

MSnbase development

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Abstract

This vignette describes the classes implemented in *MSnbase* package. It is intended as a starting point for developers or users who would like to learn more or further develop/extend pSet.

Keywords: Mass Spectrometry (MS), proteomics, infrastructure.

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Foreword

MSnbase is under active developed; current functionality is evolving and new features will be added. This software is free and open-source software. If you use it, please support the project by citing it in

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publications:

Laurent Gatto and Kathryn S. Lilley. *MSnbase - an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation*. Bioinformatics 28, 288-289 (2011).

Questions and bugs

You are welcome to contact me directly about *MSnbase*. For bugs, typos, suggestions or other questions, please file an issue in our tracking system¹ providing as much information as possible, a reproducible example and the output of `sessionInfo()`.

If you wish to reach a broader audience for general questions about proteomics analysis using R, you may want to use the Bioconductor support site: <https://support.bioconductor.org/>.

1 Introduction

This document is not a replacement for the individual manual pages, that document the slots of the *MSnbase* classes. It is a centralised high-level description of the package design.

MSnbase aims at being compatible with the *Biobase* infrastructure [1]. Many meta data structures that are used in *eSet* and associated classes are also used here. As such, knowledge of the *Biobase development and the new eSet* vignette² would be beneficial.

The initial goal is to use the *MSnbase* infrastructure for labelled quantitation using reporter ions (iTRAQ [2] and TMT [3]). Spectral counting should be trivial to apply with current features, as long as identification data is at hand. Currently, no effort is invested to streamline label-free quantitative proteomics, although some effort has been done to keep the infrastructure flexible enough to accommodate more designs.

2 MSnbase classes

All classes have a `__classVersion__` slot, of class `Versioned` from the *Biobase* package. This slot documents the class version for any instance to be used for debugging and object update purposes. Any change in a class implementation should trigger a version change.

¹<https://github.com/lgatto/MSnbase/issues>

²The vignette can directly be accessed with `vignette("BiobaseDevelopment", package="Biobase")` once *Biobase* is loaded.

2.1 pSet: a virtual class for raw mass spectrometry data and meta data

This virtual class is the main container for mass spectrometry data, i.e spectra, and meta data. It is based on the eSet implementation for genomic data. The main difference with eSet is that the assayData slot is an environment containing any number of Spectrum instances (see section 2.6).

One new slot is introduced, namely processingData, that contains one MSnProcess instance (see section 2.4). and the experimentData slot is now expected to contain MIAPE data (see section 2.5). The annotation slot has not been implemented, as no prior feature annotation is known in shotgun proteomics.

```
getClass("pSet")
Virtual Class "pSet" [package "MSnbase"]

Slots:

Name:          assayData          phenoData
Class:          environment NAnnotatedDataFrame

Name:          featureData         experimentData
Class:  AnnotatedDataFrame         MIAxE

Name:          protocolData        processingData
Class:  AnnotatedDataFrame         MSnProcess

Name:          .cache      .__classVersion__
Class:          environment          Versions

Extends: "Versioned"

Known Subclasses: "MSnExp"
```

Future work Currently, few setters have been implemented.

2.2 MSnExp: a class for MS experiments

MSnExp extends pSet to store MS experiments. It does not add any new slots to pSet. Accessors and setters are all inherited from pSet and new ones should be implemented for pSet. Methods that manipulate actual data in experiments are implemented for MSnExp objects.

```
getClass("MSnExp")
Class "MSnExp" [package "MSnbase"]
```

```

Slots:

Name:          assayData          phenoData
Class:         environment NAnnotatedDataFrame

Name:          featureData        experimentData
Class:  AnnotatedDataFrame        MIAxE

Name:          protocolData        processingData
Class:  AnnotatedDataFrame        MSnProcess

Name:          .cache      .__classVersion__
Class:         environment        Versions

Extends:
Class "pSet", directly
Class "Versioned", by class "pSet", distance 2

```

2.3 MSnSet: a class for quantitative proteomics data

This class stores quantitation data and meta data after running `quantify` on an `MSnExp` object. The quantitative data is in form of a $n \times m$ matrix, where m is the number of features/spectra originally in the `MSnExp` used as parameter in `quantify` and n is the number of reporter ions (see section 2.7).

This prompted to keep a similar implementation as the `ExpressionSet` class, while adding the proteomics-specific annotation slot introduced in the `pSet` class, namely `processingData` for objects of class `MSnProcess` (see section 2.4).

The `MSnSet` class extends the virtual `eSet` class to provide compatibility for `ExpressionSet`-like behaviour. The experiment meta-data in `experimentData` is also of class `MIAPE` (see section 2.5). The annotation slot, inherited from `eSet` is not used.

```

getClass("MSnSet")

Class "MSnSet" [package "MSnbase"]

Slots:

Name:          experimentData        processingData          qual
Class:         MIAPE                MSnProcess                data.frame

Name:          assayData          phenoData          featureData
Class:         AssayData AnnotatedDataFrame AnnotatedDataFrame

Name:          annotation          protocolData      .__classVersion__

```

```

Class:          character AnnotatedDataFrame          Versions

Extends:
Class "eSet", directly
Class "VersionedBiobase", by class "eSet", distance 2
Class "Versioned", by class "eSet", distance 3

```

2.4 MSnProcess: a class for logging processing meta data

This class aims at recording specific manipulations applied to MSnExp or MSnSet instances. The processing slot is a character vector that describes major processing. Most other slots are of class logical that indicate whether the data has been centroided, smoothed, ... although many of the functionality is not implemented yet. Any new processing that is implemented should be documented and logged here.

It also documents the raw data file from which the data originates (files slot) and the *MSnbase* version that was in use when the MSnProcess instance, and hence the MSnExp/MSnSet objects, were originally created.

```

getClass("MSnProcess")

Class "MSnProcess" [package "MSnbase"]

Slots:

Name:          files          processing          merged
Class:         character      character          logical

Name:          cleaned        removedPeaks        smoothed
Class:         logical        character          logical

Name:          trimmed        normalised        MSnbaseVersion
Class:         numeric        logical          character

Name:  __classVersion__
Class:          Versions

Extends: "Versioned"

```

2.5 MIAPE: Minimum Information About a Proteomics Experiment

The Minimum Information About a Proteomics Experiment [4, 5] MIAPE class describes the experiment, including contact details, information about the mass spectrometer and control and analysis software.

```
getClass("MIAPE")
```

```
Class "MIAPE" [package "MSnbase"]
```

```
Slots:
```

```
Name:          title          url
Class:         character      character
```

```
Name:          abstract      pubMedIds
Class:         character      character
```

```
Name:          samples      preprocessing
Class:         list         list
```

```
Name:          other      dateStamp
Class:         list       character
```

```
Name:          name          lab
Class:         character      character
```

```
Name:          contact      email
Class:         character      character
```

```
Name:          instrumentModel  instrumentManufacturer
Class:         character        character
```

```
Name:  instrumentCustomisations      softwareName
Class:         character              character
```

```
Name:          softwareVersion      switchingCriteria
Class:         character             character
```

```
Name:          isolationWidth      parameterFile
Class:         numeric             character
```

```
Name:          ionSource      ionSourceDetails
Class:         character      character
```

```
Name:          analyser      analyserDetails
Class:         character      character
```

```
Name:          collisionGas      collisionPressure
Class:         character        numeric
```

```

Name:      collisionEnergy      detectorType
Class:      character           character

Name:      detectorSensitivity  __classVersion__
Class:      character           Versions

Extends:
Class "MIAxE", directly
Class "Versioned", by class "MIAxE", distance 2

```

2.6 Spectrum et al.: classes for MS spectra

Spectrum is a virtual class that defines common attributes to all types of spectra. MS1 and MS2 specific attributes are defined in the Spectrum1 and Spectrum2 classes, that directly extend Spectrum.

```

getClass("Spectrum")

Virtual Class "Spectrum" [package "MSnbase"]

Slots:

Name:      msLevel      peaksCount      rt
Class:      integer      integer          numeric

Name:      acquisitionNum  scanIndex      tic
Class:      integer      integer          numeric

Name:      mz      intensity      fromFile
Class:      numeric      numeric      integer

Name:      centroided __classVersion__
Class:      logical      Versions

Extends: "Versioned"

Known Subclasses: "Spectrum2", "Spectrum1"

```

```

getClass("Spectrum1")

Class "Spectrum1" [package "MSnbase"]

Slots:

Name:      polarity      msLevel      peaksCount
Class:      integer      integer      integer

```

Name:	rt	acquisitionNum	scanIndex
Class:	numeric	integer	integer
Name:	tic	mz	intensity
Class:	numeric	numeric	numeric
Name:	fromFile	centroided	.__classVersion__
Class:	integer	logical	Versions

Extends:

Class "Spectrum", directly

Class "Versioned", by class "Spectrum", distance 2

```
getClass("Spectrum2")
```

Class "Spectrum2" [package "MSnbase"]

Slots:

Name:	merged	precScanNum	precursorMz
Class:	numeric	integer	numeric
Name:	precursorIntensity	precursorCharge	collisionEnergy
Class:	numeric	integer	numeric
Name:	msLevel	peaksCount	rt
Class:	integer	integer	numeric
Name:	acquisitionNum	scanIndex	tic
Class:	integer	integer	numeric
Name:	mz	intensity	fromFile
Class:	numeric	numeric	integer
Name:	centroided	.__classVersion__	
Class:	logical	Versions	

Extends:

Class "Spectrum", directly

Class "Versioned", by class "Spectrum", distance 2

2.7 ReporterIons: a class for isobaric tags

The iTRAQ and TMT (or any other peak of interest) are implemented ReporterIons instances, that essentially defines an expected MZ position for the peak and a width around this value as well a names for the reporters.

```
getClass("ReporterIons")
Class "ReporterIons" [package "MSnbase"]

Slots:

Name:          name      reporterNames      description
Class:         character  character        character

Name:          mz        col        width
Class:         numeric   character    numeric

Name:  __classVersion__
Class:      Versions

Extends: "Versioned"
```

2.8 NAnnotatedDataFrame: multiplexed AnnotatedDataFrames

The simple expansion of the AnnotatedDataFrame classes adds the multiplex and multiLabel slots to document the number and names of multiplexed samples.

```
getClass("NAnnotatedDataFrame")
Class "NAnnotatedDataFrame" [package "MSnbase"]

Slots:

Name:          multiplex      multiLabels      varMetadata
Class:         numeric        character        data.frame

Name:          data      dimLabels  __classVersion__
Class:         data.frame  character    Versions

Extends:
Class "AnnotatedDataFrame", directly
Class "Versioned", by class "AnnotatedDataFrame", distance 2
```

3 Miscellaneous

Unit tests *MSnbase* implements unit tests with the *testthat* package.

Processing methods Methods that process raw data, i.e. spectra should be implemented for Spectrum objects first and then eapply'ed (or similar) to the assayData slot of an MSnExp instance in the specific method.

4 Session information

- R version 3.2.1 (2015-06-18), x86_64-w64-mingw32
- Locale: LC_COLLATE=C, LC_CTYPE=English_United States.1252, LC_MONETARY=English_United States.1252, LC_NUMERIC=C, LC_TIME=English_United States.1252
- Base packages: base, datasets, grDevices, graphics, grid, methods, parallel, stats, stats4, utils
- Other packages: AnnotationDbi 1.30.1, Biobase 2.28.0, BiocGenerics 0.14.0, BiocParallel 1.2.6, GenomInfoDb 1.4.1, IRanges 2.2.4, MLInterfaces 1.48.0, MSnbase 1.16.2, ProtGenerics 1.0.0, Rcpp 0.11.6, RcppClassic 0.9.6, Rdisop 1.28.0, S4Vectors 0.6.0, XML 3.98-1.2, annotate 1.46.0, cluster 2.0.2, ggplot2 1.0.1, gplots 2.17.0, knitr 1.10.5, mzR 2.2.1, pRoloc 1.8.0, pRolocdata 1.6.0, reshape2 1.4.1, zoo 1.7-12
- Loaded via a namespace (and not attached): BiocInstaller 1.18.3, BiocStyle 1.6.0, BradleyTerry2 1.0-6, DBI 0.3.1, FNN 1.1, KernSmooth 2.23-14, MALDIquant 1.12, MASS 7.3-41, Matrix 1.2-1, RColorBrewer 1.1-2, RCurl 1.95-4.6, RSQLite 1.0.0, SparseM 1.6, affy 1.46.1, affyio 1.36.0, biomaRt 2.24.0, bitops 1.0-6, brglm 0.5-9, caTools 1.17.1, car 2.0-25, caret 6.0-47, class 7.3-12, codetools 0.2-11, colorspace 1.2-6, digest 0.6.8, doParallel 1.0.8, e1071 1.6-4, evaluate 0.7, foreach 1.4.2, formatR 1.2, futile.logger 1.4.1, futile.options 1.0.0, gdata 2.16.1, genefilter 1.50.0, gtable 0.1.2, gtools 3.5.0, highr 0.5, impute 1.42.0, iterators 1.0.7, kernlab 0.9-20, labeling 0.3, lambda.r 1.1.7, lattice 0.20-31, limma 3.24.11, lme4 1.1-8, lpSolve 5.6.11, magrittr 1.5, mclust 5.0.1, mgcv 1.8-6, minqa 1.2.4, munsell 0.4.2, mvtnorm 1.0-2, mzID 1.6.0, nlme 3.1-120, nloptr 1.0.4, nnet 7.3-9, pbkrtest 0.4-2, pcaMethods 1.58.0, pls 2.4-3, plyr 1.8.3, preprocessCore 1.30.0, proto 0.3-10, proxy 0.4-14, quantreg 5.11, randomForest 4.6-10, rda 1.0.2-2, rpart 4.1-9, sampling 2.6, scales 0.2.5, sfsmisc 1.0-27, snow 0.3-13, splines 3.2.1, stringi 0.5-2, stringr 1.0.0, survival 2.38-2, tools 3.2.1, vsn 3.36.0, xtable 1.7-4, zlibbioc 1.14.0

References

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