Package 'WGSmapp'

February 20, 2025

Type Package

Title Mappability tracks of Whole-genome Sequencing from the ENCODE Project

Version 1.18.0

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Description

This package provides whole-genome mappability tracks on human hg19/hg38 assembly. We employed the 100-mers mappability track from the ENCODE Project and computed weighted average of the mappability scores if multiple ENCODE regions overlap with the same bin. "Blacklist" bins, including segmental duplication regions and gaps in reference assembly from telomere, centromere, and/or heterochromatin regions are included. The dataset consists of three assembled .bam files of single-cell whole genome sequencing from 10X for illustration purposes.

Depends R (>= 3.6.0), GenomicRanges

License GPL-2

biocViews ExperimentData, SequencingData, DNASeqData, SingleCellData, Homo_sapiens_Data, Genome, ENCODE

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

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

git_branch RELEASE_3_20

git_last_commit 95d2dc5

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-02-20

Contents

mapp_hg19 *GRanges with mappability scores for hg19*

Description

GRanges of mappability track for 100-mers on the GRCh37/hg19 human reference genome from ENCODE.

Usage

```
mapp_hg19
```

Format

A GRanges object with 21591667 ranges and mappability scores

mapp_hg38 *GRanges with mappability scores for hg38*

Description

Use liftOver utility to convert hg19 coordinates to hg38

Usage

```
mapp_hg38
```

Format

A GRanges object with 21584930 ranges and mappability scores

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