Package: OHCA (via r-universe)

October 7, 2026

Title Orchestrating Hi-C analysis with Bioconductor

Version 1.9.2

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, HiContacts, HiContactsData, DNAZooData, fourDNData, plyinteractions, GenomicInteractions, WGCNA, diffHic, strawr, TopDom, GOTHiC, BSgenome.Hsapiens.UCSC.hg38, cowplot, curl, fs, knitr, BiocStyle, sessioninfo

Suggests BiocBook (>= 1.11.2), reticulate, multiHiCcompare, terra, ggbio, patchwork, HiCool

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 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 libx11-dev xz-utils zlib1g-dev

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

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

RemoteRef HEAD

RemoteSha 8ef6242d336e8c8875f4afb2164b47c4d0fbcea4