Package: OHCA (via r-universe)

May 28, 2026

Title Orchestrating Hi-C analysis with Bioconductor

Version 1.9.0

Date 2023-04-14

Description The primary aim of this book is to introduce the R user to Hi-C analysis. This book starts with key concepts important for the analysis of chromatin conformation capture and then presents Bioconductor tools that can be leveraged to process, analyze, explore and visualize Hi-C data.

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URL https://github.com/js2264/OHCA

BugReports https://github.com/js2264/OHCA/issues

Depends R (>= 4.4),

Imports HiCExperiment, HiCool, HiContacts, HiContactsData, DNAZooData, fourDNData, plyinteractions, GenomicInteractions, terra, Rfast, WGCNA, diffHic, strawr, multiHiCcompare, TopDom, GOTHiC, BSgenome.Hsapiens.UCSC.hg38, ggbio, cowplot, patchwork, fs, knitr, BiocStyle, sessioninfo

biocViews HiC, DNA3DStructure, FunctionalGenomics

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

BiocType Book

VignetteBuilder knitr

LazyData false

Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev libgdal-dev gdal-bin libgeos-dev libglpk-dev make libharfbuzz-dev libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev libproj-dev python3 libsqlite3-dev libx11-dev xz-utils zlib1g-dev

Repository https://tempbioc.r-universe.dev

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RemoteUrl https://github.com/bioc/OHCA

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RemoteSha 6b215aa360fcfa925fb096b652a2f2752551a531