

Package ‘sesameData’

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Type Package

Title Supporting Data for SeSAmE Package

Description Provides supporting annotation and test data for SeSAmE package.

Version 1.8.1

License Artistic-2.0

Depends R (>= 4.0), ExperimentHub, AnnotationHub

Suggests GenomicRanges, BiocGenerics, sesame, testthat, knitr

Imports utils, curl

biocViews ExperimentData, MicroarrayData, Genome, ExperimentHub

VignetteBuilder knitr

LazyData true

NeedsCompilation no

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sesameDataCacheAll *Cache all SeSAmE data*

Description

Cache all SeSAmE data

Usage

```
sesameDataCacheAll(dateAdded = latest_date, showProgress = FALSE)
```

Arguments

dateAdded version of the data by date added, if "all", cache all dates
showProgress whether to show progress of download

Value

TRUE

Examples

```
sesameDataCacheAll()
```

sesameDataGet *Get SeSAmE data*

Description

Get SeSAmE data

Usage

```
sesameDataGet(title, verbose = FALSE, dateAdded = latest_date)
```

Arguments

title title of the data
verbose whether to output ExperimentHub message
dateAdded version of the data by date added

Value

data object

Examples

```
result <- sesameDataGet('genomeInfo.hg38')
```

| | |
|----------------|-----------------------------|
| sesameDataList | <i>List all SeSAmE data</i> |
|----------------|-----------------------------|

Description

List all SeSAmE data

Usage

```
sesameDataList(dateAdded = latest_date)
```

Arguments

dateAdded version of the data by date added, if "all", show all dates

Value

all titles from SeSAmE Data

Examples

```
sesameDataList()
```

| | |
|---------------------|---|
| sesameDataListDates | <i>List all versions of SeSAmE data</i> |
|---------------------|---|

Description

List all versions of SeSAmE data

Usage

```
sesameDataListDates()
```

Value

sorted unique dates of SeSAmE Data

Examples

```
sesameDataListDates()
```

```
sesameDataPullManifest
```

Retrieve manifest file from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

Description

Retrieve manifest file from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

Usage

```
sesameDataPullManifest(
  platform = c("EPIC", "HM450", "HM27"),
  refversion = c("hg19", "hg38"),
  version = "current",
  probeType = c("all", "cg", "ch", "rs"),
  designType = c("all", "I", "II")
)
```

Arguments

| | |
|------------|---|
| platform | Infinium platform |
| refversion | human reference version, irrelevant for mouse array |
| version | manifest version, default to the latest/current. |
| probeType | cg, ch or rs, default to all probes |
| designType | I (Infinium-I) or II (Infinium-II), default to both |

Value

manifest file of requested probes

Examples

```
mft <- sesameDataPullManifest('HM27', 'hg38')
```

```
sesameDataPullVariantAnno_InfiniumI
```

Retrieve variant annotation file for Infinium-I probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

Description

Retrieve variant annotation file for Infinium-I probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

Usage

```
sesameDataPullVariantAnno_InfiniumI(  
  platform = c("EPIC"),  
  refversion = c("hg19", "hg38"),  
  version = "20200704"  
)
```

Arguments

| | |
|------------|---|
| platform | Infinium platform |
| refversion | human reference version, irrelevant for mouse array |
| version | manifest version, default to the latest/current. |

Value

variant annotation file of infinium I probes

Examples

```
annoI <- sesameDataPullVariantAnno_InfiniumI('EPIC', 'hg38')
```

sesameDataPullVariantAnno_SNP

Retrieve variant annotation file for explicit rs probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

Description

Retrieve variant annotation file for explicit rs probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

Usage

```
sesameDataPullVariantAnno_SNP(  
  platform = c("EPIC"),  
  refversion = c("hg19", "hg38"),  
  version = "20200704"  
)
```

Arguments

| | |
|------------|---|
| platform | Infinium platform |
| refversion | human reference version, irrelevant for mouse array |
| version | manifest version, default to the latest/current. |

Value

variant annotation file of explicit rs probes

Examples

```
annoS <- sesameDataPullVariantAnno_SNP('EPIC', 'hg38')
```

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