The R for Mass Spectrometry Initiative

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The aim of the **R for Mass Spectrometry** initiative is to provide efficient, thoroughly documented, tested and flexible R software for the analysis and interpretation of high throughput mass spectrometry assays, including proteomics and metabolomics experiments. The project formalises the longtime collaborative development efforts of its core members under the *RforMassSpectrometry* organisation to facilitate dissemination and accessibility of their work.

For more details, visit http://www.RforMassSpectrometry.org

The project is currently composed of the following packages:

RforMassSpectrometry is a meta-package that is used to manage the R for Mass Spectrometry suite of package versions in a coherent way. Users will rely on this package to install and manage the other software.

The **Spectra** package provides base classes and processing methods for raw mass spectrometry data. It is designed with efficiency, both in terms of memory footprint and processing time in mind, and can manage data in different types of formats.

The **Chromatograms** package provides base classes and processing methods for chromatographics data. It is designed with efficiency, both in terms of memory footprint and processing time in mind, and can manage data in different types of formats.

The **Features** package offers the infrastrucutre to manage and process quantitative features for high-throughput mass spectrometry assays, including proteomics and metabolomics experiments.

The **MsExperiment** package provides the infrastructure to store and manage all aspects related to a complete proteomics or metabolomics mass spectrometry experiment. It relies on the other RforMassSpectrometry core packages for the data crunching.

The **MsCoreUtils** package defines low-level functions for mass spectrometry data processing and is independent of any high-level data structures.

To install all the **R for Mass Spectrometry** packages and load the core packages:

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

Contributions to the initiative are more than welcome, whether under the form of ideas, documentation, code, packages, ... Find details about contribution guidelines and **code of conduct** on our webpage.