Package ‘OmaDB’

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Author Klara Kaleb
Maintainer Klara Kaleb <klara.kaleb18@ic.ac.uk>, Adrian Altenhoff <adrian.altenhoff@inf.ethz.ch>
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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 GO annotation information of the most similar protein to the query sequence

Examples

annotateSequence(query='MNDPSLLGYPNVGPQQQQQQQQ0HAGLLGKGTPNALQQLHMMQLTGIPPPGMNN5DVTSSNNRQLLDDQALANGANANMLN...SYINSAVYELINTGRVQIHQEGNGRDFGYMSEKNFSHNLALKSSYNCIGELPFTNFTPSFTDVIDYIWFSTHALRVRGLLGEVDPEYVSKFIGFPNDKFPSDHIPLLARFEFMKTNTGSKKV')

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 containing the GO annotation 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')
**getGenome**

**getGenome**

**Description**

The function to obtain the information available for a single entry in the database. 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**

```r
data(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**

```r
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 instead getGenomePairs.

Usage

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

Arguments

genoem_id1 an identifier for the first genome, which can be either its taxon id or UniProt species code
genoem_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.
getGenomePairs

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

```r
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 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
getHOG

**Examples**

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

---

**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 descended 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 deepest level of the most specific sub-hog for the given ID.
- `members`: boolean that when set to TRUE returns a dataframe containing 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**
```r
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**
```r
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. Attribute 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')

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/](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='MNDPSLLGYPNVGPOQQQQQQQHAGLLKGTPNALQQQLHNNDDVHTSSNNNSRQLDLLLANTANMLMNMDNNN

mapSequence(search='mixed',query='NKLLQPTDFQSHIAEASKSLVDCTMQALMEMADTLTDSKTAKKQQPTGDSSTPSGTATNSAVSTPTKIELFANG

Description

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

Usage

g getXref(pattern)

g getAnnotation(query)

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

g getData(type, id, attribute = NULL)

Details

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

g getXref

For gxRef, use searchProtein.
getAnnotation

For getAnnotation, use annotateSequence.

getGenomeAlignment

For getGenomeAlignment, use getGenomePairs.

getData

For getData, use getProtein, getGenome, getOMAGroup.

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 alignment 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
- **oma_id** oma identifier of the ortholog
- **canonical_id** canonical id 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

**Description**

This function is usually 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**

```r
resolveURL(url)
```

**Arguments**

- `url`: The url of interest

**Value**

a data.frame containing the information behind an URL

**Examples**

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

---

### searchProtein

**Description**

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

**Usage**

```r
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
sequence_annotation

Examples

```r
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=MNDPSLLGYPNVGQQQQQQQQHQAGLLKGTQNALQQQQLHMQUTGPPPLMN
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=MNDPSLLGYPNVGPQQQQQQQQQQHAGLLGKTPNALQQQLHNMQLTGIPPPGLMNNSDVHTSSNNNSRQLLDQLANG ...

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

```r
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](https://omabrowser.org/api/taxonomy/Alveolata/?type=newick)

---

### `xref`

*An example xref object.*

#### Description

An example xref object.

#### Usage

```r
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 ...
$.omadb_obj

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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