

Package ‘ewceData’

April 6, 2022

Title The ewceData package provides reference data required for ewce

Version 1.2.0

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 7.1.1

VignetteBuilder knitr

Config/testthat/edition 3

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

git_branch RELEASE_3_14

git_last_commit 16af004

git_last_commit_date 2021-10-26

Date/Publication 2022-04-06

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>

R topics documented:

all_hgnc	2
all_hgnc_wtEnsembl	3
all_mgi	3
all_mgi_wtEnsembl	4
alz_h_gwas_top100	4
cortex_mrna	5
ctd	5
ensembl_transcript_lengths_GCcontent	6
ewceData	6
example_genelist	7
hpsd_genes	7
hypothalamus_mrna	8
id_genes	8
mgi_synonym_data	9
mouse_to_human_homologs	9
rbfox_genes	10
schiz_genes	10
tt_alzh	11
tt_alzh_BA36	11
tt_alzh_BA44	12

Index	13
--------------	-----------

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

Description

all_hgnc returns the all_hgnc dataset

Usage

all_hgnc()

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()
```

Value

all_hgnc_wtEnsembl dataset

Examples

```
all_hgnc_wtEnsembl()
```

all_mgi	<i>all_mgi</i>
---------	----------------

Description

all_mgi returns the all_mgi dataset

Usage

```
all_mgi()
```

Value

all_mgi dataset

Examples

```
all_mgi()
```

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

Description

all_mgi_wtEnsembl returns the all_mgi_wtEnsembl dataset

Usage

```
all_mgi_wtEnsembl()
```

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()
```

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()

Value

cortex_mrna dataset

Examples

cortex_mrna()

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

Description

ctd returns the ctd dataset

Usage

ctd()

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()
```

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()

Value

example_genelist dataset

Examples

example_genelist()

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

Description

hpsd_genes returns the hpsd_genes dataset

Usage

hpsd_genes()

Value

hpsd_genes dataset

Examples

hpsd_genes()

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

Description

hypothalamus_mrna returns the hypothalamus_mrna dataset

Usage

hypothalamus_mrna()

Value

hypothalamus_mrna dataset

Examples

hypothalamus_mrna()

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

Description

id_genes returns the id_genes dataset

Usage

id_genes()

Value

id_genes dataset

Examples

id_genes()

<code>mgc_synonym_data</code>	<i>mgc_synonym_data</i>
-------------------------------	-------------------------

Description

`mgc_synonym_data` returns the `mgc_synonym_data` dataset

Usage

```
mgc_synonym_data()
```

Value

`mgc_synonym_data` dataset

Examples

```
mgc_synonym_data()
```

<code>mouse_to_human_homologs</code>	<i>mouse_to_human_homologs</i>
--------------------------------------	--------------------------------

Description

`mouse_to_human_homologs` returns the `mouse_to_human_homologs` dataset

Usage

```
mouse_to_human_homologs()
```

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()
```

Value

`rbfox_genes` dataset

Examples

```
rbfox_genes()
```

`schiz_genes`*schiz_genes*

Description

`schiz_genes` returns the `schiz_genes` dataset

Usage

```
schiz_genes()
```

Value

`schiz_genes` dataset

Examples

```
schiz_genes()
```

tt_alzh	<i>tt_alzh</i>
---------	----------------

Description

tt_alzh returns the tt_alzh dataset

Usage

```
tt_alzh()
```

Value

tt_alzh dataset

Examples

```
tt_alzh()
```

tt_alzh_BA36	<i>tt_alzh_BA36</i>
--------------	---------------------

Description

tt_alzh_BA36 returns the tt_alzh_BA36 dataset

Usage

```
tt_alzh_BA36()
```

Value

tt_alzh_BA36 dataset

Examples

```
tt_alzh_BA36()
```

tt_alzh_BA44	<i>tt_alzh_BA44</i>
--------------	---------------------

Description

tt_alzh_BA44 returns the tt_alzh_BA44 dataset

Usage

```
tt_alzh_BA44()
```

Value

tt_alzh_BA44 dataset

Examples

```
tt_alzh_BA44()
```

Index

* **datasets**

- [ewceData](#), [6](#)
- [all_hgnc](#), [2](#)
- [all_hgnc_wtEnsembl](#), [3](#)
- [all_mgi](#), [3](#)
- [all_mgi_wtEnsembl](#), [4](#)
- [alz_h_gwas_top100](#), [4](#)
-
- [cortex_mrna](#), [5](#)
- [ctd](#), [5](#)
-
- [ensembl_transcript_lengths_GCcontent](#),
[6](#)
- [ewceData](#), [6](#)
- [ewceData-package \(ewceData\)](#), [6](#)
- [example_genelist](#), [7](#)
-
- [hpsd_genes](#), [7](#)
- [hypothalamus_mrna](#), [8](#)
-
- [id_genes](#), [8](#)
-
- [mgi_synonym_data](#), [9](#)
- [mouse_to_human_homologs](#), [9](#)
-
- [rbfox_genes](#), [10](#)
-
- [schiz_genes](#), [10](#)
-
- [tt_alzh](#), [11](#)
- [tt_alzh_BA36](#), [11](#)
- [tt_alzh_BA44](#), [12](#)