

Package ‘ontoProc’

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Title processing of ontologies of anatomy, cell lines, and so on

Description Support harvesting of diverse bioinformatic ontologies, making particular use of the ontologyIndex package on CRAN. We provide snapshots of key ontologies for terms about cells, cell lines, chemical compounds, and anatomy, to help analyze genome-scale experiments, particularly cell x compound screens. Another purpose is to strengthen development of compelling use cases for richer interfaces to emerging ontologies.

Version 1.24.0

Imports Biobase, S4Vectors, methods, stats, utils, BiocFileCache, shiny, graph, Rgraphviz, ontologyPlot, dplyr, magrittr, DT, igraph, AnnotationHub, SummarizedExperiment

Suggests knitr, org.Hs.eg.db, org.Mm.eg.db, testthat, BiocStyle, SingleCellExperiment, celldex, rmarkdown, AnnotationDbi

Depends R (>= 4.0), ontologyIndex

License Artistic-2.0

LazyLoad yes

biocViews Infrastructure, GO

RoxygenNote 7.2.3

VignetteBuilder knitr

Encoding UTF-8

Collate bind_formal_tags.R common_classes.R data.R getOntos.R
seurTab.R CLextend.R connect_classes.R dropStop.R graphNEL.R
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mapNaive.R subset_descendants.R clfixer.R ctmarks.R
findCommonAncestors.R roots.R sym2CellOnto.R termProc.R

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BugReports <https://github.com/vjcitn/ontoProc/issues>

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allGOterms	<i>allGOterms: data.frame with ids and terms</i>
------------	--

Description

allGOterms: data.frame with ids and terms

Usage

allGOterms

Format

data.frame instance

Source

This is a snapshot of all the terms available from GO.db (3.4.2), August 2017, using keys(GO.db, keytype="TERM").

Examples

```
data(allGOterms)
head(allGOterms)
```

bind_formal_tags	<i>add mapping from informal to formal cell type tags to a Summarized-Experiment colData</i>
------------------	--

Description

add mapping from informal to formal cell type tags to a SummarizedExperiment colData

Usage

```
bind_formal_tags(se, informal, tagmap, force = FALSE)
```

Arguments

<code>se</code>	SummarizedExperiment instance
<code>informal</code>	character(1) name of colData element with uncontrolled vocabulary
<code>tagmap</code>	data.frame with columns 'informal' and 'formal'
<code>force</code>	logical(1), defaults to FALSE; if TRUE, allows clobbering existing colData variable named "formal"

Value

SummarizedExperiment instance with a new colData column 'label.ont' giving the formal tags associated with each sample

Note

This function will fail if the value of 'informal' is not among the colData variable names, or if "formal" is among the colData variable names.

c, TermSet-method *combine TermSet instances*

Description

combine TermSet instances

Usage

```
## S4 method for signature 'TermSet'
c(x, ...)
```

Arguments

<code>x</code>	TermSet instance
<code>...</code>	additional instances

Value

TermSet instance

cellTypeToGO	<i>utilities for approximate matching of cell type terms to GO categories and annotations</i>
--------------	---

Description

utilities for approximate matching of cell type terms to GO categories and annotations

Usage

```
cellTypeToGO(celltypeString, gotab, ...)  
  
cellTypeToGenes(  
  celltypeString,  
  gotab,  
  orgDb,  
  cols = c("ENSEMBL", "SYMBOL"),  
  ...  
)
```

Arguments

celltypeString	character atom to be used to search GO terms using
gotab	a data.frame with columns GO (goids) and TERM (term strings) agrep
...	additional arguments to agrep
orgDb	instances of orgDb
cols	columns to be retrieved in select operation

Value

data.frame
data.frame

Note

Very primitive, uses [agrep](#) to try to find relevant terms.

Examples

```
library(org.Hs.eg.db)  
data(allGOterms)  
head(cellTypeToGO("serotonergic neuron", allGOterms))  
head(cellTypeToGenes("serotonergic neuron", allGOterms, org.Hs.eg.db))
```

cleanCLNames	<i>obtain named character vector of terms from Cell Line Ontology, omitting obsolete and trailing 'cell'</i>
--------------	--

Description

obtain named character vector of terms from Cell Line Ontology, omitting obsolete and trailing 'cell'

Usage

```
cleanCLNames()
```

Value

character()

Examples

```
cleanCLNames()[1:10]
```

CLfeats	<i>produce a data.frame of features relevant to a Cell Ontology class</i>
---------	---

Description

produce a data.frame of features relevant to a Cell Ontology class

Usage

```
CLfeats(ont, tag = "CL:0001054", pr, go)
```

Arguments

ont	instance of ontologyIndex ontology
tag	character(1) a CL: class tag
pr	instance of ontologyIndex PRO protein ontology
go	instance of ontologyIndex GO gene ontology

Value

a data.frame instance

