

Package ‘ewceData’

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Title The ewceData package provides reference data required for ewce

Version 1.17.0

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>

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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

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Contents

all_hgnc	2
all_hgnc_wtEnsembl	3
all_mgi	3
all_mgi_wtEnsembl	4
alz_h_gwas_top100	5
cortex_mrna	5
ctd	6
ensembl_transcript_lengths_GCcontent	6
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
Index	15

all_hgnc	<i>all_hgnc</i>
----------	-----------------

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()
```

all_hgnc_wtEnsembl	<i>all_hgnc_wtEnsembl</i>
--------------------	---------------------------

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	<i>all_mgi</i>
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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()
```

<code>all_mgi_wtEnsembl</code>	<i>all_mgi_wtEnsembl</i>
--------------------------------	--------------------------

Description

`all_mgi_wtEnsembl` returns the `all_mgi_wtEnsembl` dataset

Usage

```
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

```
all_mgi_wtEnsembl()
```

alzh_gwas_top100	<i>alzh_gwas_top100</i>
------------------	-------------------------

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	<i>cortex_mrna</i>
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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	<i>ctd</i>
-----	------------

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
<i>ensembl_transcript_lengths_GCcontent</i>

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.
----------	---

Value

ensembl_transcript_lengths_GCcontent dataset

Examples

```
ensembl_transcript_lengths_GCcontent()
```

ewceData	<i>The ewceData package provides reference data required for ewce</i>
----------	---

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	<i>example_genelist</i>
------------------	-------------------------

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	<i>hpsd_genes</i>
------------	-------------------

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

```
hpsd_genes()
```

hypothalamus_mrna	<i>hypothalamus_mrna</i>
-------------------	--------------------------

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	<i>id_genes</i>
----------	-----------------

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()
```

mg_i_synonym_data	<i>mg_i_synonym_data</i>
-------------------	--------------------------

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	<i>mouse_to_human_homologs</i>
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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	<i>rbfox_genes</i>
-------------	--------------------

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	<i>schiz_genes</i>
-------------	--------------------

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()
```

tt_alzh	<i>tt_alzh</i>
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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()
```

```
tt_alzh_BA36
```

```
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
```

```
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

tt_alzh_BA44()

Index

* datasets

- ewceData, [7](#)
- all_hgnc, [2](#)
- all_hgnc_wtEnsembl, [3](#)
- all_mgi, [3](#)
- all_mgi_wtEnsembl, [4](#)
- alz_h_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](#)