

# Package ‘robStepSplitReg’

July 23, 2025

**Type** Package

**Title** Robust Stepwise Split Regularized Regression

**Version** 1.1.0

**Date** 2023-06-28

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**Description** Functions to perform robust stepwise split regularized regression. The approach first uses a robust stepwise algorithm to split the variables into the models of an ensemble. An adaptive robust regularized estimator is then applied to each subset of predictors in the models of an ensemble.

**License** GPL (>= 2)

**Encoding** UTF-8

**Biarch** true

**Imports** Rcpp (>= 1.0.9), cellWise, glmnet

**Suggests** testthat, mvnfast

**LinkingTo** Rcpp, RcppArmadillo

**RoxygenNote** 7.2.3

**NeedsCompilation** yes

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**Repository** CRAN

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coef.robStepSplitReg    *Coefficients for robStepSplitReg Object*

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**Description**

coef.robStepSplitReg returns the coefficients for a robStepSplitReg object.

**Usage**

```
## S3 method for class 'robStepSplitReg'  
coef(object, group_index = NULL, ...)
```

**Arguments**

|             |                                                                           |
|-------------|---------------------------------------------------------------------------|
| object      | An object of class robStepSplitReg                                        |
| group_index | Groups included in the ensemble. Default setting includes all the groups. |
| ...         | Additional arguments for compatibility.                                   |

**Value**

The coefficients for the robStepSplitReg object.

**Author(s)**

Anthony-Alexander Christidis, <anthony.christidis@stat.ubc.ca>

**See Also**

[robStepSplitReg](#)

**Examples**

```
# Required library  
library(mvnfast)  
  
# Simulation parameters  
n <- 50  
p <- 500  
rho <- 0.5  
p.active <- 100  
snr <- 1  
contamination.prop <- 0.2  
  
# Setting the seed  
set.seed(0)  
  
# Simulation of beta vector  
true.beta <- c(runif(p.active, 0, 5)*(-1)^rbinom(p.active, 1, 0.7), rep(0, p - p.active))
```

```

# Simulation of uncontaminated data
sigma.mat <- matrix(0, nrow = p, ncol = p)
sigma.mat[1:p.active, 1:p.active] <- rho
diag(sigma.mat) <- 1
x <- mvnfast::rmvn(n, mu = rep(0, p), sigma = sigma.mat)
sigma <- as.numeric(sqrt(t(true.beta) %*% sigma.mat %*% true.beta)/sqrt(snr))
y <- x %*% true.beta + rnorm(n, 0, sigma)

# Contamination of data
contamination_indices <- 1:floor(n*contamination.prop)
k_lev <- 2
k_slo <- 100
x_train <- x
y_train <- y
beta_cont <- true.beta
beta_cont[true.beta!=0] <- beta_cont[true.beta!=0]*(1 + k_slo)
beta_cont[true.beta==0] <- k_slo*max(abs(true.beta))
for(cont_id in contamination_indices){

  a <- runif(p, min = -1, max = 1)
  a <- a - as.numeric((1/p)*t(a) %*% rep(1, p))
  x_train[cont_id,] <- mvnfast::rmvn(1, rep(0, p), 0.1^2*diag(p)) +
    k_lev * a / as.numeric(sqrt(t(a) %*% solve(sigma.mat) %*% a))
  y_train[cont_id] <- t(x_train[cont_id,]) %*% beta_cont
}

# Ensemble models
ensemble_fit <- robStepSplitReg(x_train, y_train,
                               n_models = 5,
                               model_saturation = c("fixed", "p-value")[1],
                               alpha = 0.05, model_size = n - 1,
                               robust = TRUE,
                               compute_coef = TRUE,
                               en_alpha = 1/4)

# Ensemble coefficients
ensemble_coefs <- coef(ensemble_fit, group_index = 1:ensemble_fit$n_models)
sens_ensemble <- sum(which((ensemble_coefs[-1]!=0)) <= p.active)/p.active
spec_ensemble <- sum(which((ensemble_coefs[-1]!=0)) <= p.active)/sum(ensemble_coefs[-1]!=0)

# Simulation of test data
m <- 2e3
x_test <- mvnfast::rmvn(m, mu = rep(0, p), sigma = sigma.mat)
y_test <- x_test %*% true.beta + rnorm(m, 0, sigma)

# Prediction of test samples
ensemble_preds <- predict(ensemble_fit, newx = x_test,
                          group_index = 1:ensemble_fit$n_models,
                          dynamic = FALSE)
mspe_ensemble <- mean((y_test - ensemble_preds)^2)/sigma^2

```

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`predict.robStepSplitReg`*Predictions for robStepSplitReg Object*

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## Description

`predict.robStepSplitReg` returns the predictions for a `robStepSplitReg` object.

## Usage

```
## S3 method for class 'robStepSplitReg'  
predict(object, newx, group_index = NULL, dynamic = FALSE, ...)
```

## Arguments

|                          |                                                                                                                      |
|--------------------------|----------------------------------------------------------------------------------------------------------------------|
| <code>object</code>      | An object of class <code>robStepSplitReg</code>                                                                      |
| <code>newx</code>        | New data for predictions.                                                                                            |
| <code>group_index</code> | Groups included in the ensemble. Default setting includes all the groups.                                            |
| <code>dynamic</code>     | Argument to determine whether dynamic predictions are used based on deviating cells. Default is <code>FALSE</code> . |
| <code>...</code>         | Additional arguments for compatibility.                                                                              |

## Value

The predictions for the `robStepSplitReg` object.

## Author(s)

Anthony-Alexander Christidis, <anthony.christidis@stat.ubc.ca>

## See Also

[robStepSplitReg](#)

## Examples

```
# Required library  
library(mvnfast)  
  
# Simulation parameters  
n <- 50  
p <- 500  
rho <- 0.5  
p.active <- 100  
snr <- 1  
contamination.prop <- 0.2
```

```

# Setting the seed
set.seed(0)

# Simulation of beta vector
true.beta <- c(runif(p.active, 0, 5)*(-1)^rbinom(p.active, 1, 0.7), rep(0, p - p.active))

# Simulation of uncontaminated data
sigma.mat <- matrix(0, nrow = p, ncol = p)
sigma.mat[1:p.active, 1:p.active] <- rho
diag(sigma.mat) <- 1
x <- mvnfast::rmvn(n, mu = rep(0, p), sigma = sigma.mat)
sigma <- as.numeric(sqrt(t(true.beta) %*% sigma.mat %*% true.beta)/sqrt(snr))
y <- x %*% true.beta + rnorm(n, 0, sigma)

# Contamination of data
contamination_indices <- 1:floor(n*contamination.prop)
k_lev <- 2
k_slo <- 100
x_train <- x
y_train <- y
beta_cont <- true.beta
beta_cont[true.beta!=0] <- beta_cont[true.beta!=0]*(1 + k_slo)
beta_cont[true.beta==0] <- k_slo*max(abs(true.beta))
for(cont_id in contamination_indices){

  a <- runif(p, min = -1, max = 1)
  a <- a - as.numeric((1/p)*t(a) %*% rep(1, p))
  x_train[cont_id,] <- mvnfast::rmvn(1, rep(0, p), 0.1^2*diag(p)) +
    k_lev * a / as.numeric(sqrt(t(a) %*% solve(sigma.mat) %*% a))
  y_train[cont_id] <- t(x_train[cont_id,]) %*% beta_cont
}

# Ensemble models
ensemble_fit <- robStepSplitReg(x_train, y_train,
                               n_models = 5,
                               model_saturation = c("fixed", "p-value")[1],
                               alpha = 0.05, model_size = n - 1,
                               robust = TRUE,
                               compute_coef = TRUE,
                               en_alpha = 1/4)

# Ensemble coefficients
ensemble_coefs <- coef(ensemble_fit, group_index = 1:ensemble_fit$n_models)
sens_ensemble <- sum(which((ensemble_coefs[-1]!=0)) <= p.active)/p.active
spec_ensemble <- sum(which((ensemble_coefs[-1]!=0)) <= p.active)/sum(ensemble_coefs[-1]!=0)

# Simulation of test data
m <- 2e3
x_test <- mvnfast::rmvn(m, mu = rep(0, p), sigma = sigma.mat)
y_test <- x_test %*% true.beta + rnorm(m, 0, sigma)

# Prediction of test samples
ensemble_preds <- predict(ensemble_fit, newx = x_test,

```

```

      group_index = 1:ensemble_fit$n_models,
      dynamic = FALSE)
mspe_ensemble <- mean((y_test - ensemble_preds)^2)/sigma^2

```

---

|                 |                                                     |
|-----------------|-----------------------------------------------------|
| robStepSplitReg | <i>Robust Stepwise Split Regularized Regression</i> |
|-----------------|-----------------------------------------------------|

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## Description

robStepSplitReg performs robust stepwise split regularized regression.

## Usage

```

robStepSplitReg(
  x,
  y,
  n_models = 1,
  model_saturation = c("fixed", "p-value")[1],
  alpha = 0.05,
  model_size = NULL,
  robust = TRUE,
  compute_coef = FALSE,
  en_alpha = 1/4
)

```

## Arguments

|                  |                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------|
| x                | Design matrix.                                                                                            |
| y                | Response vector.                                                                                          |
| n_models         | Number of models into which the variables are split.                                                      |
| model_saturation | Criterion to determine if a model is saturated. Must be one of "fixed" (default) or "p-value".            |
| alpha            | P-value used to determine when the model is saturated                                                     |
| model_size       | Size of the models in the ensemble.                                                                       |
| robust           | Argument to determine if robust measures of location, scale and correlation are used. Default is TRUE.    |
| compute_coef     | Argument to determine if coefficients are computed (via adaptive PENSE) for each model. Default is FALSE. |
| en_alpha         | Elastic net mixing parameter for parameters shrinkage. Default is 1/4.                                    |

## Value

An object of class robStepSplitReg.

**Author(s)**

Anthony-Alexander Christidis, <anthony.christidis@stat.ubc.ca>

**See Also**

[coef.robStepSplitReg](#), [predict.robStepSplitReg](#)

**Examples**

```
# Required library
library(mvnfast)

# Simulation parameters
n <- 50
p <- 500
rho <- 0.5
p.active <- 100
snr <- 1
contamination.prop <- 0.2

# Setting the seed
set.seed(0)

# Simulation of beta vector
true.beta <- c(runif(p.active, 0, 5)*(-1)^rbinom(p.active, 1, 0.7), rep(0, p - p.active))

# Simulation of uncontaminated data
sigma.mat <- matrix(0, nrow = p, ncol = p)
sigma.mat[1:p.active, 1:p.active] <- rho
diag(sigma.mat) <- 1
x <- mvnfast::rmvn(n, mu = rep(0, p), sigma = sigma.mat)
sigma <- as.numeric(sqrt(t(true.beta) %*% sigma.mat %*% true.beta)/sqrt(snr))
y <- x %*% true.beta + rnorm(n, 0, sigma)

# Contamination of data
contamination_indices <- 1:floor(n*contamination.prop)
k_lev <- 2
k_slo <- 100
x_train <- x
y_train <- y
beta_cont <- true.beta
beta_cont[true.beta!=0] <- beta_cont[true.beta!=0]*(1 + k_slo)
beta_cont[true.beta==0] <- k_slo*max(abs(true.beta))
for(cont_id in contamination_indices){

  a <- runif(p, min = -1, max = 1)
  a <- a - as.numeric((1/p)*t(a) %*% rep(1, p))
  x_train[cont_id,] <- mvnfast::rmvn(1, rep(0, p), 0.1^2*diag(p)) +
    k_lev * a / as.numeric(sqrt(t(a) %*% solve(sigma.mat) %*% a))
  y_train[cont_id] <- t(x_train[cont_id,]) %*% beta_cont
}
```

```
# Ensemble models
ensemble_fit <- robStepSplitReg(x_train, y_train,
                               n_models = 5,
                               model_saturation = c("fixed", "p-value")[1],
                               alpha = 0.05, model_size = n - 1,
                               robust = TRUE,
                               compute_coef = TRUE,
                               en_alpha = 1/4)

# Ensemble coefficients
ensemble_coefs <- coef(ensemble_fit, group_index = 1:ensemble_fit$n_models)
sens_ensemble <- sum(which((ensemble_coefs[-1] != 0)) <= p.active)/p.active
spec_ensemble <- sum(which((ensemble_coefs[-1] != 0)) <= p.active)/sum(ensemble_coefs[-1] != 0)

# Simulation of test data
m <- 2e3
x_test <- mvnfast::rmvn(m, mu = rep(0, p), sigma = sigma.mat)
y_test <- x_test %*% true.beta + rnorm(m, 0, sigma)

# Prediction of test samples
ensemble_preds <- predict(ensemble_fit, newx = x_test,
                          group_index = 1:ensemble_fit$n_models,
                          dynamic = FALSE)
mspe_ensemble <- mean((y_test - ensemble_preds)^2)/sigma^2
```

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