

# Package ‘prioritylasso’

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**Type** Package

**Title** Analyzing Multiple Omics Data with an Offset Approach

**Version** 0.2.3

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**Description** Fits successive Lasso models for several blocks of (omics) data with different priorities and takes the predicted values as an offset for the next block.

**Depends** R (>= 2.10.0)

**License** GPL-2

**LazyData** TRUE

**Imports** survival, glmnet, utils

**RoxygenNote** 7.0.2

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**VignetteBuilder** knitr

**NeedsCompilation** no

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cvm\_prioritylasso      *prioritylasso with several block specifications*

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### Description

Runs prioritylasso for a list of block specifications and gives the best results in terms of cv error.

### Usage

```
cvm_prioritylasso(X, Y, weights, family, type.measure, blocks.list,
  max.coef.list = NULL, block1.penalization = TRUE,
  lambda.type = "lambda.min", standardize = TRUE, nfolds = 10,
  foldid, cvoffset = FALSE, cvoffsetnfolds = 10, ...)
```

### Arguments

X	a (nxp) matrix or data frame of predictors with observations in rows and predictors in columns.
Y	n-vector giving the value of the response (either continuous, numeric-binary 0/1, or Surv object).
weights	observation weights. Default is 1 for each observation.
family	should be "gaussian" for continuous Y, "binomial" for binary Y, "cox" for Y of type Surv.
type.measure	The accuracy/error measure computed in cross-validation. It should be "class" (classification error) or "auc" (area under the ROC curve) if family="binomial", "mse" (mean squared error) if family="gaussian" and "deviance" if family="cox" which uses the partial-likelihood.
blocks.list	list of the format <code>list(list(bp1=..., bp2=...), list(bp1=..., bp2=...), ...)</code> . For the specification of the entries, see <a href="#">prioritylasso</a> .
max.coef.list	list of max.coef vectors. The first entries are omitted if block1.penalization = FALSE. Default is NULL.
block1.penalization	whether the first block should be penalized. Default is TRUE.
lambda.type	specifies the value of lambda used for the predictions. lambda.min gives lambda with minimum cross-validated errors. lambda.1se gives the largest value of lambda such that error is within 1 standard error of the minimum. Note that lambda.1se can only be chosen without restrictions of max.coef.
standardize	logical, whether the predictors should be standardized or not. Default is TRUE.
nfolds	the number of CV procedure folds.
foldid	an optional vector of values between 1 and nfold identifying what fold each observation is in.
cvoffset	logical, whether CV should be used to estimate the offsets. Default is FALSE.
cvoffsetnfolds	the number of folds in the CV procedure that is performed to estimate the offsets. Default is 10. Only relevant if cvoffset=TRUE.
...	Other arguments that can be passed to the function <code>cv.glmnet</code> .

**Value**

object of class `prioritylasso` with the following elements. If these elements are lists, they contain the results for each penalized block of the best result.

`lambda.ind` list with indices of `lambda` for `lambda.type`.

`lambda.type` type of `lambda` which is used for the predictions.

`lambda.min` list with values of `lambda` for `lambda.type`.

`min.cvm` list with the mean cross-validated errors for `lambda.type`.

`nzero` list with numbers of non-zero coefficients for `lambda.type`.

`glmnet.fit` list of fitted `glmnet` objects.

`name` a text string indicating type of measure.

`block1unpen` if `block1.penalization = FALSE`, the results of either the fitted `glm` or `coxph` object.

`best.blocks` character vector with the indices of the best block specification.

`best.max.coef` vector with the number of maximal coefficients corresponding to `best.blocks`.

`coefficients` coefficients according to the results obtained with `best.blocks`.

`call` the function call.

**Note**

The function description and the first example are based on the R package `ipflasso`.

**Author(s)**

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**References**

Klau, S., Jurinovic, V., Hornung, R., Herold, T., Boulesteix, A.-L. (2018). Priority-Lasso: a simple hierarchical approach to the prediction of clinical outcome using multi-omics data. *BMC Bioinformatics* 19, 322

**See Also**

[pl\\_data](#), [prioritylasso](#), [cvr2.ipflasso](#)

**Examples**

```
cvm_prioritylasso(X = matrix(rnorm(50*500),50,500), Y = rnorm(50), family = "gaussian",
  type.measure = "mse", lambda.type = "lambda.min", nfolds = 5,
  blocks.list = list(list(bp1=1:75, bp2=76:200, bp3=201:500),
    list(bp1=1:75, bp2=201:500, bp3=76:200)))
```

## Not run:

```
cvm_prioritylasso(X = pl_data[,1:1028], Y = pl_data[,1029], family = "binomial",
  type.measure = "auc", standardize = FALSE, block1.penalization = FALSE,
  blocks.list = list(list(1:4, 5:9, 10:28, 29:1028),
```

```

                                list(1:4, 5:9, 29:1028, 10:28)),
max.coef.list = list(c(Inf, Inf, Inf, 10), c(Inf, Inf, 10, Inf)))
## End(Not run)

```

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pl\_data

*Simulated AML data with binary outcome*

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### Description

A data set containing the binary outcome and 1028 predictor variables of 400 artificial AML patients.

### Usage

```
pl_data
```

### Format

A data frame with 400 rows and 1029 variables:

**pl\_out:** (pl\_data[,1029]) binary outcome representing refractory status.

**b1:** (pl\_data[,1:4]) 4 binary variables representing variables with a known influence on the outcome.

**b2:** (pl\_data[,5:9]) 5 continuous variables representing clinical variables.

**b3:** (pl\_data[,10:28]) 19 binary variables representing mutations.

**b4:** (pl\_data[,29:1028]) 1000 continuous variables representing gene expression data.

### Details

We generated the data in the following way: We took the empirical correlation of 1028 variables related to 315 AML patients. This correlation served as a correlation matrix when generating 1028 multivariate normally distributed variables with the R function `rmvnorm`. Because we didn't have a positive definite matrix, we took the nearest positive definite matrix according to the function `nearPD`. The variables that should be binary were dichotomized, so that their marginal probabilities corresponded to the marginal probabilities they were based on. The coefficients were defined by

- `beta_b1 <-c(0.8,0.8,0.6,0.6)`
- `beta_b2 <-c(rep(0.5,3),rep(0,2))`
- `beta_b3 <-c(rep(0.4,4),rep(0,15))`
- `beta_b4 <-c(rep(0.5,5),rep(0.3,5),rep(0,990))`.

We included them in the vector `beta <-c(beta_b1,beta_b2,beta_b3,beta_b4)` and calculated the probability through

$$p_i = \exp(\beta * x) / (1 + \exp(\beta * x))$$

where `x` denotes our data matrix with 1028 predictor variables. Finally we got the outcome through `pl_out <-rbinom(400,size = 1,p = pi)`.

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predict.prioritylasso *Predictions from prioritylasso*

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### Description

Makes predictions for a prioritylasso object. It can be chosen between linear predictors or fitted values.

### Usage

```
## S3 method for class 'prioritylasso'  
predict(object, newdata, type = c("link",  
  "response"), ...)
```

### Arguments

object	An object of class prioritylasso.
newdata	(nnew x p) matrix or data frame with new values.
type	Specifies the type of predictions. link gives the linear predictors for all types of response and response gives the fitted values.
...	Further arguments passed to or from other methods.

### Value

Predictions that depend on type.

### Author(s)

Simon Klau

### See Also

[pl\\_data](#), [prioritylasso](#)

### Examples

```
pl_bin <- prioritylasso(X = matrix(rnorm(50*500),50,500), Y = rbinom(50,1,0.5),  
  family = "binomial", type.measure = "auc",  
  blocks = list(block1=1:13,block2=14:200, block3=201:500),  
  block1.penalization = TRUE, lambda.type = "lambda.min",  
  standardize = FALSE, nfold = 5)  
  
newdata_bin <- matrix(rnorm(30*500),30,500)  
  
predict(object = pl_bin, newdata = newdata_bin, type = "response")
```

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prioritylasso	<i>Patient outcome prediction based on multi-omics data taking practitioners' preferences into account</i>
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### Description

Fits successive Lasso models for several ordered blocks of (omics) data and takes the predicted values as an offset for the next block.

### Usage

```
prioritylasso(X, Y, weights, family, type.measure, blocks,
  max.coef = NULL, block1.penalization = TRUE,
  lambda.type = "lambda.min", standardize = TRUE, nfolds = 10,
  foldid, cvoffset = FALSE, cvoffsetnfolds = 10, ...)
```

### Arguments

X	a (n x p) matrix of predictors with observations in rows and predictors in columns.
Y	n-vector giving the value of the response (either continuous, numeric-binary 0/1, or Surv object).
weights	observation weights. Default is 1 for each observation.
family	should be "gaussian" for continuous Y, "binomial" for binary Y, "cox" for Y of type Surv.
type.measure	accuracy/error measure computed in cross-validation. It should be "class" (classification error) or "auc" (area under the ROC curve) if family="binomial", "mse" (mean squared error) if family="gaussian" and "deviance" if family="cox" which uses the partial-likelihood.
blocks	list of the format list(bp1=..., bp2=..., ...), where the dots should be replaced by the indices of the predictors included in this block. The blocks should form a partition of 1:p.
max.coef	vector with integer values which specify the number of maximal coefficients for each block. The first entry is omitted if block1.penalization = FALSE. Default is NULL.
block1.penalization	whether the first block should be penalized. Default is TRUE.
lambda.type	specifies the value of lambda used for the predictions. lambda.min gives lambda with minimum cross-validated errors. lambda.1se gives the largest value of lambda such that the error is within 1 standard error of the minimum. Note that lambda.1se can only be chosen without restrictions of max.coef.
standardize	logical, whether the predictors should be standardized or not. Default is TRUE.
nfolds	the number of CV procedure folds.
foldid	an optional vector of values between 1 and nfolds identifying what fold each observation is in.

<code>cvoffset</code>	logical, whether CV should be used to estimate the offsets. Default is FALSE.
<code>cvoffsetnfolds</code>	the number of folds in the CV procedure that is performed to estimate the offsets. Default is 10. Only relevant if <code>cvoffset=TRUE</code> .
<code>...</code>	other arguments that can be passed to the function <code>cv.glmnet</code> .

### Details

For `block1.penalization = TRUE`, the function fits a Lasso model for each block. First, a standard Lasso for the first entry of blocks (block of priority 1) is fitted. The predictions are then taken as an offset in the Lasso fit of the block of priority 2, etc. For `block1.penalization = FALSE`, the function fits a model without penalty to the block of priority 1 (recommended as a block with clinical predictors where  $p < n$ ). This is either a generalized linear model for family "gaussian" or "binomial", or a Cox model. The predicted values are then taken as an offset in the following Lasso fit of the block with priority 2, etc.

The first entry of `blocks` contains the indices of variables of the block with priority 1 (first block included in the model). Assume that `blocks = list(1:100, 101:200, 201:300)` then the block with priority 1 consists of the first 100 variables of the data matrix. Analogously, the block with priority 2 consists of the variables 101 to 200 and the block with priority 3 of the variables 201 to 300.

### Value

object of class `prioritylasso` with the following elements. If these elements are lists, they contain the results for each penalized block.

`lambda.ind` list with indices of `lambda` for `lambda.type`.

`lambda.type` type of `lambda` which is used for the predictions.

`lambda.min` list with values of `lambda` for `lambda.type`.

`min.cvm` list with the mean cross-validated errors for `lambda.type`.

`nzero` list with numbers of non-zero coefficients for `lambda.type`.

`glmnet.fit` list of fitted `glmnet` objects.

`name` a text string indicating type of measure.

`block1unpen` if `block1.penalization = FALSE`, the results of either the fitted `glm` or `coxph` object corresponding to `best.blocks`.

`coefficients` vector of estimated coefficients. If `block1.penalization = FALSE` and `family = gaussian` or `binomial`, the first entry contains an intercept.

`call` the function call.

### Note

The function description and the first example are based on the R package `ipflasso`. The second example is inspired by the example of `cv.glmnet` from the `glmnet` package.

**Author(s)**

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**References**

Klau, S., Jurinovic, V., Hornung, R., Herold, T., Boulesteix, A.-L. (2018). Priority-Lasso: a simple hierarchical approach to the prediction of clinical outcome using multi-omics data. *BMC Bioinformatics* 19, 322

**See Also**

[pl\\_data](#), [cvm\\_prioritylasso](#), [cvr.ipflasso](#), [cvr2.ipflasso](#)

**Examples**

```
# gaussian
prioritylasso(X = matrix(rnorm(50*500),50,500), Y = rnorm(50), family = "gaussian",
  type.measure = "mse", blocks = list(bp1=1:75, bp2=76:200, bp3=201:500),
  max.coef = c(Inf,8,5), block1.penalization = TRUE,
  lambda.type = "lambda.min", standardize = TRUE, nfolds = 5, cvoffset = FALSE)

## Not run:
# cox
# simulation of survival data:
n <- 50;p <- 300
nzc <- trunc(p/10)
x <- matrix(rnorm(n*p), n, p)
beta <- rnorm(nzc)
fx <- x[, seq(nzc)]%*%beta/3
hx <- exp(fx)
# survival times:
ty <- rexp(n,hx)
# censoring indicator:
tcens <- rbinom(n = n,prob = .3,size = 1)
library(survival)
y <- Surv(ty, 1-tcens)
blocks <- list(bp1=1:20, bp2=21:200, bp3=201:300)
# run prioritylasso:
prioritylasso(x, y, family = "cox", type.measure = "deviance", blocks = blocks,
  block1.penalization = TRUE, lambda.type = "lambda.min", standardize = TRUE,
  nfolds = 5)

# binomial
# using pl_data:
prioritylasso(X = pl_data[,1:1028], Y = pl_data[,1029], family = "binomial", type.measure = "auc",
  blocks = list(bp1=1:4, bp2=5:9, bp3=10:28, bp4=29:1028), standardize = FALSE)
## End(Not run)
```

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