

# arrayMvout

April 12, 2012

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ArrayOutliers-methods *ArrayOutliers – wrapper for platform-specific multivariate outlier detection for expression arrays*

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## Description

wraps functions that perform multivariate outlier detection on dimension-reduced QA statistics of expression arrays

## Methods

**data = "ANY", alpha = "missing", alphaSeq = "missing"** fails; tells user that alpha is obligatory parameter

**data = "AffyBatch", alpha = "numeric", alphaSeq = "ANY"** performs calibrated multivariate outlier detection on an AffyBatch instance using various affy-specific QA parameters

**data = "LumiBatch", alpha = "numeric", alphaSeq = "ANY"** performs calibrated multivariate outlier detection on an LumiBatch instance using various illumina-specific QA parameters

**data = "data.frame", alpha = "numeric", alphaSeq = "ANY"** performs calibrated outlier detection on QA statistics housed in data.frame – all columns of the data entity must be numeric QA statistics for the arrays.

## Examples

```
example(ArrayOutliers)
```

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ArrayOutliers *Multivariate outlier detection based on PCA of QA statistics*

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## Description

Multivariate outlier detection based on PCA of QA statistics

## Usage

```
ArrayOutliers (data, alpha, alphaSeq = c(0.01, 0.05, 0.1), ... )  
#   qcOutput = NULL, plmOutput = NULL, degOutput = NULL, prscale = TRUE,  
#   pc2use = 1:3)
```

**Arguments**

<code>data</code>	an (affy) AffyBatch instance with at least 11 samples
<code>alpha</code>	false positive rate for outlier detection, adjusting for multiple comparisons according to Caroni and Prescott's adaptation of Rosner (1983); full report based on this choice of alpha
<code>alphaSeq</code>	vector of alpha candidates to be quickly tried for short report
<code>...</code>	additional parameters, see below

**Details**

Additional parameters may be supplied

**qcOutput** optional result of `simpleaffy qc()` to speed computations

**plmOutput** optional result of `affyPLM fitPLM()` to speed computations

**degOutput** optional result of `affy AffyRNAdeg()` to speed computations

**prscale** scaling option for `prcomp`

**pc2use** selection of principal components to use for outlier detection

Data elements `afxsubDEG`, `afxsubQC`, `s12cDEG`, `s12cQC` are precomputed RNA degradation and `simpleaffy qc()` results; `s12c` is an AffyBatch with digital contamination of some samples.

Data elements `maqQA` and `itnQA` are affymetrix QC statistics on large collections of arrays. Data element `ilmQA` is derived from a LumiBatch of the Illumina-submitted MAQC raw data, 19 arrays. (Conveyed by Leming Shi, personal communication). Data element `spikQA` is a 12x9 matrix of QA parameters obtained for 12 arrays from U133A spikein dataset, with first 2 arrays digitally contaminated as described in Asare et al.

Data element `fig3map` gives the indices of the points labeled A-H in Figure 3 of the manuscript by Asare et al. associated with this package.

**Value**

an instance of `arrOutStruct` class, a list with a partition of samples into two data frames (`inl` and `outl`) with QA summary statistics

**Author(s)**

Z. Gao et al.

**Examples**

```
library(simpleaffy)
setQCEnvironment("hgu133acdf") # no CDF corresponding to tag array
if ( require("mvoutData") ) {
  data(s12c)
  data(s12cQC)
  data(s12cDEG)
  library(affyPLM)
  s12cPset = fitPLM(s12c)
  ao = ArrayOutliers(s12c, alpha=0.05, qcOut=s12cQC, plmOut=s12cPset, degOut=s12cDEG)
  ao
}
if (require("lumiBarnes")) {
  library(lumiBarnes)
```

```

data(lumiBarnes)
ArrayOutliers(lumiBarnes, alpha=0.05)
lb2 = lumiBarnes
exprs(lb2)[1:20000,1:2] = 10000*exprs(lb2)[1:20000,1:2]
ArrayOutliers(lb2, alpha=0.05)
}
data(maqcQA) # affy
ArrayOutliers(maqcQA[, -c(1:2)], alpha=.05)
ArrayOutliers(maqcQA[, -c(1:2)], alpha=.01)
data(ilmQA) # illumina
ArrayOutliers(data.frame(ilmQA), alpha=.01)
data(itnQA) # 507 arrays from ITN
ArrayOutliers(itnQA, alpha=.01)

```

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arrOutStruct-class      *Class "arrOutStruct" container for ArrayOutliers output*

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## Description

Class "arrOutStruct" container for ArrayOutliers output

## Objects from the Class

Objects can be created by calls of the form `new("arrOutStruct", ...)`. This class just extends `list` but has specialized `show` and `plot` methods.

## Extends

Class "`list`", from data part. Class "`vector`", by class "`list`", distance 2. Class `AssayData`, by class "`list`", distance 2.

## Methods

**plot** signature(x = "arrOutStruct", y = "ANY"): a biplot of QA statistics

**show** signature(object = "arrOutStruct"): summary report

## Author(s)

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## Examples

```

data(maqcQA)
f1 = ArrayOutliers(maqcQA[, -c(1:2)], alpha=0.01)
names(f1)
f1

```

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