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
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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_Modifications", "inc"), 
  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
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 i-th 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.

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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)

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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)
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.

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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 bla bla bla."
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, ...)
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.
**QcMetrics-class**

```r
qcd<signature(object = "QcMetrics", value = "list")
```

sets the qcd of object.

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

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

```r
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"): ...

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**See Also**

The `QcMetric` class for individual QC items.

**Examples**

```r
eexample(QcMetric)
show(qc)

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

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

qcm <- QcMetrics(qcd = 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

```r
signature( object = "QcMetrics", reportname = "character", type = "character", author = "character", title = "character", ... = "logical", sessioninfo = "logical", template = "character", clean = "logical", quiet = "logical", reporter, qcto, ... )
```

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. 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. Additional 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

```r
eexample(QcMetrics)
show(qcm)

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

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

## Not run:
```
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 qmetrics 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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