

# Package ‘ibh’

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**Type** Package

**Version** 1.52.0

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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

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## Contents

|                       |   |
|-----------------------|---|
| ibh-package . . . . . | 2 |
| findEntry . . . . .   | 3 |
| ibh . . . . .         | 4 |
| ibhBioGRID . . . . .  | 5 |

|   |    |
|---|----|
| ibhClusterEval . . . . .                    | 6  |
| ibhClusterEvalBioGRID . . . . .             | 7  |
| ibhForMultipleGeneLists . . . . .           | 8  |
| ibhForMultipleGeneListsBioGRID . . . . .    | 9  |
| readDirectedInteractionsFromCsv . . . . .   | 10 |
| readUndirectedInteractionsFromCsv . . . . . | 11 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>12</b> |
|--------------|-----------|

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|             |                                      |
|-------------|--------------------------------------|
| ibh-package | <i>Interaction Based Homogeneity</i> |
|-------------|--------------------------------------|

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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

$$L = \{g_1, g_2, \dots, g_n\}$$

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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Maintainer: Kircicegi Korkmaz <e102771@ceng.metu.edu.tr>

**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 | <i>Calculate interaction based homogeneity for the given gene list according to the interaction list</i> |
|-----|--|

---

**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 | <i>Calculate interaction based homogeneity for a gene list according to the BioGRID Interactions</i> |
|------------|--|

---

**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                                |
| 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, 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. |

**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 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

```
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

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 interaction 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, 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));
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, 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**

```
##-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**

|                          |  |
|--------------------------|--|
| <code>fileName</code>    | name of the CSV file containing te interactions  |
| <code>sepValue</code>    | the same as "sep" in read.csv function,it is the value of the field separator character.     |
| <code>headerValue</code> | 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**

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

# Index

## \* file

- findEntry, 3
- ibh, 4
- ibhBioGRID, 5
- ibhClusterEval, 6
- ibhClusterEvalBioGRID, 7
- ibhForMultipleGeneLists, 8
- ibhForMultipleGeneListsBioGRID, 9
- readDirectedInteractionsFromCsv,  
10
- readUndirectedInteractionsFromCsv,  
11

## \* package

- ibh-package, 2

findEntry, 3

ibh, 4, 5, 8, 9

ibh-package, 2

ibhBioGRID, 5

ibhClusterEval, 6

ibhClusterEvalBioGRID, 7

ibhForMultipleGeneLists, 5, 8

ibhForMultipleGeneListsBioGRID, 5, 9

readDirectedInteractionsFromCsv, 10

readUndirectedInteractionsFromCsv, 11