Package 'ibh'

April 24, 2024

Type Package

Version 1.51.0

Date 2012-04-27

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

git_url https://git.bioconductor.org/packages/ibh

git_branch devel

git_last_commit 5219e94

git_last_commit_date 2023-10-24

Repository Bioconductor 3.19

Date/Publication 2024-04-24

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`ibh-package` *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:

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

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

Stark C, Breitkreutz BJ, Reguly T, Boucher L, Breitkreutz A, Tyers M. *Biogrid: A General Repository for Interaction Datasets.* Nucleic Acids Res. Jan1; 34:D535-9

Examples

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

require(simpIntLists)
listofGeneList <- list(list(839226,817241, 824340, 832179, 818561, 831145, 838782, 826404),
list( 832018,
839226, 839226, 838824));
ibhForMultipleGeneListsBioGRID(listofGeneList,
 organism="arabidopsis",
 idType = "EntrezId");
listofGeneList <- list(list("YJR151C", "YBL032W",   "YAL040C",   "YBL072C",   "YCL050C",
   "YCR009C"),
list("YDR063W", "YDR074W", "YDR080W", "YDR247W", "YGR183C", "YHL033C"),
list("YOL068C" , "YOL015W" ,  "YOL009C" ,  "YOL004W" ,  "YOR065W"  ));
ibhForMultipleGeneListsBioGRID(listofGeneList, organism="yeast",
idType = "UniqueId");


require(yeastCC)
require(stats)
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")
```

`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

```
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

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

Arguments

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.
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

```
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

Stark C, Breitkreutz BJ, Reguly T, Boucher L, Breitkreutz A, Tyers M. *Biogrid: A General Repository for Interaction Datasets.* Nucleic Acids Res. Jan1; 34:D535-9

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 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

```
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 cluste

References

Stark C, Breitkreutz BJ, Reguly T, Boucher L, Breitkreutz A, Tyers M. *Biogrid: A General Repository for Interaction Datasets.* Nucleic Acids Res. Jan1; 34:D535-9

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 interactios 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 gen/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)
```

ibhForMultipleGeneListsBioGRID

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

Description

This function calculated interactios based homogeneity for multiple gene lists 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

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

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

Stark C, Breitkreutz BJ, Reguly T, Boucher L, Breitkreutz A, Tyers M. *Biogrid: A General Repository for Interaction Datasets.* Nucleic Acids Res. Jan1; 34:D535-9

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");
listofGeneList <- list(list("YJR151C", "YBL032W",   "YAL040C",   "YBL072C",
```

```
"YCL050C",
"YCR009C"), list("YDR063W", "YDR074W", "YDR080W", "YDR247W",
"YGR183C", "YHL033C"), list("YOL068C" , "YOL015W" ,
"YOL009C" , "YOL004W" , "YOR065W"  ));
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)
```

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, 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.

Author(s)

Kircicegi Korkmaz

Examples

```
##-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 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, 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.

Author(s)

Kircicegi Korkmaz

Examples

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

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