Package ‘RnBeads.hg19’

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Title RnBeads.hg19

Description Automatically generated RnBeads annotation package for the assembly hg19.

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License GPL-3

Version 1.16.0

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_9

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R topics documented:

`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 `NULL`s; 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 `NULL`s; the names of the elements correspond to the site and probe annotation tables.

`"controls"` `list` of `NULL`s; 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 `NULL`s; the names of the elements correspond to the built-in region annotation tables.

Author(s)

Yassen Assenov

`regions` *Names of the regions*

Description

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

Usage

```
regions
```

Format

`list` of `NULL`s; 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` *Example Data Set*

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` *Names of the sites*

Description

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

Usage

```
sites
```

Format

`list` of `NULL`s; the names of the elements correspond to the site and probe annotation tables.

Author(s)

Michael Scherer

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