Package ‘mdqc’

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Type Package
Title Mahalanobis Distance Quality Control for microarrays
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Description MDQC is a multivariate quality assessment method for microarrays based on quality control (QC) reports. The Mahalanobis distance of an array’s quality attributes is used to measure the similarity of the quality of that array against the quality of the other arrays. Then, arrays with unusually high distances can be flagged as potentially low-quality.
Depends R (>= 2.2.1), cluster, MASS
License LGPL (>= 2)
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NeedsCompilation no

R topics documented:

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mdqc-package  MDQC: Mahalanobis Distance Quality Control

Description

MDQC is a multivariate quality assessment method for microarrays based on quality control (QC) reports.
Details

Package: mdqc
Type: Package
Version: 1.0.0
Date: 2007-12-12
License: GPL

Author(s)

Justin Harrington <harringt@stat.ubc.ca> and Gabriela V. Cohen Freue <gcohen@stat.ubc.ca>.

References


See Also

mdqc

allQC

QC report for MLL.B

Description

A subset of arrays from a large acute lymphoblastic leukemia (ALL) study

Usage

data(allQC)

Format

A data frame with 20 observations on the following 11 variables.

Scale Factor a numeric vector
Percent Present a numeric vector
Average Background a numeric vector
Minimum Background a numeric vector
Maximum Background a numeric vector
BioB a numeric vector
BioC a numeric vector
BioD a numeric vector
CreX a numeric vector
AFFX-HSAC07/X00351.3’/5’ a numeric vector
AFFX-HUMGAPDH/M33197.3’/5’ a numeric vector
allQC

Details

Contains the QC report obtained using Bioconductor’s simpleaffy package for a subset of arrays from a large acute lymphoblastic leukemia (ALL) study (Ross et al., 2004). The QC report in allQC has been generated using the following R commands:

```r
library("affy")

## Get the raw data (see help("MLL.B") for further details)
library("ALLMLL")
data(MLL.B)

## Generate the QC metrics
library("simpleaffy")
data.all <- MLL.B[,1:20]
all.qc <- qc(data.all)

## Select relevant information
allQC <- cbind(sfs(all.qc),percent.present(all.qc)/100,
avbg(all.qc),minbg(all.qc),maxbg(all.qc),
spikeInProbes(all.qc),ratios(all.qc)[,c(1,3)])

## Specify row and column names
colnames(allQC) <- c("Scale Factor","Percent Present",
"Average Background", "Minimum Background", "Maximum Background",
"BioB", "BioC", "BioD", "CreX", "AFFX-HSAC07/X00351.3'5'",
"AFFX-HUMGAPDH/M33197.3'5'")
rownames(allQC) <- 1:20
```

Versions 1.16.0 of ‘affy’, 1.2.2 of ‘ALLMLL’, and 2.14.05 of ‘simpleaffy’ was used. Part of this dataset has been also studied by Bolstad et al. (2005) and Brettschneider et al. (2007).

Source


References


MDQC: Mahalanobis Distance Quality Control

Description

MDQC is a multivariate quality assessment method for microarrays based on quality control (QC) reports.

Usage

```r
mdqc(x, method=c("nogroups", "apriori", "global", "cluster", "loading"),
     groups=NULL, k=NULL, pc=NULL,
     robust=c("S-estimator", "MCD", "MVE"), nsamp=10*nrow(x))
```

Arguments

- `x`: a numeric matrix or data frame containing the quality measures (columns) for each array (rows). The number of rows must exceed the number of columns.
- `method`: The Mahalanobis Distances (MDs) can be computed on all the quality measures in the QC report (this is the default method given by `method="nogroups"`), on the first `k` principal components resulting from a principal component analysis (PCA) of the QC report ("global") or on subsets of quality measures in the QC report ("apriori": groups defined by the user, "cluster": groups resulting from a cluster analysis, or "loading": groups resulting from a cluster analysis in the space of the loadings of a PCA). While the first two methods compute a single MD for each array, the last three compute one MD within each created group of quality measures.
- `groups`: A list to specify the groups of quality measures when the "apriori" method is chosen. E.g. `groups = list(c(1,2), c(4,6))` puts column 1,2 as one group and 4,6 as a second.
- `k`: An integer to specify the number of clusters (or groups) to be used in the cluster analysis when "cluster" or "loading" methods are chosen.
- `pc`: An integer to specify the number of principal components analyzed from the PCA when "global" or "loading" methods are chosen.
- `robust`: A robust multivariate location/spread estimator (choice of S-estimator, MCD or MVE). The default method uses S-estimators with a 25% breakdown point.
- `nsamp`: The number of subsamples that the robust estimator should use. This defaults to 10 times the number of rows in the matrix.

Details

MDQC flags potentially low quality arrays based on the idea of outlier detection, that is, it flags those arrays whose quality attributes jointly depart from those of the bulk of the data.

This function computes a distance measure, the Mahalanobis Distance, to summarize the quality of each array. The use of this distance allows us to perform a multivariate analysis of the information in
QC reports taking the correlation structure of the quality measures into account. In addition, by using robust estimators to identify the typical quality measures of good-quality arrays, the evaluation is not affected by the measures of outlying arrays.

MDQC can be based on all the quality measures simultaneously (using \texttt{method="nogroups"}), on subsets of them (using \texttt{method="apriori"}, "cluster", or "loading"), or on a transformed space with a lower dimension (using \texttt{method="global"}).

In the “apriori” approach the user forms groups of quality measures on the basis of an a priori interpretation of them and according to the quality aspect they represent. The “cluster” and the “loading” methods are two data-driven methods to form the groups. The former groups the quality measures using clustering analysis, and the latter uses the loadings of a principal component analysis to identify the quality measures that contain similar information and group them. It is important to note that the “apriori”, the “cluster”, and the “loading” methods create groups of the original quality measures of the report and compute one MD within each group. Finally, the “global” method computes a single MD based on the reduced space of the first \( k \) principal components from a robust PCA. The number \( k \) of PCs can be chosen using a scree plot.

More details on each method are given in Cohen Freue et al. (2007)

\section*{Value}

An object of class ‘\"mdqc\"’ (with associated plot, print and summary methods) with components

\begin{itemize}
\item \texttt{ngroups} \hspace{1cm} Number of groups in which the MDs have been computed
\item \texttt{groups} \hspace{1cm} column numbers corresponding to the quality measures in each group
\item \texttt{mdqcValues} \hspace{1cm} Mahalanobis Distance(s) for each array
\item \texttt{x} \hspace{1cm} dataset containing the numeric quality measures in the report
\item \texttt{method} \hspace{1cm} method used to group or transform the quality measures before computing the MD for each array
\item \texttt{pc} \hspace{1cm} number of principal components used in the robust PCA.
\item \texttt{k} \hspace{1cm} number of clusters used in the cluster analysis.
\end{itemize}

\section*{Note}

We thank Christopher Croux for providing us a MATLAB code that we translated into R to compute the multivariate S-estimator

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Justin Harrington <harringt@stat.ubc.ca> and Gabriela V. Cohen Freue <gcohen@stat.ubc.ca>.

\section*{References}


\texttt{mdqc}

See Also

`prcomp.robust`, `pam`, `mahalanobis`, `allQC`

Examples

```r
data(allQC)

## Contains the QC report obtained using Bioconductor's simpleaffy package
## for a subset of arrays from a large acute lymphoblastic leukemia (ALL)
## study (Ross et al., 2004).
## This dataset has been also studied by Bolstad et al. (2005) and
## Brettschneider et al. (2007).
## For further information see allQC.

#### No Groups method
# Figure 2 in Cohen Freue et al. (2007):
# Results of MDQC based on all measures of the QC report.

mdout <- mdqc(allQC, method="nogroups")
plot(mdout)
print(mdout)
summary(mdout)

#### A-Priori grouping method
# Figure 3 in Cohen Freue et al. (2007):
# Results of MDQC using the apriori grouping method.

mdout <- mdqc(allQC, method="apriori", groups=list(1:5, 6:9, 10:11))
plot(mdout)

#### Global PCA method
# Figure 4 in Cohen Freue et al.(2007):
# Results of MDQC using the global PCA method.

mdout <- mdqc(allQC, method="global", pc=4)
plot(mdout)

#### Clustering grouping method
# Figure 4 in Supplementary Material of Cohen Freue et al. (2007):
# Results of MDQC using a cluster analysis to form
# 3 groups of quality measures.

mdout <- mdqc(allQC, method="cluster", k=3)
plot(mdout)
```
### Loading grouping method

Figure 4 in Supplementary Material of Cohen Freue et al. (2007): Results of MDQC using a cluster analysis on the first k=4 loading vectors from a robust PCA to form 3 groups of quality measures.

```r
mdout <- mdqc(allQC, method="loading", k=3, pc=4)
plot(mdout)
```

### To get the raw MD distances

`mdout$mdqcValues`

---

**plot.mdqc**

*The plot method for a MDQC object*

**Description**

The plot method for a MDQC object, which plots ...

**Usage**

```r
## S3 method for class 'mdqc'
plot(x, levels = c(0.9, 0.95, 0.99), xlab='', ylab='',
     mfrow=NULL, mfcol=NULL, ...)
```

**Arguments**

- `x`: An object of the class ‘mdqc’.
- `levels`: A vector or scalar between 0 and 1 for displaying critical values for outliers. See details.
- `xlab`: The label for for x-axis. Note that when there are multiple plots, the same value of this argument is used for each one.
- `ylab`: The label for the y-axis. Note that when there are multiple plots, the same value of this argument is used for each one.
- `mfrow`: Specify the arrangement of plots on the page, by rows, or leave NULL to let the function work it out
- `mfcol`: As for mcol, but arrange plots by column instead
- `...`: Other arguments passed to the default plot method.

**Details**

This plot method is for the output from the function `mdqc`, and plots the Mahalanobis distances for each array. The `levels` argument plots horizontal lines at critical values (based on the quantiles of a chi-squared distribution), and aids in identifying outliers.

For further details, see Cohen Freue et al. (2007)
prcomp.robust

Description

A function that performs PCA using the robust estimators "S-estimator", "MCD" and "MVE".

Usage

prcomp.robust(x, robust = c("S-estimator", "MCD", "MVE"),
              nsamp = 10*nrow(x), ...)
## S3 method for class 'robust'
prcomp(x, robust = c("S-estimator", "MCD", "MVE"),
       nsamp = 10*nrow(x), ...)

Arguments

x

robust

nsamp

...
Details

The calculation is done by a singular value decomposition of the robust centered and scaled data matrix, not by using `eigen` on the covariance matrix. This is generally the preferred method for numerical accuracy. The `print` method for the these objects prints the results in a nice format and the `plot` method produces a scree plot. The scree plot can be used to determine the number \( k \) of principal components preserved in the analysis, looking for the “elbow” or the first important bend in the line. A biplot can also be generated to represent the values of the first two principal components (PCs) and the contribution of each variable to these components in the same plot (see Supplementary Material of Cohen Freue et al. (2007)).

Value

`prcomp.robust` returns a list with class "prcomp" containing the following components:

- `sdev`: the standard deviations of the principal components (i.e., the square roots of the eigenvalues of the covariance matrix calculated using the `robust` argument, though the calculation is actually done with the singular values of the data matrix).
- `rotation`: the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). The function `princomp` returns this in the element `loadings`.
- `x`: the value of the rotated data (the centered and scaled) data multiplied by the `rotation` matrix is returned.

Author(s)

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References


See Also

- `mdqc`, `prcomp`

Examples

```r
data(allQC) ## Loads the dataset allQC

prout <- prcomp.robust(allQC)
screeplot(prout, type="line")
biplot(prout)

prout <- prcomp.robust(allQC, robust="MCD")
screeplot(prout, type="line")
biplot(prout)

prout <- prcomp.robust(allQC, robust="MVE")
screeplot(prout, type="line")
biplot(prout)
```
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