Package ‘ewceData’

May 28, 2026

Title The ewceData package provides reference data required for ewce

Version 1.21.0

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, rbibutils, testthat (>= 3.0.0)

biocViews ExperimentData, ExperimentHub, ExpressionData, Genome, Proteome, MicroarrayData, SequencingData, SingleCellData, RNASeqData

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

VignetteBuilder knitr

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/ewceData

git_branch devel

git_last_commit 29b7bce

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-28

Author Alan Murphy [aut] (ORCID: <`https://orcid.org/0000-0002-2487-8753`>), Hiranyamaya Dash [cre] (ORCID: <`https://orcid.org/0009-0005-5514-505X`>), Nathan Skene [aut] (ORCID: <`https://orcid.org/0000-0002-6807-3180`>)

Maintainer Hiranyamaya Dash <`hdash.work@gmail.com`>

Contents

`all_hgnc` *all_hgnc*

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` *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` *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()
```

`all_mgi_wtEnsembl` *all_mgi_wtEnsembl*

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` *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` *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` *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.

Value

ensembl_transcript_lengths_GCcontent dataset

Examples

```
ensembl_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` *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` *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

```
hpsd_genes()
```

`hypothalamus_mrna` *hypothalamus_mrna*

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` *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.

Value

id_genes dataset

Examples

```
id_genes()
```

`mgi_synonym_data` *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` *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` *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()
```

`schiz_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()
```

`tt_alzh` *tt_alzh*

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