Package 'biscuiteerData'

April 24, 2025

Type Package

Title Data Package for Biscuiteer

Description Contains default datasets used by the Bioconductor package biscuiteer.

Version 1.22.0

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 RELEASE_3_21

git_last_commit 1c14676

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-04-24

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

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

title	Title of the data
dateAdded	Version of the data (given by the date added) (DEFAULT: "2019-09-25")
verbose	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