geneslator

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`GeneslatorDb` *GeneslatorDb class*

Description

The `GeneslatorDb` class is the container for storing annotation databases in the **geneslator** package.

Usage

```
GeneslatorDb(org, release.version = "latest")
```

Arguments

`org`	A character string specifying the scientific name of the organism (e.g. "Homo sapiens") or its Taxonomy ID. See `availableDatabases()` for the list of supported organisms.
`release.version`	A character string indicating the release version of the annotation database (e.g. "2025-12"). See `availableVersions()` for the list of available releases.

Details

The `GeneslatorDb` class is the container for storing annotation databases in the `geneslator` package. It wraps an `OrgDb` object, which represents the annotation database of a specific organism.

Annotation databases used by **geneslator** are updated on a monthly basis and available as different versions of a Zenodo record at `https://doi.org/10.5281/zenodo.20448208` as SQLite files. Each release refers to a specific version of the databases. Versions are indicated as `year.month`, where `year` and `month` denote the year and the month of the publication of the release (e.g. '2026.03'). Each database in a release refers to a specific organism.

The constructor method `GeneslatorDb(org)` creates a new `GeneslatorDb` object for the annotation database of organism `org`. Once created, the object is exported to the global environment of the user as a variable having the same name of the annotation database (e.g. `org.Hsapiens.db` for Human, `org.Mmusculus.db` for Mouse). By default, the constructor method considers the latest release of the database. An older version can be specified through parameter `release.version`. See `availableDatabases()` and `availableVersions()` for the list of available databases and release versions.

When called, the constructor method first look for a copy of the SQLite file in the R cache folder of the user. If the SQLite file exists and is up-to-date, the cached copy is used to create the `GeneslatorDb` object. Otherwise, upon request by the user, the database is dowloaded from the remote release and copied in the **geneslator** package cache, before creating the object.

Value

A GeneslatorDb object.

Slots

db The annotation database represented as an OrgDb object.

Examples

```
# Create a GeneslatorDb object for Human
# First call: download human db (org.Hsapiens.db) from latest release and
# save it to R cache
GeneslatorDb("Homo sapiens")
org.Hsapiens.db
# Second call: load db from local cache
GeneslatorDb("Homo sapiens")
org.Hsapiens.db

# Create a GeneslatorDb object for Fly.
# Use taxonomy id and release version 2025.12
GeneslatorDb("7227", "2025.12")
org.Dmelanogaster.db
```

---

availableDatabases *Available databases in geneslator*

Description

availableDatabases lists all possible annotation databases that can be queried in the **geneslator** package. Databases are updated on a monthly basis and available as different versions of a Zenodo record at https://doi.org/10.5281/zenodo.20448208. Each release refer to a specific version of the databases. Versions are indicated as year.month, where year and month denote the year and the month of the publication of the release (e.g. '2026.03'). Each database in a release refer to a specific organism.

Usage

```
availableDatabases(release.version = "latest")
```

Arguments

release.version
: Release version of the databases. By default, the most recent version is considered ("latest"). Older versions must be indicated as year.month, where year and month denote the year and the month of the publication of the release (e.g. "2026.03"). See availableVersions() for the list of available release versions.

Value

availableDatabases returns a dataframe which reports, for each annotation database: database name, scientific name of the organism, Taxonomy ID of the organism, MD5 security check of the SQLite database file and release version. Database info refer to the release version specified by the version parameter.

See Also

GeneslatorDb, availableVersions.

Examples

```
# List all databases included in the current geneslator release
availableDatabases()

# List all databases included in geneslator release version 2025.12
availableDatabases("2025.12")
```

---

availableVersions *Available database versions in geneslator*

Description

availableVersions lists all possible versions of the annotation databases that can be queried in the **geneslator** package. Databases are updated on a monthly basis and available as different versions of a Zenodo record at https://doi.org/10.5281/zenodo.20448208. Each release refer to a specific version of the databases. Versions are indicated as year.month, where year and month denote the year and the month of the publication of the release (e.g. '2026.03').

Usage

```
availableVersions()
```

Value

availableVersions returns a character vector with all available versions of the geneslator annotation databases.

See Also

GeneslatorDb, availableDatabases.

Examples

```
# List all available versions of geneslator databases
availableVersions()
```

keys *List values of a column in the annotation databases of geneslator*

Description

The keys function lists of all possible values for a given column in the annotation database of a specific organism within the **geneslator** package.

Usage

```
## S4 method for signature 'GeneslatorDb'
keys(x, keytype)
```

Arguments

x	A GeneslatorDb object returned by GeneslatorDb(). It represents the annotation database to query from.
keytype	Name of the column from which the list of values should be extracted. See keytypes() for the list of available columns for the annotation database x.

Value

keys returns a character vector of all possible values of the column keytype in database x.

See Also

keytypes(), mapIds(), select()

Examples

```
# Get the list of all NCBI gene ids present in zebrafish annotation db
GeneslatorDb("Danio rerio")
geneslator::keys(org.Drerio.db, keytype = "ENTREZID")

# Get the list of all REACTOME pathways present in rat annotation db
GeneslatorDb("Rattus norvegicus")
geneslator::keys(org.Rnorvegicus.db, keytype = "REACTOMEPATH")
```

keytypes *List available columns in the annotation databases of geneslator*

Description

Functions keytypes and columns are used to access the complete lists of input and output columns that can be queried in the annotation databases of the **geneslator** package through mapIds() and select() functions.

Usage

```
## S4 method for signature 'GeneslatorDb'
keytypes(x)

## S4 method for signature 'GeneslatorDb'
columns(x)
```

Arguments

x	A GeneslatorDb object returned by GeneslatorDb(). It represents the annotation database to query from.

Details

keytypes() lists all possible columns of the annotation database x that can be used as input when querying x, i.e., all possible values of the keytype argument in mapIds() and select() functions.

columns() lists all possible columns of the annotation database x that can be used as output when querying x, i.e., all possible values of the column argument in mapIds() and select() functions.

The following is a list of columns shared by all organisms in the annotation databases of **geneslator** package. Some of these columns may be missing in one or more organisms, if no data is available for that organism.

Column	Description
SYMBOL	Official gene symbol
ALIAS	Aliases of a gene
LOCUS	Locus tag of a gene
GENETYPE	Biological type of a gene (e.g. 'protein-coding', 'ncRNA')
GENENAME	Full name or description of a gene
ENTREZID	Gene ID in NCBI Gene
ENSEMBL	Gene ID in Ensembl
UNIPROT	Uniprot IDs of proteins associated to a gene
ENTREZIDOLD	Archived IDs in NCBI Gene
ENSEMBLOLD	Archived IDs in Ensembl
ORTHO[org]	Orthologs in species [org], where [org] is the upper-case common name of one of the organism p
GO	IDs of Gene Ontology (GO) terms associated to a gene
GONAME	Names of GO terms associated to a gene
GOEVIDENCE	Evidence codes of GO terms associated to a gene
GOTYPE	Types of GO terms ('BP'=biological process, 'CC'=cellular component, 'MF'=molecular function)
KEGGPATH	IDs of KEGG pathways associated to a gene
KEGGPATHNAME	Names of KEGG pathways associated to a gene
REACTOMEPATH	IDs of Reactome pathways associated to a gene
REACTOMEPATHNAME	Names of Reactome pathways associated to a gene
WIKIPATH	IDs of Wikipathways pathways associated to a gene
WIKIPATHNAME	Names of Wikipathways pathways associated to a gene

Here is a list of the most representative species-specific IDs in in the annotation databases of **geneslator** package. Type columns(org) to retrieve the list of species-specific IDs for organism org.

Organism	Column	Description
Human	HGNC	Gene ID in HUGO Gene Nomenclature Committee

Mouse	MGI	Gene ID in Mouse Genome Informatics
Rat	RGD	Gene ID in Rat Genome Database
Yeast	SGD	Gene ID in Saccharomyces Genome Database
Worm	WORMBASE	Gene ID in WormBase database
Fly	FLYBASE	Gene ID in FlyBase database
Zebrafish	ZFIN	Gene ID in Zebrafish Information Network
Arabidopsis	TAIR	Gene ID in The Arabidopsis Information Resource

Value

keytypes() and columns() return a character vector of column names of database x.

See Also

availableDatabases, mapIds, select

Examples

```
# Get the list of available keytypes in mouse
GeneslatorDb("Mus musculus")
geneslator::keytypes(org.Mmusculus.db)

# Get the list of available columns that can be mapped to keys in yeast
GeneslatorDb("Saccharomyces cerevisiae")
geneslator::columns(org.Scerevisiae.db)
```

---

mapIds *Map data from the annotation databases of geneslator*

Description

mapIds maps key values of a column to values of another column in the annotation databases of **geneslator** package.

Usage

```
## S4 method for signature 'GeneslatorDb'
mapIds(
  x,
  keys,
  column,
  keytype,
  search.aliases = TRUE,
  search.archives = TRUE,
  ...,
  multiVals
)
```

Arguments

x	A GeneslatorDb object returned by GeneslatorDb(). It represents the annotation database to query from.
keys	Values used as keys to retrieve records from the annotation database.
column	Column to return as output of the query. See columns() for more details.
keytype	Column representing the type of values of keys parameter. See keytypes() for more details.
search.aliases	When no mapping is found using gene symbol (SYMBOL column), should select perform query using also ALIAS column? (default = TRUE). This parameter is used only in queries involving SYMBOL column.
search.archives	When no mapping is found using NCBI gene ids (ENTREZID column) and/or Ensembl gene ids (ENSEMBL column), should select perform query using also archived identifiers (columns ENTREZIDOLD and/or ENSEMBLOLD)? (default = TRUE). This parameter is used only in queries involving ENTREZID and/or ENSEMBL column.
...	Other arguments. See AnnotationDb for more info.
multiVals	What should mapIds do when there are multiple output values that could be returned for a specific input? Options include:

Option	Description
first	Return a vector object containing only the first match found for each input (default behaviour).
asNA	Return a vector object with NA values whenever there are multiple matches for a given input.
filter	Return a shorter vector object, excluding all inputs for which multiple matches have been found.
list	Return a list object with all matches found for each input.
CharacterList	Return a SimpleCharacterList object with all matches found for each input.
FUN	Supply a function to the multiVals argument for custom behaviors.

If using FUN, the function must take a single argument and return a single value. This function will be applied to all elements and will serve as a 'rule' for which item to keep when there is more than one match for a given input. For example, the following function grabs the last element in each result: `last <- function(x) { x[[length(x)]] }`.

Details

mapIds maps each key value to either a single value or a list of values of the type specified by column parameter, depending on the value of multiVals parameter.

Value

mapIds returns either a named vector, where each value is a possible mapping (if exists) for a given key, or a list of values, where each element of the list is the vector of all mappings found for a given key. The type of the return object depends on the value of the multiVals parameter.

See Also

availableDatabases, keytypes, columns

Examples

```
# Map NCBI gene ids to gene aliases in yeast.
# Return a named vector with 1st mapping found
GeneslatorDb("Saccharomyces cerevisiae")
geneslator::mapIds(org.Scerevisiae.db,
  keys = c("856781", "1466469"),
  column = "ALIAS", keytype = "ENTREZID"
)

# Map gene symbols to gene ontologies in mouse.
# Return a list with all possible mappings
GeneslatorDb("Mus musculus")
geneslator::mapIds(org.Mmusculus.db,
  keys = c("Grin2a", "Rev3l"), column = "GO",
  keytype = "SYMBOL", multiVals = "list"
)

# Map gene symbols to uniprot ids in rat. Apply a custom function to
# return the last mapping found and do not use Ensembl archive data.
GeneslatorDb("Rattus norvegicus")
last <- function(x) {
  x[[length(x)]]
}
geneslator::mapIds(org.Rnorvegicus.db,
  keys = c(
    "ENSRNOG00000003105",
    "ENSRNOG00000049505"
  ), column = "UNIPROT", keytype = "ENSEMBL",
  multiVals = "list", search.archives = FALSE
)

# Map gene symbols to reactome pathways in zebrafish.
# Return a CharacterList object with all possible mappings
GeneslatorDb("Danio rerio")
geneslator::mapIds(org.Drerio.db,
  keys = c("hoxc8a", "samhd1"),
  column = "REACTOMEPATH", keytype = "SYMBOL", multiVals = "CharacterList"
)
```

`select` *Extract data from the annotation databases of geneslator*

Description

`select` query annotation databases of **geneslator** package, by mapping different types of gene annotation data from several source of data.

Usage

```
## S4 method for signature 'GeneslatorDb'
select(
  x,
  keys,
  columns,
  keytype,
  search.aliases = TRUE,
  search.archives = TRUE,
  orthologs.mapping = "multiple",
  ...
)
```

Arguments

x	A GeneslatorDb object returned by GeneslatorDb(). It represents the annotation database to query from.
keys	Values used as keys to retrieve records from the annotation database.
columns	Columns to return as output of the query. See columns() for more details.
keytype	Column representing the type of values of keys parameter. See keytypes() for more details.
search.aliases	When no mapping is found using gene symbol (SYMBOL column), should select perform query using also ALIAS column? (default = TRUE). This parameter is used only in queries involving SYMBOL column.
search.archives	When no mapping is found using NCBI gene ids (ENTREZID column) and/or Ensembl gene ids (ENSEMBL column), should select perform query using also archived identifiers (columns ENTREZIDOLD and/or ENSEMBLOLD)? (default = TRUE). This parameter is used only in queries involving ENTREZID and/or ENSEMBL column.
orthologs.mapping	Return all orthologs ("multiple") or just the first ortholog ("single") of a gene? (default = "multiple"). Used only in queries where the output columns include ORTHO columns (e.g. ORTHOMOUSE, ORTHOYEAST).
...	Other arguments. See AnnotationDb for more info.

Details

select collects all possible mappings between values of the column specified by keytype parameter and values of the columns specified by the columns parameter.

Value

select returns a dataframe with all columns specified by keytype and columns parameters and one row for each mapping found between keys and column values.

See Also

availableDatabases, keytypes, columns

Examples

```
# Lookup NCBI gene ids for a given list of gene symbols in fly
GeneslatorDb("Drosophila melanogaster")
geneslator::select(org.Dmelanogaster.db,
  keys = c("CG14883", "GstE2"),
  columns = "ENTREZID", keytype = "SYMBOL"
)

# Lookup REACTOME pathway ids and their relative full names for a given list
# of ensembl gene ids in worm
GeneslatorDb("Caenorhabditis elegans")
geneslator::select(org.Celegans.db,
  keys = c(
    "ENSDARG00000013522",
    "ENSDARG00000103044"
  ), columns = c("REACTOMEPATH", "REACTOMEPATHNAME"),
  keytype = "ENSEMBL"
)

# Lookup mouse orthologs for a list of human gene symbols.
# Ignore aliases and return only the first ortholog found for each gene
GeneslatorDb("Homo sapiens")
geneslator::select(org.Hsapiens.db,
  keys = c("BRCA1", "PTEN"),
  columns = "ORTHOMOUSE", keytype = "SYMBOL", search.aliases = FALSE,
  orthologs.mapping = "single"
)

# Lookup gene ontologies for a list of entrez ids in arabidopsis.
# Do not use NCBI archive data
GeneslatorDb("Arabidopsis thaliana")
geneslator::select(org.Athaliana.db,
  keys = c("820005", "831939"),
  columns = c("GO", "GONAME", "GOTYPE"), keytype = "ENTREZID",
  search.archives = FALSE
)
```

---

show,GeneslatorDb-method

Show method for GeneslatorDb

Description

Show method for GeneslatorDb

Usage

```
## S4 method for signature 'GeneslatorDb'
show(object)
```

Arguments

object	A GeneslatorDb object.

Value

Invisibly returns `NULL`. Called for its side effect of printing a summary of the object to the console.

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