

Package: scOntoMatch (via r-universe)

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Type Package

Title Aligning Ontology Annotation Across Single Cell Datasets with 'scOntoMatch'

Version 0.1.1

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Description Unequal granularity of cell type annotation makes it difficult to compare scRNA-seq datasets at scale. Leveraging the ontology system for defining cell type hierarchy, 'scOntoMatch' aims to align cell type annotations to make them comparable across studies. The alignment involves two core steps: first is to trim the cell type tree within each dataset so each cell type does not have descendants, and then map cell type labels cross-studies by direct matching and mapping descendants to ancestors. Various functions for plotting cell type trees and manipulating ontology terms are also provided. In the Single Cell Expression Atlas hosted at EBI, a compendium of datasets with curated ontology labels are great inputs to this package.

Imports ontologyIndex, ontologyPlot, purrr

URL <https://github.com/Papatheodorou-Group/scOntoMatch>

BugReports <https://github.com/Papatheodorou-Group/scOntoMatch/issues>

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Depends R(>= 3.5)

Suggests knitr, devtools, SeuratObject

VignetteBuilder knitr

Repository <https://papatheodorou-group.r-universe.dev>

RemoteUrl <https://github.com/papatheodorou-group/scontomatch>

RemoteRef HEAD

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check_ontology_translate

make sure ontology names are all translated to ontology ids while warning, consider manual reannotation

Description

make sure ontology names are all translated to ontology ids while warning, consider manual reannotation

Usage

```
check_ontology_translate(obj, onts, ont, anno_col)
```

Arguments

obj	seurat rds object
onts	ontology ids from translate
ont	ontologyIndex object
anno_col	annotation column in obj@meta.data that is translated to onts ids

Value

do not return a value but output messages

fill_query	<i>Get a names list of ontology and id by id</i>
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Description

Get a names list of ontology and id by id

Usage

```
fill_query(all, query)
```

Arguments

all	all ontology id to plot tree
query	query ontology id to fill

Value

a color object to fill query in onto_plot

Examples

```
## Not run:  
fill_query(all = c("CL0000548", "CL:0000066", "CL:0000082"), query = c("CL:0000082"))  
  
## End(Not run)
```

getOntologyId	<i>Get a names list of ontology and id by name</i>
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Description

Get a names list of ontology and id by name

Usage

```
getOntologyId(ont, onto_name)
```

Arguments

ont	ontology object
onto_name	character vector of ontology names

Value

a named list mapping ontology id and ontology name

Examples

```
## Not run:
getOntologyId(onto_name = "epithelial cell of lung", ont = ont)

## End(Not run)
```

getOntologyName	<i>Get a names list of ontology and id by id</i>
-----------------	--

Description

Get a names list of ontology and id by id

Usage

```
getOntologyName(ont, onto_id)
```

Arguments

ont	ontology object
onto_id	character vector of ontology ids

Value

a named list mapping ontology id and ontology name

Examples

```
## Not run:
getOntologyName(onto_id = "epithelial cell of lung", ont = ont)

## End(Not run)
```

getOntoMapping	<i>match ontology terms by direct mapping and mapping descendants to ancestors</i>
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Description

match ontology terms by direct mapping and mapping descendants to ancestors

Usage

```
getOntoMapping(ont, onts1, onts2)
```

Arguments

ont the ontology object from get_OBO
onts1 a character vector of ontology id
onts2 a character vector of ontology id

Value

a named list for ontology id mapping looks like ontology_id:ontology_id

Examples

```
## Not run:  
getOntoMapping(ont = ont, onts1 = "CL:0000548", onts2 = c("CL0000548", "CL:0000066"))  
  
## End(Not run)
```

getOntoMinimal *match descendant terms to ancestor terms within a dataset*

Description

match descendant terms to ancestor terms within a dataset

Usage

```
getOntoMinimal(ont, onts)
```

Arguments

ont the ontology object from get_OBO
onts a character vector of ontology id

Value

a named list for ontology id mapping looks like ontology_id:ontology_id

Examples

```
## Not run:  
getOntoMinimal(ont = ont, onts = c("CL0000548", "CL:0000066", "CL:0000082"))  
  
## End(Not run)
```

getOntoMultiMapping *Match descendants to ancestors in multiple ontology id lists*

Description

Match descendants to ancestors in multiple ontology id lists

Usage

```
getOntoMultiMapping(ont, onts)
```

Arguments

ont	ontologyIndex object
onts	named list of ontology ids

Value

a named character of mapping from:mapping to

Examples

```
## Not run:  
getOntoMultiMapping(ont = ont, onts = c("CL0000548", "CL:0000066", "CL:0000082"))  
  
## End(Not run)
```

getSeuratRds *read in seurat object .rds files as a named list of seurat object*

Description

read in seurat object .rds files as a named list of seurat object

Usage

```
getSeuratRds(metadata, sep)
```

Arguments

metadata	a metadata file indicating name, path to 'seurat' rds file
sep	sep of the metadata file

Value

a named list contains data name and the corresponding 'seurat' object

Examples

```
## Not run:  
getSeuratRds(metadata = 'metadata.tsv', sep = '\t')  
  
## End(Not run)
```

ontoMinimal	<i>get the minimal ontology tree of a dataset by reducing descendant terms to ancestor terms return obj meta.data[["cell_ontology_base"]] storing the reduced ontology annotation</i>
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Description

get the minimal ontology tree of a dataset by reducing descendant terms to ancestor terms return obj meta.data[["cell_ontology_base"]] storing the reduced ontology annotation

Usage

```
ontoMinimal(obj, ont, anno_col, onto_id_col)
```

Arguments

obj	the seurat object
ont	ontologyIndex object
anno_col	the cell ontology text annotation column name
onto_id_col	if also have ontology id column for direct mapping

Value

an seurat object with meta.data[["cell_ontology_base"]]

Examples

```
## Not run:  
ontoMinimal(obj = seurat_obj, ont = ont, anno_col = 'ontology_name', onto_id_col = 'ontology_id')  
  
## End(Not run)
```

ontoMultiMatch	<i>Core function of scOntoMatch Match the ontology annotation of multiple seurat objects</i>
----------------	--

Description

Core function of scOntoMatch Match the ontology annotation of multiple seurat objects

Usage

```
ontoMultiMatch(obj_list, anno_col, onto_id_col, ont)
```

Arguments

obj_list	a named list of seurat objects to match
anno_col	the cell ontology text annotation column name
onto_id_col	if also have ontology id column for direct mapping
ont	ontologyIndex object

Value

a list of seurat objects with annotation ontology mapped to each-other in obs[['cell_ontology_mapped']]

Examples

```
## Not run:
ontoMultiMatch(seurat_obj_list, ont, "ontology_name", 'ontology_id')

## End(Not run)
```

ontoMultiMinimal	<i>get the minimal ontology tree of a list of seurat objects by reducing descendant terms to ancestor terms return a named list of seurat objects with meta.data[["cell_ontology_base"]] storing the reduced ontology annotation</i>
------------------	--

Description

get the minimal ontology tree of a list of seurat objects by reducing descendant terms to ancestor terms return a named list of seurat objects with meta.data[["cell_ontology_base"]] storing the reduced ontology annotation

Usage

```
ontoMultiMinimal(obj_list, ont, anno_col = "cell_ontology_base", onto_id_col)
```


Arguments

obj_list a named list of seurat objects
 ont ontologyIndex object
 anno_col the cell ontology text annotation column name
 onto_id_col if also have ontology id column for direct mapping

Value

a named list of seurat objects with meta.data[["cell_ontology_base"]]

Examples

```
## Not run:
ontoMultiMinimal(seurat_obj_list, ont, "cell_ontology_base", 'ontology_id')

## End(Not run)
```

ontoTranslate	<i>translate named list of obj_list to named list of cell ontology ids per obj</i>
---------------	--

Description

translate named list of obj_list to named list of cell ontology ids per obj

Usage

```
ontoTranslate(obj_list, ont, onto_id_col, anno_col)
```

Arguments

obj_list a named list of seurat object
 ont ontologyIndex object
 onto_id_col if also have ontology id column for direct mapping
 anno_col the cell ontology text annotation column name

Value

a named list of cell ontology ids

Examples

```
## Not run:
ontoTranslate(seurat_obj_list, ont, 'ontology_name', 'ontology_id')

## End(Not run)
```

plotMatchedOntoTree *Plot a ontology tree with matched ontology from ontoMatch*

Description

Plot a ontology tree with matched ontology from ontoMatch

Usage

```
plotMatchedOntoTree(  
  obj_list,  
  ont,  
  anno_col = "cell_ontology_mapped",  
  onto_id_col,  
  roots = c("CL:0000548"),  
  ...  
)
```

Arguments

obj_list	a list of seurat obj files as the output of ontoMatch
ont	ontology object
anno_col	the cell ontology text annotation column name
onto_id_col	if also have ontology id column for direct mapping
roots	root ontology in tree to plot, default "animal cells" in cell ontology
...	additional parameters for ontologyPlot::onto_plot

Value

a list of matched ontology tree plot

Examples

```
## Not run:  
plotMatchedOntoTree(seurat_obj_list, ont, 'cell_ontology_mapped', 'ontology_id')  
  
## End(Not run)
```

plotOntoTree	<i>Plot a tree representation of ontology terms</i>
--------------	---

Description

Plot a tree representation of ontology terms

Usage

```
plotOntoTree(  
  ont,  
  onts,  
  plot_ancestors = TRUE,  
  ont_query = NULL,  
  roots = c("CL:0000548"),  
  ...  
)
```

Arguments

ont	ontology object
onts	ontology ids to plot
plot_ancestors	if plot ancestors or not
ont_query	query ontology to highlight in the tree
roots	root ontology in tree, default "animal cells" in cell ontology
...	additional parameters for ontologyPlot::onto_plot

Value

an ontology tree plot

Examples

```
## Not run:  
plotOntoTree(ont = ont, onts = c("CL:0000066", "CL:0000082"), ont_query = c("CL:0000082"))  
  
## End(Not run)
```

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