Package ‘ewceData’

June 27, 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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### all_hgnc

**Description**

`all_hgnc` returns the all_hgnc dataset

**Usage**

```r
all_hgnc(localHub = FALSE)
```

**Arguments**

- `localHub` (default: `FALSE`)
  - 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.
all_hgnc_wtEnsembl

Value

all_hgnc dataset

Examples

all_hgnc()

all_hgnc_wtEnsembl

Description

all_hgnc_wtEnsembl returns the all_hgnc_wtEnsembl dataset

Usage

all_hgnc_wtEnsembl(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_hgnc_wtEnsembl dataset

Examples

all_hgnc_wtEnsembl()

all_mgi

Description

all_mgi returns the all_mgi dataset

Usage

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

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
**ctd**

**Description**

tdt 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()

**ensembl_transcript_lengths_GCcontent**

**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.
ewceData

Value

ensemble_transcript_lengths_GCcontent dataset

Examples

ensemble_transcript_lengths_GCcontent()

ewceData

The ewceData package provides reference data required for ewce

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.

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

alzh_gwas_top100()
example_genelist

Description
example_genelist returns the example_genelist dataset

Usage
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
example_genelist()

hpsd_genes

Description
hpsd_genes returns the hpsd_genes dataset

Usage
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
hypothalamus_mrna

Examples

hpsd_genes()

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.
mouse_to_human_homologs

Value
id_genes dataset

Examples
id_genes()

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()

mouse_to_human_homologs

Description
mouse_to_human_homologs returns the mouse_to_human_homologs dataset

Usage
mouse_to_human_homologs(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

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()
Description

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()

Description

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
Examples

```r
tt_alzh()
```

Description

`tt_alzh()` returns the `tt_alzh` dataset.

Usage

```r
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

Examples

```r
tt_alzh()
```

Description

`tt_alzh()` returns the `tt_alzh` dataset.

Usage

```r
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_BA44 dataset

Examples

tt_alzh_BA44()
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