Package: Metabonaut (via r-universe)

May 25, 2026

Title Exploring and Analyzing LC-MS Data

Version 1.5.0

Description This resource hosts tutorials and end-to-end workflows describing how to analyze LC-MS/MS data, from raw files to annotation, using Bioconductor packages.

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Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

Depends R (>= 4.5), BiocParallel (>= 1.8.0)

Suggests alabaster.se, missForest, MsCoreUtils, xcms (>= 4.3.4), Spectra (>= 1.11.10), MsExperiment, MsIO (>= 0.0.8), SpectriPy (>= 1.1.0), MsBackendMetaboLights, ggVennDiagram, UpSetR, readxl, limma, matrixStats, pander, ggfortify, gridExtra, AnnotationHub, CompoundDb, MetaboAnnotation, vioplot, MetaboCoreUtils, BiocStyle, rmarkdown, RColorBrewer, SummarizedExperiment, pheatmap, knitr, reticulate, quarto, MsBackendMgf, notame, notameStats, notameViz, stringr, RSQLite, MsBackendMassbank (>= 1.18.1), RuSirius, zen4R

Remotes RforMassSpectrometry/MsIO, RforMassSpectrometry/RuSirius, sirius-ms/sirius-client-openAPI/client-api_r/generated@2c983e6

URL `https://github.com/rformassspectrometry/Metabonaut/`, `https://rformassspectrometry.github.io/Metabonaut/`

BugReports `https://github.com/rformassspectrometry/Metabonaut/issues/new`

BiocType Workflow

RoxygenNote 7.3.3

VignetteBuilder quarto, knitr

SystemRequirements pandoc, python (>= 3.10), quarto

Config/pak/sysreqs python3

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

Date/Publication 2026-03-17 15:13:14 UTC

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

RemoteRef HEAD

RemoteSha 35a1a9b99fb9434348ae7c1e05ea801d754a16db

Contents

`Metabonaut` *Learning to analysis LC-MS/MS data*

Description

This resource hosts tutorials and end-to-end workflows describing how to analyze LC-MS/MS data, from raw files to annotation, using Bioconductor packages.

THe tutorials are rendered and can be found on this page Metabonaut For more information you can find the source code here

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