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,
   NetworkEnrichment
NeedsCompilation no

R topics documented:

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**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

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

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)
```

---

**ibh**

*Calculate interaction based homogeneity for the given gene list according to the interaction list*

---

**Description**

This function calculates interaction based homogeneity of the given gene list according to the interaction list.

**Usage**

```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 cerevisae (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
organism Organism name. Can be one of 'arabidopsis', 'c.elegans', 'fruitFly', 'human', 'mouse', 'yeast', 's.pombe'.
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");
geneList <- list("YJR151C", "YBL032W", "YAL040C", "YBL072C", "YCL050C", "YCR009C");
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 gen/protein and “interactors” containing the
list of genes/proteins interacting with it.

Value

A vector of floats representing interaction based homogeneity for each cluste

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), Caenerhabditis 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.
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
```
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
```
ibhForMultipleGeneLists(interactionList, listofGeneList)
```
Arguments

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.

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

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

listofGeneList  List of list of genes/proteins for which interaction based homogeneity is evaluated.
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 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");
```

readDirectedInteractionsFromCsv

Read directed interactions from csv and create the interaction list

Description

This function reads the directed 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

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

**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.

**Author(s)**
Kircicegi Korkmaz

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

---

**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);
```
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