

Package ‘ewceData’

April 13, 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>

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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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all_hgnc	<i>all_hgnc</i>
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Description

all_hgnc returns the all_hgnc dataset

Usage

```
all_hgnc()
```

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()`

Value

`all_hgnc_wtEnsembl` dataset

Examples

`all_hgnc_wtEnsembl()`

`all_mgi` *all_mgi*

Description

`all_mgi` returns the `all_mgi` dataset

Usage

`all_mgi()`

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()
```

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()
```

Value

alzh_gwas_top100 dataset

Examples

```
alzh_gwas_top100
```

`cortex_mrna`*cortex_mrna*

Description

`cortex_mrna` returns the `cortex_mrna` dataset

Usage

```
cortex_mrna()
```

Value

`cortex_mrna` dataset

Examples

```
cortex_mrna()
```

`ctd`*ctd*

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()
```

<code>example_genelist</code>	<i>example_genelist</i>
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Description

`example_genelist` returns the `example_genelist` dataset

Usage

```
example_genelist()
```

Value

`example_genelist` dataset

Examples

```
example_genelist()
```

<code>hpsd_genes</code>	<i>hpsd_genes</i>
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Description

`hpsd_genes` returns the `hpsd_genes` dataset

Usage

```
hpsd_genes()
```

Value

`hpsd_genes` dataset

Examples

```
hpsd_genes()
```

hypothalamus_mrna	<i>hypothalamus_mrna</i>
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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()
```

`mgc_synonym_data` *mgc_synonym_data*

Description

`mgc_synonym_data` returns the `mgc_synonym_data` dataset

Usage

`mgc_synonym_data()`

Value

`mgc_synonym_data` dataset

Examples

`mgc_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()`

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>
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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`*tt_alzh_BA44*

Description

`tt_alzh_BA44` returns the `tt_alzh_BA44` dataset

Usage

```
tt_alzh_BA44()
```

Value

`tt_alzh_BA44` dataset

Examples

```
tt_alzh_BA44()
```

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