MSnbase, efficient R-based access and manipulation 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. Here we present how the new *on disk* infrastructure allows the handling of hundreds on commodity hardware and present some application of the package.

Introduction

What is `MSnbase`: `MSnbase`[1] offers a solution between low level liraries such as jmzml, exclusively for the development of new applications and GUI software, that provides a limited and fixed set of functionality.

Software functionality

On disk backend

Efficient low level access: in memory vs on disk mode (using mzR), benchmarking, used in ms-based proteomics and metabolomics.

Use cases

Example applications: visualisation, ...

Discussion

To address (from guidelines):

- potential for reuse
- general limitations
- system limitations
- end-user documentation
- developer documentation
- sample data
- benchmark data set
- availability
- license information
- system requirements

Collaborative development, 11 contributors since creation (see blog post).

Count packages depending on `MSnbase`.

Future developments.

The version of `MSnbase` used in this manuscritp is version 2.9.4. The main features presented here were available since version 2.0.

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References

(1) Gatto, L.; Lilley, K. S. MSnbase - an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. *Bioinformatics* **2012**, *28*, 288–9.