Package 'RITANdata'

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Type Package

Title This package contains reference annotation and network data sets

Version 1.36.0

Description Data such as is contained in the two R data files in this package are required for the RITAN package examples. Users are highly encouraged to use their own or additional resources in conjunction with RITANdata. See the RITAN vignettes and RITAN.md for more information, such as gathering more up-to-date annotation data.

LazyData TRUE

LazyDataCompression xz

Depends R (>= 4.2)

VignetteBuilder knitr

Suggests knitr

RoxygenNote 5.0.1

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biocViews AnnotationData, Homo_sapiens

NeedsCompilation no

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Author Michael Zimmermann [aut, cre]

Maintainer Michael Zimmermann <mtzimmermann@mcw.edu>

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`RITANdata-package` *This package contains reference annotation and network data sets*

Description

Data such as is contained in the two R data files in this package are required for the RITAN package examples. Users are highly encouraged to use their own or additional resources in conjunction with RITANdata. See the RITAN vignettes and RITAN.md for more information, such as gathering more up-to-date annotation data.

`cached_coding_genes` *cached_coding_genes.RData*

Description

Gene symbols for all human protein coding genes, cached for use in RITAN vignettes. The set of all human protein coding genes is the default "background" list. This data was generated by running the load_all_protein_coding_symbols() function from RITAN and saving the resulting vector of gene symbols. By default, functions in RITAN will download the most recent list. We encourage users to use the most appropriate background for their study. See our vignettes for additional discussion.

Usage

```
cached_coding_genes
```

Format

A `chr` vector of gene symbols for all protein coding genes

Value

Chr vector of gene symbols

Author(s)

Michael T Zimmermann

Source

ftp://ftp.ebi.ac.uk/pub/databases/genenames/new/tsv/locus_groups/protein-coding_gene.txt

Examples

```
print(str(cached_coding_genes))
```

`geneset_list` *geneset_list.RData*

Description

R list object containing annotation resources and the gene sets contained in each of them.

Usage

```
geneset_list
```

Format

A `list` with one element for each annotation resource. Each element contains a varying number of gene symbols.

Value

A list of resources. Each resource contains a list of genesets.

Author(s)

Michael T Zimmermann

Source

Multiple sources used. See our table in the network vignette.

Examples

```
print(names(geneset_list))
```

network_list *network_list.RData*

Description

R list object containing network data resources and, when available, confidence scores for each interaction. Each resource was taken as-is from flat-file downloads and simplified into SIF files for expediency. Citation information for each cached resource can be accessed via attr(network_list, 'network_data_sources'). Some resources are queried using existing R packages. For example, we access STRING data through STRINGdb. Future versions of RITAN will leverage additional existing package services.

Usage

```
network_list
```

Format

A `list` of resources, one entry for each network resource. Each list element is a data.frame with 3 columns:

`p1` protein or gene 1

`edge_type` edge/interaction/connection type

`p2` protein or gene 2

Value

A `list` of netowrk resources. Each entry contains a `list` of edges as a `data.frame`.

Author(s)

Michael T Zimmermann

Source

Multiple sources used. See our table in the RITAN network vignette for citation information.

Examples

```
print(names(network_list))
```

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