Package ‘SCSBrainCellTypeCollection’
February 12, 2016

Type Package
Title anRichment-type collection of brain cell type-specific gene sets
Version 1.00
Depends anRichment
Suggests org.Hs.eg.db
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Description This package contains gene sets with genes highly expressed in broad cell types as determined in single-cell sequencing by Zeisel et al., Science (2015).
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SCSBrainCellTypeCollection

SCSBrainCellTypeCollection

Returns a collection containing gene sets of marker genes of broad brain cell types.

Description

Returns a collection containing gene sets of marker genes of broad brain cell types. The gene sets were compiled from single cell sequencing data in mouse brains.

Usage

SCSBrainCellTypeCollection(
  organism = "human",
  useHomology = TRUE,
  addOldOrganismToSetNames = FALSE,
  namePattern = ".convertedFrom.%",
  addOldOrganismToSetDescriptions = FALSE,
  descriptionPattern = " (Converted from %.)")
Arguments

organism Character string specifying the organism. Can be common name (such as "human"), scientific name ("Homo sapiens"), or scientific shorthand ("Hs"). To see all recognized organisms, use function `organismLabels`. If `NULL` or `NA`, gene sets in the collection will retain their original content and organism (in this case mouse).

useHomology logical: should genes in non-human organisms be matched by homology information (where available)? If this is `FALSE` or the homology information is not available, genes will be matched by name.

addOldOrganismToSetNames Logical: should an indication of the old organism be appended to the set name? This may be useful to indicate that the gene sets was originally constructed for a different organism and its content may not accurately reflect the new organism.

namePattern Character string giving the pattern that is to be added to the set name. The characters "%o" will be substituted by the actual organism name.

addOldOrganismToSetDescriptions Logical: should an indication of the old organism be appended to the set description?

descriptionPattern Character string giving the pattern that is to be added to the set description. The characters "%o" will be substituted by the actual organism name.

Details

SCSBrainCellType gene sets were downloaded on December 14, 2015 and correspond to version 5.0.

Value

Collection of marker genes of broad brain cell types.

Author(s)


Examples

```R
# Not run:
collection = SCSBrainCellTypeCollection(organism = "mouse");
knownGroups(collection)

# End(Not run)
```
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