Package ‘ewceData’

July 25, 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](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

```r
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.
**all_hgnc_wtEnsembl**

**Value**

all_hgnc dataset

**Examples**

```r
all_hgnc()
```

---

**Description**

all_hgnc_wtEnsembl returns the all_hgnc_wtEnsembl dataset

**Usage**

```r
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**

```r
all_hgnc_wtEnsembl()
```

---

**all_mgi**

**Description**

all_mgi returns the all_mgi dataset

**Usage**

```r
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()
alzh_gwas_top100

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

cortex_mrna

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
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()

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.
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**

```
ewceData
```

```
value

ensembl_transcript_lengths_GCcontent dataset
```

```
Examples

ensembl_transcript_lengths_GCcontent()
```

```
ewceData
```

```
The ewceData package provides reference data required for ewce
```

```
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

```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()

---

**mg_i_synonym_data**  
**mg_i_synonym_data**

**Description**

mg_i_synonym_data returns the mg_i_synonym_data dataset

**Usage**

mg_i_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**

mg_i_synonym_data dataset

**Examples**

mg_i_synonym_data()

---

**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)
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()

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

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
**tt_alzh_BA36**

**Examples**

```
tt_alzh()
```

---

**tt_alzh_BA36**

**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()
```

---

**tt_alzh_BA44**

**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

\texttt{tt_alzh_BA44()}

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