Package: rawDiag (via r-universe)

May 30, 2026

Type Package

Title Brings Orbitrap Mass Spectrometry Data to Life; Fast and Colorful

Version 1.8.0

Depends R (>= 4.4)

Imports dplyr, ggplot2 (>= 3.4), grDevices, hexbin, htmltools, BiocManager, BiocParallel, rawrr (>= 1.15.5), rlang, reshape2, scales, shiny (>= 1.5), stats, utils

Suggests BiocStyle (>= 2.28), ExperimentHub, tartare, knitr, testthat

Description Optimizing methods for liquid chromatography coupled to mass spectrometry (LC-MS) poses a nontrivial challenge. The rawDiag package facilitates rational method optimization by generating MS operator-tailored diagnostic plots of scan-level metadata. The package is designed for use on the R shell or as a Shiny application on the Orbitrap instrument PC.

License GPL-3

URL https://github.com/fgcz/rawDiag/

BugReports https://github.com/fgcz/rawDiag/issues

Encoding UTF-8

NeedsCompilation no

RoxygenNote 7.3.2

VignetteBuilder knitr

biocViews MassSpectrometry, Proteomics, Metabolomics, Infrastructure, Software, ShinyApps

Config/pak/sysreqs cmake make libicu-dev libuv1-dev zlib1g-dev

Repository https://bioc-release.r-universe.dev

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

RemoteRef RELEASE_3_23

RemoteSha 2d83a3def6b7e5d650bcd036fdb27be0b8d0925c

Contents

`.calculatioMasterScan` *Calculate Master Scan Number*

Description

calculates the MS1 master scan number of an MS2 scan and populates the MasterScanNumber with it

Usage

```
.calculatioMasterScan(x)
```

Arguments

`x`	a `data.frame` object adhering to the specified criteria for the `is.rawDiag` function.

Value

a `data.frame` containing a `MasterScanNumber` column.

Author(s)

Christian Trachsel

.cycleTime *Calculate MS Cycle Time*

Description

calculates the lock mass deviations along RT.

Usage

```
.cycleTime(x)
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.

Value

calculates the time of all ms cycles and the 95 the cycle time is defined as the time between two consecutive MS1 scans

Note

TODO: quantile part needed? If no MS1 scan is present? E.g., DIA take lowest window as cycle indicator?

Author(s)

Christian Trachsel (2017), Christian Panse (20231201) refactored

.fillNAgaps *Fill NA values with last previous value*

Description

Fill NA values with last previous value

Usage

```
.fillNAgaps(x)
```

Arguments

x	a vector of values

Value

a vector with any NA values replaced with the last previous actuall value

Author(s)

Christian Trachsel

Examples

```
c(NA, 1, 2, 3, NA, 4, 5, NA, NA, NA, 6) |>
  rawDiag:::.fillNAgaps()
```

`buildRawDiagShinyApp` *Build the rawDiag shiny application*

Description

Build the rawDiag shiny application

Usage

```
buildRawDiagShinyApp(rawDir = (dirname(rawrr::sampleFilePath())))
```

Arguments

`rawDir`	A directory containing the input raw files, default is set to the `$HOME/Downloads` directory.

Value

returns the rawDiag shiny apps

Note

launch the shiny application by embracing your command line while expecting the raw file in `$HOME/Downloads`

- MacOSX and Linux: `R -q -e "library(rawDiag); buildRawDiagShinyApp() |> shiny::runApp(launch.browse`
- Microsoft Windows: `R.exe -e "library(rawDiag); buildRawDiagShinyApp() |> shiny::runApp(launch.brows`

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |>
  dirname() |>
  rawDiag::buildRawDiagShinyApp() |>
  shiny::runApp()

 # or use your 'Download' folder
 (Sys.getenv('HOME') |>
   file.path("Downloads")) |>
   rawDiag::buildRawDiagShinyApp() |>
   shiny::runApp()
```

`checkRawrr` *Checks Bioconductor installation instructions*

Description

Checks Bioconductor installation instructions

Usage

```
checkRawrr()
```

Value

TRUE if everything is installed correctly

`is.rawDiag` *Is an Object an rawDiag Object?*

Description

Is an Object an rawDiag Object?

Usage

```
is.rawDiag(object)
```

Arguments

`object`	any R object.

Value

a boolean

Author(s)

Christian Panse 2018

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() |> rawDiag::is.rawDiag()
```

`plotChargeState` *Charge State Overview Plot*

Description

graphs the number of occurrences of all selected precursor charge states.

Usage

```
plotChargeState(x, method = "trellis")
```

Arguments

`x`	a `data.frame` object adhering to the specified criteria for the `is.rawDiag` function.
`method`	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a `ggplot` object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() -> S
S |> rawDiag::plotLockMassCorrection()
```

plotCycleLoad *Cycle Load Plot*

Description

plotting the number of MS2 per MS1 (the duty cycle) scan versus retention time. The deepskyblue colored loess curve shows the trend.

Usage

```
plotCycleLoad(x, method = "trellis")
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() -> S

S |> rawDiag::plotCycleLoad()
```

plotCycleTime *Plot Cycle Time*

Description

graphs the time difference between two consecutive MS1 scans (cycle time) with respect to RT (scatter plots) or its density (violin). A smooth curve graphs the trend. The 95th percentile is indicated by a red dashed line.

Usage

```
plotCycleTime(x, method = "trellis")
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot object.

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() |> rawDiag::plotCycleTime()
```

plotInjectionTime *Plot Injection Time*

Description

shows the injection time density of each mass spectrometry file as a violin plot. The higher the maximum number of MS2 scans is in the method, the more the density is shifted towards the maximum injection time value.

Usage

```
plotInjectionTime(x, method = "trellis")
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() |> rawDiag::plotInjectionTime()
```

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plotLockMassCorrection

Lock Mass Correction Plot

Description

Lock Mass Correction Plot

Usage

```
plotLockMassCorrection(x, method = "trellis")
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |>
  rawDiag::readRaw() |>
  rawDiag::plotLockMassCorrection()
```

`plotMassDistribution` *Mass Distribution Plot*

Description

plots the mass frequency in dependency to the charge state

Usage

```
plotMassDistribution(x, method = "trellis")
```

Arguments

`x`	a `data.frame` object adhering to the specified criteria for the `is.rawDiag` function.
`method`	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Details

displays charge state resolved frequency of precursor masses.

Value

a `ggplot` object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() |> rawDiag::plotMassDistribution('overlay')
```

plotMzDistribution *mZ Distribution Plot of Ms2 Scans*

Description

draws precursor mass vs retention time for each MS2 scan in the raw file.

Usage

```
plotMzDistribution(x, method = "trellis")
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() -> S
rawDiag::plotMzDistribution(S)
```

plotPrecursorHeatmap *Precursor Mass versus StartTime MS2 based hexagons*

Description

Precursor Mass versus StartTime MS2 based hexagons

Usage

```
plotPrecursorHeatmap(x, method = "overlay", bins = 80)
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.
bins	number of bins in both vertical and horizontal directions. default is 80.

Value

a ggplot object.

Note

TODO: define bin with dynamically as h= 2x IQR x n e-1/3 or number of bins (max-min)/h

Author(s)

Christian Trachsel (2017)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() |> rawDiag::plotPrecursorHeatmap()
```

---

plotScanTime *Scan Event Plot*

Description

Plotting the elapsed scan time for each individual scan event.

Usage

```
plotScanTime(x, method = "trellis")
```

Arguments

x	a data.frame object adhering to the specified criteria for the is.rawDiag function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot object.

Author(s)

Christian Trachsel (2017), Christian Panse (2023)

References

- rawDiag: doi:10.1021/acs.jproteome.8b00173,
- rawrr: doi:10.1021/acs.jproteome.0c00866

Examples

```
## for debugging bioconductor check
 if (Sys.info()['sysname'] %in% c("Darwin", "Linux")) {Sys.which('mono')}
 rawrr::sampleFilePath() |> rawDiag::readRaw() -> S

rawDiag::checkRawrr()

S |> rawDiag::plotScanTime()
```

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plotTicBasepeak *Total Ion Count and Base Peak Plot*

Description

displays the Total Ion Count (TIC) and the Base Peak Chromatogram of a mass spectrometry measurement. Multiple files are handled by faceting based on rawfile name.

Usage

```
plotTicBasepeak(x, method = "trellis")
```

Arguments

x	a `data.frame` object adhering to the specified criteria for the `is.rawDiag` function.
method	specifying the plot method 'trellis' | 'violin' | 'overlay'. The default is 'trellis'.

Value

a ggplot2 object for graphing the TIC and the Base Peak chromatogram.

Author(s)

Christian Trachsel (2017), Christian Panse (20231130) refactored

Examples

```
rawrr::sampleFilePath() |> rawDiag::readRaw() |> rawDiag::plotTicBasepeak()
```

rawDiagServer *rawDiag shiny module*

Description

rawDiag shiny module

Usage

```
rawDiagServer(id, vals)
```

Arguments

id	An ID string that corresponds with the ID used to call the module's UI function.
vals	containing rawfile

Value

rawDiag shiny module server

Examples

```
shiny::shiny(rawDir = (rawrr::sampleFilePath() |> dirname()))
```

rawDiagUI *rawDiag shiny module UI*

Description

rawDiag shiny module UI

Usage

```
rawDiagUI(id)
```

Arguments

id	An ID string that corresponds with the ID used to call the module's UI function.

Value

a shiny UI module

rawDiag shiny module UI

Examples

```
rawDiag::shiny(rawDir = (rawrr::sampleFilePath() |> dirname()))
```

`readRaw` *Reads selected raw file trailer information for rawDiag plot functions*

Description

implements a wrapper function using the rawrr methods `readIndex`, `readTrailer`, and `readChromatogram` to read proprietary mass spectrometer generated data using third-party libraries.

Usage

```
readRaw(
  rawfile,
  msgFUN = function(x) {
     message(x)
 }
)
```

Arguments

`rawfile`	the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.
`msgFUN`	this function is used for logging information while composing the resulting data.frame. It can also be used for shiny progress bar. The default is using the `message`.

Value

a `data.frame` containing the selected trailer information.

Note

The set up procedure for the rawrr package needs to be run in order to use this package.

Author(s)

Christian Panse (2016-2023)

References

doi:10.1021/acs.jproteome.8b00173

Examples

```
rawDiag::checkRawrr()
rawrr::sampleFilePath() |>
  rawDiag::readRaw()
```

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