

Package ‘biscuiteerData’

December 19, 2024

Type Package

Title Data Package for Biscuiteer

Description Contains default datasets used by the Bioconductor package biscuiteer.

Version 1.21.0

Date 2023-07-05

Author Tim Triche, Jr. [aut, cre], Wanding Zhou [aut], Ben Johnson [aut], Jacob Morrison [aut], Lyong Heo [aut]

Maintainer ``Jacob Morrison" <jacob.morrison@vai.org>

License GPL-3

Depends R (>= 4.1.0), ExperimentHub

Imports AnnotationHub, utils, curl, GenomicRanges

Suggests knitr, rmarkdown, markdown

biocViews ExperimentHub, ExperimentData, Genome, Homo_sapiens_Data

Encoding UTF-8

RoxygenNote 6.1.1

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

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

git_branch devel

git_last_commit 1a228b9

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-12-19

Contents

biscuiteerData-package	2
biscuiteerDataCacheAll	3
biscuiteerDataGet	3
biscuiteerDataList	4
biscuiteerDataListDates	4
PMDs.hg19	5
PMDs.hg38	5
Zhou_solo_WCGW_inCommonPMDs.hg19	5
Zhou_solo_WCGW_inCommonPMDs.hg38	6
Index	7

biscuiteerData-package

Supplementary Datasets for Biscuiteer

Description

A handful of datasets to be used in biscuiteer

Author(s)

Timothy J Triche Jr <Tim.Triche@vai.org>,
 Wanding Zhou <Wanding.Zhou@vai.org>,
 Ben Johnson <Ben.Johnson@vai.org>,
 Jacob Morrison <Jacob.Morrison@vai.org>,
 Lyong Heo <Lyong.Heo@vai.org>

See Also

Useful links:

- <https://github.com/trichelab/biscuiteer>
- Report bugs at <https://github.com/trichelab/biscuiteer/issues>

Examples

```
Zhou_solo_WCGW_inCommonPMDs.hg19 <-
  biscuiteerDataGet("Zhou_solo_WCGW_inCommonPMDs.hg19.rda")
PMDs.hg19 <- biscuiteerDataGet("PMDs.hg19.rda")
```

`biscuiteerDataCacheAll`*Cache all biscuiteer data*

Description

Cache all biscuiteer data

Usage

```
biscuiteerDataCacheAll(dateAdded = "all", showProgress = FALSE)
```

Arguments

<code>dateAdded</code>	Version of the data (given by the date added), if "all" then all dates will be cached (DEFAULT: "all")
<code>showProgress</code>	Whether to show progress of download (DEFAULT: FALSE)

Value

TRUE

Examples

```
biscuiteerDataCacheAll()
```

`biscuiteerDataGet`*Retrieve biscuiteer data*

Description

Retrieve biscuiteer data

Usage

```
biscuiteerDataGet(title, dateAdded = "2019-09-25", verbose = FALSE)
```

Arguments

<code>title</code>	Title of the data
<code>dateAdded</code>	Version of the data (given by the date added) (DEFAULT: "2019-09-25")
<code>verbose</code>	Whether to output ExperimentHub message (DEFAULT: FALSE)

Value

Data object

Examples

```
wcgws <- biscuiteerDataGet("Zhou_solo_WCGW_inCommonPMDs.hg19.rda")
```

biscuiteerDataList *List all biscuiteer data*

Description

List all biscuiteer data

Usage

```
biscuiteerDataList(dateAdded = "all")
```

Arguments

dateAdded Version of the data (given by the date added), if "all" then all dates will be shown (DEFAULT: "all")

Value

All titles from biscuiteer data

Examples

```
biscuiteerDataList()
```

biscuiteerDataListDates
 List all versions of biscuiteer data

Description

List all versions of biscuiteer data

Usage

```
biscuiteerDataListDates()
```

Value

Sorted unique dates in biscuiteer data

Examples

```
biscuiteerDataListDates()
```

PMDs.hg19

PMDs.hg19

Description

Common PMD locations in hg19 genome

Details

Source URL: http://zwdzwd.io/pmd/PMD_coordinates_hg19.bed.gz Source type: BED file Return type: GRanges

PMDs.hg38

PMDs.hg38

Description

Common PMD locations in hg38 genome

Details

Source URL: http://zwdzwd.io/pmd/PMD_coordinates_hg38.bed.gz Source type: BED file Return type: GRanges

Zhou_solo_WCGW_inCommonPMDs.hg19

Zhou_solo_WCGW_inCommonPMDs.hg19

Description

Solo WCGWs living in hg19 common PMDs

Details

Source URL: http://zwdzwd.io/pmd/solo_WCGW_inCommonPMDs_hg19.bed.gz Source type: BED file Return type: GRanges

Zhou_solo_WCGW_inCommonPMDs.hg38

Zhou_solo_WCGW_inCommonPMDs.hg38

Description

Solo WCGWs living in hg38 common PMDs

Details

Source URL: http://zwdzwd.io/pmd/solo_WCGW_inCommonPMDs_hg38.bed.gz Source type: BED
file Return type: GRanges

Index

- * **Biscuit**
 - biscuiteerData-package, [2](#)
- * **DNAMethylation**
 - biscuiteerData-package, [2](#)
- * **DataImport**
 - biscuiteerData-package, [2](#)
- * **EpigeneticsWorkflow**
 - biscuiteerData-package, [2](#)
- * **ExperimentData**
 - biscuiteerData-package, [2](#)
- * **MethylSeq**
 - biscuiteerData-package, [2](#)
- * **data**
 - PMDs.hg19, [5](#)
 - PMDs.hg38, [5](#)
 - Zhou_solo_WCGW_inCommonPMDs.hg19,
[5](#)
 - Zhou_solo_WCGW_inCommonPMDs.hg38,
[6](#)
- _PACKAGE (biscuiteerData-package), [2](#)
- biscuiteerData
 - (biscuiteerData-package), [2](#)
- biscuiteerData-package, [2](#)
- biscuiteerDataCacheAll, [3](#)
- biscuiteerDataGet, [3](#)
- biscuiteerDataList, [4](#)
- biscuiteerDataListDates, [4](#)
- PMDs.hg19, [5](#)
- PMDs.hg38, [5](#)
- Zhou_solo_WCGW_inCommonPMDs.hg19, [5](#)
- Zhou_solo_WCGW_inCommonPMDs.hg38, [6](#)