Package 'qcmetrics'

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Type Package

Title A Framework for Quality Control

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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

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URL https://github.com/lgatto/qcmetrics

biocViews Software, Bioinformatics, QualityControl, Proteomics,
Microarray, MassSpectrometry, Visualisation, ReportWriting

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

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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 log2 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_Modifica
   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 log2 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 qcReport for details.
reportname	The name of the report, in case a type is defined. If missing (default), the report will be names n15qcreport followed by the generation data and time.

Value

Invisibly returns the resulting QcMetrics instance.

Author(s)

Laurent Gatto

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psm   *15N example data*

Description

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

Usage

```
data(n15psm)
```

References

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

Examples

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

Qc2Tex   *'QcMetric' sectioning functions*

Description

These functions convert the ith QcMetric instance of the QcMetrics object into a section of the adequate format, i.e. TeX of 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)

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See Also

[qcReport](#) and the vignette.

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.

qcdata: 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 weather 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.

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

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

qcdata<- 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 qcdata 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 qcdata variables. Equivalent to qcdata(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 protocol
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)
```

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qcReport-methods   *Automatic report generation*

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 qcreprt)and type, the latter defining the output format and the extension. Possi-
ble 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 pro-
vided, 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)
```

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rnadeg   *A simple RNA degradation QC for Affymetrix arrays*

Description

A simple wrapper function that uses affy's RNA degradation curves and yaqcaffy'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 affybatch.
status	A logical of length 2 to set the respective QcMetric'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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