

Package: CopyhelpeR (via r-universe)

October 10, 2026

Type Package

Title Helper files for CopywriteR

Version 1.44.0

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

Repository Bioconductor 3.23

Date/Publication 2026-04-28 12:28:08 UTC

RemoteUrl <https://github.com/bioc/CopyhelpeR>

RemoteRef RELEASE_3_23

RemoteSha 94415d0742a6dfbe01c20935519f65cbdd05d1d0

Contents

getPathHelperFiles	2
Index	3

getPathHelperFiles	<i>CopyhelpR: Helper files for CopywriteR</i>
--------------------	---

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

CopyhelperR (getPathHelperFiles), [2](#)

getPathHelperFiles, [2](#)