Package 'CopyhelpeR'

July 10, 2025

Type Package

Title Helper files for CopywriteR

Version 1.41.0

Date 2021-11-21

Author Thomas Kuilman

Maintainer Oscar Krijgsman <o.krijgsman@nki.nl>

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.

License GPL-2

biocViews Homo_sapiens, GenomicSequence

git_url https://git.bioconductor.org/packages/CopyhelpeR

git_branch devel

git_last_commit 683ab81

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-10

Contents

---

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.

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)

Thomas Kuilman (t.kuilman@nki.nl)

Examples

```
getPathHelperFiles("hg19")
```

Index