Package 'OmnipathR'

August 11, 2019

Type Package

Title Import Omnipath network

Version 0.2.0

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Description Import data from https://www.omnipathdb.org webservice. It also includes functions to transform and print this data.

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URL https://github.com/saezlab/OmnipathR

Encoding UTF-8

LazyData true

Depends igraph, graphics, methods

Imports dplyr, tidyr

Suggests dnet, gprofiler2, BiocStyle

RoxygenNote 6.1.1

R topics documented:

`.get_annotation_databases` *Get the different annotation databases integrated in Omnipath*

Description

get the names of the databases from http://omnipath.org/annotation

Usage

```
.get_annotation_databases()
```

Value

character vector with the names of the annotation databases

See Also

import_Omnipath_annotations

Examples

```
.get_annotation_databases()
```

.get_complexes_databases *Get the different complexes databases integrated in Omnipath*

Description

get the names of the databases from http://omnipath.org/complexes

Usage

```
.get_complexes_databases()
```

Value

character vector with the names of the databases

See Also

import_Omnipath_complexes

Examples

```
.get_complexes_databases()
```

.get_interaction_databases *Get the different interaction databases*

Description

get the names of the databases from http://omnipath.org/interactions

Usage

```
.get_interaction_databases()
```

Value

character vector with the names of the interaction databases

See Also

import_AllInteractions,import_Omnipath_Interactions,import_PathwayExtra_Interactions,import_KinaseE

Examples

```
.get_interaction_databases()
```

.get_intercell_categories *Get the different intercell categories described in Omnipath*

Description

get the names of the categories from http://omnipath.org/intercell

Usage

```
.get_intercell_categories()
```

Value

character vector with the different intercell categories

See Also

import_Omnipath_intercell

Examples

```
.get_intercell_categories()
```

.get_ptms_databases *Get Post-translational modification (PTMs) databases*

Description

get the names of the different databases available for ptms databases http://omnipath.org/ptms

Usage

```
.get_ptms_databases()
```

Value

character vector with the names of the PTMs databases

See Also

import_Omnipath_PTMS

Examples

```
.get_ptms_databases()
```

get_complex_genes *Get all the molecular complexes for a given gene(s)*

Description

This function returns all the molecular complexes where an input set of genes participate. User can choose to retrieve every complex where any of the input genes participate or just retrieve these complexes where all the genes in input set participate together.

Usage

```
get_complex_genes(complexes = import_Omnipath_complexes(),
  select_genes = query_genes, total_match = FALSE)
```

Arguments

complexes	complexes data frame (obtained using import_Omnipath_complexes)
select_genes	vector containing the genes for whom complexes will be retrieved (hgnc format).
total_match	[default=FALSE] logical indicating if the user wants to get all the complexes where any of the input genes participate (FALSE) or to get only the complexes where all the input genes participate together (TRUE)

Value

data.frame of complexes

See Also

import_Omnipath_complexes)

Examples

```
complexes = import_Omnipath_complexes(filter_databases=c("CORUM", "hu.MAP"))
query_genes = c("LMNA","BANF1")
complexes_query_genes = get_complex_genes(complexes,query_genes)
```

get_signed_ptms *get signs for ptms interactions*

Description

ptms data does not contain sign (activation/inhibition), we generate this information based on the interaction network

Usage

```
get_signed_ptms(ptms = import_Omnipath_PTMS(),
  interactions = import_Omnipath_Interactions())
```

Arguments

ptms	ptms data frame generated by import_Omnipath_PTMS
interactions	interaction data frame generated by import_Omnipath_Interactions

Value

data.frame of ptms with is_inhibition and is_stimulation columns

See Also

import_Omnipath_PTMS import_Omnipath_Interactions

Examples

```
ptms = import_Omnipath_PTMS(filter_databases=c("PhosphoSite", "Signor"))
interactions = import_Omnipath_Interactions()
ptms = get_signed_ptms(ptms,interactions)
```

---

import_AllInteractions

Imports from Omnipath webservice all the available interactions from the different datasets

---

Description

Imports the dataset from: http://omnipathdb.org/interactions?datasets=omnipath,pathwayextra,kinaseextra,ligrecextra,tfregulons,mirnatarget&fields=sources,references&genesymbols=1, which contains all the different interactions available in the webserver:

Usage

```
import_AllInteractions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases(),
  select_organism = 9606)
```

Arguments

from_cache_file	path to an earlier data file
filter_databases	interactions not reported in these databases are removed. See .get_interaction_databases for more information.

select_organism
: Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse

Details

omnipath: the OmniPath data as defined in the paper, an arbitrary optimum between coverage and quality pathwayextra: activity flow interactions without literature reference kinaseextra: enzyme-substrate interactions without literature reference ligrecextra: ligand-receptor interactions without literature reference tfregulons: transcription factor (TF)-target interactions from DoRothEA mirnatarget: miRNA-mRNA and TF-miRNA interactions

Value

A dataframe containing all the datasets in the interactions query

See Also

.get_interaction_databases

Examples

```
interactions <- import_AllInteractions(filter_databases=c("HPRD","BioGRID"),
    select_organism = 9606)
```

---

import_KinaseExtra_Interactions

Imports from Omnipath webservice the interactions from kinaseextra dataset

---

Description

Imports the dataset from: http://omnipathdb.org/interactions?datasets=kinaseextra, which contains enzyme-substrate interactions without literature reference

Usage

```
import_KinaseExtra_Interactions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases(),
  select_organism = 9606)
```

Arguments

from_cache_file
: path to an earlier data file

filter_databases
: interactions not reported in these databases are removed. See .get_interaction_databases for more information.

`select_organism`
: Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse

Value

A dataframe containing enzyme-substrate interactions without literature reference

See Also

`.get_interaction_databases`, `import_AllInteractions`

Examples

```
interactions <- import_KinaseExtra_Interactions(filter_databases=c("PhosphoPoint","PhosphoSite"),
                select_organism = 9606)
```

---

import_LigrecExtra_Interactions

Imports from Omnipath webservice the interactions from ligrecextra dataset

---

Description

Imports the dataset from: http://omnipathdb.org/interactions?datasets=ligrecextra, which contains ligand-receptor interactions without literature reference

Usage

```
import_LigrecExtra_Interactions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases(),
  select_organism = 9606)
```

Arguments

`from_cache_file`
: path to an earlier data file

`filter_databases`
: interactions not reported in these databases are removed. See `.get_interaction_databases` for more information.

`select_organism`
: Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse

Value

A dataframe containing ligand-receptor interaction without literature reference

See Also

.get_interaction_databases, import_AllInteractions

Examples

```
interactions <- import_LigrecExtra_Interactions(filter_databases=c("HPRD","Guide2Pharma"),
        select_organism=9606)
```

---

import_miRNAtarget_Interactions

Imports from Omnipath webservice the interactions from miRNAtarget dataset

---

Description

Imports the dataset from: http://omnipathdb.org/interactions?datasets=mirnatarget, which contains miRNA-mRNA and TF-miRNA interactions

Usage

```
import_miRNAtarget_Interactions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases())
```

Arguments

from_cache_file	path to an earlier data file
filter_databases	interactions not reported in these databases are removed. See .get_interaction_databases for more information.

Value

A dataframe containing miRNA-mRNA and TF-miRNA interactions

See Also

.get_interaction_databases, import_AllInteractions

Examples

```
interactions <-
  import_miRNAtarget_Interactions(filter_databases=c("miRTarBase",
  "miRecords"))
```

`import_Omnipath_annotations` *Import Omnipath Annotations*

Description

imports the annotations stored in Omnipath database from http://omnipathdb.org/annotations

Usage

```
import_Omnipath_annotations(from_cache_file = NULL,
  select_genes = NULL, filter_databases = .get_annotation_databases())
```

Arguments

`from_cache_file`	path to an earlier data file
`select_genes`	vector containing the genes for whom annotations will be retrieved (hgnc format). It is also possible to donwload complexes annotations. To do so, write "COMPLEX:" right before the genesymbols of the genes integrating the complex. Check the vignette for examples.
`filter_databases`	annotations not reported in these databases are removed. See `.get_annotation_databases` for more information.

Value

A data.frame containing different gene/complex annotations

See Also

`.get_annotation_databases`

Examples

```
annotations = import_Omnipath_annotations(select_genes=c("TP53","LMNA"),
     filter_databases=c("HPA"))
```

import_Omnipath_complexes

Import Omnipath Complexes

Description

imports the complexes stored in Omnipath database from http://omnipathdb.org/complexes

Usage

```
import_Omnipath_complexes(from_cache_file = NULL,
  filter_databases = .get_complexes_databases())
```

Arguments

from_cache_file	path to an earlier data file
filter_databases	complexes not reported in these databases are removed. See .get_complexes_databases for more information.

Value

A dataframe containing information about complexes

See Also

.get_complexes_databases

Examples

```
complexes = import_Omnipath_complexes(filter_databases=c("CORUM", "hu.MAP"))
```

import_Omnipath_Interactions

Import Omnipath interaction database

Description

imports the database from http://omnipathdb.org/interactions, which contains only interactions with references. These interactions are the original ones from the first Omnipath version.

Usage

```
import_Omnipath_Interactions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases(),
  select_organism = 9606)
```

Arguments

from_cache_file
: path to an earlier data file

filter_databases
: interactions not reported in these databases are removed. See .get_interaction_databases for more information.

select_organism
: Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse

Value

A dataframe containing information about protein-protein interactions

See Also

.get_interaction_databases, import_AllInteractions

Examples

```
interactions = import_Omnipath_Interactions(filter_databases=c("SignaLink3"),
               select_organism = 9606)
```

---

import_Omnipath_intercell

Import Omnipath Intercell Data

Description

imports the intercell data stored in Omnipath database from http://omnipathdb.org/intercell. Intercell provides information on the roles in inter-cellular signaling. E.g. if a protein is a ligand, a receptor, an extracellular matrix (ECM) component, etc.

Usage

```
import_Omnipath_intercell(from_cache_file = NULL,
  select_categories = .get_intercell_categories())
```

Arguments

from_cache_file
: path to an earlier data file

select_categories
: vector containing the categories to be retrieved. All the genes belonging to that category will be returned. For furter information about the categories see .get_intercell_categories

Value

A dataframe cotaining information about roles in inter-cellular signaling.

See Also

.get_intercell_categories

Examples

```
intercell = import_Omnipath_intercell(select_categories=c("ecm"))
```

---

import_Omnipath_PTMS *Import Omnipath post-translational modifications (PTMs)*

Description

imports the PTMs database from http://omnipathdb.org/ptms

Usage

```
import_Omnipath_PTMS(from_cache_file = NULL,
  filter_databases = .get_ptms_databases(), select_organism = 9606)
```

Arguments

from_cache_file	path to an earlier data file
filter_databases	PTMs not reported in these databases are removed. See .get_ptms_databases for more information
select_organism	PTMs are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse

Value

A data frame containing the information about ptms

See Also

.get_ptms_databases,import_Omnipath_Interactions

Examples

```
ptms = import_Omnipath_PTMS(filter_databases=c("PhosphoSite", "Signor"),
       select_organism=9606)
```

`import_PathwayExtra_Interactions` *Imports from Omnipath webservice the interactions from Pathwayextra dataset*

Description

Imports the dataset from: http://omnipathdb.org/interactions?datasets=pathwayextra, which contains activity flow interactions without literature reference

Usage

```
import_PathwayExtra_Interactions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases(),
  select_organism = 9606)
```

Arguments

`from_cache_file`
: path to an earlier data file

`filter_databases`
: interactions not reported in these databases are removed. See `.get_interaction_databases` for more information.

`select_organism`
: Interactions are available for human, mouse and rat. Choose one of those: 9606 human (default), 10116 rat or 10090 Mouse

Value

A dataframe containing activity flow interactions between proteins without literature reference

See Also

`.get_interaction_databases`, `import_AllInteractions`

Examples

```
interactions <- import_PathwayExtra_Interactions(filter_databases=c("BioGRID","IntAct"),
                select_organism = 9606)
```

`import_TFregulons_Interactions` *Imports from Omnipath webservice the interactions from Dorothea dataset*

Description

Imports the dataset from: http://omnipathdb.org/interactions?datasets=tfregulons which contains transcription factor (TF)-target interactions from DoRothEA https://github.com/saezlab/DoRothEA

Usage

```
import_TFregulons_Interactions(from_cache_file = NULL,
  filter_databases = .get_interaction_databases(),
  select_organism = 9606)
```

Arguments

`from_cache_file`	path to an earlier data file
`filter_databases`	interactions not reported in these databases are removed. See `.get_interaction_databases` for more information.
`select_organism`	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse

Value

A dataframe containing TF-target interactions from DoRothEA

See Also

`.get_interaction_databases`, `import_AllInteractions`

Examples

```
interactions <- import_TFregulons_Interactions(filter_databases=c("tfact","ARACNe-GTEx"),
                select_organism=9606)
```

interaction_graph *Build Omnipath interaction graph*

Description

transforms the interactions data.frame to an igraph object

Usage

```
interaction_graph(interactions = interactions)
```

Arguments

interactions	data.frame created by import_Omnipath_Interactions, import_PathwayExtra_Interactions, import_KinaseExtra_Interactions, import_LigrecExtra_Interactions, import_TFregulons_Interactions, import_miRNAtarget_Interactions or import_AllInteractions

Value

An igraph object

See Also

import_Omnipath_Interactions, import_PathwayExtra_Interactions, import_KinaseExtra_Interactions, import_LigrecExtra_Interactions, import_TFregulons_Interactions, import_miRNAtarget_Interactions or import_AllInteractions

Examples

```
interactions = import_Omnipath_Interactions(filter_databases=c("SignaLink3"))
OPI_g = interaction_graph(interactions)
```

OmnipathR *The OmnipathR package*

Description

OmnipathR is an R package built to provide easy access to the data stored in the Omnipath webservice:

http://omnipathdb.org/

The webservice implements a very simple REST style API. This package make requests by the HTTP protocol to retreive the data. Hence, fast Internet access is required for a propser use of OmnipathR.

The package also provides some utility functions to filter, analyse and visualize the data.

Author(s)

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Examples

```
# Download post-translational modifications:
ptms = import_Omnipath_PTMS(filter_databases=c("PhosphoSite", "Signor"))

# Download protein-protein interactions
interactions = import_Omnipath_Interactions(filter_databases=c("SignaLink3"))

# Convert to igraph objects:
ptms_g = ptms_graph(ptms = ptms )
OPI_g = interaction_graph(interactions = interactions )

# Print some interactions:
print_interactions(head(ptms))

# interactions with references:
print_interactions(tail(ptms),writeRefs=TRUE)

# find interactions between kinase and substrate:
print_interactions(dplyr::filter(ptms,enzyme_genesymbol=="MAP2K1",
   substrate_genesymbol=="MAPK3"))

# find shortest paths on the directed network between proteins
printPath_es(shortest_paths(OPI_g,from = "TYRO3",to = "STAT3",
   output = 'epath')$epath[[1]],OPI_g)

# find all shortest paths between proteins
printPath_vs(all_shortest_paths(ptms_g,from = "SRC",to = "STAT1")$res,ptms_g)
```

---

printPath_es *print network paths given by edge sequence*

Description

prints the interactions in the path in a nice format

Usage

```
printPath_es(edgeSeq, G)
```

Arguments

edgeSeq	edge sequence
G	igraph object (from ptms or any interaction dataset)

See Also

printPath_vs

Examples

```
interactions = import_Omnipath_Interactions(filter_databases=c("SignaLink3"))
OPI_g = interaction_graph(interactions = interactions )
printPath_es(shortest_paths(OPI_g,from = "TYRO3",to = "STAT3", output = 'epath')$epath[[1]],OPI_g)
```

---

printPath_vs *print networks paths given by node sequence*

Description

prints the interactions in the path in a nice format

Usage

```
printPath_vs(nodeSeq, G)
```

Arguments

nodeSeq	node sequence
G	igraph object (from ptms or interactions)

See Also

printPath_es

Examples

```
interactions = import_Omnipath_Interactions(filter_databases=c("SignaLink3"))
OPI_g = interaction_graph(interactions = interactions )
printPath_vs(shortest_paths(OPI_g,from = "TYRO3",to = "STAT3")$vpath,OPI_g)

ptms = import_Omnipath_PTMS(filter_databases=c("PhosphoSite", "Signor"))
ptms_g = ptms_graph(ptms)
printPath_vs(all_shortest_paths(ptms_g,from = "SRC",to = "STAT1")$res,ptms_g)
```

print_interactions *print interactions*

Description

prints the interactions/ptms in a nice format

Usage

```
print_interactions(interDF, writeRefs = FALSE)
```

Arguments

interDF	data.frame with the interactions generated by any of the following functions: import_Omnipath_PTMS, import_Omnipath_Interactions, import_PathwayExtra_Interactions, import_KinaseExtra_Interactions, import_LigrecExtra_Interactions, import_TFregulons_Interactions, import_miRNAtarget_Interactions or import_AllInteractions
writeRefs	[FALSE] writes also the PubMed IDs if available

Examples

```
ptms = import_Omnipath_PTMS()
print_interactions(head(ptms))
print_interactions(tail(ptms),writeRefs=TRUE)
print_interactions(dplyr::filter(ptms,enzyme_genesymbol=="MAP2K1",
  substrate_genesymbol=="MAPK3"))
```

ptms_graph *Post-translational modifications (PTMs) graph*

Description

transforms the ptms interactions data.frame to igraph object

Usage

```
ptms_graph(ptms)
```

Arguments

ptms	data.frame created by import_Omnipath_PTMS

Value

An igraph object

See Also

import_Omnipath_PTMS

Examples

```
ptms = import_Omnipath_PTMS(filter_databases=c("PhosphoSite", "Signor"))
ptms_g = ptms_graph(ptms = ptms )
```

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