Package ‘CopyhelpeR’

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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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getPathHelperFiles

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.

Usage

getAddressHelperFiles(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").

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Examples

getAddressHelperFiles("hg19")
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