

# Package ‘CopyhelperR’

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**Type** Package

**Title** Helper files for CopywriteR

**Version** 1.18.0

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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.

**License** GPL-2

**biocViews** Homo\_sapiens, GenomicSequence

**git\_url** <https://git.bioconductor.org/packages/CopyhelperR>

**git\_branch** RELEASE\_3\_10

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getPathHelperFiles      *CopyhelpR: Helper files for CopywriteR*

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### 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)

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### Examples

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

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