

Package ‘OmnipathR’

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Type Package

Title OmniPath web service client and more

Version 3.0.4

Description A client for the OmniPath web service (<https://www.omnipathdb.org>) and many other resources. It also includes functions to transform and pretty print some of the downloaded data, functions to access a number of other resources such as BioPlex, ConsensusPathDB, EVEX, Gene Ontology, Guide to Pharmacology (IUPHAR/BPS), Harmonizome, HTRIdb, Human Phenotype Ontology, InWeb InBioMap, KEGG Pathway, Pathway Commons, Ramilowski et al. 2015, RegNetwork, ReMap, TF census, TRRUST and Vinayagam et al. 2011. Furthermore, OmnipathR features a close integration with the NicheNet method for ligand activity prediction from transcriptomics data, and its R implementation `nichenetr` (available only on github).

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URL <https://saezlab.github.io/OmnipathR/>

BugReports <https://github.com/saezlab/OmnipathR/issues>

biocViews GraphAndNetwork, Network, Pathways, Software, ThirdPartyClient, DataImport, DataRepresentation, GeneSignaling, GeneRegulation, SystemsBiology, Transcriptomics, SingleCell, Annotation, KEGG

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.omnipath_options_defaults

Default values for the package options

Description

These options describe the default settings for OmnipathR so you do not need to pass these parameters at each function call. Currently the only option useful for the public web service at omnipathdb.org is “omnipath.license“. If you are a for-profit user set it to “commercial“ to make sure all the data you download from OmniPath is legally allowed for commercial use. Otherwise just leave it as it is: “academic“. If you don’t use omnipathdb.org but within your organization you deployed your own pypath server and want to share data with a limited availability to outside users, you may want to use a password. For this you can use the “omnipath.password“ option. Also if you want the R package to work from another pypath server instead of omnipathdb.org, you can change the option “omnipath.url“.

Usage

```
.omnipath_options_defaults
```

Format

An object of class list of length 13.

all_uniprots

A table with all UniProt IDs

Description

Retrieves a table from UniProt with all proteins for a certain organism.

Usage

```
all_uniprots(fields = "id", reviewed = TRUE, organism = 9606)
```

Arguments

fields	Character vector of fields as defined by UniProt. For possible values please refer to https://www.uniprot.org/help/uniprotkb%5Fcolumn%5Fnames
reviewed	Retrieve only reviewed (‘TRUE‘), only unreviewed (‘FALSE‘) or both (‘NULL‘).
organism	Integer, NCBI Taxonomy ID of the organism (by default 9606 for human).

Value

Data frame (tibble) with the requested UniProt entries and fields.

Examples

```
human_swissprot_ac <- all_uniprots(fields = 'entry name')
human_swissprot_ac
# # A tibble: 20,396 x 1
#   `Entry name`
#   <chr>
# 1 OR4K3_HUMAN
# 2 O52A1_HUMAN
# 3 O2AG1_HUMAN
# 4 O10S1_HUMAN
# 5 O11G2_HUMAN
# # . with 20,386 more rows
```

ancestors

All ancestors in the ontology tree

Description

Starting from the selected nodes, recursively walks the ontology tree until it reaches the root. Collects all visited nodes, which are the ancestors (parents) of the starting nodes.

Usage

```
ancestors(
  terms,
  db_key = "go_basic",
  ids = TRUE,
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",
               "negatively_regulates")
)
```

Arguments

terms	Character vector of ontology term IDs or names. A mixture of IDs and names can be provided.
db_key	Character: key to identify the ontology database. For the available keys see omnipath_show_db .
ids	Logical: whether to return IDs or term names.
relations	Character vector of ontology relation types. Only these relations will be used.

Details

Note: this function relies on the database manager, the first call might take long because of the database load process. Subsequent calls within a short period should be faster. See [get_ontology_db](#).

Value

Character vector of ontology IDs. If the input terms are all root nodes, NULL is returned. The starting nodes won't be included in the result unless some of them are ancestors of other starting nodes.

Examples

```
ancestors('GO:0005035', ids = FALSE)
# [1] "molecular_function"
# [2] "transmembrane signaling receptor activity"
# [3] "signaling receptor activity"
# [4] "molecular transducer activity"
```

annotated_network *Network interactions with annotations*

Description

Annotations are often useful in a network context, e.g. one might want to label the interacting partners by their pathway membership. This function takes a network data frame and joins an annotation data frame from both the left and the right side, so both the source and target molecular entities will be labeled by their annotations. If one entity has many annotations these will yield many rows, hence the interacting pairs won't be unique across the data frame any more. Also if one entity has really many annotations the resulting data frame might be huge, we recommend to be careful with that. Finally, if you want to do the same but with intercell annotations, there is the [import_intercell_network](#) function.

Usage

```
annotated_network(network = NULL, annot = NULL, ...)
```

Arguments

network	Behaviour depends on type: if list, will be passed as arguments to import_omnipath_interactions to obtain a network data frame; if a data frame or tibble, it will be used as a network data frame; if a character vector, will be assumed to be a set of resource names and interactions will be queried from these resources.
annot	Either the name of an annotation resource (for a list of available resources call get_annotation_resources), or an annotation data frame. If the data frame contains more than one resources, only the first one will be used.
...	Column names selected from the annotation data frame (passed to <code>dplyr::select</code> , if empty all columns will be selected.)

Value

A data frame of interactions with annotations for both interacting entities.

Examples

```
signalink_with_pathways <-
  annotated_network('Signalink3', 'Signalink_pathway')
```

annotation_categories *Annotation categories and resources*

Description

A full list of annotation resources, keys and values.

Usage

```
annotation_categories()
```

Value

A data frame with resource names, annotation key labels and for each key all possible values.

Examples

```
annot_cat <- annotation_categories()
annot_cat
# # A tibble: 46,307 x 3
#   source      label  value
#   <chr>      <chr> <chr>
# 1 connectomeDB2020 role    ligand
# 2 connectomeDB2020 role    receptor
# 3 connectomeDB2020 location ECM
# 4 connectomeDB2020 location plasma membrane
# 5 connectomeDB2020 location secreted
# 6 KEGG-PC      pathway Alanine, aspartate and glutamate metabolism
# 7 KEGG-PC      pathway Amino sugar and nucleotide sugar metabolism
# 8 KEGG-PC      pathway Aminoacyl-tRNA biosynthesis
# 9 KEGG-PC      pathway Arachidonic acid metabolism
# 10 KEGG-PC     pathway Arginine and proline metabolism
```

`bioplex1`*Downloads the BioPlex version 1.0 interaction dataset*

Description

This dataset contains ~24,000 interactions detected in HEK293T cells using 2,594 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

Usage`bioplex1()`**Value**

Data frame (tibble) with interactions.

See Also

- [bioplex2](#)
- [bioplex3](#)
- [bioplex_hct116_1](#)
- [bioplex_all](#)

Examples

```
bioplex_interactions <- bioplex1()
nrow(bioplex_interactions)
# [1] 23744
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

`bioplex2`*Downloads the BioPlex version 2.0 interaction dataset*

Description

This dataset contains ~56,000 interactions detected in HEK293T cells using 5,891 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>

Usage`bioplex2()`

Value

Data frame (tibble) with interactions.

See Also

- [bioplex1](#)
- [bioplex3](#)
- [bioplex_hct116_1](#)
- [bioplex_all](#)

Examples

```
bioplex_interactions <- bioplex2()
nrow(bioplex_interactions)
# [1] 56553
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

bioplex3

Downloads the BioPlex version 3.0 interaction dataset

Description

This dataset contains ~120,000 interactions detected in HEK293T cells using 10,128 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

Usage

```
bioplex3()
```

Value

Data frame (tibble) with interactions.

See Also

- [bioplex1](#)
- [bioplex2](#)
- [bioplex_hct116_1](#)
- [bioplex_all](#)

Examples

```
bioplex_interactions <- bioplex3()
nrow(bioplex_interactions)
# [1] 118162
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

bioplex_all

Downloads all BioPlex interaction datasets

Description

BioPlex provides four interaction datasets: version 1.0, 2.0, 3.0 and HCT116 version 1.0. This function downloads all of them, merges them to one data frame, removes the duplicates (based on unique pairs of UniProt IDs) and separates the isoform numbers from the UniProt IDs. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

Usage

```
bioplex_all(unique = TRUE)
```

Arguments

unique	Logical. Collapse the duplicate interactions into single rows or keep them as they are. In case of merging duplicate records the maximum p value will be chosen for each record.
--------	--

Value

Data frame (tibble) with interactions.

See Also

- [bioplex1](#)
- [bioplex2](#)
- [bioplex3](#)
- [bioplex_hct116_1](#)

Examples

```

bioplex_interactions <- bioplex_all()
bioplex_interactions
# # A tibble: 195,538 x 11
#   UniprotA IsoformA UniprotB IsoformB GeneA GeneB SymbolA SymbolB
#   <chr>      <int> <chr>      <int> <dbl> <dbl> <chr>   <chr>
# 1 A0AV02      2 Q5K4L6      NA 84561 11000 SLC12A8 SLC27A3
# 2 A0AV02      2 Q8N5V2      NA 84561 25791 SLC12A8 NGEF
# 3 A0AV02      2 Q9H6S3      NA 84561 64787 SLC12A8 EPS8L2
# 4 A0AV96      2 O00425      2 54502 10643 RBM47   IGF2BP3
# 5 A0AV96      2 O00443      NA 54502 5286 RBM47   PIK3C2A
# 6 A0AV96      2 O43426      NA 54502 8867 RBM47   SYNJ1
# 7 A0AV96      2 O75127      NA 54502 26024 RBM47   PTC1D1
# 8 A0AV96      2 O95208      2 54502 22905 RBM47   EPN2
# 9 A0AV96      2 O95900      NA 54502 26995 RBM47   TRUB2
# 10 A0AV96     2 P07910      2 54502 3183 RBM47   HNRNPC
# # . with 195,528 more rows, and 3 more variables: p_wrong <dbl>,
# #   p_no_interaction <dbl>, p_interaction <dbl>

```

bioplex_hct116_1

Downloads the BioPlex HCT116 version 1.0 interaction dataset

Description

This dataset contains ~71,000 interactions detected in HCT116 cells using 5,522 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

Usage

```
bioplex_hct116_1()
```

Value

Data frame (tibble) with interactions.

See Also

- [bioplex1](#)
- [bioplex2](#)
- [bioplex3](#)
- [bioplex_all](#)

Examples

```
bioplex_interactions <- bioplex_hct116_1()
nrow(bioplex_interactions)
# [1] 70966
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

bma_motif_es

BMA motifs from a sequence of edges

Description

These motifs can be added to a BMA canvas.

Usage

```
bma_motif_es(edge_seq, G, granularity = 2)
```

Arguments

edge_seq	An igraph edge sequence.
G	An igraph graph object.
granularity	Numeric: granularity value.

Value

Character: BMA motifs as a single string.

Examples

```
interactions <- import_omnipath_interactions(resources = 'ARN')
graph <- interaction_graph(interactions)
motifs <- bma_motif_es(igraph::E(graph)[1], graph)
```

bma_motif_vs	<i>Prints a BMA motif to the screen from a sequence of nodes, which can be copy/pasted into the BMA canvas</i>
--------------	--

Description

Intended to parallel print_path_vs

Usage

```
bma_motif_vs(node_seq, G)
```

Arguments

node_seq	An igraph node sequence.
G	An igraph graph object.

Value

Character: BMA motifs as a single string.

Examples

```
interactions <- import_omnipath_interactions(resources = 'ARN')
graph <- interaction_graph(interactions)
bma_string <- bma_motif_vs(
  igraph::all_shortest_paths(
    graph,
    from = 'ULK1',
    to = 'ATG13'
  )$res,
  graph
)
```

consensuspathdb_download

Retrieves the ConsensusPathDB network

Description

Compiles a table of binary interactions from ConsensusPathDB (<http://cpdb.molgen.mpg.de/>) and translates the UniProtKB ACs to Gene Symbols.

Usage

```
consensuspathdb_download(complex_max_size = 4, min_score = 0.9)
```

Arguments

complex_max_size	Numeric: do not expand complexes with a higher number of elements than this. ConsensusPathDB does not contain conventional interactions but lists of participants, which might be members of complexes. Some records include dozens of participants and expanding them to binary interactions result thousands, sometimes hundreds of thousands of interactions from one single record. At the end, this process consumes >10GB of memory and results rather unusable data, hence it is recommended to limit the complex sizes at some low number.
min_score	Numeric: each record in ConsensusPathDB comes with a confidence score, expressing the amount of evidences. The default value, a minimum score of 0.9 retains approx. the top 30 percent of the interactions.

Value

Data frame (tibble) with interactions.

Examples

```
cpdb_data <- consensuspathdb_download(
  complex_max_size = 1,
  min_score = .99
)
nrow(cpdb_data)
# [1] 252302
colnames(cpdb_data)
# [1] "databases" "references" "uniprot_a" "confidence" "record_id"
# [6] "uniprot_b" "in_complex" "genesymbol_a" "genesymbol_b"
cpdb_data
## # A tibble: 252,302 x 9
##   databases references uniprot_a confidence record_id uniprot_b in_com
##   <chr>      <chr>      <chr>      <dbl>      <int> <chr>      <lgl>
## 1 Reactome  NA          SUMF2_HU.    1           1 SUMF1_HU. TRUE
## 2 Reactome  NA          SUMF1_HU.    1           1 SUMF2_HU. TRUE
## 3 DIP,Reac. 22210847,. STIM1_HU.    0.998       2 TRPC1_HU. TRUE
## 4 DIP,Reac. 22210847,. TRPC1_HU.    0.998       2 STIM1_HU. TRUE
## # . with 252,292 more rows, and 2 more variables: genesymbol_a <chr>,
## #   genesymbol_b <chr>
```

consensuspathdb_raw_table

Downloads interaction data from ConsensusPathDB

Description

Downloads interaction data from ConsensusPathDB

Usage

```
consensuspathdb_raw_table()
```

Value

Data frame (tibble) with interactions.

Examples

```
cpdb_raw <- consensuspathdb_raw_table()
```

descendants

All descendants in the ontology tree

Description

Starting from the selected nodes, recursively walks the ontology tree until it reaches the leaf nodes. Collects all visited nodes, which are the descendants (children) of the starting nodes.

Usage

```
descendants(  
  terms,  
  db_key = "go_basic",  
  ids = TRUE,  
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",  
               "negatively_regulates")  
)
```

Arguments

terms	Character vector of ontology term IDs or names. A mixture of IDs and names can be provided.
db_key	Character: key to identify the ontology database. For the available keys see omnipath_show_db .
ids	Logical: whether to return IDs or term names.
relations	Character vector of ontology relation types. Only these relations will be used.

Details

Note: this function relies on the database manager, the first call might take long because of the database load process. Subsequent calls within a short period should be faster. See [get_ontology_db](#).

Value

Character vector of ontology IDs. If the input terms are all leaves NULL is returned. The starting nodes won't be included in the result unless some of them are descendants of other starting nodes.

Examples

```
descendants('GO:0005035', ids = FALSE)
# [1] "tumor necrosis factor-activated receptor activity"
# [2] "TRAIL receptor activity"
# [3] "TNFSF11 receptor activity"
```

enzsub_graph	<i>Enzyme-substrate graph</i>
--------------	-------------------------------

Description

Transforms the a data frame with enzyme-substrate relationships (obtained by [import_omnipath_enzsub](#)) to an igraph graph object.

Usage

```
enzsub_graph(enzsub)
```

Arguments

enzsub Data frame created by [import_omnipath_enzsub](#)

Value

An igraph directed graph object.

See Also

- [import_omnipath_enzsub](#)
- [giant_component](#)
- [find_all_paths](#)

Examples

```
enzsub <- import_omnipath_enzsub(resources = c('PhosphoSite', 'SIGNOR'))
enzsub_g <- enzsub_graph(enzsub = enzsub)
```

evex_download

*Interactions from the EVEX database***Description**

Downloads interactions from EVEX, a versatile text mining resource (<http://evexdb.org>). Translates the Entrez Gene IDs to Gene Symbols and combines the interactions and references into a single data frame.

Usage

```
evex_download(
  min_confidence = NULL,
  remove_negatives = TRUE,
  top_confidence = NULL
)
```

Arguments

min_confidence Numeric: a threshold for confidence scores. EVEX confidence scores span roughly from -3 to 3. By providing a numeric value in this range the lower confidence interactions can be removed. If NULL no filtering performed.

remove_negatives Logical: remove the records with the "negation" attribute set.

top_confidence Confidence cutoff as quantile (a number between 0 and 1). If NULL no filtering performed.

Value

Data frame (tibble) with interactions.

Examples

```
evex_interactions <- evex_download()
evex_interactions
# # A tibble: 368,297 x 13
#   general_event_id source_entrezge. target_entrezge. confidence negation
#   <dbl> <chr> <chr> <dbl> <dbl>
# 1     98 8651     6774     -1.45     0
# 2    100 8431     6774     -1.45     0
# 3    205 6261     6263     0.370     0
# 4    435 1044     1045     -1.09     0
# . with 368,287 more rows, and 8 more variables: speculation <dbl>,
#   coarse_type <chr>, coarse_polarity <chr>, refined_type <chr>,
#   refined_polarity <chr>, source_genesymbol <chr>,
#   target_genesymbol <chr>, references <chr>
```

filter_by_resource *Filters OmniPath data by resources*

Description

Keeps only those records which are supported by any of the resources of interest.

Usage

```
filter_by_resource(data, resources = NULL)
```

Arguments

data	A data frame downloaded from the OmniPath web service (interactions, enzyme-substrate or complexes).
resources	Character vector with resource names to keep.

Value

The data frame filtered.

Examples

```
interactions <- import_omnipath_interactions()
signor <- filter_by_resource(interactions, resources = 'SIGNOR')
```

filter_intercell_network
Quality filter an intercell network

Description

The intercell database of OmniPath covers a very broad range of possible ways of cell to cell communication, and the pieces of information, such as localization, topology, function and interaction, are combined from many, often independent sources. This unavoidably result some weird and unexpected combinations which are false positives in the context of intercellular communication. [import_intercell_network](#) provides a shortcut (high_confidence) to do basic quality filtering. For custom filtering or experimentation with the parameters we offer this function.

Usage

```

filter_intercell_network(
  network,
  transmitter_topology = c("secreted", "plasma_membrane_transmembrane",
    "plasma_membrane_peripheral"),
  receiver_topology = "plasma_membrane_transmembrane",
  min_curation_effort = 2,
  min_resources = 1,
  min_references = 0,
  min_provenances = 1,
  consensus_percentile = 50,
  loc_consensus_percentile = 30,
  ligand_receptor = FALSE,
  simplify = FALSE,
  unique_pairs = FALSE,
  omnipath = TRUE,
  ligreextra = TRUE,
  kinaseextra = FALSE,
  pathwayextra = FALSE,
  ...
)

```

Arguments

network	An intercell network data frame, as provided by import_intercell_network , without simplify.
transmitter_topology	Character vector: topologies allowed for the entities in transmitter role. Abbreviations allowed: "sec", "pmtm" and "pmp".
receiver_topology	Same as transmitter_topology for the entities in the receiver role.
min_curation_effort	Numeric: a minimum value of curation effort (resource-reference pairs) for network interactions. Use zero to disable filtering.
min_resources	Numeric: minimum number of resources for interactions. The value 1 means no filtering.
min_references	Numeric: minimum number of references for interactions. Use zero to disable filtering.
min_provenances	Numeric: minimum number of provenances (either resources or references) for interactions. Use zero or one to disable filtering.
consensus_percentile	Numeric: percentile threshold for the consensus score of generic categories in intercell annotations. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each

category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.

loc_consensus_percentile	Numeric: similar to consensus_percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be TRUE only where at least 50 percent of the resources support these.
ligand_receptor	Logical. If TRUE, only <i>ligand</i> and <i>receptor</i> annotations will be used instead of the more generic <i>transmitter</i> and <i>receiver</i> categories.
simplify	Logical: keep only the most often used columns. This function combines a network data frame with two copies of the intercell annotation data frames, all of them already having quite some columns. With this option we keep only the names of the interacting pair, their intercellular communication roles, and the minimal information of the origin of both the interaction and the annotations.
unique_pairs	Logical: instead of having separate rows for each pair of annotations, drop the annotations and reduce the data frame to unique interacting pairs. See unique_intercell_network for details.
omnipath	Logical: shortcut to include the <i>omnipath</i> dataset in the interactions query.
ligreextra	Logical: shortcut to include the <i>ligreextra</i> dataset in the interactions query.
kinaseextra	Logical: shortcut to include the <i>kinaseextra</i> dataset in the interactions query.
pathwayextra	Logical: shortcut to include the <i>pathwayextra</i> dataset in the interactions query.
...	If simplify or unique_pairs is TRUE, additional column names can be passed here to <code>dplyr::select</code> on the final data frame. Otherwise ignored.

Value

An intercell network data frame filtered.

See Also

- [import_intercell_network](#)
- [unique_intercell_network](#)
- [simplify_intercell_network](#)

Examples

```
icn <- import_intercell_network()
icn_f <- filter_intercell_network(
  icn,
  consensus_percentile = 75,
  min_provenances = 3,
  simplify = TRUE
)
```

find_all_paths	<i>All paths between two groups of vertices</i>
----------------	---

Description

Finds all paths up to length 'maxlen' between specified groups of vertices. This function is needed only because igraph's 'all_shortest_paths' finds only the shortest, not any path up to a defined length.

Usage

```
find_all_paths(  
  graph,  
  start,  
  end,  
  attr = NULL,  
  mode = 'OUT',  
  maxlen = 2,  
  progress = TRUE  
)
```

Arguments

graph	An igraph graph object.
start	Integer or character vector with the indices or names of one or more start vertices.
end	Integer or character vector with the indices or names of one or more end vertices.
attr	Character: name of the vertex attribute to identify the vertices by. Necessary if 'start' and 'end' are not igraph vertex ids but for example vertex names or labels.
mode	Character: IN, OUT or ALL. Default is OUT.
maxlen	Integer: maximum length of paths in steps, i.e. if maxlen = 3, then the longest path may consist of 3 edges and 4 nodes.
progress	Logical: show a progress bar. Default is FALSE.

Value

List of vertex paths, each path is a character or integer vector.

See Also

- [interaction_graph](#)
- [enzsub_graph](#)
- [giant_component](#)

Examples

```
interactions <- import_omnipath_interactions()
graph <- interaction_graph(interactions)
paths <- find_all_paths(
  graph = graph,
  start = c('EGFR', 'STAT3'),
  end = c('AKT1', 'ULK1'),
  attr = 'name'
)
```

get_annotation_resources

Retrieves a list of available resources in the annotations database of OmniPath

Description

Get the names of the resources from <https://omnipath.org/annotations>.

Usage

```
get_annotation_resources(dataset = NULL, ...)
```

Arguments

dataset	ignored for this query type
...	optional additional arguments

Value

character vector with the names of the annotation resources

See Also

- [get_resources](#)
- [import_omnipath_annotations](#)

Examples

```
get_annotation_resources()
```

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_complex_resources` *Retrieve a list of complex resources available in Omnipath*

Description

Get the names of the resources from <https://omnipath.org/complexes>

Usage

```
get_complex_resources(dataset = NULL)
```

Arguments

`dataset` ignored for this query type

Value

character vector with the names of the databases

See Also

- [get_resources](#)
- [import_omnipath_complexes](#)

Examples

```
get_complex_resources()
```

`get_db` *Access a built in database*

Description

Databases are resources which might be costly to load but can be used many times by functions which usually automatically load and retrieve them from the database manager. Each database has a lifetime and will be unloaded automatically upon expiry.

Usage

```
get_db(key, param = NULL, reload = FALSE)
```

Arguments

key	Character: the key of the database to load. For a list of available keys see omnipath_show_db .
param	List: override the defaults or pass further parameters to the database loader function. See the loader functions and their default parameters in omnipath_show_db . If the database is already loaded with different parameters it will be reloaded with the new parameters only if the reload option is TRUE.
reload	Reload the database if param passed here is different from the parameters used the last time the database was loaded. If different functions with different parameters access the database repeatedly and request reload the frequent reloads might cost substantial time and resource use.

Value

An object with the database contents. The exact format depends on the database, most often it is a data frame or a list.

See Also

[omnipath_show_db](#).

Examples

```
goslim <- get_db('go_slim')
```

get_enzsub_resources *Retrieves a list of enzyme-substrate resources available in OmniPath*

Description

Get the names of the enzyme-substrate relationship resources available in <https://omnipath.org/enzsub>

Usage

```
get_enzsub_resources(dataset = NULL)
```

Arguments

dataset ignored for this query type

Value

character vector with the names of the enzyme-substrate resources

See Also

- [get_resources](#)
- [import_omnipath_enzsub](#)

Examples

```
get_enzsub_resources()
```

```
get_interaction_resources
```

Retrieve a list of interaction resources available in Omnipath

Description

Gets the names of the resources from <https://omnipath.org/interactions>.

Usage

```
get_interaction_resources(dataset = NULL)
```

Arguments

dataset a dataset within the interactions query type. Currently available datasets are 'omnipath', 'kinaseextra', 'pathwayextra', 'ligrecextra', 'dorothea', 'tf_target', 'tf_mirna', 'mirnatarget' and 'lncrna_mrna'

Value

character vector with the names of the interaction databases

See Also

- [get_resources](#)
- [import_all_interactions](#)
- [import_omnipath_interactions](#)
- [import_pathwayextra_interactions](#)
- [import_kinaseextra_interactions](#)
- [import_ligrecextra_interactions](#)
- [import_mirnatarget_interactions](#)
- [import_dorothea_interactions](#)

Examples

```
get_interaction_resources()
```

`get_intercell_categories`*Categories in the intercell database of OmniPath*

Description

Retrieves a list of categories from <https://omnipath.org/intercell>.

Usage

```
get_intercell_categories()
```

Value

character vector with the different intercell categories

See Also

- [import_omnipath_intercell](#)
- [get_intercell_generic_categories](#)

Examples

```
get_intercell_categories()
```

`get_intercell_generic_categories`*Retrieves a list of the generic categories in the intercell database of OmniPath*

Description

Retrieves a list of the generic categories from <https://omnipath.org/intercell>.

Usage

```
get_intercell_generic_categories()
```

Value

character vector with the different intercell main classes

See Also

- [import_omnipath_intercell](#)
- [get_intercell_categories](#)

Examples

```
get_intercell_generic_categories()
```

```
get_intercell_resources
```

Retrieves a list of intercellular communication resources available in OmniPath

Description

Retrieves a list of the databases from <https://omnipath.org/intercell>.

Usage

```
get_intercell_resources(dataset = NULL)
```

Arguments

dataset ignored at this query type

Value

character vector with the names of the databases

See Also

- [get_resources](#)
- [import_omnipath_intercell](#)

Examples

```
get_intercell_resources()
```

get_ontology_db	<i>Access an ontology database</i>
-----------------	------------------------------------

Description

Retrieves an ontology database with relations in the desired data structure. The database is automatically loaded and the requested data structure is constructed if necessary. The databases stay loaded up to a certain time period (see the option `omnipath.db_lifetime`). Hence the first one of repeated calls to this function might take long and the subsequent ones should be really quick.

Usage

```
get_ontology_db(key, rel_fmt = "tbl", child_parents = TRUE)
```

Arguments

key	Character: key of the ontology database. For the available keys see omnipath_show_db .
rel_fmt	Character: the data structure of the ontology relations. Possible values are 1) "tbl" a data frame, 2) "lst" a list or 3) "gra" a graph.
child_parents	Logical: whether the ontology relations should point from child to parents (TRUE) or from parent to children (FALSE).

Value

A list with the following elements: 1) "names" a table with term IDs and names; 2) "namespaces" a table to connect term IDs and namespaces they belong to; 3) "relations" a table with relations between terms and their parent terms; 4) "subsets" a table with terms and the subsets they are part of; 5) "obsolete" character vector with all the terms labeled as obsolete.

See Also

- [omnipath_show_db](#)
- [get_db](#)

Examples

```
go <- get_ontology_db('go_basic', child_parents = FALSE)
```

get_resources	<i>Retrieve the available resources for a given query type</i>
---------------	--

Description

Collects the names of the resources available in OmniPath for a certain query type and optionally for a dataset within that.

Usage

```
get_resources(query_type, datasets = NULL, generic_categories = NULL)
```

Arguments

query_type	one of the query types 'interactions', 'enz_sub', 'complexes', 'annotations' or 'intercell'
datasets	currently within the 'interactions' query type only, multiple datasets are available: 'omnipath', 'kinaseextra', 'pathwayextra', 'ligreextra', 'dorothea', 'tf_target', 'tf_mirna', 'mirnatarget' and 'lncrna_mrna'.
generic_categories	for the 'intercell' query type, restrict the search for some generic categories e.g. 'ligand' or 'receptor'.

Value

a character vector with resource names

Examples

```
get_resources(query_type = 'interactions')
```

get_signed_ptms	<i>Signs for enzyme-substrate interactions</i>
-----------------	--

Description

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

Usage

```
get_signed_ptms(
  enzsub = import_omnipath_enzsub(),
  interactions = import_omnipath_interactions()
)
```


Arguments

enzsub Enzyme-substrate data frame generated by [import_omnipath_enzsub](#)
interactions interaction data frame generated by [import_omnipath_interactions](#)

Value

Data frame of enzyme-substrate relationships with is_inhibition and is_stimulation columns.

See Also

- [import_omnipath_enzsub](#)
- [import_omnipath_interactions](#)

Examples

```
enzsub <- import_omnipath_enzsub(resources = c('PhosphoSite', 'SIGNOR'))  
interactions <- import_omnipath_interactions()  
enzsub <- get_signed_ptms(enzsub, interactions)
```

giant_component	<i>Giant component of a graph</i>
-----------------	-----------------------------------

Description

For an igraph graph object returns its giant component.

Usage

```
giant_component(graph)
```

Arguments

graph An igraph graph object.

Value

An igraph graph object containing only the giant component.

Examples

```
interactions <- import_post_translational_interactions()  
graph <- interaction_graph(interactions)  
graph_gc <- giant_component(graph)
```

go_annot_download *Gene annotations from Gene Ontology*

Description

Gene Ontology is an ontology of gene subcellular localizations, molecular functions and involvement in biological processes. Gene products across many organisms are annotated with the ontology terms. This function downloads the gene-ontology term associations for certain model organisms or all organisms. For a description of the columns see <http://geneontology.org/docs/go-annotation-file-gaf-format-2.2/>.

Usage

```
go_annot_download(organism = "human", aspects = c("C", "F", "P"), slim = NULL)
```

Arguments

organism	Character: either "chicken", "cow", "dog", "human", "pig" or "uniprot_all".
aspects	Character vector with some of the following elements: "C" (cellular component), "F" (molecular function) and "P" (biological process). Gene Ontology is three separate ontologies called as three aspects. By this parameter you can control which aspects to include in the output.
slim	Character: if not NULL, the name of a GOsubset (slim). instead of the full GO annotation, the slim annotation will be returned. See details at go_annot_slim . If TRUE, the "generic" slim will be used.

Value

A tibble (data frame) of annotations as it is provided by the database

Examples

```
goa_data <- go_annot_download()
goa_data
# # A tibble: 606,840 x 17
#   db      db_object_id db_object_symbol qualifier go_id  db_ref
#   <fct>  <chr>          <chr>          <fct>  <chr> <chr>
# 1 UniProt. A0A024RBG1  NUDT4B          NA      GO:000. GO_REF:00.
# 2 UniProt. A0A024RBG1  NUDT4B          NA      GO:000. GO_REF:00.
# 3 UniProt. A0A024RBG1  NUDT4B          NA      GO:004. GO_REF:00.
# 4 UniProt. A0A024RBG1  NUDT4B          NA      GO:005. GO_REF:00.
# 5 UniProt. A0A024RBG1  NUDT4B          NA      GO:005. GO_REF:00.
# # . with 606,830 more rows, and 11 more variables:
# #   evidence_code <fct>, with_or_from <chr>, aspect <fct>,
# #   db_object_name <chr>, db_object_synonym <chr>,
# #   db_object_type <fct>, taxon <fct>, date <date>,
# #   assigned_by <fct>, annotation_extension <chr>,
# #   gene_product_from_id <chr>
```

go_annot_slim

GO slim gene annotations

Description

GO slims are subsets of the full GO which "give a broad overview of the ontology content without the detail of the specific fine grained terms". In order to annotate genes with GO slim terms, we take the annotations and search all ancestors of the terms up to the root of the ontology tree. From the ancestors we select the terms which are part of the slim subset.

Usage

```
go_annot_slim(
  organism = "human",
  slim = "generic",
  aspects = c("C", "F", "P"),
  cache = TRUE
)
```

Arguments

organism	Character: either "chicken", "cow", "dog", "human", "pig" or "uniprot_all".
slim	Character: the GO subset (GO slim) name. Available GO slims are: "agr" (Alliance for Genomics Resources), "generic", "aspergillus", "candida", "drosophila", "chembl", "metagenomic", "mouse", "plant", "pir" (Protein Information Resource), "pombe" and "yeast".
aspects	Character vector with some of the following elements: "C" (cellular component), "F" (molecular function) and "P" (biological process). Gene Ontology is three separate ontologies called as three aspects. By this parameter you can control which aspects to include in the output.
cache	Logical: Load the result from cache if available.

Details

Building the GO slim is resource intensive in its current implementation. For human annotation and generic GO slim it might take around 20 minutes. The result is saved into the cache so next time loading the data from there is really quick. If the cache option is FALSE the data will be built fresh (the annotation and ontology files still might come from cache), and the newly build GO slim will overwrite the cache instance.

Value

A tibble (data frame) of genes annotated with ontology terms in in the GO slim (subset).

See Also

- [go_annot_download](#)
- [go_ontology_download](#)
- [get_db](#)

Examples

```
goslim <- go_annot_slim(organism = 'human', slim = 'generic')
goslim
# # A tibble: 276,371 x 8
#   db      db_object_id db_object_symbol go_id aspect db_object_name
#   <fct> <chr>          <chr>          <chr> <fct> <chr>
# 1 UniPr. A0A024RBG1  NUDT4B          GO:0. F      Diphosphoinosito.
# 2 UniPr. A0A024RBG1  NUDT4B          GO:0. F      Diphosphoinosito.
# 3 UniPr. A0A024RBG1  NUDT4B          GO:0. C      Diphosphoinosito.
# 4 UniPr. A0A024RBG1  NUDT4B          GO:0. C      Diphosphoinosito.
# 5 UniPr. A0A024RBG1  NUDT4B          GO:0. C      Diphosphoinosito.
# # . with 276,366 more rows, and 2 more variables:
# #   db_object_synonym <chr>, db_object_type <fct>
```

go_ontology_download *The Gene Ontology tree*

Description

The Gene Ontology tree

Usage

```
go_ontology_download(
  basic = TRUE,
  tables = TRUE,
  subset = NULL,
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",
    "negatively_regulates")
)
```

Arguments

basic Logical: use the basic or the full version of GO. As written on the GO home page: "the basic version of the GO is filtered such that the graph is guaranteed to be acyclic and annotations can be propagated up the graph. The relations included are is a, part of, regulates, negatively regulates and positively regulates. This version excludes relationships that cross the 3 GO hierarchies. This version should be used with most GO-based annotation tools."

tables	In the result return data frames or nested lists. These later can be converted to each other if necessary. However converting from table to list is faster.
subset	Character: the GO subset (GO slim) name. GO slims are subsets of the full GO which "give a broad overview of the ontology content without the detail of the specific fine grained terms". This option, if not NULL, overrides the basic parameter. Available GO slims are: "agr" (Alliance for Genomics Resources), "generic", "aspergillus", "candida", "drosophila", "chembl", "metagenomic", "mouse", "plant", "pir" (Protein Information Resource), "pombe" and "yeast".
relations	Character vector: the relations to include in the processed data.

Value

A list with the following elements: 1) "names" a list with terms as names and names as values; 2) "namespaces" a list with terms as names and namespaces as values; 3) "relations" a list with relations between terms: terms are keys, values are lists with relations as names and character vectors of related terms as values; 4) "subsets" a list with terms as keys and character vectors of subset names as values (or NULL if the term does not belong to any subset); 5) "obsolete" character vector with all the terms labeled as obsolete. If the tables parameter is TRUE, "names", "namespaces", "relations" and "subsets" will be data frames (tibbles).

Examples

```
# retrieve the generic GO slim, a small subset of the full ontology
go <- go_ontology_download(subset = 'generic')
```

guide2pharma_download *Downloads interactions from the Guide to Pharmacology database*

Description

Downloads ligand-receptor interactions from the Guide to Pharmacology (IUPHAR/BPS) database (<https://www.guidetopharmacology.org/>).

Usage

```
guide2pharma_download()
```

Value

A tibble (data frame) of interactions as it is provided by the database

Examples

```
g2p_data <- guide2pharma_download()
g2p_data
# # A tibble: 21,586 x 38
#   target target_id target_gene_sym. target_uniprot target_ensembl_
#   <chr>      <dbl> <chr>                <chr>          <chr>
# 1 12S-L.      1387 ALOX12             P18054         ENSG00000108839
# 2 15-LO.      1388 ALOX15             P16050         ENSG00000161905
# 3 15-LO.      1388 ALOX15             P16050         ENSG00000161905
# 4 15-LO.      1388 ALOX15             P16050         ENSG00000161905
# # . with 21,576 more rows, and 33 more variables: target_ligand <chr>,
# #   target_ligand_id <chr>, target_ligand_gene_symbol <chr>,
# #   ... (truncated)
```

harmonizome_download *Downloads a Harmonizome network dataset*

Description

Downloads a single network dataset from Harmonizome <https://maayanlab.cloud/Harmonizome>.

Usage

```
harmonizome_download(dataset)
```

Arguments

dataset The dataset part of the URL. Please refer to the download section of the Harmonizome webpage.

Value

Data frame (tibble) with interactions.

Examples

```
harmonizome_data <- harmonizome_download('phosphositeplus')
harmonizome_data
# # A tibble: 6,013 x 7
#   source source_desc source_id target target_desc target_id weight
#   <chr>   <chr>          <dbl> <chr> <chr>         <dbl> <dbl>
# 1 TP53    na              7157 STK17A na           9263    1
# 2 TP53    na              7157 TP53RK na          112858   1
# 3 TP53    na              7157 SMG1  na           23049   1
# 4 UPF1    na              5976 SMG1  na           23049   1
# # . with 6,003 more rows
```

hpo_download *Downloads protein annotations from Human Phenotype Ontology*

Description

Human Phenotype Ontology (HPO) provides a standardized vocabulary of phenotypic abnormalities encountered in human disease. Each term in the HPO describes a phenotypic abnormality. HPO currently contains over 13,000 terms and over 156,000 annotations to hereditary diseases. See more at <https://hpo.jax.org/app/>.

Usage

```
hpo_download()
```

Value

A tibble (data frame) of annotations as it is provided by the database

Examples

```
hpo_data <- hpo_download()
hpo_data
# # A tibble: 231,738 x 9
#   entrez_gene_id entrez_gene_symb. hpo_term_id hpo_term_name
#   <dbl> <chr> <chr> <chr>
# 1     8192 CLPP      HP:0000013 Hypoplasia of the ute.
# 2     8192 CLPP      HP:0004322 Short stature
# 3     8192 CLPP      HP:0000786 Primary amenorrhea
# 4     8192 CLPP      HP:0000007 Autosomal recessive i.
# 5     8192 CLPP      HP:0000815 Hypergonadotropic hyp.
# # . with 231,733 more rows, and 5 more variables:
# #   frequency_raw <chr>, frequency_hpo <chr>, info_gd_source <chr>,
# #   gd_source <chr>, disease_id <chr>
```

htridb_download *Downloads TF-target interactions from HTRIdb*

Description

HTRIdb (<https://www.lbbc.ibb.unesp.br/htri/>) is a database of literature curated human TF-target interactions. As the database is recently offline, the data is distributed by the OmniPath rescued data repository (<https://rescued.omnipathdb.org/>).

Usage

```
htridb_download()
```

Value

Data frame (tibble) with interactions.

Examples

```
htridb_data <- htridb_download()
htridb_data
# # A tibble: 18,630 x 7
#   OID GENEID_TF SYMBOL_TF GENEID_TG SYMBOL_TG TECHNIQUE
#   <dbl> <dbl> <chr> <dbl> <chr> <chr>
# 1 32399 142 PARP1 675 BRCA2 Electrophoretic Mobi.
# 2 32399 142 PARP1 675 BRCA2 Chromatin Immunoprec.
# 3 28907 196 AHR 1543 CYP1A1 Chromatin Immunoprec.
# 4 29466 196 AHR 1543 CYP1A1 Electrophoretic Mobi.
# 5 28911 196 AHR 1543 CYP1A1 Chromatin Immunoprec.
# # . with 18,620 more rows, and 1 more variable: PUBMED_ID <chr>
```

```
import_all_interactions
```

Imports all interaction datasets available in OmniPath

Description

The interaction datasets currently available in OmniPath:

Usage

```
import_all_interactions(
  resources = NULL,
  organism = 9606,
  dorothea_levels = c("A", "B"),
  exclude = NULL,
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  ...
)

import_AllInteractions(...)
```

Arguments

resources interactions not reported in these databases are removed. See [get_interaction_resources](#) for more information.

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

dorothea_levels	The confidence levels of the dorothea interactions (TF-target) which range from A to D. Set to A and B by default.
exclude	Character: datasets or resources to exclude.
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
...	Passed to import_all_interactions.

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
dorothea: transcription factor (TF)-target interactions from DoRoThEA
tf_target: transcription factor (TF)-target interactions from other resources
mirnatarget: miRNA-mRNA interactions
tf_mirna: TF-miRNA interactions
lncrna_mrna: lncRNA-mRNA interactions

Value

A dataframe containing all the datasets in the interactions query

See Also

- [get_interaction_resources](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <- import_all_interactions(  
  resources = c('HPRD', 'BioGRID'),  
  organism = 9606  
)
```

```
import_dorothea_interactions
```

From the OmniPath webservice imports interactions from the DoRothEA dataset

Description

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

Usage

```
import_dorothea_interactions(
  resources = NULL,
  organism = 9606,
  dorothea_levels = c("A", "B"),
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
dorothea_levels	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.
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	optional additional arguments

Value

A dataframe containing TF-target interactions from DoRothEA

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <- import_dorothea_interactions(  
  resources = c('DoRothEA', 'ARACNe-GTEx_DoRothEA'),  
  organism = 9606,  
  dorothea_levels = c('A', 'B', 'C')  
)
```

import_intercell_network

Intercellular communication network

Description

Imports an intercellular network by combining intercellular annotations and protein interactions. First imports a network of protein-protein interactions. Then, it retrieves annotations about the proteins intercellular communication roles, once for the transmitter (delivering information from the expressing cell) and second, the receiver (receiving signal and relaying it towards the expressing cell) side. These 3 queries can be customized by providing parameters in lists which will be passed to the respective methods ([import_omnipath_interactions](#) for the network and [import_omnipath_intercell](#) for the annotations). Finally the 3 data frames combined in a way that the source proteins in each interaction annotated by the transmitter, and the target proteins by the receiver categories. If undirected interactions present (these are disabled by default) they will be duplicated, i.e. both partners can be both receiver and transmitter.

Usage

```
import_intercell_network(  
  interactions_param = list(),  
  transmitter_param = list(),  
  receiver_param = list(),  
  resources = NULL,  
  entity_types = NULL,  
  ligand_receptor = FALSE,  
  high_confidence = FALSE,
```

```

simplify = FALSE,
unique_pairs = FALSE,
consensus_percentile = NULL,
loc_consensus_percentile = NULL,
omnipath = TRUE,
ligreextra = TRUE,
kinaseextra = !high_confidence,
pathwayextra = !high_confidence,
...
)

```

Arguments

interactions_param a list with arguments for an interactions query: `import_omnipath_interactions`, `import_pathwayextra_interactions`, `import_kinaseextra_interactions`, `import_ligreextra_interactions`

transmitter_param a list with arguments for `import_omnipath_intercell`, to define the transmitter side of intercellular connections

receiver_param a list with arguments for `import_omnipath_intercell`, to define the receiver side of intercellular connections

resources A character vector of resources to be applied to both the interactions and the annotations. For example, `resources = 'CellChatDB'` will download the transmitters and receivers defined by CellChatDB, connected by connections from CellChatDB.

entity_types Character, possible values are "protein", "complex" or both.

ligand_receptor Logical. If TRUE, only *ligand* and *receptor* annotations will be used instead of the more generic *transmitter* and *receiver* categories.

high_confidence Logical: shortcut to do some filtering in order to include only higher confidence interactions. The intercell database of OmniPath covers a very broad range of possible ways of cell to cell communication, and the pieces of information, such as localization, topology, function and interaction, are combined from many, often independent sources. This unavoidably result some weird and unexpected combinations which are false positives in the context of intercellular communication. This option sets some minimum criteria to remove most (but definitely not all!) of the wrong connections. These criteria are the followings: 1) the receiver must be plasma membrane transmembrane; 2) the curation effort for interactions must be larger than one; 3) the consensus score for annotations must be larger than the 50 percentile within the generic category (you can override this by `consensus_percentile`). 4) the transmitter must be secreted or exposed on the plasma membrane. 5) The major localizations have to be supported by at least 30 percent of the relevant resources (you can override this by `loc_consensus_percentile`). 6) The datasets with lower level of curation (*kinaseextra* and *pathwayextra*) will be disabled. These criteria are of medium

	stringency, you can always tune them to be more relaxed or stringent by filtering manually, using filter_intercell_network .
simplify	Logical: keep only the most often used columns. This function combines a network data frame with two copies of the intercell annotation data frames, all of them already having quite some columns. With this option we keep only the names of the interacting pair, their intercellular communication roles, and the minimal information of the origin of both the interaction and the annotations.
unique_pairs	Logical: instead of having separate rows for each pair of annotations, drop the annotations and reduce the data frame to unique interacting pairs. See unique_intercell_network for details.
consensus_percentile	Numeric: a percentile cut off for the consensus score of generic categories in intercell annotations. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_consensus_percentile	Numeric: similar to consensus_percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be TRUE only where at least 50 percent of the resources support these.
omnipath	Logical: shortcut to include the <i>omnipath</i> dataset in the interactions query.
ligreextra	Logical: shortcut to include the <i>ligreextra</i> dataset in the interactions query.
kinaseextra	Logical: shortcut to include the <i>kinaseextra</i> dataset in the interactions query.
pathwayextra	Logical: shortcut to include the <i>pathwayextra</i> dataset in the interactions query.
...	If simplify or unique_pairs is TRUE, additional column names can be passed here to <code>dplyr::select</code> on the final data frame. Otherwise ignored.

Details

By default this function creates almost the largest possible network of intercellular interactions. However, this might contain a large number of false positives. Please refer to the documentation of the arguments, especially `high_confidence`, and the [filter_intercell_network](#) function. Note: if you restrict the query to certain intercell annotation resources or small categories, it's not recommended to use the `consensus_percentile` or `high_confidence` options, instead filter the network with [filter_intercell_network](#) for more consistent results.

Value

A dataframe containing information about protein-protein interactions and the inter-cellular roles of the proteins involved in those interactions.

See Also

- [get_intercell_categories](#)
- [get_intercell_generic_categories](#)
- [import_omnipath_intercell](#)
- [import_omnipath_interactions](#)
- [import_pathwayextra_interactions](#)
- [import_kinaseextra_interactions](#)
- [import_ligrecextra_interactions](#)
- [unique_intercell_network](#)
- [simplify_intercell_network](#)
- [filter_intercell_network](#)

Examples

```
intercell_network <- import_intercell_network(  
  interactions_param = list(datasets = 'ligrecextra'),  
  receiver_param = list(categories = c('receptor', 'transporter')),  
  transmitter_param = list(categories = c('ligand', 'secreted_enzyme'))  
)
```

```
import_kinaseextra_interactions
```

Imports interactions from the 'kinase extra' dataset of OmniPath

Description

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=kinaseextra>, which contains enzyme-substrate interactions without literature reference. The enzyme-substrate interactions supported by literature references are part of the 'omnipath' dataset.

Usage

```
import_kinaseextra_interactions(  
  resources = NULL,  
  organism = 9606,  
  fields = NULL,  
  default_fields = TRUE,  
  references_by_resource = TRUE,  
  exclude = NULL,  
  ...  
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	Optional additional arguments.

Value

A dataframe containing enzyme-substrate interactions without literature reference

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-
  import_kinaseextra_interactions(
    resources = c('PhosphoPoint', 'PhosphoSite'),
    organism = 9606
  )
```

```
import_ligrecextra_interactions
```

Imports interactions from the 'ligrec extra' dataset of OmniPath

Description

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=ligrecextra>, which contains ligand-receptor interactions without literature reference. The ligand-receptor interactions supported by literature references are part of the 'omnipath' dataset.

Usage

```
import_ligrecextra_interactions(
  resources = NULL,
  organism = 9606,
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	optional additional arguments

Value

A dataframe containing ligand-receptor interactions including the ones without literature references

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <- import_ligrecextra_interactions(
  resources = c('HPRD', 'Guide2Pharma'),
  organism = 9606
)
```

```
import_lncrna_mrna_interactions
```

Imports interactions from the lncRNA-mRNA dataset of OmniPath

Description

Imports the dataset from: https://omnipathdb.org/interactions?datasets=lncrna_mrna, which contains lncRNA-mRNA interactions

Usage

```
import_lncrna_mrna_interactions(
  resources = NULL,
  organism = 9606,
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	optional additional arguments

Value

A dataframe containing lncRNA-mRNA interactions

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-  
  import_lncrna_mrna_interactions(  
    resources = c('ncRDeathDB')  
  )
```

```
import_mirnatarget_interactions
```

Imports interactions from the miRNA-target dataset of OmniPath

Description

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=mirnatarget>, which contains miRNA-mRNA interactions.

Usage

```
import_mirnatarget_interactions(  
  resources = NULL,  
  organism = 9606,  
  fields = NULL,  
  default_fields = TRUE,  
  references_by_resource = TRUE,  
  exclude = NULL,  
  ...  
)
```

Arguments

- | | |
|----------------|---|
| resources | interactions not reported in these databases are removed. See get_interaction_resources for more information. |
| organism | Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse |
| fields | The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE. |
| default_fields | whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added. |

```
references_by_resource
    if FALSE, removes the resource name prefixes from the references (PubMed
    IDs); this way the information which reference comes from which resource will
    be lost and the PubMed IDs will be unique.
exclude      Character: datasets or resources to exclude.
...         optional additional arguments
```

Value

A dataframe containing miRNA-mRNA interactions

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-
  import_mirnatarget_interactions(
    resources = c('miRTarBase', 'miRecords')
  )
```

```
import_omnipath_annotations
```

Imports annotations from OmniPath

Description

Imports protein annotations about function, localization, expression, structure and other properties of proteins from OmniPath <https://omnipathdb.org/annotations>. Note: there might be also a few miRNAs annotated; a vast majority of protein complex annotations are inferred from the annotations of the members: if all members carry the same annotation the complex inherits.

Usage

```
import_omnipath_annotations(
  proteins = NULL,
  resources = NULL,
  wide = FALSE,
  ...
)
```

Arguments

proteins	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 download annotations for protein complexes. To do so, write 'COMPLEX:' right before the genesymbols of the genes integrating the complex. Check the vignette for examples.
resources	Load the annotations only from these databases. See get_annotation_resources for possible values.
wide	Convert the annotation table to wide format, which corresponds more or less to the original resource. If the data comes from more than one resource a list of wide tables will be returned. See examples at pivot_annotations .
...	Additional arguments.

Details

Downloading the full annotations dataset 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 resources, depending on your interest. You can always download the full database from https://archive.omnipathdb.org/omnipath_webservice_annotations__recent.tsv using any standard R or readr method.

Value

A data frame containing different gene and complex annotations.

See Also

- [get_annotation_databases](#)
- [pivot_annotations](#)

Examples

```
annotations <- import_omnipath_annotations(  
  proteins = c('TP53', 'LMNA'),  
  resources = c('HPA_subcellular')  
)
```

```
import_omnipath_complexes
```

Imports protein complexes from OmniPath

Description

Imports the complexes stored in Omnipath database from <https://omnipathdb.org/complexes>.

Usage

```
import_omnipath_complexes(resources = NULL, ...)
```

Arguments

resources	complexes not reported in these databases are removed. See get_complexes_databases for more information.
...	optional additional arguments

Value

A dataframe containing information about complexes

See Also

- [get_complexes_databases](#)

Examples

```
complexes = import_omnipath_complexes(  
  resources = c('CORUM', 'hu.MAP')  
)
```

```
import_omnipath_enzsub
```

Imports enzyme-substrate relationships from OmniPath

Description

Imports the enzyme-substrate (more exactly, enzyme-PTM) relationship database from <https://omnipathdb.org/enzsub>

Usage

```
import_omnipath_enzsub(  
  resources = NULL,  
  organism = 9606,  
  fields = NULL,  
  default_fields = TRUE,  
  references_by_resource = TRUE,  
  exclude = NULL,  
  ...  
)
```

Arguments

resources	PTMs not reported in these databases are removed. See get_ptms_databases for more information.
organism	PTMs are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
fields	You can define here additional fields to be added to the result. If used, set the next argument, default_fields, to FALSE.
default_fields	Whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the fields argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	Optional additional arguments.

Value

A data frame containing the information about ptms

See Also

- [get_enzsub_resources](#)
- [import_omnipath_interactions](#)
- [enzsub_graph](#)
- [print_interactions](#)

Examples

```
enzsub <- import_omnipath_enzsub(
  resources = c('PhosphoSite', 'SIGNOR'),
  organism = 9606
)
```

```
import_omnipath_interactions
```

Imports interactions from the 'omnipath' dataset of Omnipath

Description

Imports the database from <https://omnipathdb.org/interactions>, which contains only interactions supported by literature references. This part of the interaction database compiled a similar way as it has been presented in the first paper describing OmniPath (Turei et al. 2016).

Usage

```
import_omnipath_interactions(
  resources = NULL,
  organism = 9606,
  datasets = "omnipath",
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
datasets	Names of the interaction datasets to download: omnipath (by default). Other possibilities are: pathwayextra, kinaseextra, ligreextra, dorothea,tf_target, mirnatarget, tf_mirna, lncrna_mrna. The user can select multiple datasets as for example: c('omnipath', 'pathwayextra', 'kinaseextra')
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	optional additional arguments

Value

A dataframe of protein-protein interactions

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions = import_omnipath_interactions(  
    resources = c('SignalLink3'),  
    organism = 9606  
)
```

```
import_omnipath_intercell  
    Imports OmniPath intercell annotations
```

Description

Imports the OmniPath intercellular communication role annotation database from <https://omnipathdb.org/intercell>. It 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(  
    categories = NULL,  
    resources = NULL,  
    parent = NULL,  
    scope = NULL,  
    aspect = NULL,  
    source = NULL,  
    transmitter = NULL,  
    receiver = NULL,  
    secreted = NULL,  
    plasma_membrane_peripheral = NULL,  
    plasma_membrane_transmembrane = NULL,  
    proteins = NULL,  
    topology = NULL,  
    causality = NULL,  
    consensus_percentile = NULL,  
    loc_consensus_percentile = NULL,  
    ...  
)
```

Arguments

categories	vector containing the categories to be retrieved. All the genes belonging to those categories will be returned. For further information about the categories see code get_intercell_categories .
resources	limit the query to certain resources; see the available resources by get_intercell_resources .

parent	vector containing the parent classes to be retrieved. All the genes belonging to those classes will be returned. For further information about the main classes see get_intercell_categories .
scope	either 'specific' or 'generic'
aspect	either 'locational' or 'functional'
source	either 'resource_specific' or 'composite'
transmitter	logical, include only transmitters i.e. proteins delivering signal from a cell to its environment.
receiver	logical, include only receivers i.e. proteins delivering signal to the cell from its environment.
secreted	logical, include only secreted proteins
plasma_membrane_peripheral	logical, include only plasma membrane peripheral membrane proteins.
plasma_membrane_transmembrane	logical, include only plasma membrane transmembrane proteins.
proteins	limit the query to certain proteins
topology	topology categories: one or more of 'secreted' (sec), 'plasma_membrane_peripheral' (pmp), 'plasma_membrane_transmembrane' (pmtm) (both short or long notation can be used).
causality	'transmitter' (trans), 'receiver' (rec) or 'both' (both short or long notation can be used).
consensus_percentile	Numeric: a percentile cut off for the consensus score of generic categories. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_consensus_percentile	Numeric: similar to codeconsensus_percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be true only where at least 50 percent of the resources support these.
...	Additional optional arguments, ignored.

Value

A dataframe containing information about roles in intercellular signaling.

See Also

- [get_intercell_categories](#)
- [get_intercell_generic_categories](#)
- [import_intercell_network](#)
- [intercell_consensus_filter](#)

Examples

```
intercell <- import_omnipath_intercell(categories = 'ecm')
```

```
import_pathwayextra_interactions
```

Imports interactions from the 'pathway extra' dataset of Omnipath

Description

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=pathwayextra>, which contains activity flow interactions without literature reference. The activity flow interactions supported by literature references are part of the 'omnipath' dataset.

Usage

```
import_pathwayextra_interactions(
  resources = NULL,
  organism = 9606,
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose one of those: 9606 human (default), 10116 rat or 10090 Mouse.
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.

```
references_by_resource
    if FALSE, removes the resource name prefixes from the references (PubMed
    IDs); this way the information which reference comes from which resource will
    be lost and the PubMed IDs will be unique.
exclude      Character: datasets or resources to exclude.
...         optional additional arguments
```

Value

A dataframe containing activity flow interactions between proteins without literature reference

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-
  import_pathwayextra_interactions(
    resources = c('BioGRID', 'IntAct'),
    organism = 9606
  )
```

```
import_post_translational_interactions
    Imports all post-translational interactions from OmniPath
```

Description

Imports the dataset from all post-translational datasets of OmniPath.

Usage

```
import_post_translational_interactions(
  resources = NULL,
  organism = 9606,
  exclude = NULL,
  references_by_resource = TRUE,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
exclude	Character: datasets or resources to exclude.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
...	optional additional arguments

Value

A dataframe containing post-translational interactions

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-  
  import_post_translational_interactions(  
    resources = c('BioGRID')  
  )
```

```
import_tf_mirna_interactions
```

Imports interactions from the TF-miRNA dataset of OmniPath

Description

Imports the dataset from: https://omnipathdb.org/interactions?datasets=tf_mirna, which contains transcription factor-miRNA gene interactions

Usage

```
import_tf_mirna_interactions(
  resources = NULL,
  organism = 9606,
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
fields	The user can define here the fields to be added. If used, set the next argument, 'default_fields', to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the 'fields' argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	optional additional arguments

Value

A dataframe containing TF-miRNA interactions

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-
  import_tf_mirna_interactions(
    resources = c('TransmiR')
  )
```

```
import_tf_target_interactions
```

Imports interactions from the TF-target dataset of OmniPath

Description

Imports the dataset from: https://omnipathdb.org/interactions?datasets=tf_target, which contains transcription factor-target protein coding gene interactions. Note: this is not the only TF-target dataset in OmniPath, ‘dorothea’ is the other one and the ‘tf_mirna’ dataset provides TF-miRNA gene interactions.

Usage

```
import_tf_target_interactions(
  resources = NULL,
  organism = 9606,
  fields = NULL,
  default_fields = TRUE,
  references_by_resource = TRUE,
  exclude = NULL,
  ...
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
fields	The user can define here the fields to be added. If used, set the next argument, ‘default_fields’, to FALSE.
default_fields	whether to include the default fields (columns) for the query type. If FALSE, only the fields defined by the user in the ‘fields’ argument will be added.
references_by_resource	if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.
exclude	Character: datasets or resources to exclude.
...	Optional additional arguments

Value

A dataframe containing TF-target interactions

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-  
  import_tf_target_interactions(  
    resources = c('DoRothEA', 'SIGNOR')  
  )
```

```
import_transcriptional_interactions
```

Imports all TF-target interactions from OmniPath

Description

Imports the dataset from: https://omnipathdb.org/interactions?datasets=tf_target,dorothea, which contains transcription factor-target protein coding gene interactions.

Usage

```
import_transcriptional_interactions(  
  resources = NULL,  
  organism = 9606,  
  dorothea_levels = c("A", "B"),  
  references_by_resource = TRUE,  
  exclude = NULL,  
  ...  
)
```

Arguments

resources	interactions not reported in these databases are removed. See get_interaction_resources for more information.
organism	Interactions are available for human, mouse and rat. Choose among: 9606 human (default), 10116 rat and 10090 Mouse
dorothea_levels	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.

references_by_resource
 if FALSE, removes the resource name prefixes from the references (PubMed IDs); this way the information which reference comes from which resource will be lost and the PubMed IDs will be unique.

exclude
 Character: datasets or resources to exclude.

...
 Optional additional arguments.

Value

A dataframe containing TF-target interactions.

See Also

- [get_interaction_resources](#)
- [import_all_interactions](#)
- [interaction_graph](#)
- [print_interactions](#)

Examples

```
interactions <-
  import_transcriptional_interactions(
    resources = c('PAZAR', 'ORegAnno', 'DoRothEA')
  )
```

inbiomap_download *Downloads and preprocesses network data from InWeb InBioMap*

Description

Downloads the data by [inbiomap_raw](#), extracts the UniProt IDs, Gene Symbols and scores and removes the irrelevant columns.

Usage

```
inbiomap_download(...)
```

Arguments

... Passed to [inbiomap_raw](#).

Value

A data frame (tibble) of interactions.

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

```

inbiomap_interactions <- inbiomap_download()
inbiomap_interactions

# # A tibble: 625,641 x 7
#   uniprot_a uniprot_b genesymbol_a genesymbol_b inferred score1 score2
#   <chr>     <chr>     <chr>         <chr>         <lgl>   <dbl> <dbl>
# 1 A0A5B9    P01892     TRBC2         HLA-A         FALSE   0.417 0.458
# 2 A0AUZ9    Q96CV9     KANSL1L       OPTN          FALSE   0.155 0.0761
# 3 A0AV02    P24941     SLC12A8       CDK2          TRUE    0.156 0.0783
# 4 A0AV02    Q00526     SLC12A8       CDK3          TRUE    0.157 0.0821
# 5 A0AV96    P0CG48     RBM47         UBC           FALSE   0.144 0.0494
# # . with 625,631 more rows

```

inbiomap_raw

*Downloads network data from InWeb InBioMap***Description**

Downloads the data from <https://inbio-discover.com/map.html#downloads> in tar.gz format, extracts the PSI MITAB table and returns it as a data frame.

Usage

```
inbiomap_raw(curl_verbose = FALSE)
```

Arguments

`curl_verbose` Logical. Perform CURL requests in verbose mode for debugging purposes.

Value

A data frame (tibble) with the extracted interaction table.

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

```
inbiomap_psimitab <- inbiomap_raw()
```

interaction_graph	<i>Build Omnipath interaction graph</i>
-------------------	---

Description

Transforms the interactions data frame to an igraph graph object.

Usage

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

Arguments

interactions data.frame created by

- `import_omnipath_enzsub`
- `import_omnipath_interactions`
- `import_pathwayextra_interactions`
- `import_kinaseextra_interactions`
- `import_ligreextra_interactions`
- `import_post_translational_interactions`
- `import_dorothea_interactions`
- `import_tf_target_interactions`
- `import_transcriptional_interactions`
- `import_mirnatarget_interactions`
- `import_all_interactions`

Value

An igraph graph object.

See Also

- `import_omnipath_interactions`
- `import_pathwayextra_interactions`
- `import_kinaseextra_interactions`
- `import_ligreextra_interactions`
- `import_dorothea_interactions`
- `import_mirnatarget_interactions`
- `import_all_interactions`
- `giant_component`
- `find_all_paths`

Examples

```
interactions <- import_omnipath_interactions(resources = c('Signalink3'))
g <- interaction_graph(interactions)
```

intercell_categories *Full list of intercell categories and resources*

Description

Full list of intercell categories and resources

Usage

```
intercell_categories()
```

Value

A data frame of categories and resources.

Examples

```
ic_cat <- intercell_categories()
ic_cat
# # A tibble: 1,125 x 3
#   category          parent          database
#   <chr>             <chr>             <chr>
# 1 transmembrane    transmembrane     UniProt_location
# 2 transmembrane    transmembrane     UniProt_topology
# 3 transmembrane    transmembrane     UniProt_keyword
# 4 transmembrane    transmembrane_predicted Phobius
# 5 transmembrane_phobius transmembrane_predicted Almen2009
# # . with 1,120 more rows
```

intercell_consensus_filter
Quality filter for intercell annotations

Description

Quality filter for intercell annotations

Usage

```
intercell_consensus_filter(data, percentile = NULL, loc_percentile = NULL)
```

Arguments

data	A data frame with intercell annotations, as provided by import_omnipath_intercell .
percentile	Numeric: a percentile cut off for the consensus score of composite categories. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_percentile	Numeric: similar to percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be TRUE only where at least 50 percent of the resources support these.

Value

The data frame in data filtered by the consensus scores.

Examples

```
intercell <- import_omnipath_intercell(parent = c('ligand', 'receptor'))
nrow(intercell)
# [1] 50174
intercell_q50 <- intercell_consensus_filter(intercell, 50)
nrow(intercell_q50)
# [1] 42863
```

is_ontology_id	<i>Looks like an ontology ID</i>
----------------	----------------------------------

Description

Tells if the input has the typical format of ontology IDs, i.e. a code of capital letters, a colon, followed by a numeric code.

Usage

```
is_ontology_id(terms)
```

Arguments

terms	Character vector with strings to check.
-------	---

Value

A logical vector with the same length as the input.

Examples

```
is_ontology_id(c('GO:000001', 'reproduction'))  
# [1] TRUE FALSE
```

kegg_info

Information about a KEGG Pathway

Description

Information about a KEGG Pathway

Usage

```
kegg_info(pathway_id)
```

Arguments

pathway_id Character: a KEGG Pathway identifier, e.g. "hsa04710". For a complete list of IDs see [kegg_pathway_list](#).

Value

List with the pathway information.

See Also

- [kegg_pathway_list](#)
- [kegg_picture](#)
- [kegg_open](#)

Examples

```
kegg_info('map00563')
```

kegg_open	<i>Open a KEGG Pathway diagram in the browser</i>
-----------	---

Description

Open a KEGG Pathway diagram in the browser

Usage

```
kegg_open(pathway_id)
```

Arguments

pathway_id Character: a KEGG Pathway identifier, e.g. "hsa04710". For a complete list of IDs see [kegg_pathway_list](#).

Details

To open URLs in the web browser the "browser" option must to be set to a a valid executable. You can check the value of this option by `getOption("browser")`. If your browser is firefox and the executable is located in the system path, you can set the option to point to it: `options(browser = "firefox")`. To make it a permanent setting, you can also include this in your `.Rprofile` file.

Value

Returns NULL.

See Also

- [kegg_pathway_list](#)
- [kegg_picture](#)
- [kegg_info](#)

Examples

```
if(any(getOption('browser') != '')) kegg_open('hsa04710')
```

`kegg_pathways_download`*Download the KEGG Pathways database*

Description

Downloads all pathway diagrams in the KEGG Pathways database in KGML format and processes the XML to extract the interactions.

Usage

```
kegg_pathways_download(max_expansion = NULL, simplify = FALSE)
```

Arguments

`max_expansion` Numeric: the maximum number of relations derived from a single relation record. As one entry might represent more than one molecular entities, one relation might yield a large number of relations in the processing. This happens in a combinatorial way, e.g. if the two entries represent 3 and 4 entities, that results 12 relations. If NULL, all relations will be expanded.

`simplify` Logical: remove KEGG's internal identifiers and the pathway annotations, keep only unique interactions with direction and effect sign.

Value

A data frame (tibble) of interactions.

See Also

- [kegg_pathway_list](#)
- [kegg_process](#)
- [kegg_pathway_download](#)

Examples

```
kegg_pw <- kegg_pathways_download(simplify = TRUE)
kegg_pw
# # A tibble: 6,765 x 6
#   uniprot_source uniprot_target type effect genesymbol_source
#   <chr>          <chr>      <chr> <chr> <chr>
# 1 Q03113        Q15283      PPre1 activ. GNA12
# 2 Q9Y4G8        P62070      PPre1 activ. RAPGEF2
# 3 Q13972        P62070      PPre1 activ. RASGRF1
# 4 O95267        P62070      PPre1 activ. RASGRP1
# 5 P62834        P15056      PPre1 activ. RAP1A
# # . with 6,760 more rows, and 1 more variable: genesymbol_target <chr>
```

kegg_pathway_download *Download one KEGG pathway*

Description

Downloads one pathway diagram from the KEGG Pathways database in KGML format and processes the XML to extract the interactions.

Usage

```
kegg_pathway_download(  
  pathway_id,  
  process = TRUE,  
  max_expansion = NULL,  
  simplify = FALSE  
)
```

Arguments

pathway_id	Character: a KEGG pathway identifier, for example "hsa04350".
process	Logical: process the data or return it in raw format. processing means joining the entries and relations into a single data frame and adding UniProt IDs.
max_expansion	Numeric: the maximum number of relations derived from a single relation record. As one entry might represent more than one molecular entities, one relation might yield a large number of relations in the processing. This happens in a combinatorial way, e.g. if the two entries represent 3 and 4 entities, that results 12 relations. If NULL, all relations will be expanded.
simplify	Logical: remove KEGG's internal identifiers and the pathway annotations, keep only unique interactions with direction and effect sign.

Value

A data frame (tibble) of interactions if process is TRUE, otherwise a list with two data frames: "entries" is a raw table of the entries while "relations" is a table of relations extracted from the KGML file.

See Also

- [kegg_process](#)
- [kegg_pathways_download](#)
- [kegg_pathway_list](#)

Examples

```
tgf_pathway <- kegg_pathway_download('hsa04350')
tgf_pathway

# # A tibble: 50 x 12
#   source target type effect arrow relation_id kegg_id_source
#   <chr> <chr> <chr> <chr> <chr> <chr> <chr>
# 1 51 49 PPre1 activ. --> hsa04350:1 hsa:7040 hsa:.
# 2 57 55 PPre1 activ. --> hsa04350:2 hsa:151449 hs.
# 3 34 32 PPre1 activ. --> hsa04350:3 hsa:3624 hsa:.
# 4 20 17 PPre1 activ. --> hsa04350:4 hsa:4838
# 5 60 46 PPre1 activ. --> hsa04350:5 hsa:4086 hsa:.
# # . with 45 more rows, and 5 more variables: genesymbol_source <chr>,
# # uniprot_source <chr>, kegg_id_target <chr>,
# # genesymbol_target <chr>, uniprot_target <chr>
```

kegg_pathway_list *List of KEGG pathways*

Description

Retrieves a list of available KEGG pathways.

Usage

```
kegg_pathway_list()
```

Value

Data frame of pathway names and identifiers.

See Also

- [kegg_process](#)
- [kegg_pathway_download](#)
- [kegg_pathways_download](#)
- [kegg_open](#)
- [kegg_picture](#)
- [kegg_info](#)

Examples

```
kegg_pws <- kegg_pathway_list()
kegg_pws
# # A tibble: 521 x 2
#   id      name
#   <chr>   <chr>
# 1 map01100 Metabolic pathways
# 2 map01110 Biosynthesis of secondary metabolites
# 3 map01120 Microbial metabolism in diverse environments
# 4 map01200 Carbon metabolism
# 5 map01210 2-Oxocarboxylic acid metabolism
# 6 map01212 Fatty acid metabolism
# 7 map01230 Biosynthesis of amino acids
# # . with 514 more rows
```

kegg_picture

Download a pathway diagram as a picture

Description

Downloads a KEGG Pathway diagram as a PNG image.

Usage

```
kegg_picture(pathway_id, path = NULL)
```

Arguments

pathway_id	Character: a KEGG Pathway identifier, e.g. "hsa04710". For a complete list of IDs see kegg_pathway_list .
path	Character: save the image to this path. If NULL, the image will be saved in the current directory under the name <pathway_id>.png.

Value

Invisibly returns the path to the downloaded file.

See Also

[kegg_pathway_list](#)

- [kegg_pathway_list](#)
- [kegg_open](#)
- [kegg_info](#)

Examples

```
kegg_picture('hsa04710')
kegg_picture('hsa04710', path = 'foo/bar')
kegg_picture('hsa04710', path = 'foo/bar/circadian.png')
```

kegg_process	<i>Interactions from KGML</i>
--------------	-------------------------------

Description

Processes KEGG Pathways data extracted from a KGML file. Joins the entries and relations into a single data frame and translates the Gene Symbols to UniProt IDs.

Usage

```
kegg_process(entries, relations, max_expansion = NULL, simplify = FALSE)
```

Arguments

entries	A data frames with entries extracted from a KGML file by kegg_pathway_download .
relations	A data frames with relations extracted from a KGML file by kegg_pathway_download .
max_expansion	Numeric: the maximum number of relations derived from a single relation record. As one entry might represent more than one molecular entities, one relation might yield a large number of relations in the processing. This happens in a combinatorial way, e.g. if the two entries represent 3 and 4 entities, that results 12 relations. If NULL, all relations will be expanded.
simplify	Logical: remove KEGG's internal identifiers and the pathway annotations, keep only unique interactions with direction and effect sign.

Value

A data frame (tibble) of interactions. In rare cases when a pathway doesn't contain any relation, returns NULL.

See Also

- [kegg_pathway_download](#)
- [kegg_pathways_download](#)
- [kegg_pathway_list](#)

Examples

```

hsa04350 <- kegg_pathway_download('hsa04350', process = FALSE)
tgf_pathway <- kegg_process(hsa04350$entries, hsa04350$relations)
tgf_pathway

# # A tibble: 50 x 12
#   source target type effect arrow relation_id kegg_id_source
#   <chr> <chr> <chr> <chr> <chr> <chr> <chr>
# 1 51 49 PPre1 activ. --> hsa04350:1 hsa:7040 hsa:.
# 2 57 55 PPre1 activ. --> hsa04350:2 hsa:151449 hs.
# 3 34 32 PPre1 activ. --> hsa04350:3 hsa:3624 hsa:.
# 4 20 17 PPre1 activ. --> hsa04350:4 hsa:4838
# 5 60 46 PPre1 activ. --> hsa04350:5 hsa:4086 hsa:.
# # . with 45 more rows, and 5 more variables: genesymbol_source <chr>,
# # uniprot_source <chr>, kegg_id_target <chr>,
# # genesymbol_target <chr>, uniprot_target <chr>

```

load_db

*Load a built in database***Description**

Load a built in database

Usage

```
load_db(key, param = list())
```

Arguments

key	Character: the key of the database to load. For a list of available keys see omnipath_show_db .
param	List: override the defaults or pass further parameters to the database loader function. See the loader functions and their default parameters in omnipath_show_db .

Details

This function loads a database which is stored within the package namespace until its expiry. The loaded database is accessible by [get_db](#) and the loading process is typically initiated by [get_db](#), not by the users directly.

Value

Returns NULL.

See Also

[omnipath_show_db](#).

Examples

```
load_db('go_slim')
omnipath_show_db()
```

nichenet_build_model *Construct a NicheNet ligand-target model*

Description

Construct a NicheNet ligand-target model

Usage

```
nichenet_build_model(optimization_results, networks, use_weights = TRUE)
```

Arguments

optimization_results	The outcome of NicheNet parameter optimization as produced by nichenet_optimization .
networks	A list with NicheNet format signaling, ligand-receptor and gene regulatory networks as produced by nichenet_networks .
use_weights	Logical: whether to use the optimized weights.

Value

A named list with two elements: 'weighted_networks' and 'optimized_parameters'.

Examples

```
expression <- nichenet_expression_data()

networks <- nichenet_networks()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)
```

nichenet_expression_data

Expression data from ligand-receptor perturbation experiments used by NicheNet

Description

NicheNet uses expression data from a collection of published ligand or receptor KO or perturbation experiments to build its model. This function retrieves the original expression data, deposited in Zenodo (<https://zenodo.org/record/3260758>).

Usage

```
nichenet_expression_data()
```

Value

Nested list, each element contains a data frame of processed expression data and key variables about the experiment.

Examples

```
exp_data <- nichenet_expression_data()
head(names(exp_data))
# [1] "bmp4_tgfb"      "tgfb_bmp4"      "nodal_Nodal"    "spectrum_IL4"
# [5] "spectrum_Tnf"  "spectrum_Ifng"
purrr::map_chr(head(exp_data), 'from')
#   bmp4_tgfb      tgfb_bmp4      nodal_Nodal    spectrum_IL4  spectrum_Tnf
#   "BMP4"        "TGFB1"        "NODAL"        "IL4"        "TNF"
# spectrum_Ifng
#   "IFNG"
```

nichenet_gr_network

Builds a NicheNet gene regulatory network

Description

Builds gene regulatory network prior knowledge for NicheNet using multiple resources.

Usage

```
nichenet_gr_network(  
  omnipath = list(),  
  harmonizome = list(),  
  regnetwork = list(),  
  htridb = list(),  
  remap = list(),  
  evex = list(),  
  pathwaycommons = list(),  
  trrust = list(),  
  only_omnipath = FALSE  
)
```

Arguments

omnipath	List with paramaters to be passed to nichenet_gr_network_omnipath .
harmonizome	List with paramaters to be passed to nichenet_gr_network_harmonizome .
regnetwork	List with paramaters to be passed to nichenet_gr_network_regnetwork .
htridb	List with paramaters to be passed to nichenet_gr_network_htridb .
remap	List with paramaters to be passed to nichenet_gr_network_remap .
evex	List with paramaters to be passed to nichenet_gr_network_evex .
pathwaycommons	List with paramaters to be passed to nichenet_gr_network_pathwaycommons .
trrust	List with paramaters to be passed to nichenet_gr_network_trrust .
only_omnipath	Logical: a shortcut to use only OmniPath as network resource.

Value

A network data frame (tibble) with gene regulatory interactions suitable for use with NicheNet.

See Also

- [nichenet_gr_network_evex](#)
- [nichenet_gr_network_harmonizome](#)
- [nichenet_gr_network_htridb](#)
- [nichenet_gr_network_omnipath](#)
- [nichenet_gr_network_pathwaycommons](#)
- [nichenet_gr_network_regnetwork](#)
- [nichenet_gr_network_remap](#)
- [nichenet_gr_network_trrust](#)

Examples

```
# load everything with the default parameters:
gr_network <- nichenet_gr_network()

# less targets from ReMap, not using RegNetwork:
gr_network <- nichenet_gr_network(
  # I needed to disable ReMap here due to some issues
  # of one of the Bioconductor build servers
  # remap = list(top_targets = 200),
  remap = NULL,
  regnetwork = NULL,
)

# use only OmniPath:
gr_network_omnipath <- nichenet_gr_network(only_omnipath = TRUE)
```

nichenet_gr_network_evex

NicheNet gene regulatory network from EVEX

Description

Builds a gene regulatory network using data from the EVEX database and converts it to a format suitable for NicheNet.

Usage

```
nichenet_gr_network_evex(
  top_confidence = 0.75,
  indirect = FALSE,
  regulation_of_expression = FALSE
)
```

Arguments

top_confidence Double, between 0 and 1. Threshold based on the quantile of the confidence score.

indirect Logical: whether to include indirect interactions.

regulation_of_expression Logical: whether to include also the "regulation of expression" type interactions.

Value

Data frame of interactions in NicheNet format.
Data frame with gene regulatory interactions in NicheNet format.

See Also

- [nichenet_gr_network](#)
- [evex_download](#)

Examples

```
# use only the 10% with the highest confidence:
evex_gr_network <- nichenet_gr_network_evex(top_confidence = .9)
```

```
nichenet_gr_network_harmonizome
NicheNet gene regulatory network from Harmonizome
```

Description

Builds gene regulatory network prior knowledge for NicheNet using Harmonizome

Usage

```
nichenet_gr_network_harmonizome(
  datasets = c("cheappi", "encodetfppi", "jasparpwm", "transfac", "transfacpwm",
    "motifmap", "geotf", "geokinase", "geogene"),
  ...
)
```

Arguments

datasets	The datasets to use. For possible values please refer to default value and the Harmonizome webpage.
...	Ignored.

Value

Data frame with gene regulatory interactions in NicheNet format.

See Also

- [nichenet_gr_network](#)
- [harmonizome_download](#)

Examples

```
# use only JASPAR and TRANSFAC:
hz_gr_network <- nichenet_gr_network_harmonizome(
  datasets = c('jasparpwm', 'transfac', 'transfacpwm')
)
```

`nichenet_gr_network_htridb`*NicheNet gene regulatory network from HTRIdb*

Description

Builds a gene regulatory network using data from the HTRIdb database and converts it to a format suitable for NicheNet.

Usage

```
nichenet_gr_network_htridb()
```

Value

Data frame with gene regulatory interactions in NicheNet format.

See Also

[htridb_download](#), [nichenet_gr_network](#)

Examples

```
htri_gr_network <- nichenet_gr_network_htridb()
```

`nichenet_gr_network_omnipath`*Builds gene regulatory network for NicheNet using OmniPath*

Description

Retrieves network prior knowledge from OmniPath and provides it in a format suitable for NicheNet. This method never downloads the ‘ligreextra’ dataset because the ligand-receptor interactions are supposed to come from [nichenet_lr_network_omnipath](#).

Usage

```
nichenet_gr_network_omnipath(min_curation_effort = 0, ...)
```

Arguments

`min_curation_effort`

Lower threshold for curation effort

`...`

Passed to [import_transcriptional_interactions](#)

Value

A network data frame (tibble) with gene regulatory interactions suitable for use with NicheNet.

See Also

- [nichenet_gr_network_evex](#)
- [nichenet_gr_network_harmonizome](#)
- [nichenet_gr_network_htridb](#)
- [nichenet_gr_network_omnipath](#)
- [nichenet_gr_network_pathwaycommons](#)
- [nichenet_gr_network_regnetwork](#)
- [nichenet_gr_network_remap](#)
- [nichenet_gr_network_trrust](#)

Examples

```
# use interactions up to confidence level "C" from DoRothEA:
op_gr_network <- nichenet_gr_network_omnipath(
  dorothea_levels = c('A', 'B', 'C')
)
```

nichenet_gr_network_pathwaycommons

NicheNet gene regulatory network from PathwayCommons

Description

Builds gene regulation prior knowledge for NicheNet using PathwayCommons.

Usage

```
nichenet_gr_network_pathwaycommons(
  interaction_types = "controls-expression-of",
  ...
)
```

Arguments

interaction_types

Character vector with PathwayCommons interaction types. Please refer to the default value and the PathwayCommons webpage.

... Ignored.

Value

Data frame with gene regulatory interactions in NicheNet format.

See Also

- [nichenet_gr_network](#)
- [pathwaycommons_download](#)

Examples

```
pc_gr_network <- nichenet_gr_network_pathwaycommons()
```

nichenet_gr_network_regnetwork

NicheNet gene regulatory network from RegNetwork

Description

Builds a gene regulatory network using data from the RegNetwork database and converts it to a format suitable for NicheNet.

Usage

```
nichenet_gr_network_regnetwork()
```

Value

Data frame with gene regulatory interactions in NicheNet format.

See Also

- [regnetwork_download](#)
- [nichenet_gr_network](#)

Examples

```
regn_gr_network <- nichenet_gr_network_regnetwork()
```

`nichenet_gr_network_remap`*NicheNet gene regulatory network from ReMap*

Description

Builds a gene regulatory network using data from the ReMap database and converts it to a format suitable for NicheNet.

Usage

```
nichenet_gr_network_remap(  
  score = 100,  
  top_targets = 500,  
  only_known_tfs = TRUE  
)
```

Arguments

<code>score</code>	Numeric: a minimum score between 0 and 1000, records with lower scores will be excluded. If NULL no filtering performed.
<code>top_targets</code>	Numeric: the number of top scoring targets for each TF. Essentially the maximum number of targets per TF. If NULL the number of targets is not restricted.
<code>only_known_tfs</code>	Logical: whether to exclude TFs which are not in TF census.

Value

Data frame with gene regulatory interactions in NicheNet format.

See Also

- [remap_filtered](#)
- [nichenet_gr_network](#)

Examples

```
# use only max. top 100 targets for each TF:  
remap_gr_network <- nichenet_gr_network_remap(top_targets = 100)
```

`nichenet_gr_network_trrust`*NicheNet gene regulatory network from TRRUST*

Description

Builds a gene regulatory network using data from the TRRUST database and converts it to a format suitable for NicheNet.

Usage

```
nichenet_gr_network_trrust()
```

Value

Data frame with gene regulatory interactions in NicheNet format.

See Also

- [trrust_download](#)
- [nichenet_gr_network](#)

Examples

```
trrust_gr_network <- nichenet_gr_network_trrust()
```

`nichenet_ligand_activities`*Calls the NicheNet ligand activity analysis*

Description

Calls the NicheNet ligand activity analysis

Usage

```
nichenet_ligand_activities(  
  ligand_target_matrix,  
  lr_network,  
  expressed_genes_transmitter,  
  expressed_genes_receiver,  
  genes_of_interest,  
  background_genes = NULL,  
  n_top_ligands = 42,  
  n_top_targets = 250  
)
```

Arguments

ligand_target_matrix	A matrix with rows and columns corresponding to ligands and targets, respectively. Produced by <code>nichenet_ligand_target_matrix</code> or <code>nichenetr::construct_ligand_target_ma</code>
lr_network	A data frame with ligand-receptor interactions, as produced by <code>nichenet_lr_network</code> .
expressed_genes_transmitter	Character vector with the gene symbols of the genes expressed in the cells transmitting the signal.
expressed_genes_receiver	Character vector with the gene symbols of the genes expressed in the cells receiving the signal.
genes_of_interest	Character vector with the gene symbols of the genes of interest. These are the genes in the receiver cell population that are potentially affected by ligands expressed by interacting cells (e.g. genes differentially expressed upon cell-cell interaction).
background_genes	Character vector with the gene symbols of the genes to be used as background.
n_top_ligands	How many of the top ligands to include in the ligand-target table.
n_top_targets	For each ligand, how many of the top targets to include in the ligand-target table.

Value

A named list with 'ligand_activities' (a tibble giving several ligand activity scores; following columns in the tibble: \$test_ligand, \$aucroc, \$aupr and \$pearson) and 'ligand_target_links' (a tibble with columns ligand, target and weight (i.e. regulatory potential score)).

Examples

```
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)
lt_matrix <- nichenet_ligand_target_matrix(
  nichenet_model$weighted_networks,
  networks$lr_network,
  nichenet_model$optimized_parameters
)
ligand_activities <- nichenet_ligand_activities(
  ligand_target_matrix = lt_matrix,
  lr_network = networks$lr_network,
  # the rest of the parameters should come
  # from your transcriptomics data:
  expressed_genes_transmitter = expressed_genes_transmitter,
  expressed_genes_receiver = expressed_genes_receiver,
  genes_of_interest = genes_of_interest
)
```

nichenet_ligand_target_links

Compiles a table with weighted ligand-target links

Description

A wrapper around `nichenetr::get_weighted_ligand_target_links` to compile a data frame with weighted links from the top ligands to their top targets.

Usage

```
nichenet_ligand_target_links(
  ligand_activities,
  ligand_target_matrix,
  genes_of_interest,
  n_top_ligands = 42,
  n_top_targets = 250
)
```

Arguments

`ligand_activities` Ligand activity table as produced by `nichenetr::predict_ligand_activities`.

`ligand_target_matrix` Ligand-target matrix as produced by `nichenetr::construct_ligand_target_matrix` or the wrapper around it in the current package: `nichenet_ligand_target_matrix`.

`genes_of_interest` Character vector with the gene symbols of the genes of interest. These are the genes in the receiver cell population that are potentially affected by ligands expressed by interacting cells (e.g. genes differentially expressed upon cell-cell interaction).

`n_top_ligands` How many of the top ligands to include in the ligand-target table.

`n_top_targets` For each ligand, how many of the top targets to include in the ligand-target table.

Value

A tibble with columns `ligand`, `target` and `weight` (i.e. regulatory potential score).

Examples

```
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)
lt_matrix <- nichenet_ligand_target_matrix(
  nichenet_model$weighted_networks,
  networks$l_r_network,
```



```

    nichenet_model$optimized_parameters
  )
  ligand_activities <- nichenet_ligand_activities(
    ligand_target_matrix = lt_matrix,
    lr_network = networks$lr_network,
    # the rest of the parameters should come
    # from your transcriptomics data:
    expressed_genes_transmitter = expressed_genes_transmitter,
    expressed_genes_receiver = expressed_genes_receiver,
    genes_of_interest = genes_of_interest
  )
  lt_links <- nichenet_ligand_target_links(
    ligand_activities = ligand_activities,
    ligand_target_matrix = lt_matrix,
    genes_of_interest = genes_of_interest,
    n_top_ligands = 20,
    n_top_targets = 100
  )

```

nichenet_ligand_target_matrix

Creates a NicheNet ligand-target matrix

Description

Creates a NicheNet ligand-target matrix

Usage

```

nichenet_ligand_target_matrix(
  weighted_networks,
  lr_network,
  optimized_parameters,
  use_weights = TRUE,
  construct_ligand_target_matrix_param = list()
)

```

Arguments

weighted_networks	Weighted networks as provided by nichenet_build_model .
lr_network	A data frame with ligand-receptor interactions, as produced by nichenet_lr_network .
optimized_parameters	The outcome of NicheNet parameter optimization as produced by nichenet_build_model .
use_weights	Logical: whether the network sources are weighted. In this function it only affects the output file name.
construct_ligand_target_matrix_param	Override parameters for <code>nichenetr::construct_ligand_target_matrix</code> .

Value

A matrix containing ligand-target probability scores.

Examples

```
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)
lt_matrix <- nichenet_ligand_target_matrix(
  nichenet_model$weighted_networks,
  networks$lr_network,
  nichenet_model$optimized_parameters
)
```

nichenet_lr_network *Builds a NicheNet ligand-receptor network*

Description

Builds ligand-receptor network prior knowledge for NicheNet using multiple resources.

Usage

```
nichenet_lr_network(
  omnipath = list(),
  guide2pharma = list(),
  ramilowski = list(),
  only_omnipath = FALSE,
  quality_filter_param = list()
)
```

Arguments

omnipath List with paramaters to be passed to [nichenet_lr_network_omnipath](#).

guide2pharma List with paramaters to be passed to [nichenet_lr_network_guide2pharma](#).

ramilowski List with paramaters to be passed to [nichenet_lr_network_ramilowski](#).

only_omnipath Logical: a shortcut to use only OmniPath as network resource.

quality_filter_param
Arguments for [filter_intercell_network](#) (quality filtering of the OmniPath ligand-receptor network). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

Value

A network data frame (tibble) with ligand-receptor interactions suitable for use with NicheNet.

See Also

- [nichenet_lr_network_omnipath](#)
- [nichenet_lr_network_guide2pharma](#)
- [nichenet_lr_network_ramilowski](#)
- [filter_intercell_network](#)

Examples

```
# load everything with the default parameters:
lr_network <- nichenet_lr_network()

# don't use Ramilowski:
lr_network <- nichenet_lr_network(ramilowski = NULL)

# use only OmniPath:
lr_network_omnipath <- nichenet_lr_network(only_omnipath = TRUE)
```

nichenet_lr_network_guide2pharma
Ligand-receptor network from Guide to Pharmacology

Description

Downloads ligand-receptor interactions from the Guide to Pharmacology database and converts it to a format suitable for NicheNet.

Usage

```
nichenet_lr_network_guide2pharma()
```

Value

Data frame with ligand-receptor interactions in NicheNet format.

See Also

[nichenet_lr_network_guide2pharma_download](#)

Examples

```
g2p_lr_network <- nichenet_lr_network_guide2pharma()
```

`nichenet_lr_network_omnipath`*Builds ligand-receptor network for NicheNet using OmniPath*

Description

Retrieves network prior knowledge from OmniPath and provides it in a format suitable for NicheNet. This method never downloads the ‘ligreextra’ dataset because the ligand-receptor interactions are supposed to come from [nichenet_lr_network_omnipath](#).

Usage

```
nichenet_lr_network_omnipath(quality_filter_param = list(), ...)
```

Arguments

`quality_filter_param`

List with arguments for [filter_intercell_network](#). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

`...`

Passed to [import_intercell_network](#)

Value

A network data frame (tibble) with ligand-receptor interactions suitable for use with NicheNet.

See Also

- [nichenet_lr_network](#)
- [import_intercell_network](#)

Examples

```
# use only ligand-receptor interactions (not for example ECM-adhesion):
op_lr_network <- nichenet_lr_network_omnipath(ligand_receptor = TRUE)

# use only CellPhoneDB and Guide to Pharmacology:
op_lr_network <- nichenet_lr_network_omnipath(
  resources = c('CellPhoneDB', 'Guide2Pharma')
)

# only interactions where the receiver is a transporter:
op_lr_network <- nichenet_lr_network_omnipath(
  receiver_param = list(parent = 'transporter')
)
```

`nichenet_lr_network_ramilowski`*Ligand-receptor network from Ramilowski 2015*

Description

Downloads ligand-receptor interactions from Supplementary Table 2 of the paper 'A draft network of ligand-receptor-mediated multicellular signalling in human' (Ramilowski et al. 2015, <https://www.nature.com/articles/ncomms8866>). It converts the downloaded table to a format suitable for NicheNet.

Usage

```
nichenet_lr_network_ramilowski(  
  evidences = c("literature supported", "putative")  
)
```

Arguments

`evidences` Character: evidence types, "literature supported", "putative" or both.

Value

Data frame with ligand-receptor interactions in NicheNet format.

See Also

- [nichenet_lr_network](#)
- [ramilowski_download](#)

Examples

```
# use only the literature supported data:  
rami_lr_network <- nichenet_lr_network_ramilowski(  
  evidences = 'literature supported'  
)
```

nichenet_main	<i>Executes the full NicheNet pipeline</i>
---------------	--

Description

Builds all prior knowledge data required by NicheNet. For this it calls a multitude of methods to download and combine data from various databases according to the settings. The content of the prior knowledge data is highly customizable, see the documentation of the related functions. After the prior knowledge is ready, it performs parameter optimization to build a NicheNet model. This results a weighted ligand- target matrix. Then, considering the expressed genes from user provided data, a gene set of interest and background genes, it executes the NicheNet ligand activity analysis.

Usage

```
nichenet_main(
  only_omnipath = FALSE,
  expressed_genes_transmitter = NULL,
  expressed_genes_receiver = NULL,
  genes_of_interest = NULL,
  background_genes = NULL,
  use_weights = TRUE,
  n_top_ligands = 42,
  n_top_targets = 250,
  signaling_network = list(),
  lr_network = list(),
  gr_network = list(),
  small = FALSE,
  tiny = FALSE,
  make_multi_objective_function_param = list(),
  objective_function_param = list(),
  mlrmo_optimization_param = list(),
  construct_ligand_target_matrix_param = list(),
  results_dir = NULL,
  quality_filter_param = list()
)
```

Arguments

only_omnipath Logical: use only OmniPath for network knowledge. This is a simple switch for convenience, further options are available by the other arguments. By default we use all available resources. The networks can be customized on a resource by resource basis, as well as providing custom parameters for individual resources, using the parameters 'signaling_network', 'lr_network' and 'gr_network'.

expressed_genes_transmitter Character vector with the gene symbols of the genes expressed in the cells transmitting the signal.

expressed_genes_receiver	Character vector with the gene symbols of the genes expressed in the cells receiving the signal.
genes_of_interest	Character vector with the gene symbols of the genes of interest. These are the genes in the receiver cell population that are potentially affected by ligands expressed by interacting cells (e.g. genes differentially expressed upon cell-cell interaction).
background_genes	Character vector with the gene symbols of the genes to be used as background.
use_weights	Logical: calculate and use optimized weights for resources (i.e. one resource seems to be better than another, hence the former is considered with a higher weight).
n_top_ligands	How many of the top ligands to include in the ligand-target table.
n_top_targets	How many of the top targets (for each of the top ligands) to consider in the ligand-target table.
signaling_network	A list of parameters for building the signaling network, passed to nichenet_signaling_network .
lr_network	A list of parameters for building the ligand-receptor network, passed to nichenet_lr_network .
gr_network	A list of parameters for building the gene regulatory network, passed to nichenet_gr_network .
small	Logical: build a small network for testing purposes, using only OmniPath data. It is also a high quality network, it is reasonable to try the analysis with this small network.
tiny	Logical: build an even smaller network for testing purposes. As this involves random subsetting, it's not recommended to use this network for analysis.
make_multi_objective_function_param	Override parameters for <code>smoof::makeMultiObjectiveFunction</code> .
objective_function_param	Override additional arguments passed to the objective function.
mlrmo_optimization_param	Override arguments for <code>nichenetr::mlrmo_optimization</code> .
construct_ligand_target_matrix_param	Override parameters for <code>nichenetr::construct_ligand_target_matrix</code> .
results_dir	Character: path to the directory to save intermediate and final outputs from NicheNet methods.
quality_filter_param	Arguments for filter_intercell_network (quality filtering of the OmniPath ligand-receptor network). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

Details

About *small* and *tiny* networks: Building a NicheNet model is computationally demanding, taking several hours to run. As this is related to the enormous size of the networks, to speed up testing we

can use smaller networks, around 1,000 times smaller, with few thousands of interactions instead of few millions. Random subsetting of the whole network would result disjunct fragments, instead we load only a few resources. To run the whole pipeline with tiny networks use [nichenet_test](#).

Value

A named list with the intermediate and final outputs of the pipeline: 'networks', 'expression', 'optimized_parameters', 'weighted_networks' and 'ligand_target_matrix'.

See Also

- [nichenet_networks](#)
- [nichenet_signaling_network](#)
- [nichenet_lr_network](#)
- [nichenet_gr_network](#)
- [nichenet_test](#)
- [nichenet_workarounds](#)
- [nichenet_results_dir](#)

Examples

```
nichenet_results <- nichenet_main(  
  # altering some network resource parameters, the rest  
  # of the resources will be loaded according to the defaults  
  signaling_network = list(  
    cpdb = NULL, # this resource will be excluded  
    inbiomap = NULL,  
    evex = list(min_confidence = 1.0) # override some parameters  
  ),  
  gr_network = list(only_omnipath = TRUE),  
  n_top_ligands = 20,  
  # override the default number of CPU cores to use  
  mlrmo_optimization_param = list(ncores = 4)  
)
```

nichenet_networks	<i>Builds NicheNet network prior knowledge</i>
-------------------	--

Description

Builds network knowledge required by NicheNet. For this it calls a multitude of methods to download and combine data from various databases according to the settings. The content of the prior knowledge data is highly customizable, see the documentation of the related functions.

Usage

```
nichenet_networks(
  signaling_network = list(),
  lr_network = list(),
  gr_network = list(),
  only_omnipath = FALSE,
  small = FALSE,
  tiny = FALSE,
  quality_filter_param = list()
)
```

Arguments

signaling_network	A list of parameters for building the signaling network, passed to nichenet_signaling_network
lr_network	A list of parameters for building the ligand-receptor network, passed to nichenet_lr_network
gr_network	A list of parameters for building the gene regulatory network, passed to nichenet_gr_network
only_omnipath	Logical: a shortcut to use only OmniPath as network resource.
small	Logical: build a small network for testing purposes, using only OmniPath data. It is also a high quality network, it is reasonable to try the analysis with this small network.
tiny	Logical: build an even smaller network for testing purposes. As this involves random subsetting, it's not recommended to use this network for analysis.
quality_filter_param	Arguments for filter_intercell_network (quality filtering of the OmniPath ligand-receptor network). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

Value

A named list with three network data frames (tibbles): the signaling, the ligand-receptor (lr) and the gene regulatory (gr) networks.

See Also

- [nichenet_signaling_network](#)
- [nichenet_lr_network](#)
- [nichenet_gr_network](#)

Examples

```
networks <- nichenet_networks()
dplyr::sample_n(networks$gr_network, 10)
# # A tibble: 10 x 4
#   from   to     source      database
#   <chr> <chr> <chr>      <chr>
```

```

# 1 MAX    ALG3    harmonizome_ENCODE    harmonizome
# 2 MAX    IMPDH1  harmonizome_ENCODE    harmonizome
# 3 SMAD5   LCP1    Remap_5                Remap
# 4 HNF4A   TNFRSF19 harmonizome_CHEA      harmonizome
# 5 SMC3    FAP     harmonizome_ENCODE    harmonizome
# 6 E2F6    HIST1H1B harmonizome_ENCODE    harmonizome
# 7 TFAP2C  MAT2B   harmonizome_ENCODE    harmonizome
# 8 USF1    TBX4    harmonizome_TRANSFAC  harmonizome
# 9 MIR133B FETUB   harmonizome_TRANSFAC  harmonizome
# 10 SP4    HNRNP2  harmonizome_ENCODE    harmonizome

# use only OmniPath:
omnipath_networks <- nichenet_networks(only_omnipath = TRUE)

```

nichenet_optimization *Optimizes NicheNet model parameters*

Description

Optimize NicheNet method parameters, i.e. PageRank parameters and source weights, based on a collection of experiments where the effect of a ligand on gene expression was measured.

Usage

```

nichenet_optimization(
  networks,
  expression,
  make_multi_objective_function_param = list(),
  objective_function_param = list(),
  mlrmo_optimization_param = list()
)

```

Arguments

networks	A list with NicheNet format signaling, ligand-receptor and gene regulatory networks as produced by nichenet_networks .
expression	A list with expression data from ligand perturbation experiments, as produced by nichenet_expression_data .
make_multi_objective_function_param	Override parameters for <code>smoof::makeMultiObjectiveFunction</code> .
objective_function_param	Override additional arguments passed to the objective function.
mlrmo_optimization_param	Override arguments for <code>nichenetr::mlrmo_optimization</code> .

Value

A result object from the function 'mlrMBO::mbo'. Among other things, this contains the optimal parameter settings, the output corresponding to every input etc.

Examples

```
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)
```

nichenet_remove_orphan_ligands

Removes experiments with orphan ligands

Description

Removes from the expression data the perturbation experiments involving ligands without connections.

Usage

```
nichenet_remove_orphan_ligands(expression, lr_network)
```

Arguments

expression Expression data as returned by [nichenet_expression_data](#).
lr_network A NicheNet format ligand-receptor network data frame as produced by [nichenet_lr_network](#).

Value

The same list as 'expression' with certain elements removed.

Examples

```
lr_network <- nichenet_lr_network()
expression <- nichenet_expression_data()
expression <- nichenet_remove_orphan_ligands(expression, lr_network)
```

nichenet_results_dir *Path to the current NicheNet results directory*

Description

Path to the directory to save intermediate and final outputs from NicheNet methods.

Usage

```
nichenet_results_dir()
```

Value

Character: path to the NicheNet results directory.

Examples

```
nichenet_results_dir()
# [1] "nichenet_results"
```

nichenet_signaling_network
Builds a NicheNet signaling network

Description

Builds signaling network prior knowledge for NicheNet using multiple resources.

Usage

```
nichenet_signaling_network(  
  omnipath = list(),  
  pathwaycommons = list(),  
  harmonizome = list(),  
  vinayagam = list(),  
  cpdb = list(),  
  evex = list(),  
  inbiomap = list(),  
  only_omnipath = FALSE  
)
```

Arguments

omnipath	List with paramaters to be passed to nichenet_signaling_network_omnipath .
pathwaycommons	List with paramaters to be passed to nichenet_signaling_network_pathwaycommons .
harmonizome	List with paramaters to be passed to nichenet_signaling_network_harmonizome .
vinayagam	List with paramaters to be passed to nichenet_signaling_network_vinayagam .
cpdb	List with paramaters to be passed to nichenet_signaling_network_cpdb .
evex	List with paramaters to be passed to nichenet_signaling_network_evex .
inbiomap	List with paramaters to be passed to nichenet_signaling_network_inbiomap .
only_omnipath	Logical: a shortcut to use only OmniPath as network resource.

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

See Also

- [nichenet_signaling_network_omnipath](#)
- [nichenet_signaling_network_pathwaycommons](#)
- [nichenet_signaling_network_harmonizome](#)
- [nichenet_signaling_network_vinayagam](#)
- [nichenet_signaling_network_cpdb](#)
- [nichenet_signaling_network_evex](#)
- [nichenet_signaling_network_inbiomap](#)

Examples

```
# load everything with the default parameters:
# we don't load inBio Map due to the - hopefully
# temporary - issues of their server
sig_network <- nichenet_signaling_network(inbiomap = NULL)

# override parameters for some resources:
sig_network <- nichenet_signaling_network(
  omnipath = list(resources = c('SIGNOR', 'Signalink3', 'SPIKE')),
  pathwaycommons = NULL,
  harmonizome = list(datasets = c('phosphositeplus', 'depod')),
  cpdb = list(complex_max_size = 1, min_score = .98),
  evex = list(min_confidence = 1.5),
  inbiomap = NULL
)

# use only OmniPath:
sig_network_omnipath <- nichenet_signaling_network(only_omnipath = TRUE)
```

`nichenet_signaling_network_cpdb`*Builds signaling network for NicheNet using ConsensusPathDB*

Description

Builds signaling network prior knowledge using ConsensusPathDB (CPDB) data. Note, the interactions from CPDB are not directed and many of them comes from complex expansion. Find out more at <http://cpdb.molgen.mpg.de/>.

Usage

```
nichenet_signaling_network_cpdb(...)
```

Arguments

... Passed to [consensuspathdb_download](#).

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

See Also

- [nichenet_signaling_network](#)
- [consensuspathdb_download](#)

Examples

```
# use some parameters stricter than default:
cpdb_signaling_network <- nichenet_signaling_network_cpdb(
  complex_max_size = 2,
  min_score = .99
)
```

`nichenet_signaling_network_evex`*NicheNet signaling network from EVEX*

Description

Builds signaling network prior knowledge for NicheNet from the EVEX database.

Usage

```
nichenet_signaling_network_evex(top_confidence = 0.75, indirect = FALSE, ...)
```

Arguments

top_confidence Double, between 0 and 1. Threshold based on the quantile of the confidence score.

indirect Logical: whether to include indirect interactions.

... Ignored.

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

See Also

- [evex_download](#)
- [nichenet_signaling_network](#)

Examples

```
ev_signaling_network <- nichenet_signaling_network_evex(  
  top_confidence = .9  
)
```

nichenet_signaling_network_harmonizome
NicheNet signaling network from Harmonizome

Description

Builds signaling network prior knowledge for NicheNet using Harmonizome

Usage

```
nichenet_signaling_network_harmonizome(  
  datasets = c("phosphositeplus", "kea", "depod"),  
  ...  
)
```

Arguments

datasets The datasets to use. For possible values please refer to default value and the Harmonizome webpage.

... Ignored.

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

Examples

```
# use only KEA and PhosphoSite:
hz_signaling_network <- nichenet_signaling_network_harmonizome(
  datasets = c('kea', 'phosphositeplus')
)
```

nichenet_signaling_network_inbiomap

NicheNet signaling network from InWeb InBioMap

Description

Builds signaling network prior knowledge for NicheNet from the InWeb InBioMap database.

Usage

```
nichenet_signaling_network_inbiomap(...)
```

Arguments

... Ignored.

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

See Also

[nichenet_signaling_network](#), [inbiomap_download](#)

Examples

```
ib_signaling_network <- nichenet_signaling_network_inbiomap()
```

`nichenet_signaling_network_omnipath`*Builds signaling network for NicheNet using OmniPath*

Description

Retrieves network prior knowledge from OmniPath and provides it in a format suitable for NicheNet. This method never downloads the ‘ligreextra’ dataset because the ligand-receptor interactions are supposed to come from [nichenet_lr_network_omnipath](#).

Usage

```
nichenet_signaling_network_omnipath(min_curation_effort = 0, ...)
```

Arguments`min_curation_effort`

Lower threshold for curation effort

`...`Passed to [import_post_translational_interactions](#)**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

See Also

- [nichenet_signaling_network](#)

Examples

```
# use interactions with at least 2 evidences (reference or database)
op_signaling_network <- nichenet_signaling_network_omnipath(
  min_curation_effort = 2
)
```

`nichenet_signaling_network_pathwaycommons`*NicheNet signaling network from PathwayCommons*

Description

Builds signaling network prior knowledge for NicheNet using PathwayCommons.

Usage

```
nichenet_signaling_network_pathwaycommons(
  interaction_types = c("catalysis-precedes", "controls-phosphorylation-of",
    "controls-state-change-of", "controls-transport-of", "in-complex-with",
    "interacts-with"),
  ...
)
```

Arguments

```
interaction_types
  Character vector with PathwayCommons interaction types. Please refer to the
  default value and the PathwayCommons webpage.
...
  Ignored.
```

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

Examples

```
# use only the "controls-transport-of" interactions:
pc_signaling_network <- nichenet_signaling_network_pathwaycommons(
  interaction_types = 'controls-transport-of'
)
```

```
nichenet_signaling_network_vinayagam
```

NicheNet signaling network from Vinayagam

Description

Builds signaling network prior knowledge for NicheNet using Vinayagam 2011 Supplementary Table S6. Find out more at <https://doi.org/10.1126/scisignal.2001699>.

Usage

```
nichenet_signaling_network_vinayagam(...)
```

Arguments

```
...
  Ignored.
```

Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

Examples

```
vi_signaling_network <- nichenet_signaling_network_vinayagam()
```

nichenet_test

Run the NicheNet pipeline with a little dummy network

Description

Loads a tiny network and runs the NicheNet pipeline with low number of iterations in the optimization process. This way the pipeline runs in a reasonable time in order to test the code. Due to the random subsampling disconnected networks might be produced sometimes. If you see an error like "Error in if (sd(prediction_vector) == 0) ... missing value where TRUE/FALSE needed", the random subsampled input is not appropriate. In this case just interrupt and call again. This test ensures the computational integrity of the pipeline. If it fails during the optimization process, try to start it over several times, even restarting R. The unpredictability is related to codemlrMBO and nichenetr not being prepared to handle certain conditions, and it's also difficult to find out which conditions lead to which errors. At least 3 different errors appear time to time, depending on the input. It also seems like restarting R sometimes helps, suggesting that the entire system might be somehow stateful. You can ignore the Parallelization was not stopped warnings on repeated runs.

Usage

```
nichenet_test(...)
```

Arguments

... Passed to [nichenet_main](#).

Value

A named list with the intermediate and final outputs of the pipeline: 'networks', 'expression', 'optimized_parameters', 'weighted_networks' and 'ligand_target_matrix'.

Examples

```
nnt <- nichenet_test()
```

nichenet_workarounds *Workarounds using NicheNet without attaching the package*

Description

NicheNet requires the availability of some lazy loaded external data which are not available if the package is not loaded and attached. Also, the `BBmisc::convertToShortString` used for error reporting in `mlrMBO::evalTargetFun.OptState` is patched here to print longer error messages. Maybe it's a better solution to attach `nichenetr` before running the NicheNet pipeline. Alternatively you can try to call this function in the beginning. Why we don't call this automatically is just because we don't want to load datasets from another package without the user knowing about it.

Usage

```
nichenet_workarounds()
```

Value

Returns NULL.

Examples

```
nichenet_workarounds()
```

obo_parser *Generic OBO parser*

Description

Reads the contents of an OBO file and processes it into data frames or a list based data structure.

Usage

```
obo_parser(  
  path,  
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",  
               "negatively_regulates"),  
  shorten_namespace = TRUE,  
  tables = TRUE  
)
```

Arguments

path	Path to the OBO file.
relations	Character vector: process only these relations.
shorten_namespace	Logical: shorten the namespace to a single letter code (as usual for Gene Ontology, e.g. cellular_component = "C").
tables	Logical: return data frames (tibbles) instead of nested lists.

Value

A list with the following elements: 1) "names" a list with terms as names and names as values; 2) "namespaces" a list with terms as names and namespaces as values; 3) "relations" a list with relations between terms: terms are keys, values are lists with relations as names and character vectors of related terms as values; 4) "subsets" a list with terms as keys and character vectors of subset names as values (or NULL if the term does not belong to any subset); 5) "obsolete" character vector with all the terms labeled as obsolete. If the tables parameter is TRUE, "names", "namespaces", "relations" and "subsets" will be data frames (tibbles).

See Also

- [relations_list_to_table](#)
- [relations_table_to_list](#)
- [swap_relations](#)

Examples

```
goslim_url <-
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"
path <- tempfile()
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))
obo <- obo_parser(path, tables = FALSE)
unlink(path)
names(obo)
# [1] "names"      "namespaces" "relations"  "subsets"    "obsolete"
head(obo$relations, n = 2)
# $`GO:0000001`
# $`GO:0000001`$is_a
# [1] "GO:0048308" "GO:0048311"
#
# $`GO:0000002`
# $`GO:0000002`$is_a
# [1] "GO:0007005"
```

Description

OmnipathR is an R package built to provide easy access to the data stored in the OmniPath web service:

<https://omnipathdb.org/>

And a number of other resources, such as BioPlex, ConsensusPathDB, EVEX, Guide to Pharmacology (IUPHAR/BPS), Harmonizome, HTRIdb, InWeb InBioMap, KEGG Pathway, Pathway Commons, Ramilowski et al. 2015, RegNetwork, ReMap, TF census, TRRUST and Vinayagam et al. 2011.

The OmniPath web service 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. Furthermore, OmnipathR features a close integration with the NicheNet method for ligand activity prediction from transcriptomics data, and its R implementation nichenetr (available in CRAN).

Author(s)

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Examples

```
# Download post-translational modifications:
enzsub <- import_omnipath_enzsub(resources = c("PhosphoSite", "SIGNOR"))

# Download protein-protein interactions
interactions <- import_omnipath_interactions(resources = c("SignalLink3"))

# Convert to igraph objects:
enzsub_g <- enzsub_graph(enzsub = enzsub)
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
```

```
print_path_es(shortest_paths(OPI_g, from = "TYR03", to = "STAT3",
  output = 'epath')$epath[[1]], OPI_g)

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

omnipath_cache_autoclean

Keeps only the latest versions of complete downloads

Description

Removes the old versions, the failed downloads and the files in the cache directory which are missing from the database. For more flexible operations use [omnipath_cache_remove](#) and [omnipath_cache_clean](#).

Usage

```
omnipath_cache_autoclean()
```

Value

Invisibl returns the cache database (list of cache records).

Examples

```
omnipath_cache_autoclean()
```

omnipath_cache_clean *Removes the items from the cache directory which are unknown by the cache database*

Description

Removes the items from the cache directory which are unknown by the cache database

Usage

```
omnipath_cache_clean()
```

Value

Returns 'NULL'.

Examples

```
omnipath_cache_clean()
```

```
omnipath_cache_clean_db
```

Removes the cache database entries without existing files

Description

Removes the cache database entries without existing files

Usage

```
omnipath_cache_clean_db(...)
```

Arguments

... Ignored.

Value

Returns 'NULL'.

Examples

```
omnipath_cache_clean_db()
```

`omnipath_cache_download_ready`*Sets the download status to ready for a cache item*

Description

Sets the download status to ready for a cache item

Usage

```
omnipath_cache_download_ready(version, key = NULL)
```

Arguments

<code>version</code>	Version of the cache item. If does not exist a new version item will be created
<code>key</code>	Key of the cache item

Value

Character: invisibly returns the version number of the cache version item.

Examples

```
bioc_url <- 'https://bioconductor.org/'
# request a new version item (or retrieve the latest)
new_version <- omnipath_cache_latest_or_new(url = bioc_url)
# check if the version item is not a finished download
new_version$status
# [1] "unknown"
# download the file
httr::GET(bioc_url, httr::write_disk(new_version$path, overwrite = TRUE))
# report to the cache database that the download is ready
omnipath_cache_download_ready(new_version)
# now the status is ready:
version <- omnipath_cache_latest_or_new(url = bioc_url)
version$status
# "ready"
version$dl_finished
# [1] "2021-03-09 16:48:38 CET"
omnipath_cache_remove(url = bioc_url) # cleaning up
```

`omnipath_cache_filter_versions`*Filters the versions from one cache record*

Description

Filters the versions based on multiple conditions: their age and status

Usage

```
omnipath_cache_filter_versions(  
  record,  
  latest = FALSE,  
  max_age = NULL,  
  min_age = NULL,  
  status = CACHE_STATUS$READY  
)
```

Arguments

<code>record</code>	A cache record
<code>latest</code>	Return the most recent version
<code>max_age</code>	The maximum age in days (e.g. 5: 5 days old or more recent)
<code>min_age</code>	The minimum age in days (e.g. 5: 5 days old or older)
<code>status</code>	Character vector with status codes. By default only the versions with 'ready' (completed download) status are selected

Value

Character vector with version IDs, NA if no version satisfies the conditions.

Examples

```
# creating an example cache record  
bioc_url <- 'https://bioconductor.org/'  
version <- omnipath_cache_latest_or_new(url = bioc_url)  
httr::GET(bioc_url, httr::write_disk(version$path, overwrite = TRUE))  
omnipath_cache_download_ready(version)  
record <- dplyr::first(omnipath_cache_search('biocond'))  
  
# only the versions with status "ready"  
version_numbers <- omnipath_cache_filter_versions(record, status = 'ready')  
omnipath_cache_remove(url = bioc_url) # cleaning up
```

omnipath_cache_get *Retrieves one item from the cache directory*

Description

Retrieves one item from the cache directory

Usage

```
omnipath_cache_get(  
  key = NULL,  
  url = NULL,  
  post = NULL,  
  payload = NULL,  
  create = TRUE,  
  ...  
)
```

Arguments

key	The key of the cache record
url	URL pointing to the resource
post	HTTP POST parameters as a list
payload	HTTP data payload
create	Create a new entry if doesn't exist yet
...	Passed to omnipath_cache_record (internal function)

Value

Cache record: an existing record if the entry already exists, otherwise a newly created and inserted record

Examples

```
# create an example cache record  
bioc_url <- 'https://bioconductor.org/'  
version <- omnipath_cache_latest_or_new(url = bioc_url)  
omnipath_cache_remove(url = bioc_url) # cleaning up  
  
# retrieve the cache record  
record <- omnipath_cache_get(url = bioc_url)  
record$key  
# [1] "41346a00fb20d2a9df03aa70cf4d50bf88ab154a"  
record$url  
# [1] "https://bioconductor.org/"
```

omnipath_cache_key *Generates a hash which identifies an element in the cache database*

Description

Generates a hash which identifies an element in the cache database

Usage

```
omnipath_cache_key(url, post = NULL, payload = NULL)
```

Arguments

url	Character vector with URLs
post	List with the HTTP POST parameters or a list of lists if the url vector is longer than 1. NULL for queries without POST parameters.
payload	HTTP data payload. List with multiple items if the url vector is longer than 1. NULL for queries without data.

Value

Character vector of cache record keys.

Examples

```
bioc_url <- 'https://bioconductor.org/'
omnipath_cache_key(bioc_url)
# [1] "41346a00fb20d2a9df03aa70cf4d50bf88ab154a"
```

omnipath_cache_latest_or_new
The latest or a new version of a cache record

Description

Looks up a record in the cache and returns its latest valid version. If the record doesn't exist or no valid version available, creates a new one.

Usage

```
omnipath_cache_latest_or_new(
  key = NULL,
  url = NULL,
  post = NULL,
  payload = NULL,
  create = TRUE,
  ...
)
```

Arguments

key	The key of the cache record
url	URL pointing to the resource
post	HTTP POST parameters as a list
payload	HTTP data payload
create	Logical: whether to create and return a new version. If FALSE only the latest existing valid version is returned, if available.
...	Passed to omnipath_cache_get

Value

A cache version item.

Examples

```
# retrieve the latest version of the first cache record
# found by the search keyword "bioplex"
latest_bioplex <-
  omnipath_cache_latest_or_new(
    names(omnipath_cache_search('bioplex'))[1]
  )

latest_bioplex$dl_finished
# [1] "2021-03-09 14:28:50 CET"
latest_bioplex$path
# [1] "/home/denes/.cache/OmnipathR/378e0def2ac97985f629-1.rds"

# create an example cache record
bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
omnipath_cache_remove(url = bioc_url) # cleaning up
```

omnipath_cache_latest_version

Finds the most recent version in a cache record

Description

Finds the most recent version in a cache record

Usage

```
omnipath_cache_latest_version(record)
```

Arguments

record A cache record

Value

Character: the version ID with the most recent download finished time

omnipath_cache_load *Loads an R object from the cache*

Description

Loads the object from RDS format.

Usage

```
omnipath_cache_load(
  key = NULL,
  version = NULL,
  url = NULL,
  post = NULL,
  payload = NULL
)
```

Arguments

key Key of the cache item

version Version of the cache item. If does not exist or NULL, the latest version will be retrieved

url URL of the downloaded resource

post HTTP POST parameters as a list

payload HTTP data payload

Value

Object loaded from the cache RDS file.

See Also

[omnipath_cache_save](#)

Examples

```
# works only if you have already this item in the cache
intercell_data <- omnipath_cache_load(url = paste0(
  'https://omnipathdb.org/intercell?resources=Adhesome,Almen2009,',
  'Baccin2019,CSPA,CellChatDB&license=academic'
))
class(intercell_data)
# [1] "data.frame"
nrow(intercell_data)
# [1] 16622
attr(intercell_data, 'origin')
# [1] "cache"

# basic example of saving and loading to and from the cache:
bioc_url <- 'https://bioconductor.org/'
bioc_html <- readChar(url(bioc_url), nchars = 99999)
omnipath_cache_save(bioc_html, url = bioc_url)
bioc_html <- omnipath_cache_load(url = bioc_url)
```

omnipath_cache_move_in

Moves an existing file into the cache

Description

Either the key or the URL (with POST and payload) must be provided.

Usage

```
omnipath_cache_move_in(
  path,
  key = NULL,
  version = NULL,
  url = NULL,
  post = NULL,
  payload = NULL,
  keep_original = FALSE
)
```

Arguments

path	Path to the source file
key	Key of the cache item
version	Version of the cache item. If does not exist a new version item will be created
url	URL of the downloaded resource
post	HTTP POST parameters as a list
payload	HTTP data payload
keep_original	Whether to keep or remove the original file

Value

Character: invisibly returns the version number of the cache version item.

See Also

[omnipath_cache_save](#)

Examples

```
omnipath_cache_move_in('some/file.zip', url = 'the_download_address')
```

```
# basic example of moving a file to the cache:
```

```
bioc_url <- 'https://bioconductor.org/'  
html_file <- tempfile(fileext = '.html')  
httr::GET(bioc_url, httr::write_disk(html_file, overwrite = TRUE))  
omnipath_cache_move_in(path = html_file, url = bioc_url)  
omnipath_cache_remove(url = bioc_url) # cleaning up
```

omnipath_cache_remove *Removes contents from the cache directory*

Description

According to the parameters, it can remove contents older than a certain age, or contents having a more recent version, one specific item, or wipe the entire cache.

Usage

```
omnipath_cache_remove(key = NULL, url = NULL, post = NULL,  
  payload = NULL, max_age = NULL, min_age = NULL, status = NULL,  
  only_latest = FALSE, wipe = FALSE, autoclean = TRUE)
```


Arguments

key	The key of the cache record
url	URL pointing to the resource
post	HTTP POST parameters as a list
payload	HTTP data payload
max_age	Age of cache items in days. Remove everything that is older than this age
min_age	Age of cache items in days. Remove everything more recent than this age
status	Remove items having any of the states listed here
only_latest	Keep only the latest version
wipe	Logical: if TRUE, removes all files from the cache and the cache database. Same as calling omnipath_cache_wipe .
autoclean	Remove the entries about failed downloads, the files in the cache directory which are missing from the cache database, and the entries without existing files in the cache directory

Value

Invisibly returns the cache database (list of cache records).

See Also

- [omnipath_cache_wipe](#)
- [omnipath_cache_clean](#)
- [omnipath_cache_autoclean](#)

Examples

```
# remove all cache data from the BioPlex database
cache_records <- omnipath_cache_search(
  'bioplex',
  ignore.case = TRUE
)
omnipath_cache_remove(names(cache_records))

# remove a record by its URL
regnetwork_url <- 'http://www.regnetworkweb.org/download/human.zip'
omnipath_cache_remove(url = regnetwork_url)

# remove all records older than 30 days
omnipath_cache_remove(max_age = 30)

# for each record, remove all versions except the latest
omnipath_cache_remove(only_latest = TRUE)

bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
```

```
httr::GET(bioc_url, httr::write_disk(version$path, overwrite = TRUE))
omnipath_cache_download_ready(version)
key <- omnipath_cache_key(bioc_url)
omnipath_cache_remove(key = key)
```

omnipath_cache_save *Saves an R object to the cache*

Description

Exports the object in RDS format, creates new cache record if necessary.

Usage

```
omnipath_cache_save(  
  data,  
  key = NULL,  
  version = NULL,  
  url = NULL,  
  post = NULL,  
  payload = NULL  
)
```

Arguments

data	An object
key	Key of the cache item
version	Version of the cache item. If does not exist a new version item will be created
url	URL of the downloaded resource
post	HTTP POST parameters as a list
payload	HTTP data payload

Value

Returns invisibly the data itself.

Invisibly returns the 'data'.

See Also

[omnipath_cache_move_in](#)

Examples

```
mydata <- data.frame(a = c(1, 2, 3), b = c('a', 'b', 'c'))
omnipath_cache_save(mydata, url = 'some_dummy_address')
from_cache <- omnipath_cache_load(url = 'some_dummy_address')
from_cache
#   a b
# 1 1 a
# 2 2 b
# 3 3 c
attr(from_cache, 'origin')
# [1] "cache"

# basic example of saving and loading to and from the cache:
bioc_url <- 'https://bioconductor.org/'
bioc_html <- readChar(url(bioc_url), nchars = 99999)
omnipath_cache_save(bioc_html, url = bioc_url)
bioc_html <- omnipath_cache_load(url = bioc_url)
```

omnipath_cache_search *Searches for cache items*

Description

Searches the cache records by matching the URL against a string or regexp.

Usage

```
omnipath_cache_search(pattern, ...)
```

Arguments

pattern	String or regular expression.
...	Passed to grep

Value

List of cache records matching the pattern.

Examples

```
# find all cache records from the BioPlex database
bioplex_cache_records <- omnipath_cache_search(
  'bioplex',
  ignore.case = TRUE
)
```

`omnipath_cache_set_ext`*Sets the file extension for a cache record*

Description

Sets the file extension for a cache record

Usage

```
omnipath_cache_set_ext(key, ext)
```

Arguments

<code>key</code>	Character: key for a cache item, alternatively a version entry.
<code>ext</code>	Character: the file extension, e.g. "zip".

Value

Returns 'NULL'.

Examples

```
bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
version$path
# [1] "/home/denes/.cache/OmnipathR/41346a00fb20d2a9df03-1"
httr::GET(bioc_url, httr::write_disk(version$path, overwrite = TRUE))
key <- omnipath_cache_key(url = bioc_url)
omnipath_cache_set_ext(key = key, ext = 'html')
version <- omnipath_cache_latest_or_new(url = bioc_url)
version$path
# [1] "/home/denes/.cache/OmnipathR/41346a00fb20d2a9df03-1.html"
record <- omnipath_cache_get(url = bioc_url)
record$ext
# [1] "html"
omnipath_cache_remove(url = bioc_url) # cleaning up
```

`omnipath_cache_update_status`*Updates the status of an existing cache record*

Description

Updates the status of an existing cache record

Usage

```
omnipath_cache_update_status(key, version, status,  
                             dl_finished = NULL)
```

Arguments

<code>key</code>	Key of the cache item
<code>version</code>	Version of the cache item. If does not exist a new version item will be created
<code>status</code>	The updated status value
<code>dl_finished</code>	Timestamp for the time when download was finished, if 'NULL' the value remains unchanged

Value

Character: invisibly returns the version number of the cache version item.

Examples

```
bioc_url <- 'https://bioconductor.org/'  
latest_version <- omnipath_cache_latest_or_new(url = bioc_url)  
key <- omnipath_cache_key(bioc_url)  
omnipath_cache_update_status(  
  key = key,  
  version = latest_version$number,  
  status = 'ready',  
  dl_finished = Sys.time()  
)  
omnipath_cache_remove(url = bioc_url) # cleaning up
```

omnipath_cache_wipe *Permanently removes all the cache contents*

Description

After this operation the cache directory will be completely empty, except an empty cache database file.

Usage

```
omnipath_cache_wipe(...)
```

Arguments

... Ignored.

Value

Returns 'NULL'.

See Also

[omnipath_cache_remove](#)

Examples

```
omnipath_cache_wipe()
# the cache is completely empty:
print(omnipath.env$cache)
# list()
list.files(omnipath_get_cachedir())
# [1] "cache.json"
```

omnipath_get_config_path
 Current config file path

Description

Current config file path

Usage

```
omnipath_get_config_path(user = FALSE)
```

Arguments

`user` Logical: prioritize the user level config even if a config in the current working directory is available.

Value

Character: path to the config file.

Examples

```
omnipath_get_config_path()
```

`omnipath_load_config` *Load the package configuration from a config file*

Description

Load the package configuration from a config file

Usage

```
omnipath_load_config(path = NULL, title = "default", user = FALSE, ...)
```

Arguments

`path` Path to the config file.

`title` Load the config under this title. One config file might contain multiple configurations, each identified by a title. If the title is not available the first section of the config file will be used.

`user` Force to use the user level config even if a config file exists in the current directory. By default, the local config files have priority over the user level config.

`...` Passed to `yaml::yaml.load_file`.

Value

Invisibly returns the config as a list.

Examples

```
# load the config from a custom config file:
omnipath_load_config(path = 'my_custom_omnipath_config.yml')
```

omnipath_log	<i>Browse the current OmnipathR log file</i>
--------------	--

Description

Browse the current OmnipathR log file

Usage

```
omnipath_log()
```

Value

Returns 'NULL'.

See Also

[omnipath_logfile](#)

Examples

```
omnipath_log()
# then you can browse the log file, and exit with `q`
```

omnipath_logfile	<i>Path to the current OmnipathR log file</i>
------------------	---

Description

Path to the current OmnipathR log file

Usage

```
omnipath_logfile()
```

Value

Character: path to the current logfile, or NULL if no logfile is available.

See Also

[omnipath_log](#)

Examples

```
omnipath_logfile()
# [1] "/home/denes/omnipathr/omnipathr-log/omnipathr-20210309-1642.log"
```

omnipath_msg

Dispatch a message to the OmnipathR logger

Description

Any package or script can easily send log messages and establish a logging facility with the fantastic ‘logger’ package. This function serves the only purpose if you want to inject messages into the logger of OmnipathR. Otherwise we recommend to use the ‘logger’ package directly.

Usage

```
omnipath_msg(level, ...)
```

Arguments

level	Character, numeric or class loglevel. A log level, if character one of the followings: "fatal", "error", "warn", "success", "info", "trace".
...	Arguments for string formatting, passed <code>sprintf</code> or <code>str_glue</code> .

Value

Returns ‘NULL’.

Examples

```
omnipath_msg(
  level = 'success',
  'Talking to you in the name of OmnipathR, my favourite number is %d',
  round(runif(1, 1, 10))
)
```

`omnipath_reset_config` *Restores the built-in default values of all config parameters*

Description

Restores the built-in default values of all config parameters

Usage

```
omnipath_reset_config(save = NULL, reset_all = FALSE)
```

Arguments

<code>save</code>	If a path, the restored config will be also saved to this file. If TRUE, the config will be saved to the current default config path (see omnipath_get_config_path).
<code>reset_all</code>	Reset to their defaults also the options already set in the R options.

Value

The config as a list.

See Also

[omnipath_load_config](#), [omnipath_save_config](#)

Examples

```
# restore the defaults and write them to the default config file:
omnipath_reset_config()
omnipath_save_config()
```

`omnipath_save_config` *Save the current package configuration*

Description

Save the current package configuration

Usage

```
omnipath_save_config(path = NULL, title = "default", local = FALSE)
```

Arguments

path	Path to the config file. Directories and the file will be created if don't exist.
title	Save the config under this title. One config file might contain multiple configurations, each identified by a title.
local	Save into a config file in the current directory instead of a user level config file. When loading, the config in the current directory has priority over the user level config.

Value

Returns 'NULL'.

Examples

```
# after this, all downloads will default to commercial licenses
# i.e. the resources that allow only academic use will be excluded:
options(omnipath.license = 'commercial')
omnipath_save_config()
```

omnipath_set_cachedir *Change the cache directory*

Description

Change the cache directory

Usage

```
omnipath_set_cachedir(path = NULL)
```

Arguments

path	Character: path to the new cache directory. If don't exist, the directories will be created. If the path is an existing cache directory, the package's cache database for the current session will be loaded from the database in the directory. If NULL, the cache directory will be set to its default path.
------	--

Value

Returns NULL.

Examples

```
tmp_cache <- tempdir()
omnipath_set_cachedir(tmp_cache)
# restore the default cache directory:
omnipath_set_cachedir()
```

omnipath_set_console_loglevel
Sets the log level for the console

Description

Use this method to change during a session which messages you want to be printed on the console. Before loading the package, you can set it also by the config file, with the `omnipath.console_loglevel` key.

Usage

```
omnipath_set_console_loglevel(level)
```

Arguments

`level` Character or class 'loglevel'. The desired log level.

Value

Returns 'NULL'.

See Also

[omnipath_set_logfile_loglevel](#)

Examples

```
omnipath_set_console_loglevel('warn')
# or:
omnipath_set_console_loglevel(logger::WARN)
```


Value

Returns 'NULL'.

Examples

```
omnipath_set_loglevel(logger::FATAL, target = 'console')
```

omnipath_show_db	<i>Built in database definitions</i>
------------------	--------------------------------------

Description

Databases are resources which might be costly to load but can be used many times by functions which usually automatically load and retrieve them from the database manager. Each database has a lifetime and will be unloaded automatically upon expiry.

Usage

```
omnipath_show_db()
```

Value

A data frame with the built in database definitions.

Examples

```
database_definitions <- omnipath_show_db()
database_definitions
# # A tibble: 14 x 10
#   name      last_used      lifetime package loader loader_p.
#   <chr>    <dtm>          <dbl> <chr> <chr> <list>
# 1 Gene Onto. 2021-04-04 20:19:15    300 Omnipat. go_ontol. <named l.
# 2 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# 3 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# 4 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# 5 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# ... (truncated)
# # . with 4 more variables: latest_param <list>, loaded <lgl>, db <list>,
# #   key <chr>
```

`omnipath_unlock_cache_db`*Removes the lock file from the cache directory*

Description

A lock file in the cache directory avoids simultaneous write and read. It's supposed to be removed after each read and write operation. This might not happen if the process crashes during such an operation. In this case you can manually call this function.

Usage`omnipath_unlock_cache_db()`**Value**

Logical: returns TRUE if the cache was locked and now is unlocked; FALSE if it was not locked.

Examples`omnipath_unlock_cache_db()`

`ontology_ensure_id` *Only ontology IDs*

Description

Converts a mixture of ontology IDs and names to only IDs. If an element of the input is missing from the chosen ontology it will be dropped. This can happen if the ontology is a subset (slim) version, but also if the input is not a valid ID or name.

Usage`ontology_ensure_id(terms, db_key = "go_basic")`**Arguments**

<code>terms</code>	Character: ontology IDs or term names.
<code>db_key</code>	Character: key to identify the ontology database. For the available keys see omnipath_show_db .

Value

Character vector of ontology IDs.

Examples

```
ontology_ensure_id(c('mitochondrion inheritance', 'GO:0001754'))
# [1] "GO:0000001" "GO:0001754"
```

ontology_ensure_name *Only ontology term names*

Description

Converts a mixture of ontology IDs and names to only names. If an element of the input is missing from the chosen ontology it will be dropped. This can happen if the ontology is a subset (slim) version, but also if the input is not a valid ID or name.

Usage

```
ontology_ensure_name(terms, db_key = "go_basic")
```

Arguments

terms Character: ontology IDs or term names.

db_key Character: key to identify the ontology database. For the available keys see [omnipath_show_db](#).

Value

Character vector of ontology term names.

Examples

```
ontology_ensure_name(c('reproduction', 'GO:0001754', 'foo bar'))
# [1] "eye photoreceptor cell differentiation" "reproduction"
```

ontology_name_id *Translate between ontology IDs and names*

Description

Makes sure that the output contains only valid IDs or term names. The input can be a mixture of IDs and names. The order of the input won't be preserved in the output.

Usage

```
ontology_name_id(terms, ids = TRUE, db_key = "go_basic")
```


Arguments

terms Character: ontology IDs or term names.
 ids Logical: the output should contain IDs or term names.
 db_key Character: key to identify the ontology database. For the available keys see [omnipath_show_db](#).

Value

Character vector of ontology IDs or term names.

Examples

```
ontology_name_id(c('mitochondrion inheritance', 'reproduction'))
# [1] "GO:0000001" "GO:0000003"
ontology_name_id(c('GO:0000001', 'reproduction'), ids = FALSE)
# [1] "mitochondrion inheritance" "reproduction"
```

pathwaycommons_download

Interactions from PathwayCommons

Description

PathwayCommons (<http://www.pathwaycommons.org/>) provides molecular interactions from a number of databases, in either BioPAX or SIF (simple interaction format). This function retrieves all interactions in SIF format. The data is limited to the interacting pair and the type of the interaction.

Usage

```
pathwaycommons_download()
```

Value

A data frame (tibble) with interactions.

Examples

```
pc_interactions <- pathwaycommons_download()
pc_interactions
# # A tibble: 1,884,849 x 3
#   from type to
#   <chr> <chr> <chr>
# 1 A1BG controls-expression-of A2M
# 2 A1BG interacts-with ABCC6
# 3 A1BG interacts-with ACE2
# 4 A1BG interacts-with ADAM10
# 5 A1BG interacts-with ADAM17
```

```
# # . with 1,884,839 more rows
```

```
pivot_annotations      Converts annotation tables to a wide format
```

Description

Use this method to reconstitute the annotation tables into the format of the original resources. With the 'wide=TRUE' option `import_omnipath_annotations` applies this function to the downloaded data.

Usage

```
pivot_annotations(annotations)
```

Arguments

`annotations` A data frame of annotations downloaded from the OmniPath web service by `import_omnipath_annotations`.

Value

A wide format data frame (tibble) if the provided data contains annotations from one resource, otherwise a list of wide format tibbles.

See Also

[import_omnipath_annotations](#)

Examples

```
# single resource: the result is a data frame
disgenet <- import_omnipath_annotations(resources = 'DisGeNet')
disgenet <- pivot_annotations(disgenet)
disgenet
# # A tibble: 119,551 x 10
#   uniprot genesymbol entity_type disease score dsi dpi nof_pmids
#   <chr>   <chr>       <chr>      <chr> <chr> <chr> <chr> <chr>
# 1 P04217 A1BG      protein    Schizo... 0.3  0.857 0.172 1
# 2 P04217 A1BG      protein    Hepato... 0.3  0.857 0.172 1
# 3 P01023 A2M       protein    alpha-... 0.31 0.564 0.724 0
# 4 P01023 A2M       protein    Fibros... 0.3  0.564 0.724 1
# 5 P01023 A2M       protein    Hepato... 0.3  0.564 0.724 1
# # . with 119,541 more rows, and 2 more variables: nof_snps <chr>,
# #   source <chr>

# multiple resources: the result is a list
annotations <- import_omnipath_annotations(
```

```

resources = c('DisGeNet', 'Signalink_function', 'DGIdb', 'kinase.com')
)
annotations <- pivot_annotations(annotations)
names(annotations)
# [1] "DGIdb"           "DisGeNet"       "kinase.com"
# [4] "Signalink_function"
annotations$kinase.com
## # A tibble: 825 x 6
#   uniprot genesymbol entity_type group family subfamily
#   <chr>   <chr>       <chr>   <chr> <chr> <chr>
# 1 P31749 AKT1         protein AGC   Akt   NA
# 2 P31751 AKT2         protein AGC   Akt   NA
# 3 Q9Y243 AKT3         protein AGC   Akt   NA
# 4 O14578 CIT          protein AGC   DMPK  CRIK
# 5 Q09013 DMPK         protein AGC   DMPK  GEK
## # . with 815 more rows

```

print_bma_motif_es *Prints BMA motifs to the screen from a sequence of edges*

Description

The motifs can be copy-pasted into a BMA canvas.

Usage

```
print_bma_motif_es(edge_seq, G, granularity = 2)
```

Arguments

edge_seq An igraph edge sequence.
G An igraph graph object.
granularity Numeric: granularity value.

Value

Returns 'NULL'.

Examples

```

interactions <- import_omnipath_interactions(resources = 'ARN')
graph <- interaction_graph(interactions)
print_bma_motif_es(igraph::E(graph)[1], graph)
# {"Model": {
#   "Name": "Omnipath motif",
#   "Variables": [{
#     "Name": "ULK1",
#     "Id": 1,

```

```
#      "RangeFrom":0,  
#      "RangeTo":2,  
#      "Formula":""  
#    },  
#    {  
#      "Name":"ATG13",  
#      ...  
#    }],  
# ... (truncated)  
# }}}
```

print_bma_motif_vs *Prints BMA motifs to the screen from a sequence of nodes*

Description

The motifs can be copy-pasted into a BMA canvas.

Usage

```
print_bma_motif_vs(node_seq, G)
```

Arguments

node_seq An igraph node sequence.
G An igraph graph object.

Value

Returns 'NULL'.

Examples

```
interactions <- import_omnipath_interactions(resources = 'ARN')  
graph <- interaction_graph(interactions)  
print_bma_motif_vs(  
  igraph::all_shortest_paths(  
    graph,  
    from = 'ULK1',  
    to = 'ATG13'  
  )$res,  
  graph  
)
```

print_interactions *Print OmniPath interactions*

Description

Prints the interactions or enzyme-substrate relationships 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_enzsub`
- `import_omnipath_interactions`
- `import_pathwayextra_interactions`
- `import_kinaseextra_interactions`
- `import_ligrecextra_interactions`
- `import_post_translational_interactions`
- `import_dorothea_interactions`
- `import_tf_target_interactions`
- `import_transcriptional_interactions`
- `import_mirnatarget_interactions`
- `import_all_interactions`

writeRefs [FALSE] writes also the PubMed IDs if available

Value

Returns 'NULL'.

Examples

```
enzsub <- import_omnipath_enzsub()
print_interactions(head(enzsub))
print_interactions(tail(enzsub), writeRefs = TRUE)
print_interactions(
  dplyr::filter(
    enzsub,
    enzyme_genesymbol == 'MAP2K1',
    substrate_genesymbol == 'MAPK3'
  )
)

signor <- import_omnipath_interactions(resources = 'SIGNOR')
print_interactions(head(signor))
```

#	source	interaction	target	n_resources
# 6	MAPK14 (Q16539)	==(+)==>	MAPKAPK2 (P49137)	23
# 4	TRPM7 (Q96QT4)	==(+)==>	ANXA1 (P04083)	10
# 1	PRKG1 (Q13976)	==(-)==>	TRPC3 (Q13507)	8
# 2	PTPN1 (P18031)	==(-)==>	TRPV6 (Q9H1D0)	6
# 5	PRKACA (P17612)	==(-)==>	MCOLN1 (Q9GZU1)	6
# 3	RACK1 (P63244)	==(-)==>	TRPM6 (Q9BX84)	2

print_path_es

Prints network paths in an edge sequence

Description

Pretty prints the interactions in a path.

Usage

```
print_path_es(edgeSeq, G)
```

Arguments

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

Value

Returns 'NULL'.

See Also

- [print_path_vs](#)

Examples

```
interactions <- import_omnipath_interactions(resources = c('Signalink3'))
OPI_g <- interaction_graph(interactions = interactions)
print_path_es(
  suppressWarnings(igraph::shortest_paths(
    OPI_g,
    from = 'TYR03',
    to = 'STAT3',
    output = 'epath'
  ))$path[[1]],
  OPI_g
)
```

print_path_vs	<i>Print networks paths given by node sequence</i>
---------------	--

Description

Prints the interactions in the path in a nice format.

Usage

```
print_path_vs(nodeSeq, G)
```

Arguments

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

Value

Returns 'NULL'.

See Also

[print_path_es](#)

Examples

```
interactions <- import_omnipath_interactions(resources=c('SignalLink3'))
OPI_g <- interaction_graph(interactions = interactions)
print_path_vs(
  igraph::all_shortest_paths(
    OPI_g,
    from = 'TYRO3',
    to = 'STAT3'
  )$vpath,
  OPI_g
)
enzsub <- import_omnipath_enzsub(resources=c('PhosphoSite', 'SIGNOR'))
enzsub_g <- enzsub_graph(enzsub)
print_path_vs(
  igraph::all_shortest_paths(
    enzsub_g,
    from = 'SRC',
    to = 'STAT1'
  )$res,
  enzsub_g
)
```

ramilowski_download *Downloads ligand-receptor interactions from Ramilowski et al. 2015*

Description

Curated ligand-receptor pairs from Supplementary Table 2 of the article "A draft network of ligand-receptor mediated multicellular signaling in human" (<https://www.nature.com/articles/ncomms8866>).

Usage

```
ramilowski_download()
```

Value

A data frame (tibble) with interactions.

Examples

```
rami_interactions <- ramilowski_download()
rami_interactions
# # A tibble: 2,557 x 16
#   Pair.Name Ligand.Approved. Ligand.Name Receptor.Approv.
#   <chr>      <chr>              <chr>      <chr>
# 1 A2M_LRP1  A2M                    alpha-2-ma. LRP1
# 2 AANAT_MT. AANAT                  aralkylami. MTNR1A
# 3 AANAT_MT. AANAT                  aralkylami. MTNR1B
# 4 ACE_AGTR2 ACE                    angiotensi. AGTR2
# 5 ACE_BDKR. ACE                    angiotensi. BDKRB2
# # . with 2,547 more rows, and 12 more variables: Receptor.Name <chr>,
# #   DLRP <chr>, HPMR <chr>, IUPHAR <chr>, HPRD <chr>,
# #   STRING.binding <chr>, STRING.experiment <chr>, HPMR.Ligand <chr>,
# #   HPMR.Receptor <chr>, PMID.Manual <chr>, Pair.Source <chr>,
# #   Pair.Evidence <chr>
```

regnetwork_directions *Transcription factor effects from RegNetwork*

Description

Transcription factor effects from RegNetwork

Usage

```
regnetwork_directions(organism = "human")
```


Arguments

organism Character: either human or mouse.

Value

A data frame (tibble) of TF-target interactions with effect signs.

Examples

```
reg_dir <- regnetwork_directions()
reg_dir
# # A tibble: 3,954 x 5
#   source_genesymb. source_entrez target_genesymb. target_entrez
#   <chr>             <chr>             <chr>             <chr>
# 1 AHR                196                CDKN1B            1027
# 2 APLNR              187                PIK3C3            5289
# 3 APLNR              187                PIK3R4            30849
# 4 AR                 367                KLK3              354
# 5 ARNT               405                ALDOA             226
# # . with 3,944 more rows, and 1 more variable: effect <dbl>
```

regnetwork_download *Interactions from RegNetwork*

Description

Downloads transcriptional and post-transcriptional regulatory interactions from the RegNetwork database (<http://www.regnetworkweb.org/>). The information about effect signs (stimulation or inhibition), provided by [regnetwork_directions](#) are included in the result.

Usage

```
regnetwork_download(organism = "human")
```

Arguments

organism Character: either human or mouse.

Value

Data frame with interactions.

Examples

```

regn_interactions <- regnetwork_download()
regn_interactions
# # A tibble: 372,778 x 7
#   source_genesymb. source_entrez target_genesymb. target_entrez
#   <chr>             <chr>             <chr>             <chr>
# 1 USF1              7391              S100A6            6277
# 2 USF1              7391              DUSP1             1843
# 3 USF1              7391              C4A               720
# 4 USF1              7391              ABCA1             19
# 5 TP53              7157              TP73              7161
# # . with 372,768 more rows, and 3 more variables: effect <dbl>,
# #   source_type <chr>, target_type <chr>

```

```
relations_list_to_table
```

Table from a nested list of ontology relations

Description

Converting the nested list to a table is a more costly operation, it takes a few seconds. Best to do it only once, or pass `tables = TRUE` to `obo_parser`, and convert the data frame to list, if you also need it in list format.

Usage

```
relations_list_to_table(relations, direction = NULL)
```

Arguments

<code>relations</code>	A nested list of ontology relations (the "relations" element of the list returned by <code>obo_parser</code> in case its argument 'tables' is FALSE).
<code>direction</code>	Override the direction (i.e. child -> parents or parent -> children). The nested lists produced by functions in the current package add an attribute "direction" thus no need to pass this value. If the attribute and the argument are both missing, the column will be named simply "side2" and it won't be clear whether the relations point from "term" to "side2" or the other way around. The direction should be a character vector of length 2 with the values "parents" and "children".

Value

The relations converted to a data frame (tibble).

See Also

- [swap_relations](#)
- [relations_table_to_list](#)
- [obo_parser](#)

Examples

```
goslim_url <-  
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"  
path <- tempfile()  
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))  
obo <- obo_parser(path, tables = FALSE)  
unlink(path)  
rel_tbl <- relations_list_to_table(obo$relations)
```

relations_table_to_graph

Graph from a table of ontology relations

Description

Graph from a table of ontology relations

Usage

```
relations_table_to_graph(relations)
```

Arguments

relations A data frame of ontology relations (the "relations" element of the list returned by [obo_parser](#) in case its argument 'tables' is TRUE).

Details

By default the relations point from child to parents, the edges in the graph will be of the same direction. Use [swap_relations](#) on the data frame to reverse the direction.

Value

The relations converted to an igraph graph object.

Examples

```
go <- get_db('go_basic')  
go_graph <- relations_table_to_graph(go$relations)
```

`relations_table_to_list`*Nested list from a table of ontology relations*

Description

Nested list from a table of ontology relations

Usage

```
relations_table_to_list(relations)
```

Arguments

`relations` A data frame of ontology relations (the "relations" element of the list returned by [obo_parser](#) in case its argument 'tables' is TRUE).

Value

The relations converted to a nested list.

See Also

- [relations_list_to_table](#)
- [swap_relations](#)
- [obo_parser](#)

Examples

```
goslim_url <-  
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"  
path <- tempfile()  
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))  
obo <- obo_parser(path, tables = TRUE)  
unlink(path)  
rel_list <- relations_table_to_list(obo$relations)
```

`remap_dorothea_download`*Downloads TF-target interactions from ReMap*

Description

ReMap (<http://remap.univ-amu.fr/>) is a database of ChIP-Seq experiments. It provides raw and merged peaks and CRMs (cis regulatory motifs) with their associations to regulators (TFs). TF-target relationships can be derived as it is written in Garcia-Alonso et al. 2019: "For ChIP-seq, we downloaded the binding peaks from ReMap and scored the interactions between each TF and each gene according to the distance between the TFBSs and the genes' transcription start sites. We evaluated different filtering strategies that consisted of selecting only the top-scoring 100, 200, 500, and 1000 target genes for each TF." (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/#s1title>). This function returns the top TF-target relationships as used in DoRothEA: https://github.com/saezlab/dorothea/blob/master/inst/scripts/02_chip_seq.R).

Usage

```
remap_dorothea_download()
```

Value

Data frame with TF-target relationships.

See Also

[remap_tf_target_download](#)

Examples

```
remap_interactions <- remap_dorothea_download()
remap_interactions
# # A tibble: 136,988 x 2
#   tf      target
#   <chr> <chr>
# 1 ADNP  ABCC1
# 2 ADNP  ABCC6
# 3 ADNP  ABHD5
# 4 ADNP  ABT1
# 5 ADNP  AC002066.1
# # . with 136,978 more rows
```

remap_filtered	<i>Downloads TF-target interactions from ReMap</i>
----------------	--

Description

Downloads the ReMap TF-target interactions as processed by Garcia-Alonso et al. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/#s1title>) and filters them based on a score threshold, the top targets and whether the TF is included in the TF census (Vaquerizas et al. 2009). The code for filtering is adapted from DoRothEA, written by Christian Holland.

Usage

```
remap_filtered(score = 100, top_targets = 500, only_known_tfs = TRUE)
```

Arguments

score	Numeric: a minimum score between 0 and 1000, records with lower scores will be excluded. If NULL no filtering performed.
top_targets	Numeric: the number of top scoring targets for each TF. Essentially the maximum number of targets per TF. If NULL the number of targets is not restricted.
only_known_tfs	Logical: whether to exclude TFs which are not in TF census.

Value

Data frame with TF-target relationships.

See Also

- [remap_tf_target_download](#)
- [remap_filtered](#)
- [tfcensus_download](#)

Examples

```
remap_interactions <- remap_filtered()
nrow(remap_interactions)
# [1] 145680

remap_interactions <- remap_filtered(top_targets = 100)
remap_interactions
# # A tibble: 30,330 x 2
#   source_genesymbol target_genesymbol
#   <chr>              <chr>
# 1 ADNP              ABCC1
# 2 ADNP              ABT1
# 3 ADNP              AC006076.1
# 4 ADNP              AC007792.1
```

```
# 5 ADNP AC011288.2
# # . with 30,320 more rows
```

```
remap_tf_target_download
```

Downloads TF-target interactions from ReMap

Description

ReMap (<http://remap.univ-amu.fr/>) is a database of ChIP-Seq experiments. It provides raw and merged peaks and CRMs (cis regulatory motifs) with their associations to regulators (TFs). TF-target relationships can be derived as it is written in Garcia-Alonso et al. 2019: "For ChIP-seq, we downloaded the binding peaks from ReMap and scored the interactions between each TF and each gene according to the distance between the TFBSs and the genes' transcription start sites. We evaluated different filtering strategies that consisted of selecting only the top-scoring 100, 200, 500, and 1000 target genes for each TF." (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/#s1title>). This function retrieves the full processed TF-target list from the data deposited in <https://zenodo.org/record/3713238>.

Usage

```
remap_tf_target_download()
```

Value

Data frame with TF-target relationships.

See Also

- [remap_dorothea_download](#)
- [remap_filtered](#)

Examples

```
remap_interactions <- remap_tf_target_download()
remap_interactions
# # A tibble: 9,546,470 x 4
#   source_genesymbol target_genesymbol target_ensembl score
#   <chr>             <chr>             <chr>         <dbl>
# 1 ADNP              PTPRS             ENSG00000105426.16 1000
# 2 AFF4              PRKCH             ENSG00000027075.14 1000
# 3 AHR               CTNND2            ENSG00000169862.18 1000
# 4 AR                PDE4D             ENSG00000113448.18 1000
# 5 ARID1A           PLEC              ENSG00000178209.14 1000
# # . with 9,546,460 more rows
```

resources_colname	<i>Name of the column with the resources</i>
-------------------	--

Description

Unfortunately the column title is different across the various query types in the OmniPath web service, so we need to guess.

Usage

```
resources_colname(data)
```

Arguments

data	A data frame downloaded by any <code>import_...</code> function in the current package.
------	---

Value

Character: the name of the column, if any of the column names matches.

Examples

```
co <- import_omnipath_complexes()
resources_colname(co)
# [1] "sources"
```

simplify_intercell_network	<i>Simplify an intercell network</i>
----------------------------	--------------------------------------

Description

The intercellular communication network data frames, created by [import_intercell_network](#), are combinations of a network data frame with two copies of the intercell annotation data frames, all of them already having quite some columns. Here we keep only the names of the interacting pair, their intercellular communication roles, and the minimal information of the origin of both the interaction and the annotations. Optionally further columns can be selected.

Usage

```
simplify_intercell_network(network, ...)
```

Arguments

network	An intercell network data frame, as provided by import_intercell_network .
...	Optional, further columns to select.

Value

An intercell network data frame with some columns removed.

See Also

- [import_intercell_network](#)
- [unique_intercell_network](#)
- [filter_intercell_network](#)

Examples

```
icn <- import_intercell_network()
icn_s <- simplify_intercell_network(icn)
```

swap_relations	<i>Reverse the direction of ontology relations</i>
----------------	--

Description

Reverse the direction of ontology relations

Usage

```
swap_relations(relations)
```

Arguments

relations The ‘relations’ component of the data returned by [obo_parser](#) or any ‘...ontology_download’ function such as [go_ontology_download](#). Depending on the `tables` argument of those functions the ‘relations’ can be a data frame or a nested list.

Value

Same type as the input, but the relations swapped: if in the input these pointed from each child to the parents, in the output they point from each parent to their children, and vice versa.

See Also

- [relations_list_to_table](#)
- [relations_table_to_list](#)
- [obo_parser](#)

Examples

```

goslim_url <-
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"
path <- tempfile()
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))
obo <- obo_parser(path)
unlink(path)
rel_swapped <- swap_relations(obo$relations)

```

tfcensus_download	<i>Downloads the list of transcription factors from TF census</i>
-------------------	---

Description

Vaquerizas et al. published in 2009 a list of transcription factors. This function retrieves Supplementary Table 2 from the article (<http://www.nature.com/nrg/journal/v10/n4/index.html>).

Usage

```
tfcensus_download()
```

Value

A data frame (tibble) listing transcription factors.

Examples

```

tfcensus <- tfcensus_download()
tfcensus
# # A tibble: 1,987 x 7
#   Class `Ensembl ID` `IPI ID` `Interpro DBD` `Interpro DNA-b.
#   <chr> <chr>          <chr>      <chr>          <chr>
# 1 a     ENSG000000000. IPI0021. NA           IPR001289
# 2 a     ENSG000000000. IPI0004. IPR000047;IPR. NA
# 3 a     ENSG000000000. IPI0001. IPR001356;IPR. NA
# 4 a     ENSG000000000. IPI0029. IPR000910;IPR. NA
# 5 a     ENSG000000000. IPI0001. IPR007087;IPR. IPR006794
# # . with 1,977 more rows, and 2 more variables: `HGNC symbol` <chr>,
# # `Tissue-specificity` <chr>

```

translate_ids	<i>Translate gene and protein identifiers</i>
---------------	---

Description

Translates a vector of identifiers, resulting a new vector, or a column of identifiers in a data frame by creating another column with the target identifiers.

Usage

```
translate_ids(  
  d,  
  ...,  
  uploadlists = FALSE,  
  keep_untranslated = TRUE,  
  return_df = FALSE,  
  organism = 9606,  
  reviewed = TRUE  
)
```

Arguments

d	Character vector or data frame.
...	At least two arguments, with or without names. The first of these arguments describes the source identifier, the rest of them describe the target identifier(s). The values of all these arguments must be valid identifier types as shown in Details. The names of the arguments are column names. In case of the first (source) ID the column must exist. For the rest of the IDs new columns will be created with the desired names. For ID types provided as arguments without names, the name of the ID type will be used for column name.
uploadlists	Force using the uploadlists service from UniProt. By default the plain query interface is used (implemented in uniprot_full_id_mapping_table in this package). If any of the provided ID types is only available in the uploadlists service, it will be automatically selected. The plain query interface is preferred because in the long term, with caching, it requires less download and data storage.
keep_untranslated	In case the output is a data frame, keep the records where the source identifier could not be translated. At these records the target identifier will be NA.
return_df	Return a data frame even if the input is a vector.
organism	Integer, NCBI Taxonomy ID of the organism (by default 9606 for human). Matters only if uploadlists is FALSE.
reviewed	Translate only reviewed (TRUE), only unreviewed (FALSE) or both (NULL) UniProt records. Matters only if uploadlists is FALSE.

Details

This function, depending on the `uploadlists` parameter, uses either the `uploadlists` service of UniProt or plain UniProt queries to obtain identifier translation tables. The possible values for `from` and `to` are the identifier type abbreviations used in the UniProt API, please refer to the table here: https://www.uniprot.org/help/api_idmapping. In addition, simple synonyms are available which realize a uniform API for the `uploadlists` and UniProt query based backends. These are the followings:

OmnipathR	Uploadlists	UniProt query
uniprot	ACC	id
uniprot_entry	ID	entry name
genesymbol	GENENAME	genes(PREFERRED)
genesymbol_syn		genes(ALTERNATIVE)
hgnc	HGNC_ID	database(HGNC)
entrez	P_ENTREZGENEID	database(geneid)
ensg	ENSEMBLGENOME_ID	
enst	ENSEMBL_TRS_ID	database(ensembl)
ensp	ENSEMBL_PRO_ID	
ensgt	ENSEMBLGENOME_TRS_ID	
ensgp	ENSEMBLGENOME_PRO_ID	
ensembl	ENSEMBL_ID	
protein_name		protein names
refseqp	P_REFSEQ_AC	database(refseq)
refseqn	REFSEQ_NT_ID	
embl	EMBL	database(embl)
embl_id	EMBL_ID	
gi	P_GI	
pir	PIR	
pdb	PDB_ID	

The mapping between identifiers can be ambiguous. In this case one row in the original data frame yields multiple rows or elements in the returned data frame or vector(s).

Value

- Data frame: if the input is a data frame or the input is a vector and `return_df` is TRUE.
- Vector: if the input is a vector, there is only one target ID type and `return_df` is FALSE.
- List of vectors: if the input is a vector, there are more than one target ID types and `return_df` is FALSE. The names of the list will be ID types (as they were column names, see the description of the `...` argument), and the list will also include the source IDs.

See Also

- [uniprot_id_mapping_table](#)
- [uniprot_full_id_mapping_table](#)

Examples

```
d <- data.frame(uniprot_id = c('P00533', 'Q9ULV1', 'P43897', 'Q9Y2P5'))
d <- translate_ids(d, uniprot_id = uniprot, genesymbol)
d
#   uniprot_id genesymbol
# 1   P00533      EGFR
# 2   Q9ULV1      FZD4
# 3   P43897      TSFM
# 4   Q9Y2P5    SLC27A5
```

trrust_download	<i>Downloads TF-target interactions from TRRUST</i>
-----------------	---

Description

TRRUST v2 (<https://www.grnpedia.org/trrust/>) is a database of literature mined TF-target interactions for human and mouse.

Usage

```
trrust_download(organism = "human")
```

Arguments

organism Character: either "human" or "mouse".

Value

A data frame of TF-target interactions.

Examples

```
trrust_interactions <- trrust_download()
trrust_interactions
# # A tibble: 11,698 x 4
#   source_genesymbol target_genesymbol effect reference
#   <chr>              <chr>          <dbl> <chr>
# 1 AATF                BAX              -1 22909821
# 2 AATF                CDKN1A           0 17157788
# 3 AATF                KLK3             0 23146908
# 4 AATF                MYC              1 20549547
# 5 AATF                TP53             0 17157788
# 6 ABL1                BAX              1 11753601
# 7 ABL1                BCL2            -1 11753601
# # . with 11,688 more rows
```

`uniprot_full_id_mapping_table`*Creates an ID translation table from UniProt data*

Description

Creates an ID translation table from UniProt data

Usage

```
uniprot_full_id_mapping_table(  
  to,  
  from = "id",  
  reviewed = TRUE,  
  organism = 9606  
)
```

Arguments

<code>to</code>	Character or symbol: target ID type. See Details for possible values.
<code>from</code>	Character or symbol: source ID type. See Details for possible values.
<code>reviewed</code>	Translate only reviewed (TRUE), only unreviewed (FALSE) or both (NULL) UniProt records.
<code>organism</code>	Integer, NCBI Taxonomy ID of the organism (by default 9606 for human).

Details

For both source and target ID type, this function accepts column codes used by UniProt and some simple shortcuts defined here. For the UniProt codes please refer to <https://www.uniprot.org/help/uniprotkb>. The shortcuts are `entrez`, `genesymbol`, `genesymbol_syn` (synonym gene symbols), `hgnc`, `embl`, `refseqp` (RefSeq protein), `enst` (Ensembl transcript), `uniprot_entry` (UniProtKB AC, e.g. EGFR_HUMAN), `protein_name` (full name of the protein), `uniprot` (UniProtKB ID, e.g. P00533). For a complete table please refer to [translate_ids](#).

Value

A data frame (tibble) with columns 'From' and 'To', UniProt IDs and the corresponding foreign IDs, respectively.

See Also

[translate_ids](#)

Examples

```
uniprot_entrez <- uniprot_full_id_mapping_table(to = 'entrez')
uniprot_entrez
# # A tibble: 20,723 x 2
#   From To
#   <chr> <chr>
# 1 Q96R72 NA
# 2 Q9UKL2 23538
# 3 Q9H205 144125
# 4 Q8NGN2 219873
# 5 Q8NGC1 390439
# # . with 20,713 more rows
```

uniprot_id_mapping_table

Retrieves an identifier translation table from the UniProt uploadlists service

Description

Retrieves an identifier translation table from the UniProt uploadlists service

Usage

```
uniprot_id_mapping_table(identifiers, from, to, chunk_size = 5000)
```

Arguments

identifiers	Character vector of identifiers
from	Character or symbol: type of the identifiers provided. See Details for possible values.
to	Character or symbol: identifier type to be retrieved from UniProt. See Details for possible values.
chunk_size	Integer: query the identifiers in chunks of this size. If you are experiencing download failures, try lower values.

Details

This function uses the uploadlists service of UniProt to obtain identifier translation tables. The possible values for 'from' and 'to' are the identifier type abbreviations used in the UniProt API, please refer to the table here: https://www.uniprot.org/help/api_idmapping or the table of synonyms supported by the current package: [translate_ids](#). Note: if the number of identifiers is larger than the chunk size the log message about the cache origin is not guaranteed to be correct (most of the times it is still correct).

Value

A data frame (tibble) with columns 'From' and 'To', the identifiers provided and the corresponding target IDs, respectively.

See Also

[translate_ids](#)

Examples

```
uniprot_genesymbol <- uniprot_id_mapping_table(
  c('P00533', 'P23771'), uniprot, genesymbol
)
uniprot_genesymbol
# # A tibble: 2 x 2
#   From To
#   <chr> <chr>
# 1 P00533 EGFR
# 2 P23771 GATA3
```

unique_intercell_network

Unique intercellular interactions

Description

In the intercellular network data frames produced by [import_intercell_network](#), by default each pair of annotations for an interaction is represented in a separate row. This function drops the annotations and keeps only the distinct interacting pairs.

Usage

```
unique_intercell_network(network, ...)
```

Arguments

network	An intercellular network data frame as produced by import_intercell_network .
...	Additional columns to keep. Note: if these have multiple values for an interacting pair, only the first row will be preserved.

Value

A data frame with interacting pairs and interaction attributes.

See Also

- [import_intercell_network](#)
- [simplify_intercell_network](#)
- [filter_intercell_network](#)

Examples

```
icn <- import_intercell_network()
icn_unique <- unique_intercell_network(icn)
```

vinayagam_download *Protein-protein interactions from Vinayagam 2011*

Description

Retrieves the Supplementary Table S6 from Vinayagam et al. 2011. Find out more at <https://doi.org/10.1126/scisignal.2001699>.

Usage

```
vinayagam_download()
```

Value

A data frame (tibble) with interactions.

Examples

```
vinayagam_interactions <- vinayagam_download()
vinayagam_interactions
# # A tibble: 34,814 x 5
#   `Input-node Gen.` `Input-node Gen.` `Output-node Ge.` `Output-node Ge.`
#   <chr>             <dbl> <chr>             <dbl>
# 1 C1orf103          55791 MNAT1           4331
# 2 MAST2            23139 DYNLL1           8655
# 3 RAB22A           57403 APPL2          55198
# 4 TRAP1            10131 EXT2           2132
# 5 STAT2            6773  COPS4           51138
# # . with 34,804 more rows, and 1 more variable:
# # `Edge direction score` <dbl>
```

walk_ontology_tree *All nodes of a subtree starting from the selected nodes*

Description

Starting from the selected nodes, recursively walks the ontology tree until it reaches either the root or leaf nodes. Collects all visited nodes.

Usage

```
walk_ontology_tree(  
  terms,  
  ancestors = TRUE,  
  db_key = "go_basic",  
  ids = TRUE,  
  method = "gra",  
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",  
               "negatively_regulates")  
)
```

Arguments

terms	Character vector of ontology term IDs or names. A mixture of IDs and names can be provided.
ancestors	Logical: if FALSE the ontology tree is traversed towards the leaf nodes; if TRUE, the tree is traversed until the root. The former returns the ancestors (parents), the latter the descendants (children).
db_key	Character: key to identify the ontology database. For the available keys see omnipath_show_db .
ids	Logical: whether to return IDs or term names.
method	Character: either "gra" or "lst". The implementation to use for traversing the ontology tree. The graph based implementation is faster than the list based, the latter will be removed in the future.
relations	Character vector of ontology relation types. Only these relations will be used.

Details

Note: this function relies on the database manager, the first call might take long because of the database load process. Subsequent calls within a short period should be faster. See [get_ontology_db](#).

Value

Character vector of ontology IDs. If the input terms are all leaves or roots NULL is returned. The starting nodes won't be included in the result unless they fall onto the traversal path from other nodes.

See Also

- [omnipath_show_db](#)
- [get_ontology_db](#)

Examples

```
walk_ontology_tree(c('GO:0006241', 'GO:0044211'))
# [1] "GO:0006139" "GO:0006220" "GO:0006221" "GO:0006241" "GO:0006725"
# [6] "GO:0006753" "GO:0006793" "GO:0006796" "GO:0006807" "GO:0008150"
# ... (truncated)
walk_ontology_tree(c('GO:0006241', 'GO:0044211'), ancestors = FALSE)
# [1] "GO:0044210" "GO:0044211"
walk_ontology_tree(
  c('GO:0006241', 'GO:0044211'),
  ancestors = FALSE,
  ids = FALSE
)
# [1] "'de novo' CTP biosynthetic process" "CTP salvage"
```

zenodo_download

Retrieves data from Zenodo

Description

Zenodo is a repository of large scientific datasets. Many projects and publications make their datasets available at Zenodo. This function downloads an archive from Zenodo and extracts the requested file.

Usage

```
zenodo_download(
  path,
  reader = NULL,
  reader_param = list(),
  url_key = NULL,
  zenodo_record = NULL,
  zenodo_fname = NULL,
  url_param = list(),
  url_key_param = list(),
  ...
)
```

Arguments

path Character: path to the file within the archive.

reader Optional, a function to read the connection.

reader_param	List: arguments for the reader function.
url_key	Character: name of the option containing the URL
zenodo_record	The Zenodo record ID, either integer or character.
zenodo_fname	The file name within the record.
url_param	List: variables to insert into the URL string (which is returned from the options).
url_key_param	List: variables to insert into the 'url_key'.
...	Passed to archive_extractor

Value

A connection

Examples

```
# an example from the OmnipathR::remap_tf_target_download function:
remap_dorothea <- zenodo_download(
  zenodo_record = 3713238,
  zenodo_fname = 'tf_target_sources.zip',
  path = (
    'tf_target_sources/chip_seq/remap/gene_tf_pairs_genesymbol.txt'
  ),
  reader = read_tsv,
  reader_param = list(
    col_names = c(
      'source_genesymbol',
      'target_genesymbol',
      'target_ensembl',
      'score'
    ),
    col_types = cols(),
    progress = FALSE
  ),
  resource = 'ReMap'
)
```

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