Package ‘CopyhelpeR’

Type Package
Title Helper files for CopywriteR
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Depends R(>= 2.10)
Suggests BiocStyle
Description This package contains the helper files that are required to run the Bioconductor package CopywriteR. It contains pre-assembled 1kb bin GC-content and mappability files for the reference genomes hg18, hg19, hg38, mm9 and mm10. In addition, it contains a blacklist filter to remove regions that display CNV. Files are stored as GRanges objects from the GenomicRanges Bioconductor package.
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biocViews Homo_sapiens, GenomicSequence
NeedsCompilation no

R topics documented:

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getPathHelperFiles          CopyhelpeR: Helper files for CopywriteR

Description

This package contains the helper files that are required to run the CopywriteR R package (see https://github.com/PeeperLab/CopywriteR/releases). It contains pre-assembled 1kb bin GC-content and mappability files for the reference genomes hg18, hg19, hg38, mm9 and mm10. In addition, it contains a blacklist filter to remove regions that display CNV. Files are stored as GRanges objects from the GenomicRanges Bioconductor package.
**getPathHelperFiles**

**Usage**

`getPathHelperFiles(ref.genome)`

**Arguments**

- `ref.genome` - the reference genome for which the helper files are required.

**Details**

The `getPathHelperFiles()` function returns the full path to the helper files folder for the relevant reference genomes ("hg18", "hg19", "hg38", "mm9" or "mm10").

**Value**

Returns the full path to the helper files folder for the relevant reference genomes ("hg18", "hg19", "hg38", "mm9" or "mm10").

**Author(s)**

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**Examples**

`getPathHelperFiles("hg19")`
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