Package ‘RnBeads.hg19’

September 30, 2015

Title RnBeads.hg19

Description Annotation tables and mappings for hg19 used by RnBeads

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Version 1.0.0

Depends R (>= 2.15), GenomicRanges

Suggests RnBeads (>= 0.99.0), BSgenome.Hsapiens.UCSC.hg19,

License GPL-3

biocViews Homo_sapiens

NeedsCompilation no

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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)

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