Package ‘LRcellTypeMarkers’

September 3, 2024

Type Package

Title Marker gene information for LRcell R Bioconductor package

Version 1.13.0

Date 2020-02-25

BugReports https://github.com/marvinquiet/LRcellTypeMarkers/issues

GitURL https://github.com/marvinquiet/LRcellTypeMarkers

Description This is an external ExperimentData package for LRcell. This data package contains the gene enrichment scores calculated from scRNA-seq dataset which indicates the gene enrichment of each cell type in certain brain region. LRcell package is used to identify specific sub-cell types that drives the changes observed in a bulk RNA-seq differential gene expression experiment. For more details, please visit: https://github.com/marvinquiet/LRcell.

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Encoding UTF-8

biocViews ExperimentData, ExperimentHub, RNASeqData, SingleCellData, ExpressionData, PackageTypeData

Depends R (>= 4.1)

Imports ExperimentHub

Suggests LRcell, BiocStyle, knitr, rmarkdown, roxygen2, testthat

VignetteBuilder knitr

RoxygenNote 7.1.1

git_url https://git.bioconductor.org/packages/LRcellTypeMarkers

git_branch devel

git_last_commit b651f2f

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-09-03

Author Wenjing Ma [cre, aut] (<https://orcid.org/0000-0001-8757-651X>)

Maintainer Wenjing Ma <wenjing.ma@emory.edu>

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Description

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Details

See the vignette for examples of extracting and using these data.

browseVignettes("LRcellTypeMarkers")

Details of how these data were created are in the scripts/ directory of the source package.

The current release includes the following datasets:

Mouse Whole Brain Marker Genes Gene enrichment scores calculated from Mouse Adult Whole Brain scRNA-seq dataset. The dataset contains 15,976 common genes among 9 brain regions. According to original cell type annotation, we computed the gene enrichment scores for each brain region. The 9 brain regions are: Frontal Cortex (EH4548), Cerebellum (EH4549), Entopeduncular (EH4550), Globus Pallidus (EH4551), Posterior Cortex (EH4552), Striatum (EH4553), Substantia Nigra (EH4554), Thalamus (EH4555) and Hippocampus (EH4556).

Human Prefrontal Cortex Marker Genes Gene enrichment scores calculated from healthy human prefrontal cortex scRNA-seq dataset (EH4557). Original paper annotated the cell types based on prior knowledge which contains 26 valid sub-cell types (clusters).

References

Saunders et al. (2018). Molecular Diversity and Specializations among the Cells of the Adult Mouse Brain. *Cell* 174(4), 1015-1030

Nagy et al. (2020) Single-nucleus transcriptomics of the prefrontal cortex in major depressive disorder implicates oligodendrocyte precursor cells and excitatory neurons. *Nature Neuroscience* 1-11

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
myfiles <- query(eh, "LRcellTypeMarkers")
## download resource
myfiles[[1]]  ## load the first resource
myfiles[['EH4548']]  ## load by EH id
```

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