# Package 'CopyhelpeR'

April 24, 2025

**Type** Package

**Title** Helper files for CopywriteR

**Version** 1.40.0

**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** RELEASE_3_21

**git_last_commit** 881df90

**git_last_commit_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-04-24

## Contents

getPathHelperFiles . . . . . 2

**Index** **3**

`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

CopyhelpeR *(*getPathHelperFiles*)*, 2

getPathHelperFiles, 2