

Package ‘NFP’

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Type Package

Title Network Fingerprint Framework in R

Version 0.99.4

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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

LazyDataCompression xz

NeedsCompilation no

RoxygenNote 7.1.1

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

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

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calc_sim_score	<i>Calculating the similarity scores</i>
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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 exemplar 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

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	<i>Human KEGG signal pathway maps</i>
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Description

A dataset containing the human signal pathway maps of KEGG

Format

A `NFPRefnet` object, more details see [NFPRefnet-class](#)

See Also

[NFPRefnet-class](#)

load_KEGG_refnet	<i>Load the the reference molecular networks</i>
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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 help users to load kegg pathway maps as the basic networks.

Appanrently, 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](#)

net-methods

Basic networks of 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

The NFP package

Description

This package implementation the applications of network finger print method.

NFP-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

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

- subnet, signature(object = "NFPretnet"): subset basic networks, e.g. a group of a networks or same networks of a given group
- refnet_name, signature(object = "NFPretnet"): the names of basic networks
- show, signature(object = "NFPretnet"): display methods for S4 classes NFPretnet, 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 *Plot NFP results*

Description

Function for visualization NFP results.

Usage

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

```
## S4 method for signature 'NFP'  
plot_NFP(  
  object,  
  type = c("matchstick", "line", "point"),  
  p_size = 2,  
  l_size = 0.5  
)
```

Arguments

object,	NFP class
type,	types of the visaulization of <i>NFP</i> 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. #' @aliases plot_NFP plot_NFP-methods

See Also

[NFP-class](#)

plot_NFPlist *Plot multiple NFPs.*

Description

Function for visualization multiple NFPs.

Usage

```
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	<i>The show generic function</i>
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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	<i>Show an Object</i>
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Description

show method short for NFPRefnet object, see [show](#)

Usage

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

Arguments

object, NFPRefnet class

subnet-methods *Subset the basic networks*

Description

Extract or Replace parts of the NFP basic networks.

Usage

```
subnet(object, group_name, index = NULL)
```

```
## S4 method for signature 'NFPRefnet'
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](#)

sub_NFP-methods *subset of NFP object*

Description

This function extract the subsets of NFP-class.

Usage

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

```
## 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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