Package ‘CTDquerier’

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Title Package for CTDbase data query, visualization and downstream analysis

Version 2.10.0

Description Package to retrieve and visualize data from the Comparative Toxicogenomics Database (http://ctdbase.org/). The downloaded data is formatted as DataFrames for further downstream analyses.

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Author Carles Hernandez-Ferrer [aut], Juan R. Gonzalez [aut], Xavier Escribà-Montagut [cre]

Maintainer Xavier Escribà-Montagut <xavier.escriba@isglobal.org>
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### CTDdata

Class CTDdata

**Description**

Class resulting of `query_ctd_gene`, `query_ctd_chem` and `query_ctd_dise`. It is used to encapsulate all the information in `CTDbase` for given set of genes, chemicals or diseases.

**Usage**

```r
# S4 method for signature 'CTDdata'
enrich(x, y, universe, use = "curated", warnings = TRUE, ...)

# S4 method for signature 'CTDdata'
get_table(object, index_name, ...)

# S4 method for signature 'CTDdata'
get_terms(object)

# S4 method for signature 'CTDdata,ANY'
plot(x, y, index_name = "base", representation = "heatmap", ...)
```

**Arguments**

- `x` Object of class `CTDdata`.
- `y` NOT USED
CTDdata

- **universe**: String vector of genes used as universe. If not provided, all genes in CTDbase are used.
- **use**: Select if all or only curated relations are used.
- **warnings**: Shows or hiddes warnings.
- **object**: Object of class CTDdata.
- **index_name**: Name of the plot to be draw. See CTDdata's detail section for more information on 'CTDdata-class' representation.
- **representation**: Can take values "heatmap" or "network".

**Details**

CTDdata objects provides with a summarized representation of the downloaded data obtained from the standard show method. For instance, a CTDdata created using query_ctd_chem shows:

```
Object of class 'CTDdata'
-------------------------
. Type: CHEMICAL
. Length: 2
. Items: IRON, ..., AIR POLLUTANTS
. Diseases: 1755 (203 / 3322)
. Chemical-gene interactions: 2070 (2799)
. KEGG pathways: 637 (637)
. GO terms: 3641 (3641)
```

The information shown corresponds to:

- **Type**: Indicates the source (chemical, gene or disease) used to create the object.
- **Creation**: Shows the time-stamp from the creation time.
- **Length**: Shows the number of terms used to create the object.
- **Items**: Shows some of the terms used to create the object.
- **Diseases**: Corresponds to the unique number of diseases obtained in the query. In parenthesis: number of curated chemical-diseases and total number of chemical-diseases association.
- **Chemical-gene interactions**: Indicates the unique number of chemical-gene interactions. In parenthesis the total number of chemical-gene interactions.
- **KEGG pathways**: Shows the unique number of KEGG pathway versus chemical associations. In parenthesis the total number of associations.
- **GO terms**: Shows the unique number of GO terms versus chemical associations. In parenthesis the total number of associations.

CTDdata objects allows many types of representation according to the different sources (chemical, gene or disease). The used method is plot, matching the argument x with a CTDdata object. The argument index_name indicates the type of plot to be draw. The default value of index_name is "base".
• "base": shows a bar-plot indicating the number of lost & found terms for the given object.

For gene queries, index_name can take values:

• "disease": (argument representation must be "heatmap") shows shows the inference score that associates the given genes with diseases according to CTDBase.
• "chemical interactions": (argument representation must be "heatmap") shows the number of reference that cites the association between the given genes and chemicals.
• "gene-gene interaction": (argument representation can be "network" and "heatmap") in the network representation teh original genes are dark-colored while the other genes are light-colored. Both plots allows to to explore the gene-gene interactions.
• "kegg pathways": (argument representation must be "network") shows the linked between genes and KEGG pathways.
• "go terms": (argument representation must be "network") shows the links between genes and GO terms.

For chemical queries, index_name can take values:

• "gene interactions": (argument representation can be "network" and "heatmap") shows the gene-chemical interactions. Network representation includes the "mechanism" of the interactions.
• "disease": (argument representation can be "network" and "heatmap") shows the inference score of the link between chemicals and diseases.
• "kegg pathways": (argument representation must be "network") shows the P-Value of relation between KEGG pathways and chemicals.
• "go terms": (argument representation must be "network") shows the P-Value of relation between GO terms and chemicals.

For disease queries, index_name can take values:

• "gene": (argument representation must be "heatmap") shows the number of references linking a set of genes with a set of diseases.
• "chemical": (argument representation must be "heatmap"): shows the inference-score linking diseases with chemicals.
• "kegg pathways": (argument representation must be "network") shows the pathways linked to a set of diseases.

The other arguments of plot functions follows:

• subset.chemical: filters the chemicals to be include into the plot.
• subset.gene: filters the genes to be include into the plot.
• subset.pathway: filters the KEGG pathways or GO terms included into the plot.
• subset.source: filters the origin in gene-gene interaction network.
• subset.target: filters the end in gene-gene interaction network.
• field.score: can take values "Inference" or "Reference" depending of the used source and representation.
• filter.score: allows to filter the relations to be included into the plot in base of the set of field.score.
• max.length: indicates the maximum number of characters of the names of each "item" in the plot.
• ontology: for the KEGG pathways, allows to filter the pathways in base of their ontology. By default: c("Biological Process", "Cellular Component", "Molecular Function").
• main: title to be displayed in network representations. For heatmap representations use: + ggtitle("TITLE").

Value

An object of class CTDdata

Methods (by generic)

• enrich(CTDdata): Method to perform enrichment analysis given two object of class CTDdata.
• get_table(CTDdata): Method to obtain a specific inner table from an CTDdata object.
• get_terms(CTDdata): Return a list with the terms found to create the object.
• plot(x = CTDdata, y = ANY): Generates a basic plot showing the number of terms that can be used to query CTDbase.

Slots

timestamp Character with the timestamp.
type Character saving "GENE", "CHEMICAL" or "DISEASE" depending if it was created using query_ctd_gene, query_ctd_chem or query_ctd_dise
terms DataFrame with the genes, chemicals or diseases used to create the object.
losts Character with the terms used to create the object but that were nor present in CTDbase.
gene_interactions (Only for chemicals) Table with a relation of the genes interacting with the given chemicals.
chemicals_interactions (Only for genes) Table with a relation of the chemicals interacting with the given genes.
diseases Table with a relation of the diseases associated with given genes or chemicals.
gen_gene_interactions (Only for genes) Table with a relation of the genes interacting with the given genes.
kegg Table with a relation of the KEGG pathways affected by the given chemicals or where the given genes play a role.
go Table with a relation of the GO terms affected by the given chemicals or where the given genes play a role.

See Also

query_ctd_gene to create a CTDdata from a set of genes, query_ctd_chem to create a CTDdata from a set of chemicals, query_ctd_dise to create a CTDdata from a set of diseases, get_table to retrieve encapsulated data and plot to get nice plots from stored data.
CTDquerier

Package for CTDbase data query, data visualization and data analysis.

Description

It can retrieve information related to genes, chemicals and diseases.

Data Download

CTDquerier offers two functions to query CTDbase (http://ctdbase.org): `query_ctd_gene` to query CTDbase given a set of genes; and `query_ctd_chem` to query CTDbase given a set of chemicals. Both functions return CTDdata objects. Raw downloaded information can be retrieved from CTDdata using method `get_table`.

Data Visualization

CTDdata objects offers basic visualization of the downloaded information using standard `plot` method.

download_ctd_chem

Function to download chemicals available in CTDbase

Description

This function download the "Chemical vocabulary" file (CTD_chemicals.tsv.gz) from http://ctdbase.org/downloads.

Usage

download_ctd_chem(verbsoe = FALSE, ask = TRUE)

Arguments

verbose (default FALSE) If set to TRUE is shows relevant information of each step.
ask (default TRUE) If TRUE it asks the the persistent location must be used.

Details

The field included in the file (CTD_chemicals.tsv.gz) are:

1. ChemicalName
2. ChemicalID (MeSH identifier)
3. CasRN (CAS Registry Number, if available)
4. Definition
5. ParentIDs (identifiers of the parent terms; '\' delimited list),
download_ctd_dise

6. TreeNumbers (identifiers of the chemical’s nodes; 'l'-delimited list),
7. ParentTreeNumbers (identifiers of the parent nodes; 'l'-delimited list),
8. Synonyms ('l'-delimited list)
9. DrugBankIDs ('l'-delimited list)

Value
Passed name into filename argument if it could be download 1 otherwise.

Examples

download_ctd_chem()
file.exists( "CTD_chemicals.tsv.gz" )

download_ctd_dise

Function to download diseases available in CTDbase

Description
This function download the "Disease vocabulary" file (CTD_diseases.tsv.gz) from http://ctdbase.org/downloads.

Usage

download_ctd_dise( verbose = FALSE, ask = TRUE )

Arguments

verbose (default FALSE) If set to TRUE is shows relevant information of each step.
ask (default TRUE) If TRUE it asks the the persistent location must be used.

Details
The field included in the file (CTD_diseases.tsv.gz) are:

1. DiseaseName
2. DiseaseID (MeSH or OMIM identifier)
3. Definition
4. AltDiseaseIDs (alternative identifiers; 'l'-delimited list)
5. ParentIDs (identifiers of the parent terms; 'l'-delimited list)
6. TreeNumbers (identifiers of the disease’s nodes; 'l'-delimited list)
7. ParentTreeNumbers (identifiers of the parent nodes; 'l'-delimited list)
8. Synonyms ('l'-delimited list)
9. SlimMappings (MEDIC-Slim mappings; 'l'-delimited list)
download_ctd_genes

Value
Passed name into filename argument if it could be download 1 otherwise.

Examples


download_ctd_dise()
file.exists( "CTD_diseases.tsv.gz" )


download_ctd_genes     Function to download genes available in CTDbase

Description
This function download the "Gene vocabulary" file (CTD_genes.tsv.gz) from http://ctdbase.org/downloads.

Usage

download_ctd_genes( verbose = FALSE, ask = TRUE )

Arguments

verbose (default FALSE) If set to TRUE is shows relevant information of each step.

ask (default TRUE) If TRUE it asks the the persistent location must be used.

Details
The field included in the file (CTD_genes.tsv.gz) are:
1. GeneSymbol
2. GeneName
3. GeneID (NCBI Gene identifier)
4. AltGeneIDs (alternative NCBI Gene identifiers; '|' delimited list)
5. Synonyms ( '|' -delimited list)
6. BioGRIDIDs ( '|' -delimited list)
7. PharmGKBIDs ( '|' -delimited list)
8. UniprotIDs ( '|' -delimited list)

Value
Passed name into filename argument if it could be download 1 otherwise.

Examples

download_ctd_genes()
enrich

\textit{Method to perform enrichment analysis using two CTDdata objects}

\textbf{Description}

This method performs a fisher test using the genes in two objects of class \texttt{CTDdata}. The object in 'x' is used as source while the object on 'y' is used as universe. When object 'x' corresponds to an object created with \texttt{query_ctd_gene}, the used genes are the found terms in CTDbase. In the other cases (chemicals and disease \texttt{CTDdata}), the genes from the 'gene interactions' table are used. If universe is missing, all genes in CTDbase are used as universe.

\textbf{Usage}

\begin{verbatim}
enrich(x, y, universe, use = "curated", warnings = TRUE, ...)
\end{verbatim}

\textbf{Arguments}

- \texttt{x} Object of class \texttt{CTDdata}.
- \texttt{y} Object of class \texttt{CTDdata}.
- \texttt{universe} Vector of strings corresponding to the genes to be used as universe.
- \texttt{use} (default: "curated") It can take values "curated" or "all" to filter or not filter for curated the genes into the CTDdata objects.
- \texttt{warnings} (default: TRUE).
- \texttt{...} NOT USED

\textbf{Value}

A list with class \texttt{htest}. Check \texttt{fisher.test} for more information.

\textbf{Examples}

\begin{verbatim}
# Example in a tryCatch, since we are performing a connection to a server we might
# get a refused connection due to a server rejection. Evaluate the received HTTP
# message to understand if the server is not available or if your IP address is temporarily restricted
tryCatch({
data("gala")
air <- query_ctd_chem( terms = "Air Pollutants" )
hgnc_universe <- readRDS(paste0(path.package("CTDquerier"), "/extdata/universe.RDS"))
enrich(gala, air, hgnc_universe)
}, error = function(w){NULL})
\end{verbatim}
Description

CTDdata with information of 258 genes downloaded from CTDbase. The object was created from
the genes obtained from the scientific article entitled "Case-control admixture mapping in
Latino populations enriches for known asthma-associated genes" (Table E1) by Torgerson et. al.
The genes were used to query CTDbase using `query_ctd_genes` function.

Usage

data("gala")

Format

An object of class `CTDdata` of length 1.

Value

An `CTDdata` object.

Examples

```r
data("gala")
gala
```

get_table

*Method to obtain a specific inner table from a `CTDdata` object.*

Description

Obtain the raw data from a `CTDdata` object, result from a query to CTDbase.

Usage

get_table(object, index_name, ...)

Arguments

- **object**: Object of class `CTDdata`.
- **index_name**: String indicating the type of data to obtain.
- **...**: NOT USED
Details

Available tables are (index_name):

1. "gene interactions": (Only for chemicals) Table with a relation of the genes interacting with the given chemicals.
2. "chemical interactions": (Only for genes) Table with a relation of the chemicals interacting with the given genes.
3. "diseases": Table with a relation of the diseases associated with given genes or chemicals.
4. "gene-gene interactions": (Only for genes) Table with a relation of the genes interacting with the given genes.
5. "kegg pathways": Table with a relation of the KEGG pathways affected by the given chemicals or where the given genes play a role.
6. "go terms": Table with a relation of the GO terms affected by the given chemicals or where the given genes play a role.

Value

A DataFrame containing the raw result from CTDdata.

Examples

```r
data("gala")
get_table(gala, "diseases")[1:3, ]
```

---

**get_terms**

Getter to obtain the terms used to perform a query into CTDbase

Description

Getter to obtain the terms used to perform a query into CTDbase

Usage

```r
get_terms(object)
```

Arguments

- **object**: Object of class **CTDdata**.

Value

A list with two accessors: "used" for the terms that exists in CTDbase, and "lost" with the terms that do not exists in CTDbase.

Examples

```r
data("gala")
get_terms(gala)[["lost"]]
```
Function to create a leaf plot

Description
This function takes a data.frame and returns a gtable with three plots. The left-leafes, the axis names and the right-leafes.

Usage
leaf_plot(
  dta, label = "name", valueLeft = "var1", valueRight = "var2",
  titleLeft = NULL, titleRight = NULL,
  colorLeft = "#FF7F50", colorRight = "#20B2AA"
)

Arguments
dta data.frame with, at least, three columns corresponding to the axis labels, the left values and the right values.
label (default "name") Name of the column in dta with the labels.
valueLeft (default "var1") Name of the column with the values for the left plot.
valueRight (default "var2") Name of the column with the values for the right plot.
titleLeft (default NULL) Character used as a title for the left plot.
titleRight (default NULL) Character used as a title for the right plot.
colorLeft (default "#FF7F50") Color for left plot bars.
colorRight (default "#20B2AA") Color for right plot bars.

Value
A ggplot2 object.

Examples
data <- data.frame(
  labels = LETTERS[1:15],
  right = runif(n = 15) * 11,
  left = runif(n = 15) * 9
)
leaf_plot(data, "labels", "left", "right", "runif09", "runif11")
load_ctd_chem

Function to load the .tsv.gz file for chemicals

Description

Function to load the .tsv.gz file for chemicals

Usage

load_ctd_chem(verbose = FALSE)

Arguments

verbose (default FALSE) If set to TRUE messages and warnings are raised.

Details

The field included in the file (CTD_chemicals.tsv.gz) are:

1. ChemicalName
2. ChemicalID (MeSH identifier)
3. CasRN (CAS Registry Number, if available)
4. Definition
5. ParentIDs (identifiers of the parent terms; '|' delimited list),
6. TreeNumbers (identifiers of the chemical's nodes; '|' delimited list),
7. ParentTreeNumbers (identifiers of the parent nodes; '|' delimited list),
8. Synonyms ('|'-delimited list)
9. DrugBankIDs ('|'-delimited list)

Value

A data.frame with the content of the file "CTD_genes.tsv.gz"

Examples

if(download_ctd_chem()){
  fdl <- load_ctd_chem()
  dim( fdl )
}
load_cpd_dise

Function to load the .tsv.gz file for disease

Description

Function to load the .tsv.gz file for disease

Usage

load_cpd_dise(verbose = FALSE)

Arguments

verbose (default FALSE) If set to TRUE messages and warnings are raised.

Details

The field included in the file (CTD_diseases.tsv.gz) are:

1. DiseaseName
2. DiseaseID (MeSH or OMIM identifier)
3. Definition
4. AltDiseaseIDs (alternative identifiers; '|' delimited list)
5. ParentIDs (identifiers of the parent terms; '|' delimited list)
6. TreeNumbers (identifiers of the disease’s nodes; '|' delimited list)
7. ParentTreeNumbers (identifiers of the parent nodes; '|' delimited list)
8. Synonyms ('|'-delimited list)
9. SlimMappings (MEDIC-Slim mappings; '|' delimited list)

Value

A data.frame with the content of the file "CTD_genes.tsv.gz"

Examples

```r
if(download_cpd_dise()){
  fdl <- load_cpd_dise()
  dim( fdl )
}
```
load_ctd_gene

Function to load the .tsv.gz file for genes

Description

This function works in pair with download_ctd_genes. This function loads into the R session the downloaded "CTD_genes.tsv.gz" file.

Usage

load_ctd_gene(verbose = FALSE)

Arguments

verbose (default FALSE) If set to TRUE messages and warnings are raised.

Details

The field included in the file (CTD_genes.tsv.gz) are:

1. GeneSymbol
2. GeneName
3. GeneID (NCBI Gene identifier)
4. AltGeneIDs (alternative NCBI Gene identifiers; '|' delimited list)
5. Synonyms ('|'-delimited list)
6. BioGRIDIDs ('|'-delimited list)
7. PharmGKBIDs ('|'-delimited list)
8. UniprotIDs ('|'-delimited list)

Value

A data.frame with the content of the file "CTD_genes.tsv.gz"

Examples

if(download_ctd_genes()){
  fd1 <- load_ctd_gene()
  dim(fdl)
}
**query_ctd_chem**

*Function to query CTDbase using chemical terminology (Chemical Name)*

**Description**

This function checks for CTDbase gene vocabulary and query CTDbase for each one, downloading chemical-genes interactions, associated diseases, associated KEGG pathways and associated GO terms.

**Usage**

```r
query_ctd_chem(terms, max.distance = 10, ask = FALSE, verbose = FALSE)
```

**Arguments**

- `terms` Character vector with the chemicals used in the query.
- `max.distance` (default 10) Maximum distance allowed between a given element in terms argument and a possible match in CTDbase.
- `ask` (default TRUE) If TRUE it asks the the persistent location must be used to save the vocabulary if it was not downloaded previously.
- `verbose` (default FALSE) If set to TRUE is shows relevant information of each step.

**Value**

An object of class `CTDdata`.

**Examples**

```r
# Example in a tryCatch, since we are performing a connection to a server we might
# get a refused connection due to a server rejection. Evaluate the received HTTP
# message to understand if the server is not available or if your IP adress is temporarily restricted
rst <- tryCatch({query_ctd_chem(terms = c("Iron", "Air Pollutants"), verbose = TRUE)}, error = function(w)NULL)
```

**query_ctd_dise**

*Function to query CTDbase using disease terminology*

**Description**

This function checks for CTDbase disease vocabulary and query CTDbase for each one, downloading disease-gene interactions, chemicals interactions, associated diseases, associated KEGG pathways and associated GO terms.

**Usage**

```r
query_ctd_dise(terms, ask = TRUE, verbose = FALSE)
```
query_ctd_gene

Arguments

- terms: Character vector with the diseases used in the query.
- ask: (default TRUE) If TRUE it asks the the persistent location must be used to save the vocabulary if it was not downloaded previously.
- verbose: (default FALSE) If set to TRUE is shows relevant information of each step.

Value

An object of class CTDdata.

Examples

```r
# Example in a tryCatch, since we are performing a connection to a server we might get a refused connection due to a server rejection. Evaluate the received HTTP message to understand if the server is not available or if your IP address is temporarily restricted rst <- tryCatch({query_ctd_dise( terms = "Asthma", verbose = TRUE )}, error = function(w){NULL})
```

query_ctd_gene

Function to query CTDbase using gene terminology (Gene Symbol)

Description

This function checks for CTDbase gene vocabulary and query CTDbase for each one, downloading gene-gene interactions, chemicals interactions, associated disease, associated KEGG pathways and associated GO terms.

Usage

```
query_ctd_gene(terms, ask = TRUE, verbose = FALSE)
```

Arguments

- terms: Character vector with the genes used in the query.
- ask: (default TRUE) If TRUE it asks the the persistent location must be used to save the vocabulary if it was not downloaded previously.
- verbose: (default FALSE) If set to TRUE is shows relevant information of each step.

Value

An object of class CTDdata.

Examples

```
# Example in a tryCatch, since we are performing a connection to a server we might get a refused connection due to a server rejection. Evaluate the received HTTP message to understand if the server is not available or if your IP address is temporarily restricted rst <- tryCatch({query_ctd_gene( terms = c( "APP", "HMOX1A", "hmox1" ), verbose = TRUE )}, error = function(w){NULL})
```
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