yaqcaffy

April 20, 2011

`bio-methods` *Returns the 'bio' hybridization probes of YaqcControlProbes or YaqcBioProbes objects.*

Description

The 'bio' method can be called with ojects of classes `YaqcBioProbes` or `YaqcControlProbes` (the latter containing the former) to get the labelling probes (BioB3, BioB5, BioBM, BioC5,...).

Methods

`signature(object = "YaqcControlProbes")` Returns the labelling probes as an instance of the `YaqcBioProbes`.

`signature(object = "YaqcBioProbes")` Returns the labelling probes as characters.

`deg-methods` *Returns the degradation probes of YaqcControlProbes or YaqcDegProbes objects.*

Description

The 'deg' method can be called with ojects of classes `YaqcDegProbes` or `YaqcControlProbes` (the latter containing the former) to get the labelling probes (actin3, actin5, actinM, gapdh5,...).

Methods

`signature(object = "YaqcControlProbes")` Returns the degratation probes as an instance of the `YaqcDegProbes`.

`signature(object = "YaqcDegProbes")` Returns the degradation probes as characters.

`getAllInt` *Get the summerized MAS5 values for a given spike probe*

Description

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

Usage

```
getAllInt(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

```
## load a dataset
library(affydata)
data(Dilution)
## perform quality control
qc <- yaqc(Dilution)
## get intensities for the biob
## spikes probe sets
getAllInt(qc,"biob")
## or
getAllInt(qc,"b[3|5|m]")
```

`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(object,onlyFirst)
```

Arguments

- `object` An object of type "`AffyBatch`" or "`ExpressionSet`"
- `onlyFirst` Boolean defining of only first or all instances found should be returned. Default is set to TRUE. Warnings are returned if more than one probe is found. The function stops with an error if no probe is found.

Value

An object of type "`character`" with the Affymetrix hybridation (bio) probe names for the given chip type.

Author(s)

Laurent Gatto

See Also

getSpikeProbes,getRatioProbes

Examples

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

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

Description

This function retrives the outliers fot 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)
```

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

```
## load data
library(MAQCsubsetAFX)
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,onlyFirst)
```

Arguments

`object`	An object of class "`AffyBatch`" or "`ExpressionSet`"
`onlyFirst`	Boolean defining of only first or all instances found should be returned. Default is set to TRUE. Warnings are returned if more than one probe is found. The function stops with an error if no probe is found.

Value

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

Author(s)

Laurent Gatto

See Also

getSpikeProbes,getBioProbes

Examples

```
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

```
getSpikeProbes(object,onlyFirst)
```

Arguments

`object`	An object of type `AffyBatch` or `ExpressionSet`.
`onlyFirst`	Boolean defining of only first or all instances found should be returned. Default is set to TRUE. Warnings are returned if more than one probe is found. The function stops with an error if no probe is found.

Value

An object of class `character` containing all (hybridization and labelling) Affymetrix spike probe names.

Author(s)

Laurent Gatto

See Also

getBioProbes,getRatiosProbes

Examples

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

probeSelectionInterface

Tcltk Interface to Generate an Instance of YaqcControlProbes for a given Chip Set

Description

probeSelectionInterface starts a tcltk graphical user interface (GUI) that allows the user to choose the probes to be used for subsequent quality analyses with the yaqcaffy package. The probes are selected on basis of the features of a given set of Affymetrix Genechips provided as input. The list of probes can be pre-filtered to display only control probes (i.e starting by AFFX) or all probes on the Genechip can be shown.

Usage

```
probeSelectionInterface(object,
returnVar="yaqcControlProbes",
filter=TRUE)
```

Arguments

object	an object of class linkS4Class{AffyBatch} or linkS4Class{ExpressionSet}.
returnVar	a string defining the name of the variable the returned object will be saved as in the global environment. The default variable name is 'yaqcControlProbes'. If such a variable name already exists, a warning will be issued and the user can cancel the function.
filter	logical value. If 'TRUE', the feature names of the input object are filtered out (see details). If 'FALSE', all features are listed for all control probes.

Details

Three tabs are displayed, one for the hybridization (bio) probes, labelling probes (dap, phe, thr and lys) and the degradation probes (actin and gapdh) respectively. If the user uses the 'Close' button, no return object is saved in the global environment. An object is saved as returnVar if the user presses 'Ok'. If such a variable name already exists, a warning will be issued and the user can close the interface and cancel the function.

If filtering is applied, the hybridization menus will list probes that match the given probe (BioB, BioC or BioD) and position (5, 3 or M). Similarly, only matching labelling probes (dap, phe, thr and lys) and positions will be displayed. As the pattern for the degradation probes are less strict, all the 'AFFX' probes, except those already selected as hybridization and labelling probes, will be displayed in the drop-down menus.

Value

Returns an object of class YaqcBioProbes.

Author(s)

Laurent Gatto

Examples

```
 ## Not run:
   library(affydata)
   data(Dilution)
   probeSelectionInterface(Dilution)

## End(Not run)
```

---

reprodPlot *Plot human whole genome GeneChips reproductibility*

Description

Compares Affymetrix Human Genome U133 Plus 2.0 Arrays to a subset of the MAQC arrays for a RNA reference.

Usage

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

Arguments

`userAffyBatchObject`
: a set of Human Genomue 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 imlplemented in the **affy** library), `gcrma` for GCRMA (as imlplemented in the `gcrma` library), `mas5` for MAS5 (as imlplemented 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.

Details

The plot shows all the pairwise scatterplots (plotted with **graphics**)'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

```
  ## 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)
```

---

spk-methods *Returns the labelling probes of YaqcControlProbes or YaqcSpkProbes objects.*

Description

The 'spk' method can be called with ojects of classes YaqcSpkProbes or YaqcControlProbes (the latter containing the former) to get the hybridization probes (dap3, dap5, dapM, phe5,...).

Methods

`signature(object = "YaqcControlProbes")` Returns the hybridization probes as an instance of the YaqcSpkProbes.

`signature(object = "YaqcSpkProbes")` Returns the hybridization probes as characters.

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yaqc.affy *Generate QC Stats from an AffyBatch Object*

Description

Generate YAQC metrics for Affymetrix data.

Usage

```
 yaqc.affy(object,
myYaqcControlProbes=NULL,
alphas=NULL,
tgt=100,
tau=0.015,
logged,
verbose)
```

Arguments

`object` a object of type `AffyBatch` or `ExpressionSet`.

`myYaqcControlProbes` an object of type `YaqcControlProbes`. If none is supplied (default behaviour), the control probes are selected automatically. See the `YaqcControlProbes` class for more details `probeSelectionInterface` to generate such an object.

`alphas` a numeric of length 2 with the alpha1 and alpha2 values. Alpha1 and alpha2 are thresholds used to define if a given probe shoudl be called present (p<alpha1), marginal (alpha1<p<alpha2) or absent (alpha2<p), where p is the p-value from the Wilcoxon Signed Rank test used in MAS5. The default is to get these values from simpleaffy's qcdef files (see simpleaffy's vignette for more details) or to use 0.04 and 0.06 as default values.

`tgt` the target intensity to which the chips should be scaled (used to calculated the MAS5 intensitiy values).

`tau` used for detection p-value.

`logged` to be used with an `ExpressionSet` object, defining if the expression intensities are logged.

`verbose` logical value. If 'TRUE', it writes out some messages indicating progress. If 'FALSE' nothing should be printed.

Details

Affymetrix recommends 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 computes MAS5 intensity values, expression calls(see `call.exprs`) and other quality-related metrics to generate an YAQCStats. If an `ExpressionSet` object is provided, only the β-actin, GAPDH and internal control values are computed.

Value

An YAQCStats object describing the input object

Author(s)

Laurent Gatto

Examples

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

YaqcControlProbes-class *Class "YaqcControlProbes"*

Description

The YAQCStats class stores the probes used for the quality control as a special class, namely the YaqcControlProbes class. This class encapsulated the probe names that are used the generate an YAQCStats-class object. Objects of this class are created with the probeSelectionInterface function. The hybridization, labelling and degradation probes are encapsulated in YaqcBioProbes, YaqcSpkProbes and YaqcDegProbes objects respectively. These can be retrieved as described in bio-methods, spk-methods and deg-methods. Furthermore, an info function allows to retrive or set a free text slot to describe the current object.

Slots

`bio`: Object of class `"YaqcBioProbes"` encapsulating the 'bio' (BioB5, BioB3, BioBM, BioC5,...) hybridization probes.

`spk`: Object of class `"YaqcSpkProbes"` encapsulating the labelling probes (dap5, dap3, dap3, phe5,...).

`deg`: Object of class `"YaqcDegProbes"` encapsulating the degradation probes used to assess the 3'/5' ratio.

`info`: Object of class `"character"` providing general information about the `YaqcControlProbes` object.

Methods

bio `signature(object = "YaqcControlProbes")`: returns the 'bio' (BioB5, BioB3, BioBM, BioC5,...) hybridization probes of the current object.

spk `signature(object = "YaqcControlProbes")`: returns the labelling probes (dap5, dap3, dap3, phe5,...) of the current object.

deg `signature(object = "YaqcControlProbes")`: returns the degradation probes used to assess the 3'/5'ratio.

info `signature(object = "YaqcControlProbes")`: returns the inforation slot of the current object.

info<- `signature(object = "YaqcControlProbes")`: sets the information slot of the current object.

show `signature(object = "YaqcControlProbes")`: shows the current object.

Author(s)

Laurent Gatto

See Also

probeSelectionInterface, bio-methods, spk-methods, deg-methods, YAQCStats

Examples

```
showClass("YaqcControlProbes")
showClass("YaqcBioProbes")
showClass("YaqcSpkProbes")
showClass("YaqcDegProbes")
```

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.plot *Plots a YAQCStats object*

Description

Generates a visual summary of the various Affymetrix QC statistics.

Usage

```
yaqc.plot(YAQCStatsObject, which,...)
```

Arguments

YAQCStatsObject
an object of class "YAQCStats".

which which quality metrics should be plotted (all by default).

... 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 metircs 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.

Individual plots can also be generated with the `which` argument: 'sfs' for the scale factor, 'avbg' and 'avns' for the average background and noise, 'pp' for the percentage of present calls, 'gapdh' and 'actin' for the GAPDH and β-actin ratios, 'bio' for the hybridization controls and 'spikes' for the retro-transciption spiked controls.

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)
```

`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 respectivley 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 YACQStats object (see `yaqc` for more details). objectVersion: Returns the version of the `yaqcaffy` package used to create the given object getYaqcControlProbes: Returns the probes used to generate the current object as instance of the `YaqcControlProbes` class.

Usage

```
isLog(object)
avns(object)
moreSpikeInProbes(object)
gcosProbes(object)
bioCalls(object)
objectVersion(object)
getYaqcControlProbes(object)
```

Arguments

`object`	an object of class `"YAQCStats"`

Author(s)

Laurnet Gatto

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 super-class.

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 .

`objectVersion` Character describing the version of the library used to generate the `YAQCStats` object.

`yaqcControlProbes` Object of class `YaqcControlProbes` that defines the different probes used for the quality control.

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.

summary `signature(object = "YAQCStats")`: data frame summary of the outliers.

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")`: shows the array names of an YAQCStats objects.

objectVersion `signature(object = "YAQCStats")`: shows the library verison used to generate the `YAQCStats` object.

getYaqcControlProbes `signature(object = "YAQCStats")`: returns the `YaqcControlProbes` object that has been used to generate the current `YAQCStats` object.

Author(s)

Laurent Gatto

See Also

QCStats-class,YaqcControlProbes-class

`yaqc.summary` *Summarizes YAQCStats object outliers*

Description

Generates a data frame of QC outliers.

Usage

```
yaqc.summary(YAQCStatsObject,latex)
```

Arguments

`YAQCStatsObject`
: an object of class `"YAQCStats"`.

`latex` logical value. If 'TRUE', the data frame is returned as a latex table.

Details

The outliers of the `YAQCStatsObject` quality control metrics are summerized and returned as a data frame. The internal probe (bioB, bioC and bioD) and poly-A controls (dap, thr, phe and lys) are summerized in two rows.

If `latex` is set to 'TRUE', the data frame is returned as a latex table (requires the `xtable` library).

Note: not tested if the YAQCStatsObject has been generated with an Expression Set objects.

Author(s)

Laurent Gatto

Examples

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

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