Package ‘ewceData’

May 9, 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

Config/testthat/edition  3

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Repository  Bioconductor 3.19

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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()

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**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**

```r
all_mgi()
```

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**Description**

`all_mgi_wtEnsembl` returns the all_mgi_wtEnsembl dataset

**Usage**

```r
all_mgi_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_mgi_wtEnsembl dataset

**Examples**

```r
all_mgi_wtEnsembl()
```
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()

ctd

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()
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 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 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**

```r
hpsd_genes()
```

**Description**

`hypothalamus_mrna` returns the hypothalamus_mrna dataset.

**Usage**

```r
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**

```r
hypothalamus_mrna()
```

### id_genes

**Description**

`id_genes` returns the id_genes dataset.

**Usage**

```r
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)
**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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**rbfox_genes**

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

```
rFOX_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

```
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()*
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