Spectra: A Flexible Infrastructure for Mass Spectrometry Data

Sebastian Gibb[1], Laurent Gatto[2] and Johannes Rainer[3]

[1] Department of Anaesthesiology and Intensive Care, University Medicine Greifswald, Germany
[2] de Duve Institute, UCLouvain, Brussels, Belgium
[3] Institute for Biomedicine, Eurac Research, Italy

Mass Spectrometry (MS) Data

- Paired measurements:
  - intensity (counts) vs m/z (mass-to-charge ratio).
  - intensity vs retention time.
- Additional various metatdata.

Problems

- Vendor-specific, closed file formats.
- Various open-formats, e.g. mzML, mzXML, mz5, CDF, MGF, CSV.
- Spectra libraries/Annotation information in databases, e.g. SQL.
- Multiple R -packages require different file formats and/or data structures.
- Larger experiments don't fit into RAM.

Solution: Spectra[1]

- Common, flexible data structure and interface.
- Supports various file formats by different backends.

Spectra class

- Handles one or multiple MS spectra.
- Implements typical processing functionality.
- Isolation from type of data storage (handled by backend classes)

MsBackend classes

- Isolation from spectra handling and processing.
- Specific class for each type of data storage.

class	source.files	storage	writeable
MsBackendDataFrame[1]	manual	in-memory	yes
MsBackendHdf5Peaks[1]	hdf5	on-disk	yes
MsBackendMzR[1]	mzML, mzXML and CDF	on-disk	no
MsBackendHmdbXml[2]	XML	on-disk	yes
MsBackendRawFileReader[3]	Thermo .raw	on-disk	no

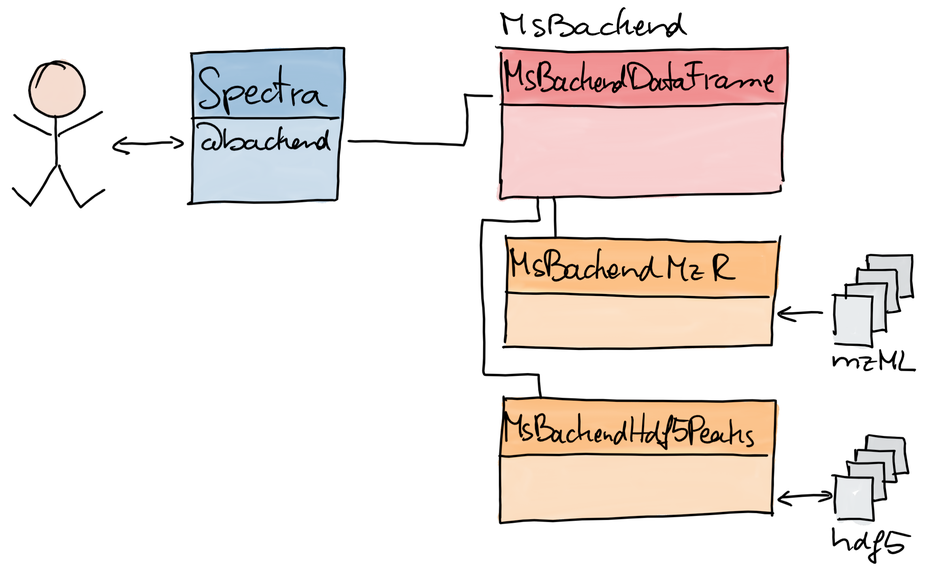

Figure 1: The user interacts with a Spectra object. It takes care of the data storage by different backend classes.

Example

```
# Load packages
library("Spectra")
library("magrittr")

# Import data
#sps <- Spectra("data/20191107_Mix2_CE20.mzML", back
sps <- Spectra()

# Select all MS2 spectra for a [M+Na]+ ion of Fructo

mzr <- 203.0526
mzr <- 156.07675 # Histidine
fruct <- sps %>%
    filterMsLevel(2) %>%
    filterPrecursorMz(
        mz = mzr + ppm(c(-mzr, mzr), 20)
    )

# Centroid and clean spectra.

fruct <- fruct %>%
    pickPeaks() %>%
    removePeaks(threshold = 500) %>%
    clean(all = TRUE)

# Change backend: load data in memory.

#fruct <- setBackend(fruct, MsBackendDataFrame())
```

Contact

- https://github.com/rformassspectrometry/Spectra
- https://rformassspectrometry.org
- https://twitter.com/search?q=%23rformassspec

References

Laurent Gatto, Johannes Rainer, and Sebastian Gibb.
Spectra: Spectra Infrastructure for Mass Spectrometry Data.
R package version 0.3.0.

Laurent Gatto, Johannes Rainer, and Sebastian Gibb.
MsBackendHmdb: Mass spectrometry data backends for The Human Metabolome Database, 2019.
R package version 0.1.0.

Christian Panse and Tobias Kockmann.
MsBackendRawFileReader: Bridging Spectra and ThermoFinnigan raw files, 2019.
R package version 0.0.1.

To use the Spectra package install the **R for Mass Spectrometry** packages and load the core packages:

```
BiocManager::install("RforMassSpectrometry/RforMassSpectrometry")
library("RforMassSpectrometry")
```