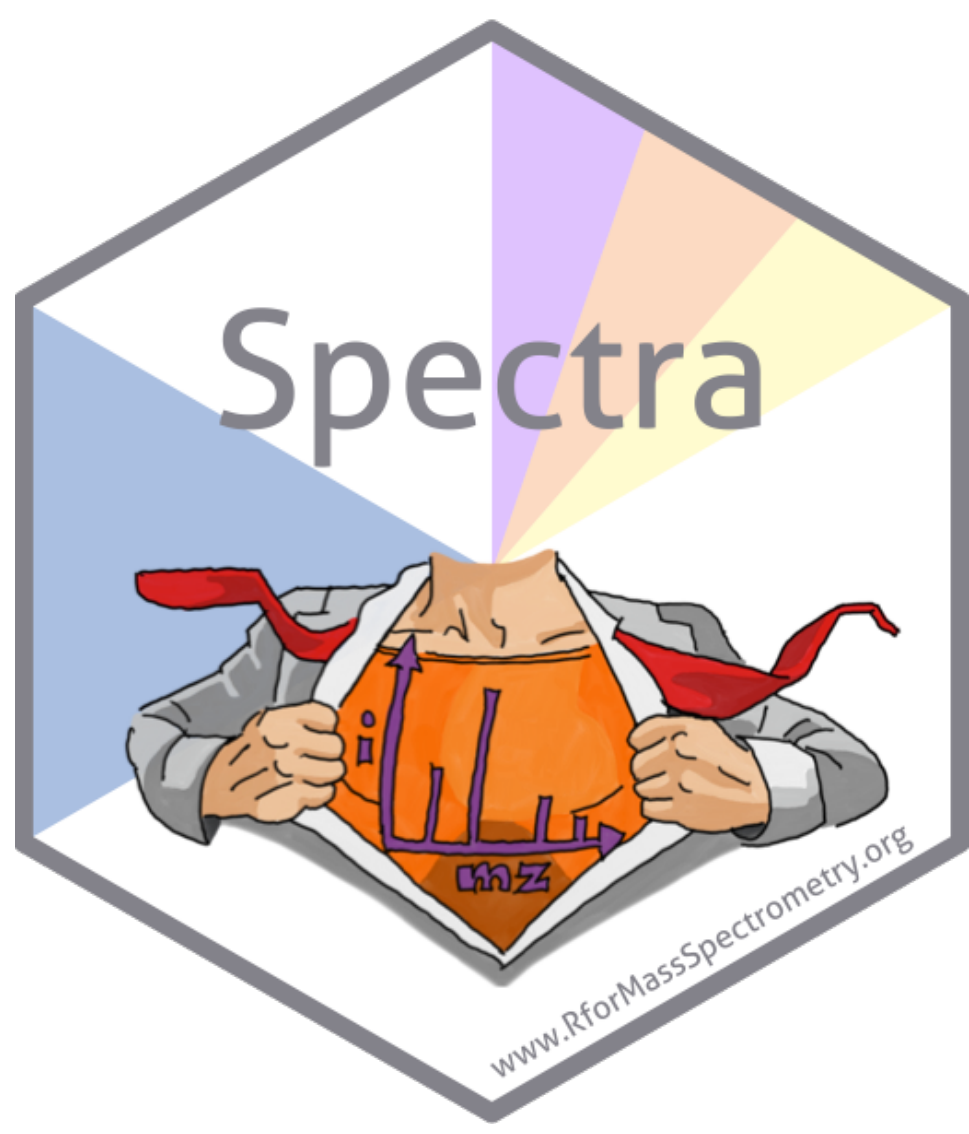


# Spectra: A Flexible Infrastructure for Mass Spectrometry Data



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## 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.
- Lazy and parallel evaluation.
- 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

## Example

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

# Import data
sps <- Spectra(
  "20191107_Mix2_CE20.mzML",
  backend = MsBackendMzR()
)

# Select all MS2 spectra for a [M+H]+ ion of
# Histidine
mzr <- 156.07675 # Histidine
his <- sps %>%
  filterMsLevel(2) %>%
  filterPrecursorMz(
    mz = mzr + ppm(c(-mzr, mzr), 20)
  )

# Centroid and clean spectra.
his <- fruct %>%
  pickPeaks() %>%
  removePeaks(threshold = 500) %>%
  clean(all = TRUE)

## Error in eval(lhs, parent, parent): object 'fruct' not found

# Change backend: load data in memory.
his <- setBackend(his, MsBackendDataFrame())
```

## Contact

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

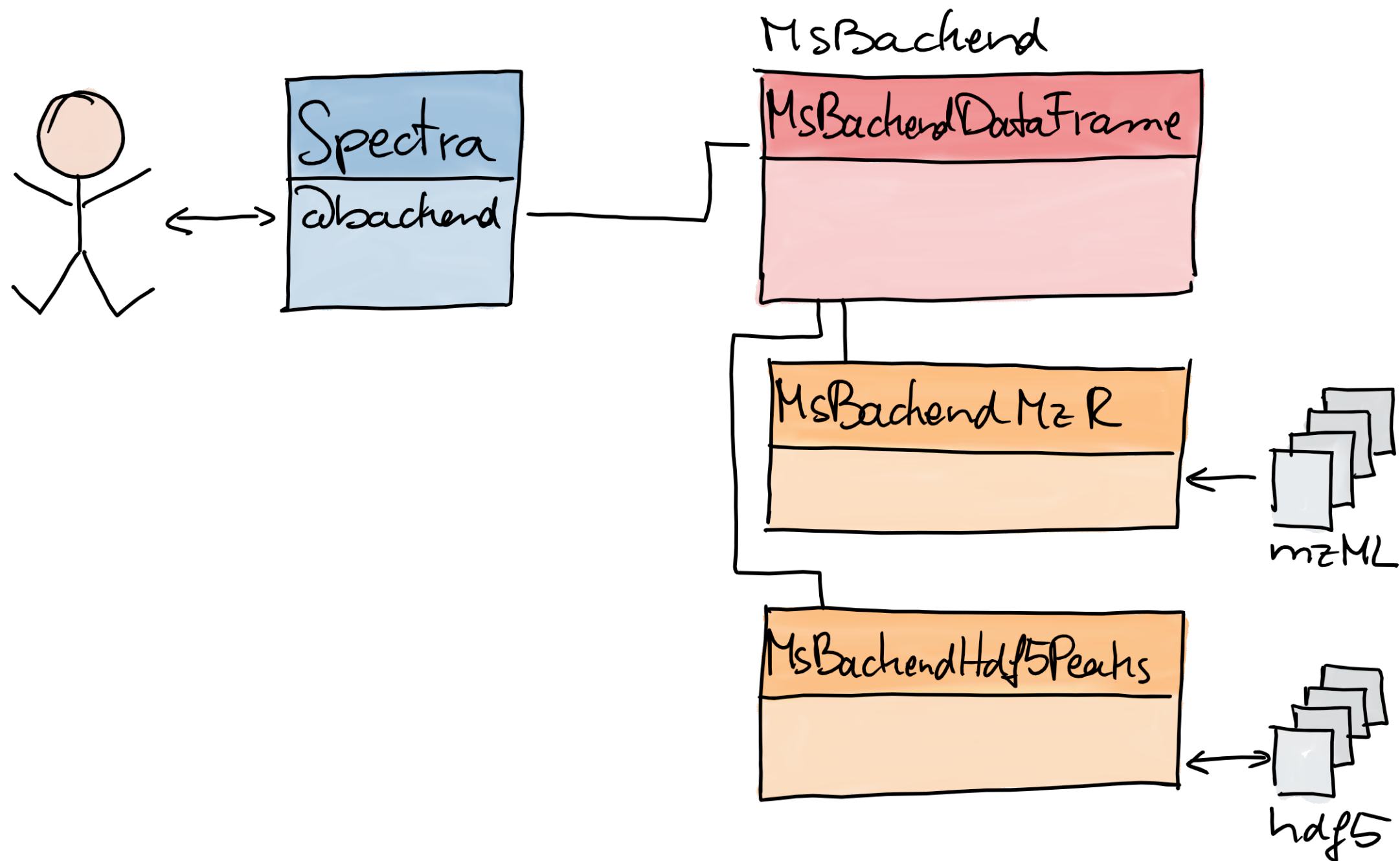
## References

[1] Laurent Gatto, Johannes Rainer, and Sebastian Gibb. *Spectra: Spectra Infrastructure for Mass Spectrometry Data*, 2019. R package version 0.3.0.

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

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

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



To install all the R for Mass Spectrometry packages:

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