Package ‘ewceData’

August 8, 2024

Title The ewceData package provides reference data required for ewce

Version 1.12.0

Description This package provides reference data required for ewce. Expression Weighted Celltype Enrichment (EWCE) is used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies. The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

URL https://github.com/neurogenomics/ewceData

License Artistic-2.0

Encoding UTF-8

Depends R (>= 4.1), ExperimentHub

Suggests knitr, BiocStyle, ggplot2, cowplot, rmarkdown, markdown, testthat (>= 3.0.0)

biocViews ExperimentData, ExperimentHub, ExpressionData, Genome, Proteome, MicroarrayData, SequencingData, SingleCellData, RNASEqData

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

VignetteBuilder knitr

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Content

all_hgnc returns the all_hgnc dataset

Usage

all_hgnc(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
Description

all_hgnc_wtEnsembl returns the \textit{all_hgnc_wtEnsembl} dataset

Usage

\texttt{all_hgnc_wtEnsembl(localHub = FALSE)}

Arguments

\begin{itemize}
  \item \texttt{localHub} If working offline, add argument \texttt{localHub=TRUE} to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
\end{itemize}

Value

\textit{all_hgnc_wtEnsembl} dataset

Examples

\texttt{all_hgnc_wtEnsembl()}

Description

\textit{all_mgi} returns the \textit{all_mgi} dataset

Usage

\texttt{all_mgi(localHub = FALSE)}
Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

all_mgi dataset

Examples

all_mgi()
Description

alzh_gwas_top100 returns the alzh_gwas_top100 dataset

Usage

alzh_gwas_top100(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

alzh_gwas_top100 dataset

Examples

alzh_gwas_top100

Description
cortex_mrna returns the cortex_mrna dataset

Usage
cortex_mrna(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value
cortex_mrna dataset
Examples

cortex_mrna()

Description

ctd returns the ctd dataset

Usage

ctd(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

ctd dataset

Examples

ctd()

Description

ensembl_transcript_lengths_GCcontent returns the ensembl_transcript_lengths_GCcontent dataset

Usage

ensembl_transcript_lengths_GCcontent(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
The `ewceData` package provides reference data required for ewce. Expression Weighted Celltype Enrichment (EWCE) is used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies. The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

**Arguments**

- `metadata`  
  Logical value indicating whether metadata only should be returned or if the resource should be loaded. Default behavior (metadata=FALSE) loads the data.

**Value**

These accessor functions return differing dataset types

**Source**

These datasets have been sourced from various repositories, see the ExperimentHub database for details

**Examples**

`ensembl_transcript_lengths_GCcontent()`  
`alzh_gwas_top100()`
### example_genelist

**Description**

example_genelist returns the example_genelist dataset

**Usage**

```r
example_genelist(localHub = FALSE)
```

**Arguments**

- `localHub` If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

example_genelist dataset

**Examples**

```r
example_genelist()
```

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### hpsd_genes

**Description**

hpsd_genes returns the hpsd_genes dataset

**Usage**

```r
hpsd_genes(localHub = FALSE)
```

**Arguments**

- `localHub` If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

hpsd_genes dataset
Examples

hpsd_genes()

hypothalamus_mrna

Description

hypothalamus_mrna returns the hypothalamus_mrna dataset

Usage

hypothalamus_mrna(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

hypothalamus_mrna dataset

Examples

hypothalamus_mrna()

id_genes

Description

id_genes returns the id_genes dataset

Usage

id_genes(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
Value

id_genes dataset

Examples

id_genes()

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mgi_synonym_data        mgi_synonym_data

Description

mgi_synonym_data returns the mgi_synonym_data dataset

Usage

mgi_synonym_data(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

mgi_synonym_data dataset

Examples

mgi_synonym_data()

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mouse_to_human_homologs

mouse_to_human_homologs

Description

mouse_to_human_homologs returns the mouse_to_human_homologs dataset

Usage

mouse_to_human_homologs(localHub = FALSE)
rbfox_genes

Arguments

localHub

If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

mouse_to_human_homologs dataset

Examples

mouse_to_human_homologs()

Description

rbfox_genes returns the rbfox_genes dataset

Usage

rbfox_genes(localHub = FALSE)

Arguments

localHub

If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

rbfox_genes dataset

Examples

rbfox_genes()
schiz_genes returns the schiz_genes dataset

Usage

schiz_genes(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

schiz_genes dataset

Examples

schiz_genes()

tt_alzh returns the tt_alzh dataset

Usage

tt_alzh(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

Value

tt_alzh dataset
tt_alzh_BA36

Examples

tt_alzh()

Description
tt_alzh_BA36 returns the tt_alzh_BA36 dataset

Usage
tt_alzh_BA36(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-
updated hub; It will only have resources available that have previously been
downloaded. If offline, Please also see BiocManager vignette section on offline
use to ensure proper functionality.

Value
tt_alzh_BA36 dataset

Examples
tt_alzh_BA36()

Description

tt_alzh_BA44 returns the tt_alzh_BA44 dataset

Usage
tt_alzh_BA44(localHub = FALSE)

Arguments

localHub If working offline, add argument localHub=TRUE to work with a local, non-
updated hub; It will only have resources available that have previously been
downloaded. If offline, Please also see BiocManager vignette section on offline
use to ensure proper functionality.
Value

- `tt_alzh_BA44` dataset

Examples

- `tt_alzh_BA44()`
Index

* datasets
  ewceData, 7
all_hgnc, 2
all_hgnc_wtEnsembl, 3
all_mgi, 3
all_mgi_wtEnsembl, 4
alzh_gwas_top100, 5
cortex_mrna, 5
ctd, 6

ensemble_transcript_lengths_GCcontent,
  6
ewceData, 7
ewceData-package (ewceData), 7
example_genelist, 8

hpsd_genes, 8
hypothalamus_mrna, 9

id_genes, 9

mgi_synonym_data, 10
mouse_to_human_homologs, 10

rbfox_genes, 11

schiz_genes, 12

tt_alzh, 12
tt_alzh_BA36, 13
tt_alzh_BA44, 13