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

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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

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_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_Kina

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,get_intercell_classes

Examples

```
get_intercell_categories()
```

---

get_intercell_classes *Get the different intercell main classes described in Omnipath*

Description

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

Usage

```
get_intercell_classes()
```

Value

character vector with the different intercell main classes

See Also

import_Omnipath_intercell,get_intercell_categories

Examples

```
get_intercell_classes()
```

---

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_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 = NULL,
  force_full_download = FALSE,
  ...
)
```

Arguments

from_cache_file	Path to an earlier data file
select_genes	Vector containing the genes or proteins for whom annotations will be retrieved (UniProt IDs or HGNC Gene Symbols or miRBase IDs). It is also possible to donwload annotations for protein complexes. To do so, write "COMPLEX:" right before the genesymbols of the genes integrating the complex. Check the vignette for examples.
filter_databases	Load the annotations only from these databases. See get_annotation_databases for possible values.
force_full_download	Force the download of the entire annotations dataset. This is disabled by default because the size of this data is around 1GB. We recommend to retrieve the annotations for a set of proteins or only from a few databases, depending on your interest.
...	Additional arguments.

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_subcellular"))
```

---

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(),
  select_classes = get_intercell_classes()
)
```

Arguments

`from_cache_file` path to an earlier data file

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

`select_classes` vector containing the main classes to be retrieved. All the genes belonging to those classes will be returned. For furter information about the main classes see get_intercell_classes

Value

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

See Also

get_intercell_categories

Examples

```
intercell = import_Omnipath_intercell()
```

`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,
  confidence_level = c("A", "B")
)
```

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

`confidence_level`
: Vector detailing the confidence levels of the interactions to be downloaded. In dorothea, every TF-target interaction has a confidence score ranging from A to E, being A the most reliable interactions. By default we take A and B level interactions (`c(A,B)`). It is to note that E interactions are not available in OmnipathR.

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 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.

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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)

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` *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)

Value

Interactions displayed in a nice format

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_Interactior 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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