

# Package ‘arrayMvout’

April 26, 2026

**Title** multivariate outlier detection for expression array QA

**Version** 1.69.0

**Author** Z. Gao, A. Asare, R. Wang, V. Carey

**Description** This package supports the application of diverse quality metrics to AffyBatch instances, summarizing these metrics via PCA, and then performing parametric outlier detection on the PCs to identify aberrant arrays with a fixed Type I error rate

**Depends** R (>= 2.6.0), tools, methods, utils, parody, Biobase, affy

**Suggests** MAQCsubset, mvoutData, lumiBarnes, affyPLM, affydata, hgu133atagcdf

**Imports** mdqc, affyContam, lumi

**Maintainer** V. Carey <stvjc@channing.harvard.edu>

**License** Artistic-2.0

**LazyLoad** yes

**biocViews** Infrastructure, Microarray, QualityControl

**RoxygenNote** 7.1.1

**git\_url** <https://git.bioconductor.org/packages/arrayMvout>

**git\_branch** devel

**git\_last\_commit** 285aeb3

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.24

**Date/Publication** 2026-04-26

## Contents

ArrayOutliers . . . . .	2
ArrayOutliers-methods . . . . .	3
arrOutStruct-class . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

ArrayOutliers

*Multivariate outlier detection based on PCA of QA statistics*


---

## 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 `maqcQA` 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**

```
## Not run:
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)

## End(Not run)
```

---

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

---

**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)
```

---

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

---

**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)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

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

# Index

- \* **classes**
  - arrOutStruct-class, [4](#)
- \* **methods**
  - ArrayOutliers-methods, [3](#)
- \* **models**
  - ArrayOutliers, [2](#)

afxsubDEG (ArrayOutliers), [2](#)  
afxsubQC (ArrayOutliers), [2](#)  
ArrayOutliers, [2](#)  
ArrayOutliers, AffyBatch, numeric, ANY-method  
(ArrayOutliers-methods), [3](#)  
ArrayOutliers, ANY, missing, missing-method  
(ArrayOutliers-methods), [3](#)  
ArrayOutliers, data.frame, numeric, ANY-method  
(ArrayOutliers-methods), [3](#)  
ArrayOutliers, LumiBatch, numeric, ANY-method  
(ArrayOutliers-methods), [3](#)  
ArrayOutliers-methods, [3](#)  
arrOutStruct-class, [4](#)  
AssayData, [4](#)

fig3map (ArrayOutliers), [2](#)

ILM1 (ArrayOutliers), [2](#)  
ilmQA (ArrayOutliers), [2](#)  
itnQA (ArrayOutliers), [2](#)

list, [4](#)

maqQA (ArrayOutliers), [2](#)

plot, arrOutStruct, ANY-method  
(arrOutStruct-class), [4](#)

s12c (ArrayOutliers), [2](#)  
s12cDEG (ArrayOutliers), [2](#)  
s12cQC (ArrayOutliers), [2](#)  
show, arrOutStruct-method  
(arrOutStruct-class), [4](#)  
spikQA (ArrayOutliers), [2](#)

vector, [4](#)