

Package ‘MsBackendRawFileReader’

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Type Package

Title Mass Spectrometry Backend for Reading Thermo Fisher Scientific
raw Files

Version 1.2.0

Depends R (>= 4.1), methods, Spectra (>= 1.5.8)

Imports MsCoreUtils, S4Vectors, IRanges, rawrr (>= 1.3.6), utils,
BiocParallel

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

Description implements a MsBackend for the Spectra package using
Thermo Fisher Scientific's NewRawFileReader .Net libraries.
The package is generalizing the functionality introduced by the rawrr package
(Kockmann T. et al. (2020) <[doi:10.1101/2020.10.30.362533](https://doi.org/10.1101/2020.10.30.362533)>)
Methods defined in this package are supposed to extend the Spectra
Bioconductor package.

URL <https://github.com/fgcz/MsBackendRawFileReader>

BugReports <https://github.com/fgcz/MsBackendRawFileReader/issues>

Encoding UTF-8

NeedsCompilation yes

biocViews MassSpectrometry, Proteomics, Metabolomics

RoxygenNote 7.1.2

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.

VignetteBuilder knitr

Collate 'hidden_aliases.R' 'AllGenerics.R'
'MsBackendRawFileReader-functions.R' 'MsBackendRawFileReader.R'
'benchmark.R' 'zzz.R'

git_url <https://git.bioconductor.org/packages/MsBackendRawFileReader>

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ioBenchmark	<i>RawFileReader_read_peaks benchmark</i>
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Description

derives numbers to evaluate time performance for reading a single spectrum in dependency from the chunk size (how many spectra are read in one function call) for reading different numbers of overall spectra.

Usage

```
ioBenchmark(
  nv = c(1000, 5000, 10000),
  sizev = c(8, 16, 32, 64, 128, 256, 8, 16, 32, 64, 128, 256, 8, 16, 32, 64, 128, 256,
  8, 16, 32, 64, 128, 256, 8, 16, 32, 64, 128, 256, 8, 16, 32, 64, 128, 256),
  rawfile
)
```

Arguments

nv	number of spectra to be read.
sizev	number of spectra write and parsed in one single junk.
rawfile	the Thermo Fisher Scientific raw file.

Value

data.frame

Examples

```
eh <- ExperimentHub::ExperimentHub()
EH4547 <- normalizePath(eh[["EH4547"]])
(rawfileEH4547 <- paste0(EH4547 , ".raw"))
if (!file.exists(rawfileEH4547 )){
  file.link(EH4547 , rawfileEH4547)
}
S <- ioBenchmark(1000, c(128, 256, 128, 256), rawfile=rawfileEH4547)
```

MsBackendRawFileReader

MsBackendRawFileReader

Description

MsBackendRawFileReader

Usage

```
MsBackendRawFileReader()

## S4 method for signature 'MsBackendRawFileReader'
filterScan(object, filter = character(), ...)

## S4 method for signature 'MsBackendRawFileReader'
scanType(object, ...)
```

Arguments

object	MsBackendRawFileReader object
filter	filter string
...	Arguments to be passed to methods.

Value

a MsBackendRawFileReader object.
a character vector of scan types.

Examples

```
beRaw <- Spectra::backendInitialize(MsBackendRawFileReader::MsBackendRawFileReader(),
  files = rawrr::sampleFilePath())
beRaw |> MsBackendRawFileReader::filterScan('Ms')
beRaw <- Spectra::backendInitialize(MsBackendRawFileReader::MsBackendRawFileReader(),
  files = rawrr::sampleFilePath())
scanType(beRaw) |> head()
```

MsBackendRawFileReader-class

RawFileReader-based backend

Description

The ‘MsBackendRawFileReader’ inherits all slots and methods from the base ‘MsBackendDataFrame’ (in-memory) backend. It overrides the base ‘mz’ and ‘intensity’ methods as well as ‘peaksData’ to read the respective data from the original raw data files.

The validator function has to ensure that the files exist and that required column names are present.

The ‘backendInitialize’ method reads the header data from the raw files and hence fills the ‘spectra-Data’ slot.

Author(s)

Christian Panse (2019-2021)

Examples

```
beRaw <- Spectra::backendInitialize(MsBackendRawFileReader::MsBackendRawFileReader(),
  files = rawrr::sampleFilePath())
beRaw
Spectra::msLevel(beRaw)
```

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