed proteins, divided by the number of iterations.

Usage

```r
ppiPermTest(pnet, pepdat, pepinfo, pepColName, pi_colName, pi_edges,
            threshold, iterations)
```
Arguments

- **pnet**: procona network object
- **pepdat**: the data matrix with peptides as columns.
- **pepinfo**: Maps peptides to proteins ... same format as in ppiTable
- **pepColName**: The column in pepinfo with peptide IDs... as in pepdat (the peptide data matrix)
- **pi_colName**: The column in pepinfo that maps peptides to unit found in pi_edges
- **pi_edges**: Must be two columns A-B ... sort out evidence levels (in vivo or in vitro) in advance
- **threshold**: Minimum peptide correlation with module eigenvector.
- **iterations**: Number of repetitions

Value

returns list of test results.

Author(s)

David L Gibbs

Examples

data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=12)
ppis <- data.frame(A=sample(masstagdb$Reference, 50), B=sample(masstagdb$Reference, 50))
ppiPermTest(net1, peptideData, masstagdb, "Mass_Tag_ID", "Reference", ppis, 0.33, 100)

printNet

Description

Prints general information about the network object.

Usage

printNet(object)

Arguments

- **object**: The procona network object.

Value

None.

Author(s)

David L Gibbs
ProCoNA-Data

## Not run:
data(ProCoNA_Data)
net1 <- buildProconaNetwork("peptide network", peptideData)
printNet(net1)

## End(Not run)

### Description

The mass tag database, which would be used to identify peptides, simply maps peptide IDs to peptide sequences and protein matches.

This simulated peptide dataset was generated using OpenMS's MSSimulator. A set of proteins was randomly sampled, and used to generate a likely set of observed peptides. Then data for a co-expression network was simulated with WGCNA's simulation function, and columns were named with simulated peptides.

The mass tag database, which would be used to identify peptides, simply maps peptide IDs to peptide sequences and protein matches. This represents a mapping to Entrez IDs.

The matrix annotates the biological samples according to ... phenotypic observations!

The two network objects are included to avoid rebuilding them in the other man page examples.

### proconaNet-class

**proconaNet S4 class**

#### Description

The main ProCoNA object - holder of data.

#### Objects from the Class

Objects can be created by calls of the form `new(proconaNet ...)`

#### Slots

- **networkName**: A name describing the data or experiment used to build the network. "character"
- **samples**: The names of samples used in building the network. "character"
- **adj**: The adjacency matrix. "matrix"
- **TOM**: The topological overlap matrix or TOM. "matrix"
- **peptides**: The names of peptides used in the network, also the node names. "character"
- **pepTree**: The network dendrogram. "hclust"
- **dynamicColors**: The module labels on each node (or peptide). "numeric"
- **MEs**: The module eigenvectors (or eigen-peptides). "data.frame"
- **mergedMEs**: The module eigenvectors after merging similar modules. "data.frame"
mergedColors: The module labels after merging similar modules. "numeric"
colorOrder: Modules are ordered by size, these labels correspond to that order. "character"
power: The soft thresholding power used in scaling the adjacency matrix. "numeric"
networkType: Either a signed or unsigned network regarding the method used in computing the initial correlations between nodes. "character"
permtest: The results of the permutation test on significance of topological overlap within modules. "matrix"
proconaVersion: Returns the version number of the software that built the object. "character"

Methods

show signature(x = "proconaNet"): Shows info about the network.
print signature(x = "proconaNet"): Prints info about the network.

Author(s)

David L Gibbs

---

**proconaVersionFun**

| proconaVersionFun | Procona Software Version |

**Description**

Returns the current version of the software.

**Usage**

proconaVersionFun()

**Value**

returns the version

**Author(s)**

David L Gibbs
runningStats

**Description**
Computing the running mean and variance

**Usage**
```r
runningStats(newMat, runningMean, Mk1, Sk1, k)
```

**Arguments**
- `newMat`: The matrix from resampled data
- `runningMean`: The running mean matrix
- `Mk1`: Matrix used in calculation of mean
- `Sk1`: Matrix used in calculation of sd
- `k`: Current resampling iteration

**Value**
returns the list of `runningMean`, `runningSD`, `Mk`, `Sk`

**Author(s)**
David L. Gibbs

subsetModCors

**Description**
subsets the module-phenotype correlation matrix which has funny rownames

**Usage**
```r
subsetModCors(modCors, modules)
```

**Arguments**
- `modCors`: The matrix of module-phenotype correlations
- `modules`: Which modules are desired.

**Author(s)**
David L. Gibbs
subsetPeptideData

Description
Given a matrix of peptide data, omit columns with excess missing data, specified by NAs.

Usage
subsetPeptideData(pepdat, numNAsAllowed = NULL, percentageNAsAllowed = 0.05)

Arguments
- pepdat: The peptide matrix, with peptides in columns and samples in rows.
- numNAsAllowed: The maximum count of missing values for each peptide (counts NAs).
- percentageNAsAllowed: The percentage of missing data allowed for each peptide over samples.

Value
Returns a matrix.

Author(s)
David L. Gibbs

Examples
data(ProCoNA_Data)
subsetPeptideData(peptideData, percentageNAsAllowed=0.2)

toPermTest

Description
Uses the procona network object, the data with peptides as columns, samples in rows. And the power that the net was built at the number of permutations to do... Modules are permuted and mean topological overlap is recorded, constructing the null. The number of random permutations with mean TO greater than observed provides the p-value.

Usage
toPermTest(pnet, numPermutates)

Arguments
- pnet: ProCoNA network object.
- numPermutates: The number of permutations to perform
utri

Value
returns the network obj with the perm test

Author(s)
David L. Gibbs

Examples
data(ProCoNA_Data)
#net1 <- buildProconaNetwork("peptide network", peptideData, pow=12)
toPermTest(net1, 100)

Description
The upper triangle of a matrix

Usage
utri(mat)

Arguments
mat A matrix

Value
Returns a vector

Author(s)
David L. Gibbs

Examples
m <- matrix(rnorm(9), nrow=3, ncol=3)
utri(m)
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