

# Package ‘OutlierD’

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**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>

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## R topics documented:

lcms . . . . .	1
OutlierD . . . . .	2
<b>Index</b>	<b>3</b>

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lcms	<i>LCMS data</i>
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## Description

This data set consists of LCMS data with two samples.

## Usage

```
data(lcms)
```

**Format**

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

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

\*Topic **datasets**

lcms, [1](#)

\*Topic **models**

OutlierD, [2](#)

lcms, [1](#)

OutlierD, [2](#)