RobLoxBioC-package

Infinitesimally robust estimators for preprocessing omics data

Description

Functions for the determination of optimally robust influence curves and estimators for preprocessing omics data, in particular gene expression data.

Details

Package: RobLoxBioC
Version: 0.9
Date: 2013-09-12
Depends: R(>= 2.14.0), methods, Biobase, affy, beadarray, distr, RobLox, lattice, RColorBrewer
LazyLoad: yes
LazyCompile: yes
License: LGPL-3
URL: http://robast.r-forge.r-project.org/
SVNRevision: 696
Encoding: latin1

Package versions

Note: The first two numbers of package versions do not necessarily reflect package-individual development, but rather are chosen for the RobAStXXX family as a whole in order to ease updating "depends" information.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

Maintainer: Matthias Kohl <matthias.kohl@stamats.de>

References


**See Also**
- roblox, rowRoblox

**Examples**
```
library(RobLoxBioC)
```

---

### KolmogorovMinDist

**Generic Function for Computing Minimum Kolmogorov Distance for Biological Data**

**Description**

Generic function for computing minimum Kolmogorov distance for biological data.

**Usage**

```
KolmogorovMinDist(x, D, ...)  
```

#### S4 method for signature 'matrix,Norm'

```
KolmogorovMinDist(x, D, mad0 = 1e-4)
```

#### S4 method for signature 'AffyBatch,AbscontDistribution'

```
KolmogorovMinDist(x, D, bg.correct = TRUE, pmcorrect = TRUE, verbose = TRUE)
```

#### S4 method for signature 'BeadLevelList,AbscontDistribution'

```
KolmogorovMinDist(x, D, log = FALSE, imagesPerArray = 1, what = "G", probes = NULL, arrays = NULL)
```

**Arguments**

- **x**: biological data.
- **D**: object of class "UnivariateDistribution".
- **...**: additional parameters.
- **mad0**: scale estimate used if computed MAD is equal to zero. Median and MAD are used as start parameter for optimization.
- **bg.correct**: if TRUE MAS 5.0 background correction is performed; confer bg.correct.mas.
- **pmcorrect**: if TRUE log2(PM/MM) is used. If FALSE only log2(PM) is used.
- **verbose**: logical: if TRUE, some messages are printed.
- **log**: if TRUE, then the log2 intensities for each bead-type are summarized.
imagesPerArray  Specifies how many images (strips) there are per array. Normally 1 for a SAM and 1 or 2 for a BeadChip. The images (strips) from the same array will be combined so that each column in the output represents a sample.

what  character string specifying which intensities/values to summarize.

probes  Specify particular probes to summarize. If left NULL then all the probes on the first array are used.

arrays  integer (scalar or vector) specifying the strips/arrays to summarize. If NULL, then all strips/arrays are summarized.

Details  

The minimum Kolmogorov distance is computed for each row of a matrix, each Affymetrix probe, or each Illumina bead, respectively.

So far, only the minimum distance to the set of normal distributions can be computed.

Value  

List with components dist containing a numeric vector or matrix with minimum Kolmogorov distances and n a numeric vector or matrix with the corresponding sample sizes.

Author(s)  

Matthias Kohl <Matthias.Kohl@stamats.de>

References  


See Also  

KolmogorovDist, MDEstimator

Examples  

set.seed(123) # to have reproducible results for package checking

## matrix method for KolmogorovMinDist
ind <- rbinom(200, size=1, prob=0.05)
X <- matrix(rnorm(200, mean=ind*3, sd=(1-ind) + ind*9), nrow = 2)
KolmogorovMinDist(X, D = Norm())

## using Affymetrix-Data
data(SpikeIn)
probes <- log2(pm(SpikeIn))
(res <- KolmogorovMinDist(probes, Norm()))
boxplot(res$dist)

## Not run:
## robloxbioc

**Generic Function for Preprocessing Biological Data**

### Description


### Usage

```r
robloxbioc(x, ...)  
```

*## S4 method for signature 'matrix'*

```r
robloxbioc(x, eps = NULL, eps.lower = 0, eps.upper = 0.05, steps = 3L, fscor = TRUE, mad0 = 1e-4)  
```

*## S4 method for signature 'AffyBatch'*

```r
robloxbioc(x, ...)  
```
robloxbioc(x, bg.correct = TRUE, pmcorrect = TRUE, normalize = FALSE,
            add.constant = 32, verbose = TRUE, eps = NULL,
            eps.lower = 0, eps.upper = 0.05, steps = 3L, fsCor = TRUE,
            mad0 = 1e-4, contrast.tau = 0.03, scale.tau = 10,
            delta = 2^(-20), sc = 500)

## S4 method for signature 'beadLevelData'
robloxbioc(x, channelList = list(greenChannel), probeIDs = NULL,
            useSampleFac = FALSE, sampleFac = NULL, weightNames = "wts",
            removeUnMappedProbes = TRUE, eps = NULL, eps.lower = 0,
            eps.upper = 0.05, steps = 3L, fsCor = TRUE, mad0 = 1e-4)

Arguments

x                  biological data.
...
eps                positive real (0 < eps <= 0.5): amount of gross errors. See details below.
eps.lower          positive real (0 <= eps.lower <= eps.upper): lower bound for the amount of gross errors. See details below.
eps.upper          positive real (eps.lower <= eps.upper <= 0.5): upper bound for the amount of gross errors. See details below.
steps              positive integer. k-step is used to compute the optimally robust estimator.
fsCor              logical: perform finite-sample correction. See function finiteSampleCorrection.
mad0               scale estimate used if computed MAD is equal to zero
bg.correct         if TRUE MAS 5.0 background correction is performed; confer bg.correct.mas
pmcorrect          method used for PM correction; TRUE calls an algorithm which is comparable to the algorithm of MAS 5.0; confer pmcorrect.mas. If FALSE only the PM intensities are used.
normalize          logical: if TRUE, Affymetrix scale normalization is performed.
add.constant       constant added to the MAS 5.0 expression values before the normalization step. Improves the variance of the measure one no longer devides by numbers close to 0 when computing fold-changes.
verbose            logical: if TRUE, some messages are printed.
contrast.tau       a number denoting the contrast tau parameter; confer the MAS 5.0 PM correction algorithm.
scale.tau          a number denoting the scale tau parameter; confer the MAS 5.0 PM correction algorithm.
delta              a number denoting the delta parameter; confer the MAS 5.0 PM correction algorithm.
sc                 value at which all arrays will be scaled to.
channelList        List of objects of class illuminaChannel that defines the summarisation to be performed where in our setup only the slots transFun and name have an effect on the computations. Setting the slots outlierFun, exprFun, and varFun has no effect. In any case rmx estimators are applied.
probeIDs Vector of ArrayAddressIDs to be included in the summarized object. The default is to summarize all probes.

useSampleFac if TRUE sections belonging to the same biological sample will be combined. The default is to summarize each section separately.

sampleFac optional character vector giving which a sample identifier for each section

weightNames name of column in the beadLevelData to take extract weights

removeUnMappedProbes if TRUE and annotation information is stored in the beadLevelData object, any ArrayAddressIDs that cannot be mapped to ILMN IDs will be removed.

Details

The optimally-robust resp. the radius-minimax (rmx) estimator for normal location and scale is used to preprocess biological data. The computation uses a k-step construction with median and MAD as starting estimators; cf. Rieder (1994) and Kohl (2005).

If the amount of gross errors (contamination) is known, it can be specified by eps. The radius of the corresponding infinitesimal contamination neighborhood (infinitesimal version of Tukey’s gross error model) is obtained by multiplying eps by the square root of the sample size.

If the amount of gross errors (contamination) is unknown, which is typically the case, try to find a rough estimate for the amount of gross errors, such that it lies between eps.lower and eps.upper.

If eps is NULL, the radius-minimax (rmx) estimator in sense of Rieder et al. (2001, 2008), respectively Section 2.2 of Kohl (2005) is used.

The algorithm used for Affymetrix data is similar to MAS 5.0 (cf. Affymetrix (2002)). The main difference is the substitution of the Tukey one-step estimator by our rmx k-step (k >= 1) estimator in the PM/MM correction step. The optional scale normalization is performed as given in Affymetrix (2002).

In case of Illumina data, the rmx estimator is used to summarize the bead types. The implementation for the most part copies summarize from beadarray.

For sample size <= 2, median and MAD are used for estimation.

If eps = 0, mean and sd are computed.

Value

Return value depends on the class of x. In case of "matrix" a matrix with columns "mean" and "sd" is returned. In case of "AffyBatch" an object of class "ExpressionSet" is returned. In case of "BeadLevelData" an object of class "ExpressionSetIllumina" is returned.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>,
update for beadarray versions >= 2.0.0 with support by Mark Dunnings and Andy Lynch
References


See Also

`roblox`, `rowRoblox`, `AffyBatch-class`, `generateExprVal.method.mas`, `ExpressionSet-class`, `summarize`

Examples

```r
set.seed(123) # to have reproducible results for package checking

## similar to rowRoblox of package RobLox
ind <- rbinom(200, size=1, prob=0.05)
X <- matrix(rnorm(200, mean=ind*3, sd=(1-ind) + ind*9), nrow = 2)
robloxbioc(X)
robloxbioc(X, steps = 5)
robloxbioc(X, eps = 0.05)
robloxbioc(X, eps = 0.05, steps = 5)

## Don't run to reduce check time on CRAN
## Not run:
## the function is designed for large scale problems
X <- matrix(rnorm(50000*20, mean = 1), nrow = 50000)
system.time(robloxbioc(X))

## using Affymetrix-Data
## confer example to generateExprVal.method.mas
## A more worked out example can be found in the scripts folder
## of the package.
data(SpikeIn)
probes <- pm(SpikeIn)
mas <- generateExprVal.method.mas(probes)
rl <- 2^robloxbioc(log2(t(probes)))
concentrations <- as.numeric(colnames(SpikeIn))
plot(concentrations, mas$exprs, log="xy", ylim=c(50,100000), type="b",
     ylab = "expression measures")
points(concentrations, rl[,1], pch = 20, col="orange", type="b")
legend("topleft", c("MAS", "roblox"), pch = c(1, 20))
```
require(affydata)
data(Dilution)
eset <- robloxbioc(Dilution)
## Affymetrix scale normalization
eset1 <- robloxbioc(Dilution, normalize = TRUE)
## "Not run" just because of computation time
require(beadarrayExampleData)
data(exampleBData)
res <- robloxbioc(exampleBData, eps.upper = 0.5)
res
## End(Not run)

---

**SimStudies**

**Perform Monte-Carlo Study.**

**Description**

The function AffySimStudy can be used to perform Monte-Carlo studies comparing Tukey’s bi-weight and rmx estimators for normal location and scale. The function IlluminaSimStudy can be used to perform Monte-Carlo studies comparing Illumina’s default method - a Huber-type skipped mean and sd (cf. Hampel (1985)) - and rmx estimators for normal location and scale. In addition, maximum likelihood (ML) estimators (mean and sd) and median and MAD are computed. The comparison is based on the empirical MSE.

**Usage**

\[
\text{AffySimStudy}(n, M, \text{eps}, \text{seed} = 123, \text{eps.lower} = 0, \text{eps.upper} = 0.05, \\
\text{steps} = 3L, \text{fsCor} = \text{TRUE}, \text{contD}, \text{plot1} = \text{FALSE}, \\
\text{plot2} = \text{FALSE}, \text{plot3} = \text{FALSE})
\]

\[
\text{IlluminaSimStudy}(n, M, \text{eps}, \text{seed} = 123, \text{eps.lower} = 0, \text{eps.upper} = 0.05, \\
\text{steps} = 3L, \text{fsCor} = \text{TRUE}, \text{contD}, \text{plot1} = \text{FALSE}, \\
\text{plot2} = \text{FALSE}, \text{plot3} = \text{FALSE})
\]

**Arguments**

- **n** integer; sample size, should be at least 3.
- **M** integer; Monte-Carlo replications.
- **eps** amount of contamination in [0, 0.5].
- **seed** random seed.
- **eps.lower** used by rmx estimator.
- **eps.upper** used by rmx estimator.
- **steps** integer; steps used for estimator construction.
- **fsCor** logical; use finite-sample correction.
- **contD** object of class "UnivariateDistribution": contaminating distribution.
plot1  logical; plot cdf of ideal and real distribution.
plot2  logical; plot 20 (or M if M < 20) randomly selected samples.
plot3  logical; generate boxplots of the results.

Details

Normal location and scale with mean = 0 and sd = 1 is used as ideal model (without restriction due to equivariance).

Since there is no estimator which yields reliable results if 50 percent or more of the observations are contaminated, we use a modification where we re-simulate all samples including at least 50 percent contaminated data.

We use function \texttt{rowRoblox} for the computation of the rmx estimator.

Value

Data.frame including empirical MSE (standardized by sample size n) and relMSE with respect to the rmx estimator.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

\texttt{rowRoblox}

Examples

set.seed(123) # to have reproducible results for package checking

\texttt{AffySimStudy(n = 11, M = 100, eps = 0.02, contD = Norm(mean = 0, sd = 3),
plot1 = TRUE, plot2 = TRUE, plot3 = TRUE)}

\texttt{IlluminaSimStudy(n = 30, M = 100, eps = 0.02, contD = Norm(mean = 0, sd = 3),
plot1 = TRUE, plot2 = TRUE, plot3 = TRUE)}
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