Package: ontoProc2 (via r-universe)

November 25, 2026

Date 2026-08-28

Title Ontology Facilities Based on INCAtools Semantic SQL

Version 1.0.0

Description This package provides ontology facilities based on INCAtools Semantic SQL. Tooling is provided to retrieve and cache SQLite databases representing curated ontologies. ontologyIndex ontology_index instances can be produced. Anthropic's Claude was used in the development of S7 classes and methods and in the production of documentation.

License Artistic-2.0

Encoding UTF-8

Depends R (>= 4.5.0)

Imports RSQLite, DBI, BiocFileCache, R.utils, dplyr, ontologyIndex, ontologyPlot, graph, Rgraphviz, igraph, ggraph, ggplot2, graphlayouts, grid, methods, S7, utils, httr2, xml2, digest

Suggests knitr, testthat, BiocStyle, DT, GO.db, AnnotationDbi, stringr

VignetteBuilder knitr

biocViews Infrastructure, DataRepresentation, Pathways, SingleCell

URL https://github.com/vjcitn/ontoProc2

BugReports https://github.com/vjcitn/ontoProc2/issues

Config/roxygen2/version 8.1.0

Roxygen list(markdown = TRUE)

Config/pak/sysreqs libfontconfig1-dev libfreetype6-dev libglpk-dev libicu-dev libxml2-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:56:26 UTC

RemoteUrl https://github.com/bioc/ontoProc2

RemoteRef RELEASE_3_24

RemoteSha de4bfc3da6d62815f82d8e8601b6685c71469d05

Contents

bbop_sqlite_db_gz . . . 3
cells_with_pmp . . . 4
cn2tag . . . 4
count_by_prefix . . . 5
count_descendants . . . 5
describe_table . . . 6
disconnect . . . 7
find_by_restriction . . . 7
find_intersection . . . 8
get_ancestors . . . 9
get_ancestors_partonomy . . . 10
get_definition . . . 10
get_descendants . . . 11
get_descendants_partonomy . . . 12
get_direct_edges . . . 12
get_direct_subclasses . . . 13
get_direct_superclasses . . . 14
get_label . . . 14
get_prefix . . . 15
get_present_pmp . . . 16
get_restrictions . . . 16
get_synonyms . . . 17
get_term_info . . . 18
improve_nodes . . . 18
is_connected . . . 19
label_igraph_nodes . . . 20
list_tables . . . 20
make_graphNEL_from_ontology_plot . . . 21
make_igraph_from_ontology_plot . . . 22
ncit_map . . . 22
onto_plot2 . . . 23
onto_plot2_params . . . 24
onto_plot2_stress . . . 25
onto_plot2_sugiyama . . . 26
PREDICATES . . . 26
print . . . 27
reconnect . . . 28
report . . . 28
retrieve_semsql_conn . . . 29
run_query . . . 30
search_labels . . . 31
semsql_connect . . . 31
semsql_to_oi . . . 32
semsql_url . . . 33
SemsqlConn . . . 34
tag2cn . . . 34

with_connection 35

Index **36**

`bbop_sqlite_db_gz` *retrieve and cache all filenames of Semantic SQL ontologies available, checking for updated content relative to cache via ETag*

Description

retrieve and cache all filenames of Semantic SQL ontologies available, checking for updated content relative to cache via ETag

Usage

```
bbop_sqlite_db_gz(
  url = "https://semanticsql.berkeleybop.io/",
  bfc = BiocFileCache::BiocFileCache(),
  rname = "bbop_sqlite_listing",
  timeout_connect = 5,
  timeout_total = 15
)
```

Arguments

`url`	source address
`bfc`	an instance of BiocFileCache
`rname`	a string to use to identify the cached listing
`timeout_connect`	passed to httr2::req_options connecttimeout parameter
`timeout_total`	passed to httr2::req_options seconds parameter

Value

a character vector

Note

There is no real etag discipline for the metadata, so full metadata content is extracted on each call, digested, and compared to digest in cache. Cache is updated when there is a discrepancy, except there is a guard against rewriting cache with corrupted or zero-length data at endpoint. Note this code was negotiated at length with claude.ai Sonnet 4.6.

Examples

```
gzs = bbop_sqlite_db_gz()
head(gzs)
length(gzs)
```

cells_with_pmp *produce a table with cells exhibiting given proteins on plasma membrane according to CL*

Description

produce a table with cells exhibiting given proteins on plasma membrane according to CL

Usage

```
cells_with_pmp(curies)
```

Arguments

curies	a character vector in format "PR:nnnnnnnnn"

Value

a data.frame with columns cl, celltype, pr, protein

Examples

```
# 2064: microsialin, 1874: KLRB1-like protein
cells_with_pmp(c("PR:000002064", "PR:000001874"))
```

cn2tag *a named vector with mapping from cell type phrase to CURIE for CL.owl*

Description

a named vector with mapping from cell type phrase to CURIE for CL.owl

Usage

```
data(cn2tag)
```

Format

names character vector

Note

creation is detailed in unexported function makeBundledMaps

Examples

```
data("cn2tag", package = "ontoProc2")
cn2tag["Kupffer cell"]
```

count_by_prefix *Count labeled terms grouped by CURIE prefix*

Description

Count labeled terms grouped by CURIE prefix

Usage

```
count_by_prefix(x, ...)
```

Arguments

x	A SemsqlConn object.
...	not used.

Value

data.frame with columns prefix and n, ordered by n descending.

Examples

```
goref <- semsql_connect(ontology = "go")
count_by_prefix(goref)
disconnect(goref)
```

count_descendants *Count the number of descendants of a term*

Description

Count the number of descendants of a term

Usage

```
count_descendants(x, term_id, predicate = "rdfs:subClassOf", ...)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
predicate	character(1) predicate to traverse (default "rdfs:subClassOf").
...	not used

Value

integer(1).

Examples

```
goref <- semsql_connect(ontology = "go")
count_descendants(goref, "GO:0006915") # all apoptosis subtypes
disconnect(goref)
```

`describe_table` *Describe the columns of a table in a SemsqlConn database*

Description

Describe the columns of a table in a SemsqlConn database

Usage

```
describe_table(x, table_name, ...)
```

Arguments

`x`	A `SemsqlConn` object.
`table_name`	character(1) name of the table.
`...`	not used

Value

data.frame with PRAGMA table_info output (columns: cid, name, type, notnull, dflt_value, pk).

Examples

```
goref <- semsql_connect(ontology = "go")
describe_table(goref, "rdfs_label_statement")
disconnect(goref)
```

disconnect *Disconnect a SemsqlConn from its database*

Description

Disconnect a SemsqlConn from its database

Usage

```
disconnect(x, quiet = FALSE, ...)
```

Arguments

x	A SemsqlConn object.
quiet	logical(1) if TRUE suppresses the disconnection message (default FALSE).
...	not used

Value

The SemsqlConn object invisibly.

find_by_restriction *Find terms that have a given OWL someValuesFrom restriction*

Description

Find terms that have a given OWL someValuesFrom restriction

Usage

```
find_by_restriction(
  x,
  property,
  filler,
  include_filler_descendants = FALSE,
  ...
)
```

Arguments

x	A SemsqlConn object.
property	character(1) property CURIE (e.g. "BFO:0000050" for part-of).
filler	character(1) filler class CURIE.
include_filler_descendants	logical(1) if TRUE also match subclasses of filler (default FALSE).
...	not used

Value

data.frame with columns `id` and `label`.

Examples

```
goref <- semsql_connect(ontology = "go")
# cellular components that are part_of nucleus (GO:0005634)
find_by_restriction(goref, "BFO:0000050", "GO:0005634")
disconnect(goref)
```

`find_intersection` *Find terms that are descendants of a superclass and have a given restriction*

Description

Find terms that are descendants of a superclass and have a given restriction

Usage

```
find_intersection(x, superclass_id, relation_property, related_to_id, ...)
```

Arguments

`x`	A `SemsqlConn` object.
`superclass_id`	character(1) CURIE of the superclass.
`relation_property`	character(1) property CURIE for the restriction.
`related_to_id`	character(1) filler CURIE for the restriction.
`...`	not used

Value

data.frame with columns `id` and `label`.

Examples

```
goref <- semsql_connect(ontology = "go")
# CC terms (GO:0005575) that are part_of nucleus (GO:0005634)
find_intersection(goref, "GO:0005575", "BFO:0000050", "GO:0005634")
disconnect(goref)
```

`get_ancestors` *Get all ancestors of a term via entailed edges*

Description

Get all ancestors of a term via entailed edges

Usage

```
get_ancestors(
  x,
  term_id,
  predicates = "rdfs:subClassOf",
  include_self = FALSE,
  ...
)
```

Arguments

`x`	A `SemsqlConn` object.
`term_id`	character(1) CURIE.
`predicates`	character vector of predicate CURIEs to follow. Defaults to `"rdfs:subClassOf"`. See `PREDICATES()` for common values.
`include_self`	logical(1) whether to include the term itself (default `FALSE`).
`...`	not used

Value

data.frame with columns `id`, `label`, `predicate`.

Examples

```
goref <- semsql_connect(ontology = "go")
get_ancestors(goref, "GO:0006915")
disconnect(goref)
```

get_ancestors_partonomy *Get ancestors traversing both is-a and part-of relationships*

Description

Convenience wrapper around `get_ancestors()` that follows both `rdfs:subClassOf` and `BFO:0000050` (part-of) edges.

Usage

```
get_ancestors_partonomy(conn, term_id, include_self = FALSE)
```

Arguments

`conn`	A `SemsqlConn` object.
`term_id`	character(1) CURIE.
`include_self`	logical(1) whether to include the term itself (default `FALSE`).

Value

data.frame with columns `id`, `label`, `predicate`.

Examples

```
goref <- semsql_connect(ontology = "go")
get_ancestors_partonomy(goref, "GO:0005739") # mitochondrion
disconnect(goref)
```

get_definition *Get the text definition for a term*

Description

Get the text definition for a term

Usage

```
get_definition(x, term_id, ...)
```

Arguments

`x`	A `SemsqlConn` object.
`term_id`	character(1) CURIE.
`...`	not used

Value

character(1) definition text, or NA_character_ if not found.

Examples

```
goref <- semsql_connect(ontology = "go")
get_definition(goref, "GO:0006915")
disconnect(goref)
```

---

get_descendants *Get all descendants of a term via entailed edges*

Description

Get all descendants of a term via entailed edges

Usage

```
get_descendants(
  x,
  term_id,
  predicates = "rdfs:subClassOf",
  include_self = FALSE,
  ...
)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
predicates	character vector of predicate CURIEs to follow. Defaults to "rdfs:subClassOf".
include_self	logical(1) whether to include the term itself (default FALSE).
...	not used

Value

data.frame with columns id, label, predicate.

Examples

```
goref <- semsql_connect(ontology = "go")
get_descendants(goref, "GO:0006915")
disconnect(goref)
```

get_descendants_partonomy *Get descendants traversing both is-a and has-part relationships*

Description

Convenience wrapper around `get_descendants()` that follows both `rdfs:subClassOf` and `BFO:0000051` (has-part) edges.

Usage

```
get_descendants_partonomy(conn, term_id, include_self = FALSE)
```

Arguments

`conn`	A `SemsqlConn` object.
`term_id`	character(1) CURIE.
`include_self`	logical(1) whether to include the term itself (default `FALSE`).

Value

data.frame with columns `id`, `label`, `predicate`.

Examples

```
goref <- semsql_connect(ontology = "go")
get_descendants_partonomy(goref, "GO:0005634") # nucleus sub-components
disconnect(goref)
```

get_direct_edges *Get direct edges in the ontology graph for a term*

Description

Get direct edges in the ontology graph for a term

Usage

```
get_direct_edges(
  x,
  term_id,
  direction = c("outgoing", "incoming", "both"),
  ...
)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
direction	character(1) one of "outgoing", "incoming", "both".
...	not used

Value

data.frame with columns subject, subject_label, predicate, predicate_label, object, object_label.

Examples

```
goref <- semsql_connect(ontology = "go")
get_direct_edges(goref, "GO:0006915")
get_direct_edges(goref, "GO:0006915", direction = "both")
disconnect(goref)
```

---

get_direct_subclasses *Get direct subclasses of a term*

Description

Get direct subclasses of a term

Usage

```
get_direct_subclasses(x, term_id, ...)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
...	not used

Value

data.frame with columns id and label, ordered by label.

Examples

```
goref <- semsql_connect(ontology = "go")
# direct children of "apoptotic process" (GO:0006915)
get_direct_subclasses(goref, "GO:0006915")
disconnect(goref)
```

get_direct_superclasses *Get direct superclasses of a term*

Description

Get direct superclasses of a term

Usage

```
get_direct_superclasses(x, term_id, ...)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
...	not used

Value

data.frame with columns id and label, ordered by label.

Examples

```
goref <- semsql_connect(ontology = "go")
get_direct_superclasses(goref, "GO:0006915")
disconnect(goref)
```

get_label *Get the rdfs:label for a term*

Description

Get the rdfs:label for a term

Usage

```
get_label(x, term_id, ...)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE, e.g. "GO:0006915".
...	not used

Value

character(1) label, or NA_character_ if not found.

Examples

```
goref <- semsql_connect(ontology = "go")
get_label(goref, "GO:0006915") # "apoptotic process"
disconnect(goref)
```

`get_prefix` *Retrieve the ontology prefix from a SemsqlConn*

Description

Retrieve the ontology prefix from a SemsqlConn

Usage

```
get_prefix(x, ...)
```

Arguments

x	A SemsqlConn object.
...	not used

Value

character(1) the primary ontology prefix (e.g. "GO").

Examples

```
goref <- semsql_connect(ontology = "go")
get_prefix(goref)
disconnect(goref)
```

get_present_pmp *produce a table with list of proteins from protein ontology identified as present on cell membranes for input cell type CURIEs*

Description

produce a table with list of proteins from protein ontology identified as present on cell membranes for input cell type CURIEs

Usage

```
get_present_pmp(curies)
```

Arguments

curies	a character vector in format "CL:nnnnnnn"

Value

a data.frame with columns cl, celltype, pr, protein

Examples

```
get_present_pmp(c("CL:0000091", "CL:0000926"))
```

get_restrictions *Get OWL someValuesFrom restrictions for a term*

Description

Get OWL someValuesFrom restrictions for a term

Usage

```
get_restrictions(x, term_id, ...)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
...	not used

Value

data.frame with columns restriction_id, property, property_label, filler, filler_label.

Examples

```
goref <- semsql_connect(ontology = "go")
# mitochondrion (GO:0005739) has part-of restrictions to cell
get_restrictions(goref, "GO:0005739")
disconnect(goref)
```

`get_synonyms` *Get synonyms for a term*

Description

Get synonyms for a term

Usage

```
get_synonyms(
  x,
  term_id,
  type = c("all", "exact", "broad", "narrow", "related"),
  ...
)
```

Arguments

`x`	A `SemsqlConn` object.
`term_id`	character(1) CURIE.
`type`	character(1) synonym scope: one of `"all"`, `"exact"`, `"broad"`, `"narrow"`, `"related"`.
`...`	not used

Value

data.frame with columns `subject`, `predicate`, `synonym`.

Examples

```
goref <- semsql_connect(ontology = "go")
get_synonyms(goref, "GO:0006915")
get_synonyms(goref, "GO:0006915", type = "exact")
disconnect(goref)
```

get_term_info *Retrieve a summary of information about a term*

Description

Retrieve a summary of information about a term

Usage

```
get_term_info(x, term_id, ...)
```

Arguments

x	A SemsqlConn object.
term_id	character(1) CURIE.
...	not used

Value

list with elements id, label, definition, synonyms, superclasses, subclasses.

Examples

```
goref <- semsql_connect(ontology = "go")
info <- get_term_info(goref, "GO:0006915")
info$label
info$superclasses
disconnect(goref)
```

improve_nodes *inject linefeeds for node names for graph, with textual annotation from ontology*

Description

inject linefeeds for node names for graph, with textual annotation from ontology

Usage

```
improve_nodes(g, ont)
```

Arguments

g	graphNEL instance
ont	instance of ontology from ontologyIndex

Value

graphNEL instance

Examples

```
requireNamespace("Rgraphviz")
requireNamespace("graph")
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
p3k <- ontologyPlot::onto_plot(cl, cl3k)
gnel <- make_graphNEL_from_ontology_plot(p3k)
head(graph::nodes(gnel)) # before improving
gnel <- improve_nodes(gnel, cl)
head(graph::nodes(gnel))
```

---

is_connected *Test whether a SemsqlConn has a valid open connection*

Description

Test whether a SemsqlConn has a valid open connection

Usage

```
is_connected(x, ...)
```

Arguments

x	A SemsqlConn object.
...	not used

Value

logical(1).

Examples

```
goref <- semsql_connect(ontology = "go")
is_connected(goref) # TRUE
disconnect(goref)
is_connected(goref) # FALSE
```

label_igraph_nodes *Add term labels as a vertex attribute to an ontology igraph*

Description

Add term labels as a vertex attribute to an ontology igraph

Usage

```
label_igraph_nodes(g, ont, sep = "\n")
```

Arguments

g	igraph directed graph whose vertex names are ontology term IDs
ont	ontology_index instance (from ontologyIndex)
sep	character(1) separator between term name and ID, defaults to "\n"

Value

igraph with a "label" vertex attribute

Examples

```
requireNamespace("igraph")
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
p3k <- ontologyPlot::onto_plot(cl, cl3k)
ig <- make_igraph_from_ontology_plot(p3k)
ig <- label_igraph_nodes(ig, cl)
igraph::V(ig)$label
```

list_tables *List tables in a SemsqlConn database*

Description

List tables in a SemsqlConn database

Usage

```
list_tables(x, ...)
```

Arguments

x	A SemsqlConn object.
...	not used

Value

character vector of table names.

Examples

```
goref <- semsql_connect(ontology = "go")
list_tables(goref)
disconnect(goref)
```

---

make_graphNEL_from_ontology_plot

obtain graphNEL from ontology_plot instance of ontologyPlot

Description

obtain graphNEL from ontology_plot instance of ontologyPlot

Usage

```
make_graphNEL_from_ontology_plot(x)
```

Arguments

x	instance of S3 class ontology_plot

Value

instance of S4 graphNEL class

Examples

```
requireNamespace("Rgraphviz")
requireNamespace("graph")
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
p3k <- ontologyPlot::onto_plot(cl, cl3k)
gnel <- make_graphNEL_from_ontology_plot(p3k)
gnel <- improve_nodes(gnel, cl)
graph::graph.par(list(nodes = list(shape = "plaintext", cex = .8)))
gnel <- Rgraphviz::layoutGraph(gnel)
Rgraphviz::renderGraph(gnel)
```

make_igraph_from_ontology_plot *Convert an ontology_plot instance to an igraph object*

Description

Convert an ontology_plot instance to an igraph object

Usage

```
make_igraph_from_ontology_plot(x)
```

Arguments

x	instance of S3 class ontology_plot (from ontologyPlot::onto_plot)

Value

an igraph directed graph

Examples

```
requireNamespace("igraph")
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
p3k <- ontologyPlot::onto_plot(cl, cl3k)
ig <- make_igraph_from_ontology_plot(p3k)
ig
```

ncit_map *a named vector with values rdfs labels in NCI thesaurus, and names the corresponding formal ontology tags*

Description

a named vector with values rdfs labels in NCI thesaurus, and names the corresponding formal ontology tags

Usage

```
data(ncit_map)
```

Format

named character vector

Note

creation is detailed in unexported function makeBundledMaps

Examples

```
data("ncit_map", package = "ontoProc2")
head(ncit_map)
```

---

onto_plot2 *high-level use of graph/Rgraphviz for rendering ontology relations*

Description

high-level use of graph/Rgraphviz for rendering ontology relations

Usage

```
onto_plot2(ont, terms2use, cex = 0.8, ...)
```

Arguments

ont	instance of ontology from ontologyIndex
terms2use	character vector
cex	numeric(1) defaults to .8, supplied to Rgraphviz::graph.par
...	passed to onto_plot of ontologyPlot

Value

graphNEL instance (invisibly)

Examples

```
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
onto_plot2(cl, cl3k)
```

`onto_plot2_params` *Visual parameters for ggraph-based ontology plots*

Description

Returns a named list of default visual parameters consumed by `onto_plot2_sugiyama` and `onto_plot2_stress`. Modify individual fields before passing to control the appearance without touching every argument.

Usage

```
onto_plot2_params(
  label_size = 3,
  edge_colour = "grey60",
  arrow_length_mm = 3,
  end_cap_mm = 10,
  node_colour = "black",
  bg_fill = "white",
  arc_strength = 0.15,
  node_fill = "steelblue",
  label_corner_r = 0.3
)
```

Arguments

`label_size`	numeric(1) node label text size, default 3
`edge_colour`	character(1) edge colour, default "grey60"
`arrow_length_mm`	numeric(1) arrowhead length in mm, default 3
`end_cap_mm`	numeric(1) radius mm of circular buffer at arrow tip (controls clearance between arrowhead and node text), default 10
`node_colour`	character(1) node text colour, default "black"
`bg_fill`	character(1) plot background fill colour, default "white"
`arc_strength`	numeric(1) curvature of arcs in stress layout (0 = straight), default 0.15
`node_fill`	character(1) fill colour for node label boxes in stress layout, default "steelblue"
`label_corner_r`	numeric(1) corner rounding radius in lines for node label boxes in stress layout, default 0.3

Value

named list of visual parameters

Examples

```
p <- onto_plot2_params()
p$end_cap_mm <- 14
p$edge_colour <- "navy"
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
onto_plot2_sugiyama(cl, cl3k, params = p)
```

---

onto_plot2_stress *Plot ontology relations using ggraph with a stress-minimisation layout*

Description

Produces a ggplot2-based directed graph using ggraph and the graphlayouts stress layout, which places nodes to minimise visual stress. Useful when the hierarchy is shallow or you prefer a force-directed look. Visual parameters are controlled via `onto_plot2_params()`.

Usage

```
onto_plot2_stress(ont, terms2use, params = onto_plot2_params(), ...)
```

Arguments

`ont`	ontology_index instance (from ontologyIndex / semsql_to_oi)
`terms2use`	character vector of ontology term IDs to include
`params`	named list of visual parameters from `onto_plot2_params()`
`...`	passed to ontologyPlot::onto_plot

Value

a ggplot object (printed as a side effect); the igraph is returned invisibly

Examples

```
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
onto_plot2_stress(cl, cl3k)
```

onto_plot2_sugiyama *Plot ontology relations using ggraph with a Sugiyama (hierarchical) layout*

Description

Produces a ggplot2-based directed graph using ggraph and igraph's Sugiyama layout, which respects the DAG structure of ontology hierarchies. Visual parameters are controlled via `onto_plot2_params()`.

Usage

```
onto_plot2_sugiyama(ont, terms2use, params = onto_plot2_params(), ...)
```

Arguments

`ont`	ontology_index instance (from ontologyIndex / semsql_to_oi)
`terms2use`	character vector of ontology term IDs to include
`params`	named list of visual parameters from `onto_plot2_params()`
`...`	passed to ontologyPlot::onto_plot

Value

a ggplot object (printed as a side effect); the igraph is returned invisibly

Examples

```
clcon <- retrieve_semsql_conn("cl")
cl <- semsql_to_oi(clcon)
cl3k <- c(
  "CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
  "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556"
)
onto_plot2_sugiyama(cl, cl3k)
```

PREDICATES *Standard predicate CURIEs used in OBO ontologies*

Description

A named list of commonly used predicate CURIEs in OBO-format ontologies, for use with `get_ancestors()`, `get_descendants()`, and related functions.

Usage

```
PREDICATES
```

Format

A named list with elements `subclass_of`, `part_of`, `has_part`, `develops_from`, `located_in`, `has_characteristic`.

Value

a named list

Examples

```
goref <- semsql_connect(ontology = "go")
# apoptotic process (GO:0006915) ancestors via is-a and part-of
anc <- get_ancestors(goref, "GO:0006915",
  predicates = c(PREDICATES$subclass_of, PREDICATES$part_of)
)
head(anc)
disconnect(goref)
```

---

print *Show method for SemsqlConn. Concise one-line summary displayed when a* `SemsqlConn` *object is auto-printed at the R prompt.*

Description

Show method for SemsqlConn. Concise one-line summary displayed when a `SemsqlConn` object is auto-printed at the R prompt.

Usage

```
## S7 method for class <ontoProc2::SemsqlConn>
print(x, ...)
```

Arguments

`x`	A `SemsqlConn` object.
`...`	not used

Value

x, invisibly

reconnect *Reconnect a SemsqlConn to its database*

Description

Attempts to reconnect a disconnected `SemsqlConn` object to its database. Returns a new `SemsqlConn`; the original cannot be modified in place due to S7 value semantics.

Usage

```
reconnect(x, ...)
```

Arguments

`x`	A `SemsqlConn` object.
`...`	not used

Value

A new `SemsqlConn` object with an active connection.

Examples

```
goref <- semsql_connect(ontology = "go")
disconnect(goref)
goref <- reconnect(goref)
disconnect(goref)
```

report *Display a detailed report of a SemsqlConn object*

Description

Displays a verbose, formatted representation of a `SemsqlConn` object including connection status, database statistics (labeled terms, edges, definitions), prefix breakdown, and available key tables. More informative than `print()`, intended for interactive exploration.

Usage

```
report(object, ...)

## S7 method for class <ontoProc2::SemsqlConn>
report(object, ...)
```

Arguments

object	A SemsqlConn object.
...	additional arguments (currently unused)

Value

The SemsqlConn object invisibly.

Examples

```
goref <- semsql_connect(ontology = "go")
report(goref)
disconnect(goref)
```

---

retrieve_semsql_conn *return a SQLite connection (read only) to an INCAtools Semantic SQL ontology*

Description

return a SQLite connection (read only) to an INCAtools Semantic SQL ontology

Usage

```
retrieve_semsql_conn(
  ontology = "efo",
  cache = BiocFileCache::BiocFileCache(),
  cacheid = NULL,
  ...
)
```

Arguments

ontology	character(1) short string prefixing .db.gz in the INCAtools collection
cache	a BiocFileCache instance, defaulting to BiocFileCache::BiocFileCache()
cacheid	character(1) or NULL; if non-null, the associated SQLite resource will be used from cache
...	passed to download.file

Value

an RSQLite DBI connection instance

Note

When the cache is searched, the string given as 'ontology' will be prefixed with '^'. This helps avoid confusion between pcl.db and cl.db, for example.

Examples

```
# first time will involve a download and decompression
aionto <- retrieve_semsql_conn("aio")
head(DBI::dbListTables(aionto))
dplyr::tbl(aionto, "class_node") |> head()
```

`run_query` *Run an arbitrary SQL query against a SemsqlConn database*

Description

Run an arbitrary SQL query against a SemsqlConn database

Usage

```
run_query(x, sql, ...)
```

Arguments

`x`	A `SemsqlConn` object.
`sql`	character(1) SQL query string.
`...`	not used

Value

data.frame with query results.

Examples

```
goref <- semsql_connect(ontology = "go")
run_query(
  goref,
  "SELECT subject, value AS label FROM rdfs_label_statement LIMIT 5"
)
disconnect(goref)
```

search_labels *Search term labels in a SemsqlConn database*

Description

Search term labels in a SemsqlConn database

Usage

```
search_labels(x, pattern, limit = 20L)
```

Arguments

x	A SemsqlConn object.
pattern	character(1) substring to match against rdfs:label values (SQL LIKE pattern, case-insensitive on most SQLite builds).
limit	integer(1) maximum number of rows to return (default 20).

Value

data.frame with columns subject and label.

Examples

```
goref <- semsql_connect(ontology = "go")
search_labels(goref, "apoptosis")
disconnect(goref)
```

semsql_connect *Create a SemsqlConn connection*

Description

Opens a connection to a SemanticSQL SQLite database, either by supplying a direct file path or by referencing a short ontology name that is retrieved and cached via BiocFileCache.

Usage

```
semsql_connect(
  db_path = NULL,
  ontology_prefix = NULL,
  ontology = NULL,
  cache = BiocFileCache::BiocFileCache(),
  validate = TRUE,
  ...
)
```

Arguments

db_path	character(1) or NULL. Path to an existing SQLite database file. Either db_path or ontology must be supplied.
ontology_prefix	character(1) or NULL. Primary CURIE prefix for the ontology (e.g. "CL"). If NULL and ontology is supplied, defaults to toupper(ontology); otherwise auto-detected from the database.
ontology	character(1) or NULL. Short name of an INCAtools ontology (e.g. "cl", "go"). If supplied, retrieve_semsql_conn() is called to locate or download the cached database.
cache	a BiocFileCache instance used when ontology is supplied. Defaults to BiocFileCache::BiocFileCacl
validate	logical(1) if TRUE (the default value) the ontology code is checked against available Semantic SQL resources at INCAtools. Set to FALSE if using off line.
...	passed to retrieve_semsql_conn() and ultimately to utils::download.file().

Value

A SemsqlConn() object.

Note

The connection has flag SQLITE_RO for read-only access. There will be an attempt to validate the ontology tag that is supplied, against all available Semantic SQL resources available at INCAtools bucket. Function fails if a match cannot be made, which in general requires network access.

Examples

```
# by ontology short name (downloads if not cached)
goref <- semsql_connect(ontology = "go")
goref
disconnect(goref)
```

---

semsql_to_oi *produce an ontology_index instance from semantic sql sqlite connection*

Description

produce an ontology_index instance from semantic sql sqlite connection

Usage

```
semsql_to_oi(con)
```

Arguments

con	DBI::dbConnect value for sqlite table

Value

result of ontologyIndex::ontology_index evaluated for the labels and parent-child relations in tables statements and edge of the semantic sql resource

Examples

```
## Not run:
conn <- semsql_connect(ontology = "aio")
oi <- suppressWarnings(semsql_to_oi(conn@con))
names(oi)

## End(Not run)
```

---

semsql_url *produce INCAtools distribution URL*

Description

produce INCAtools distribution URL

Usage

```
semsql_url(ontology = "efo")
```

Arguments

ontology	short string that is the prefix to .db.gz in the bbop-sqlite collection

Value

a string with URL for INCAtools resource

Examples

```
semsql_url("cl")
```

SemsqlConn — *SemsqlConn: S7 connection wrapper for SemanticSQL databases*

Description

An S7 class that encapsulates a SQLite connection to an ontology database following the SemanticSQL schema. Provides methods for common ontology queries including label lookup, ancestor/descendant traversal, and relationship queries.

Properties:

con The DBI connection object (SQLiteConnection)

db_path character(1) path to the SQLite database file

ontology_prefix character(1) primary ontology prefix, e.g. `"CL"` for the Cell Ontology

Usage

```
SemsqlConn(con = NULL, db_path = character(0), ontology_prefix = character(0))
```

Arguments

`con`	DBI connection object
`db_path`	character path to SQLite database file
`ontology_prefix`	character, e.g., 'CL' for cell ontology

Value

wrapped connection

tag2cn — *a named vector with mapping from CURIE to cell type phrase for CL.owl*

Description

a named vector with mapping from CURIE to cell type phrase for CL.owl

Usage

```
data(tag2cn)
```

Format

names character vector

Note

creation is detailed in unexported function makeBundledMaps

Examples

```
data("tag2cn", package = "ontoProc2")
tag2cn[c("CL:0000000", "CL:0000006")]
```

---

with_connection *Execute code with an automatically managed SemsqlConn*

Description

Opens a connection, evaluates an expression with `conn` bound to the open `SemsqlConn`, then closes the connection even if an error occurs. Analogous to Python's context manager (`with` statement).

Usage

```
with_connection(db_path, expr)
```

Arguments

`db_path`	character(1) path to the SQLite database.
`expr`	an expression to evaluate; `conn` is bound to the open `SemsqlConn` within this expression.

Value

the value of `expr`.

Examples

```
## Not run:
result <- with_connection("cl.db", {
  get_ancestors(conn, "CL:0000540")
})

## End(Not run)
```

Index

∗ **datasets**
    cn2tag, 4
    ncit_map, 22
    tag2cn, 34

bbop_sqlite_db_gz, 3

cells_with_pmp, 4
cn2tag, 4
count_by_prefix, 5
count_descendants, 5

describe_table, 6
disconnect, 7

find_by_restriction, 7
find_intersection, 8

get_ancestors, 9
get_ancestors(), *10*, *26*
get_ancestors_partonomy, 10
get_definition, 10
get_descendants, 11
get_descendants(), *12*, *26*
get_descendants_partonomy, 12
get_direct_edges, 12
get_direct_subclasses, 13
get_direct_superclasses, 14
get_label, 14
get_prefix, 15
get_present_pmp, 16
get_restrictions, 16
get_synonyms, 17
get_term_info, 18

improve_nodes, 18
is_connected, 19

label_igraph_nodes, 20
list_tables, 20

make_graphNEL_from_ontology_plot, 21
make_igraph_from_ontology_plot, 22

ncit_map, 22

onto_plot2, 23
onto_plot2_params, 24
onto_plot2_stress, 25
onto_plot2_sugiyama, 26

PREDICATES, 26
PREDICATES(), *9*
print, 27

reconnect, 28
report, 28
report,ontoProc2::SemsqlConn-method
    *(*report*)*, 28
retrieve_semsql_conn, 29
retrieve_semsql_conn(), *32*
run_query, 30

search_labels, 31
semsql_connect, 31
semsql_to_oi, 32
semsql_url, 33
SemsqlConn, 34
SemsqlConn(), *32*

tag2cn, 34

utils::download.file(), *32*

with_connection, 35