Package ‘NFP’

October 14, 2019

Type Package

Title Network Fingerprint Framework in R

Version 0.99.3

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Description An implementation of the network fingerprint framework that introduced in paper "Network fingerprint: a knowledge-based characterization of biomedical networks" (Cui, 2015) <doi:10.1038/srep13286>. This method worked by making systematic comparisons to a set of well-studied "basic networks", measuring both the functional and topological similarity. A biological could be characterized as a spectrum-like vector consisting of similarities to basic networks. It shows great potential in biological network study.

Depends R (>= 3.2.0), graph

Imports igraph, stringr, magrittr, plyr, ggplot2, apcluster, KEGGgraph, dplyr, tidyr, methods

Suggests knitr, testthat, graphite, NFPdata, rmarkdown

Additional_repositories https://yiluheihei.github.io/datarepo/

VignetteBuilder knitr

License GPL (>= 2)

LazyData yes

NeedsCompilation no

RoxygenNote 6.1.1

URL https://github.com/yiluheihei/NFP

BugReports https://github.com/yiluheihei/NFP/issues

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Repository CRAN

Date/Publication 2019-10-14 10:10:08 UTC
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- calc_sim_score ........................................ 2

Description

This function was used to calculate the similarity scores between a network and the reference network.

Usage

calc_sim_score(net, NFPnet, nperm = 100, ...)

Arguments

- net, a graphNel object to represent the query biological networks, for more details see graphNEL
- NFPnet, a NFPRefnet object, one or more kegg pathway map, or customized networks. For more details see NFPRefnet-class.
- nperm, number of random networks for similarity score standardization
- ..., arguments passed to apcluster

Value

a similarity scoring vector, length is the same as the number of networks
See Also

NFPRefnet-class.

cluster_info-methods

Extract the cluster information of NFP.

Description

This function extract the cluster information of network fingerprint.

Usage

cluster_info(object)

## S4 method for signature 'NFP'
cluster_info(object)

Arguments

object NFP object

Value

a list which contains the number, the examplar and some other cluster properties.

See Also

NFP

group-methods

Group information of NFPRefnet

Description

This function extract the group information NFP basic networks.

Usage

group(object)

## S4 method for signature 'NFPRefnet'
group(object)

Arguments

object, NFPRefnet class
install_data_package

Value

a list which contains the group number and names of basic networks, as well as the size of each group

See Also

NFPRefnet-class

install_data_package  
Install NFP data package NFPdata

Description

Downloads and Install the NFPdata Package to use with the NFP package

Usage

install_data_package(type = "ONL", loc = NULL)

Arguments

type  
A string with value "ONL" or "LOCAL"

loc  
A string that contains the file location.

Details

The NFPdata Package contains data that from kegg gene similarity based on gene ontology and is approximately a 16.4 MB download.

Examples

## Not run:
# Online install
install_data_package()

## End(Not run)
**kegg_refnet**

Human KEGG signal pathway maps

**Description**
A dataset containing the human signal pathway maps of KEGG

**Format**
A NFPRefnet object, more details see NFPRefnet-class

**See Also**
NFPRefnet-class

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**load_KEGG_refnet**

Load the reference molecular networks

**Description**
This function generates the well-studied "basic networks".

**Usage**
load_KEGG_refnet(organism = "hsa")

**Arguments**
organism, a character indicating to which organism's pathway map was taken as the basic network. e.g. hsa.

**Details**
KEGG pathway is a well-studied and the most widely used biological networks database. This function helps users to load KEGG pathway maps as the basic networks. Apparently, users can also load their customized biological networks as the basic networks by creating a new NFPRefnet object.

**Value**
a NFPRefnet object

**See Also**
NFPRefnet-class
Description

This function extract the basic networks of NFPRefnet class.

Usage

net(object)

## S4 method for signature 'NFPRefnet'
net(object)

Arguments

object, NFPRefnet class

Value

a igraph list of all basic networks

See Also

NFPRefnet-class
NFP-class

Description

An S4 object for storing network fingerprint similarity score information.

Slots

raw_score, a numeric vector, network fingerprint based on reference networks before standardization.

randomized_score, a data frame, the permulated similarity score.

standardized_score, a numeric vector, the final standardized network fingerprint.

cluster, an APResult list, more details see package *apcluster*, each element provides a cluster information of a biological network based on one reference networks. #’@section method:

• perm_score, signature(object = "NFP"): extract the randomized similarity score
• cluster_info, signature(object = "NFP"): extract the cluster information
• sub_NFP, signature(object = "NFP"): subset of NFP object
• plot, signature(object,type = "character",p_size = "numeric",l_size = 'numeric'): plot NFP results
• show, signature(object = "NFP"): display methods for S4 classes NFP, see also show

See Also

show-methods, plot-methods, perm_score-methods, cluster_info-methods, sub_NFP-methods

NFPRefnet-class

Description

An S4 object for storing NFP reference network information.

Slots

Refnet, object of graphNEL list represents the basic networks, and each elements contains a group of basic networks.

group, a character vector whose length is the same with Refnet, the group names of basic networks.

name, names of the basic networks, with the same data structure with Refnet.

organism, character, indicating the activation organism of basic networks. #’@section method:

• net, signature(object = "NFPRefnet"): extract the basic networks
• group, signature(object = "NFPRefnet"): extract group information
perm_score-methods

- subnet, signature(object = "NFPRefnet"): subset basic networks, e.g. a group of a networks or same networks of a given group
- refnet_name, signature(object = "NFPRefnet"): the names of basic networks
- show, signature(object = "NFPRefnet"): display methods for S4 classes NFPRefnet, see also show

See Also

  show-methods, net-methods, refnet_name-methods, group-methods, subnet-methods

perm_score-methods  Extract the randomized similarity score

Description

This function extract the randomized similarity score for standardization.

Usage

perm_score(object)

## S4 method for signature 'NFP'
perm_score(object)

Arguments

  object,       NFP class

Value

  a data frame, each col (elements) represents once permutation similarity score, each row indicate a reference basic network.

See Also

  NFP
plot_NFP-methods

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**plot_NFP-methods**

**Plot NFP results**

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**Description**

Function for visualization NFP results.

**Usage**

```r
plot_NFP(object, type = c("matchstick", "line", "point"), p_size = 2, l_size = 0.5)
```

## S4 method for signature 'NFP'

```r
plot_NFP(object, type = c("matchstick", "line", "point"), p_size = 2, l_size = 0.5)
```

**Arguments**

- `object`, NFP class
- `type`, types of the visualization of NFP object, point or line. Default is point.
- `p_size`, point size of plot, default is 2.
- `l_size`, line size of plot, default is 0.5.

**See Also**

- `NFP-class`

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**plot_NFPlist**

**Plot multiple NFPs.**

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**Description**

Function for visualization multiple NFPs.

**Usage**

```r
plot_NFPlist(object, l_size = 0.5)
```

**Arguments**

- `object`, NFP class list.
- `l_size`, line size of plot, default is 0.5.

**See Also**

- `NFP-class`
refnet_name-methods  Names of basic networks

Description

This function extract names of NFP basic networks.

Usage

refnet_name(object)

## S4 method for signature 'NFPRefnet'
refnet_name(object)

Arguments

object,  NFPRefnet class

Value

a list

See Also

NFPRefnet-class

show,NFP-method  The show generic function

Description

Show a short summary for NFP object, see show.

Usage

## S4 method for signature 'NFP'
show(object)

Arguments

object,  NFP object
**show,NFPRefnet-method**  
*Show an Object*

### Description
show method short for NFPRefnet object, see show

### Usage
```r
## S4 method for signature 'NFPRefnet'
show(object)
```

### Arguments
- `object`, NFPRefnet class

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**subnet-methods**  
*Subset the basic networks*

### Description
Extract or Replace parts of the NFP basic networks.

### Usage
```r
subnet(object, group_name, index = NULL)
```

### Arguments
- `object`, NFPRefnet class.
- `group_name`, character, indicating the groups to subset.
- `index`, numeric, character or NA, indices specifying elements to extract. This parameter only works while `group_name` is a length-one character. Default is `NULL`, indicating extract all the networks of a group. See details for more information.

### Details
This function help users to extract the specific networks for customized analysis, which could be of entire group networks or some part of a specific group networks.subsequent analysis.

Note, the index argument is only worked while one argument is consideration, which means `group_name` is a length-one character. And default is `NULL`, indicating extract the entire group basic networks.
See Also

`NFPRefnet-class`

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**Description**

This function extract the subsets of NFP-class.

**Usage**

```r
sub_NFP(object, i)
```

```r
## S4 method for signature 'NFP'
sub_NFP(object, i)
```

**Arguments**

- `object`, NFP class
- `i`, numeric or character indicating the index or the names of the reference network

**Value**

An similar NFP object contain just the selected elements.

**See Also**

`NFP-class`
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