Package 'rawDiag'

September 26, 2024

Type Package

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

Version 1.0.0

Depends R (>= 4.3)

Imports dplyr, ggplot2 (>= 3.4), grDevices, hexbin, htmltools, BiocManager, BiocParallel, rawrr (>= 1.10), 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 7.3.1

VignetteBuilder knitr

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

SystemRequirements mono 4.x or higher on OSX / Linux, .NET 4.x or higher on Windows, 'msbuild' and 'nuget' available in the path

git_url https://git.bioconductor.org/packages/rawDiag

git_branch RELEASE_3_19

git_last_commit 4b0e5b5

git_last_commit_date 2024-04-30

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Maintainer Christian Panse <cp@fgcz.ethz.ch>

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rawDiag-package	*rawDiag: Brings Orbitrap Mass Spectrometry Data to Life; Fast and Colorful*

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.

Author(s)

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Authors:

- Christian Trachsel <Christian.Trachsel@fgcz.ethz.ch>
- Tobias Kockmann <Tobias.Kockmann@fgcz.ethz.ch>

See Also

Useful links:

- https://github.com/fgcz/rawDiag/
- Report bugs at https://github.com/cpanse/rawDiag/issues

.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` func-
                        tion.

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 func-
            tion.

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](https://doi.org/10.1021/acs.jproteome.8b00173),
- rawrr: [doi:10.1021/acs.jproteome.0c00866](https://doi.org/10.1021/acs.jproteome.0c00866)

Examples

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

S|>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|> 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() |> readRaw() |> 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() |> readRaw() |> plotInjectionTime()
```

---

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() |>
  readRaw() |>
  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](https://doi.org/10.1021/acs.jproteome.8b00173),
- rawrr: [doi:10.1021/acs.jproteome.0c00866](https://doi.org/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 func-
            tion.

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](https://doi.org/10.1021/acs.jproteome.8b00173),
- rawrr: [doi:10.1021/acs.jproteome.0c00866](https://doi.org/10.1021/acs.jproteome.0c00866)

Examples

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

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

S|> plotScanTime()
```

---

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() |> readRaw() |> 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

```
rawDiag::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

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

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