

arrayQualityMetrics

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addXYfromGAL

Computing the coordinates of the spots on a slide

Description

From the coordinates of the blocks of a microarray slide and the Row and Column locations of the spots within the blocks, `addXYfromGAL` computes the X and Y coordinates of the spots of a slide.

Usage

```
addXYfromGAL(x, gal.file, nBlocks, skip, ...)
```

Arguments

<code>x</code>	is an <code>AnnotatedDataFrame</code> representing the <code>featureData</code> of an object.
<code>gal.file</code>	name of the file <code>.gal</code> that contains the coordinates of the blocks.
<code>nBlocks</code>	number of blocks on the slide.
<code>skip</code>	number of header lines to skip when reading the <code>gal.file</code> .
<code>...</code>	Arguments that get passed on to <code>read.table</code> .

Value

The object `x` of class `AnnotatedDataFrame` will be returned with two added columns: X and Y corresponding to the absolute position of the probes on the array.

Author(s)

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```
arrayQualityMetrics
```

Quality metrics on microarray experiments

Description

arrayQualityMetrics performs quality metrics on [ExpressionSet](#), [AffyBatch](#), [NChannelSet](#), [BeadLevelList](#), [RGList](#), [MAList](#), [marrayRaw](#) or [marrayNorm](#) containing microarray data from any platforms, one or two channels. The results, presented in a HTML report, are designated to allow the user to rapidly assess the quality of a set of arrays.

Usage

```
## S4 method for signature 'ExpressionSet':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)

arrayQualityMetrics(expressionset,
                     outdir = getwd(),
                     force = FALSE,
                     do.logtransform = FALSE,
                     split.plots = FALSE,
                     intgroup = "Covariate",
                     grouprep = FALSE)

## S4 method for signature 'AffyBatch':
arrayQualityMetrics(expressionset, outdir, force,
do.logtransform, split.plots, intgroup, grouprep)
## S4 method for signature 'NChannelSet':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)
## S4 method for signature 'BeadLevelList':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)
## S4 method for signature 'RGList':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)
## S4 method for signature 'MAList':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)
## S4 method for signature 'marrayRaw':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)
## S4 method for signature 'marrayNorm':
arrayQualityMetrics(expressionset, outdir,
force, do.logtransform, split.plots, intgroup, grouprep)
```

Arguments

expressionset

is an object of class [ExpressionSet](#), [AffyBatch](#), [NChannelSet](#), [BeadLevelList](#), [RGList](#), [MAList](#), [marrayRaw](#) or [marrayNorm](#).

<code>outdir</code>	is the name of the directory in which the results are created.
<code>force</code>	if TRUE, <code>outdir</code> will be overwritten if it already exists.
<code>do.logtransform</code>	If TRUE, the data are log transformed before the analysis.
<code>split.plots</code>	If the number of studied array is more than 50 it is advised to define a number of experiments to represent on the density plots.
<code>intgroup</code>	Name of the column of the <code>phenoData</code> to be used to draw a color side bar next to the heatmap.
<code>grouprep</code>	Decide if you want the boxplots and density plots to be coloured function of the groups set by <code>'intgroup'</code> . The default is FALSE meaning that the boxplot and density plots will not be represented function of the groups of <code>'intgroup'</code> .

Value

A directory `outdir` containing a HTML report named `QMreport.html` and all the PNG and PDF plots is created.

Author(s)

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Examples

```
## Not run:
library(ALLMLL)
data(MLL.A)
arrayQualityMetrics(expressionset = MLL.A,
                    outdir = "MLL",
                    do.logtransform = TRUE,
                    split.plots = 10)
# "QMreport.html" is a report created in the "MLL" directory
# on the logarithm expression data of the MLL.A AffyBatch.
# 10 experiments are represented by density plots.

## End(Not run)
```

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