

# Package ‘qqqMS’

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**Type** Package

**Title** Peak Detection for MRM-MS data

**Version** 0.0.99

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**Description** Simple wrappers for post-acquisition processing of Multiple Reaction Monitoring (MRM) Mass Spectrometry (MS) data using xcms.

**License** GPL (>= 3)

**Depends** xcms, methods

**Imports** MSnbase

**Suggests** testthat, covr

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**NeedsCompilation** no

## R topics documented:

extract_targets . . . . .	<a href="#">1</a>
integrate_peaks . . . . .	<a href="#">2</a>

<b>Index</b>	<a href="#">3</a>
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extract_targets	<i>Extract Targets</i>
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## Description

Use a user-defined list of MRM-MR targets to create a filtered feature values matrix

**Usage**

```
extract_targets(features, targets)
```

**Arguments**

- |          |  |
|----------|--|
| features | a list which has been produced using the <a href="#">integrate_peaks</a> function  |
| targets  | a data.frame of MRM-MS targets to extract the the xcms processed object. targets must contain the following columns; <ul style="list-style-type: none"> <li>• <b>name</b> the generic name of the target</li> <li>• <b>mz</b> the m/z value of the target (as it appears in the raw file)</li> <li>• <b>rt</b> the approximate retention time of the target</li> </ul> |

**Value**

a data.frame of feature values for only those which corresponds to an identified target

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integrate_peaks	<i>Detect and integrate MRM-MS features</i>
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**Description**

Use the matchedFilter algorithm xcms for feature detection in MRM-MS which have been converted to LC-MS style .mzML files.

**Usage**

```
integrate_peaks(files, phenoData, pol)
```

**Arguments**

- |           |   |
|-----------|---|
| files     | a character vector of .mzML files which have been converted from MRM-MS .mzML to LC-MS style .mzML files using MRMConverter   |
| phenoData | a data.frame. phenoData must contain the following columns; <ul style="list-style-type: none"> <li>• <b>fileName</b> file name</li> <li>• <b>name</b> sample name</li> </ul> Providing these two columns are present; phenoData can contain as many other columns as the user wishes. |
| pol       | a character string of either 1 for positive mode or -1 for negative mode. If input data only contains one polarity mode, then polarity can be NULL  |

**Value**

a list of two elements

- values values for the integrated peak areas of all features detected
- definitions a data.frame of feature definitions. See [XCMSnExp-class](#) for more details

# Index

extract\_targets, [1](#)

integrate\_peaks, [2](#), [2](#)