OutlierD

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`lcms`	*LCMS data*

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`	*Outlier dectection using quantile regression on the M-A scatterplots of high-throughput data*

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-tranformation, 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")
```

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