Package 'sesameData'

April 13, 2022

Type Package

Title Supporting Data for SeSAMe Package

Description Provides supporting annotation and test data for SeSAMe package. This includes chip tango addresses, mapping information, performance annotation, and trained predictor for Infinium array data. This package provides user access to essential annotation data for working with many generations of the Infinium DNA methylation array. Current we support human array (HM27, HM450, EPIC), mouse array (MM285) and the Horvath-MethylChip40 (Mammal40) array.

Version 1.12.0

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Depends R (>= 4.1), ExperimentHub, AnnotationHub, rmarkdown

Suggests GenomicRanges, BiocGenerics, sesame, testthat, knitr

Imports utils, curl

biocViews ExperimentData, MicroarrayData, Genome, ExperimentHub, MethylationArrayData

VignetteBuilder knitr

NeedsCompilation no

RoxygenNote 7.1.2

git_url https://git.bioconductor.org/packages/sesameData

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R **topics documented:**

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df_master   *Master data frame for all object to cache*

Description

This is an internal object which will be updated on every new release library(ExperimentHub) eh =
query(ExperimentHub(localHub=FALSE), c("sesameData", "v1.11.7")) data.frame(name=eh$title,
eh=names(eh))

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sesameDataCache   *Cache SeSAMe data for specific platform*

Description

Cache SeSAMe data for specific platform

Usage

```
sesameDataCache(platform = NULL, keyword = NULL)
```

Arguments

platform   EPIC, HM450, MM285, etc.

keyword   keyword used to filter records

Value

TRUE

Examples

```
if(FALSE) { sesameDataCache("MM285") }
```

---

sesameDataCacheAll   *Cache all SeSAMe data*

Description

Cache all SeSAMe data

Usage

```
sesameDataCacheAll()
```

Value

TRUE

Examples

```
if(FALSE) { sesameDataCacheAll() }
```

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sesameDataDownload   *Download auxiliary data for sesame function and documentation*

Description

Download auxiliary data for sesame function and documentation

Usage

```
sesameDataDownload(file_name, dest_dir = NULL)
```

Arguments

file_name	name of file to download
dest_dir	directory to hold downloaded file. use the temporary directory if not given

Value

a list with url, dest_dir, dest_file and file_name

Examples

```
if(FALSE) { sesameDataDownload("3999492009_R01C01_Grn.idat") }
```

---

sesameDataGet	*Get SeSAMe data*

Description

Get SeSAMe data

Usage

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

Arguments

title	title of the data
verbose	whether to output ExperimentHub message

Value

data object

Examples

```
sesameDataCache("HM27")
genomeInfo.hg38 <- sesameDataGet('genomeInfo.hg38')
```

---

sesameDataGetAnno	*Retrieve manifest file from the supporting web-site at http://zwdzwd.github.io/InfiniumAnnotation and https://github.com/zhou-lab/InfiniumAnnotation*

Description

Retrieve manifest file from the supporting website at http://zwdzwd.github.io/InfiniumAnnotation and https://github.com/zhou-lab/InfiniumAnnotation

Usage

```
sesameDataGetAnno(title)
```

Arguments

title	title of the annotation file

Value

annotation file

Examples

```
mft = sesameDataGetAnno("HM27/HM27.hg19.manifest.tsv.gz")
annoS = sesameDataGetAnno("EPIC/EPIC.hg19.typeI_overlap_b151.rds")
```

---

sesameDataList   *List all SeSAMe data*

Description

List all SeSAMe data

Usage

```
sesameDataList()
```

Value

all titles from SeSAMe Data

Examples

```
sesameDataList()
```

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sesameDataPullVariantAnno_InfiniumI

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

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Description

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

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 support-*
> *ing 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/InfiniumAnnotati

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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