

Package ‘OmnipathR’

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Type Package

Title Import Omnipath network

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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>

biocViews GraphAndNetwork, Network, Pathways, Software,
ThirdPartyClient, DataImport, DataRepresentation

Encoding UTF-8

Depends igraph, graphics, methods, utils

Imports dplyr, rlang

Suggests tidy, dnet, gprofiler2, BiocStyle, testthat

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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_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,  
  total_match = FALSE  
)
```

Arguments

<code>complexes</code>	complexes data frame (obtained using import_Omnipath_complexes)
<code>select_genes</code>	vector containing the genes for whom complexes will be retrieved (hgnc format).
<code>total_match</code>	[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_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_Kinase](#)

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	<i>Get Post-translational modification (PTMs) databases</i>
--------------------	---

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_signed_ptms	<i>get signs for ptms interactions</i>
-----------------	--

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,ligreextra,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
ligreextra: ligand-receptor interactions without literature reference
tfregulons: transcription factor (TF)-target interactions from DoRothEA
mir-target: 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 ligreextra dataset

Description

Imports the dataset from: <http://omnipathdb.org/interactions?datasets=ligreextra>, 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 download 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 further information about the categories see [get_intercell_categories](#)

Value

A dataframe containing 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("DoRothEA_A",
    "ARACNe-GTex_DoRothEA"), 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 retrieve the data. Hence, fast Internet access is required for a proper use of OmnipathR.

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

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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	<i>print network paths given by edge sequence</i>
--------------	---

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)

Value

Interactions displayed in a nice format

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	<i>print networks paths given by node sequence</i>
--------------	--

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)

Value

Interactions displayed in a nice format

See Also[printPath_es](#)**Examples**

```
interactions = import_Omnipath_Interactions(filter_databases=c("SignalLink3"))
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

Value

Interactions displayed in a nice format

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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