Package: GOxploreR (via r-universe)

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Type Package

Title Structural Exploration of the Gene Ontology (GO) Knowledge Base

Version 0.99.0

Description It provides an effective, efficient, and fast way to explore the Gene Ontology (GO). Given a set of genes, the package contains functions to assess the GO and obtain the terms associated with the genes and the levels of the GO terms. The package provides functions for the three different GO ontology. We discussed the methods explicitly in the following article <doi:10.1038/s41598-020-73326-3>.

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degreeDistBP — *Degree distribution of the GO biological process (BP) terms on a GO-level*

Description

For a directed graph, the in-degree nodes are the nodes which have edges coming into them and the out-degree nodes are those which have edges going out of them. The degreeDistBP function shows the distribution of these degrees over a particular GO-level. A bar plot is obtain which shows how many nodes in the GO-level have a certain degree k.

Usage

```
degreeDistBP(level)
```

Arguments

level	A numeric value for the GO-level

Value

A plot showing the degree distribution

Examples

```
# Degree distribution of GO-terms on level 3
degreeDistBP(level = 3)

# Degree distribution of GO-terms on level 9
degreeDistBP(level = 9)
```

degreeDistCC — *Degree distribution of the GO cellular component (CC) terms on a GO level*

Description

For a directed graph, the in-degree nodes are the nodes which have edges coming into them and the out-degree nodes are those which have edges going out of them. The degreeDistCC function shows the distribution of these degrees over a particular GO level. A bar plot is obtain which shows how many nodes in the GO level have a certain degree k.

Usage

```
degreeDistCC(level)
```

Arguments

level	A numeric value for the GO level

Value

A plot showing the degree distribution

Examples

```
# Degree distribution of GO terms on level 8
degreeDistCC(level = 8)

# Degree distribution of GO terms on level 6
degreeDistCC(level = 6)
```

---

degreeDistMF — *Degree distribution of the GO molecular function (MF) terms on a GO-level*

Description

For a directed graph, the in-degree nodes are the nodes which have edges coming into them and the out-degree nodes are those which have edges going out of them. The degreeDistMF function shows the distribution of these degrees over a particular GO-level. A bar plot is obtain which shows how many nodes in the GO-level have a certain degree k.

Usage

```
degreeDistMF(level)
```

Arguments

level	A numeric value for the GO-level

Value

A plot showing the degree distribution

Examples

```
# Degree distribution of GO-terms on level 3
degreeDistMF(level = 3)

# Degree distribution of GO-terms on level 10
degreeDistMF(level = 10)
```

distRankingGO *Provides ranking of GO-terms according to distance*

Description

distRankingGO returns the ranking of GO-terms based on the GO-terms hierarchy level and the maximal depth of paths in the GO-DAG passing through these GO-terms.

Usage

```
distRankingGO(goterm, domain = "BP", plot = TRUE)
```

Arguments

goterm	A list of GO-terms to be ordered
domain	The ontology of the GO-terms. The default is "BP"
plot	If FALSE the visualisation of the ordering is not provided. The default is TRUE.

Value

The function returns the ordered GO-terms, the indices corresponding to these GO-terms, the distance between the GO-terms hierarchy level and the maximal depth of paths in the GO-DAG passing through these GO-terms and a plot of the visualisaiton by default.

Examples

```
goterm <- c("GO:0000278","GO:0006414","GO:0022403","GO:0006415",
"GO:0045047","GO:0072599","GO:0006613","GO:0000184","GO:0070972",
"GO:0006413","GO:0000087","GO:0000280","GO:0000279","GO:0006612",
"GO:0000956","GO:0048285","GO:0019080","GO:0019083","GO:0043624",
"GO:0006402","GO:0032984","GO:0006401","GO:0072594","GO:0019058",
"GO:0051301","GO:0016071","GO:0006412","GO:0002682","GO:0022411",
"GO:0006614")

#The GO-terms in the list are ordered
distRankingGO(goterm = goterm, domain = "BP", plot = TRUE)
```

`Gene2GOTermAndLevel` *Get the Gene Ontology (GO) terms associated with a gene(s) and their levels*

Description

Retrieves the gene association GO-terms, also, the ontology of the terms as well as the respective levels based on the directed acyclic graph (DAG) are returned. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Gene2GOTermAndLevel(genes, organism, domain = NULL)
```

Arguments

`genes`	A character vector of entrezgene id's belonging to an organism of interest
`organism`	An object of class character. A character string that defines the scientific / common name of the organism eg. Homo sapiens, Mouse.
`domain`	An optional object of class character. GO-terms have three domains .i.e. biological process (BP), molecular function (MF) and cellular component (CC). This character string identifies which of the three GO categories associated with the genes to return. GO-terms from one domain can be returned at a time. If NULL the biological process GO-terms will be obtained (default).

Value

A data.frame object that contains the genes, GO terms, ontology and GO-levels

Note

This function is similar to `Gene2GOTermAndLevel_ON`, the difference is that the function do not query the Ensembl database for GO terms (It is relatively faster) which means the results from Gene2GOTermAndLevel_ON function is always up to date.

Examples

```
 # human genes
v <- c(6713,4605,55143,10615,10212,4001,2146,11130,983,4085,9833,9134)

# No value for domain is given so the default ("BP") is used
Gene2GOTermAndLevel(genes = v, organism = "Homo sapiens")

# The scientific names of the species can also be used
Gene2GOTermAndLevel(genes = v, organism = "Homo sapiens", domain = "CC")
```

```
Gene2GOTermAndLevel(genes = v, organism = "Human", domain = "MF")
```

`Gene2GOTermAndLevel_ON` *Get the Gene Ontology (GO) terms associated with a gene(s) and their levels*

Description

Retrieves the gene association GO-terms, also, the ontology of the terms as well as the respective levels based on the directed acyclic graph (DAG) are returned. A fast internet connection is needed for this funciton execution. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly".

Usage

```
Gene2GOTermAndLevel_ON(genes, organism, domain = NULL)
```

Arguments

`genes`	A character vector of entrezgene id's belonging to an organism of interest
`organism`	An object of class character. A character string that defines the scientific / common name of the organism eg. Homo sapiens, Mouse.
`domain`	An optional object of class character. GO-terms have three domains .i.e. biological process (BP), molecular function (MF) and cellular component (CC). This character string identifies which of the three GO categories associated with the genes to return. GO terms from one domain can be returned at a time. If NULL the biological process GO-terms will be obtained (default)

Value

A data.frame object that contains the genes, GO-terms, ontology and GO-levels

Note

This function does not provide support for Escherichia coli.

Examples

```
# human genes
v <- c(6713,4605, 10212, 9833, 6713)

# No value for domain is given so the default ("BP") is used
Gene2GOTermAndLevel_ON(genes = v, organism = "Human")

# The scientific names of the species can also be used
Gene2GOTermAndLevel_ON(genes = v, organism = "Homo sapiens", domain = "CC")

Gene2GOTermAndLevel_ON(genes = v, organism = "Human", domain = "MF")
```

GetDAG *Organism-specific GO-DAG edgelist*

Description

Derive the organism gene association GO-terms as an edgelist. It indicates how the terms are linked together. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish","Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", " Escherichia coli / E.coli"

Usage

```
GetDAG(organism, domain = "BP")
```

Arguments

organism	An object of class character that represents the organism. If the organism option is "BP", "MF" or "CC" the biological process, molecular function and cellular component general GO edgelist are obtained respectively
domain	The ontology of the GO-terms. The default is BP.

Value

A two-column matrix of the nodes and the edges to which they are connected

Examples

```
# Edgelist for entire GO BP ontology

GetDAG(organism = "BP")

# Edgelist for cellular component gene association GO-terms for organism Yeast
```

```
GetDAG(organism = "Yeast", domain = "CC")

# Edgelist for molecular function gene association GO-terms for organism Zebrafish
GetDAG(organism = "Zebrafish", domain = "MF")
```

---

getGOcategory *GO-term category getter*

Description

Get the category of a GO-term. It checks if a GO-term is a jump node (RN), regular node (RN) or leaf node (LN).

Usage

```
getGOcategory(goterm)
```

Arguments

goterm	An object with a category

Value

A data.frame object containing the terms, category and ontology.

Examples

```
goterm <- c("GO:0106003","GO:0032991","GO:1990429","GO:0002133","GO:0089713",
"GO:1990666","GO:0036125")


getGOcategory(goterm)
```

GetLeafNodesBP *All the BP GO-DAG leaf nodes*

Description

Returns all the leaf nodes from a particular organism-specific GO-DAG. If empty (or if "BP"), all the general BP GO-DAG leaf nodes will be returned. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
GetLeafNodesBP(organism = NULL)
```

Arguments

organism	An object of class character that represents an organism

Value

A two-coloum matrix of all the leaf nodes in the organism-specific DAG and their respective levels

Examples

```
# General GO BP leaf nodes
GetLeafNodesBP("BP")

# Human BP GO-DAG leaf nodes
GetLeafNodesBP(organism = "Human")

# Mouse BP GO-DAG leaf nodes
GetLeafNodesBP(organism = "DANIO RERIO")
```

GetLeafNodesCC *All the CC GO-DAG leaf nodes*

Description

Returns all the leaf nodes from a particular organism-specific GO-DAG. If empty (or if "CC"), all the general CC GO-DAG leaf nodes are returned. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
GetLeafNodesCC(organism = NULL)
```

Arguments

organism	An object of class character that represents an organism

Value

A two-coloum matrix of all leaf nodes in the organism-specific DAG and their respective levels

Examples

```
# Zebrafish CC GO-DAG leaf nodes
 GetLeafNodesCC("Danio rerio")

# Mouse CC GO-DAG leaf nodes
GetLeafNodesCC("Zebrafish")
```

GetLeafNodesMF *All the MF GO-DAG leaf nodes*

Description

Returns all the leaf nodes from a particular organism-specific GO-DAG. If empty (or if "MF"), all the general MF GO-DAG leaf nodes are returned. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
GetLeafNodesMF(organism = NULL)
```

Arguments

organism	An object of class character that represents an organism.

Value

A two-coloum matrix of all the leaf nodes in the organism-specific DAG and their respective levels

Examples

```
# Mouse MF GO-DAG leaf nodes
GetLeafNodesMF(organism = "Human")

# Arabidopsis thaliana MF GO-DAG leaf nodes
GetLeafNodesMF(organism = "Arabidopsis thaliana")

# Drosophila melanogaster MF GO-DAG leaf nodes
GetLeafNodesMF(organism = "Drosophila melanogaster")
```

GO2DecBP *GO biological process (BP) descendant GO-terms as an Edgelist*

Description

The GO2DecBP function provides a simple way to represent the biological process (BP) GO term. The function returns the descendant child nodes of a GO-term. In other words we begin from an ancestor term and find it's descendant child terms.

Usage

```
GO2DecBP(goterm)
```

Arguments

goterm	A string object of BP GO-term

Value

A vector comprising of GO-terms and the nodes they are linked to

Examples

```
v <- "GO:0000070" # BP GO term
GO2DecBP(v)
x <- "GO:0006725"
GO2DecBP(x)
```

GO2DecCC *GO cellular component (CC) descendant GO-terms as an Edgelist*

Description

The GO2DecCC function provides a simple way to represent the cellular component (CC) GO-terms. The function returns the descendant child nodes of a GO-term. In other words we begin from an ancestor term and find it's descendant child terms.

Usage

```
GO2DecCC(goterm)
```

Arguments

goterm	A string object of CC GO-terms

Value

A vector comprising of GO-terms and the nodes they are linked to

Examples

```
v <- "GO:0000799" # CC GO term
GO2DecCC(v)
x <- "GO:0043231"
GO2DecCC(x)
```

GO2DecMF *GO molecular function (MF) descendant GO-terms as an Edgelist*

Description

The GO2DecMF function provides a simple way to represent the molecular function (MF) GO-terms. TThe function returns the descedant child nodes of a GO term. In other words we begin from an ancestor term and find it's descendant child terms.

Usage

```
GO2DecMF(goterm)
```

Arguments

goterm	A string object of MF GO-terms

Value

A vector comprising of GO-terms and the nodes they are linked to

Examples

```
v <- "GO:0001228" # MF GO term
GO2DecMF(v)
x <- "GO:0005515"
GO2DecMF(x)
```

GO4Organism *All gene association GO-terms for an organism*

Description

The function contains all the GO-terms associated with the genes of an organism and their levels. If "BP", "MF" or "CC" the GO-terms from the whole ontology is return and their levels. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
GO4Organism(organism, domain = "BP")
```

Arguments

organism	The organism supported by the package. Both the scientific / common name of the organism can be use
domain	The ontology of the GO-terms. The default is BP.

Value

A two-column matrix that contains the GO-terms and their GO-levels

Examples

```
# Return all the BP GO-terms associated with organism Homo sapiens
GO4Organism(organism = "Homo sapiens")

# Return all the CC GO-terms associated with organism Rat
GO4Organism(organism = "Rat", domain = "CC")
```

GOTermBP2ChildLevel *Get the level of a biological process (BP) GO term's children*

Description

This function retrieves a GO BP term children's level i.e. for a GO-term it's children level are derived.

Usage

```
GOTermBP2ChildLevel(goterm)
```

Arguments

goterm	A character string of a valid gene ontology id e.g "GO:0097278"

Value

A list of children terms and their respective levels

Examples

```
# Retrieve "GO:0097278" children's level
GOTermBP2ChildLevel(goterm = "GO:0097278")

# Retrieve "GO:0051775" children's level
GOTermBP2ChildLevel(goterm = "GO:0051775")
```

GOTermBPOnLevel *GO biological process (BP) terms level getter*

Description

Gets the level of a GO biological process (BP) term based on the directed acyclic graph (DAG).

Usage

```
GOTermBPOnLevel(goterm)
```

Arguments

goterm	An object of class character. A character string of GO biological process (BP) term id. The object can be a GO-term or a vector of GO-terms

Value

A two-column matrix of the GO-terms and the level they map to

Note

The Gene Ontology (GO) biological process (BP) tree was built using the root node "GO:0001850"

Examples

```
# A vector of biological process GO terms
goterms <- c("GO:0006805","GO:0009083","GO:0006631")

GOTermBPOnLevel(goterms)

GOTermBPOnLevel("GO:0006629")
```

GOTermCC2ChildLevel *Get the level of a cellular component (CC) GO term's children*

Description

This function retrieves a GO CC term children's level i.e. for a GO-term it's children level are derived.

Usage

```
GOTermCC2ChildLevel(goterm)
```

Arguments

goterm	A character string of a valid gene ontology id e.g "GO:0005737"

Value

A list of children terms and their respective levels

Examples

```
# Retrieve "GO:0005737" children's level
GOTermCC2ChildLevel("GO:0005737")

# Retrieve "GO:0099568" children's level
GOTermCC2ChildLevel("GO:0099568")
```

GOTermCCOnLevel *GO cellular component (CC) terms level getter*

Description

Get the level of a GO cellular component (CC) term based on the directed acyclic graph (DAG)

Usage

```
GOTermCCOnLevel(goterm)
```

Arguments

goterm	An object of class character. A character string of GO cellular component (CC) terms. The object can be a GO-term or a vector of GO-terms

Value

A two-column matrix of the GO-terms and the level they map to

Note

The Gene Ontology (GO) cellular component (CC) tree was built using the root node "GO:0005575"

Examples

```
# Cellular component GO terms
goterms <- c("GO:0005634", "GO:0005737", "GO:0016020", "GO:0005743", "GO:0005739",
"GO:0005759", "GO:0005829")

GOTermCCOnLevel(goterms)

GOTermCCOnLevel("GO:0005730")
```

GOTermMF2ChildLevel *Get the level of a molecular function (MF) GO term's children*

Description

This function retrieves a GO MF term children's level i.e. for a GO-term it's children level are derived.

Usage

```
GOTermMF2ChildLevel(goterm)
```

Arguments

goterm	A character string of a valid gene ontology id e.g "GO:0004518"

Value

A list of children terms and their respective levels

Examples

```
# Retrieve "GO:0000978" children's level
GOTermMF2ChildLevel(goterm = "GO:0000978")

# Retrieve "GO:0004518" children's level
GOTermMF2ChildLevel(goterm = "GO:0004518")
```

GOTermMFOnLevel *GO molecular function (MF) term level getter*

Description

Gets the level of a molecular function (MF) term based on the directed acyclic graph (DAG) defined by the Gene Ontology consortium

Usage

```
GOTermMFOnLevel(goterm)
```

Arguments

goterm	An object of class character. A character string of GO molecular function (MF) terms. The object can be a GO-term or a vector of GO-terms

Value

A two-column matrix of the GO-terms and the level they map to

Note

The Gene Ontology (GO) molecular function (MF) tree was built using the root node "GO:0003674"

Examples

```
# molecular function GO terms

goterms <- c("GO:0003674","GO:0005515","GO:0003712","GO:0002039","GO:0000978","GO:0016740")

GOTermMFOnLevel(goterms)

GOTermMFOnLevel("GO:0005542")
```

Level2GOTermBP *GO biological process (BP) terms on a level*

Description

Gets all the biological process (BP) GO-terms on a GO-level. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2GOTermBP(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	The organism of interest. If NULL the results will be from the general GO BP tree

Value

A list of GO-terms from the level

Note

The Gene Ontology (GO) biological process (BP) tree was built using the root node GO:0001850

Examples

```
# Gene association GO-terms for organism Yeast on level 6
Level2GOTermBP(level = 6, organism = "Yeast")

# Gene association GO-terms for organism Fruit fly on level 2
Level2GOTermBP(level = 2, organism = "Fruit fly")
```

Level2GOTermCC *GO cellular component (CC) terms on a level*

Description

Gets all the biological process (CC) GO-terms on a GO-level. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2GOTermCC(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	The organism of interest. If NULL the results will be from the general GO CC tree

Value

A list of GO-terms from the level

Note

The Gene Ontology (GO) cellular component (CC) tree was built using the root node GO:0005575

Examples

```
# Gene association GO-terms for organism Rat on level 4
Level2GOTermCC(level = 4, organism = "Rat")

# Gene association GO-terms for the General GO CC tree
Level2GOTermCC(level = 7)
```

Level2GOTermMF *GO molecular function (MF) terms on a level*

Description

Gets all the molecular function (MF) GO-terms on a GO-level. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2GOTermMF(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	The organism of interest. If NULL the results will be from the general GO MF tree

Value

A list of GO-terms from the level

Note

The Gene Ontology (GO) molecular function (MF) tree was built using the root node GO:0003674

Examples

```
# Gene association GO-terms for organism Mouse on level 9
Level2GOTermMF(level = 9, organism = "mouse")

# Gene association GO-terms for organism Zebrafish on level 10
Level2GOTermMF(level = 10, organism = "zebrafish")
```

`Level2JumpNodeBP` *Jump nodes from a GO BP level*

Description

The function retrieves the Jump nodes (JNs) from a GO-level. JNs are those GO-terms which have at least one child term not present in the level below it. If the optional parameter "organism" is missing then the results are from the general GO tree. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2JumpNodeBP(level, organism = NULL)
```

Arguments

`level`	A numeric value for the GO-level
`organism`	Organism of interest that is supported by the package

Value

All jump nodes from the level

Examples

```
# Jump nodes from level 3
Level2JumpNodeBP(level = 3, organism = "Homo sapiens")

# Jump nodes from level 6
Level2JumpNodeBP(level = 6, organism = "Arabidopsis thaliana")
```

Level2JumpNodeCC *Jump nodes from a GO CC level*

Description

The function retrieves the Jump nodes (JNs) from a GO-level. JNs are those GO-terms which have at least one child term not present in the level below it. If the optional parameter "organism" is missing then the result are from the general GO tree. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2JumpNodeCC(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	Organism of interest that is supported by the package

Value

All jump nodes from the level

Examples

```
# Jump nodes on level 5
Level2JumpNodeCC(level = 5, organism = "Saccharomyces cerevisiae" )

# Jump nodes on level 3
Level2JumpNodeCC(level = 3, organism = "Schizosaccharomyces pombe" )
```

Level2JumpNodeMF *Jump nodes from a GO MF level*

Description

The function retrieves the Jump nodes (JNs) from a GO-level. JNs are those GO-terms which have at least one child term not present in the level below it. If the optional parameter "organism" is missing then the results are from the general GO tree. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2JumpNodeMF(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	Organism of interest that is supported by the package

Value

All jump nodes from the level

Examples

```
# Jump nodes on level 3
Level2JumpNodeMF(level = 3, organism = "Danio rerio" )

# Jump nodes on level 6
Level2JumpNodeMF(level = 6, organism = "Caenorhabditis elegans" )
```

Level2LeafNodeBP *GO biological process (BP) level leaf nodes getter*

Description

Derive all the leaf nodes from a GO BP level. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2LeafNodeBP(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	An organism of interest from the list of supported organism. If the parameter is NULL the results are from the general GO-DAG (default).

Value

All leaf nodes on the level.

Examples

```
# level 2 leaf nodes for Drosophila melanogaster GO-DAG
Level2LeafNodeBP(2, "Drosophila melanogaster")

# level 10 leaf nodes for Drosophila melanogaster GO-DAG
Level2LeafNodeBP(10, "Drosophila melanogaster")
```

Level2LeafNodeCC *GO cellular component (CC) level leaf nodes getter*

Description

Derive all the leaf nodes from a GO CC level. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2LeafNodeCC(level, organism = NULL)
```

Arguments

`level`	A numeric value for the GO level
`organism`	An organism of interest from the list of supported organism. If the argument is NULL the results are from the general GO-DAG (default).

Value

All leaf nodes on the level

Examples

```
# level 6 leaf nodes for Yeast GO-DAG
Level2LeafNodeCC(6, "Yeast")

# level 4 leaf nodes for Mouse GO-DAG
Level2LeafNodeCC(4, "Mouse")
```

Level2LeafNodeMF *GO molecular function (MF) level leaf nodes getter*

Description

Derive all the leaf nodes from a GO MF level. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2LeafNodeMF(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	An organism of interest from the list of supported organism. If NULL the results are from the general GO-DAG (default).

Value

All leaf nodes on the level

Examples

```
# level 9 leaf nodes for Human GO-DAG
Level2LeafNodeMF(9, "Human")

# level 5 leaf nodes for Mouse GO-DAG
Level2LeafNodeMF(5, "Mouse")
```

Level2NoLeafNodeBP *Non-leaf GO-terms on a GO BP level*

Description

This function returns all the non-leaf GO-terms on a particular GO BP level. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm", "Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli"

Usage

```
Level2NoLeafNodeBP(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	The organism of interest from the list of supported organism. If NULL the results are from the general GO-DAG (default)

Value

A set of non-leaf GO-terms

Examples

```
# Non-leaf nodes from level 13 GO-DAG
Level2NoLeafNodeBP(13)

# Non-leaf nodes from level 3 for Rat BP GO-DAG
Level2NoLeafNodeBP(3, "Rattus norvegicus")
```

Level2NoLeafNodeCC *Non-leaf GO-terms on a GO CC level*

Description

This function returned all the non-leaf GO terms on a particular GO CC level. The supported organism are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli"

Usage

```
Level2NoLeafNodeCC(level, organism = NULL)
```

Arguments

level	A numeric value for the GO level
organism	The organism of interest from the list of supported organism. If NULL the results are from the general GO-DAG (default)

Value

A set of non-leaf GO terms

Examples

```
# Non-leaf nodes from level 16 for Yeast CC GO-DAG
Level2NoLeafNodeCC(level = 16, "Yeast")

# Non-leaf nodes from level 10 for Mouse CC GO-DAG
Level2NoLeafNodeCC( 10, "Mus musculus")
```

Level2NoLeafNodeMF *Non-leaf GO-terms on a GO MF level*

Description

This function returned all the non-leaf GO-terms on a particular GO MF level that are not. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2NoLeafNodeMF(level, organism = NULL)
```

Arguments

`level`	A numeric value for the GO-level
`organism`	The organism of interest from the list of supported organism. If null the results are from the general GO-DAG (default)

Value

A set of non-leaf GO-terms

Examples

```
# Non-leaf nodes on level 15
Level2NoLeafNodeMF(15)

# Non-leaf nodes from level 10 for Rat MF GO-DAG
Level2NoLeafNodeMF(10, "Rat")
```

Level2RegularNodeBP *Regular nodes from a GO BP level*

Description

The function retrieves the Regular nodes (RNs) from a GO-level. RNs are those GO-terms which have all their children term in the next GO-level (i.e level of parent + 1). If the optional parameter "organism" is missing then the result will be from the general GO tree instead of from a particular organism. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2RegularNodeBP(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	Organism of interest that is supported by the package

Value

Regular nodes from the GO-level

Examples

```
# Regular nodes on level 3
Level2RegularNodeBP(level = 3, organism = "Human" )

# Regular nodes on level 6
Level2RegularNodeBP(level = 6, organism = "Mus musculus" )
```

Level2RegularNodeCC *Regular nodes from a GO CC level*

Description

The function retrieves the Regular nodes (RNs) from a GO-level. RNs are those GO-terms which have all their children in the next GO-level (i.e level = level of parent + 1). If the optional parameter "organism" is missing then the result will be from the general GO tree instead of from a particular organism. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2RegularNodeCC(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	Organism of interest that is supported by the package

Value

Regular nodes from the GO-level

Examples

```
# Regualar nodes on level 5
Level2RegularNodeCC(level = 5, organism = "Yeast")

# Regular nodes on level 9
Level2RegularNodeCC(level = 9, organism = "Rat")
```

Level2RegularNodeMF *Regular nodes from a GO MF level*

Description

The function retrieves the Regular nodes (RNs) from a GO-level. RNs are those GO-terms which have all their children in the next GO-level (i.e level = level of parent + 1). If the optional parameter "organism" is missing then the result will be from the general GO tree instead of from a particular organism. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
Level2RegularNodeMF(level, organism = NULL)
```

Arguments

level	A numeric value for the GO-level
organism	Organism of interest that is supported by the package

Value

Regular nodes from the GO-level

Examples

```
# Regular nodes on level 3
Level2RegularNodeMF(level = 3, organism = "Human" )

# Regular nodes on level 6
Level2RegularNodeMF(level = 6, organism = "MUS MUSCULUS" )
```

`prioritizedGOTerms` *prioritization of a lists of GO-terms*

Description

Given a vector of GO-terms, this function prioritizes the GO-terms by expoiting the structure of a DAG. Starting from the GO-term on the highest level and searching all the paths to the root node iteratively. If any GO-terms in the input vector are found along this path, these GO-terms are removed. This is because the GO-term at the end of a path is more specific than the GO-terms along the path. For an organism, the GO-terms of that organism are used for the prioritization. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
prioritizedGOTerms(lst = NULL, organism = NULL, sp = TRUE, domain = "BP")
```

Arguments

`lst`	The GO ids we want to prioritize
`organism`	If organism is given then only the gene association GO-terms of that organism are considered during the prioritization otherwise, all the (non-retired) GO-terms from a particular ontology are used in the ranking.
`sp`	If the argument "sp" is TRUE, only shortest paths are used, otherwise all paths
`domain`	Ontology of the GO-terms. The default is BP.

Value

A list containing the prioritize GO-terms, their ranking, original GO-terms and their GO-levels is given.

Examples

```
Terms <-c("GO:0000278", "GO:0006414","GO:0022403","GO:0006415","GO:0006614",
 "GO:0045047","GO:0022411","GO:0001775","GO:0046649","GO:045321")
prioritizedGOTerms(Terms, organism = "Human", sp=TRUE, domain = "BP")
```

scoreRankingGO *Provides ranking of GO-terms according to a score*

Description

scoreRankingGO provides ranking for a given list of GO-terms according to a score.

Usage

```
scoreRankingGO(goterm, domain = "BP", plot = TRUE)
```

Arguments

goterm	A list of GO-terms to be ordered
domain	The ontology of the GO-terms. The default is "BP"
plot	If FALSE the visualisation of the ordering is not provided. The default is TRUE.

Value

The function returns the ordered GO-terms, the indices corresponding to these GO-terms, the score of each GO-term and a plot of the visualization by default.

Examples

```
goterm <- c( "GO:0000278","GO:0006414","GO:0022403","GO:0006415",
"GO:0045047","GO:0072599","GO:0006613","GO:0000184","GO:0070972",
"GO:0006413","GO:0000087","GO:0000280","GO:0000279","GO:0006612",
"GO:0000956","GO:0048285","GO:0019080","GO:0019083",
"GO:0006402","GO:0032984","GO:0006401","GO:0072594","GO:0019058",
"GO:0051301","GO:0016071","GO:0006412","GO:0002682","GO:0022411",
"GO:0006614")

#The GO-terms in the list are ordered according to a score
scoreRankingGO(goterm = goterm, domain = "BP", plot = TRUE)
```

visRDAGBP *Species-specific biological process GO-DAG*

Description

A sub-dag of biological process terms for a certain species e.g DAG of the gene association GO-terms for Arabidopsis thaliana. The label "J","R" and "L" on the right side of the plot gives the number of connections between the regular node (RN) on the level and the nodes right below it (RN are nodes that have all their children nodes represented in the next level) .The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
visRDAGBP(organism, plot = TRUE)
```

Arguments

organism	The organism supported by the package. Both the scientific / common name of the organism can be use to derive the Sub-DAG. If this argument is "BP" the reduced BP GO-DAG is visualised.
plot	If TRUE, both the reduced DAG and the GO-terms contained in each node are derived

Value

A list containing the plot of the DAG and all the GO terms presents in each node

Examples

```
# Reduced GO-DAG for Human
visRDAGBP(organism = "Homo sapiens")

# Reduced GO-DAG for Rat
visRDAGBP(organism = "Rat")

# RN GO-terms on level 2 can be access as follows
visRDAGBP(organism = "Human", plot = FALSE)$"L2 RN"

# JN GO-terms on level 16 can be access as follows
visRDAGBP(organism = "Human", plot = FALSE)$"L16 JN"

# LN GO-terms on level 18 can be access as follows
visRDAGBP(organism = "Human", plot = FALSE)$"L18 LN"
```

visRDAGCC *Species-specific cellular component GO-DAG*

Description

A sub-dag of cellular component terms for a certain species e.g DAG of the gene association terms for Arabidopsis thaliana.The label "J","R" and "L" on the right side of the plot gives the number of connections between the regular node (RN) on the level and the nodes right below it (RN are nodes that have all their children nodes represented in the next level). The supported organisms are "Homo sapiens / human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
visRDAGCC(organism, plot = TRUE)
```

Arguments

organism	The organism supported by the package. Both the scientific / common name of the organism can be use to derive the Sub-DAG. If this argument is "CC" the general CC GO-DAG is visualised.
plot	If TRUE, both the reduced DAG and the GO-terms contained in each node is derived

Value

A list containing the plot of the DAG and all the GO-terms presents in each node

Examples

```
# Reduced GO-DAG for Arabidopsis thaliana
visRDAGCC(organism = "Arabidopsis thaliana")

# Reduced GO-DAG for Saccharomyces cerevisiae
visRDAGCC(organism = "Worm")

# RN GO-terms on level 2 can be access as follows
visRDAGCC(organism = "Human", plot = FALSE)$"L2 RN"

# JN GO-terms on level 12 can be access as follows
visRDAGCC(organism = "Human", plot = FALSE)$"L12 JN"

# LN GO-terms on level 16 can be access as follows
visRDAGCC(organism = "Human", plot = FALSE)$"L16 LN"
```

visRDAGMF *Species-specific molecular function GO-DAG*

Description

A sub-dag of molecular function terms for a certain species e.g DAG of the gene association GO-terms for Arabidopsis thaliana. The label "J","R" and "L" on the right side of the plot gives the number of connections between the regular node (RN) on the level and the nodes right below it (RN are nodes that have all their children nodes represented in the next level). The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
visRDAGMF(organism, plot = TRUE)
```

Arguments

organism	The organism supported by the package. Both the scientific / common name of the organism can be use to derive the Sub-DAG. If this argument is "MF" the reduced MF GO-DAG is visualised.
plot	If TRUE, both the reduced DAG and the GO-terms contained in each node is derived

Value

A list containing the plot of the DAG and all the GO terms presents in each node

Examples

```
# Reduced GO-DAG for Zebrafish
visRDAGMF(organism = "Zebrafish")

# Reduced GO-DAG for Caenorhabditis elegans
visRDAGMF(organism = "Caenorhabditis elegans")

# RN GO-terms on level 1 can be access as follows
visRDAGMF(organism = "Caenorhabditis elegans", plot = FALSE)$"L1 RN"

# JN GO-terms on level 9 can be access as follows
visRDAGMF(organism = "Caenorhabditis elegans", plot = FALSE)$"L9 JN"

# LN GO-terms on level 14 can be access as follows
visRDAGMF(organism = "Caenorhabditis elegans", plot = FALSE)$"L14 LN"
```

visRsubDAGBP *Visualise the GO-DAG for a specific organism based on certain GO-terms*

Description

A category in the organism specific DAG is regarded as important if it contains at least one GO-terms from the vector supplied. The function does not visualise the entire organism's DAG, it accepts a range of GO-terms and DAG categories that contains these GO-terms are visualise. We refer to these categories as the important and everything else is faded out. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
visRsubDAGBP(goterm, organism)
```

Arguments

goterm	A vector of biological process GO-terms
organism	The organism whose DAG we want to visualise based on the GO-terms supplied. If this argument is "BP" the general reduced GO BP tree is used.

Value

Returns a plot highlighting the important categories i.e. the categories containing the GO-terms of interest

Examples

```
Terms <- c("GO:0000278", "GO:0006414","GO:0022403","GO:0006415",
"GO:0006614","GO:0045047","GO:0072599","GO:0000279")

# Visualised Human GO-DAG based on the GO-terms given
visRsubDAGBP(goterm = Terms, organism = "Human")
```

visRsubDAGCC *Visualise the GO-DAG for a specific organism based on certain GO-terms*

Description

A category in the organism-specific DAG is regarded as important if it contains at least one GO-terms from the vector given. The function does not visualise the entire organism's DAG, it accepts a range of GO-terms and DAG categories that contains these GO-terms are visualise. We refer to these categories as the important and everything else is faded out. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
visRsubDAGCC(goterm, organism)
```

Arguments

goterm	A vector of cellular component GO-terms
organism	The organism whose DAG we want to visualise based on the GO-terms supplied

Value

Returns a plot highlighting the important categories i.e. the categories containing the GO-terms of interest. If this argument is "CC" the general reduced GO CC tree is used.

Examples

```
# Visualised Human GO-DAG based on the GO-terms given
Terms <- c("GO:0030054","GO:0045171","GO:0043204")

visRsubDAGCC(goterm = Terms, organism = "Human")
```

visRsubDAGMF *Visualise the GO-DAG for a specific organism based on certain GO-terms*

Description

A category in the organism-specific DAG is regarded as important if it contains at least one GO-terms from the vector supplied. The function does not visualise the entire organism's DAG, it accepts a range of GO-terms and DAG categories that contains these GO-terms are visualise. We refer to these categories as the important and everything else is faded out. The supported organisms are "Homo sapiens / Human", "Rattus norvegicus / Rat", "Mus musculus / Mouse", "Danio rerio / Zebrafish", "Caenorhabditis elegans / Worm" ,"Arabidopsis thaliana / Cress", "Saccharomyces cerevisiae / Yeast", "Schizosaccharomyces pombe / Fission yeast", "Drosophila melanogaster / Fruit fly", "Escherichia coli / E.coli".

Usage

```
visRsubDAGMF(goterm, organism)
```

Arguments

goterm	A vector of molecular function GO-terms
organism	The organism whose DAG we want to visualise based on the GO-terms supplied. If this argument is "MF" the general reduced GO MF tree is used.

Value

Returns a plot highlighting the important categories i.e. the categories containing the GO-terms of interest

Examples

```
Terms <- c("GO:0034040","GO:0008374" ,"GO:0003777","GO:0003674","GO:0015440","GO:0005464")
visRsubDAGMF(Terms, "Human")
```

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