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

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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
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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

```
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
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, 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
require(simpIntLists)
data(ArabidopsisBioGRIDInteractionEntrezId)
geneList <- list(839226, 817241, 824340, 832179, 818561, 831145, 838782, 826404);
ibh(ArabidopsisBioGRIDInteractionEntrezId, geneList);
ibhBioGRID

ibhBioGRID  Calculate interaction based homogeneity for a gene list according to the BioGRID Interactions

Description

This function calculated interactions based homogeneity for a gene list 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

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 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), 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.
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)
ibhForMultipleGeneListsBioGRID

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

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

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");
listOfGeneList <- list(list("YJR151C", "YBL032W", "YAL040C", "YBL072C", "YCL050C", "YCR009C"),
list("YDR063W", "YDR074W", "YDR088W", "YDR247W", "YGR183C", "YHL033C"),
list("YOL068C", "YOL015W", "YOL009C", "YOL004W", "YOR065W" ));
ibhForMultipleGeneListsBioGRID(listOfGeneList,
organism="yeast", idType = "UniqueId");

readDirectedInteractionsFromCsv(fileName, sepValue, headerValue)

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)`
Author(s)
Kircicegi Korkmaz

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