

Package ‘OutlierD’

September 27, 2020

Version 1.52.0

Date 2007-08-02

Title Outlier detection using quantile regression on the M-A scatterplots of high-throughput data

Author HyungJun Cho <hj4cho@korea.ac.kr>

Maintainer Sukwoo Kim <s4kim@korea.ac.kr>

Depends R (>= 2.3.0), Biobase, quantreg

Description This package detects outliers using quantile regression on the M-A scatterplots of high-throughput data.

License GPL (>= 2)

URL <http://www.korea.ac.kr/~stat2242/>

biocViews Microarray

git_url <https://git.bioconductor.org/packages/OutlierD>

git_branch RELEASE_3_11

git_last_commit d96d66b

git_last_commit_date 2020-04-27

Date/Publication 2020-09-27

R topics documented:

lcms	1
OutlierD	2
Index	3

lcms	<i>LCMS data</i>
------	------------------

Description

This data set consists of LCMS data with two samples.

Usage

```
data(lcms)
```

Format

a matrix for LCMS data, rows=peptides, columns=samples

OutlierD	<i>Outlier detection using quantile regression on the M-A scatterplots of high-throughput data</i>
----------	----------------------------------------------------------------------------------------------------

Description

This detects outliers using quantile regression on the M-A scatterplots of high-throughput data.

Usage

```
OutlierD(x1, x2, k=1.5, method="nonlin")
```

Arguments

x1	one n-by-1 vector for data (n= number of peptides, proteins, or genes)
x2	the other n-by-1 vector for data (n= number of peptides, proteins, or genes)
k	parameter in $Q1-k*IQR$ and $Q3+k*IQR$, $IQR=Q3-Q1$, $k=1.5$ (default)
method	one of constant, linear, nonlinear, and nonparametric quantile regression

Value

x	data and results for outliers
---	-------------------------------

Author(s)

HyungJun Cho

Examples

```
data(lcms)
x <- log2(lcms) #log2-transformation, do normalization if necessary

fit1 <- OutlierD(x1=x[,1], x2=x[,2], method="constant")
fit2 <- OutlierD(x1=x[,1], x2=x[,2], method="linear")
fit3 <- OutlierD(x1=x[,1], x2=x[,2], method="nonlin")
fit4 <- OutlierD(x1=x[,1], x2=x[,2], method="nonpar")

fit3$x[1:10,]

plot(fit3$x$A, fit3$x$M, pch=".", xlab="A", ylab="M")
i <- sort.list(fit3$x$A)
lines(fit3$x$A[i], fit3$x$Q3[i], lty=2); lines(fit3$x$A[i], fit3$x$Q1[i], lty=2)
lines(fit3$x$A[i], fit3$x$LB[i]); lines(fit3$x$A[i], fit3$x$UB[i])
title("Nonlinear")
```

Index

* **datasets**

lcms, 1

* **models**

OutlierD, 2

lcms, 1

OutlierD, 2