moreSpikeInProbes  Accessor Methods for YAQCStats class

Description

The Microarray Quality Control Consortium guidelines and reference datasets are applied to analyse some of the QC metrics recommended by Affymetrix. These guidelines, datasets and QC metrics are discussed in detail in the package vignette.

Each of these functions queries a YAQCStats object to retrieve one of these QC metrics. The YAQCStats class is a subclass of the QCStats object as defined in the simpleaffy package. sfs, avbg and percent.present methods access to the scale.factors, average.background and percent.present attributes respectively are defined in the superclass.

Briefly:
isLog: Returns a logical saying if the expression intensities are in log2 from. target: Returns the target value (for MAS 5.0 normalization). moreSpikeInProbes: Returns a table of intensities for the internal spike probes. gcosProbes: Returns a table of intensities for GAPDH and β-actin probes. avbg: Returns a vector of the average background levels for each array. minbg: Returns a vector of the minimum background levels for each array. percent.present: Returns a vector listing the percentage of probesets called present on each array. sfs: Returns a vector of scale factors for each array (as produced by the MAS 5.0 algorithm). bioCalls: Returns a table of Present/Marginal/Absent calls for the spike probes. arrays: Returns the names of the arrays in the YAQCStats object. plot: Plots the YAQCStats object (see yaqc for more details).

Usage

isLog(object)
avns(object)
moreSpikeInProbes(object)
gcosProbes(object)
bioCalls(object)

Arguments

object an object of class "YAQCStats"

Author(s)

Laurnet Gatto
YAQCStats-class

See Also

yaqc, QCStats

YAQCStats-class Class "YAQCStats"

Description

Holds Quality Control data for a set of Affymetrix arrays

Objects from the Class

Objects can be created by calls of the form yaqc(object) where object is of class AffyBatch of ExpressionSet. YAQCStats is a subclass of QCStats and uses the scale.factor, average.background and percent.present, arraytype and target attributes of it's subclass.

Slots

log: Object of class "logical" that specifies if expression values are in log2 form
average.noise: Object of class "numeric" The average noise for the arrays
morespikes: Object of class "matrix" More spiked in probes (e.g. r2biob5, r2biob3,...)
gcos.probes: Object of class "matrix" GAPDH and β-actin qc probes (e.g. gapdh 3,5,M,...) containing the GCOS values
bio.calls: Object of class "matrix" BioB 5',3',M and BioC, BioC 5',3' present/absent/marginal calls

Methods

isLog signature(object = "YAQCStats"): are intensities in log2 form
avns signature(object = "YAQCStats"): average noise
moreSpikeInProbes signature(object = "YAQCStats"): more spike-in probes
gcosProbes signature(object = "YAQCStats"): GCOS values of gapdh and actin QC probes
bioCalls signature(object = "YAQCStats"): P/M/A calls for BioB, BioC and BioD spikes
arrays signature(object = "YAQCStats"): shows the array names composing the YAQCStats object
plot signature(object = "YAQCStats"): visual representation of the qc metrics
show signature(object = "YAQCStats"): displays the content of the object as a data frame
merge signature(object = "YAQCStats"): merges two compatible YAQCStats objects, i.e. that have the same values for the log, target and arraytype slots.
arrays signature(object = "YAQCStats"): show the array names of an YAQCStats objects.
getAllInt

Author(s)
Laurent Gatto

See Also
QCStats-class

---

### getAllInt

*Get the GCOS values for a given spike probe*

#### Description

This function retrieves the expression intensities provided by the object of class "YAQCStats" for the probe which names are compatible with the given pattern and return their mean value.

#### Usage

```r
ggetAllInt(YAQCStatsObject,pattern)
```

#### Arguments

- **YAQCStatsObject**
  - an object of type "YAQCStats"
- **pattern**
  - a pattern used to select the probe names to be used

#### Value

An object of type "numeric" in which the mean expression intensities of each array are given.

#### Author(s)
Laurent Gatto

#### Examples

```r
## load a dataset
library(affydata)
data(Dilution)
## perform quality control
qc <- yaqc(Dilution)
## get intensities for the biob
## spikes probe sets
getAllInt(qc,"biob")
```
**getBioProbes**  
*Get the names of the Bio spike probes on the array*

**Description**
This function returns all the AFFX-Bio probes names that are located on the given GeneChip.

**Usage**
```
getBioProbes(affyBatchObject)
```

**Arguments**
- `affyBatchObject`  
  An object of type "AffyBatch"

**Value**
An object of type "character" with all the Affymetrix Bio probe names.

**Author(s)**
Laurent Gatto

**See Also**
getSpikeProbes, getRatioProbes

**Examples**
```r
## load a dataset
library(affydata)
data(Dilution)
getBioProbes(Dilution)
```

---

**getOutliers**  
*Get outliers for the different YAQCStatsObject slots*

**Description**
This function retrieves the outliers for the different quality control metrics stored in a YAQCStatsObject. Outliers are defined as being outside of the mean +/- 2 stdev range or mean/2, mean*1.5 for the scale factor.

**Usage**
```
getOutliers(YAQCStatsObject, slot)
```
getOutliers

Arguments

YAQCStatsObject

an object of type "YAQCStats"

slot

an object of type string describing the slot for which the outliers should be retrieved (see details for possible slot strings)

Details

The slot strings that can be used are:

- **scale factor** "sfs"
- **average background** "avbg"
- **average noise** "avns"
- **percentage present** "pp"
- **β-actin 3'/5' ratio** "actin"
- **GAPDH 3'/5' ratio** "gapdh"
- **internal bioB control** "biob"
- **internal bioC control** "bioc"
- **internal bioD control** "biod"
- **Dap spike control** "dap"
- **Thr spike control** "thr"
- **Phe spike control** "phe"
- **Lys spike control** "lys"

Value

An object of type "numeric" giving the outliers names and values

Author(s)

Laurent Gatto

Examples

```r
## load data
library(MAQCSsubsetAFX)
data(refA)
## create the yaqc object
qobj <- yaqc(refA[,3:5])
## get outliers for the scale factor
getOutliers(qobj,"sfs")
```
getQCRatios

Compute qc probe ratios using GCOS intensity values

Description
This function computes the 3’/5’ ratios of the GAPDh and β-actin qc probes using the GCOS intensity values.

Usage
getQCRatios(YAQCStatsObject)

Arguments
YAQCStatsObject
an object of class YAQCStats

Value
An object of type "matrix" with two qc ratios per array.

Author(s)
Laurent Gatto

See Also
getRatioProbes

Examples
## load a dataset
library(affydata)
data(Dilution)
## create yaqc object
qobj <- yaqc(Dilution)
getQCRatios(qobj)

getRatioProbes

Get the names of degradation control probes on the array

Description
This function returns the probes names used for degradation control that are located on the given GeneChip.

Usage
getRatioProbes(object)
**getSpikeProbes**

**Arguments**

Object  
An object of class "AffyBatch" or "ExpressionSet"

**Value**

An object of type "character" with all the Affymetrix degradation control probe names.

**Author(s)**

Laurent Gatto

**See Also**

getSpikeProbes, getBioProbes

**Examples**

```r
library(yaqcaffy)
## load a dataset
library(affydata)
data(Dilution)
getRatioProbes(Dilution)
```

getSpikeProbes  
Get the names of all spike probes on the array

**Description**

This function returns all the spike probes (i.e. BioB-3', BioD-5', Lys-3, ...) that are located on the given GeneChip.

**Usage**

```r
getSpikeProbes(object)
```

**Arguments**

Object  
An object of type AffyBatch or ExpressionSet.

**Value**

An object of class character containing all Affymetrics spike probe names.

**Author(s)**

Laurent Gatto

**See Also**

getBioProbes, getRatiosProbes
## Examples

```r
## load a dataset
library(affydata)
data(Dilution)
getSpikeProbes(Dilution)
```

<table>
<thead>
<tr>
<th>morespikes</th>
<th>The name of more spike probes</th>
</tr>
</thead>
</table>

### Description

The name of more spike probes for each array (e.g. biob-3, biob-5, etc.)

### Format

A CSV file, with a column for each spike.

### See Also

spikes

---

## reprodPlot

### Description

Plot human whole genome GeneChips reproducibility

### Usage

```r
reprodPlot(userAffyBatchObject, ref,
           normalize=c("rma","gcrma","mas5","none"),
           main="MAQC reference reproducibility",
           cex,...)
```

### Arguments

- **userAffyBatchObject**: a set of Human Genome U133 Plus 2.0 arrays provided as an AffBatch object,
- **ref**: a string ("refA", "refB", "refC", or "refD") defining the RNA reference to compare the userAffyBatchObject to,
- **normalize**: a string defining the algorithm used for data normalization: *rma* (default) for RMA (as implemented in the *affy* library), *gcrma* for GCRMA (as implemented in the *gcrma* library), *mas5* for MAS5 (as implemented in the *affy* library) or 'none' for no normalization,
- **main**: an overall title for the plot,
- **cex**: size of text on the plot,
- **...**: other arguments.
yaqc-methods

Details

The plot shows all the pairwise scatterplots (plotted with `geneplotter`'s `smoothScatter` function) with Pearson's correlation factor and MAplots (plotted with `affy`'s `ma.plot` function). The subset of the MAQC arrays are 1 randomly chosen .CEL file out of the 5 replicates for the 6 different test site.

Value

Outputs a graph on the available graphical device

Author(s)

Laurent Gatto

Examples

```r
## Not run:
## loading data
library(MAQCsubsetAFX)
data(refB)
d<-refB[,1]
## testing the reproductibility against ref A
reprodPlot(d,"refA",normalize="rma")
## End(Not run)
```

yaqc-methods  

Create an YAQCStat object

Description

Create an YAQCStats qc object for an AffyBatch (or ExpressionSet) input

Methods

- `object="eSet"` Create a full YAQCStats object for an AffyBatch input or a light YAQCStats object for an ExpressionSet input.

See Also

- yaqc.affy
yaqc.affy  
Generate QC stats from an AffyBatch object

Description

Generate YAQC metrics for Affymetrix data.

Usage

yaqc.affy(object, tgt=100, tau=0.015, logged=FALSE)

Arguments

object a object of type AffyBatch or ExpressionSet
tgt the target intensity to which the chips should be scaled (used to calculated the GCOS intensities)
tau used by detection p value
logged to be used with an ExpressionSet object, defining if the expression intensities are logged

Details

Affymetrix recommend a set of quality control metrics to check the quality of GeneChips expression arrays. This function applies the guidelines described in the Affymetrix Microarray Quality Control Consortium (MAQC) protocols to asses the succes of the hybridization. See the package vignette for more details.

This function takes a raw (unnormalised) AffyBatch object or an ExpressionSet object. In the first case, it computess GCOS intensity values, MAS expression calls(see call.exprs) and other quality-related metrics to generate an YAQCStats. If an ExpressionSet object is provided, only the \( \beta \)-actin, GAPDH and internal control values are computed.

Value

An YAQCStats object describing the input object

Author(s)

Laurent Gatto

Examples

```r
## loading data
library(affydata)
data(Dilution)
## qc analysis
qobj <- yaqc(Dilution)
show(qobj)
```
yaqc.plot

Plots a YAQCStats object

Description
Generates a visual summary of the various Affymetrix QC statistics.

Usage
yaqc.plot(YAQCStatsObject,...)

Arguments
YAQCStatsObject
an object of class "YAQCStats".

... other arguments.

Details
The quality control metrics of the YAQCStatsObject are plotted in a serie of graphs with the recommended ranges.

The scale factors are represented through a dot chart and the upper and lower limits are defined with vertical red lines. The other qc metrics are shown using dot plots. For the upper row box plots (average background, average noise, percent present and β-actin and GAPDH ratios, the mean is represented by a dashed red line and the mean +/- 2 stdev by red dotted lines. For the lower box plots, featuring the internal controls, grey boxes defines the mean (middle segment) +/- 2 stdev.

If the YAQCStatsObject has been generated with an Expression Set objects, the scale factors, average noise and background and percent present can not be computed and the respective plots are removed from the final graph.

Author(s)
Laurent Gatto

Examples
## load data
library(affydata)
data(Dilution)
## create the yaqc object
## and plot it
qobj<-yaqc(Dilution)
plot(qobj)
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