

Package ‘RnBeads.hg19’

October 16, 2021

Title RnBeads.hg19

Description Automatically generated RnBeads annotation package for the assembly hg19.

Author RnBeadsAnnotationCreator

Maintainer RnBeadsAnnotationCreator <rnbeads@mpi-inf.mpg.de>

Date 2018-07-30

License GPL-3

Version 1.24.0

Depends R (>= 3.0.0), GenomicRanges

Suggests RnBeads

NeedsCompilation no

RoxygenNote 6.0.1

git_url <https://git.bioconductor.org/packages/RnBeads.hg19>

git_branch RELEASE_3_13

git_last_commit 01cc87d

git_last_commit_date 2021-05-19

Date/Publication 2021-10-16

R topics documented:

hg19	2
regions	2
rnb.set.example	3
sites	3
Index	4

hg19

*HG19 - Annotation tables***Description**

Scaffold of annotation tables for HG19. This structure is automatically loaded upon initialization of the annotation, that is, by the first valid call to any of the following functions: [rnb.get.assemblies](#), [rnb.get.chromosomes](#), [rnb.get.annotation](#), [rnb.set.annotation](#), [rnb.get.mapping](#), [rnb.annotation.size](#). Adding an annotation amounts to attaching its table(s) and mapping structures to this scaffold.

Format

list of four elements - "regions", "sites", "controls" and "mappings". These elements are described below.

"regions" list of NULLs; the names of the elements correspond to the built-in region annotation tables. Once the default annotations are loaded, the attribute "builtin" is a logical vector storing, for each region annotation, whether it is the default (built-in) or custom.

"sites" list of NULLs; the names of the elements correspond to the site and probe annotation tables.

"controls" list of NULLs; the names of the elements correspond to the control probe annotation tables. The attribute "sites" is a character vector pointing to the site annotation that encompasses the respective control probes.

"mappings" list of NULLs; the names of the elements correspond to the built-in region annotation tables.

Author(s)

Yassen Assenov

regions

*Names of the regions***Description**

This is a list of all regions available for the annotation.

Usage

regions

Format

list of NULLs; the names of the elements correspond to the built-in region annotation tables. Once the default annotations are loaded, the attribute "builtin" is a logical vector storing, for each region annotation, whether it is the default (built-in) or custom.

Author(s)

Michael Scherer

rnb.set.example	<i>Example Data Set</i>
-----------------	-------------------------

Description

A small example dataset for testing RnBeads' basic functionality.

Usage

```
data(small.example.object)
```

Format

`RnBeadRawSet-class` object with 12 samples and 1,736 sites. It is an example object obtained from Illumina Infinium 450K BeadChip and contains coverage, intensity, and detection p-values. No preprocessing steps have been performed.

Author(s)

Michael Scherer

sites	<i>Names of the sites</i>
-------	---------------------------

Description

This a a list of all sites available for the annotation.

Usage

```
sites
```

Format

list of NULLs; the names of the elements correspond to the site and probe annotation tables.

Author(s)

Michael Scherer

Index

* datasets

hg19, [2](#)

regions, [2](#)

rnb.set.example, [3](#)

sites, [3](#)

hg19, [2](#)

regions, [2](#)

rnb.annotation.size, [2](#)

rnb.get.annotation, [2](#)

rnb.get.assemblies, [2](#)

rnb.get.chromosomes, [2](#)

rnb.get.mapping, [2](#)

rnb.set.annotation, [2](#)

rnb.set.example, [3](#)

sites, [3](#)