Package: StashSpectra (via r-universe)

June 3, 2026

Title Serialize and restore Spectra objects in interoperable file formats

Version 0.97.0

Description The serialization mechanism of R allows to save and load R data objects in a binary format, that can however not be read by other programming languages or software. The StashSpectra package implements the serialization methods from the MsStash package for Spectra objects and its MsBackend classes. A variety of different file formats and types, including HDF5 and JSON-based formats defined by the Bioconductor *alabaster* package are supported. The file type can be defined and configured through a second argument `param` of the save/read methods.

Depends R (>= 4.6.0)

Imports methods, MsStash

Suggests BiocStyle, alabaster.base, testthat

License Artistic-2.0

Encoding UTF-8

VignetteBuilder knitr

BugReports `https://github.com/RforMassSpectrometry/StashSpectra/issues`

URL `https://github.com/RforMassSpectrometry/StashSpectra`

biocViews Infrastructure, MassSpectrometry, Metabolomics, DataImport, Proteomics

Roxygen list(markdown=TRUE)

RoxygenNote 7.3.3

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

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RemoteUrl https://github.com/rformassspectrometry/StashSpectra

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