

Package: liftOver (via r-universe)

October 11, 2026

Title Changing genomic coordinate systems with rtracklayer::liftOver

Version 1.37.0

Date 2017-09-05

Description The liftOver facilities developed in conjunction with the UCSC browser track infrastructure are available for transforming data in GRanges formats. This is illustrated here with an image of the EBI/NHGRI GWAS catalog that is, as of May 10 2017, distributed with coordinates defined by NCBI build hg38.

Depends R (>= 3.3.0), gwascat, GenomeInfoDb, GenomicRanges, rtracklayer, Homo.sapiens, BiocGenerics

License Artistic-2.0

Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews Workflow, BasicWorkflow

Suggests knitr, rmarkdown, BiocStyle

NeedsCompilation no

URL <https://www.bioconductor.org/help/workflows/liftOver/>

RoxygenNote 7.3.2

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

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

RemoteRef HEAD

RemoteSha 1d1315664c5eeca3732929b426faeb983685aa8