

Package: biscuiteerData (via r-universe)

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Type Package

Title Data Package for Biscuiteer

Description Contains default datasets used by the Bioconductor package
biscuiteer.

Version 1.27.0

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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>

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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

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository <https://bioc.r-universe.dev>

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RemoteUrl <https://github.com/bioc/biscuiteerData>

RemoteRef HEAD

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biscuiteerData-package
<i>Supplementary Datasets for Biscuiteer</i>

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>,
L Yong Heo <L Yong.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	<i>List all biscuiteer data</i>
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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")
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Value

All titles from biscuiteer data

Examples

```
biscuiteerDataList()
```

biscuiteerDataListDates	<i>List all versions of biscuiteer data</i>
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Description

List all versions of biscuiteer data

Usage

```
biscuiteerDataListDates()
```

Value

Sorted unique dates in biscuiteer data

Examples

```
biscuiteerDataListDates()
```

PMDs.hg19	<i>PMDs.hg19</i>
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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	<i>PMDs.hg38</i>
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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	<i>Zhou_solo_WCGW_inCommonPMDs.hg19</i>
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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

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