

Package: msdata (via r-universe)

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Title Various Mass Spectrometry raw data example files

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Depends R (>= 2.10)

Suggests xcms, mzR, MSnbase

ZipData no

Description Ion Trap positive ionization mode data in mzML file
format. Subset from 500-850 m/z and 1190-1310 seconds, incl.
MS2 and MS3, intensity threshold 100.000. Extracts from FTICR
Apex III, m/z 400-450. Subset of UPLC - Bruker micrOTOFq data,
both mzML and mz5. LC-MSMS and MRM files from proteomics
experiments. PSI mzIdentML example files for various search
engines.

biocViews ExperimentData, MassSpectrometryData

License GPL (>= 2)

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CE-MS

*CE-MS test data***Description**

The CE-MS test files consist of two files, i.e. "CEMS_10ppm.mzML" and "CEMS_25ppm.mzML". The data contains CE-MS runs of a standard mixture that contains e.g. Lysine (at 10 ppm and 25 ppm, respectively) and the neutral EOF marker Paracetamol (50 ppm). The data was acquired on a 7100 capillary electrophoresis system from Agilent Technologies, coupled to an Agilent 6560 IM-QToF-MS. CE Separation was performed using a 80 cm fused silica capillary with an internal diameter of 50 μ m and external diameter of 365 μ m. The Background Electrolyte was 10 % acetic acid and separation was performed at +30 kV and a constant pressure of 50 mbar. MS detection was performed in positive ionization mode.

The raw data were then converted to an open-source ".mzML" format (Proteowizzard) and load into R via the MSnBase::readMSData() function. In order to reduce data size, the test data was subsequently cutted in migration time and mz range using filterRt(rt = c(400, 900)) and filterMz(mz = c(147.1, 152.0)) from MSnBase

Author(s)

Liesa Salzer

msdata

*Sample FTICR, LC/MS and MSⁿ data***Description**

x object containing a subset of LC/MS raw data from a Thermo Finnigan LCQ Deca XP The data is a subset from 500-850 m/z and 1190-1310 seconds, incl. MS2 and MS3, intensity threshold 100.000. It was collected in positive ionization mode.

xs object containing a subset of FTICR data from a Bruker APex III FTICR. The data is a subset from 400-450 m/z, collected in positive ionization mode.

Usage

data(xs)

Format

The format is:

xs

Details

The corresponding raw mzML files are located in the `fticr-mzML` and `iontrap` subdirectory of this package.

See Also

[xcmsSet](#), [xcmsRaw](#)

Examples

```
## The directory with the mzML LC/MS files
data(xs)
mzMLpath <- file.path(find.package("msdata"), "iontrap")
mzMLpath
files <- list.files(mzMLpath, recursive = TRUE, full.names = TRUE)
files

if (require(xcms)) {

  ## xcmsSet Summary
  show(xs)

  ## Access raw data file
  x <- xcmsRaw(files[1])
  x

}
```

proteomics

Proteomics data in msdata

Description

This function returns proteomics mass spectrometry files. These files are all stored in the `proteomics` directory in the `msdata` package. Each file/data is described in more details below.

Usage

```
proteomics(...)
```

Arguments

`...` Additional arguments passed to [list.files](#).

Value

A character with file names.

Author(s)

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See Also

For more access to mass spectrometry-based proteomics data, see the rpx and MsDataHub packages.

sciexdata

AB Sciex LC-MS data files

Description

The mzML files in the sciex directory in the msdata package represent profile-mode LC-MS data of pooled human serum samples (the same pool being measured). The samples were analyzed by ultra high-performance liquid chromatography (UHPLC; Agilent 1290) coupled to a Q-TOF mass spectrometer (TripleTOF 5600+ AB Sciex). The chromatographic separation was based in hydrophilic interaction liquid chromatography (HILIC) and performed using an Waters Acquity BEH Amide, 100 x 2.1 mm column.

The mass spectrometer was operated in full scan mode in the mass range from 50 to 1000 m/z and with an accumulation time of 250 ms. The files represent a subset of spectra/scans from m/z 105 to 134 and from retention time 0 to 260 seconds. The files were generated in the same LC-MS run, but from different injections. Details on the individual files are provided below.

Details

- 20171016_POOL_POS_1_105-134.mzML profile-mode LC-MS data of pooled human serum samples. Injection index: 1.
- 20171016_POOL_POS_3_105-134.mzML profile-mode LC-MS data of pooled human serum samples. Injection index: 19.

Author(s)

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Examples

```
## List the files in the sciex folder
dir(system.file("sciex", package = "msdata"))
```

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