

# MSnbase, efficient and elegant R-based processing and visualisation of raw mass spectrometry data

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## Abstract

We present version 2 of the MSnbase R/Bioconductor package. MSnbase provides infrastructure for the manipulation, processing and visualisation of mass spectrometry data. We focus on the new *on-disk* infrastructure, that allows the handling of large raw mass spectrometry experiment on commodity hardware and illustrate how the package is used for elegant data processing, method development, and visualisation.

## Introduction

Mass spectrometry is a powerful technology to assay chemical and biological samples. It is used in routine applications with well characterised protocols such as diagnostics, as well as a

development platform, ~~with the aim~~ to improve on existing ~~methods~~ ~~protocols~~ and devise new ones. The complexity and diversity of mass spectrometry yield data that is itself complex and often times of considerable size, that require non trivial processing before producing interpretable results. ~~This is particularly relevant, and can~~ ~~The complexity and size of these~~ ~~data~~ constitute a significant challenge for ~~method~~ ~~protocol~~ development: in addition to the development of sample processing and mass spectrometry methods ~~that yield the raw data,~~ ~~it is essential~~ ~~there is a need~~ to process, analyse, interpret and assess these new data to demonstrate the improvement in the technical, analytical and computational workflows.

Practitioners have a diverse catalogue of software tools to explore, process and interpret mass spectrometry data at their disposal. These range from low level software libraries that are aimed at programmers to enable development of new applications, to more user-oriented applications with graphical user interfaces which provide a more limited set of functionalities to address a defined scope. Examples of software libraries include Java-based jmzML<sup>1</sup> or C/C++-based ProteoWizard.<sup>2</sup> ~~ProteomeDiscoverer (Thermo Scientific)~~ ~~Thermo Scientific~~ ~~Proteome Discoverer (Thermo Fisher Scientific)~~, MaxQuant<sup>3</sup> and PeptideShaker<sup>4</sup> are among the most widely used user-centric applications.

In this software note, we present version 2 of the MSnbase<sup>5</sup> software, available from the Bioconductor<sup>6</sup> project. The package, like other software such as Python-based pyOpenMS,<sup>7</sup> spectrum\_utils<sup>8</sup> or Pyteomics,<sup>9</sup> offers a platform that lies between low level libraries and end-user software. MSnbase provides a flexible R<sup>10</sup> command-line environment for metabolomics and proteomics mass spectrometry-based applications. It lays out a sound infrastructure to work with raw mass spectrometry ~~data from MS files in mzML, mzXML, mzData or ANDI-MS/netCDF format as well as~~ quantitative and proteomics identification data. The package enables manipulation (for example subsetting, filtering, or accessing specific parts thereof), detailed step-by-step processing (for example smoothing and centroiding of ~~raw~~ ~~profile-mode~~ ~~MS~~ data, or normalisation and imputation of quantitative data), analysis and visualisation of these data and the development of novel computational mass spectrometry methods.<sup>11</sup>

Extensive documentation and use cases are provided in *package vignettes*<sup>12</sup> and *workflows*.<sup>13</sup>

Here, we focus on the new developments pertaining to raw mass spectrometry data handling and processing.

## Infrastructure for raw data

In **MSnbase**, mass spectrometry experiments are handled as **MSnExp** objects. While the implementation is more complex, it is useful to schematise a raw data experiment as being composed of raw data, i.e. a collection of individual spectra, as well as spectra-level metadata (Figure 1). Each spectrum is composed of  $m/z$  values and associated intensities. The metadata are represented by a **single** table with variables along the columns and each row associated to a spectrum. Among the metadata available for each spectrum, there are MS level, acquisition number, retention time, precursor  $m/z$  and intensity (for MS level 2 and above), and many more. **MSnbase** **relies on the mzR package**<sup>2</sup> to import raw mass spectrometry data from one of the many community-maintained open standards formats (mzML, mzXML, mzData or ANDI-MS/netCDF) and provides a rich interface to manipulate such objects. The code chunk below illustrates such an object as displayed in the R console and an enumeration of the metadata fields.

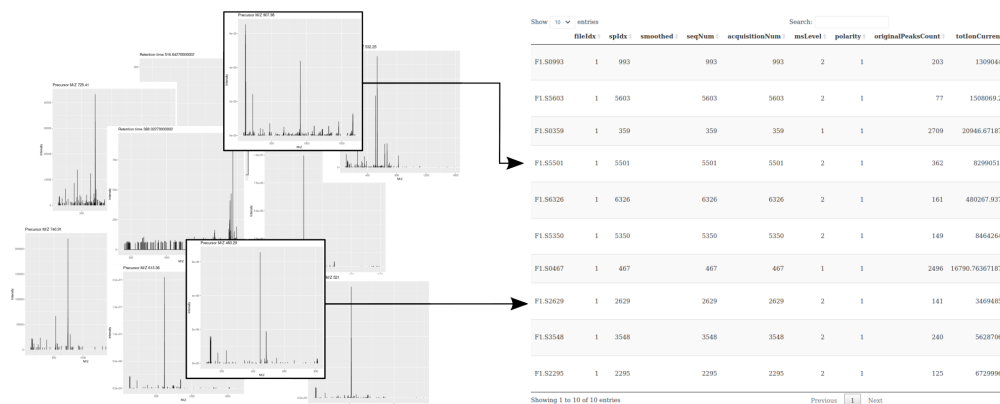


Figure 1: Schematic representation of what is referred to by *raw data*: a collection of mass spectra and a table containing spectrum-level annotations along the lines. Raw data is contained in one of the many community-maintained open standards formats (mzML, mzXML, mzData or ANDI-MS/netCDF).

```

> show(ms)
MSn experiment data ("OnDiskMSnExp")
Object size in memory: 0.54 Mb
- - - Spectra data - - -
MS level(s): 1 2 3
Number of spectra: 994
MSn retention times: 45:27 - 47:6 minutes
- - - Processing information - - -
Data loaded [Sun Apr 26 15:40:58 2020]
MSnbase version: 2.13.6
- - - Meta data - - -
phenoData
  rowNames: MS3TMT11.mzML
  varLabels: sampleNames
  varMetadata: labelDescription
Loaded from:
  MS3TMT11.mzML
protocolData: none
featureData
  featureNames: F1.S001 F1.S002 ... F1.S994 (994 total)
  fvarLabels: fileIdx spIdx ... spectrum (35 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
> fvarLabels(ms)
[1] "fileIdx"          "spIdx"
[3] "smoothed"         "seqNum"
[5] "acquisitionNum"   "msLevel"

```

[7]	"polarity"	"originalPeaksCount"
[9]	"totIonCurrent"	"retentionTime"
[11]	"basePeakMZ"	"basePeakIntensity"
[13]	"collisionEnergy"	"ionisationEnergy"
[15]	"lowMZ"	"highMZ"
[17]	"precursorScanNum"	"precursorMZ"
[19]	"precursorCharge"	"precursorIntensity"
[21]	"mergedScan"	"mergedResultScanNum"
[23]	"mergedResultStartScanNum"	"mergedResultEndScanNum"
[25]	"injectionTime"	"filterString"
[27]	"spectrumId"	"centroided"
[29]	"ionMobilityDriftTime"	"isolationWindowTargetMZ"
[31]	"isolationWindowLowerOffset"	"isolationWindowUpperOffset"
[33]	"scanWindowLowerLimit"	"scanWindowUpperLimit"
[35]	"spectrum"	

In the following sections, we describe ~~MSnbase's ability to efficiently handle very large mass spectrometry data and experiments and how it~~ **how MSnbase** can be used for data processing and visualisation. **An example of its ability to efficiently handle also very large mass spectrometry experiments (in this case with 5,773,464 spectra in 1,182 mzXML files) is provided as supplementary information.** We will also illustrate how it makes use of the forward-pipe operator (`%>%`) defined in the `magrittr` package. This operator has proved useful to develop non-trivial analyses by combining individual functions into easily readable pipelines.

## On-disk backend

The main feature in version 2 of the `MSnbase` package was the addition of different backends for raw data storage, namely *in-memory* and *on-disk*. The following code chunk demonstrates how to create two `MSnExp` objects **importing data from an mzML file and storing data them** either in-memory or on-disk.

```
library("MSnbase")  
  
raw_mem <- readMSData("file.mzML", mode = "inMemory")  
raw_dsk <- readMSData("file.mzML", mode = "onDisk")
```

Both modes rely on the `mzR`<sup>2</sup> package to access the spectra (using the `mzR::peaks()` function) and the metadata (using the `mzR::header()` function) in the data files. The former is the legacy storage mode, implemented in the first version of the package, that loads all the raw data and the metadata into memory upon creation of the in-memory `MSnExp` object. This solution doesn't scale for modern large dataset, and was complemented by the on-disk backend. The on-disk backend only loads the metadata into memory when the on-disk `MSnExp` is created and accesses the spectra data (i.e.  $m/z$  and intensity values) in the original files on disk only when needed (see below and Figure 2 (d)), such as for example for plotting. There are two direct benefits using the on-disk backend, namely faster reading and reduced memory footprint. Figure 2 shows 5-fold faster reading times (a) and over a 10-fold reduction in memory usage (b).

**Because the on-disk backend does not hold all the data in memory, direct data manipulations are not possible. We thus implemented a *lazy processing* mechanism for this backend that caches any data manipulation operations in a processing queue in the object itself. Only when the user accesses  $m/z$  or intensity values are these operations are applied. The on-disk backend also offers efficient data manipulation by way of *lazy processing* in the object itself. Operations on the raw data are stored in a processing queue and only effectively applied when the user accesses  $m/z$  or intensity values. As an additional advantage, operations**

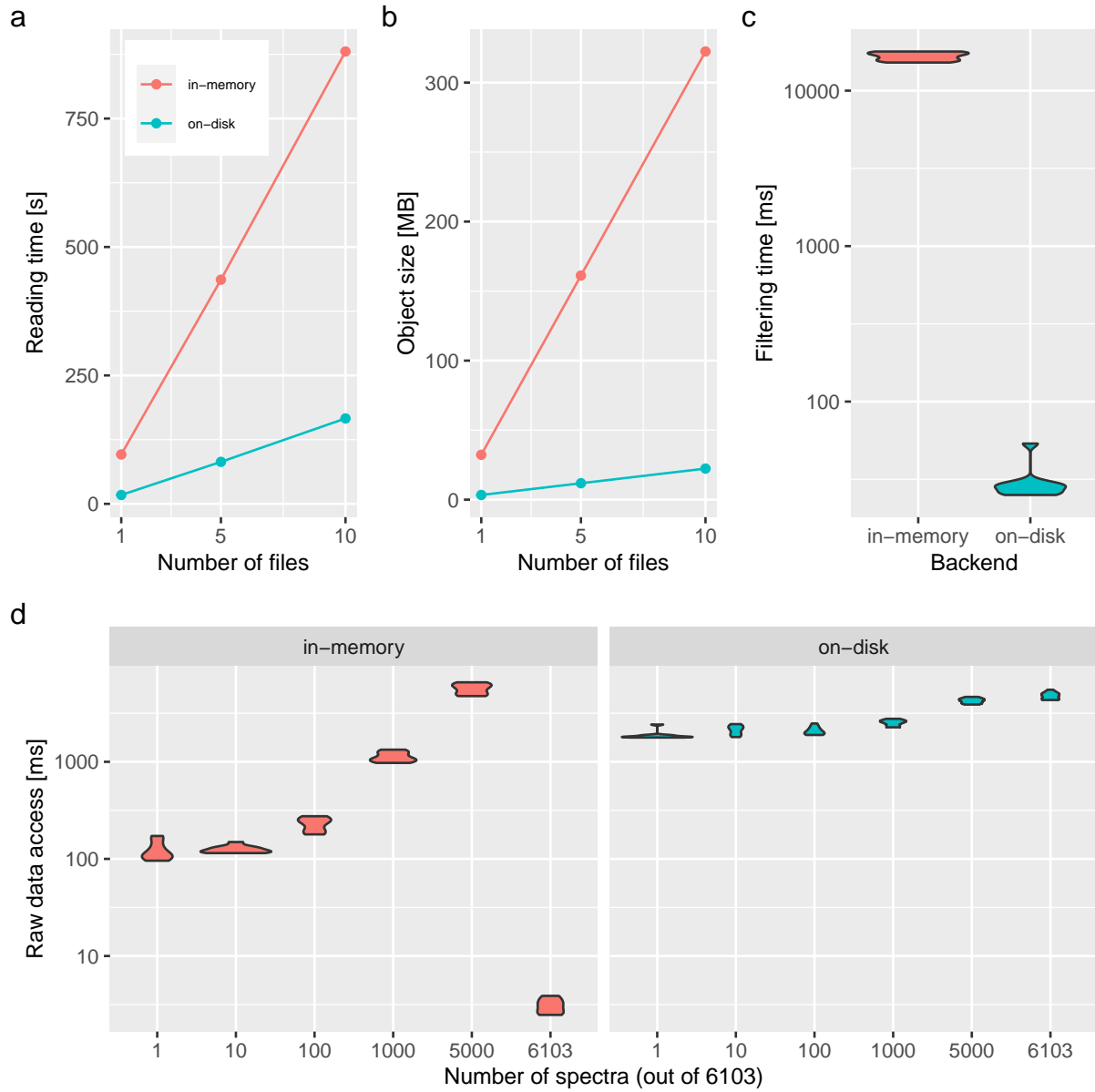


Figure 2: (a) Reading time (in seconds) and (b) data size in memory (in MB) to read/store 1, 5 and 10 files containing 1431 MS1 (on-disk only) and 6103 MS2 (on-disk and in-memory) spectra. (c) Filtering benchmark assessed over 10 interactions on in-memory and on-disk data containing 6103 MS2 spectra. (d) Access time to spectra for the in-memory (left) and on-disk (right) backends for 1, 10, 100 1000, 5000 and all 6103 spectra. Benchmarks were performed on a Dell XPS laptop with an Intel i5-8250U processor 1.60 GHz (4 cores, 8 threads), 7.5 GB RAM running Ubuntu 18.04.4 LTS 64-bit **and SSD drive**.

on subsets of the data become much faster since data manipulations are applied only to data subsets instead of the full data set at once. Also, data access in on-disk backends is parallelized by data file ensuring a higher performance of this backend over conventional in-memory data representations. As an example, the following short analysis pipeline, that can equally be applied to in-memory or on-disk data, retains MS2 spectra acquired between 1000 and 3000 seconds, extracts the m/z range corresponding to the TMT 6-plex range and focuses on the MS2 spectra with a precursor intensity greater than  $11 \times 10^6$  (the median precursor intensity).

```
ms <- ms %>%
  filterRt(c(1000, 3000)) %>%
  filterMz(120, 135)
ms[precursorIntensity(ms) > 11e6, ]
```

As shown on Figure 2 (c), this lazy mechanism is significantly faster than its application on in-memory data. The advantageous reading and execution times and memory footprint of the on-disk backend are possible by retrieving only spectra data from the selected subset hence avoiding access to the full raw data. Once access to the spectra m/z and intensity values become mandatory (for example for plotting), then the in-memory backend becomes more efficient, as illustrated on Figure 2 (d). This gain is maximal when the whole dataset is accessed (i.e. all spectra are already in memory) and negligible when only subsets of the data are requested.

## Prototyping

The MSnExp data structure and its interface constitute an efficient prototyping environment for computational method development. We illustrate this by demonstrating how to implement the BoxCar<sup>14</sup> acquisition method. In a nutshell, BoxCar acquisition aims at improving the detection of intact precursor ions by distributing the charge capacity over multiple nar-



row  $m/z$  segments and thus limiting the proportion of highly abundant precursors in each segment. A full scan is reconstructed by combining the respective adjacent segments of the BoxCar acquisitions. The `MSnbaseBoxCar` package<sup>15</sup> is a small package that demonstrates this. The simple method is composed of three steps is described below and illustrated with code from `MSnbaseBoxCar` in the following code chunk.

1. Identify and filter the groups of spectra that represent adjacent BoxCar acquisitions (Figure 3 (b)). This can be done using the *filterString* metadata variable that identifies BoxCar spectra by their adjacent  $m/z$  segments with the `bc_groups()` function and filtering relevant spectra with the `filterBoxCar()`.
2. Remove any signal outside the BoxCar segments using the `bc_zero_out_box()` function from `MSnbaseBoxCar` (Figures 3 (c) and (d)).
3. Using the `combineSpectra` function from the `MSnbase`, combine the cleaned BoxCar spectra into a new, full spectrum (Figure 3 (e)).

```
bc <- readMSData("boxcar.mzML", mode = "onDisk") %>%
  bc_groups() %>%      ## identify BoxCar groups (creates 'bc_groups')
  filterBoxCar() %>%   ## keep only BoxCar spectra
  bc_zero_out_box() %>% ## remove signal outside of BoxCar segments
  combineSpectra(fcol = "bc_groups", ## reconstruct full spectrum
                 method = boxcarCombine)
```

After processing of the BoxCar data, the final object can either be further analysed in `R` using `MSnbase` or written back to disk as an `mzML` file using `writeMSData()` for processing with other tools.

All the functions for the processing of BoxCar spectra and segments in `MSnbaseBoxCar` were developed using existing functionality implemented in `MSnbase`, illustrating the flexibil-

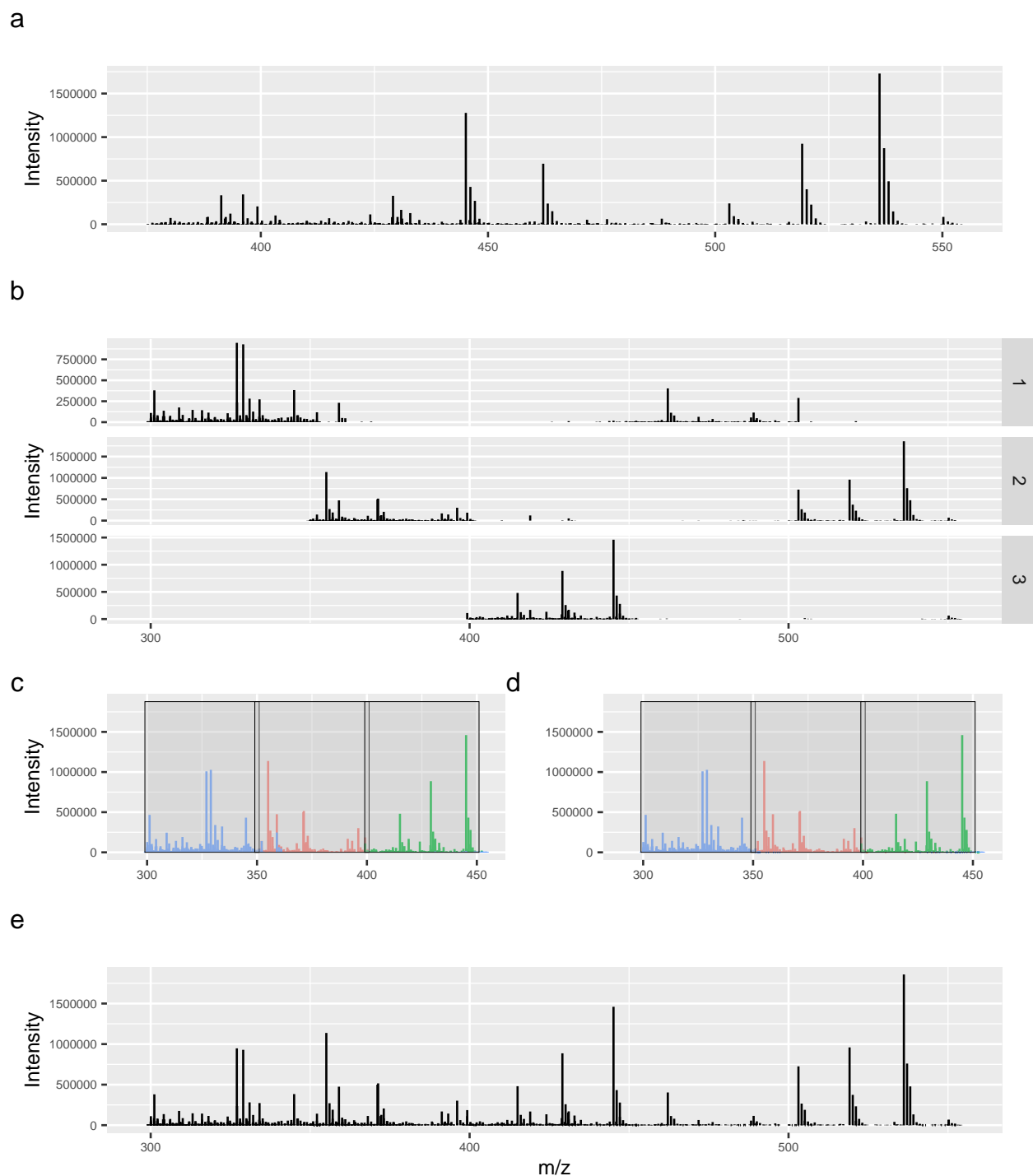


Figure 3: BoxCar processing with MSnbase. (a) Standard full scan with (b) three corresponding BoxCar scans showing the adjacent segments. Figure (c) shows the overlapping intact BoxCar segments and (d) the same segments after cleaning, i.e. where peaks outside of the segments were removed. The reconstructed full scan is shown on panel (e). Spectra visualisation, as shown here, rely on the `ggplot2`<sup>16</sup> package.

ity and adaptability of the **MSnbase** package for computational mass spectrometry method development.

## Visualisation

The R environment is well known for the quality of its visualisation capacity. This also holds true for mass spectrometry.<sup>17–20</sup> Here, we conclude the overview of version 2 of the **MSnbase** package by highlighting the flexibility of the software to visualise and assess the efficiency of raw data processing. Figure 4 compares the raw MS profile data **imported from an mzML file** for the serine and the same data after smoothing, centroiding and m/z refinement, as illustrated in the code chunk below. Detailed execution and description of these operations can be found in the *MSnbase: centroiding of profile-mode MS data* **MSnbase** vignette.

```
serine_mz <- 106.049871
serine_proc <- ms %>%
  smooth(method = "SavitzkyGolay", halfWindowSize = 4L) %>%
  pickPeaks(refineMz = "descendPeak") %>%
  filterMz(c(serine_mz - 0.01, serine_mz + 0.01)) %>%
  filterRt(c(175, 187))
```

## Discussion

We have presented here some important functionality of **MSnbase** version 2. The new on-disk infrastructure enables large scale data analyses,<sup>21</sup> either using **MSnbase** directly or through packages that rely on it, such as **xcms**. We have also illustrated how **MSnbase** can be used for standard data analysis and visualisation, and how it can be used for method development and prototyping.

The first public commit to the **MSnbase** GitHub repository was in October 2010. Since

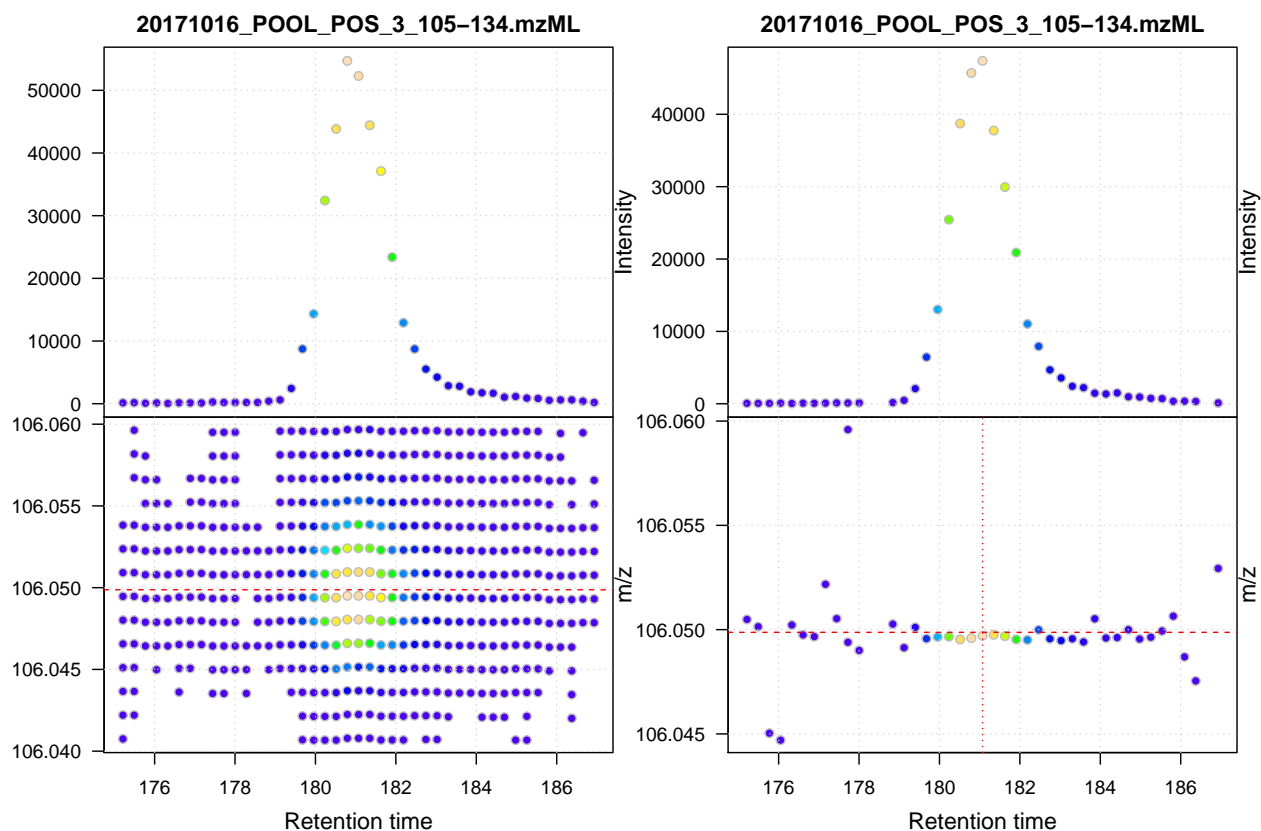


Figure 4: Visualisation of data smoothing and  $m/z$  refinement using MSnbase. (a) Raw MS profile data for serine. Upper panel shows the base peak chromatogram (BPC), lower panel the individual signals in the retention time -  $m/z$  space. The horizontal dashed red line indicates the theoretical  $m/z$  of the  $[M+H]^+$  adduct of serine. (b) Smoothed and centroided data for serine with  $m/z$  refinement. The horizontal red dashed line indicates the theoretical  $m/z$  for the  $[M+H]^+$  ion and the vertical red dotted line the position of the maximum signal.

then, the package benefited from 12 contributors<sup>22</sup> that added various features, some particularly significant ones such as the on-disk backend described herein. According to **MSnbase**'s Bioconductor page, there are 36 Bioconductor packages that depend, import or suggest it. Among these are **pRoloc**<sup>23</sup> to analyse mass spectrometry-based spatial proteomics data, **msmsTests**,<sup>24</sup> **DEP**,<sup>25</sup> **DAPAR** and **ProStaR**<sup>26</sup> for the statistical analysis for **of** quantitative proteomics data, **RMassBank**<sup>27</sup> to process metabolomics tandem MS files and build MassBank records, **MSstatsQC**<sup>28</sup> for longitudinal system suitability monitoring and quality control of targeted proteomic experiments and the widely used **xcms**<sup>29</sup> package for the processing and analysis of metabolomics data. **MSnbase** is also used in non-R/Bioconductor software, such as for example IsoProt,<sup>30</sup> that provides a reproducible workflow for iTRAQ/TMT experiments. **MSnbase** currently ranks 101 out of 1823 packages based on the monthly downloads from unique IP addresses, tallying over 1000 downloads from unique IP addresses each months.

As is custom with Bioconductor packages, **MSnbase** comes with ample documentation. Every user-accessible function is documented in a dedicated manual page. In addition, the package offers 5 vignettes, including one aimed at developers. The package is checked nightly on the Bioconductor servers: it implements unit tests covering 72% of the code base and, through its vignettes, also provides integration testing. Questions from users and developers are answered on the Bioconductor support forum as well as on the package GitHub page. The package provides several sample and benchmarking datasets, and relies on other dedicated *experiment packages* such as **msdata**<sup>31</sup> for raw data or **pRolocdata**<sup>23</sup> for quantitative data. **MSnbase** is available on Windows, Mac OS and Linux under the open source Artistic 2.0 license and easily installable using standard installation procedures.

The version of **MSnbase** used in this manuscript is 2.14.2. The main features presented here were available since version 2.0. The code to reproduce the analyses and figures in this article is available at <https://github.com/lgatto/2020-msnbase-v2/>.

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