

# Package ‘ewceData’

August 8, 2024

**Title** The ewceData package provides reference data required for ewce

**Version** 1.13.0

**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

**git\_url** <https://git.bioconductor.org/packages/ewceData>

**git\_branch** devel

**git\_last\_commit** aec1c88

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-08-08

**Author** Alan Murphy [cre] (<<https://orcid.org/0000-0002-2487-8753>>),  
Nathan Skene [aut] (<<https://orcid.org/0000-0002-6807-3180>>)

**Maintainer** Alan Murphy <alanmurph94@hotmail.com>

## 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
<b>Index</b>	<b>15</b>

---

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      *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	<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>
-------------	--------------------

---

**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	<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      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()
```

---

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	<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>
---------	----------------

---

**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](#)
- [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](#)