Package 'OmaDB'

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Title R wrapper for the OMA REST API

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Description A package for the orthology prediction data download from OMA database.

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`OmaDB-package` *OmaDB: A package for the orthology prediction data download from OMA database.*

Description

OmaDB is a wrapper for the REST API for the Orthologous MAtrix project (OMA) which is a database for the inference of orthologs among complete genomes. For more details on the OMA project, see https://omabrowser.org/.

OmaDB functions

The package contains a range of functions that are used to query the database. Some of the main functions are listed below:

- getProtein()
- getHOG()
- getOMAGroup()
- getGenomePairs()
- getTaxonomy()
- mapSequence()
- annotateSequence()
- searchProtein()

In addition to these, OmaDB features a range of functions that are used to format the retrieved data into some commonly used Bioconductor objects using packages such as GenomicRanges, Biostrings, topGO and ggtree. Some of them are listed below:

- formatTopGO()
- getGRanges()

The above functions are described in more detail in the package vignette's listed below:

- Get started with OmaDB
- Exploring Hierarchical orthologous groups with OmaDB
- Exploring Taxonomic trees with OmaDB
- Sequence Analysis with OmaDB

`annotateSequence` *Map GO annotation to a sequence that is not available in the OMA Browser*

Description

This function obtain Gene Ontology annotation for a given sequence that does not need to exist in the OMA Browser so far. The query sequence will analysed and a fast homology detection approach based on kmers will be used to detect the closest sequences in OMA. GO annotations for these top hits will be used to annotated the query sequence.

Usage

```
annotateSequence(query)
```

Arguments

query	the sequence to be annotated, it can be either a string or an AAString object from the Biostrings package

Value

a data.frame containing the the GO annotation information of the most similar protein to the query sequence

Examples

```
annotateSequence(query='MNDPSLLGYPNVGPQQQQQQQQQQHAGLLGKGTPNALQQQLHMNQLTGIPPPGLMNNSDVHTSSNNNSRQLLDQLANGNANMLNMN
```

---

formatTopGO *Format the GO annotations data*

Description

The function to create a list of GO annotations that is compatible with topGO from protein objects in roma

Usage

```
formatTopGO(geneList, format)
```

Arguments

geneList	the list of OmaDB protein objects or a dataframe of ontologies to be included in the analysis - this is where the GO annotations are extracted from.
format	format for the data to be returned in - either 'GO2geneID' or 'geneID2GO'

Value

a list containing the GO2geneID or geneID2GO information

Examples

```
geneList = list(getProtein(id='YEAST01'),getProtein(id='YEAST03'))
annotations = formatTopGO(geneList,format='geneID2GO')
```

getAnnotation-deprecated *Get GO annotation for a sequence Function*

Description

This function should no longer be used. Use instead annotateSequence.

Usage

```
getAnnotation(query)
```

Arguments

query	the sequence to be annotated, it can be either a string or an AAString object from the Biostrings package

Value

a data.frame containg the GO annotaition information linked to the query sequence

See Also

OmaDB-deprecated

getAttribute *Get the value for the Object Attribute*

Description

The function to obtain the value for an object attribute.

Usage

```
getAttribute(obj, attribute)
```

Arguments

obj	the object of interest
attribute	the attribute of interest

Value

an value for a given object attribute

Examples

```
members = getAttribute(getOMAGroup(id ='YEAST58'),'members')
```

getData-deprecated *Get the Data Function*

Description

The function to obtain the information available for a single entry in the datase. This function should no longer be used. It has been divided into several functions: Use the following functions instead.

- `getProtein` to obtain proteins (former `type='protein'`)
- `getGenome` to obtain genomes (former `type='genome'`)
- `getOMAGroup` to obtain genomes (former `type='group'`)

Usage

```
getData(type, id, attribute = NULL)
```

Arguments

`type`	the type for the entry to be returned - either protein, genome or group
`id`	an identifier for the entry to be returned. For more information, see the 'Get started with OmaDB' vignette.
`attribute`	an extra attribute

Value

an object containing the JSON keys as attributes

See Also

`OmaDB-deprecated`

getGenome *Retrieve a genome from the OMA Browser database*

Description

This function obtains the basic information for one specific genome available on the OMA Browser, or - if no id is provided - a dataframe with all available genomes.

Usage

```
getGenome(id = NULL, attribute = NULL)
```

Arguments

id	A genome identifier. By default, all available genomes will be returned.
attribute	An extra attribute to be returned (proteins)

Details

Ids can be either the scientific name of a species, the NCBI taxonomy id or the UniProtKB mnemonic species code.

The optional argument attribute can be used to directly load the proteins belonging to the genome. Alternatively, you can access the proteins attribute of the result which will transparently load the proteins from the OMA Browser.

Value

an object containing the JSON keys as attributes or a dataframe

Examples

```
getGenome()
getGenome(id='HUMAN')
getGenome(id=9606)
getGenome(id='HUMAN',attribute='proteins')
```

---

getGenomeAlignment-deprecated

Get Whole Genome Alignment Function

Description

This function should no longer be used. Use instaed `getGenomePairs`.

Usage

```
getGenomeAlignment(genome1, genome2, chr1 = NULL, chr2 = NULL,
  rel_type = NULL)
```

Arguments

genome_id1	an identifier for the first genome, which can be either its taxon id or UniProt species code
genome_id2	an an identifier for the second genome, which can be either its taxon id or UniProt species code
chr1	the chromosome of interest for the first genome
chr2	the chromosome of interest for the second genome
rel_type	the pairs relationship type
per_page	the number of instances to be returned or 'all'. default is set to a 100.

Value

a dataframe containing information about both the entries in the orthologous pair and their relationship

See Also

OmaDB-deprecated

`getGenomePairs` *Retrieves the pairwise relations among two genomes*

Description

This function retrieves the pairwise relations among two genomes from the OMA Browser database. The relations are orthologs in case the genomes are different and "close paralogs" and "homoeologs" in case they are the same.

Usage

```
getGenomePairs(genome_id1, genome_id2, chr1 = NULL, chr2 = NULL,
  rel_type = NULL, ...)
```

Arguments

`genome_id1`	an identifier for the first genome, which can be either its taxon id or UniProt species code
`genome_id2`	an an identifier for the second genome, which can be either its taxon id or UniProt species code
`chr1`	the chromosome of interest for the first genome
`chr2`	the chromosome of interest for the second genome
`rel_type`	the pairs relationship type
`...`	qwargs

Details

By using the parameters chr1 and chr2, one can limit the relations to a certain chromosome for one or both genomes. The id of the chromosome corresponds to the chromosome ids from the `getGenome` result.

The rel_type parameter further limits the returned relations to a specific subtype of orthologs (i.e. "1:1", "1:n", "m:1", "m:n") or - within a genome to either "close paralogs" or "homeologs".

Value

a dataframe containing information about both the entries in the orthologous pair and their relationship

Examples

```
getGenomePairs(genome_id1='YEAST',genome_id2='ASHGO')
```

---

getHOG *Retrieve a HOG from the OMA Browser*

Description

The function retrieves a specific Hierarchical Orthologous Group (HOG) from the OMA Browser database. A HOG is a set of genes that have all decendet from a single ancestral gene at a specific taxonomic level.

Usage

```
getHOG(id, level = NULL, members = FALSE)
```

Arguments

id	an identifier for the HOG to be returned - either its HOG ID or a protein id.
level	a specific level for the HOG to be restricted to. level can either be 'root', or the name of a taxonomic level that is part of the HOG, e.g. 'Fungi'. By default it will retrieve the depest level of the most specific subhog for the given ID.
members	boolean that when set to TRUE returns a dataframe containg the protein members at a given hog level

Details

A HOG can be identified by its member proteins and a taxonomic level, or a HOG ID. As a taxonomic level, you can use either 'root' to retrieve the HOG at its deepest level, or the name of NCBI taxonomy level, or leave it out in which case the deepest level that doesn't include a duplication node is used.

The function either returns a single hog object or a list of hog objects. The later happens if the HOG ID you provide has already split into several sub-hogs at the level you indicate.

Value

an object containing HOG attributes, or a list of those

Examples

```
getHOG(id = 'YEAST590')
getHOG(id = 'YEAST590', level='root')
getHOG(id = 'YEAST590', level='Saccharomycetaceae', members=TRUE)
```

getLocus *Get loci for a given list of proteins*

Description

Function to obtain loci in genomic range format for a given list of proteins

Usage

```
getLocus(proteins)
```

Arguments

proteins	the dataframe or a list of dataframes containing the protein data of interest. this can either be the members df or a list of protein ids.

Value

genomic range object from the GenomicRanges package in Bioconductor

Examples

```
loci = getLocus(proteins = getOMAGroup('YEAST58')['members'])
```

getObjectAttributes *Get the Object Attributes*

Description

The function to obtain the attributes and their data types for the object created.

Usage

```
getObjectAttributes(obj)
```

Arguments

obj	the object of interest

Value

an list of object attributes and their data classes

Examples

```
attributes = getObjectAttributes(getOMAGroup(id ='YEAST58'))
```

getOMAGroup *Retrieve an OMA Group from the OMA Browser*

Description

This function obtains an OMA Group from the OMA Browser database. An OMA Group is defined to be a clique of proteins that are all orthologous to each other, i.e. they are all related through speciation events only. An OMA Group can thus by definition not contain any inparalogs. It is a very stringent orthology grouping approach. OMA Groups are mostly useful to infer phylogenetic species tree where they can be used as marker genes.

Usage

```
getOMAGroup(id, attribute = NULL)
```

Arguments

id	An identifier for the group. See above for possible types of IDs.
attribute	an extra attribute to be returned (close_groups)

Details

Retrieving an OMA Group can be done using a group nr as id, its fingerprint (a 7mer AA sequence which is unique to proteins in that group), a member protein id or any sequence pattern that is unique to the group.

Value

an object containing the JSON keys as attributes or a dataframe

Examples

```
getOMAGroup(id='58')
getOMAGroup(id='P12345')
getOMAGroup(id='NNRRGRI')
getOMAGroup(id='58', attribute='close_groups')
```

getProtein *Retrieve a protein from the OMA Browser*

Description

This function enables to retrieve information on one or several proteins from the OMA Browser database.

Usage

```
getProtein(id, attribute = NULL)
```

Arguments

id	Identifier(s) for the entry or entries to be returned. a character string if single entry or a vector if multiple.
attribute	Instead of the protein, return the attribute property of the protein. Attriute needs to be one of 'domains', 'orthologs', 'gene_ontology', 'locus', or 'homoeologs'.

Details

In its simplest form the function returns the base data of the query protein. The query protein can be selected with any unique id, for example with a UniProtKB accession (P12345), an OMA id (YEAST00012), or a RefSeq id (NP_001226). To retrieve more than one protein, you should pass a vector of IDs.

Non-scalar properties of proteins such as their domains, GO annotations, orthologs or homeologs will get loaded upon accessing them, or if you only need this information you can set the attribute parameter to the property name and retrieve this information directly.

Value

An object containing the JSON keys as attributes or a dataframe containing the non-scalar protein property.

See Also

For non-unique non-unique IDs or partial ID lookup, use searchProtein instead.

Examples

```
getProtein(id='YEAST00001')
getProtein(id='YEAST00001', attribute='orthologs')
getProtein(id=c('YEAST00001','YEAST00002','YEAST00012'))
getProtein(id=c('YEAST00001','YEAST00002','YEAST00012'), attribute='gene_ontology')
```

---

getTaxonomy *Get the Taxonomic tree function*

Description

The function to obtain the taxonomic tree from the database in the newick format that can be plugged into phylo.io for visualisation.

Usage

```
getTaxonomy(root = NULL, members = NULL, newick = TRUE)
```

Arguments

root	optional parameter, the root of the node of interest
members	optional parameter, list of member ncbi taxon or UniProt IDs that should be included in the induced taxonomy.
newick	optional parameter, boolean default set to TRUE

Value

an object containing the JSON keys as attributes

Examples

```
getTaxonomy()
getTaxonomy(members='YEAST,ASHGO')
getTaxonomy(root='Alveolata')
```

---

getTopGO *Get the topGO Object function*

Description

The function to create a topGO object containing the GO annotations for the given protein list.

Usage

```
getTopGO(annotations, format, foregroundGenes, ontology)
```

Arguments

annotations	list of GO annoatations obtained from the formatTopGO()
format	Format for the data to be returned in - either 'GO2geneID' or 'geneID2GO'
foregroundGenes	List of identifiers for the foreground genes
ontology	The ontology for which the enrichment should be done. This parameter is passed directly to the topGOdata constructor.

Value

topGO object

Examples

```
geneList = list(getProtein(id='YEAST58'),getProtein(id='YEAST00059'))
annotations = formatTopGO(geneList,format='geneID2GO')
library(topGO)
getTopGO(annotations, foregroundGenes = list('YEAST00058'), format = 'geneID2GO', ontology = 'BP')
```

getTree *Get the Tree Object*

Description

A convenience function to obtain a tree object from newick tree, essentially wraps read.tree from the ape package.

Usage

```
getTree(newick)
```

Arguments

newick	The newick tree to be instantiated.

Value

a tree object

Examples

```
taxonomy = getTaxonomy(root='Alveolata')
getTree(newick=taxonomy$newick)
```

getVersion *Get the API and database version function*

Description

The function to obtain the API and database version that the package is using.

Usage

```
getVersion()
```

Value

S3 object

Examples

```
getVersion()
```

getXref-deprecated *Get the CrossReferences in the OMA database for a pattern*

Description

This function is should no longer be used. Use instead `searchProtein`.

Usage

```
getXref(pattern)
```

Arguments

`pattern`	the pattern to query the OMA database with - needs to be at least 3 characters long

Value

a data.frame containing information on the cross references for a given pattern

See Also

`OmaDB-deprecated`

group *An example OMA group object.*

Description

An object containing information for the OMA group number 737636.

Usage

```
group
```

Format

An S3 object with 4 variables:

group_nr group number, not stable across releases

fingerprint fingerprint of the oma group, stable across releases

related_groups url to the endpoint containing the list of oma groups that share some of the orthologs with this oma group

members list of protein members of this oma group ...

Source

`https://omabrowser.org/api/group/YEAST58/`

hog *An example HOG object.*

Description

An object containing information for the HOG:0273533.1b.

Usage

```
hog
```

Format

An S3 object with 8 variables:

hog_id hog identifier

level the taxonomic level of this hog

levels_url url pointer to the hog information at a given level

members_url url pointer to the list of gene members for this hog

alternative_members a dataframe object containing the rest of the taxonomic levels in this hog

roothog_id the root taxonomic level of this hog

parent_hogs a dataframe containing information on the parent hogs to the current hogs

children_hogs a dataframe containing information on the children hogs to the current hogs ...

Source

https://omabrowser.org/api/hog/HOG:0273533.1b/

mapSequence *Map the Protein Sequence Function*

Description

The function to identify a sequence.

Usage

```
mapSequence(query, search = NULL, full_length = FALSE)
```

Arguments

query	the sequence to be searched, it can be either a string or an AAString object from the Biostrings package
search	argument to choose search strategy. Can be set to 'exact', 'approximate' or 'mixed'. Defaults to 'mixed', meaning first tries to find exact match. If no target can be found, uses approximate search strategy to identify query sequence in database.
full_length	a boolean indicating whether or not for exact matches, the query sequence must be matching the full target sequence. By default, a partial exact match is also reported as exact match.

Value

a data.frame containing the information of matches for the query sequence

Examples

```
mapSequence(query='MNDPSLLGYPNVGPQQQQQQQQQQHAGLLGKGTPNALQQQLHMNQLTGIPPPGLMNNSDVHTSSNNNSRQLLDQLANGNANMLNMNMDNNN
mapSequence(search='mixed',query='NKLLQPTDFQQSHIAEASKSLVDCTKQALMEMADTLTDSKTAKKQQPTGDSTPSGTATNSAVSTPLTPKIELFANG
```

`OmaDB-deprecated` *Deprecated functions in package* **OmaDB**.

Description

These functions are provided for compatibility with older versions of **OmaDB** only, and will be defunct at the next release.

Usage

```
getXref(pattern)

getAnnotation(query)

getGenomeAlignment(genome1, genome2, chr1 = NULL, chr2 = NULL,
  rel_type = NULL)

getData(type, id, attribute = NULL)
```

Details

The following functions are deprecated and will be made defunct; use the replacement indicated below:

`getXref`

For `getXref`, use `searchProtein`.

getAnnotation

For getAnnotation, use annotateSequence.

getGenomeAlignment

For getGenomeAlignment, use getGenomePairs.

getData

For getData, use getProtein, getGenome, getOMAGroup.

---

orthologs *An example orthologs object.*

Description

A dataframe containing information for the orthologs of protein YEAST00058.

Usage

```
orthologs
```

Format

A dataframe object with 15 variables:

entry_nr entry number of the ortholog

omaid oma identifier of the ortholog

canonicalid canonicalid of the ortholog

sequence_md5 sequence_md5 of the ortholog

oma_group oma_group of the ortholog

oma_hog_id hog id of the ortholog

chromosome chromosomal location of the ortholog

locus.start start locus of the ortholog

locus.end end locus of the ortholog

locus.strand locus strand of the ortholog

is_main_isoform true/false

rel_type relationship type of the ortholog to the gene

distance ortholog distance

score ortholog score ...

Source

https://omabrowser.org/api/protein/YEAST00058/orthologs

`pairs` *An example genome alignment object.*

Description

A dataframe containing information for the whole genome aligment of YEAST and ASHGO.

Usage

```
pairs
```

Format

A dataframe object with 12 variables for each member of the pair, as well some 3 additional variables:

entry_nr entry number of the ortholog

omaid oma identifier of the ortholog

canonicalid canonicalid of the ortholog

sequence_md5 sequence_md5 of the ortholog

oma_group oma_group of the ortholog

oma_hog_id hog id of the ortholog

chromosome chromosomal location of the ortholog

locus.start start locus of the ortholog

locus.end end locus of the ortholog

locus.strand locus strand of the ortholog

is_main_isoform true/false

rel_type relationship type of the ortholog to the gene

distance ortholog distance

score ortholog score ...

Source

https://omabrowser.org/api/pairs/YEAST/ASHGO/

`protein` *An example protein object.*

Description

An object containing information for the YEAST00058 protein.

Usage

```
protein
```

Format

A S3 object with 23 variables:

entry_nr entry number of the protein
entry_url url pointer to the protein
omaid oma identifier of the protein
canonicalid canonicalid of the protein
sequence_md5 sequence_md5 of the protein
oma_group oma_group of the protein
oma_hog_id hog id of the protein
chromosome chromosomal location of the protein
locus GRanges object with the locus information for the protein
is_main_isoform true/false
roothog_id root taxonomic level of the relevant hog
roothog_id taxonomic levels of the hog in which the protein is present
sequence_length length of the protein sequence
sequence AAString of the protein sequence
cdna DNAString of the protein sequence
domains url pointer to the list of protein domains
xref url pointer to the list of protein cross references
orthologs url pointer to the list of protein orthologs
homeologs url pointer to the list of protein homeologs
gene_ontology url pointer to the list of protein GO ontologies
oma_group_url url pointer to the protein oma group
oma_hog_members url pointer to the protein hog members
alternative_isoforms_urls list of url pointers to the protein isoforms ...

Source

https://omabrowser.org/api/protein/6633022/

resolveURL *Load data for a given url from the OMA Browser API.*

Description

This function is usualy not needed by users. In most circumstances an attribute containing a URL is automatically loaded when accessed. However, in case the data is transformed into a dataframe, this will no longer be true, in which case one can access the data behind this attribute using this function.

Usage

```
resolveURL(url)
```

Arguments

url	The url of interest

Value

a data.frame containing the information behind an URL

Examples

```
resolveURL('http://omabrowser.org/api/protein/YEAST58/gene_ontology/')
```

searchProtein *Get the CrossReferences in the OMA database for a pattern*

Description

The function to list all the crossreferences that match a certain defined pattern.

Usage

```
searchProtein(pattern)
```

Arguments

pattern	the pattern to query the OMA database with - needs to be at least 3 characters long

Value

a data.frame containing information on the cross references for a given pattern

Examples

```
searchProtein(pattern='MAL')
```

`sequence_annotation` *An example dataframe containing GO annotations identified from a given sequence.*

Description

An example dataframe containing GO annotations identified from a given sequence.

Usage

```
sequence_annotation
```

Format

A dataframe with 13 variables:

Qualifier qualifier of the annotation

GO_ID GO term for the annotation

With GO term for the annotation

Evidence evidence for the annotation

Date date

DB_Object_Type identified object type

DB_Object_Name identified object name

Aspect aspect

Assigned_By assignment of the annotation

GO_name GO term name

DB database

DB.Reference database reference

Synonym synonym ...

Source

https://omabrowser.org/api/function/?query=MNDPSLLGYPNVGPQQQQQQQQQQHAGLLGKGTPNALQQQLHMNQLTGIPPPGLMN

sequence_map — *An example dataframe containing proteins identified from a given sequence.*

Description

An example dataframe containing proteins identified from a given sequence.

Usage

```
sequence_map
```

Format

A dataframe with 3 variables:

query sequence that was queried

identified_by type of identification

targets list of protein targets identified ...

Source

https://omabrowser.org/api/sequences/?query=MNDPSLLGYPNVGPQQQQQQQQQQHAGLLGKGTPNALQQQLHMNQLTGIPPPGLM

setAPI — *Set the url to the OMA Browser API*

Description

Function to set the base url to the OMA Browser API. If no url is specified, the default OMA Browser API url is used.

Usage

```
setAPI(url)
```

Arguments

url	Base url to the API

taxonomy *An example newick format taxonomy object.*

Description

An example newick format taxonomy object.

Usage

```
taxonomy
```

Format

An S3 with 2 variables:

root_taxon sequence that was queried

newick taxonomy newick ...

Source

https://omabrowser.org/api/taxonomy/Alveolata/?type=newick

xref *An example xref object.*

Description

An example xref object.

Usage

```
xref
```

Format

A dataframe with 8 variables:

xref cross reference

source source of the cross reference

entry_nr oma database entry number

oma_id oma id of the cross reference

genome.code genome_id of the cross reference

genome.taxon_id taxon_id of the cross reference

genome.species species of the cross reference

genome.genome_url genome url pointer of the cross reference ...

Source

https://omabrowser.org/api/xref/?search=MAL

`$.omadb_obj` *Resolve URLs automatically when accessed*

Description

The function to obtain further information from a given url.

Usage

```
## S3 method for class 'omadb_obj'
x$name
```

Arguments

`x`	object
`name`	attribute

Value

API response behind the URL

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