Package ‘ewceData’

May 16, 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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Repository Bioconductor 3.19

Date/Publication 2024-05-16
Description

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.
Value

*all_hgnc* dataset

Examples

*all_hgnc()*

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()*

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

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

cortex_mrna dataset

Examples

alzh_gwas_top100

cortex_mrna

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
ctd

description

crd returns the ctd dataset

usage

crd(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

crd dataset

examples

crd()

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()

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
**Examples**

```r
hpsd_genes()
```

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**Description**

`hpsd_genes()` returns the `hpsd_genes` dataset

**Usage**

```r
hpsd_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.

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**Value**

`hpsd_genes` dataset

**Examples**

```r
hpsd_genes()
```

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**id_genes**

**Description**

`id_genes()` returns the `id_genes` dataset

**Usage**

```r
id_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
  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)
*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()*

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**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

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()

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tt_alzh

Description

tt_alzh returns the tt_alzh dataset

Usage

tt_alzh(localHub = FALSE)

Argument

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_BA36` returns the `tt_alzh_BA36` dataset

Usage

```r
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

```r
tt_alzh_BA36()
```

Description

`tt_alzh_BA44` returns the `tt_alzh_BA44` dataset

Usage

```r
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

ensembl_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