Package ‘ibh’

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Type Package
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Title Interaction Based Homogeneity for Evaluating Gene Lists
Depends simpIntLists
Suggests yeastCC, stats
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Description This package contains methods for calculating Interaction
Based Homogeneity to evaluate fitness of gene lists to an
interaction network which is useful for evaluation of
clustering results and gene list analysis. BioGRID interactions
are used in the calculation. The user can also provide their
own interactions.
License GPL (>= 2)
biocViews QualityControl, DataImport, GraphAndNetwork,
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NeedsCompilation no

R topics documented:

ibh-package ................................................................. 2
findEntry ................................................................. 3
ibh ................................................................. 4
ibhBioGRID ................................................................. 5
ibhClusterEval ............................................................... 6
ibhClusterEvalBioGRID .................................................. 6
ibhForMultipleGeneLists ................................................ 7
ibhForMultipleGeneListsBioGRID ...................................... 8
readDirectedInteractionsFromCsv ................................... 9
readUndirectedInteractionsFromCsv .................................. 10

Index 12
Interaction Based Homogeneity

Description

This package contains methods for evaluating Interaction Based Homogeneity for lists of genes. Given a gene list of n genes, we first form an adjacency matrix A whose rows and columns are genes in the list where

\[ A_{ij} = 1 \]

if genes i and j have an interaction in the network and

\[ A_{ij} = 0 \]

otherwise. The Interaction Based Homogeneity for a gene list

\[ L = \{g_1, g_2, ..., g_n\} \]

of size n is then calculated as:

\[
\text{InteractionBasedHomogeneity}(L) = \frac{\sum_{i=1}^{n} \sum_{j=1}^{n} A_{ij}}{n^2}
\]

Details

- Package: ibh
- Type: Package
- Version: 1.0.0
- Date: 2011-01-19
- License: GPL (version 2 or newer)
- LazyLoad: yes

The user can provide his own interaction list or can use predefined gene lists which are created based on the BioGRID Interactions. Both gene lists and result of clustering methods such as kmeans or hclust can be used as inputs. Entrez identifiers, unique ids (systematic names) or official names can be used as gene/protein identifiers.

Author(s)

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References


Examples

```r
require(simpIntLists)
```
findEntry

Find the index of an entry in an interaction list

Description
Find the index of an entry in an interaction list, used mostly for internal purposes

Usage
findEntry(interactionList, name)

Arguments
interactionList
  list of interactions

name
  name to be searched in the interaction list

Value
an integer that is the index of name in the interaction list
Examples

```r
require(simpIntLists)
data(ArabidopsisBioGRIDInteractionEntrezId)
findEntry(ArabidopsisBioGRIDInteractionEntrezId, 832179)
```

```r
ibh(interactionList, geneList)
```

Arguments

- `interactionList` : List containing the interactions. For each gene/protein, there is an entry in the list with "name" containing name of the gen/protein and "interactors" containing the list of genes/proteins interacting with it.
- `geneList` : List of genes/proteins for which interaction based homogeneity is evaluated.

Value

Interaction based homogeneity value as float

Author(s)

Kircicegi Korkmaz

See Also

`ibhForMultipleGeneLists`

Examples

```r
require(simpIntLists)
data(ArabidopsisBioGRIDInteractionEntrezId)
geneList <- list(839226, 817241, 824340, 832179, 818561, 831145, 838782, 826404);
ibh(ArabidopsisBioGRIDInteractionEntrezId, geneList);
```
ibhBioGRID  Calculate interaction based homogeneity for a gene list according to the BioGRID Interactions

Description
This function calculated interactios based homogeneity for a gene list according to the BioGRID Interactions for seven organisms: Arabidopsis thaliana(arabidopsis), Caenerhabditis elegans(c.elegans), Drosophila melanogaster (fruitFly), Homo sapiens (human), Mus musculus (mouse), Saccharomyces cerevisiae (yeast), Schizosaccharomyces pombe (s.pombe). Unique ids(systematic names), official names or Entrez ids can be used as identifier type.

Usage
ibhBioGRID(geneList, organism, idType = “EntrezId”)

Arguments
geneList list of genes/proteins for which interaction based homogeneity is evaluated
idType Type of identifier used. Can be one of ‘EntrezId’, ‘Official’ and ‘UniqueId’

Value
Float representing interaction based homogeneity for each list

References

See Also
ibh,ibhForMultipleGeneListsBioGRID

Examples
require(simpIntLists)
geneList <- list(839226,817241, 824340, 832179, 818561, 831145, 838782, 826404);
ibhBioGRID(geneList, organism="arabidopsis", idType = "EntrezId");
ibhBioGRID(geneList, organism="yeast", idType = "UniqueId");
ibhClusterEval  
Evaluate clustering with interaction based homogeneity

Description

This function calculated interaction based homogeneity for a clustering result.

Usage

ibhClusterEval(cluster, allGenesList, interactionList)

Arguments

cluster  
result of clustering

allGenesList  
list of genes in the same order of clustering object

interactionList  
list containing the interactions. For each gene/protein, the is an entry in the list 
with "name" containing name of the gene/protein and "interactors" containing the 
list of genes/proteins interacting with it.

Value

A vector of floats representing interaction based homogeneity for each cluster

Examples

require(yeastCC)
require(stats)
data(yeastCC)
require(simpIntLists)
data(YeastBioGRIDInteractionUniqueId)

subset <- exprs(yeastCC)[1:50,]
d <- dist(subset, method="euclidean")
k <- kmeans(d, 3);
ibhClusterEval(k$cluster, rownames(subset),
YeastBioGRIDInteractionUniqueId)

ibhClusterEvalBioGRID  
Evaluate clustering with interaction based homogeneity using BioGRID Interactions

Description

This function calculated interaction based homogeneity for a clustering result to the BioGRID Inter-
actions for seven organisms: Arabidopsis thaliana (arabidopsis), Caenhabditis elegans (c.elegans),
Drosophila melanogaster (fruitFly), Homo sapiens (human), Mus musculus (mouse), Saccharomyces
cerevisae (yeast), Schizosaccharomyces pombe (s.pombe). Unique ids (systematic names), official 
names or Entrez ids can be used as identifier type.
ibhForMultipleGeneLists

**Usage**

```r
ibhClusterEvalBioGRID(cluster, allGenesList, organism, idType = "EntrezId")
```

**Arguments**

- `cluster`: result of clustering
- `allGenesList`: list of genes in the same order of clustering object
- `organism`: organism name, can be one of 'arabidopsis', 'c.elegans', 'fruitFly', 'human', 'mouse', 'yeast', 's.pombe'.
- `idType`: type of identifier, can be one of 'EntrezId', 'Official' and 'UniqueId'.

**Value**

A vector of floats representing interaction based homogeneity for each cluster.

**References**


**Examples**

```r
require(yeastCC)
require(stats)
require(simpIntLists)
data(yeastCC)
subset <- exprs(yeastCC)[1:50,]
d <- dist(subset, method="euclidean")
k <- kmeans(d, 3);
ibhClusterEvalBioGRID(k$cluster, rownames(subset), organism="yeast", idType="UniqueId")
```

---

**ibhForMultipleGeneLists**

*Calculate interaction based homogeneity for multiple gene lists according to the interaction list*

**Description**

This function calculated interactions based homogeneity for multiple gene lists according to the interaction list

**Usage**

```r
ibhForMultipleGeneLists(interactionList, listofGeneList)
```
Arguments

interactionList
List containing the interactions. For each gene/protein, there is an entry in the list with "name" containing name of the gene/protein and "interactors" containing the list of genes/proteins interacting with it.

listofGeneList
List of list of genes/proteins for which interaction based homogeneity is evaluated.

Value
A vector of floats representing interaction based homogeneity for each list

Author(s)
Kircicegi Korkmaz

See Also
ibh

Examples

```r
require(simpIntLists)
data(ArabidopsisBioGRIDInteractionEntrezId)
listofGeneList <- list(list(839226, 817241, 824340, 832179, 818561, 831145, 838782, 826404),
                          list(832018, 839226, 839226, 838824));
ibhForMultipleGeneListsBioGRID(ArabidopsisBioGRIDInteractionEntrezId, listofGeneList)
```

ibhForMultipleGeneListsBioGRID

*Calculate interaction based homogeneity for multiple gene lists according to the BioGRID Interactions*

Description

This function calculates interaction based homogeneity for multiple gene lists according to the BioGRID Interactions for seven organisms: Arabidopsis thaliana (arabidopsis), Caenorhabditis elegans (c.elegans), Drosophila melanogaster (fruitFly), Homo sapiens (human), Mus musculus (mouse), Saccharomyces cerevisiae (yeast), Schizosaccharomyces pombe (s.pombe). Unique ids (systematic names), official names or Entrez ids can be used as identifier type.

Usage

```r
ibhForMultipleGeneListsBioGRID(listofGeneList, organism, idType = "EntrezId")
```
Arguments

listofGeneList List of list of genes/proteins for which interaction based homogeneity is evaluated.


idType Type of identifier. Can be one of ‘EntrezId’, ‘Official’ and ‘UniqueId’.

Value

A vector of floats representing interaction based homogeneity for each list

References


See Also

ibh

Examples

require(simpIntLists)
listofGeneList <- list(list(839226, 817241, 824340, 832179, 818561, 831145, 838782, 826404),
list(832018, 839226, 839226, 838824));
ibhForMultipleGeneListsBioGRID(listofGeneList,
organism = "arabidopsis", idType = "EntrezId");
ibhForMultipleGeneListsBioGRID(listofGeneList,
organism = "yeast", idType = "UniqueId");
readUndirectedInteractionsFromCsv

Arguments

fileName  name of the CSV file containing te interactions
sepValue  the same as "sep" in read.csv function, it is the value of the field separator character.
headerValue  whether the CSV file has a header or not, TRUE if the file has a header row, FALSE otherwise

Value

A list containing the interactions. For each gene/protein, there is an entry in the list with "name" containing name of the gen/protein and "interactors" containing the list of genes/proteins interacting with it.

Author(s)

Kircicegi Korkmaz

Examples

```r
## interactionList <- readDirectedInteractionsFromCsv("Arabidopsis_BioGRID-1.72.entrezid.csv"," ", FALSE);
```

readUndirectedInteractionsFromCsv

Read undirected interactions from csv and create the interaction list

Description

This function reads the undirected interactions from a csv file and creates the interaction list. The csv file must contain two names: first gene/protein name, second the interactor.

Usage

```
readUndirectedInteractionsFromCsv(fileName, sepValue, headerValue)
```

Arguments

fileName  name of the CSV file containing the interactions
sepValue  the same as "sep" in read.csv function, it is the value of the field separator character.
headerValue  whether the CSV file has a header or not, TRUE if the file has a header row, FALSE otherwise

Value

A list containing the interactions. For each gene/protein, there is an entry in the list with "name" containing name of the gene/protein and "interactors" containing the list of genes/proteins interacting with it.
readUndirectedInteractionsFromCsv

Author(s)
Kircicegi Korkmaz

Examples
```r
##-interactionList <- readUndirectedInteractionsFromCsv("Arabidopsis_BioGRID-3.1.72.entrezid.csv", " ", FALSE);
```
Index

*Topic file
  findEntry, 3
  ibh, 4
  ibhBioGRID, 5
  ibhClusterEval, 6
  ibhClusterEvalBioGRID, 6
  ibhForMultipleGeneLists, 7
  ibhForMultipleGeneListsBioGRID, 8
  readDirectedInteractionsFromCsv, 9
  readUndirectedInteractionsFromCsv, 10

*Topic package
  ibh-package, 2

findEntry, 3
  ibh, 4, 5, 8, 9
  ibh-package, 2
  ibhBioGRID, 5
  ibhClusterEval, 6
  ibhClusterEvalBioGRID, 6
  ibhForMultipleGeneLists, 4, 7
  ibhForMultipleGeneListsBioGRID, 5, 8

  readDirectedInteractionsFromCsv, 9
  readUndirectedInteractionsFromCsv, 10