Package 'enetLTS'

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Type Package

Title Robust and Sparse Methods for High Dimensional Linear and
Logistic Regression

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Description Fully robust versions of the elastic net estimator are introduced for linear and logistic regression, in particular high dimensional data by Kurnaz, Hoffmann and Filzmoser (2017) <DOI:10.1016/j.chemolab.2017.11.017>. The algorithm searches for outlier free subsets on which the classical elastic net estimators can be applied.

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Imports ggplot2, glmnet, robustHD, grid, reshape, parallel, cvTools,
stats

NeedsCompilation no

Repository CRAN

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R topics documented:

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coef.enetLTS   *coefficients from the* enetLTS *object*

Description

A numeric vector which extracts model coefficients from object returned by regression model.

Usage

```
   ## S3 method for class 'enetLTS'
coef(object,vers,zeros,...)
```

Arguments

object	fitted enetLTS model object.
vers	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.
zeros	a logical indicating whether to keep zero coefficients (TRUE, the default) or to omit them (FALSE).
...	additional arguments from the enetLTS object if needed.

Value

a numeric vector containing the requested coefficients.

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See Also

[enetLTS](), [predict.enetLTS](), [nonzeroCoef.enetLTS]()

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                          # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1           # 10% nonzero coefficients
sigma <- 0.5                               # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
```

```
e <- rnorm(n,0,1)                          # error terms
eps <- 0.1                                 # contamination level
m <- ceiling(eps*n)                        # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10     # vertical outliers
yout <- c(x %*% beta + sigma * eout)       # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10   # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
coef(fit1)
coef(fit1,vers="raw")
coef(fit1,vers="reweighted",zeros=FALSE)



## for binomial

eps <-0.05                                 # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;      # class 0
yout <- y                                  # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
coef(fit2)
coef(fit2,vers="reweighted")
coef(fit2,vers="raw",zeros=FALSE)
```

---

cv.enetLTS   *Cross-validation for the* enetLTS *object*

Description

Does k-fold cross-validation for enetLTS, produces a plot, and returns optimal values for alpha and lambda.

Usage

```
cv.enetLTS(index=NULL,xx,yy,family,h,alphas,lambdas,nfold,repl,ncores,plot=TRUE)
```

Arguments

index	A user supplied index. The default is NULL.
xx	matrix xx as in enetLTS.
yy	response yy as in enetLTS.
family	a description of the error distribution and link function to be used in the model. "gaussian" and "binomial" options are available.

h	a user supplied numeric value giving how many observations will be used.
alphas	a user supplied alpha sequence for the elastic net penalty, which is the mixing proportion of the ridge and lasso penalties and takes value in [0,1]. Here $\alpha = 1$ is the lasso penalty, and $\alpha = 0$ the ridge penalty.
lambdas	a user supplied lambda sequence for the strength of the elastic net penalty.
nfold	a user supplied numeric value for fold number of k-fold cross-validation which used in varied functions of the algorithm. The default is 5-fold cross-validation.
repl	a user supplied posiitive number for more stable results, repeat the k-fold CV repl times and take the average of the corresponding evaluation measure. The default is 5.
ncores	a positive integer giving the number of processor cores to be used for parallel computing. The default is 4.
plot	a logical indicating if produces a plot for k-fold cross-validation based on alpha and lambda combinations. The default is TRUE.

Value

produces a plot, and returns optimal values for `alpha` and `lambda`

Note

This is an internal function. But, it is also available for direct usage to obtain optimal values of alpha and lambda for user supplied index set.

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---

enetLTS   *Robust and sparse estimation for linear and logistic regression*

Description

Compute fully robust versions of the elastic net estimator, which allows for sparse model estimates, for linear and logistic regression.

Usage

```
enetLTS(xx, yy, family=c("gaussian","binomial"),
alphas, lambdas, lambdaw, hsize=0.75,
intercept=TRUE, nsamp=500, s1=10, nCsteps=20, nfold=5,
seed=NULL, plot=TRUE, repl=5, para=TRUE, ncores=1,
del=0.0125, tol=-1e6, scal=TRUE, type=c("response","class"))
```

Arguments

xx	a numeric matrix containing the predictor variables.
yy	response variable. Quantitative for `family="gaussian"`. For `family="binomial"` should be a factor with two levels which is coded as `0` and `1`.
family	a description of the error distribution and link function to be used in the model. `"gaussian"` and `"binomial"` options are available.
alphas	a user supplied alpha sequence for the elastic net penalty, which is the mixing proportion of the ridge and lasso penalties and takes value in [0,1]. $\alpha = 1$ is the lasso penalty, and $\alpha = 0$ the ridge penalty. If not provided a sequence, default is 41 equally spaced values.
lambdas	a user supplied lambda sequence for the strength of the elastic net penalty. If not provided a sequence, default is chosen with steps of size -0.025 lambda0 with $0 \leq \lambda \leq lambda0$ for linear regression and -0.025 lambda00 with $0 \leq \lambda \leq lambda00$ for logistic regression. lambda0 is determined based on the Pearson correlation between y and the jth predictor variable x_j on winsorized data for linear regression. In lambda00 for logistic regression, the Pearson correlation is replaced by a robustified point-biserial correlation.
lambdaw	a user supplied lambda sequence for reweighting step. If not provided, default is computed by using k-fold cross-validation via `cv.glmnet` function.
hsize	a user supplied numeric value giving the percentage of the residuals for which the elastic net penalized sum of squares for linear regression or for which the elastic net penalized sum of deviances for logistic regression should be minimized. The default is 0.75.
intercept	a logical indicating whether a constant term should be included in the model (the default is `TRUE`).
scal	a logical indicating whether scale the predictors by their arithmetic means and standard deviations. For `family="gaussian"`, it also indicates if mean-center the response variable or not. The default is `TRUE`. Note that scaling is performed on the subsamples rather than the full data set.
nsamp	a numeric vector giving the number of subsamples to be used in the beginning of the algorithm, which gives the number of initial subsamples to be used. The default is to first perform C-steps on 500 initial subsamples, and then to keep the s1 subsamples with the lowest value (or highest value based on which model is used - `"gaussian"` or `"binomial"`) of the objective function for additional C-steps until convergence.
s1	a number of subsamples to keep after perform C-steps on `nsamp` initial subsets. For those remaining subsets, additional C-steps are performed until convergence. The default is 10.
nCsteps	a positive integer giving the number of C-steps to perform on determined s1 subsamples. The default is 20.
nfold	a user supplied numeric value for fold number of k-fold cross-validation which used in varied functions of the algorithm. The default is 5-fold cross-validation.
seed	optional initial seed for the random number generator (see `.Random.seed`) when determine initial subsets at the beginning of the algorithm. The default is NULL.

plot	a logical indicating if produces a plot for k-fold cross-validation based on alpha and lambda combinations. The default is TRUE.
repl	a user supplied positive number for more stable results, repeat the k-fold CV `repl` times and take the average of the corresponding evaluation measure. The default is 5.
para	if TRUE, use parallel to fit each fold. Must register parallel before hand, such as doMC or others.
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 prediction error estimation, parallel computing is implemented on the R level using package **parallel**.
del	The default is 0.0125.
tol	a small numeric value for convergence. The default is -1e6.
type	type of prediction required. `type="response"` gives the fitted probabilities for `"binomial"` and gives the fitted values for `"gaussian"`. `type="class"` is available only for `"binomial"` model, and produces the class label corresponding to the maximum probability.

Details

The idea of repeatedly applying the non-robust classical elastic net estimators to data subsets only is used for linear and logistic regression. The algorithm starts with 500 elemental subsets only for one combination of α and λ, and takes the warm start strategy for subsequent combinations. This idea saves the computation time. To choose the elastic net penalties, k-fold cross-validation is used and the replication option is provided for more stable results. Robustness has been achieved by using trimming idea, therefore a reweighting step is introduced in order to improve the efficiency. The outliers are identified according to current model. For `family="gaussian"`, standardized residuals are used. For `family="binomial"`, the Pearson residuals which are approximately standard normally distributed is used. Then the weights are defined by the binary weight function using `del=0.0125`, which allows to be flagged as outliers of the 2.5% of the observations in the normal model. Therefore, binary weight function produces a clear distinction between the "good observations" and "outliers".

Value

objective	a numeric vector giving the respective values of the enetLTS objective function, i.e., the elastic net penalized sums of the h smallest squared residuals from the raw fits for `family="gaussian"` and the elastic net penalized sums of the h deviances from the raw fits for `family="binomial"`.
best	an integer vector containing the respective best subsets of h observations found and used for computing the raw estimates.
raw.wt	an integer vector containing binary weights that indicate outliers from the respective raw fits, i.e., the weights used for the reweighted fits.
wt	an integer vector 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.

a00	intercept term obtained from the raw fit.
raw.coefficients	
	a numeric vector containing the respective coefficient estimates from the raw fit.
a0	intercept term obtained from the reweighted fit.
coefficients	a numeric vector containing the respective coefficient estimates from the reweighted fit.
alpha	an optimal elastic net mixing parameter value obtained with k-fold cross-validation.
lambda	an optimal value for the strength of the elastic net penalty obtained with k-fold cross-validation.
lambdaw	an optimal value for the strength of the elastic net penalty re-obtained with k-fold cross-validation for reweighted fit.
num.nonzerocoef	
	the number of the nonzero coefficients in the model.
h	the number of observations used to compute the raw estimates.
raw.residuals	a numeric vector containing the respective residuals from the raw fits.
residuals	a numeric vector containing the respective residuals from the reweighted fits.
raw.fitted.values	
	a numeric vector containing the respective fitted values of the response from the raw fits.
fitted.values	a numeric vector containing the respective fitted values of the response from the reweighted fits.
raw.rmse	root mean squared error for raw fit, which is available for only family="gaussian".
rmse	root mean squared error for reweighted fit, which is available for only family ="gaussian".
classnames	class names for logistic model, which is available for only family="binomial".
classize	class sizes for logisitic model, which is available for only family="binomial".
inputs	all inputs used in the function enetLTS.R.
call	the matched function call.

Author(s)

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References

Kurnaz, F.S., Hoffmann, I. and Filzmoser, P. (2017) Robust and sparse estimation methods for high dimensional linear and logistic regression. *Chemometrics and Intelligent Laboratory Systems.*

See Also

[print](), [predict](), [coef](), [nonzeroCoef.enetLTS](), [plot](), [plotCoef.enetLTS](), [plotResid.enetLTS](), [plotDiagnostic.enetLTS](), [residuals](), [fitted](), [weights]()

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                              # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1               # 10% nonzero coefficients
sigma <- 0.5                                   # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                              # error terms
eps <- 0.1                                     # contamination level
m <- ceiling(eps*n)                            # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10         # vertical outliers
yout <- c(x %*% beta + sigma * eout)           # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10       # bad leverage points


fit <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
# determine user supplied alpha and lambda sequences
# alphas=seq(0,1,length=11)
# l0 <- robustHD::lambda0(xout,yout)         # use # lambda0 function from robustHD package
# lambdas <- seq(l0,0,by=-0.1*l0)
# fit <- enetLTS(xout,yout,alphas=alphas,lambdas=lambdas)


## for binomial

eps <-0.05                                     # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;          # class 0
yout <- y                                      # wrong classification for vertical outliers


fit <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
# determine user supplied alpha and lambda sequences
# l00 <- lambda00(xout,yout,normalize=TRUE,intercept=TRUE)
# lambdas <-  seq(l00,0,by=-0.01*l00)
# fit <- enetLTS(xout,yout,family="binomial",alphas=alphas,lambdas=lambdas)
```

---

fitted.enetLTS   *the fitted values from the* "enetLTS" *object.*

Description

A numeric vector which extract fitted values from the current model.

Usage

```
   ## S3 method for class 'enetLTS'
fitted(object,vers=c("reweighted","raw","both"),type=c("response","class"),...)
```

Arguments

`object`	the model fit from which to extract fitted values.
`vers`	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.
`type`	type of prediction required. `type="response"` gives the fitted probabilities for `"binomial"` and gives the fitted values for `"gaussian"`. `type="class"` is available only for `"binomial"` model, and produces the class label corresponding to the maximum probability.
`...`	additional arguments from the `enetLTS` object if needed.

Value

A numeric vector containing the requested fitted values.

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See Also

[enetLTS](), [predict.enetLTS](), [residuals.enetLTS]()

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                        # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1         # 10% nonzero coefficients
sigma <- 0.5                             # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                        # error terms
eps <- 0.1                               # contamination level
m <- ceiling(eps*n)                      # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10   # vertical outliers
yout <- c(x %*% beta + sigma * eout)     # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10 # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
fitted(fit1)
fitted(fit1,vers="raw")
fitted(fit1,vers="both")
fitted(fit1,vers="reweighted",type="response")

## for binomial
eps <-0.05                                   # %10 contamination to only class 0
```

```
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;          # class 0
yout <- y                                      # wrong classification for vertical outliers



fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
fitted(fit2)
fitted(fit2,vers="raw")
fitted(fit2,vers="both",type="class")
fitted(fit2,vers="both")
fitted(fit2,vers="reweighted",type="class")
```

---

lambda00   *Upper limit of the penalty parameter for* family="binomial"

Description

Use bivariate winsorization to estimate the smallest value of the upper limit for the penalty parameter.

Usage

```
lambda00(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 or not (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 (the default is 2).
prob	numeric; probability for the quantile of the χ^2 distribution to be used in bivariate winsorization (the default is 0.95).
tol	a small positive numeric value used to determine singularity issues in the computation of correlation estimates for bivariate winsorization.
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 if needed.

Details

The estimation procedure is done with similar approach as in Alfons et al. (2013). But the Pearson correlation between y and the jth predictor variable xj on winsorized data is replaced to a robustified point-biserial correlation for logistic regression.

Value

A robust estimate of the smallest value of the penalty parameter for enetLTS regression (for family="binomial").

Note

For linear regression, we take exactly same procedure as in Alfons et al., which is based on the Pearson correlation between y and the jth predictor variable xj on winsorized data. See Alfons et al. (2013).

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References

Kurnaz, F.S., Hoffmann, I. and Filzmoser, P. (2017) Robust and sparse estimation methods for high dimensional linear and logistic regression. *Chemometrics and Intelligent Laboratory Systems.*

Alfons, A., Croux, C. and Gelper, S. (2013) Sparse least trimmed squares regression for analyzing high-dimensional large data sets. *The Annals of Applied Statistics*, 7(1), 226–248.

See Also

enetLTS, sparseLTS, lambda0

Examples

```
set.seed(86)
n <- 100; p <- 25                       # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1        # 10% nonzero coefficients
sigma <- 0.5                            # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                       # error terms
eps <-0.05                              # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;   # class 0
yout <- y                               # wrong classification for vertical outliers

# compute smallest value of the upper limit for the penalty parameter
l00 <- lambda00(xout,yout)
```

---

nonzeroCoef.enetLTS | *nonzero coefficients indices from the* "enetLTS" *object*

Description

A numeric vector which gives the indices of nonzero coefficients from the current model.

Usage

```
nonzeroCoef.enetLTS(beta)
```

Arguments

beta   Coefficient vector

Value

A numeric vector containing the requeste.

Author(s)

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See Also

enetLTS, predict.enetLTS, coef.enetLTS

Examples

```
## for gaussian
set.seed(86)
n <- 100; p <- 25                        # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1         # 10% nonzero coefficients
sigma <- 0.5                             # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                        # error terms
eps <- 0.1                               # contamination level
m <- ceiling(eps*n)                      # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10   # vertical outliers
yout <- c(x %*% beta + sigma * eout)     # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10 # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
beta1 <- coef(fit1)
nonzeroCoef.enetLTS(beta1)

## for binomial
```

```
eps <-0.05                                  # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;       # class 0
yout <- y                                   # wrong classification for vertical outliers



fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
beta1 <- coef(fit2,vers="raw")
nonzeroCoef.enetLTS(beta1)
```

---

plot.enetLTS   *plots from the* "enetLTS" *object*

Description

Produce plots for the coefficients, residuals, and diagnostics of the current model.

Usage

```
## S3 method for class 'enetLTS'
plot(x,method=c("coefficients","resid","diagnostic"),
        vers=c("reweighted","raw"),...)
```

Arguments

x	object of class enetLTS, the model fit to be plotted.
method	a character string specifying the type of plot. Possible values are "coefficients" to plot the coefficients via plotCoef.enetLTS, "resid" to plot the residuals via plotResid.enetLTS, or "diagnostic" for diagnostic plot via plotDiagnostic.enetLTS.
vers	a character string denoting which model to use for the plots. Possible values are "reweighted" (the default) for plots from the reweighted fit, and "raw" for plots from the raw fit.
...	additional arguments from the enetLTS object if needed.

Value

An object of class "ggplot" (see [ggplot](#)).

Note

For method, the choices are:

method="coefficients" - coefficients vs indices.

method="resid" - residuals vs indices. (for both family="binomial" and family="gaussian").

- additionally, residuals vs fitted values (for only family="gaussian").

method="diagnostics" - fitted values vs indices.

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References

Kurnaz, F.S., Hoffmann, I. and Filzmoser, P. (2017) Robust and sparse estimation methods for high dimensional linear and logistic regression. *Chemometrics and Intelligent Laboratory Systems*.

See Also

ggplot, enetLTS, coef.enetLTS, predict.enetLTS, residuals.enetLTS, fitted.enetLTS

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                        # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1         # 10% nonzero coefficients
sigma <- 0.5                             # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                        # error terms
eps <- 0.1                               # contamination level
m <- ceiling(eps*n)                      # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10   # vertical outliers
yout <- c(x %*% beta + sigma * eout)     # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10 # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
plot(fit1)
plot(fit1,method="resid",vers="raw")
plot(fit1,method="coefficients",vers="reweighted")
plot(fit1,method="diagnostic")

## for binomial
eps <-0.05                                # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;     # class 0
yout <- y                                 # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
plot(fit2)
plot(fit2,method="resid",vers="raw")
plot(fit2,method="coefficients",vers="reweighted")
plot(fit2,method="diagnostic")
```

---

plotCoef.enetLTS	*coefficients plots from the* "enetLTS" *object*

Description

Produce plots for the coefficients of the current model.

Usage

```
plotCoef.enetLTS(object,vers=c("reweighted","raw"),colors=NULL,...)
```

Arguments

object	the model fit to be plotted.
vers	a character string denoting which model to use for the plots. Possible values are "reweighted" (the default) for plots from the reweighted fit, and "raw" for plots from the raw fit.
colors	optional parameter, list object with list names bars, errorbars, background, abline, scores, cutc each containing a string referring to a color.
...	additional arguments from the enetLTS object if needed.

Value

An object of class "ggplot" (see [ggplot](#)).

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References

Kurnaz, F.S., Hoffmann, I. and Filzmoser, P. (2017) Robust and sparse estimation methods for high dimensional linear and logistic regression. *Chemometrics and Intelligent Laboratory Systems*.

See Also

[ggplot](#), [enetLTS](#), [coef.enetLTS](#), [predict.enetLTS](#)

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                        # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1         # 10% nonzero coefficients
sigma <- 0.5                             # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
```

```
e <- rnorm(n,0,1)                           # error terms
eps <- 0.1                                  # contamination level
m <- ceiling(eps*n)                         # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10      # vertical outliers
yout <- c(x %*% beta + sigma * eout)        # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10    # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
plotCoef.enetLTS(fit1)
plotCoef.enetLTS(fit1,vers="raw")

## for binomial
eps <-0.05                                  # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;       # class 0
yout <- y                                   # wrong classification for vertical outliers



fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
plotCoef.enetLTS(fit2)
plotCoef.enetLTS(fit2,vers="raw")
```

---

plotDiagnostic.enetLTS

diagnostics plots from the "enetLTS" *object*

Description

Produce plots for the diagnostics of the current model.

Usage

```
plotDiagnostic.enetLTS(object,vers=c("reweighted","raw"),...)
```

Arguments

object	the model fit to be plotted.
vers	a character string denoting which model to use for the plots. Possible values are "reweighted" (the default) for plots from the reweighted fit, and "raw" for plots from the raw fit.
...	additional arguments from the enetLTS object if needed.

Value

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

Note

gives the plot of fitted values vs indices.

Author(s)

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References

Kurnaz, F.S., Hoffmann, I. and Filzmoser, P. (2017) Robust and sparse estimation methods for high dimensional linear and logistic regression. *Chemometrics and Intelligent Laboratory Systems*.

See Also

ggplot, enetLTS, coef.enetLTS, predict.enetLTS, residuals.enetLTS, fitted.enetLTS

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                       # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1        # 10% nonzero coefficients
sigma <- 0.5                            # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                       # error terms
eps <- 0.1                              # contamination level
m <- ceiling(eps*n)                     # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10  # vertical outliers
yout <- c(x %*% beta + sigma * eout)    # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10    # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
plotDiagnostic.enetLTS(fit1)
plotDiagnostic.enetLTS(fit1,vers="raw")

## for binomial

eps <-0.05                              # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;       # class 0
yout <- y                               # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
plotDiagnostic.enetLTS(fit2)
plotDiagnostic.enetLTS(fit2,vers="raw")
```

plotResid.enetLTS   *residuals plots from the* "enetLTS" *object*

Description

Produce plots for the residuals of the current model.

Usage

```
plotResid.enetLTS(object,vers=c("reweighted","raw"), ...)
```

Arguments

object	the model fit to be plotted.
vers	a character string denoting which model to use for the plots. Possible values are "reweighted" (the default) for plots from the reweighted fit, and "raw" for plots from the raw fit.
...	additional arguments from the enetLTS object if needed.

Value

An object of class "ggplot" (see [ggplot](#)).

Note

gives the plot of - residuals vs indices. (for both family="binomial" and family="gaussian").

- additionally, residuals vs fitted values (for only family="gaussian").

Author(s)

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References

Kurnaz, F.S., Hoffmann, I. and Filzmoser, P. (2017) Robust and sparse estimation methods for high dimensional linear and logistic regression. *Chemometrics and Intelligent Laboratory Systems*.

See Also

[ggplot](#), [enetLTS](#), [predict.enetLTS](#), [residuals.enetLTS](#), [fitted.enetLTS](#)

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                            # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1             # 10% nonzero coefficients
sigma <- 0.5                                 # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                            # error terms
eps <- 0.1                                   # contamination level
m <- ceiling(eps*n)                          # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10       # vertical outliers
yout <- c(x %*% beta + sigma * eout)         # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10     # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
plotResid.enetLTS(fit1)
plotResid.enetLTS(fit1,vers="raw")


## for binomial

eps <-0.05                                   # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;        # class 0
yout <- y                                    # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
plotResid.enetLTS(fit2)
plotResid.enetLTS(fit2,vers="raw")
```

---

predict.enetLTS   *make predictions from the "*enetLTS*" object.*

Description

Similar to other predict methods, this function predicts fitted values, logits, coefficients and nonzero coefficients from a fitted "enetLTS" object.

Usage

```
## S3 method for class 'enetLTS'
predict(object,newX,vers=c("reweighted","raw","both"),
    type=c("response","coefficients","nonzero","class"),...)
```

Arguments

`object`	the model fit from which to make predictions.
`newX`	new values for the predictor matrix X. Must be a matrix; can be sparse as in `Matrix` package. This argument is not used for type=c("coefficients","nonzero").
`vers`	a character string denoting which fit to use for the 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.
`type`	type of prediction required. type="response" gives the fitted probabilities for "binomial" and gives the fitted values for "gaussian". type="coefficients" computes the coefficients from the fitted model. type="nonzero" returns a list of the indices of the nonzero coefficients. type="class" is available only for "binomial" model, and produces the class label corresponding to the maximum probability.
`...`	additional arguments from the enetLTS object if needed.

Details

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

coef.enetLTS(...) is equivalent to predict.enetLTS(object,newX,type="coefficients",...), where newX argument is the matrix as in enetLTS.

Value

The requested predicted values are returned.

Author(s)

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See Also

enetLTS, coef.enetLTS, nonzeroCoef.enetLTS

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                          # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1           # 10% nonzero coefficients
sigma <- 0.5                               # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                          # error terms
eps <- 0.1                                 # contamination level
m <- ceiling(eps*n)                        # observations to be contaminated
```

```
eout <- e; eout[1:m] <- eout[1:m] + 10        # vertical outliers
yout <- c(x %*% beta + sigma * eout)          # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10      # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
predict(fit1,newX=xout)
predict(fit1,newX=xout,type="coefficients",vers="both")
predict(fit1,newX=xout,type="nonzero",vers="raw")
# provide new X matrix
newX <- matrix(rnorm(n*p, sigma),nrow=n)
predict(fit1,newX=newX,type="response",vers="both")
predict(fit1,newX=newX,type="coefficients")
predict(fit1,newX=newX,type="nonzero",vers="both")


## for binomial

eps <-0.05                                    # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;         # class 0
yout <- y                                     # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
predict(fit2,newX=xout)
predict(fit2,newX=xout,type="coefficients",vers="both")
predict(fit2,newX=xout,type="nonzero",vers="raw")
predict(fit2,newX=newX,type="class",vers="both")
predict(fit2,newX=newX,type="coefficients",vers="raw")
predict(fit2,newX=newX,type="nonzero",vers="both")
```

---

print.enetLTS	*print from the* "enetLTS" *object*

Description

Print a summary of the enetLTS object.

Usage

```
## S3 method for class 'enetLTS'
print(x,vers=c("reweighted","raw"),zeros=FALSE,...)
```

Arguments

x	fitted enetLTS object
vers	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.
zeros	a logical indicating whether to keep zero coefficients (FALSE, the default) or to keep them (TRUE).
...	additional arguments from the enetLTS object if needed.

Details

The call that produced the enetLTS object is printed, followed by the coefficients, the number of nonzero coefficients and penalty parameters.

Value

The produced object, the coefficients, the number of nonzero coefficients and penalty parameters are returned.

Author(s)

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See Also

enetLTS, predict.enetLTS, coef.enetLTS

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                        # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1         # 10% nonzero coefficients
sigma <- 0.5                             # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                        # error terms
eps <- 0.1                               # contamination level
m <- ceiling(eps*n)                      # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10   # vertical outliers
yout <- c(x %*% beta + sigma * eout)     # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10 # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
print(fit1)
print(fit1,vers="raw")
print(fit1,vers="raw",zeros=TRUE)
print(fit1,zeros=TRUE)
```

```
## for binomial

eps <-0.05                                # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;      # class 0
yout <- y                                  # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
print(fit2)
print(fit2,vers="raw")
print(fit2,vers="raw",zeros=TRUE)
print(fit2,zeros=TRUE)
```

---

residuals.enetLTS   *the residuals from the* "enetLTS" *object*

Description

A numeric vector which returns residuals from the enetLTS object.

Usage

```
## S3 method for class 'enetLTS'
residuals(object,vers=c("reweighted","raw","both"),...)
```

Arguments

object   the model fit from which to extract residuals.

vers   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.

...   additional arguments from the enetLTS object.

Value

A numeric vector containing the requested residuals.

Author(s)

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See Also

enetLTS, fitted.enetLTS, predict.enetLTS, coef.enetLTS

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                           # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1            # 10% nonzero coefficients
sigma <- 0.5                                # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                           # error terms
eps <- 0.1                                  # contamination level
m <- ceiling(eps*n)                         # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10      # vertical outliers
yout <- c(x %*% beta + sigma * eout)        # response
xout <- x; xout[1:m,] <- xout[1:m,] + 10    # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
residuals(fit1)
residuals(fit1,vers="raw")
residuals(fit1,vers="both")


## for binomial

eps <-0.05                                  # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;       # class 0
yout <- y                                   # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
residuals(fit2)
residuals(fit2,vers="raw")
residuals(fit2,vers="both")
```

---

weights.enetLTS   *binary weights from the* "enetLTS" *object*

Description

Extract binary weights that indicate outliers from the current model.

Usage

```
## S3 method for class 'enetLTS'
weights(object,vers=c("reweighted","raw","both"),index=FALSE,...)
```

Arguments

object   the model fit from which to extract outlier weights.

vers   a character string specifying for which estimator to extract outlier weights. Pos-
              sible 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.

index   a logical indicating whether the indices of the weight vector should be included
              or not (the default is FALSE).

...   additional arguments from the enetLTS object if needed.

Value

A numeric vector containing the requested outlier weights.

Note

The weights are 1 for observations with reasonably small residuals and 0 for observations with
large residuals. Here, residuals represent standardized residuals for linear regression and Pearson
residuals for logistic residuals.

Use weights with or without index is available.

Author(s)

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See Also

[enetLTS](#)

Examples

```
## for gaussian

set.seed(86)
n <- 100; p <- 25                        # number of observations and variables
beta <- rep(0,p); beta[1:6] <- 1         # 10% nonzero coefficients
sigma <- 0.5                             # controls signal-to-noise ratio
x <- matrix(rnorm(n*p, sigma),nrow=n)
e <- rnorm(n,0,1)                        # error terms
eps <- 0.1                               # contamination level
m <- ceiling(eps*n)                      # observations to be contaminated
eout <- e; eout[1:m] <- eout[1:m] + 10   # vertical outliers
yout <- c(x %*% beta + sigma * eout)     # response
```

```
xout <- x; xout[1:m,] <- xout[1:m,] + 10        # bad leverage points


fit1 <- enetLTS(xout,yout,alphas=0.5,lambdas=0.05,plot=FALSE)
weights(fit1)
weights(fit1,vers="raw",index=TRUE)
weights(fit1,vers="both",index=TRUE)


## for binomial

eps <-0.05                                 # %10 contamination to only class 0
m <- ceiling(eps*n)
y <- sample(0:1,n,replace=TRUE)
xout <- x
xout[y==0,][1:m,] <- xout[1:m,] + 10;      # class 0
yout <- y                                  # wrong classification for vertical outliers


fit2 <- enetLTS(xout,yout,family="binomial",alphas=0.5,lambdas=0.05,plot=FALSE)
weights(fit2)
weights(fit2,vers="raw",index=TRUE)
weights(fit2,vers="both",index=TRUE)
```

Index