arrayQualityMetrics

April 20, 2011

`aqm.boxplot`	*Compute boxplots, density plots, heatmap, PCA biplot on a aqmobj.prepdata object.*

Description

The functions do boxplots, density plots, heatmap, PCA biplot and produce output objects ready for rendering by `aqm.plot`.

Usage

```
aqm.boxplot(expressionset, dataprep, intgroup, subsample = 10000, ...)
aqm.density(expressionset, dataprep, intgroup, outliers, ...)
aqm.heatmap(expressionset, dataprep, intgroup, ...)
aqm.pca(expressionset, dataprep, intgroup, outliers, ...)
```

Arguments

`expressionset, dataprep, intgroup`
Same as for the function `arrayQualityMetrics`

`outliers` Indicates arrays to be highlighted as potential outliers in the plots.

`subsample` For the boxplot computations, if the arrays have more features than indicates by this number, then randomly subsample that number of them.

`...` These arguments get passed on to `bwplot` (in the case of `aqm.boxplot`), `xyplot` (in the case of `aqm.density`), `levelplot` (in the case of `aqm.heatmap`)

Details

See `aqm.prepdata` and the `aqm` Vignette.

Value

An object of class `aqmobj.box`, `aqmobj.dens` or `aqmobj.heat`, respectively.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqm.prepdata, aqmobj.prepdata, aqmobj.box

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aqm.maplot *Performs MA-plots on aqmobj.prepdata objects.*

Description

aqm.maplot performs MA-plots, outlier detection from it and formats the output for aqm.plot usage.

Usage

```
aqm.maplot(dataprep, ...)
```

Arguments

dataprep	An object of class aqmobj.prepdata
...	Any arguments to panel.smoothScatter

Details

See aqm.prepdata and the aqm Vignette.

Value

An object of class aqmobj.ma.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqm.prepdata, aqmobj.prepdata, aqmobj.ma

---

aqm.meansd *Performs Mean/SD plot on aqmobj.prepdata objects.*

Description

aqm.meansd performs Mean/SD plot, and formats the output for aqm.plot usage.

Usage

```
aqm.meansd(dataprep, ...)
```

Arguments

`dataprep`	An object of class `aqmobj.prepdata`
`...`	Any arguments to `meanSdPlot`

Details

See `aqm.prepdata` and the `aqm` Vignette.

Value

An object of class `aqmobj.msd`.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.prepdata`, `aqmobj.prepdata`, `aqmobj.msd`

`aqmobj.box-class` *Class to contain data generated from the aqm.boxplot, aqm.heatmap, aqm.maplot, aqm.spatial, aqm.nuse and aqm.rle functions.*

Description

Class to contain data generated from `aqm.boxplot`, `aqm.heatmap`, `aqm.maplot`, `aqm.spatial`, `aqm.nuse` and `aqm.rle`.

Details

See `aqm.prepdata`, `aqm.prepaffy` and the `aqm` Vignette.

Slots

- `plot`**:** In the case of `aqmobj.box` or `aqmobj.spatial`, an object of class `trellis.object` if one channel arrays and a list of trellis.object if several channels arrays. In the case of `aqmobj.heat`, `aqmobj.ma` , `aqmobj.nuse` or `aqmobj.rle`, an object of class `trellis.object`.
- `section`**:** A character string with a name for the section the plot belongs to in the report.
- `title`**:** A character string with the title of the plot to be written in the report.
- `legend`**:** A character string with the legend of the plot to be written in the report.
- `scores`**:** A numeric for each array corresponding to the scores assessed from the plot.
- `outliers`**:** List or integer of the arrays that are outliers using the function `boxplot.stats` on the scores.
- `shape`**:** A character "square" or "rect" depending on the aspect ratio desired in the report.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqm.boxplot, aqm.heatmap, aqm.maplot, aqm.spatial, aqm.nuse, aqm.rle, aqm.plot

aqmobj.dens-class *Class to contain data generated from aqm.density, aqm.pca, aqm.spatialbg, aqm.probesmap, aqm.qcs.*

Description

Class to contain data generated from aqm.density, aqm.pca, aqm.spatialbg, aqm.probesmap, aqm.qcs.

Details

See the aqm.prepdata help or the aqm Vignette for example of this object.

Slots

plot: In the case of aqmobj.dens or aqmobj.spatialbg, an object of class trellis.object if one channel arrays and a list of trellis.object if several channels arrays. In the case of aqmobj.pca, aqmobj.probesmap or aqmobj.qcs, an object of class trellis.object.

section: A character string with a name for the section the plot belongs to in the report.

title: A character string with the title of the plot to be written in the report.

legend: A character string with the legend of the plot to be written in the report.

shape: A character "square" or "rect" depending on the aspect ratio desired in the report.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqm.density, aqm.pca, aqm.spatialbg, aqm.probesmap, aqm.qcstats, aqm.plot

aqmobj.msd-class *Class to contain data generated from aqm.meansd.*

Description

Class to contain data generated from aqm.meansd.

Details

See aqm.prepdata and the aqm Vignette.

Slots

- `plot`: A matrix to be represented calling the `meanSdPlot` function.
- `section`: A character string with a name for the section the plot belongs to in the report.
- `title`: A character string with the title of the plot to be written in the report.
- `legend`: A character string with the legend of the plot to be written in the report.
- `shape`: A character "square" or "rect" depending on the aspect ratio desired in the report.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.meansd`, `aqm.plot`

`aqmobj.pmmm-class` *Class to contain data generated from aqm.pmmm.*

Description

Class to contain data generated from `aqm.pmmm`.

Details

See `aqm.pmmm` and the `aqm` Vignette.

Slots

- `plot`: A list to be represented calling the `aqm.plot` function.
- `section`: A character string with a name for the section the plot belongs to in the report.
- `title`: A character string with the title of the plot to be written in the report.
- `legend`: A character string with the legend of the plot to be written in the report.
- `shape`: A character "square" or "rect" depending on the aspect ratio desired in the report.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.pmmm`, `aqm.plot`

aqmobj.prepaffy-class *Class to contain data generated from aqm.prepaffy.*

Description

Container for the output of aqm.prepaffy and for the input of the aqm.rle and aqm.nuse functions.

Details

See aqm.prepaffy and the aqm Vignette.

Slots

dataPLM: A PLMset.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

aqmobj.prepdata-class *Class to contain data generated from aqm.prepdata.*

Description

Container for the output of aqm.prepdata and for the input of the aqm functions.

Details

See aqm.prepdata and the aqm Vignette.

Slots

M: A matrix of the M values (log-ratio). The log-ratio is computed with the second channel being the median of the intensities across arrays in the case of one channel arrays.

A: A matrix of the A values. The A value is the mean of the two intensities. The second channel is computed as for the M values in the case of one channel arrays.

dat: A matrix with the log-ratio if two channels or the intensities if one channel.

rc: A matrix with the red channel intensities in the case of two channels arrays. NULL if one colour arrays.

gc: A matrix with the green channel intensities in the case of two channels arrays. NULL if one colour arrays.

rcb: A matrix with the red channel background intensities if two channels arrays and if available. NULL if one colour arrays.

gcb: A matrix with the green channel background intensities if two channels arrays and if available. NULL if one colour arrays.

- `outM`: The distance between each pairs of arrays, computed using `dist2` from the `genefilter` package.
- `sN`: Integers numbering the arrays to be used to label the plots.
- `numArrays`: An integer giving the number of arrays.
- `nchannels`: A numeric giving the number of channels.
- `logtransformed`: A logical telling if the data have been log transformed by the function aqm.prepdata.
- `classori`: A character string of the class of the object that was given as an input of the aqm.prepdata function.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.prepdata`, `aqm.boxplot`, `aqm.density`, `aqm.heatmap`, `aqm.maplot`, `aqm.meansd`, `aqm.probesmap`, `aqm.spatial`, `aqm.spatialbg`

`aqmobj.rnadeg-class` *Class to contain data generated from aqm.rnadegplot.*

Description

Class to contain data generated from `aqm.rnadegplot`.

Details

See `aqm.prepdata` and the `aqm` Vignette.

Slots

- `plot`: A list to be represented calling the `plotAffyRNAdeg` function.
- `section`: A character string with a name for the section the plot belongs to in the report.
- `title`: A character string with the title of the plot to be written in the report.
- `legend`: A character string with the legend of the plot to be written in the report.
- `shape`: A character "square" or "rect" depending on the aspect ratio desired in the report.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.rnadeg`, `aqm.plot`

`aqm.plot` *Performs plots from aqm objects.*

Description

`aqm.plot` performs plots.

Usage

```
aqm.plot(obj)
```

Arguments

`obj`	an object of class `aqmobj`

Details

See the aqm.prepdata help or the aqm Vignette for example of this object.

Value

A plot in the x11 device.

Author(s)

Audrey Kauffmann Maintainer: <kauffmann@bergonie.org>

`aqm.pmmm` *Performs perfect match versus mismatch density plots.*

Description

`aqm.pmmm` performs PM MM density curves on objects of class `AffyBatch` and formats the output for `aqm.plot` usage.

Usage

```
aqm.pmmm(expressionset, ...)
```

Arguments

`expressionset`	is an object of class `AffyBatch`
`...`	Any arguments to `density`

Value

An object of class `aqmobj.pmmm`.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqmobj.pmmm

Examples

```
library("ALLMLL")
data("MLL.A")
pm = aqm.pmmm(MLL.A)
class(pm)
aqm.plot(pm)
```

aqm.prepaffy *Preparation of Affymetrix experiments for RLE and NUSE.*

Description

aqm.prepaffy performs data preprocessing on AffyBatch and formats the output for aqm.rle and aqm.nuse usage.

Usage

```
aqm.prepaffy(expressionset)
```

Arguments

expressionset
is an object of class AffyBatch

Value

A preprocessed affy object of class aqmobj.prepaffy.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqm.rle, aqm.nuse

Examples

```
library(ALLMLL)
data(MLL.A)
MLLprep = aqm.prepdata(MLL.A, do.logtransform = TRUE)
MLLaffyprep = aqm.prepaffy(MLL.A)
nuse = aqm.nuse(MLL.A, MLLprep, MLLaffyprep)
class(nuse)
aqm.plot(nuse)
```

aqm.prepdata *Generate an object aqmobj.prepdata to be called by the aqm functions.*

Description

aqm.prepdata formats an ExpressionSet, an AffyBatch, a NChannelSet, or a BeadLevelList into a aqmobj.prepdata object which can be used as an input of the aqm functions.

Usage

```
aqm.prepdata(expressionset, do.logtransform = TRUE)
```

Arguments

expressionset
: An object of class ExpressionSet for one colour non Affymetrix data, AffyBatch for Affymetrix data, NChannelSet for two colour arrays, or BeadLevelList for Illumina bead arrays.

do.logtransform
: TRUE or FALSE whether or not you want to log transform the data.

Value

An object of class aqmobj.prepdata.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqmobj.prepdata, aqm.boxplot, aqm.density, aqm.heatmap, aqm.maplot, aqm.meansd, aqm.probesmap, aqm.spatial, aqm.spatialbg

Examples

```
## Load an example of a NChannelSet
library("CCl4")
data("CCl4")

## Normalization of CCl4 using vsn
library("vsn")
CCl4norm = justvsn(CCl4, subsample=2000)

## Add a column in the phenoData to annotate samples
cond = paste(pData(CCl4norm)$RIN.Cy3,pData(CCl4norm)$RIN.Cy5,sep="/")
poor = grep(cond,pattern="2.5")
medium = grep(cond,pattern="^5/|/5")
good = grep(cond,pattern="9.7")
cov = rep(0, length = nrow(pData(CCl4norm)))
cov[good] = "Good"
cov[medium] = "Medium"
cov[poor] = "Poor"
```

```
phenoData(CCl4norm)$RNAintegrity = cov

## Add X and Y columns in the featureData to allow spatial representations
featureData(CCl4norm)$X = featureData(CCl4norm)$Row
featureData(CCl4norm)$Y = featureData(CCl4norm)$Column

## Add a hasTarget column in the featureData to call aqm.probesmap
featureData(CCl4norm)$hasTarget = (regexpr("^NM",
                                   featureData(CCl4norm)$Name)> 0)


## Prepare the data for aqm.xxx calls
CCl4prep = aqm.prepdata(CCl4norm, do.logtransform = FALSE)

## Draw MA plots
ma = aqm.maplot(dataprep = CCl4prep)
class(ma)
aqm.plot(ma)

## Draw heatmap making use of the RNAintegrity
## column of the phenoData
hm = aqm.heatmap(expressionset = CCl4norm,
                 dataprep = CCl4prep,
                 intgroup = "RNAintegrity")
class(hm)
aqm.plot(hm)

## Draw probes mapping density curves making use of the hasTarget
## column of the featureData
sp = aqm.spatial(expressionset = CCl4norm,
                 dataprep = CCl4prep,
                 scale = "Rank")
class(sp)
aqm.plot(sp)

## Draw probes mapping density curves making use of the hasTarget
## column of the featureData
pm = aqm.probesmap(expressionset = CCl4norm, dataprep = CCl4prep)
class(pm)
aqm.plot(pm)
```

`aqm.probesmap` *Performs probes mapping on aqmobj.prepdata objects.*

Description

`aqm.probesmap` performs probes mapping, and formats the output for `aqm.plot` usage.

Usage

```
aqm.probesmap(expressionset, dataprep, ...)
```

Arguments

`expressionset`
Same input as for the function `arrayQualityMetrics`

`dataprep` An object of class `aqmobj.prepdata`

`...` Any arguments to `densityplot`

Details

See `aqm.prepdata` and the `aqm` Vignette.

Value

An object of class `aqmobj.probesmap`

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

`aqm.qcstats` *Performs QCstats plot on AffyBatch.*

Description

`aqm.qcstats` performs QCstats on objects of class `AffyBatch` and formats the output for `aqm.plot` usage.

Usage

```
aqm.qcstats(expressionset, ...)
```

Arguments

`expressionset`
is an object of class `AffyBatch`

`...` Any arguments to `qc`

Value

An object of class `aqmobj.qcs`.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqmobj.qcs`

Examples

```
library(ALLMLL)
data(MLL.A)
qm = aqm.qcstats(MLL.A)
class(qm)
aqm.plot(qm)
```

`aqm.rle` *Performs RLE and NUSE plots on aqmobj.prepaffy objects.*

Description

The functions do RLE boxplots and NUSE boxplots and produce output objects ready for rendering by `aqm.plot`.

Usage

```
aqm.rle(expressionset, dataprep, affyproc, intgroup, subsample = 10000, ...)
aqm.nuse(expressionset, dataprep, affyproc, intgroup, subsample = 10000, ...)
```

Arguments

`expressionset, dataprep, intgroup`	Same as for the function `arrayQualityMetrics`
`affyproc`	An object of class `aqmobj.prepaffy`
`subsample`	Same as for the function `aqm.boxplot`
`...`	These arguments get passed on to `bwplot`

Details

See `aqm.prepaffy` and the `aqm` Vignette.

Value

An object of class `aqmobj.rle` or `aqmobj.nuse`

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.prepaffy`, `aqmobj.prepaffy`, `aqmobj.rle`, `aqmobj.nuse`

aqm.rnadeg *Computes RNA degradation plot on AffyBatch.*

Description

aqm.rnadeg performs RNA degradation on objects of class AffyBatch and formats the output for aqm.plot usage.

Usage

```
aqm.rnadeg(expressionset)
```

Arguments

expressionset
An object of class AffyBatch

Details

See aqm.prepdata and the aqm Vignette.

Value

An object of class aqmobj.rnadeg.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

aqmobj.rnadeg

aqm.spatialbg *Performs spatial distribution representation of background intensities of the arrays from aqmobj.prepdata objects.*

Description

aqm.spatialbg performs representation of the spatial distribution of the background intensities on the arrays, outlier detection and formats the output for aqm.plot usage.

Usage

```
aqm.spatialbg(expressionset, dataprep, scale)
```

Arguments

`expressionset`
: Same input as for the function `arrayQualityMetrics`

`dataprep` An object of class `aqmobj.prepdata`

`scale` The spatial distribution can be represented on the rank of the intensities or on the logarithm scale. Possible options are thus 'Rank' and 'Log'.

Details

See `aqm.prepdata` and the `aqm` Vignette.

Value

An object of class `aqmobj.spatialbg`.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.prepdata`, `aqmobj.prepdata`, `aqmobj.spatialbg`

`aqm.spatial` *Performs spatial distribution representation of the arrays from aqmobj.prepdata objects.*

Description

`aqm.spatial` performs representation of the spatial distribution of the intensities on the arrays, outlier detection and formats the output for `aqm.plot` usage.

Usage

```
aqm.spatial(expressionset, dataprep, scale)
```

Arguments

`expressionset`
: Same input as for the function `arrayQualityMetrics`

`dataprep` An object of class `aqmobj.prepdata`

`scale` The spatial distribution can be represented on the rank of the intensities or on the logarithm scale. Possible options are thus 'Rank' and 'Log'.

Details

See `aqm.prepdata` and the `aqm` Vignette.

Value

An object of class `aqmobj.spatial`.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

See Also

`aqm.prepdata`, `aqmobj.prepdata`, `aqmobj.spatial`

`aqm.writereport` *Writes a report from objects produced with aqm.xxx functions.*

Description

`aqm.writereport` performs an html report from a list of aqmobj objects. It includes a summary with the outliers detected, titles, plots and legends.

Usage

```
aqm.writereport(name, expressionset, obj)
```

Arguments

`name`	A name to customize the title of the report that will be "name quality metrics report"
`expressionset`	The expressionset on which the metrics have been run
`obj`	A list of aqmobj.xxx objects

Details

See the `aqm` Vignette.

Value

An html report named 'QMreport.html' in the working directory.

Author(s)

Audrey Kauffmann <kauffmann@bergonie.org>

arrayQualityMetrics

Quality metrics for microarray experiments

Description

arrayQualityMetrics reports quality metrics on ExpressionSet, AffyBatch, NChannelSet, BeadLevelList, RGList, MAList, aqmInputObj, 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

```
arrayQualityMetrics(expressionset,
                    outdir = getwd(),
                    force = FALSE,
                    do.logtransform = FALSE,
                    intgroup = NULL,
                    grouprep,
    spatial = TRUE,
                    reporttitle = paste("Quality metrics report for", deparse(su
```

Arguments

expressionset
: an object of class ExpressionSet, AffyBatch, NChannelSet, BeadLevelList, RGList, MAList, marrayRaw, marrayNorm or aqmInputObj

outdir
: the name of the directory in which the report is created; a character of length 1.

force
: if the directory named by outdir already exists, then, if force is TRUE, the directory is overwritten, otherwise an error is thrown; if the directory does not exist, the value of force is irrelevant; a logical of length 1.

do.logtransform
: indicates whether the data should be logarithm transformed before the analysis; a logical of length 1.

intgroup
: the name of the sample covariate(s) used to draw a colour side bar next to the heatmap. The first element of intgroup is also used define sample groups in other plots (boxplots, densities). intgroup should be a character vector, and its elements need to match the columns names of phenoData(expressionset). If NULL or of length 0, then the plots are not decorated with sample covariate information.

grouprep
: deprecated. Use argument intgroup instead.

spatial
: indicates whether spatial plots should be made; a logical of length 1. This can be useful for large arrays (like Affymetrix hgu133Plus2) when CPU time and RAM resources of the machine would be limiting.

reporttitle
: title for the report (character of length 1).

Details

See the arrayQualityMetrics vignette for examples of this function.

Value

A side effect of the function is the creation of directory named by `outdir` containing a HTML report `QMreport.html` and PNG and PDF files with figures. The function also returns a list with R objects containing the report elements for subsequent programmatic processing.

Author(s)

Audrey Kauffmann.

`ksOutliers` *Function for outlier determing potential outliers*

Description

`ksOutliers` determines potential outlier arrays based on the value of the `ks.test` test statistic between each array and the pooled distribution of all arrays.

Usage

```
ksOutliers(x, subsamp = 300, theta = 2)
```

Arguments

`x`	A matrix whose columns correspond to arrays, rows the array features.
`subsamp`	If `x` has more than `subsamp` rows, use only a random subsample of size `subsamp` for calling `ks.test`.
`theta`	An array is called an outlier if its `ks.test` test statistic is more than `theta` standard deviations larger than the test statistics.

Details

The function is very simple, have a look at its code.

Value

An integer vector of indices (see `which`).

Author(s)

Wolfgang Huber <whuber@embl.de>

See Also

`ks.test`.

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

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

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)

Audrey Kauffmann, Wolfgang Huber. Maintainer: <kauffmann@bergonie.org>

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