Package ‘SLOPE’

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Title Sorted L1 Penalized Estimation
Version 0.3.3
Description Efficient implementations for Sorted L-One Penalized Estimation (SLOPE): generalized linear models regularized with the sorted L1-norm (Bogdan et al. (2015) <doi:10/gfgwzt>). Supported models include ordinary least-squares regression, binomial regression, multinomial regression, and Poisson regression. Both dense and sparse predictor matrices are supported. In addition, the package features predictor screening rules that enable fast and efficient solutions to high-dimensional problems.
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Description

This data set contains observations of abalones, the common name for any of a group of sea snails. The goal is to predict the age of an individual abalone given physical measurements such as sex, weight, and height.

Usage

abalone
Format
A list with two items representing 211 observations from 9 variables

sex sex of abalone, 1 for female
infant indicates that the person is an infant
length longest shell measurement in mm
diameter perpendicular to length in mm
height height in mm including meat in shell
weight_whole weight of entire abalone
weight_shucked weight of meat
weight_viscera weight of viscera
weight_shell weight of shell
rings rings. +1.5 gives the age in years

Details
Only a stratified sample of 211 rows of the original data set are used here.

Source

See Also
Other datasets: bodyfat, heart, student, wine

bodyfat

<table>
<thead>
<tr>
<th>bodyfat</th>
<th>Bodyfat</th>
</tr>
</thead>
</table>

Description
The response (y) corresponds to estimates of percentage of body fat from application of Siri’s 1956 equation to measurements of underwater weighing, as well as age, weight, height, and a variety of body circumference measurements.

Usage
bodyfat
Format

A list with two items representing 252 observations from 14 variables:

- **age** age (years)
- **weight** weight (lbs)
- **height** height (inches)
- **neck** neck circumference (cm)
- **chest** chest circumference (cm)
- **abdomen** abdomen circumference (cm)
- **hip** hip circumference (cm)
- **thigh** thigh circumference (cm)
- **knee** knee circumference (cm)
- **ankle** ankle circumference (cm)
- **biceps** biceps circumference (cm)
- **forearm** forearm circumference (cm)
- **wrist** wrist circumference (cm)

Source

http://lib.stat.cmu.edu/datasets/bodyfat
https://www.csie.ntu.edu.tw/~cjlin/libsvmtools/datasets/regression.html

See Also

Other datasets: abalone, heart, student, wine

caretSLOPE

Model objects for model tuning with caret

Description

This function can be used in a call to `caret::train()` to enable model tuning using caret. Note that this function does not properly work with sparse feature matrices and standardization due to the way resampling is implemented in caret. So for these cases, please check out `trainSLOPE()` instead.

Usage

caretSLOPE()

Value

A model description list to be used in the `method` argument in `caret::train()`.
**Description**

This function returns coefficients from a model fit by `SLOPE()`.

**Usage**

```r
## S3 method for class 'SLOPE'
coef(object, alpha = NULL, exact = FALSE, simplify = TRUE, sigma, ...)
```

**Arguments**

- `object`: an object of class 'SLOPE'.
- `alpha`: penalty parameter for SLOPE models; if NULL, the values used in the original fit will be used.
- `exact`: if TRUE and the given parameter values differ from those in the original fit, the model will be refit by calling `stats::update()` on the object with the new parameters. If FALSE, the predicted values will be based on interpolated coefficients from the original penalty path.
- `simplify`: if TRUE, `base::drop()` will be called before returning the coefficients to drop extraneous dimensions.
- `sigma`: deprecated. Please use `alpha` instead.
- `...`: arguments that are passed on to `stats::update()` (and therefore also to `SLOPE()`) if `exact = TRUE` and the given penalty is not in `object`.

**Details**

If `exact = FALSE` and `alpha` is not in `object`, then the returned coefficients will be approximated by linear interpolation. If coefficients from another type of penalty sequence (with a different `lambda`) are required, however, please use `SLOPE()` to refit the model.

**Value**

Coefficients from the model.

**See Also**

`predict.SLOPE()`, `SLOPE()`

Other SLOPE-methods: `deviance.SLOPE()`, `plot.SLOPE()`, `predict.SLOPE()`, `print.SLOPE()`, `score()`
Examples

```r
fit <- SLOPE(mtcars$mpg, mtcars$vs, path_length = 1)
coef(fit)
```

---

**deviance.SLOPE**

*Model deviance*

### Description

Model deviance

### Usage

```r
## S3 method for class 'SLOPE'
deviance(object, ...)
```

### Arguments

- `object`: an object of class 'SLOPE'.
- `...`: ignored

### Value

For Gaussian models this is twice the residual sums of squares. For all other models, two times the negative loglikelihood is returned.

### See Also

-SLOPE()

Other SLOPE-methods: coef.SLOPE(), plot.SLOPE(), predict.SLOPE(), print.SLOPE(), score()

### Examples

```r
fit <- SLOPE(abalone$x, abalone$y, family = "poisson")
deviance(fit)
```
Description

Diagnostic attributes of patients classified as having heart disease or not.

Usage

heart

Format

270 observations from 17 variables represented as a list consisting of a binary factor response vector y, with levels 'absence' and 'presence' indicating the absence or presence of heart disease and x: a sparse feature matrix of class 'dgCMatrix' with the following variables:

- **age** age
- **bp** diastolic blood pressure
- **chol** serum cholesterol in mg/dl
- **hr** maximum heart rate achieved
- **old_peak** ST depression induced by exercise relative to rest
- **vessels** the number of major blood vessels (0 to 3) that were colored by fluoroscopy
- **sex** sex of the participant: 0 for male, 1 for female
- **angina** a dummy variable indicating whether the person suffered angina-pectoris during exercise
- **glucose_high** indicates a fasting blood sugar over 120 mg/dl
- **cp_typical** typical angina
- **cp_atypical** atypical angina
- **cp_nonanginal** non-anginal pain
- **ecg_abnormal** indicates a ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV)
- **ecg_estes** probable or definite left ventricular hypertrophy by Estes’ criteria
- **slope_flat** a flat ST curve during peak exercise
- **slope_downsloping** a downwards-sloping ST curve during peak exercise
- **thal_reversible** reversible defect
- **thal_fixed** fixed defect

Preprocessing

The original dataset contained 13 variables. The nominal of these were dummycoded, removing the first category. No precise information regarding variables chest_pain, thal and ecg could be found, which explains their obscure definitions here.
plot.SLOPE

Description

Plot the fitted model’s regression coefficients along the regularization path.

Usage

## S3 method for class 'SLOPE'
plot(
  x, 
  intercept = FALSE,
  x_variable = c("alpha", "deviance_ratio", "step"),
  ... 
)

Arguments

  x an object of class "SLOPE"
  intercept whether to plot the intercept
  x_variable what to plot on the x axis. "alpha" plots the scaling parameter for the sequence, "deviance_ratio" plots the fraction of deviance explained, and "step" plots step number.
  ... parameters that will be used to modify the call to lattice::xyplot()

Value

An object of class "trellis", which will be plotted on the current device unless stored in a variable.

See Also

lattice::xyplot(), SLOPE(), plotDiagnostics()

Other SLOPE-methods: coef.SLOPE(), deviance.SLOPE(), predict.SLOPE(), print.SLOPE(), score()
Examples

```r
fit <- SLOPE(heart$x, heart$y)
plot(fit)
```

Description

Plot results from cross-validation

Usage

```r
## S3 method for class 'TrainedSLOPE'
plot(
  x,
  measure = c("auto", "mse", "mae", "deviance", "auc", "misclass"),
  plot_min = TRUE,
  ci_alpha = 0.2,
  ci_border = FALSE,
  ci_col = lattice::trellis.par.get("superpose.line")$col,
  ...
)
```

Arguments

- `x`: an object of class 'TrainedSLOPE', typically from a call to `trainSLOPE()`
- `measure`: any of the measures used in the call to `trainSLOPE()`. If `measure = "auto"` then deviance will be used for binomial and multinomial models, whilst mean-squared error will be used for Gaussian and Poisson models.
- `plot_min`: whether to mark the location of the penalty corresponding to the best prediction score
- `ci_alpha`: alpha (opacity) for fill in confidence limits
- `ci_border`: color (or flag to turn off and on) the border of the confidence limits
- `ci_col`: color for border of confidence limits
- `...`: other arguments that are passed on to `lattice::xyplot()`

Value

An object of class "trellis" is returned and, if used interactively, will most likely have its print function `lattice::print.trellis()` invoked, which draws the plot on the current display device.

See Also

- `trainSLOPE()`, `lattice::xyplot()`, `lattice::panel.xyplot()`
- Other model-tuning: `caretSLOPE()`, `trainSLOPE()`
Examples

# Cross-validation for a SLOPE binomial model
set.seed(123)
tune <- trainSLOPE(subset(mtcars, select = c("mpg", "drat", "wt")),
                   mtcars$hp,
                   q = c(0.1, 0.2),
                   number = 10)
plot(tune, ci_col = "salmon", col = "black")

plotDiagnostics

Plot results from diagnostics collected during model fitting

Description

This function plots various diagnostics collected during the model fitting resulting from a call to SLOPE() provided that diagnostics = TRUE.

Usage

plotDiagnostics(
  object, # an object of class "SLOPE".
  ind = max(object$diagnostics$penalty), # either "last"
  xvar = c("time", "iteration"), # what to place on the x axis. iteration plots each iteration, time plots the
  yvar, # wall-clock time.
  ...
)

Arguments

- object: an object of class "SLOPE".
- ind: either "last"
- xvar: what to place on the x axis. iteration plots each iteration, time plots the
  wall-clock time.
- yvar: deprecated (and ignored)
- ...: other arguments that will be used to modify the call to lattice::xyplot()

Value

An object of class "trellis", which, unless stored in a variable, will be plotted when its default
print() method is called.

See Also

SLOPE()
**Examples**

```r
x <- SLOPE(abalone$x, abalone$y, alpha = 2, diagnostics = TRUE)
plotDiagnostics(x)
```

---

**predict.SLOPE**

*Generate predictions from SLOPE models*

**Description**

Return predictions from models fit by `SLOPE()`.

**Usage**

```r
## S3 method for class 'SLOPE'
predict(object, x, alpha = NULL, type = "link", simplify = TRUE, sigma, ...)

## S3 method for class 'GaussianSLOPE'
predict(
  object,
  x,
  sigma = NULL,
  type = c("link", "response"),
  simplify = TRUE,
  ...
)

## S3 method for class 'BinomialSLOPE'
predict(
  object,
  x,
  sigma = NULL,
  type = c("link", "response", "class"),
  simplify = TRUE,
  ...
)

## S3 method for class 'PoissonSLOPE'
predict(
  object,
  x,
  sigma = NULL,
  type = c("link", "response"),
  exact = FALSE,
  simplify = TRUE,
  ...
)
```
predict.SLOPE

## S3 method for class 'MultinomialSLOPE'
predict(
  object,
  x,
  sigma = NULL,
  type = c("link", "response", "class"),
  exact = FALSE,
  simplify = TRUE,
  ...
)

Arguments

object an object of class "SLOPE", typically the result of a call to SLOPE()
x new data
alpha penalty parameter for SLOPE models; if NULL, the values used in the original fit will be used
type type of prediction; "link" returns the linear predictors, "response" returns the result of applying the link function, and "class" returns class predictions.
simplify if TRUE, base::drop() will be called before returning the coefficients to drop extraneous dimensions
sigma deprecated. Please use alpha instead.
... ignored and only here for method consistency
exact if TRUE and the given parameter values differ from those in the original fit, the model will be refit by calling stats::update() on the object with the new parameters. If FALSE, the predicted values will be based on interpolated coefficients from the original penalty path.

Value

Predictions from the model with scale determined by type.

See Also

stats::predict(), stats::predict.glm(), coef.SLOPE()

Other SLOPE-methods: coef.SLOPE(), deviance.SLOPE(), plot.SLOPE(), print.SLOPE(), score()

Examples

```r
fit <- with(mtcars, SLOPE(cbind(mpg, hp), vs, family = "binomial"))
predict(fit, with(mtcars, cbind(mpg, hp)), type = "class")
```
print.SLOPE

Print results from SLOPE fit

Description

Print results from SLOPE fit

Usage

## S3 method for class 'SLOPE'
print(x, ...)

## S3 method for class 'TrainedSLOPE'
print(x, ...)

Arguments

x an object of class 'SLOPE' or 'TrainedSLOPE'
...
other arguments passed to print()

Value

Prints output on the screen

See Also

SLOPE(), print.SLOPE()

Other SLOPE-methods: coef.SLOPE(), deviance.SLOPE(), plot.SLOPE(), predict.SLOPE(), score()

Examples

fit <- SLOPE(wine$x, wine$y, family = "multinomial")
print(fit, digits = 1)

score

Compute one of several loss metrics on a new data set

Description

This function is a unified interface to return various types of loss for a model fit with SLOPE().
Usage

score(object, x, y, measure)

## S3 method for class 'GaussianSLOPE'
score(object, x, y, measure = c("mse", "mae"))

## S3 method for class 'BinomialSLOPE'
score(object, x, y, measure = c("mse", "mae", "deviance", "misclass", "auc"))

## S3 method for class 'MultinomialSLOPE'
score(object, x, y, measure = c("mse", "mae", "deviance", "misclass"))

## S3 method for class 'PoissonSLOPE'
score(object, x, y, measure = c("mse", "mae"))

Arguments

object an object of class "SLOPE"

x feature matrix

y response

measure type of target measure. "mse" returns mean squared error. "mae" returns mean absolute error, "misclass" returns misclassification rate, and "auc" returns area under the ROC curve.

Value

The measure along the regularization path depending on the value in measure.

See Also

SLOPE(), predict.SLOPE()

Other SLOPE-methods: coef.SLOPE(), deviance.SLOPE(), plot.SLOPE(), predict.SLOPE(), print.SLOPE()

Examples

x <- subset(infert, select = c("induced", "age", "pooled.stratum"))
y <- infert$case

fit <- SLOPE(x, y, family = "binomial")
score(fit, x, y, measure = "auc")
SLOPE

Sorted L-One Penalized Estimation

Description

Fit a generalized linear model regularized with the sorted L1 norm, which applies a non-increasing regularization sequence to the coefficient vector ($\beta$) after having sorted it in decreasing order according to its absolute values.

Usage

SLOPE(
  x, 1
  y, 1
  family = c("gaussian", "binomial", "multinomial", "poisson"), 1
  intercept = TRUE, 1
  center = !inherits(x, "sparseMatrix"), 1
  scale = c("l2", "l1", "sd", "none"), 1
  alpha = c("path", "estimate"), 1
  lambda = c("bh", "gaussian", "oscar"), 1
  alpha_min_ratio = if (NROW(x) < NCOL(x)) 0.01 else 1e-04, 1
  path_length = if (alpha[1] == "estimate") 1 else 20, 1
  q = 0.1 * min(1, NROW(x)/NCOL(x)), 1
  screen = TRUE, 1
  screen_alg = c("strong", "previous"), 1
  tol_dev_change = 1e-05, 1
  tol_dev_ratio = 0.995, 1
  max_variables = NROW(x), 1
  solver = c("fista", "admm"), 1
  max_passes = 1e+06, 1
  tol_abs = 1e-05, 1
  tol_rel = 1e-04, 1
  tol_rel_gap = 1e-05, 1
  tol_infeas = 0.001, 1
  tol_rel_coef_change = 0.001, 1
  diagnostics = FALSE, 1
  verbosity = 0, 1
  sigma, 1
  n_sigma, 1
  lambda_min_ratio 1
)

Arguments

x
the design matrix, which can be either a dense matrix of the standard matrix class, or a sparse matrix inheriting from Matrix::sparseMatrix. Data frames will be converted to matrices internally.
y

the response, which for family = "gaussian" must be numeric; for family = "binomial" or family = "multinomial", it can be a factor.

family

model family (objective); see Families for details.

intercept

whether to fit an intercept

center

whether to center predictors or not by their mean. Defaults to TRUE if x is dense and FALSE otherwise.

scale

type of scaling to apply to predictors.

• "l1" scales predictors to have L1 norms of one.
• "l2" scales predictors to have L2 norms of one.
• "sd" scales predictors to have a population standard deviation one.
• "none" applies no scaling.

alpha

scale for regularization path: either a decreasing numeric vector (possibly of length 1) or a character vector; in the latter case, the choices are:

• "path", which computes a regularization sequence where the first value corresponds to the intercept-only (null) model and the last to the almost-saturated model, and
• "estimate", which estimates a single alpha using Algorithm 5 in Bogdan et al. (2015).

When a value is manually entered for alpha, it will be scaled based on the type of standardization that is applied to x. For scale = "l2", alpha will be scaled by $\sqrt{n}$. For scale = "sd" or "none", alpha will be scaled by $n$, and for scale = "l1" no scaling is applied. Note, however, that the alpha that is returned in the resulting value is the unstandardized alpha.

lambda

either a character vector indicating the method used to construct the lambda path or a numeric non-decreasing vector with length equal to the number of coefficients in the model; see section Regularization sequences for details.

alpha_min_ratio

smallest value for lambda as a fraction of lambda_max; used in the selection of alpha when alpha = "path".

path_length

length of regularization path; note that the path returned may still be shorter due to the early termination criteria given by tol_dev_change, tol_dev_ratio, and max_variables.

q

parameter controlling the shape of the lambda sequence, with usage varying depending on the type of path used and has no effect in a custom lambda sequence is used.

screen

whether to use predictor screening rules (rules that allow some predictors to be discarded prior to fitting), which improve speed greatly when the number of predictors is larger than the number of observations.

screen_alg

what type of screening algorithm to use.

• "strong" uses the set from the strong screening rule and check against the full set
• "previous" first fits with the previous active set, then checks against the strong set, and finally against the full set if there are no violations in the strong set
tol_dev_change  the regularization path is stopped if the fractional change in deviance falls below this value; note that this is automatically set to 0 if a alpha is manually entered

tol_dev_ratio  the regularization path is stopped if the deviance ratio \(1 - \text{deviance}/(\text{null} - \text{deviance})\) is above this threshold

max_variables  criterion for stopping the path in terms of the maximum number of unique, nonzero coefficients in absolute value in model. For the multinomial family, this value will be multiplied internally with the number of levels of the response minus one.

solver  type of solver use, either "fista" or "admm"; all families currently support FISTA but only family = "gaussian" supports ADMM.

max_passes  maximum number of passes (outer iterations) for solver

tol_abs  absolute tolerance criterion for ADMM solver

tol_rel  relative tolerance criterion for ADMM solver

tol_rel_gap  stopping criterion for the duality gap; used only with FISTA solver.

tol_infeas  stopping criterion for the level of infeasibility; used with FISTA solver and KKT checks in screening algorithm.

tol_rel_coef_change  relative tolerance criterion for change in coefficients between iterations, which is reached when the maximum absolute change in any coefficient divided by the maximum absolute coefficient size is less than this value.

diagnostics  whether to save diagnostics from the solver (timings and other values depending on type of solver)

verbosity  level of verbosity for displaying output from the program. Setting this to 1 displays basic information on the path level, 2 a little bit more information on the path level, and 3 displays information from the solver.

sigma  deprecated; please use alpha instead

n_sigma  deprecated; please use path_length instead

lambda_min_ratio  deprecated; please use alpha_min_ratio instead

Details

SLOPE() solves the convex minimization problem

\[ f(\beta) + \alpha \sum_{j=1}^{p} \lambda_j |\beta(j)|, \]

where \(f(\beta)\) is a smooth and convex function and the second part is the sorted L1-norm. In ordinary least-squares regression, \(f(\beta)\) is simply the squared norm of the least-squares residuals. See section Families for specifics regarding the various types of \(f(\beta)\) (model families) that are allowed in SLOPE().

By default, SLOPE() fits a path of models, each corresponding to a separate regularization sequence, starting from the null (intercept-only) model to an almost completely unregularized model. These regularization sequences are parameterized using \(\lambda\) and \(\alpha\), with only \(\alpha\) varying along the path. The length of the path can be manually, but will terminate prematurely depending on arguments tol_dev_change, tol_dev_ratio, and max_variables. This means that unless these arguments are modified, the path is not guaranteed to be of length path_length.
Value
An object of class "SLOPE" with the following slots:

- **coefficients**: a three-dimensional array of the coefficients from the model fit, including the intercept if it was fit. There is one row for each coefficient, one column for each target (dependent variable), and one slice for each penalty.
- **nonzeros**: a three-dimensional logical array indicating whether a coefficient was zero or not
- **lambda**: the lambda vector that when multiplied by a value in alpha gives the penalty vector at that point along the regularization path
- **alpha**: vector giving the (unstandardized) scaling of the lambda sequence
- **class_names**: a character vector giving the names of the classes for binomial and multinomial families
- **passes**: the number of passes the solver took at each step on the path
- **violations**: the number of violations of the screening rule at each step on the path; only available if diagnostics = TRUE in the call to SLOPE().
- **active_sets**: a list where each element indicates the indices of the coefficients that were active at that point in the regularization path
- **unique**: the number of unique predictors (in absolute value)
- **deviance_ratio**: the deviance ratio (as a fraction of 1)
- **null_deviance**: the deviance of the null (intercept-only) model
- **family**: the name of the family used in the model fit
- **diagnostics**: a data.frame of objective values for the primal and dual problems, as well as a measure of the infeasibility, time, and iteration; only available if diagnostics = TRUE in the call to SLOPE().
- **call**: the call used for fitting the model

Families

**Gaussian**
The Gaussian model (Ordinary Least Squares) minimizes the following objective:

$$ \frac{1}{2} \| y - X\beta \|_2^2 $$

**Binomial**
The binomial model (logistic regression) has the following objective:

$$ \sum_{i=1}^{n} \log \left( 1 + \exp \left( -y_i \left( x_i^T \beta + \beta_0 \right) \right) \right) $$

with $y \in \{-1, 1\}$.

**Poisson**
In poisson regression, we use the following objective:
- \sum_{i=1}^{n} \left( y_i \left( x_i^T \beta + \beta_0 \right) - \exp \left( x_i^T \beta + \beta_0 \right) \right)

**Multinomial**

In multinomial regression, we minimize the full-rank objective

- \sum_{i=1}^{n} \left( \sum_{k=1}^{m-1} y_{ik} (x_i^T \beta_k + \beta_{0,k}) - \log \sum_{k=1}^{m-1} \exp \left( x_i^T \beta_k + \beta_{0,k} \right) \right)

with \( y_{ik} \) being the element in a \( n \) by \( (m-1) \) matrix, where \( m \) is the number of classes in the response.

**Regularization sequences**

There are multiple ways of specifying the \( \lambda \) sequence in \texttt{SLOPE()} . It is, first of all, possible to select the sequence manually by using a non-increasing numeric vector, possible of length one, as argument instead of a character. If all \( \lambda \) are the same value, this will lead to the ordinary lasso penalty. The greater the differences are between consecutive values along the sequence, the more clustering behavior will the model exhibit. Note, also, that the scale of the \( \lambda \) vector makes no difference if \( \alpha = \text{NULL} \), since \( \alpha \) will be selected automatically to ensure that the model is completely sparse at the beginning and almost unregularized at the end. If, however, both \( \alpha \) and \( \lambda \) are manually specified, both of the scales will matter.

Instead of choosing the sequence manually, one of the following automatically generated sequences may be chosen.

**BH (Benjamini–Hochberg)**

If \( \lambda = \text{"bh"} \), the sequence used is that referred to as \( \lambda^{(BH)} \) by Bogdan et al, which sets \( \lambda \) according to

\[ \lambda_i = \Phi^{-1} \left( 1 - iq/(2p) \right), \]

for \( i = 1, \ldots, p \), where \( \Phi^{-1} \) is the quantile function for the standard normal distribution and \( q \) is a parameter that can be set by the user in the call to \texttt{SLOPE()} .

**Gaussian**

This penalty sequence is related to BH, such that

\[ \lambda_i = \lambda_i^{(BH)} \sqrt{1 + w(i-1) \cdot \text{cumsum}(\lambda^2)}, \]

for \( i = 1, \ldots, p \), where \( w(k) = 1/(n-k-1) \). We let \( \lambda_1 = \lambda_1^{(BH)} \) and adjust the sequence to make sure that it’s non-increasing. Note that if \( p \) is large relative to \( n \), this option will result in a constant sequence, which is usually not what you would want.

**OSCAR**

This sequence comes from Bondell and Reich and is a linearly non-increasing sequence such that

\[ \lambda_i = q(p-i) + 1. \]

for \( i = 1, \ldots, p \).
Solvers
There are currently two solvers available for SLOPE: FISTA (Beck and Teboulle 2009) and ADMM (Boyd et al. 2008). FISTA is available for families but ADMM is currently only available for family = "gaussian".

References

See Also
plot.SLOPE(), plotDiagnostics(), score(), predict.SLOPE(), trainSLOPE(), coef.SLOPE(), print.SLOPE(), print.SLOPE(), deviance.SLOPE()

Examples
# Gaussian response, default lambda sequence
fit <- SLOPE(bodyfat$x, bodyfat$y)

# Poisson response, OSCAR-type lambda sequence
fit <- SLOPE(abalone$x,
              abalone$y,
              family = "poisson",
              lambda = "oscar",
              q = 0.4)

# Multinomial response, custom alpha and lambda
m <- length(unique(wine$y)) - 1
p <- ncol(wine$x)
alpha <- 0.005
lambda <- exp(seq(log(2), log(1.8), length.out = p*m))

fit <- SLOPE(wine$x,
             wine$y,
             family = "multinomial",
             lambda = lambda,
             alpha = alpha)
Description

A data set of the attributes of 382 students in secondary education collected from two schools. The goal is to predict the grade in math and Portugese at the end of the third period. See the cited sources for additional information.

Usage

student

Format

382 observations from 13 variables represented as a list consisting of a binary factor response matrix } with two responses: portugese and math for the final scores in period three for the respective subjects. The list also contains }: a sparse feature matrix of class 'dgCMatrix' with the following variables:

- school_ms  student’s primary school, 1 for Mousinho da Silveira and 0 for Gabriel Pereira
- sex  sex of student, 1 for male
- age  age of student
- urban  urban (1) or rural (0) home address
- large_family  whether the family size is larger than 3
- cohabitation  whether parents live together
- Medu  mother’s level of education (ordered)
- Fedu  fathers’s level of education (ordered)
- Mjob_health  whether the mother was employed in health care
- Mjob_other  whether the mother was employed as something other than the specified job roles
- Mjob_services  whether the mother was employed in the service sector
- Mjob_teacher  whether the mother was employed as a teacher
- Fjob_health  whether the father was employed in health care
- Fjob_other  whether the father was employed as something other than the specified job roles
- Fjob_services  whether the father was employed in the service sector
- Fjob_teacher  whether the father was employed as a teacher
- reason_home  school chosen for being close to home
- reason_other  school chosen for another reason
- reason_rep  school chosen for its reputation
- nursery  whether the student attended nursery school
- internet  Pwhether the student has internet access at home
Preprocessing

All of the grade-specific predictors were dropped from the data set. (Note that it is not clear from the source why some of these predictors are specific to each grade, such as which parent is the student’s guardian.) The categorical variables were dummy-coded. Only the final grades (G3) were kept as dependent variables, whilst the first and second period grades were dropped.

Source


See Also

Other datasets: abalone, bodyfat, heart, wine

---

**trainSLOPE**  
*Train a SLOPE model*

**Description**

This function trains a model fit by SLOPE() by tuning its parameters through cross-validation.

**Usage**

```r
trainSLOPE(
  x,
  y,
  q = 0.2,
  number = 10,
  repeats = 1,
  measure = c("mse", "mae", "deviance", "missclass", "auc"),
  ...
)
```

**Arguments**

- `x`  
  the design matrix, which can be either a dense matrix of the standard `matrix` class, or a sparse matrix inheriting from `Matrix::sparseMatrix`. Data frames will be converted to matrices internally.

- `y`  
  the response, which for `family = "gaussian"` must be numeric; for `family = "binomial"` or `family = "multinomial"`, it can be a factor.
trainSLOPE

- **q**: parameter controlling the shape of the lambda sequence, with usage varying depending on the type of path used and has no effect if a custom lambda sequence is used.
- **number**: number of folds (cross-validation)
- **repeats**: number of repeats for each fold (for repeated k-fold cross validation)
- **measure**: measure to try to optimize, note that you may supply multiple values here and that, by default, all the possible measures for the given model will be used.
- **...**: other arguments to pass on to SLOPE()

**Details**

Note that by default this method matches all of the available metrics for the given model family against those provided in the argument measure. Collecting these measures is not particularly demanding computationally so it is almost always best to leave this argument as is and then choose which argument to focus on in the call to plot.TrainedSLOPE().

**Value**

An object of class "TrainedSLOPE", with the following slots:

- **summary**: a summary of the results with means, standard errors, and 0.95 confidence levels
- **data**: the raw data from the model training
- **optima**: a data.frame of the best (mean) values for the different metrics and their corresponding parameter values
- **measure**: a data.frame listing the used metrics and their labels
- **model**: the model fit to the entire data set
- **call**: the call

**Parallel operation**

This function uses the foreach package to enable parallel operation. To enable this, simply register a parallel backend using, for instance, doParallel::registerDoParallel() from the doParallel package before running this function.

**See Also**

foreach::foreach(), plot.TrainedSLOPE()

Other model-tuning: caretSLOPE(), plot.TrainedSLOPE()

**Examples**

```r
# 8-fold cross-validation repeated 5 times
tune <- trainSLOPE(subset(mtcars, select = c("mpg", "drat", "wt")),
                    mtcars$hp,
                    q = c(0.1, 0.2),
                    number = 8,
                    repeats = 5)
```

### Description

A data set of results from chemical analysis of wines grown in Italy from three different cultivars.

### Usage

```r
wine
```

### Format

178 observations from 13 variables represented as a list consisting of a categorical response vector `y` with three levels: `A`, `B`, and `C` representing different cultivars of wine as well as `x`: a sparse feature matrix of class 'dgCMatrix' with the following variables:

- `alcohol` alcoholic content
- `malic` malic acid
- `ash` ash
- `alcalinity` alcalinity of ash
- `magnesium` magnesium
- `phenols` total phenols
- `flavanoids` flavanoids
- `nonflavanoids` nonflavanoid phenols
- `proanthocyanins` proanthocyanins
- `color` color intensity
- `hue` hue
- `dilution` OD280/OD315 of diluted wines
- `proline` proline

### Source


[https://raw.githubusercontent.com/hadley/rminds/master/1-data/wine.csv](https://raw.githubusercontent.com/hadley/rminds/master/1-data/wine.csv)

[https://www.csie.ntu.edu.tw/~cjlin/libsvmtools/datasets/multiclass.html#wine](https://www.csie.ntu.edu.tw/~cjlin/libsvmtools/datasets/multiclass.html#wine)

### See Also

Other datasets: `abalone, bodyfat, heart, student`
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