Package ‘BrainDiseaseCollection’

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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Author Peter Langfelder (R code); Jason Chen (gene lists); Verge Genomics team
Maintainer Peter Langfelder <Peter.Langfelder@gmail.com>
Description This package contains gene sets implicated in neurological diseases.
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BrainDiseaseCollection

Returns a collection containing gene sets implicated in neurological diseases.

Description

Returns a collection containing gene sets implicated in neurological diseases.

Usage

BrainDiseaseCollection(
  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 gene sets implicated in neurological diseases.

## Author(s)

Code by Peter Langfelder, gene sets compiled by Jason Chen from on-line sources.

## Examples

```r
## Not run:
collection = BrainDiseaseCollection(organism = "mouse");
knownGroups(collection)

## End(Not run)
```
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