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Author(s)

Andreas Alfons [aut, cre]
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AIC.seqModel  Information criteria for a sequence of regression models

Description

Compute the Akaike or Bayes information criterion for a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.
Usage

```r
### S3 method for class 'seqModel'
AIC(object, ..., k = 2)

### S3 method for class 'sparseLTS'
AIC(object, ...,
    fit = c("reweighted", "raw", "both"), k = 2)

### S3 method for class 'seqModel'
BIC(object, ...)

### S3 method for class 'sparseLTS'
BIC(object, ...)
```

Arguments

- `object` the model fit for which to compute the information criterion.
- `...` for the BIC method, additional arguments to be passed down to the AIC method. For the AIC method, additional arguments are currently ignored.
- `fit` a character string specifying for which fit to compute the information criterion. Possible values are "reweighted" (the default) for the information criterion of the reweighted fit, "raw" for the information criterion of the raw fit, or "both" for the information criteria of both fits.
- `k` a numeric value giving the penalty per parameter to be used. The default is to use 2 as in the classical definition of the AIC.

Details

The information criteria are computed as \( n(\log(2\pi) + 1 + \log(\hat{\sigma}^2)) + dfk \), where \( n \) denotes the number of observations, \( \hat{\sigma} \) is the robust residual scale estimate, \( df \) is the number of nonzero coefficient estimates, and \( k \) is penalty per parameter. The usual definition of the AIC uses \( k = 2 \), whereas the BIC uses \( k = \log(n) \). Consequently, the former is used as the default penalty of the AIC method, whereas the BIC method calls the AIC method with the latter penalty.

Value

A numeric vector or matrix giving the information criteria for the requested model fits.

Note

Computing information criteria for several objects supplied via the `...` argument (as for the default methods of `AIC` and `BIC`) is currently not implemented.

Author(s)

Andreas Alfons
References


See Also

AIC, rlars, sparseLTS

Examples

```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100        # number of observations
p <- 25         # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5    # controls signal-to-noise ratio
epsilon <- 0.1   # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)                  # error terms
i <- 1:ceiling(epsilon*n)     # observations to be contaminated
e[i] <- e[i] + 5              # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5            # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
# compute AIC and BIC
AIC(fitRlars)
BIC(fitRlars)

## fit sparse LTS model over a grid of values for lambda
frac <- seq(0.2, 0.05, by = -0.05)
fitSparseLTS <- sparseLTS(x, y, lambda = frac, mode = "fraction")
# compute AIC and BIC
AIC(fitSparseLTS)
BIC(fitSparseLTS)
```

---

`coef.seqModel`  
*Extract coefficients from a sequence of regression models*
Description

Extract coefficients from a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

Usage

```r
## S3 method for class 'seqModel'
coef(object, s = NA, zeros = TRUE, 
     drop = !is.null(s), ...)
```

```r
## S3 method for class 'sparseLTS'
coef(object, s = NA, 
     fit = c("reweighted", "raw", "both"), zeros = TRUE, 
     drop = !is.null(s), ...)
```

Arguments

- **object**: the model fit from which to extract coefficients.
- **s**: for the "seqModel" method, an integer vector giving the steps of the submodels for which to extract coefficients (the default is to use the optimal submodel). For the "sparseLTS" method, an integer vector giving the indices of the models for which to extract coefficients. If `fit` is "both", this can be a list with two components, with the first component giving the indices of the reweighted fits and the second the indices of the raw fits. The default is to use the optimal model for each of the requested estimators. Note that the optimal models may not correspond to the same value of the penalty parameter for the reweighted and the raw estimator.
- **fit**: a character string specifying which coefficients to extract. Possible values are "reweighted" (the default) for the coefficients from the reweighted estimator, "raw" for the coefficients from the raw estimator, or "both" for the coefficients from both estimators.
- **zeros**: a logical indicating whether to keep zero coefficients (TRUE, the default) or to omit them (FALSE).
- **drop**: a logical indicating whether to reduce the dimension to a vector in case of only one submodel.
- **...**: additional arguments are currently ignored.

Value

A numeric vector or matrix containing the requested regression coefficients.

Author(s)

Andreas Alfons
**coefPlot**

Coefficient plot of a sequence of regression models

**Description**

Produce a plot of the coefficients from a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

**Examples**

```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100  # number of observations
p <- 25  # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5  # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5*t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)  # error terms
i <- 1:ceiling(epsilon*n)  # observations to be contaminated
e[i] <- e[i] + 5  # vertical outliers
y <- c(x %*% beta + sigma * e)  # response
x[i,] <- x[i,] + 5  # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, smax = 10)
# extract coefficients
coefficients(fitRlars, zeros = FALSE)
coefficients(fitRlars, s = 1:5, zeros = FALSE)

## sparse LTS over a grid of values for lambda
# fit model
frac <- seq(0.2, 0.05, by = -0.05)
fitSparseLTS <- sparseLTS(x, y, lambda = frac, mode = "fraction")
# extract coefficients
coefficients(fitSparseLTS, zeros = FALSE)
coefficients(fitSparseLTS, fit = "both", zeros = FALSE)
coefficients(fitSparseLTS, s = NULL, zeros = FALSE)
coefficients(fitSparseLTS, fit = "both", s = NULL, zeros = FALSE)
```

**See Also**

`coef`, `rlars`, `sparseLTS`
Usage

```
coefPlot(x, ...)
## S3 method for class 'seqModel'
coefPlot(x,  
  abscissa = c("step", "df"), zeros = FALSE,  
  size = c(0.5, 2, 4), labels, offset = 1, ...)
## S3 method for class 'sparseLTS'
coefPlot(x,  
  fit = c("reweighted", "raw", "both"),  
  abscissa = c("step", "df"), zeros = FALSE,  
  size = c(0.5, 2, 4), labels, offset = 1, ...)
```

Arguments

- **x**: the model fit to be plotted.
- **fit**: a character string specifying for which estimator to produce the plot. Possible values are "reweighted" (the default) for the reweighted fits, "raw" for the raw fits, or "both" for both estimators.
- **abscissa**: a character string specifying what to plot on the x-axis. Possible values are "step" for the step number (the default), or "df" for the degrees of freedom.
- **zeros**: a logical indicating whether predictors that never enter the model and thus have zero coefficients should be included in the plot (TRUE) or omitted (FALSE, the default). This is useful if the number of predictors is much larger than the number of observations, in which case many coefficients are never nonzero.
- **size**: a numeric vector of length three giving the line width, the point size and the label size, respectively.
- **labels**: an optional character vector containing labels for the predictors. Plotting labels can be suppressed by setting this to NULL.
- **offset**: an integer giving the offset of the labels from the corresponding coefficient values from the last step (i.e., the number of blank characters to be prepended to the label).
- **...**: for the generic function, additional arguments to be passed down to methods. For the "seqModel" and "sparseLTS" methods, additional arguments to be passed down to `geom_line` and `geom_point`.

Value

An object of class "ggplot" (see `ggplot`).

Author(s)

Andreas Alfons
corHuber

**See Also**
ggplot, rlars, sparseLTS

**Examples**

```r
## generate data
# example is not high-dimensional to keep computation time low
library(mvtnorm)
set.seed(1234)  # for reproducibility
n <- 100  # number of observations
p <- 25  # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5  # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)  # error terms
i <- 1:ceiling(epsilon*n)  # observations to be contaminated
e[i] <- e[i] + 5  # vertical outliers
y <- c(x %*% beta + sigma * e)  # response
x[i,] <- x[i,] + 5  # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
# create plot
coeffPlot(fitRlars)

## sparse LTS over a grid of values for lambda
# fit model
frac <- seq(0.2, 0.05, by = -0.05)
fitSparseLTS <- sparseLTS(x, y, lambda = frac, mode = "fraction")
# create plot
coeffPlot(fitSparseLTS)
coeffPlot(fitSparseLTS, fit = "both")
```

---

corHuber  
**Robust correlation based on winsorization.**

**Description**

Compute a robust correlation estimate based on winsorization, i.e., by shrinking outlying observations to the border of the main part of the data.
Usage

```r
corHuber(x, y,
  type = c("bivariate", "adjusted", "univariate"),
  standardized = FALSE, centerFun = median,
  scaleFun = mad, const = 2, prob = 0.95,
  tol = .Machine$double.eps*0.5, ...)
```

Arguments

- `x`: a numeric vector.
- `y`: a numeric vector.
- `type`: a character string specifying the type of winsorization to be used. Possible values are "univariate" for univariate winsorization, "adjusted" for adjusted univariate winsorization, or "bivariate" for bivariate winsorization.
- `standardized`: a logical indicating whether the data are already robustly standardized.
- `centerFun`: a function to compute a robust estimate for the center to be used for robust standardization (defaults to `median`). Ignored if `standardized` is `TRUE`.
- `scaleFun`: a function to compute a robust estimate for the scale to be used for robust standardization (defaults to `mad`). Ignored if `standardized` is `TRUE`.
- `const`: numeric; tuning constant to be used in univariate or adjusted univariate winsorization (defaults to 2).
- `prob`: numeric; probability for the quantile of the \( \chi^2 \) distribution to be used in bivariate winsorization (defaults to 0.95).
- `tol`: a small positive numeric value. This is used in bivariate winsorization to determine whether the initial estimate from adjusted univariate winsorization is close to 1 in absolute value. In this case, bivariate winsorization would fail since the points form almost a straight line, and the initial estimate is returned.
- `...`: additional arguments to be passed to `robstandardize`.

Details

The borders of the main part of the data are defined on the scale of the robustly standardized data. In univariate winsorization, the borders for each variable are given by \(+/−\text{const}\), thus a symmetric distribution is assumed. In adjusted univariate winsorization, the borders for the two diagonally opposing quadrants containing the minority of the data are shrunken by a factor that depends on the ratio between the number of observations in the major and minor quadrants. It is thus possible to better account for the bivariate structure of the data while maintaining fast computation. In bivariate winsorization, a bivariate normal distribution is assumed and the data are shrunken towards the boundary of a tolerance ellipse with coverage probability `prob`. The boundary of this ellipse is thereby given by all points that have a squared Mahalanobis distance equal to the quantile of the \( \chi^2 \) distribution given by `prob`. Furthermore, the initial correlation matrix required for the Mahalanobis distances is computed based on adjusted univariate winsorization.

Value

The robust correlation estimate.
critPlot

Author(s)
Andreas Alfons, based on code by Jafar A. Khan, Stefan Van Aelst and Ruben H. Zamar

References

See Also
winsorize

Examples
```r
## generate data
library("mvtnorm")
set.seed(1234)  # for reproducibility
Sigma <- matrix(c(1, 0.6, 0.6, 1), 2, 2)
xy <- rmvnorm(100, sigma=Sigma)
x <- xy[, 1]
y <- xy[, 2]

## introduce outlier

## compute correlation
cor(x, y)
corHuber(x, y)
```

---

critPlot

Optimality criterion plot of a sequence of regression models

Description
Produce a plot of the values of the optimality criterion for a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

Usage
critPlot(x, ...)

## S3 method for class 'seqModel'
critPlot(x, size = c(0.5, 2), ...)

## S3 method for class 'perrySeqModel'
critPlot(x, ...)
critPlot

## S3 method for class 'sparseLTS'
critPlot(x, 
    fit = c("reweighted", "raw", "both"), size = c(0.5, 2), 
    ...) 

## S3 method for class 'perrySparseLTS'
critPlot(x, 
    fit = c("reweighted", "raw", "both"), ...) 

### Arguments

- **x**: the model fit to be plotted.
- **fit**: a character string specifying for which estimator to produce the plot. Possible values are "reweighted" (the default) for the reweighted fits, "raw" for the raw fits, or "both" for both estimators.
- **size**: a numeric vector of length two giving the line width and the point size, respectively.
- **...**: for the generic function, additional arguments to be passed down to methods. For the "seqModel" and "sparseLTS" methods, additional arguments to be passed down to `geom_line` and `geom_point`. For the "perrySeqModel" and "perrySparseLTS" methods, additional arguments to be passed down to `perryPlot`.

### Value

An object of class "ggplot" (see `ggplot`).

### Author(s)

Andreas Alfons

### See Also

`ggplot`, `perryPlot`, `rlars`, `sparseLTS`

### Examples

```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100  # number of observations
p <- 25  # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5  # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)  # error terms
i <- 1:ceiling(epsilon*n)  # observations to be contaminated
```
diagnosticPlot

Diagnostic plots for a sequence of regression models

Description

Produce diagnostic plots for a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter. Four plots are currently implemented.

Usage

```r
diagnosticPlot(x, y)
```

## S3 method for class 'seqModel'
diagnosticPlot(x, s = NA, y)

## S3 method for class 'perrySeqModel'
diagnosticPlot(x, y)

## S3 method for class 'sparseLTS'
diagnosticPlot(x, s = NA, fit = c("reweighted", "raw", "both"), y)

## S3 method for class 'perrySparseLTS'
diagnosticPlot(x, y)

## Default S3 method:
diagnosticPlot(x,
```
which = c("all", "rqq", "rindex", "rfit", "rdiag"),
ask = (which == "all"), facets = attr(x, "facets"),
size = c(2, 4), id.n = NULL, ...)

Arguments

x
the model fit for which to produce diagnostic plots, or a data frame containing all
necessary information for plotting (as generated by the corresponding fortify
method).

s
for the "seqModel" method, an integer vector giving the steps of the submodels
for which to produce diagnostic plots (the default is to use the optimal sub-
model). For the "sparseLTS" method, an integer vector giving the indices of
the models for which to produce diagnostic plots (the default is to use the opti-
mal model for each of the requested fits).

fit
a character string specifying for which fit to produce diagnostic plots. Possible
values are "reweighted" (the default) for diagnostic plots for the reweighted
fit, "raw" for diagnostic plots for the raw fit, or "both" for diagnostic plots for
both fits.

which
a character string indicating which plot to show. Possible values are "all" (the
default) for all of the following, "rqq" for a normal Q-Q plot of the standard-
ized residuals, "rindex" for a plot of the standardized residuals versus their
index, "rfit" for a plot of the standardized residuals versus the fitted values, or
"rdiag" for a regression diagnostic plot (standardized residuals versus robust
Mahalanobis distances of the predictor variables).

ask
a logical indicating whether the user should be asked before each plot (see
devAskNewPage). The default is to ask if all plots are requested and not ask
otherwise.

facets
a faceting formula to override the default behavior. If supplied, facet_wrap or
facet_grid is called depending on whether the formula is one-sided or two-
sided.

size
a numeric vector of length two giving the point and label size, respectively.

id.n
an integer giving the number of the most extreme observations to be identified
by a label. The default is to use the number of identified outliers, which can be
different for the different plots. See “Details” for more information.

... for the generic function, additional arguments to be passed down to methods.
For the "perrySeqModel" and "perrySparseLTS" method, additional argu-
ments to be passed down to the "seqModel" and "sparseLTS" method, respec-
tively. For the "seqModel" and "sparseLTS" methods, additional arguments
to be passed down to the default method. For the default method, additional
arguments to be passed down to geom_point.

Details

In the normal Q-Q plot of the standardized residuals, a reference line is drawn through the first and
third quartile. The id.n observations with the largest distances from that line are identified by a
label (the observation number). The default for id.n is the number of regression outliers, i.e., the
number of observations whose residuals are too large (cf. wt).
In the plots of the standardized residuals versus their index or the fitted values, horizontal reference lines are drawn at 0 and +/-2.5. The id.n observations with the largest absolute values of the standardized residuals are identified by a label (the observation number). The default for id.n is the number of regression outliers, i.e., the number of observations whose absolute residuals are too large (cf. wt).

For the regression diagnostic plot, the robust Mahalanobis distances of the predictor variables are computed via the MCD based on only those predictors with non-zero coefficients (see covMcd). Horizontal reference lines are drawn at +/-2.5 and a vertical reference line is drawn at the upper 97.5% quantile of the $\chi^2$ distribution with $p$ degrees of freedom, where $p$ denotes the number of predictors with non-zero coefficients. The id.n observations with the largest absolute values of the standardized residuals and/or largest robust Mahalanobis distances are identified by a label (the observation number). The default for id.n is the number of all outliers: regression outliers (i.e., observations whose absolute residuals are too large, cf. wt) and leverage points (i.e., observations with robust Mahalanobis distance larger than the 97.5% quantile of the $\chi^2$ distribution with $p$ degrees of freedom).

**Value**

If only one plot is requested, an object of class "ggplot" (see ggplot), otherwise a list of such objects.

**Author(s)**

Andreas Alfons

**See Also**

ggplot, rlars, sparseLTS, plot.lts

**Examples**

```r
## generate data
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100       # number of observations
p <- 25        # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5   # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)                  # error terms
i <- 1:ceiling(epsilon*n)     # observations to be contaminated
e[i] <- e[i] + 5               # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5             # bad leverage points

## robust LARS
# fit model
```
fitted.seqModel

Extract fitted values from a sequence of regression models

Description

Extract fitted values from a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

Usage

```r
## S3 method for class 'seqModel'
fitted(object, s = NA,
        drop = !is.null(s), ...)

## S3 method for class 'sparseLTS'
fitted(object, s = NA,
        fit = c("reweighted", "raw", "both"),
        drop = !is.null(s), ...)
```

Arguments

- **object**
  the model fit from which to extract fitted values.

- **s**
  for the "seqModel" method, an integer vector giving the steps of the submodels for which to extract the fitted values (the default is to use the optimal submodel). For the "sparseLTS" method, an integer vector giving the indices of the models for which to extract fitted values. If `fit` is "both", this can be a list with two components, with the first component giving the indices of the reweighted fits and the second the indices of the raw fits. The default is to use the optimal model for each of the requested estimators. Note that the optimal models may not correspond to the same value of the penalty parameter for the reweighted and the raw estimator.

- **fit**
  a character string specifying which fitted values to extract. Possible values are "reweighted" (the default) for the fitted values from the reweighted estimator, "raw" for the fitted values from the raw estimator, or "both" for the fitted values from both estimators.
drop a logical indicating whether to reduce the dimension to a vector in case of only one step.

... additional arguments are currently ignored.

Value

A numeric vector or matrix containing the requested fitted values.

Author(s)

Andreas Alfons

See Also

fitted, rlars, sparseLTS

Examples

```r
## generate data
data <- example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100       # number of observations
p <- 25        # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5   # controls signal-to-noise ratio
epsilon <- 0.1 # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)               # error terms
i <- 1:ceiling(epsilon*n)   # observations to be contaminated
e[i] <- e[i] + 5            # vertical outliers
y <- c(x * beta + sigma * e) # response
x[i,] <- x[i,] + 5          # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
# extract fitted values
fitted(fitRlars)
head(fitted(fitRlars, s = 1:5))

## sparse LTS over a grid of values for lambda
# fit model
frac <- seq(0.2, 0.05, by = -0.05)
fitsparselts <- sparselts(x, y, lambda = frac, mode = "fraction")
# extract fitted values
fitted(fitsparselts)
head(fitted(fitsparselts, fit = "both"))
head(fitted(fitsparselts, s = NULL))
```
fortify.seqModel

Convert a sequence of regression models into a data frame for plotting

Description

Supplement the fitted values and residuals of a sequence of regression models (such as robust least angle regression models or sparse least trimmed squares regression models) with other useful information for diagnostic plots.

Usage

```r
## S3 method for class 'seqModel'
fortify(model, data, s = NA, ...)
```

```r
## S3 method for class 'sparselTS'
fortify(model, data, s = NA,
        fit = c("rewighted", "raw", "both"), ...)
```

Arguments

- `model` the model fit to be converted.
- `data` currently ignored.
- `s` for the "seqModel" method, an integer vector giving the steps of the submodels to be converted (the default is to use the optimal submodel). For the "sparselTS" method, an integer vector giving the indices of the models to be converted (the default is to use the optimal model for each of the requested fits).
- `fit` a character string specifying which fit to convert. Possible values are "rewighted" (the default) to convert the reweighted fit, "raw" to convert the raw fit, or "both" to convert both fits.
- `...` currently ignored.

Value

A data frame containing the columns listed below, as well as additional information stored in the attributes "qqLine" (intercepts and slopes of the respective reference lines to be displayed in residual Q-Q plots), "q" (quantiles of the Mahalanobis distribution used as cutoff points for detecting leverage points), and "facets" (default faceting formula for the diagnostic plots).

- `step` the steps (for the "seqModel" method) or indices (for the "sparselTS" method) of the models (only returned if more than one model is requested).
- `fit` the model fits (only returned if both the reweighted and raw fit are requested in the "sparselTS" method).
- `index` the indices of the observations.
fortify.seqModel

fitted  the fitted values.
residual the standardized residuals.
theoretical the corresponding theoretical quantiles from the standard normal distribution.
qdd     the absolute distances from a reference line through the first and third sample and theoretical quartiles.
rd      the robust Mahalanobis distances computed via the MCD (see covMcd).
xyd     the pairwise maxima of the absolute values of the standardized residuals and the robust Mahalanobis distances, divided by the respective other outlier detection cutoff point.
weight  the weights indicating regression outliers.
leverage logicals indicating leverage points (i.e., outliers in the predictor space).
classification a factor with levels "outlier" (regression outliers) and "good" (data points following the model).

Author(s)
Andreas Alfons

See Also
fortify, diagnosticPlot, sparseLTS, sparseLTS

Examples

## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100        # number of observations
p <- 25         # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5    # controls signal-to-noise ratio
epsilon <- 0.1   # contamination level
Sigma <- 0.5*t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)                  # error terms
i <- 1:ceiling(epsilon*n)     # observations to be contaminated
e[i] <- e[i] + 5              # vertical outliers
y <- c(x %% beta + sigma * e) # response
x[1,] <- x[1,] + 5            # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
# convert to data for plotting
head(fortify(fitRlars))
getScale

Extract the residual scale of a robust regression model

Description

Extract the robust scale estimate of the residuals from a robust regression model.

Usage

getScale(x, ...)

## S3 method for class 'sparseLTS'
getScale(x, s = NA,
         fit = c("reweighted", "raw", "both"), ...)

Arguments

x
  the model fit from which to extract the robust residual scale estimate.

s
  an integer vector giving the indices of the models from which to extract the robust residual scale estimate. If fit is "both", this can be a list with two components, with the first component giving the indices of the reweighted fits and the second the indices of the raw fits. The default is to use the optimal model for each of the requested estimators. Note that the optimal models may not correspond to the same value of the penalty parameter for the reweighted and the raw estimator.

fit
  a character string specifying from which fit to extract the robust residual scale estimate. Possible values are "reweighted" (the default) for the residual scale of the reweighted fit, "raw" for the residual scale of the raw fit, or "both" for the residual scale of both fits.

...
  additional arguments to be passed down to methods.

Details

Methods are implemented for models of class "lmrob" (see lmrob), "lts" (see ltsReg), "rlm" (see rlm), "seqModel" (see rlars) and "sparseLTS" (see sparseLTS). The default method computes the MAD of the residuals.

Value

A numeric vector or matrix giving the robust residual scale estimates for the requested model fits.
Author(s)

Andreas Alfons

See Also

AIC, lmrob, ltsReg, rlm, rlars, sparseLTS

Examples

```r
data("coleman")
fit <- lmrob(Y ~ ., data=coleman)
getScale(fit)
```

Description

Use bivariate winsorization to estimate the smallest value of the penalty parameter for sparse least trimmed squares regression that sets all coefficients to zero.

Usage

```r
lambda0(x, y, normalize = TRUE, intercept = TRUE,
        const = 2, prob = 0.95, tol = .Machine$double.eps^0.5,
        eps = .Machine$double.eps, ...)
```

Arguments

- `x` a numeric matrix containing the predictor variables.
- `y` a numeric vector containing the response variable.
- `normalize` a logical indicating whether the winsorized predictor variables should be normalized to have unit $L_2$ norm (the default is `TRUE`).
- `intercept` a logical indicating whether a constant term should be included in the model (the default is `TRUE`).
- `const` numeric; tuning constant to be used in univariate winsorization (defaults to 2).
- `prob` numeric; probability for the quantile of the $\chi^2$ distribution to be used in bivariate winsorization (defaults to 0.95).
- `tol` a small positive numeric value used to determine singularity issues in the computation of correlation estimates for bivariate winsorization (see `corHuber`).
- `eps` a small positive numeric value used to determine whether the robust scale estimate of a variable is too small (an effective zero).
- `...` additional arguments to be passed to `robStandardize`.  

Penalty parameter for sparse LTS regression
Details

The estimation procedure is inspired by the calculation of the respective penalty parameter in the first step of the classical LARS algorithm. First, two-dimensional data blocks consisting of the response with each predictor variable are cleaned via bivariate winsorization. For each block, the following computations are then performed. If an intercept is included in the model, the cleaned response is centered and the corresponding cleaned predictor is centered and scaled to have unit norm. Otherwise the variables are not centered, but the predictor is scaled to have unit norm. Finally, the dot product of the response and the corresponding predictor is computed. The largest absolute value of those dot products, rescaled to fit the parametrization of the sparse LTS definition, yields the estimate of the smallest penalty parameter that sets all coefficients to zero.

Value

A robust estimate of the smallest value of the penalty parameter for sparse LTS regression that sets all coefficients to zero.

Author(s)

Andreas Alfons

References


See Also

`sparselts`, `winsorize`

Examples

```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100   # number of observations
p <- 25    # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5   # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)  # error terms
i <- 1:ceiling(epsilon*n)  # observations to be contaminated
e[i] <- e[i] + 5  # vertical outliers
y <- c(x %*% beta + sigma * e)  # response
```
x[i,] <- x[i,] + 5  # bad leverage points

## estimate smallest value of the penalty parameter
## that sets all coefficients to 0
lambda0(x, y)

---

**Description**

Estimate the prediction error of a previously fit sequential regression model such as a robust least angle regression model or a sparse least trimmed squares regression model.

**Usage**

```r
## S3 method for class 'seqModel'
perry(object, splits = foldControl(),
       cost, ncores = 1, cl = NULL, seed = NULL, ...)

## S3 method for class 'sparseLTS'
perry(object,
       splits = foldControl(),
       fit = c("reweighted", "raw", "both"), cost = rtmspe,
       ncores = 1, cl = NULL, seed = NULL, ...)
```

**Arguments**

- **object**: the model fit for which to estimate the prediction error.
- **splits**: an object of class "cvFolds" (as returned by `cvFolds`) or a control object of class "foldControl" (see `foldControl`) defining the folds of the data for (repeated) K-fold cross-validation, an object of class "randomSplits" (as returned by `randomSplits`) or a control object of class "splitControl" (see `splitControl`) defining random data splits, or an object of class "bootSamples" (as returned by `bootSamples`) or a control object of class "bootControl" (see `bootControl`) defining bootstrap samples.
- **fit**: a character string specifying for which fit to estimate the prediction error. Possible values are "reweighted" (the default) for the prediction error of the reweighted fit, "raw" for the prediction error of the raw fit, or "both" for the prediction error of both fits.
- **cost**: a cost function measuring prediction loss. It should expect vectors to be passed as its first two arguments, the first corresponding to the observed values of the response and the second to the predicted values, and must return a non-negative scalar value. The default is to use the root mean squared prediction error for non-robust models and the root trimmed mean squared prediction error for robust models (see `cost`).
ncores  a positive integer giving the number of processor cores to be used for parallel computing (the default is 1 for no parallelization). If this is set to NA, all available processor cores are used.

cl  a parallel cluster for parallel computing as generated by makeCluster. If supplied, this is preferred over ncores.

seed  optional initial seed for the random number generator (see .Random.seed). Note that also in case of parallel computing, resampling is performed on the manager process rather than the worker processes. On the parallel worker processes, random number streams are used and the seed is set via clusterSetRNGStream.

...  additional arguments to be passed to the prediction loss function cost.

details

The prediction error can be estimated via (repeated) $K$-fold cross-validation, (repeated) random splitting (also known as random subsampling or Monte Carlo cross-validation), or the bootstrap. In each iteration, the optimal model is thereby selected from the training data and used to make predictions for the test data.

value

An object of class "perry" with the following components:

pe  a numeric vector containing the estimated prediction errors for the requested model fits. In case of more than one replication, this gives the average value over all replications.

se  a numeric vector containing the estimated standard errors of the prediction loss for the requested model fits.

reps  a numeric matrix in which each column contains the estimated prediction errors from all replications for the requested model fits. This is only returned in case of more than one replication.

splits  an object giving the data splits used to estimate the prediction error.

y  the response.

yHat  a list containing the predicted values from all replications.

call  the matched function call.

Author(s)

Andreas Alfons

See Also

rlars, sparseLTS, predict, perry, cost
Examples

```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234) # for reproducibility
n <- 100 # number of observations
p <- 25 # number of variables
beta <- rep.int(c(1, 0), c(5, p-5)) # coefficients
sigma <- 0.5 # controls signal-to-noise ratio
epsilon <- 0.1 # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma) # predictor matrix
e <- rnorm(n) # error terms
i <- 1:ceiling(epsilon*n) # observations to be contaminated
e[i] <- e[i] + 5 # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5 # bad leverage points

## fit and evaluate robust LARS model
fitRlars <- rlars(x, y, sMax = 10)
perry(fitRlars)

## fit and evaluate sparse LTS model
frac <- seq(0.2, 0.05, by = -0.05)
fitSparseLTS <- sparseLTS(x, y, lambda = frac, mode = "fraction")
perry(fitSparseLTS)
```

plot.seqModel

Plot a sequence of regression models

Description

Produce a plot of the coefficients, the values of the optimality criterion, or diagnostic plots for a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

Usage

```r
## S3 method for class 'seqModel'
plot(x,
     method = c("coefficients", "crit", "diagnostic"), ...)

## S3 method for class 'perrySeqModel'
plot(x,
     method = c("crit", "diagnostic"), ...)

## S3 method for class 'sparseLTS'
plot(x,
```
method = c("coefficients", "crit", "diagnostic"), ...)

## S3 method for class 'perrySparseLTS'
plot(x, 
method = c("crit", "diagnostic"), ...)

Arguments

x the model fit to be plotted.

method a character string specifying the type of plot. Possible values are "coefficients" to plot the coefficients from the submodels via coefPlot (only for the "seqModel" and "sparseLTS" methods), "crit" to plot the values of the optimality criterion for the submodels via critPlot, or "diagnostic" for diagnostic plots via diagnosticPlot.

... additional arguments to be passed down.

Value

An object of class "ggplot" (see ggplot).

Author(s)

Andreas Alfons

See Also

ccoefPlot, critPlot, diagnosticPlot, rlars, sparseLTS

Examples

## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100  # number of observations
p <- 25   # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5  # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5*tr(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)                  # error terms
i <- 1:ceiling(epsilon*n)     # observations to be contaminated
e[i] <- e[i] + 5              # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5            # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
predict.seqModel

# create plots
plot(fitRlars, method = "coef")
plot(fitRlars, method = "crit")
plot(fitRlars, method = "diagnostic")

### sparse LTS over a grid of values for lambda
# fit model
frac <- seq(0.2, 0.05, by = -0.05)
fitSparseLTS <- sparseLTS(x, y, lambda = frac, mode = "fraction")
# create plots
plot(fitSparseLTS, method = "coef")
plot(fitSparseLTS, method = "crit")
plot(fitSparseLTS, method = "diagnostic")

predict.seqModel

Predict from a sequence of regression models

Description

Make predictions from a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

Usage

### S3 method for class 'seqModel'
predict(object, newdata, s = NA, ...)

### S3 method for class 'sparseLTS'
predict(object, newdata, s = NA,
        fit = c("reweighted", "raw", "both"), ...)

Arguments

- **object**: the model fit from which to make predictions.
- **newdata**: new data for the predictors. If the model fit was computed with the formula method, this should be a data frame from which to extract the predictor variables. Otherwise this should be a matrix containing the same variables as the predictor matrix used to fit the model (including a column of ones to account for the intercept).
- **s**: for the "seqModel" method, an integer vector giving the steps of the submodels for which to make predictions (the default is to use the optimal submodel). For the "sparseLTS" method, an integer vector giving the indices of the models for which to make predictions. If `fit` is "both", this can be a list with two components, with the first component giving the indices of the reweighted fits and the second the indices of the raw fits. The default is to use the optimal model for each of the requested estimators. Note that the optimal models may
not correspond to the same value of the penalty parameter for the reweighted
and the raw estimator.

`fit` a character string specifying for which fit to make predictions. Possible values
are "reweighted" (the default) for predicting values from the reweighted fit,
"raw" for predicting values from the raw fit, or "both" for predicting values
from both fits.

... additional arguments to be passed down to the respective method of `coef`.

Details

The `newdata` argument defaults to the matrix of predictors used to fit the model such that the fitted
values are computed.

Value

A numeric vector or matrix containing the requested predicted values.

Author(s)

Andreas Alfons

See Also

`predict.rlars`, `sparseLTS`

Examples

```r
# generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234) # for reproducibility
n <- 100 # number of observations
p <- 25 # number of variables
beta <- rep.int(c(1, 0), c(5, p-5)) # coefficients
sigma <- 0.5 # controls signal-to-noise ratio
epsilon <- 0.1 # contamination level
Sigma <- 0.5*t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma) # predictor matrix
e <- rnorm(n) # error terms
i <- 1:ceiling(epsilon*n) # observations to be contaminated
e[i] <- e[i] + 5 # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5 # bad leverage points

# robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
# compute fitted values via predict method
predict(fitRlars)
head(predict(fitRlars, s = 1:5))
```
## residuals.seqModel

Extract residuals from a sequence of regression models

### Description

Extract residuals from a sequence of regression models, such as submodels along a robust least angle regression sequence, or sparse least trimmed squares regression models for a grid of values for the penalty parameter.

### Usage

```r
## S3 method for class 'seqModel'
residuals(object, s = NA,
    standardized = FALSE, drop = !is.null(s), ...)

## S3 method for class 'sparselts'
residuals(object, s = NA,
    fit = c("reweighted", "raw", "both"),
    standardized = FALSE, drop = !is.null(s), ...)
```

### Arguments

- `object`  
  the model fit from which to extract residuals.

- `s`  
  for the "seqModel" method, an integer vector giving the steps of the submodels for which to extract the residuals (the default is to use the optimal submodel). For the "sparselts" method, an integer vector giving the indices of the models for which to extract residuals. If `fit` is "both", this can be a list with two components, with the first component giving the indices of the reweighted fits and the second the indices of the raw fits. The default is to use the optimal model for each of the requested estimators. Note that the optimal models may not correspond to the same value of the penalty parameter for the reweighted and the raw estimator.

- `fit`  
  a character string specifying which residuals to extract. Possible values are "reweighted" (the default) for the residuals from the reweighted estimator, "raw" for the residuals from the raw estimator, or "both" for the residuals from both estimators.
standardized  a logical indicating whether the residuals should be standardized (the default is FALSE).

drop  a logical indicating whether to reduce the dimension to a vector in case of only one step.

... additional arguments are currently ignored.

Value

A numeric vector or matrix containing the requested residuals.

Author(s)

Andreas Alfons

See Also

residuals, rlars, sparseLTS

Examples

## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100  # number of observations
p <- 25  # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5  # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5*t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)  # error terms
i <- 1:ceiling(epsilon*n)  # observations to be contaminated
e[i] <- e[i] + 5  # vertical outliers
y <- c(x %% beta + sigma * e)  # response
x[i,] <- x[i,] + 5  # bad leverage points

## robust LARS
# fit model
fitRlars <- rlars(x, y, sMax = 10)
# extract residuals
residuals(fitRlars)
head(residuals(fitRlars, s = 1:5))

## sparse LTS over a grid of values for lambda
# fit model
frac <- seq(0.2, 0.05, by = -0.05)
fitSparseLTS <- sparseLTS(x, y, lambda = frac, mode = "fraction")
# extract residuals
RLARS

Robust least angle regression

Description

Robustly sequence candidate predictors according to their predictive content and find the optimal model along the sequence.

Usage

rlars(x, ...)

### S3 method for class 'formula'
rlars(formula, data, ...)

### Default S3 method:
rlars(x, y, sMax = NA,
    centerFun = median, scaleFun = mad, winsorize = FALSE,
    pca = FALSE, const = 2, prob = 0.95, fit = TRUE,
    s = c(0, sMax), regFun = lmrob, regArgs = list(),
    crit = c("BIC", "PE"), splits = foldControl(),
    cost = rtmse, costArgs = list(),
    selectBest = c("hastie", "min"), seFactor = 1,
    ncores = 1, cl = NULL, seed = NULL, model = TRUE,
    tol = .Machine$double.eps^0.5, ...)

Arguments

formula a formula describing the full model.
data an optional data frame, list or environment (or object coercible to a data frame by as.data.frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which rlars is called.
x a matrix or data frame containing the candidate predictors.
y a numeric vector containing the response.
sMax an integer giving the number of predictors to be sequenced. If it is NA (the default), predictors are sequenced as long as there are twice as many observations as predictors.
centerFun a function to compute a robust estimate for the center (defaults to median).
scaleFun a function to compute a robust estimate for the scale (defaults to mad).
winsorize a logical indicating whether to clean the full data set by multivariate winsorization, i.e., to perform data cleaning RLARS instead of plug-in RLARS (defaults to FALSE).

pca a logical indicating whether a robust PCA step should be performed when computing the data cleaning weights for multivariate winsorization (defaults to FALSE). The distances of the observations are then computed on the PCA scores rather than the original observations, which makes data cleaning RLARS applicable for high-dimensional data. If TRUE or NA, components are computed as long as the robust correlation matrix of the scores can be inverted, and all components with an eigenvalue larger than or equal to 1 are retained. Alternatively, an integer giving the maximum number of components can be supplied.

cost numeric; tuning constant to be used in the initial correlation estimates based on adjusted univariate winsorization (defaults to 2).

prob numeric; probability for the quantile of the $\chi^2$ distribution to be used in bivariate or multivariate winsorization (defaults to 0.95).

fit a logical indicating whether to fit submodels along the sequence (TRUE, the default) or to simply return the sequence (FALSE).

s an integer vector of length two giving the first and last step along the sequence for which to compute submodels. The default is to start with a model containing only an intercept (step 0) and iteratively add all variables along the sequence (step $s_{\text{Max}}$). If the second element is NA, predictors are added to the model as long as there are twice as many observations as predictors. If only one value is supplied, it is recycled.

regFun a function to compute robust linear regressions along the sequence (defaults to lmrob).

regArgs a list of arguments to be passed to regFun.

crit a character string specifying the optimality criterion to be used for selecting the final model. Possible values are "BIC" for the Bayes information criterion and "PE" for resampling-based prediction error estimation.

splits an object giving data splits to be used for prediction error estimation (see perry).

cost a cost function measuring prediction loss (see perry for some requirements). The default is to use the root trimmed mean squared prediction error (see cost).

costArgs a list of additional arguments to be passed to the prediction loss function cost.

selectBest,... arguments specifying a criterion for selecting the best model (see perrySelect). The default is to use a one-standard-error rule.

ncores a positive integer giving the number of processor cores to be used for parallel computing (the default is 1 for no parallelization). If this is set to NA, all available processor cores are used. For fitting models along the sequence and for prediction error estimation, parallel computing is implemented on the R level using package parallel. Otherwise parallel computing for some of the more computer-intensive computations in the sequencing step is implemented on the C++ level via OpenMP (http://openmp.org/).

cl a parallel cluster for parallel computing as generated by makeCluster. This is preferred over ncores for tasks that are parallelized on the R level, in which case ncores is only used for tasks that are parallelized on the C++ level.
seed

optional initial seed for the random number generator (see \texttt{Random.seed}). This is useful because many robust regression functions (including \texttt{lmrob}) involve randomness, or for prediction error estimation. On parallel R worker processes, random number streams are used and the seed is set via \texttt{clusterSetRNGStream}.

model

a logical indicating whether the model data should be included in the returned object.

tol

a small positive numeric value. This is used in bivariate winsorization to determine whether the initial estimate from adjusted univariate winsorization is close to 1 in absolute value. In this case, bivariate winsorization would fail since the points form almost a straight line, and the initial estimate is returned.

... additional arguments to be passed down. For the default method, additional arguments to be passed down to \texttt{robStandardize}.

Value

If fit is FALSE, an integer vector containing the indices of the sequenced predictors.

Else if crit is "PE", an object of class "perrySeqModel" (inheriting from class "perrySelect", see \texttt{perrySelect}). It contains information on the prediction error criterion, and includes the final model as component finalModel.

Otherwise an object of class "rlars" (inheriting from class "seqModel") with the following components:

\begin{itemize}
  \item \textbf{active} an integer vector containing the indices of the sequenced predictors.
  \item \textbf{s} an integer vector containing the steps for which submodels along the sequence have been computed.
  \item \textbf{coefficients} a numeric matrix in which each column contains the regression coefficients of the corresponding submodel along the sequence.
  \item \textbf{fitted.values} a numeric matrix in which each column contains the fitted values of the corresponding submodel along the sequence.
  \item \textbf{residuals} a numeric matrix in which each column contains the residuals of the corresponding submodel along the sequence.
  \item \textbf{df} an integer vector containing the degrees of freedom of the submodels along the sequence (i.e., the number of estimated coefficients).
  \item \textbf{robust} a logical indicating whether a robust fit was computed (TRUE for "rlars" models).
  \item \textbf{scale} a numeric vector giving the robust residual scale estimates for the submodels along the sequence.
  \item \textbf{crit} an object of class "bicSelect" containing the BIC values and indicating the final model (only returned if argument crit is "BIC" and argument s indicates more than one step along the sequence).
  \item \textbf{mux} a numeric vector containing the center estimates of the predictors.
  \item \textbf{sigmaX} a numeric vector containing the scale estimates of the predictors.
  \item \textbf{muY} numeric; the center estimate of the response.
  \item \textbf{sigmaY} numeric; the scale estimate of the response.
\end{itemize}
x  the matrix of candidate predictors (if model is TRUE).
y  the response (if model is TRUE).
w  a numeric vector giving the data cleaning weights (if winsorize is TRUE).
call  the matched function call.

Author(s)
Andreas Alfons, based on code by Jafar A. Khan, Stefan Van Aelst and Ruben H. Zamar

References

See Also
ccoef, fitted, plot, predict, residuals, lmrob

Examples
```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100  # number of observations
p <- 25   # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5  # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5*diag(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)  # error terms
i <- ceiling(epsilon*n)  # observations to be contaminated
e[i] <- e[i] + 5  # vertical outliers
y <- c(x, y, x[i] * e)  # response
x[i,] <- x[i,] + 5  # bad leverage points

## fit robust LARS model
rlars(x, y, sMax = 10)
```
Usage

sparseLTSGrid(x, ...)

## S3 method for class 'formula'
sparseLTSGrid(formula, data, ...)

## Default S3 method:
sparseLTSGrid(x, y, lambda,
   mode = c("lambda", "fraction"), ...)

Arguments

formula a formula describing the model.
data an optional data frame, list or environment (or object coercible to a data frame by \texttt{as.data.frame}) containing the variables in the model. If not found in data, the variables are taken from \texttt{environment(formula)}, typically the environment from which \texttt{sparseLTSGrid} is called.
x a numeric matrix containing the predictor variables.
y a numeric vector containing the response variable.
lambda a numeric vector of non-negative values to be used as penalty parameter.
mode a character string specifying the type of penalty parameter. If "lambda", lambda gives the grid of values for the penalty parameter directly. If "fraction", the smallest value of the penalty parameter that sets all coefficients to 0 is first estimated based on bivariate winsorization, then lambda gives the fractions of that estimate to be used (hence all values of lambda should be in the interval \([0,1]\) in that case).
... additional arguments to be passed down, eventually to \texttt{sparseLTS}.

Details

\texttt{sparseLTSGrid()} is a wrapper function for \texttt{sparseLTS} that only differs in the default values for the penalty parameter lambda.

Author(s)

Andreas Alfons

See Also

\texttt{Deprecated}
sparseLTS

Sparse least trimmed squares regression

Description

Compute least trimmed squares regression with an $L_1$ penalty on the regression coefficients, which allows for sparse model estimates.

Usage

sparseLTS(x, ...)

## S3 method for class 'formula'
 sparseLTS(formula, data, ...)

## Default S3 method:
 sparseLTS(x, y, lambda,
          mode = c("lambda", "fraction"), alpha = 0.75,
          normalize = TRUE, intercept = TRUE, nsamp = c(500, 10),
          initial = c("sparse", "hyperplane", "random"),
          nstep = 2, use.correction = TRUE,
          tol = .Machine$double.eps*0.5,
          eps = .Machine$double.eps, use.Gram,
          crit = c("BIC", "PE"), splits = foldControl(),
          cost = rtmspe, costArgs = list(),
          selectBest = c("hastie", "min"), seFactor = 1,
          ncores = 1L, cl = NULL, seed = NULL, model = TRUE, ...)

Arguments

formula a formula describing the model.
data an optional data frame, list or environment (or object coercible to a data frame by as.data.frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which sparseLTS is called.
x a numeric matrix containing the predictor variables.
y a numeric vector containing the response variable.
lambda a numeric vector of non-negative values to be used as penalty parameter.
mode a character string specifying the type of penalty parameter. If "lambda", lambda gives the grid of values for the penalty parameter directly. If "fraction", the smallest value of the penalty parameter that sets all coefficients to 0 is first estimated based on bivariate winsorization, then lambda gives the fractions of that estimate to be used (hence all values of lambda should be in the interval [0,1] in that case).
alpha a numeric value giving the percentage of the residuals for which the $L_1$ penalized sum of squares should be minimized (the default is 0.75).
normalize a logical indicating whether the predictor variables should be normalized to have unit $L_2$ norm (the default is TRUE). Note that normalization is performed on the subsamples rather than the full data set.

intercept a logical indicating whether a constant term should be included in the model (the default is TRUE).

nsamp a numeric vector giving the number of subsamples to be used in the two phases of the algorithm. The first element gives the number of initial subsamples to be used. The second element gives the number of subsamples to keep after the first phase of ncstep C-steps. For those remaining subsets, additional C-steps are performed until convergence. The default is to first perform ncstep C-steps on 500 initial subsamples, and then to keep the 10 subsamples with the lowest value of the objective function for additional C-steps until convergence.

initial a character string specifying the type of initial subsamples to be used. If "sparse", the lasso fit given by three randomly selected data points is first computed. The corresponding initial subsample is then formed by the fraction alpha of data points with the smallest squared residuals. Note that this is optimal from a robustness point of view, as the probability of including an outlier in the initial lasso fit is minimized. If "hyperplane", a hyperplane through $p$ randomly selected data points is first computed, where $p$ denotes the number of variables. The corresponding initial subsample is then again formed by the fraction alpha of data points with the smallest squared residuals. Note that this cannot be applied if $p$ is larger than the number of observations. Nevertheless, the probability of including an outlier increases with increasing dimension $p$. If "random", the initial subsamples are given by a fraction alpha of randomly selected data points. Note that this leads to the largest probability of including an outlier.

ncstep a positive integer giving the number of C-steps to perform on all subsamples in the first phase of the algorithm (the default is to perform two C-steps).

use.correction currently ignored. Small sample correction factors may be added in the future.

tol a small positive numeric value giving the tolerance for convergence.

eps a small positive numeric value used to determine whether the variability within a variable is too small (an effective zero).

use.Gram a logical indicating whether the Gram matrix of the explanatory variables should be precomputed in the lasso fits on the subsamples. If the number of variables is large, computation may be faster when this is set to FALSE. The default is to use TRUE if the number of variables is smaller than the number of observations in the subsamples and smaller than 100, and FALSE otherwise.

crit a character string specifying the optimality criterion to be used for selecting the final model. Possible values are "BIC" for the Bayes information criterion and "PE" for resampling-based prediction error estimation.

splits an object giving data splits to be used for prediction error estimation (see perryTuning).

cost a cost function measuring prediction loss (see perryTuning for some requirements). The default is to use the root trimmed mean squared prediction error (see cost).

costArgs a list of additional arguments to be passed to the prediction loss function cost.
selectBest, seFactor
arguments specifying a criterion for selecting the best model (see perryTuning). The default is to use a one-standard-error rule.

cores a positive integer giving the number of processor cores to be used for parallel computing (the default is 1 for no parallelization). If this is set to NA, all available processor cores are used. For prediction error estimation, parallel computing is implemented on the R level using package parallel. Otherwise parallel computing is implemented on the C++ level via OpenMP (http://openmp.org/).

cl a parallel cluster for parallel computing as generated by makeCluster. This is preferred over cores for prediction error estimation, in which case cores is only used on the C++ level for computing the final model.

seed optional initial seed for the random number generator (see .Random.seed). On parallel R worker processes for prediction error estimation, random number streams are used and the seed is set via clusterSetRNGStream.

model a logical indicating whether the data x and y should be added to the return object. If intercept is TRUE, a column of ones is added to x to account for the intercept.

... additional arguments to be passed down.

Value

If crit is "PE", an object of class "perrySparseLTS" (inheriting from class "perryTuning", see perryTuning). It contains information on the prediction error criterion, and includes the final model with the optimal tuning parameter as component finalModel.

Otherwise an object of class "sparseLTS" with the following components:

lambda a numeric vector giving the values of the penalty parameter.

best an integer vector or matrix containing the respective best subsets of h observations found and used for computing the raw estimates.

objective a numeric vector giving the respective values of the sparse LTS objective function, i.e., the $L_1$ penalized sums of the h smallest squared residuals from the raw fits.

coefficients a numeric vector or matrix containing the respective coefficient estimates from the reweighted fits.

fitted.values a numeric vector or matrix containing the respective fitted values of the response from the reweighted fits.

residuals a numeric vector or matrix containing the respective residuals from the reweighted fits.

center a numeric vector giving the robust center estimates of the corresponding reweighted residuals.

scale a numeric vector giving the robust scale estimates of the corresponding reweighted residuals.

cnp2 a numeric vector giving the respective consistency factors applied to the scale estimates of the reweighted residuals.
sparseLTS

an integer vector or matrix containing binary weights that indicate outliers from the respective reweighted fits, i.e., the weights are 1 for observations with reasonably small reweighted residuals and 0 for observations with large reweighted residuals.

df

an integer vector giving the respective degrees of freedom of the obtained reweighted model fits, i.e., the number of nonzero coefficient estimates.

intercept

a logical indicating whether the model includes a constant term.

alpha

a numeric value giving the percentage of the residuals for which the $L_1$ penalized sum of squares was minimized.

quan

the number $h$ of observations used to compute the raw estimates.

raw.coefficients

a numeric vector or matrix containing the respective coefficient estimates from the raw fits.

raw.fitted.values

a numeric vector or matrix containing the respective fitted values of the response from the raw fits.

raw.residuals

a numeric vector or matrix containing the respective residuals from the raw fits.

raw.center

a numeric vector giving the robust center estimates of the corresponding raw residuals.

raw.scale

a numeric vector giving the robust scale estimates of the corresponding raw residuals.

raw.cnp2

a numeric value giving the consistency factor applied to the scale estimate of the raw residuals.

raw.wt

an integer vector or matrix containing binary weights that indicate outliers from the respective raw fits, i.e., the weights used for the reweighted fits.

crit

an object of class "bicSelect" containing the BIC values and indicating the final model (only returned if argument crit is "BIC" and argument lambda contains more than one value for the penalty parameter).

x

the predictor matrix (if model is TRUE).

y

the response variable (if model is TRUE).

call

the matched function call.

Note

Package robustHD has a built-in back end for sparse least trimmed squares using the C++ library Armadillo. Another back end is available through package sparseLTSEigen, which uses the C++ library Eigen. The latter is faster, currently does not work on 32-bit R for Windows.

For both C++ back ends, parallel computing is implemented via OpenMP (http://openmp.org/).

Author(s)

Andreas Alfons
References


See Also

`coef`, `fitted`, `plot`, `predict`, `residuals`, `wt.ltsReg`

Examples

```r
## generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234)  # for reproducibility
n <- 100        # number of observations
p <- 25         # number of variables
beta <- rep.int(c(1, 0), c(5, p-5))  # coefficients
sigma <- 0.5    # controls signal-to-noise ratio
epsilon <- 0.1  # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma)  # predictor matrix
e <- rnorm(n)                  # error terms
i <- 1:ceiling(epsilon*n)      # observations to be contaminated
e[i] <- e[i] + 5               # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5             # bad leverage points

## fit sparse LTS model for one value of lambda
sparseLTS(x, y, lambda = 0.05, mode = "fraction")

## fit sparse LTS models over a grid of values for lambda
frac <- seq(0.2, 0.05, by = -0.05)
sparseLTS(x, y, lambda = frac, mode = "fraction")
```

---

**standardize**  
**Data standardization**

**Description**

Standardize data with given functions for computing center and scale.

**Usage**

```r
standardize(x, centerFun = mean, scaleFun = sd)

robStandardize(x, centerFun = median, scaleFun = mad,
               fallback = FALSE, eps = .Machine$double.eps, ...)
```
Arguments

- **x**: a numeric vector, matrix or data frame to be standardized.
- **centerFun**: a function to compute an estimate of the center of a variable (defaults to `mean`).
- **scaleFun**: a function to compute an estimate of the scale of a variable (defaults to `sd`).
- **fallback**: a logical indicating whether standardization with `mean` and `sd` should be performed as a fallback mode for variables whose robust scale estimate is too small. This is useful, e.g., for data containing dummy variables.
- **eps**: a small positive numeric value used to determine whether the robust scale estimate of a variable is too small (an effective zero).
- **...**: currently ignored.

Details

`robStandardize` is a wrapper function for robust standardization, hence the default is to use `median` and `mad`.

Value

An object of the same type as the original data `x` containing the centered and scaled data. The center and scale estimates of the original data are returned as attributes "center" and "scale", respectively.

Note

The implementation contains special cases for the typically used combinations `mean/sd` and `median/mad` in order to reduce computation time.

Author(s)

Andreas Alfons

See Also

`scale`, `sweep`

Examples

```r
## generate data
set.seed(1234)  # for reproducibility
x <- rnorm(10)  # standard normal
x[1] <- x[1] * 10  # introduce outlier

## standardize data
x
standardize(x)  # mean and sd
robStandardize(x)  # median and MAD
```
winsorize

Data cleaning by winsorization

Description

Clean data by means of winsorization, i.e., by shrinking outlying observations to the border of the main part of the data.

Usage

winsorize(x, ...)

## Default S3 method:

winsorize(x, standardized = FALSE,
          centerFun = median, scaleFun = mad, const = 2,
          return = c("data", "weights"), ...)

## S3 method for class 'matrix'

winsorize(x, standardized = FALSE,
          centerFun = median, scaleFun = mad, const = 2,
          prob = 0.95, tol = .Machine$double.eps^0.5,
          return = c("data", "weights"), ...)

## S3 method for class 'data.frame'

winsorize(x, ...)

Arguments

x a numeric vector, matrix or data frame to be cleaned.
standardized a logical indicating whether the data are already robustly standardized.
centerFun a function to compute a robust estimate for the center to be used for robust standardization (defaults to median). Ignored if standardized is TRUE.
scaleFun a function to compute a robust estimate for the scale to be used for robust standardization (defaults to mad). Ignored if standardized is TRUE.
const numeric; tuning constant to be used in univariate winsorization (defaults to 2).
prob numeric; probability for the quantile of the \( \chi^2 \) distribution to be used in multivariate winsorization (defaults to 0.95).
tol a small positive numeric value used to determine singularity issues in the computation of correlation estimates based on bivariate winsorization (see corHuber).
return character string; if standardized is TRUE, this specifies the type of return value. Possible values are "data" for returning the cleaned data, or "weights" for returning data cleaning weights.
... for the generic function, additional arguments to be passed down to methods. For the "data.frame" method, additional arguments to be passed down to the "matrix" method. For the other methods, additional arguments to be passed down to robStandardize.
Details

The borders of the main part of the data are defined on the scale of the robustly standardized data. In the univariate case, the borders are given by $\pm \text{const}$, thus a symmetric distribution is assumed. In the multivariate case, a normal distribution is assumed and the data are shrunken towards the boundary of a tolerance ellipse with coverage probability $\text{prob}$. The boundary of this ellipse is thereby given by all points that have a squared Mahalanobis distance equal to the quantile of the $\chi^2$ distribution given by $\text{prob}$.

Value

If `standardize` is `TRUE` and `return` is "weights", a set of data cleaning weights. Multiplying each observation of the standardized data by the corresponding weight yields the cleaned standardized data.

Otherwise an object of the same type as the original data $x$ containing the cleaned data is returned.

Note

Data cleaning weights are only meaningful for standardized data. In the general case, the data need to be standardized first, then the data cleaning weights can be computed and applied to the standardized data, after which the cleaned standardized data need to be backtransformed to the original scale.

Author(s)

Andreas Alfons, based on code by Jafar A. Khan, Stefan Van Aelst and Ruben H. Zamar

References


See Also

corHuber

Examples

```r
## generate data
set.seed(1234)  # for reproducibility
x <- rnorm(10)  # standard normal
x[1] <- x[1] * 10  # introduce outlier

## winsorize data
x
winsorize(x)
```
Extract outlier weights from sparse LTS regression models

Description
Extract binary weights that indicate outliers from sparse least trimmed squares regression models.

Usage
wt(object, ...)  

## S3 method for class 'sparseLTS'
wt(object, s = NA,  
    fit = c("reweighted", "raw", "both"),  
    drop = !is.null(s), ...)

Arguments

- **object**: the model fit from which to extract outlier weights.
- **s**: an integer vector giving the indices of the models for which to extract outlier weights. If `fit` is "both", this can be a list with two components, with the first component giving the indices of the reweighted fits and the second the indices of the raw fits. The default is to use the optimal model for each of the requested estimators. Note that the optimal models may not correspond to the same value of the penalty parameter for the reweighted and the raw estimator.
- **fit**: a character string specifying for which estimator to extract outlier weights. Possible values are "reweighted" (the default) for weights indicating outliers from the reweighted fit, "raw" for weights indicating outliers from the raw fit, or "both" for the outlier weights from both estimators.
- **drop**: a logical indicating whether to reduce the dimension to a vector in case of only one model.
- ... currently ignored.

Value

A numeric vector or matrix containing the requested outlier weights.

Note

The weights are 1 for observations with reasonably small residuals and 0 for observations with large residuals.

Author(s)
Andreas Alfons
See Also

sparseLTS

Examples

```r
# generate data
# example is not high-dimensional to keep computation time low
library("mvtnorm")
set.seed(1234) # for reproducibility
n <- 100    # number of observations
p <- 25     # number of variables
beta <- rep.int(c(1, 0), c(5, p-5)) # coefficients
sigma <- 0.5 # controls signal-to-noise ratio
epsilon <- 0.1 # contamination level
Sigma <- 0.5^t(sapply(1:p, function(i, j) abs(i-j), 1:p))
x <- rmvnorm(n, sigma=Sigma) # predictor matrix
e <- rnorm(n) # error terms
i <- 1:ceiling(epsilon*n) # observations to be contaminated
e[i] <- e[i] + 5 # vertical outliers
y <- c(x %*% beta + sigma * e) # response
x[i,] <- x[i,] + 5 # bad leverage points

# sparse LTS over a grid of values for lambda
# fit model
frac <- seq(0.2, 0.05, by = -0.05)
fitGrid <- sparseLTS(x, y, lambda = frac, mode = "fraction") # extract outlier weights
wt(fitGrid)
head(wt(fitGrid, fit = "both"))
head(wt(fitGrid, s = NULL))
head(wt(fitGrid, fit = "both", s = NULL))
```
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