Package: savingBiocObjects (via r-universe)

November 25, 2026

Title Saving Bioconductor Objects for Sharing

Version 1.0.0

Description Documentation and guidance on strategies for saving and sharing Bioconductor objects, covering RDS serialization, HDF5-backed storage, the alabaster ecosystem for cross-language interoperability, exporting genomic ranges to standard formats, and preserving object metadata.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

BiocType Workflow

biocViews BasicWorkflow

Suggests SummarizedExperiment, SingleCellExperiment, GenomicRanges, HDF5Array, anndataR, alabaster.base, alabaster.se, rtracklayer, plyranges, jsonlite, BiocManager, knitr, quarto

SystemRequirements Quarto (https://quarto.org)

VignetteBuilder quarto

URL https://mikelove.github.io/savingBiocObjects, https://bioconductor.org/packages/savingBiocObjects/

BugReports https://github.com/mikelove/savingBiocObjects/issues

Config/roxygen2/version 8.0.0

Repository Bioconductor 3.24

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