

# Package ‘qcmetrics’

April 15, 2017

**Type** Package

**Title** A Framework for Quality Control

**Version** 1.12.0

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**Description** The package provides a framework for generic quality control of data. It permits to create, manage and visualise individual or sets of quality control metrics and generate quality control reports in various formats.

**Depends** R (>= 2.10)

**Imports** Biobase, methods, knitr, tools, Nozzle.R1, xtable, pander, S4Vectors

**Suggests** affy, MSnbase, ggplot2, lattice, yaqcaffy, MAQCsubsetAFX, RforProteomics, AnnotationDbi, mzR, hgu133plus2cdf, BiocStyle

**License** GPL-2

**URL** <https://github.com/lgatto/qcmetrics>

**biocViews** Software, QualityControl, Proteomics, Microarray, MassSpectrometry, Visualization, ReportWriting

**VignetteBuilder** knitr

**NeedsCompilation** no

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n15qc

*N15 labelling QC report***Description**

A simple wrapper for the QC of 15N labelling. The respective QC items are the distribution of PSM incorporation rates, distribution of log<sub>2</sub> fold-changes and number of identified features. See the vignette for details.

**Usage**

```
n15qc(object,
      fcol = c("Protein_Accession", "Peptide_Sequence", "Number_Of_Unique_Peptides", "Variable_Modifications"),
      inctr = 97.5, lfctr = c(-0.5, 0.5), type, reportname)
```

**Arguments**

object	An MSnSet to be quality controlled.
fcol	The name of the feature variables for the protein identifiers (accession numbers for example), the peptide sequences, the number of unique peptides for each identified protein, the variable modifications identified on the peptides and the N15 incorporation rate. These must be provided in that order. Defaults are Protein_Accession, Peptide_Sequence, Number_Of_Unique_Peptides, Variable_Modifications, and inc.
inctr	The minimum level of median incorporation rate to set the QC item status to TRUE. Default is 97.5.
lfctr	The range of accepted median PSM log <sub>2</sub> fold-change for the QC item status to be set to TRUE. Default is c(-0.5, 0.5).
type	The type of report to be saved. If missing (default), no report is generated. See <a href="#">qcReport</a> for details.
reportname	The name of the report, in case a type is defined. If missing (default), the report will be named n15qcreport followed by the generation data and time.

**Value**

Invisibly returns the resulting QcMetrics instance.

**Author(s)**

Laurent Gatto

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psm	<i>15N example data</i>
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**Description**

An example data for <sup>15</sup>N metabolic labelling, distributed as an MSnSet to illustrate <sup>15</sup>N QC.

**Usage**

```
data(n15psm)
```

**References**

See MSnSet and the MSnbase-demo vignette in the MSnbase package.

**Examples**

```
library("MSnbase")
data(n15psm)
psm
```

---

Qc2Tex	<i>'QcMetric' sectioning functions</i>
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**Description**

These functions convert the *i*th QcMetric instance of the QcMetrics object into a section of the adequate format, i.e. TeX or R markdown.

**Usage**

```
Qc2Tex(object, i)
Qc2Tex2(object, i)
Qc2Tex3(object, i)
Qc2Rmd(object, i)
```

**Arguments**

object	An instance of class QcMetrics with at least one QC item.
i	A numeric of length 1 indicating the index of the item to be converted into text section.

**Value**

A character representing the QC item section.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

[qcReport](#) and the vignette.

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QcMetadata-class      *The "QcMetadata" class*

---

**Description**

The QcMetadata class is a simple interface to metadata. The objects can be displayed with `show` for a summary and `print` for the content.

**Objects from the Class**

Objects can be created by calls of the form `QcMetadata(...)`.

**Slots**

**metadata**: Object of class "list" that stores the metadata variables. The list must be named. NA and empty characters are not allowed.

**Methods**

[ signature(x = "QcMetadata"): subsets x as a new QcMetadata instance.

[[ signature(x = "QcMetadata"): extracts a single element of x.

**metadata** signature(x = "QcMetadata"): return the object's metadata list. Also available as `mdata`.

**metadata<-** signature(x = "QcMetadata", value = "list"): sets the objects metadata. Also available as `mdata`.

**length** signature(x = "QcMetadata"): returns the number of metadata variables.

**names** signature(x = "QcMetadata"): returns the names of the metadata variables.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
QcMetadata(metadata =
  list(name = "John Doe",
        lab = "Big Lab in Big Uni"))
## less typing
qmd <- QcMetadata(list(name = "John Doe",
                      lab = "Big Lab in Big Uni"))

mdata(qmd)
show(qmd)
print(qmd)
```

---

QcMetric-class                      *The "QcMetric" class for QC items*

---

## Description

Data structure for individual QC metrics items.

## Objects from the Class

Objects can be created using the constructor `QcMetric(...)`, where slots are assigned individually. See example below.

## Slots

**name:** Object of class "character" of length 1 naming the object.

**description:** Object of class "character" of arbitrary length describing the qc metric in more details.

**qcddata:** Object of class "environment" that stores the actual data.

**plot:** Object of class "function" to graphically represent the data and infer quality status.

**show:** Object of class "function" to print a short textual representation of the object. A reasonable default value is provided.

**status:** Object of class "logical" that indicates whether the data passes (TRUE) or fails (FALSE) the metric or has not yet been evaluated.

## Methods

**name** signature(object = "QcMetric"): retrieves the name of the object.

**name<-** signature(object = "QcMetric", value = "character"): set the name of the object.

**description** signature(object = "QcMetric"): retrieves the description of the object.

**description<-** signature(object = "QcMetric", value = "character"): set the description of the object.

**status** signature(object = "QcMetric"): retrieves the status of the object.

**status<-** signature(object = "QcMetric", value = "logical"): sets the status of the objects.

**qcddata** signature(object = "QcMetric", x = "missing"): lists all the data objects that are associated with the objects.

**qcddata** signature(object = "QcMetric", x = "character"): retrieves the variable x for the object.

**qcddata<-** signature(object = "QcMetric", var): creates or overwrites (with a message) the data variable var by assigning the RHS value. If var is missing and the RHS expression is an environment, then qcddata is reset with all the variables in value.

**qcenv** signature(object = "QcMetric"): return the environment that stores the QC data.

**qcenv<-** signature(object = "QcMetric"): Set all variable in the RHS environment as qcddata variables. Equivalent to `qcddata(object) <- x` where x is an environment.

**show** signature(object = "QcMetric"): shows a textual summary of object. The default show implementation is available as the qcshow{object, qcdata} function. The second argument is a logical (default is TRUE) that specifies whether qcdata(object) should be displayed.

**show<-** signature(object = "QcMetric", value = "function"): sets a custom show method for object.

**plot** signature(x = "QcMetric", y = "missing"): plots the object using the provide show method.

**plot<-** signature(object = "QcMetric", value = "function"): sets a custom plot method for object.

**qcReport** signature(x = "QcMetric", ...): to generate quality reports. See [qcReport](#) for details.

### Author(s)

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### See Also

The [QcMetrics](#) class to bundle a set of QcMetric instances.

### Examples

```
(qc <- QcMetric())
qcdata(qc)
try(qcdata(qc, "x"))

x <- rnorm(10)
qcdata(qc, "qc1") <- x
qcdata(qc, "qc2") <- 1:10
qcdata(qc)
all.equal(qcdata(qc, "qc1"), x)
all.equal(qcdata(qc, "qc2"), 1:10)
name(qc) <- "My test QcMetric"
description(qc) <- "This qc metric describes bla bla bla, indicating possible issues in the third step of prot"
status(qc) <- FALSE
qc

## or
e <- new.env()
e$qc1 <- rnorm(100)
e$qc2 <- 1:100
qcdata(qc) <- e
length(qcdata(qc, "qc1"))
head(qcdata(qc, "qc2"))

show(qc)
show(qc) <- function(object) cat("Updated show method\n")
show(qc)
show(qc) <- qcshow
qc

plot(qc)
plot(qc) <-
  function(object, ...)
```

```

        plot(qcdata(object, "qc2"),
             qcdata(object, "qc1"),
             xlab = "qc1",
             ylab = "qc2",
             ...)
plot(qc)
plot(qc, col = "red", pch = 19)

## Not run:
## generate a report
qcReport(qcm)

## End(Not run)

```

---

QcMetrics-class

*The "QcMetrics" class for collections of QC items*


---

## Description

Data structure for storing lists of QcMetric items.

## Objects from the Class

Objects can be created using the constructor `QcMetrics(...)`, where slots are assigned individually. See example below.

In a standardised quality control pipeline, the `QcMetrics` and `QcMetric` object are not generated manually. Their creation is delegated to a wrapper function that reads a specific type of files, parses the data, produces the individual `QcMetric` instances and, eventually, the `QcMetric` object. See the package vignette for details and examples.

## Slots

**metadata:** Object of class `QcMetadata` storing the metadata of the object. This list would typically contain the input file the data was read from, the date the object was generated, ... or fully fledged *minimum information* descriptions (see `MIAXE`), when available.

**qcdata:** Object of class "list" storing all the individual `QcMetric` instances.

## Methods

[ signature(x = "QcMetrics"): subsets x as a new `QcMetrics` instance.

[[ signature(x = "QcMetrics"): extracts a single `QcMetric` instance.

**length** signature(x = "QcMetrics"): returns the number of `QcMetric` instances populate x.

**metadata** signature(x = "QcMetrics"): return the object's metadata list. Also available as `mdata`.

**metadata<-** signature(x = "QcMetrics", value = "list"): sets the objects metadata. Also available as `mdata`.

**metadata<-** signature(x = "QcMetric", value = "QcMetadata"): sets the objects metadata. Also available as `mdata`.

**name** signature(object = "QcMetrics"): returns a character vector of length `length(object)` with the names of the `QcMetric` instances.

**qcdata** signature(object = "QcMetrics", x = "missing"): returns a list of all QcMetric instances.

**qcdata<-** signature(object = "QcMetrics", value = "list"): sets the qcdata of object.

**show** signature(object = "QcMetrics"): prints a short textual description of object.

**status** signature(object = "QcMetrics"): returns a vector of quality statuses (logicals).

**status<-** signature(object = "QcMetrics", value = "logical"): sets the quality statuses. Length of value and object must be identical.

**as** signature(object = "QcMetrics", "data.frame"): coerces object as a length(object) by 2 data frame with the respective QcMetric instances names and statuses.

**qcReport** signature(object = "QcMetrics"): ...

### Author(s)

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### See Also

The [QcMetric](#) class for individual QC items.

### Examples

```
example(QcMetric)
show(qc)

qc2 <- QcMetric(name = "My other metric", status = TRUE)
qcdata(qc2, "x") <- rnorm(100)
qcdata(qc2, "k") <- rep(LETTERS[1:2], 50)

plot(qc2) <- function(object, ...) {
  require("lattice")
  d <- data.frame(x = qcdata(object, "x"),
                 k = qcdata(object, "k"))
  bwplot(x ~ k, data = d)
}

qcm <- QcMetrics(qcdata = list(qc, qc2))
qcm

qcm[1] ## a QcMetrics instance
qcm[[1]] ## a single QcMetric

metadata(qcm)
metadata(qcm) <- QcMetadata(list(name = "Prof. Who",
                                lab = "Cabin University"))
## or, shorter but equivalent
metadata(qcm) <- list(name = "Prof. Who",
                    lab = "Cabin University")
metadata(qcm) ## or mdata(qcm)
## update metadata
metadata(qcm) <- list(lab = "Big lab", ## updated
                    uni = "Cabin University") ## added
mdata(qcm)
```



## Description

The `qcReport` method generates report in various formats taking a `QcMetrics` instance as input. Each individual quality control item produces a section with description of the item and a assessment figure.

## Details

The reporting functions take a `QcMetrics` instance as input, generate the source of the report and compile it into the final format that are currently available are `reporting_pdf`, `reporting_tex`, `reporting_rmd`, `reporting_html` and `reporting_nozzle`. See `qcto` for details about the sectioning functions, that convert individual `QcMetric` objects into adequate report sections.

The package vignette documents the report generation in more details and describes possibilities for customisation.

## Methods

`signature( object = "QcMetrics", reportname = "character", type = "character", author = "character")` generates a report for the `QcMetrics` object. The report will be named according the `reportname` (default is `qcprpt`) and `type`, the latter defining the output format and the extension. Possible types are `pdf` (default), `"tex"`, `"Rmd"`, `"html"` (all generated using the package `knitr`) and `"nozzle"` (generated using the package `Nozzle.R1` package.) A custom title can be provided; default is "Quality control report generated with `qcmetrics`". If no author is provided, the default value (`Sys.getenv("USER")`) is used. The addition of a table of contents (default is `FALSE`), a metadata section, a summary section and the session information can be controlled with the `toc`, `metadata`, `summary` and `sessioninformation` arguments. The metadata section is added to the report when present and the other have `TRUE` as default.

It is possible to supply custom templates using the `template` arguments. Intermediate files are deleted, unless `clean` is set to `FALSE` and verbose output can be turned on by setting `quiet` to `FALSE`.

The `reporter` and `qcto` arguments are used to convert `QcMetric` and `QcMetrics` objects into report source. See Details and the package vignette for details.

Addition parameters can be passed to inner functions. For the `pdf` report, passed to `texi2pdf`; for `html`, passed to `markdown::markdownToHTML`.

The method invisibly returns the name of the report that was generated.

## Examples

```
example(QcMetrics)
show(qcm)

destdir <- tempdir()
(report <- file.path(destdir, "testQCReport"))

## pdf report
qcReport(qcm, reportname = report)

## Not run:
```

```

## use pdflatex to generate the pdf file
qcReport(qcm, reportname = report, texi2dvi = "pdflatex")

## End(Not run)

## default html report
html <- qcReport(qcm, reportname = report, type = "html")
html
if (interactive())
  browseURL(html)

## using a custom css templates
writeLines("
body {
  font-size: 14pt;
  width: 650px;
  background: #789855;
  margin-left: auto;
  margin-right: auto;
  margin-top: 20px;
  margin-bottom: 20;
  text-align: justify;
}", con = "style.css")

html2 <- qcReport(qcm, reportname = "customreport", template = "style.css", type = "html")
if (interactive())
  browseURL(html2)

```

---

rnadeg

*A simple RNA degradation QC for Affymetrix arrays*


---

## Description

A simple wrapper function that uses *affy*'s RNA degradation curves and *yaqc*'s actin and GAPDH 3'/5' ratios to generate a simple RNA degradation *QcMetrics* results. Optionally generates a QC report. See the *qcmetrics* vignette for an explanation of the function and an example.

## Usage

```
rnadeg(input, status, type,
       reportname = "rnadegradation")
```

## Arguments

input	A character of CEL file names or an instance of class <i>affybatch</i> .
status	A logical of length 2 to set the respective <i>QcMetric</i> 's statuses.
type	The type of the report to be generated. Is missing, no report is generated.
reportname	The name of the report.

## Value

Invisibly return the *QcMetrics* for the input.

**Author(s)**

Laurent Gatto

**See Also**

[QcMetric](#) and [QcMetrics](#) for details about the QC infrastructure and [qcReport](#) for information about the report generation.

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