

# Package ‘rawrr’

December 9, 2023

**Type** Package

**Title** Direct Access to Orbitrap Data and Beyond

**Version** 1.10.2

**Depends** R (>= 4.1)

**Imports** grDevices, graphics, stats, utils

**Suggests** BiocStyle (>= 2.5), ExperimentHub, knitr, protViz (>= 0.7),  
rmarkdown, tartare (>= 1.5), testthat

**Description** This package wraps the functionality of the RawFileReader .NET assembly. Within the R environment, spectra and chromatograms are represented by S3 objects. The package provides basic functions to download and install the required third-party libraries. The package is developed, tested, and used at the Functional Genomics Center Zurich, Switzerland.

**License** GPL-3

**SystemRequirements** mono-runtime 4.x or higher (including System.Data library) on Linux/macOS, .Net Framework (>= 4.5.1) on Microsoft Windows.

**URL** <https://github.com/fgcz/rawrr/>

**BugReports** <https://github.com/fgcz/rawrr/issues>

**Encoding** UTF-8

**NeedsCompilation** no

**RoxygenNote** 7.2.3

**biocViews** MassSpectrometry, Proteomics, Metabolomics

**VignetteBuilder** knitr

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**Author** Christian Panse [aut, cre] (<<https://orcid.org/0000-0003-1975-3064>>),  
Tobias Kockmann [aut] (<<https://orcid.org/0000-0002-1847-885X>>)

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

## R topics documented:

.checkDllInMonoPath . . . . .	3
.thermofisherIsmsUrl . . . . .	3
auc.rawrrChromatogram . . . . .	4
basePeak . . . . .	4
buildRawrrExe . . . . .	5
dependentScan . . . . .	6
faimsVoltageOn . . . . .	6
filter . . . . .	7
installRawFileReaderDLLs . . . . .	7
installRawrrExe . . . . .	9
is.rawrrChromatogram . . . . .	10
is.rawrrSpectrum . . . . .	10
is.rawrrSpectrumSet . . . . .	11
makeAccessor . . . . .	11
massRange . . . . .	12
masterScan . . . . .	13
new_rawrrSpectrum . . . . .	13
plot.rawrrChromatogram . . . . .	14
plot.rawrrChromatogramSet . . . . .	15
plot.rawrrSpectrum . . . . .	15
print.rawrrSpectrum . . . . .	16
rawrrAssemblyPath . . . . .	17
rawrrSpectrum . . . . .	18
readChromatogram . . . . .	18
readFileHeader . . . . .	20
readIndex . . . . .	21
readSpectrum . . . . .	22
readTrailer . . . . .	25
sampleFilePath . . . . .	25
scanNumber . . . . .	26
summary.rawrrChromatogram . . . . .	27
summary.rawrrSpectrum . . . . .	27
tic . . . . .	28
validate_rawrrIndex . . . . .	29
validate_rawrrSpectrum . . . . .	29

**Index**

**31**

---

*.checkDllInMonoPath*    *Check if a file is contained in the environment variable MONO\_PATH.*

---

**Description**

Check if a file is contained in the environment variable MONO\_PATH.

**Usage**

```
.checkDllInMonoPath(dll = "ThermoFisher.CommonCore.Data.dll")
```

**Arguments**

dll                    a file name.

**Value**

a boolean

---

*.thermofisher1smsUrl*    *URL for Thermo Fisher .NET assemblies*

---

**Description**

URL for Thermo Fisher .NET assemblies

**Usage**

```
.thermofisher1smsUrl()
```

**Value**

an URL

auc.rawrrChromatogram *deriving area under the curve (AUC)*

---

**Description**

deriving area under the curve (AUC)

**Usage**

```
auc.rawrrChromatogram(x)
```

**Arguments**

x                    an rawrrChromatogram object contains x\$times and x\$intensities. x\$times is assumed to be in minutes.

**Value**

A numeric value.

---

basePeak            *Base peak of a spectrum*

---

**Description**

Base peak of a spectrum

**Usage**

```
basePeak(x)
```

**Arguments**

x                    A rawrrSpectrum object

**Value**

A double vector of length two. The first component is the base peak position (m/z). The second component is the base peak intensity.

**Examples**

```
S <- readSpectrum(rawfile = sampleFilePath(), 1)
basePeak(S[[1]])
```

---

buildRawrrExe	<i>Build rawrr.exe console application.</i>
---------------	---

---

### Description

builds rawrr.exe file from C# source code requiring xbuild or msbuild tools. The console application rawrr.exe is used by the package's reader functions through a [system2](#) call.

### Usage

```
buildRawrrExe()
```

### Details

The rawrr package implementation consists of two language layers, the top R layer and the hidden C# layer. Specifically, R functions requesting access to data stored in binary raw files invoke compiled C# wrapper methods using a [system2](#) call. Calling a wrapper method typically results in the execution of methods defined in the RawFileReader dynamic link library provided by Thermo Fisher Scientific. Our precompiled wrapper methods are bundled in the rawrr.exe executable file (.NET assembly) and shipped with the released R package. Running rawrr.exe requires the <https://www.mono-project.com/> environment on non-Microsoft operating systems. Mono is a cross platform, open source .NET framework. On Microsoft Windows the Microsoft .NET framework is typically already installed and sufficient. Our package also contains the C# source code rawrr.cs. In order to return extracted data back to the R layer we use file I/O. More specifically, the extracted information is written to a temporary location on the harddrive, read back into memory and parsed into R objects.

### Value

the return value of the system2 command.

### Author(s)

Tobias Kockmann, Christian Panse <cp@fgcz.ethz.ch>, 2021

### References

- <https://www.mono-project.com/docs/advanced/assemblies-and-the-gac/>
- <https://planetorbitrap.com/rawfilereader>
- <https://docs.microsoft.com/en-us/dotnet/csharp/language-reference/compiler-options/advanced>
- [doi:10.1021/acs.jproteome.0c00866](https://doi.org/10.1021/acs.jproteome.0c00866)

### See Also

[installRawrrExe](#) and [installRawFileReaderDLLs](#)

---

dependentScan	<i>Retrieve dependent scan(s) of a scan listed in scan index</i>
---------------	--

---

**Description**

Retrieve dependent scan(s) of a scan listed in scan index

**Usage**

```
dependentScan(x, scanNumber)
```

**Arguments**

x	A scan index returned by readIndex.
scanNumber	The scan number that should be inspected for dependent scans.

**Value**

The scan number of the dependent scan(s).

**Examples**

```
Idx <- readIndex(rawfile = sampleFilePath())  
dependentScan(Idx, scanNumber = 1)
```

---

faimsVoltageOn	<i>Is FAIMS Voltage on?</i>
----------------	-----------------------------

---

**Description**

Is FAIMS Voltage on?

**Usage**

```
faimsVoltageOn(x)
```

**Arguments**

x	A rawrrSpectrum object
---	------------------------

**Value**

A boolean

**Examples**

```
S <- readSpectrum(rawfile = sampleFilePath(), 1:10)  
try(faimsVoltageOn(S[[1]]))
```

---

filter	<i>derive scans number which match a specified filter</i>
--------	---

---

**Description**

derive scans number which match a specified filter

**Usage**

```
filter(rawfile, filter = "ms", precision = 10, tmpdir = tmpdir())
```

**Arguments**

rawfile	the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.
filter	scan filter string, e.g., ms or ms2
precision	mass precision, default is 10.
tmpdir	defines the directory used to store temporary data generated by the .NET assembly rawrr.exe. The default uses the output of tmpdir().

**Value**

a vector of integer values.

---

installRawFileReaderDLLs

*Download and install the New RawFileReader from Thermo Fisher Scientific .Net assemblies i*

---

**Description**

Download and install the New RawFileReader from Thermo Fisher Scientific .Net assemblies in the directory provided by rawrrAssemblyPath().

**Usage**

```
installRawFileReaderDLLs(sourceUrl = .thermofisher1smsUrl(), ...)
```

**Arguments**

sourceUrl	url of New RawFileReader from Thermo Fisher Scientific assemblies.
...	other parameter for download.file

## Details

The console application assembly `rawrr.exe` requires three assemblies:

- `ThermoFisher.CommonCore.Data.dll`,
- `ThermoFisher.CommonCore.MassPrecisionEstimator.dll`, and
- `ThermoFisher.CommonCore.RawFileReader.dll`

The `rawrr.exe` assembly can be built from C# source code by using the `msbuild` tool shipped by the <https://www.mono-project.com> or by Microsoft's .NET SDK <https://dotnet.microsoft.com> on Linux, Microsoft, and macOS.

If no build tool and C# compiler (`csc` or `mcs`) are available or the build process fails, you can download `rawrr.exe` assembly from the authors' site.

## Value

An (invisible) vector of integer code, 0 for success and non-zero for failure. For the "wget" and "curl" methods this is the status code returned by the external program.

## Author(s)

Christian Panse <cp@fgcz.ethz.ch>, 2021

## References

- <https://www.mono-project.com/docs/advanced/assemblies-and-the-gac/>
- <https://planetorbitrap.com/rawfilereader>
- [doi:10.1021/acs.jproteome.0c00866](https://doi.org/10.1021/acs.jproteome.0c00866)

## See Also

[buildRawrrExe](#) and [installRawrrExe](#)

## Examples

```
# to install all assemblies

rawrr::installRawFileReaderDLLs()
rawrr::buildRawrrExe() || rawrr::installRawrrExe()
```



---

installRawrrExe	<i>Download and install the rawrr.exe console application</i>
-----------------	---

---

## Description

downloads and installs the rawrr.exe .Net assembly in the directory provided by rawrrAssemblyPath().

## Usage

```
installRawrrExe(  
    sourceUrl = "https://github.com/fgcz/rawrr/releases/download/1.9.2/rawrr.1.9.2.exe",  
    ...  
)
```

## Arguments

sourceUrl	url of rawrr.exe assembly.
...	other parameter for download.file.

## Details

The console application rawrr.exe is used by the package's reader functions through a [system2](#) call.

## Value

An integer code, 0 for success and non-zero for failure. For the "wget" and "curl" methods this is the status code returned by the external program.

## References

[doi:10.1021/acs.jproteome.0c00866](https://doi.org/10.1021/acs.jproteome.0c00866)

## See Also

[buildRawrrExe](#)

---

is.rawrrChromatogram *Function to check if an object is an instance of class rawrrChromatogram*

---

**Description**

Function to check if an object is an instance of class rawrrChromatogram

**Usage**

```
is.rawrrChromatogram(x)
```

**Arguments**

x                    x any R object to be tested.

**Value**

TRUE or FALSE

**Author(s)**

Tobias Kockmann, 2020.

**Examples**

```
rawfile <- sampleFilePath()
C <- readChromatogram(rawfile, mass = 445.1181, tol = 10)
is.rawrrChromatogram(C[[1]])
```

---

is.rawrrSpectrum        *Function to check if an object is an instance of class rawrrSpectrum*

---

**Description**

Function to check if an object is an instance of class rawrrSpectrum

**Usage**

```
is.rawrrSpectrum(x)
```

**Arguments**

x                    any R object to be tested.

**Value**

TRUE or FALSE

**Examples**

```
S <- rawrr::sampleFilePath() |> rawrr::readSpectrum(scan = 1:10)
rawrr::is.rawrrSpectrum(S[[1]])
```

---

is.rawrrSpectrumSet    *Function to check if an object is an instance of class rawrrSpectrumSet*

---

**Description**

Function to check if an object is an instance of class rawrrSpectrumSet

**Usage**

```
is.rawrrSpectrumSet(x)
```

**Arguments**

x                    any R object to be tested.

**Value**

TRUE or FALSE

**Examples**

```
rawrr::sampleFilePath() |>
  rawrr::readSpectrum(scan = 1:10) |>
  rawrr::is.rawrrSpectrumSet()
```

---

makeAccessor            *Make accessor function for key value pair returned by RawFileReader*

---

**Description**

Make accessor function for key value pair returned by RawFileReader

**Usage**

```
makeAccessor(key, returnType = "integer")
```

**Arguments**

key                    An object name found in instance of class rawrrSpectrum  
returnType            The type used for casting of values

**Details**

This function factory creates accessor functions for class rawrrSpectrum.

**Value**

An accessor function

**Author(s)**

Tobias Kockmann, 2020

**Examples**

```
S <- readSpectrum(rawfile = sampleFilePath(), 1:10)
maxIonTime <- makeAccessor(key = "Max. Ion Time (ms):", returnType = "double")
maxIonTime(S[[1]])
```

---

massRange

*Acquisition/scan range of spectrum*

---

**Description**

Acquisition/scan range of spectrum

**Usage**

```
massRange(x)
```

**Arguments**

x                    A rawrrSpectrum object

**Value**

A double vector of length two. The first component is the start m/z, the second is the stop m/z value used by the detector during data acquisition. Also referred to as scan range.

**Examples**

```
S <- readSpectrum(rawfile = sampleFilePath(), 1)
massRange(S[[1]])
```

---

masterScan	<i>Retrieve master scan of scan listed in scan index</i>
------------	--

---

**Description**

Retrieve master scan of scan listed in scan index

**Usage**

```
masterScan(x, scanNumber)
```

**Arguments**

x	A scan index returned by readIndex.
scanNumber	The scan number that should be inspected for the presence of a master scan.

**Value**

Returns the scan number of the master scan or NA if no master scan exists.

**Examples**

```
rawrr::sampleFilePath() |> rawrr::readIndex() |> rawrr::masterScan(scanNumber = 1)
```

---

new_rawrrSpectrum	<i>Create instances of class rawrrSpectrum</i>
-------------------	--

---

**Description**

Developer function.

**Usage**

```
new_rawrrSpectrum(  
  scan = numeric(),  
  massRange = numeric(),  
  scanType = character(),  
  StartTime = numeric(),  
  centroidStream = logical(),  
  mZ = numeric(),  
  intensity = numeric()  
)
```

**Arguments**

scan	scan number
massRange	Mass range covered by spectrum
scanType	Character string describing the scan type.
StartTime	Retention time in minutes
centroidStream	Logical indicating if centroided data is available
mZ	m/z values
intensity	Intensity values

**Value**

Object of class rawrrSpectrum

**Author(s)**

Tobias Kockmann, 2020.

---

plot.rawrrChromatogram

*Plot rawrrChromatogram objects*

---

**Description**

Plot rawrrChromatogram objects

**Usage**

```
## S3 method for class 'rawrrChromatogram'  
plot(x, legend = TRUE, ...)
```

**Arguments**

x	A rawrrChromatogram object to be plotted.
legend	Should legend be printed?
...	Passes additional arguments.

**Value**

This function creates a plot.

**Author(s)**

Tobias Kockmann, 2020.

**Examples**

```
rawfile <- sampleFilePath()
C <- readChromatogram(rawfile, mass = 445.1181, tol = 10)
plot(C[[1]])
```

---

plot.rawrrChromatogramSet

*Plot rawrrChromatogramSet objects*

---

**Description**

Plot rawrrChromatogramSet objects

**Usage**

```
## S3 method for class 'rawrrChromatogramSet'
plot(x, diagnostic = FALSE, ...)
```

**Arguments**

x	A rawrrChromatogramSet object to be plotted.
diagnostic	Show diagnostic legend?
...	Passes additional arguments.

**Value**

This function creates a plot.

**Author(s)**

Tobias Kockmann, 2020.

---

plot.rawrrSpectrum

*Basic plotting function for instances of rawrrSpectrum*

---

**Description**

Plot method for objects of class rawrrSpectrum.

**Usage**

```
## S3 method for class 'rawrrSpectrum'
plot(
  x,
  relative = TRUE,
  centroid = FALSE,
  SN = FALSE,
  legend = TRUE,
  diagnostic = FALSE,
  ...
)
```

**Arguments**

x	an object of class rawrrSpectrum.
relative	If set to TRUE enforces plotting of relative intensities rather than absolute.
centroid	Should centroided data be used for plotting?
SN	Should Signal/Noise be used for plotting?
legend	Should legend be printed?
diagnostic	Should this option be applied? The default is FALSE.
...	function passes arbitrary additional arguments.

**Details**

plot.rawrrSpectrum is a low level function that calls base::plot for plotting rawrrSpectrum objects. It passes all additional arguments to plot()

Is usually called by method dispatch.

**Value**

This function creates a plot.

**Author(s)**

Tobias Kockmann, 2020.

---

print.rawrrSpectrum *Print method imitate the look and feel of Thermo Fisher Scientific FreeStyle's output*

---

**Description**

Print method imitate the look and feel of Thermo Fisher Scientific FreeStyle's output



### Usage

```
## S3 method for class 'rawrrSpectrum'  
print(x, ...)
```

### Arguments

x                    an rawrrSpectrum object.  
...                  Arguments to be passed to methods.

### Value

This function creates a print message.

### Author(s)

Christian Panse and Tobias Kockmann, 2020.

---

rawrrAssemblyPath      *Derives the path where all .NET assemblies are stored.*

---

### Description

Derives the path where all .NET assemblies are stored.

### Usage

```
rawrrAssemblyPath()
```

### Value

path

### See Also

installRawFileReaderDLLs and installRawrrExe

### Examples

```
rawrrAssemblyPath()
```

---

rawrrSpectrum	<i>Create rawrrSpectrum objects</i>
---------------	-------------------------------------

---

**Description**

High-level constructor for instances of class `rawrrSpectrum`, also named helper function. Currently, mainly to support testing and for demonstration.

**Usage**

```
rawrrSpectrum(sim = "TESTPEPTIDE")
```

**Arguments**

`sim` Either `example_1` or `TESTPEPTIDE`

**Value**

Function returns a validated `rawrrSpectrum` object

**Author(s)**

Tobias Kockmann, 2020.

**Examples**

```
plot(rawrrSpectrum(sim = "TESTPEPTIDE"))
rawrrSpectrum(sim = "example_1")
```

---

readChromatogram	<i>Extracts chromatographic data from a raw file.</i>
------------------	---

---

**Description**

Extracts chromatographic data from a raw file.

**Usage**

```
readChromatogram(  
  rawfile,  
  mass = NULL,  
  tol = 10,  
  filter = "ms",  
  type = "xic",  
  tmpdir = tempdir()  
)
```

### Arguments

rawfile	the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.
mass	a vector of mass values iff type = 'xic'.
tol	mass tolerance in ppm iff type = 'xic'.
filter	defines the scan filter, default is filter="ms" if a wrong filter is set the function will return NULL and draws a warning.
type	c(xic, bpc, tic) for extracted ion , base peak or total ion chromatogram.
tmpdir	defines the directory used to store temporary data generated by the .NET assembly rawrr.exe. The default uses the output of tmpdir().

### Details

Chromatograms come in different flavors but are always signal intensity values as a function of time. Signal intensities can be point estimates from scanning detectors or plain intensities from non-scanning detectors, e.g., UV trace. Scanning detector (mass analyzers) point estimates can be defined in different ways by, for instance, summing all signals of a given spectrum (total ion chromatogram or TIC), or by extracting signal around an expected value (extracted ion chromatogram = XIC), or by using the maximum signal contained in a spectrum (base peak chromatogram = BPC). On top, chromatograms can be computed from pre-filtered lists of scans. A total ion chromatogram (TIC), for instance, is typically generated by iterating over all MS1-level scans.

### Value

chromatogram object(s) containing of a vector of times and a corresponding vector of intensities.

### Author(s)

Christian Trachsel, Tobias Kockmann and Christian Panse <cp@fgz.ethz.ch> 2018, 2019, 2020.

### References

Automated quality control sample 1 (autoQC01) analyzed across different Thermo Scientific mass spectrometers, [MSV000086542](#).

### See Also

- The Thermo Fisher Scientific RawFileReader C# code snippets <https://planetorbitrap.com/rawfilereader>.
- <https://CRAN.R-project.org/package=protViz>
- <https://massive.ucsd.edu/ProteoSAFe/dataset.jsp?accession=MSV000086542>

## Examples

```
# Example 1: not meaningful but proof-of-concept
(rawfile <- rawrr::sampleFilePath())

rawrr::readChromatogram(rawfile, mass=c(669.8381, 726.8357), tol=1000) |>
  plot()
rawrr::readChromatogram(rawfile, type='bpc') |> plot()
rawrr::readChromatogram(rawfile, type='tic') |> plot()

# Example 2: extract iRT peptides
if (require(ExperimentHub) & require(protViz)){
iRTpeptide <- c("LGGNEQVTR", "YILAGVENS", "GTFIIDPGGVIR", "GTFIIDPAAVIR",
  "GAGSSEPVTGLDAK", "TPVISGGPYEYR", "VEATFGVDESN",
  "TPVITGAPYEYR", "DGLDAASYAPVR", "ADVTPADFSEWSK",
  "LFLQFGAQGSPFLK")

# fetch via ExperimentHub
library(ExperimentHub)
eh <- ExperimentHub::ExperimentHub()
EH4547 <- normalizePath(eh[["EH4547"]])

(rawfile <- paste0(EH4547, ".raw"))
if (!file.exists(rawfile)){
  file.link(EH4547, rawfile)
}
op <- par(mfrow=c(2,1))
readChromatogram(rawfile, type='bpc') |> plot()
readChromatogram(rawfile, type='tic') |> plot()
par(op)

# derive [2H+] ions
((protViz::parentIonMass(iRTpeptide) + 1.008) / 2) |>
  readChromatogram(rawfile=rawfile) |>
  plot()
}
```

---

readFileHeader

*read file header Information*

---

## Description

This function extracts the meta information from a given raw file.

## Usage

```
readFileHeader(rawfile)
```

**Arguments**

rawfile            the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.

**Value**

A list object containing the following entries: RAW file version, Creation date, Operator, Number of instruments, Description, Instrument model, Instrument name, Serial number, Software version, Firmware version, Units, Mass resolution, Number of scans, Number of ms2 scans, Scan range, Time range, Mass range, Scan filter (first scan), Scan filter (last scan), Total number of filters, Sample name, Sample id, Sample type, Sample comment, Sample vial, Sample volume, Sample injection volume, Sample row number, Sample dilution factor, or Sample barcode.

**Author(s)**

Tobias Kockmann and Christian Panse 2018, 2019, 2020.

**References**

Thermo Fisher Scientific's NewRawfileReader C# code snippets <https://planetorbitrap.com/rawfilereader>.

**Examples**

```
rawrr::sampleFilePath() |> readFileHeader()
```

---

<code>readIndex</code>	<i>Read scan index</i>
------------------------	------------------------

---

**Description**

Read scan index

**Usage**

```
readIndex(rawfile, tmpdir = tmpdir())
```

**Arguments**

rawfile            the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.

tmpdir            defines the directory used to store temporary data generated by the .NET assembly rawrr.exe. The default uses the output of tmpdir().

**Value**

returns a data.frame with the column names scan, scanType, StartTime, precursorMass, MSOrder, charge, masterScan, and dependencyType of all spectra.

**Author(s)**

Tobias Kockmann and Christian Panse <cp@fgz.ethz.ch>, 2020, 2021

**Examples**

```
Idx <- rawrr::sampleFilePath() |> rawrr::readIndex()
table(Idx$scanType)
plot(Idx$StartTime, Idx$precursorMass, col=as.factor(Idx$charge), pch=16)

table(Idx$MSOrder)
```

---

readSpectrum

*Reads spectral data from a raw file.*

---

**Description**

The function derives spectra of a given raw file and a given vector of scan numbers.

**Usage**

```
readSpectrum(
  rawfile,
  scan = NULL,
  tmpdir = tmpdir(),
  validate = FALSE,
  mode = ""
)
```

**Arguments**

rawfile	the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.
scan	a vector of requested scan numbers.
tmpdir	defines the directory used to store temporary data generated by the .NET assembly rawrr.exe. The default uses the output of tmpdir().
validate	boolean default is FALSE.
mode	if mode = "barebone" only mZ (centroidStream.Masses), intensity (centroidStream.Intensities), pepmass, StartTime and charge state is returned. As default mode is "".

## Details

All mass spectra are recorded by scanning detectors (mass analyzers) that log signal intensities for ranges of mass to charge ratios ( $m/z$ ), also referred to as position. These recordings can be of continuous nature, so-called profile data (p), or appear centroided (c) in case discrete information (tuples of position and intensity values) are sufficient. This heavily compacted data structure is often called a peak list. In addition to signal intensities, a peak list can also cover additional peak attributes like peak resolution (R), charge (z), or local noise estimates. In short, the additional attributes further described the nature of the original profile signal or help to group peak lists with respect to their molecular nature or processing history. A well-known example is the assignment of peaks to peak groups that constitute isotope patterns (M, M+1, M+2, ...). The names of objects encapsulated within `rawrrSpectrum` instances are keys returned by the Thermo Fisher Scientific New RawFileReader API and the corresponding values become data parts of the objects, typically vectors.

## Value

a nested list of `rawrrSpectrum` objects containing more than 50 values of scan information, e.g., the charge state, two vectors containing the  $mZ$  and its corresponding intensity values or the AGC information, mass calibration, ion optics ...

## Author(s)

Tobias Kockmann and Christian Panse <cp@fgz.ethz.ch> 2018, 2019, 2020, 2021

## References

- C# code snippets of the NewRawfileReader library <https://planetorbitrap.com/rawfilereader>.
- rawrr: [doi:10.1021/acs.jproteome.0c00866](https://doi.org/10.1021/acs.jproteome.0c00866)
- Universal Spectrum Explorer: <https://www.proteomicsdb.org/use/doi:10.1021/acs.jproteome.1c00096>

## See Also

<https://massive.ucsd.edu/ProteoSAFe/dataset.jsp?accession=MSV000086542>

## Examples

```
# Example 1
S <- rawrr::sampleFilePath() |> rawrr::readSpectrum(scan = 1:9)

S[[1]]

names(S[[1]])

plot(S[[1]])

# Example 2 - find best peptide spectrum match using the |> pipe operator
# fetch via ExperimentHub
```

```

if (require(ExperimentHub) & require(protViz)){
  eh <- ExperimentHub::ExperimentHub()
  EH4547 <- normalizePath(eh[["EH4547"]])

  (rawfile <- paste0(EH4547, ".raw"))
  if (!file.exists(rawfile)){
    file.link(EH4547, rawfile)
  }

  GAG <- "GAGSSEPVTGLDAK"

  .bestPeptideSpectrumMatch <- function(rawfile,
    sequence="GAGSSEPVTGLDAK"){
    readIndex(rawfile) |>
      subset(abs((1.008 + (protViz::parentIonMass(sequence) - 1.008) / 2) -
        precursorMass) < 0.001, select = scan) |>
      unlist() |>
      readSpectrum(rawfile = rawfile) |>
      lapply(function(x) {
        y <- protViz::psm(sequence = GAG, spec=x, plot=FALSE);
        y$scan <- x$scan; y
      }) |>
      lapply(FUN= function(x){
        score <- sum(abs(x$mZ.Da.error) < 0.01);
        cbind(scan=x$scan, score=score)
      }) |>
      (function(x) as.data.frame(Reduce(rbind, x)))() |>
      subset(score > 0) |>
      (function(x) x[order(x$score, decreasing = TRUE),
        'scan'])() |>
      head(1)
  }

  start_time <- Sys.time()
  bestMatch <- .bestPeptideSpectrumMatch(rawfile, GAG) |>
    rawrr::readSpectrum(rawfile=rawfile) |>
    lapply(function(x) protViz::peakplot(peptideSequence = GAG, x))

  end_time <- Sys.time()
  end_time - start_time

  # Example 3
  # using proteomicsdb \doi{10.1101/2020.09.08.287557}
  # through https://www.proteomicsdb.org/use/

  .UniversalSpectrumExplorer <- function(x, sequence){
    m <- protViz::psm( sequence, x)
    cat(paste(x$mZ[m$idx], "\t", x$intensity[m$idx]), sep = "\n")
  }

  rawrr::readSpectrum(rawfile=rawfile, 11091) |>
    lapply(function(x).UniversalSpectrumExplorer(x, sequence = GAG))
}

```



---

readTrailer	<i>Read and extract scan trailer from TFS raw files.</i>
-------------	--

---

**Description**

Read and extract scan trailer from TFS raw files.

**Usage**

```
readTrailer(rawfile, label = NULL, tmpdir = tempdir(), verbose = FALSE)
```

**Arguments**

rawfile	the name of the raw file containing the mass spectrometry data from the Thermo Fisher Scientific instrument.
label	if NULL; the function scans for all available labels.
tmpdir	defines the directory used to store temporary data generated by the .NET assembly rawrr.exe. The default uses the output of tempdir().
verbose	print message of temp files; default is FALSE.

**Value**

an vector of trailers or values of a given trailer. Of note, the values are usually returned as a character.

**Examples**

```
rawrr::sampleFilePath() |> rawrr::readTrailer()
rawrr::sampleFilePath() |> rawrr::readTrailer("AGC:") |> head()
```

---

sampleFilePath	<i>A small file size sample.raw BLOB</i>
----------------	--

---

**Description**

The binary example file sample.raw, shipped with the package, contains 574 Fourier-transformed Orbitrap spectra (FTMS) recorded on a Thermo Fisher Scientific Q Exactive HF-X. The mass spectrometer was operated in line with a nano electrospray source (NSI) in positive mode (+). All spectra were written to disk after applying centroiding (c) and lock mass correction.

**Usage**

```
sampleFilePath()
```

**Details**

Thermo Fisher Scientific Q Exactive HF-X raw file of size 1.5M bytes and checksum MD5 (sample.raw) = fe67058456c79af7442316c474d20e96. Additional raw data for demonstration and extended testing is available through [MSV000086542](#) and the [tartare](#) package. **Lions love raw meat!**

**Value**

file path of the sample.raw location.

**Author(s)**

Tobias Kockmann, 2018, 2019.

**References**

- Bioconductor [tartare](#) package.
- Automated quality control sample 1 (autoQC01) analyzed across different Thermo Fisher Scientific mass spectrometers, [MSV000086542](#).

**Examples**

```
sampleFilePath()
```

---

scanNumber	<i>Accessor function for scan number of rawrrSpectrum objects</i>
------------	---

---

**Description**

Accessor function for scan number of rawrrSpectrum objects

**Usage**

```
scanNumber(x)
```

**Arguments**

x                    A rawrrSpectrum object

**Details**

This accessor function returns the scan number of a mass spectrum stored as rawrrSpectrum object. Scan numbers are equal to the scan index  $j$  running from 1 to  $n$  with  $n$  being the last scan of a raw file.

**Value**

The scan number of type integer

**Examples**

```
S <- readSpectrum(rawfile = sampleFilePath(), 1:10)
scanNumber(S[[1]])
```

---

```
summary.rawrrChromatogram
```

*Text summary of chromatogram*

---

**Description**

Text summary of chromatogram

**Usage**

```
## S3 method for class 'rawrrChromatogram'
summary(object, ...)
```

**Arguments**

object	A rawrrChromatogram object
...	Function passes additional arguments.

**Value**

A rawrrChromatogram object

**Examples**

```
C <- readChromatogram(rawfile = sampleFilePath(),
mass = c(445.1181, 519.1367))
summary(C[[1]])
summary(C[[2]])
```

---

```
summary.rawrrSpectrum Basic summary function
```

---

**Description**

Basic summary function

**Usage**

```
## S3 method for class 'rawrrSpectrum'
summary(object, ...)
```

**Arguments**

object            an rawrrSpectrum object.  
...                Arguments to be passed to methods.

**Value**

This function creates a print message.

**Author(s)**

Christian Panse and Tobias Kockmann, 2020.

---

tic                            *Total ion current of a spectrum*

---

**Description**

Total ion current of a spectrum

**Usage**

```
tic(x)
```

**Arguments**

x                            A rawrrSpectrum object

**Value**

A double vector of length one.

**Examples**

```
S <- readSpectrum(rawfile = sampleFilePath(), 1)
tic(S[[1]])
```

---

validate\_rawrrIndex     *Validate output of the readIndex function*

---

**Description**

Checks the validity of an readIndex returned object.

**Usage**

```
validate_rawrrIndex(x)
```

**Arguments**

x                    object to be validated.

**Value**

Validated data.frame of readIndex object

**Author(s)**

Tobias Kockmann and Christian Panse, 2020-12-09.

**Examples**

```
rawrr::sampleFilePath() |> rawrr::readIndex() |> rawrr::validate_rawrrIndex()
```

---

validate\_rawrrSpectrum     *Validate instance of class rawrrSpectrum*

---

**Description**

Checks the validity of rawrrSpectrum object attributes.

**Usage**

```
validate_rawrrSpectrum(x)
```

**Arguments**

x                    object to be validated.

**Value**

Validated rawrrSpectrum object

**Author(s)**

Tobias Kockmann and Christian Panse, 2020.

**Examples**

```
S <- rawrr::sampleFilePath() |>  
  rawrr::readSpectrum(scan = 1:9, validate=TRUE)
```

# Index

.checkDllInMonoPath, 3  
.thermofisherLsmsUrl, 3  
auc.rawrrChromatogram, 4  
basePeak, 4  
buildRawrrExe, 5, 8, 9  
dependentScan, 6  
faimsVoltageOn, 6  
filter, 7  
installRawFileReaderDLLs, 5, 7  
installRawrrExe, 5, 8, 9  
is.rawrrChromatogram, 10  
is.rawrrSpectrum, 10  
is.rawrrSpectrumSet, 11  
makeAccessor, 11  
massRange, 12  
masterScan, 13  
new\_rawrrSpectrum, 13  
plot.rawrrChromatogram, 14  
plot.rawrrChromatogramSet, 15  
plot.rawrrSpectrum, 15  
print.rawrrSpectrum, 16  
rawrr (readSpectrum), 22  
rawrr.exe (installRawrrExe), 9  
rawrrAssemblyPath, 17  
rawrrSpectrum, 18  
readChromatogram, 18  
readFileHeader, 20  
readIndex, 21  
readSpectrum, 22  
readTrailer, 25  
sample.raw (sampleFilePath), 25  
sampleFilePath, 25  
scanNumber, 26  
summary.rawrrChromatogram, 27  
summary.rawrrSpectrum, 27  
system2, 5, 9  
Thermo (installRawFileReaderDLLs), 7  
ThermoFisher  
    (installRawFileReaderDLLs), 7  
ThermoFisherScientific  
    (installRawFileReaderDLLs), 7  
tic, 28  
validate\_rawrrIndex, 29  
validate\_rawrrSpectrum, 29