Package ‘glmnet’

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Type Package

Title Lasso and Elastic-Net Regularized Generalized Linear Models

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Depends R (>= 3.6.0), Matrix (>= 1.0-6)

Imports methods, utils, foreach, shape, survival, Rcpp

Suggests knitr, lars, testthat, xfun, rmarkdown

SystemRequirements C++17

Description Extremely efficient procedures for fitting the entire lasso or elastic-net regularization path for linear regression, logistic and multinomial regression models, Poisson regression, Cox model, multiple-response Gaussian, and the grouped multinomial regression; see <doi:10.18637/jss.v033.i01> and <doi:10.18637/jss.v039.i05>. There are two new and important additions. The family argument can be a GLM family object, which opens the door to any programmed family (<doi:10.18637/jss.v106.i01>). This comes with a modest computational cost, so when the built-in families suffice, they should be used instead. The other novelty is the relax option, which refits each of the active sets in the path unpenalized. The algorithm uses cyclical coordinate descent in a path-wise fashion, as described in the papers cited.

License GPL-2

VignetteBuilder knitr

Encoding UTF-8

URL https://glmnet.stanford.edu

RoxygenNote 7.2.3

LinkingTo RcppEigen, Rcpp

NeedsCompilation yes

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R topics documented:

- glmnet-package
- assess.glmnet
- beta_CVX
- bigGlm
- BinomialExample
- Cindex
- coef.glmnet
- cox.fit
- cox.path
- CoxExample
- coxgrad
- coxnet.deviance
- cox_obj_function
- cv.glmnet
- deviance.glmnet
- dev_function
- elnet.fit
- fid
- get_cox_lambda_max
- get_eta
- get_start
- glmnet
- glmnet.control
- glmnet.fit
- glmnet.measures
- glmnet.path
- makeX
- MultiGaussianExample
- MultinomialExample
- mycoxph
- mycoxpred
- na.replace
- obj_function
- pen_function
- plot.cv.glmnet
- plot.glmnet
- PoissonExample
- predict.cv.glmnet
- predict.glmnetfit
Elastic net model paths for some generalized linear models

**Description**

This package fits lasso and elastic-net model paths for regression, logistic and multinomial regression using coordinate descent. The algorithm is extremely fast, and exploits sparsity in the input x matrix where it exists. A variety of predictions can be made from the fitted models.

**Details**

- **Package:** glmnet
- **Type:** Package
- **Version:** 1.0
- **Date:** 2008-05-14
- **License:** What license is it under?

Very simple to use. Accepts x, y data for regression models, and produces the regularization path over a grid of values for the tuning parameter lambda. Only 5 functions: glmnet

predict.glmnet
plot.glmnet
print.glmnet
coef.glmnet

**Author(s)**

Jerome Friedman, Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

**References**


Glmnet webpage with four vignettes: https://glmnet.stanford.edu.

**Examples**

```r
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
g2 = sample(1:2, 100, replace = TRUE)
g4 = sample(1:4, 100, replace = TRUE)
fit1 = glmnet(x, y)
predict(fit1, newx = x[1:5, ], s = c(0.01, 0.005))
predict(fit1, type = "coef")
plot(fit1, xvar = "lambda")
fit2 = glmnet(x, g2, family = "binomial")
predict(fit2, type = "response", newx = x[2:5, ])
predict(fit2, type = "nonzero")
fit3 = glmnet(x, g4, family = "multinomial")
predict(fit3, newx = x[1:3, ], type = "response", s = 0.01)
```

**assess.glmnet**

assess performance of a 'glmnet' object using test data.

**Description**

Given a test set, produce summary performance measures for the glmnet model(s)

**Usage**

```r
assess.glmnet(
  object,
  newx = NULL,
  newy,
  weights = NULL,
  family = c("gaussian", "binomial", "poisson", "multinomial", "cox", "mgaussian"),
  ...)
```
assess.glmnet

confusion.glmnet(
  object,
  newx = NULL,
  newy,
  family = c("binomial", "multinomial"),
  ...
)

roc.glmnet(object, newx = NULL, newy, ...)

Arguments

object Fitted "glmnet" or "cv.glmnet", "relaxed" or "cv.relaxed" object, OR a matrix of predictions (for roc.glmnet or assess.glmnet). For roc.glmnet the model must be a 'binomial', and for confusion.glmnet must be either 'binomial' or 'multinomial'

newx If predictions are to made, these are the 'x' values. Required for confusion.glmnet

newy required argument for all functions; the new response values

weights For observation weights for the test observations

family The family of the model, in case predictions are passed in as 'object'

... additional arguments to predict.glmnet when "object" is a "glmnet" fit, and predictions must be made to produce the statistics.

Details

assess.glmnet produces all the different performance measures provided by cv.glmnet for each of the families. A single vector, or a matrix of predictions can be provided, or fitted model objects or CV objects. In the case when the predictions are still to be made, the ... arguments allow, for example, 'offsets' and other prediction parameters such as values for 'gamma' for 'relaxed' fits.

roc.glmnet produces for a single vector a two column matrix with columns TPR and FPR (true positive rate and false positive rate). This object can be plotted to produce an ROC curve. If more than one predictions are called for, then a list of such matrices is produced. confusion.glmnet produces a confusion matrix tabulating the classification results. Again, a single table or a list, with a print method.

Value

assess.glmnet produces a list of vectors of measures. roc.glmnet a list of 'roc' two-column matrices, and confusion.glmnet a list of tables. If a single prediction is provided, or predictions are made from a CV object, the latter two drop the list status and produce a single matrix or table.

Author(s)

Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

See Also

cv.glmnet, glmnet.measures and vignette("relax",package="glmnet")
Examples

data(QuickStartExample)
x <- QuickStartExample$x; y <- QuickStartExample$y
set.seed(11)
train = sample(seq(length(y)),70,replace=FALSE)
fit1 = glmnet(x[train,], y[train])
assess.glmnet(fit1, newx = x[-train,], newy = y[-train])
preds = predict(fit1, newx = x[-train,], s = c(1, 0.25))
assess.glmnet(preds, newy = y[-train], family = "gaussian")
fit1c = cv.glmnet(x, y, keep = TRUE)
fit1a = assess.glmnet(fit1c$fit.preval, newy=y,family="gaussian")
plot(fit1c$lambda, log="x",fit1a$mae,xlab="Log Lambda",ylab="Mean Absolute Error")
abline(v=fit1c$lambda.min, lty=2, col="red")
data(BinomialExample)
x <- BinomialExample$x; y <- BinomialExample$y
fit2 = glmnet(x[train,], y[train], family = "binomial")
assess.glmnet(fit2,newx = x[-train,], newy=y[-train], s=0.1)
plot(roc.glmnet(fit2, newx = x[-train,], newy=y[-train])[[10]])
fit2c = cv.glmnet(x, y, family = "binomial", keep=TRUE)
idmin = match(fit2c$lambda.min, fit2c$lambda)
plot(roc.glmnet(fit2c$fit.preval, newy = y)[[idmin]])
data(MultinomialExample)
x <- MultinomialExample$x; y <- MultinomialExample$y
set.seed(103)
train = sample(seq(length(y)),100,replace=FALSE)
fit3 = glmnet(x[train,], y[train], family = "multinomial")
confusion.glmnet(fit3, newx = x[-train,], newy = y[-train], s = 0.01)
fit3c = cv.glmnet(x, y, family = "multinomial", type.measure="class", keep=TRUE)
idmin = match(fit3c$lambda.min, fit3c$lambda)
confusion.glmnet(fit3c$fit.preval, newy = y, family="multinomial")[[idmin]]

Simulated data for the glmnet vignette

Description

Simple simulated data, used to demonstrate the features of glmnet

Format

Data objects used to demonstrate features in the glmnet vignette

Details

These datasets are artificial, and are used to test out some of the features of glmnet.
bigGlm

Examples

data(QuickStartExample)
x <- QuickStartExample$x; y <- QuickStartExample$y
glmnet(x, y)

bigGlm fit a glm with all the options in glmnet

Description

Fit a generalized linear model as in glmnet but unpenalized. This allows all the features of glmnet such as sparse x, bounds on coefficients, offsets, and so on.

Usage

bigGlm(x, ..., path = FALSE)

Arguments

x input matrix
... Most other arguments to glmnet that make sense
path Since glmnet does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with unpenalized fits. With path=TRUE, the fit computed with pathwise lasso regularization. The current implementation does this twice: the first time to get the lambda sequence, and the second time with a zero attached to the end). Default is path=FALSE.

Details

This is essentially the same as fitting a "glmnet" model with a single value lambda=0, but it avoids some edge cases. CAVEAT: If the user tries a problem with N smaller than or close to p for some models, it is likely to fail (and maybe not gracefully!) If so, use the path=TRUE argument.

Value

It returns an object of class "bigGlm" that inherits from class "glmnet". That means it can be predicted from, coefficients extracted via coef. It has its own print method.

Author(s)

Trevor Hastie
Maintainer: Trevor Hastie <hastie@stanford.edu>

See Also

print, predict, and coef methods.
Examples

```r
# Gaussian
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
fit1 = bigGlm(x, y)
print(fit1)

fit2 = bigGlm(x, y > 0, family = "binomial")
print(fit2)
fit2p = bigGlm(x, y > 0, family = "binomial", path = TRUE)
print(fit2p)
```

BinomialExample Synthetic dataset with binary response

Description

Randomly generated data for binomial regression example.

Usage

data(BinomialExample)

Format

List containing the following elements:

- **x** 100 by 30 matrix of numeric values.
- **y** Numeric vector of length 100 containing 44 zeros and 56 ones.

Cindex compute C index for a Cox model

Description

Computes Harrel's C index for predictions from a "coxnet" object.

Usage

```r
Cindex(pred, y, weights = rep(1, nrow(y)))
```
Arguments

- **pred**: Predictions from a "coxnet" object
- **y**: A survival response object - a matrix with two columns "time" and "status"; see documentation for "glmnet"
- **weights**: Optional observation weights

Details

Computes the concordance index, taking into account censoring.

Author(s)

Trevor Hastie hastie@stanford.edu

References


See Also

cv.glmnet

Examples

```r
set.seed(10101)
N = 1000
p = 30
nzc = p/3
x = matrix(rnorm(N * p), N, p)
beta = rnorm(nzc)
fx = x[, seq(nzc)] %*% beta/3
hx = exp(fx)
ty = rexp(N, hx)
tcens = rbinom(n = N, prob = 0.3, size = 1)  # censoring indicator
y = cbind(time = ty, status = 1 - tcens)  # y=Surv(ty,1-tcens) with library(survival)
fit = glmnet(x, y, family = "cox")
pred = predict(fit, newx = x)
apply(pred, 2, Cindex, y=y)
cv.glmnet(x, y, family = "cox", type.measure = "C")
```
coef.glmnet

Extract coefficients from a glmnet object

Description

Similar to other predict methods, this functions predicts fitted values, logits, coefficients and more from a fitted "glmnet" object.

Usage

## S3 method for class 'glmnet'
coef(object, s = NULL, exact = FALSE, ...)

## S3 method for class 'glmnet'
predict(
  object,
  newx,
  s = NULL,
  type = c("link", "response", "coefficients", "nonzero", "class"),
  exact = FALSE,
  newoffset,
  ...
)

## S3 method for class 'relaxed'
predict(
  object,
  newx,
  s = NULL,
  gamma = 1,
  type = c("link", "response", "coefficients", "nonzero", "class"),
  exact = FALSE,
  newoffset,
  ...
)

Arguments

object

Fitted "glmnet" model object or a "relaxed" model (which inherits from class "glmnet").

s

Value(s) of the penalty parameter lambda at which predictions are required. Default is the entire sequence used to create the model.

exact

This argument is relevant only when predictions are made at values of s (lambda) different from those used in the fitting of the original model. Not available for "relaxed" objects. If exact=FALSE (default), then the predict function uses linear interpolation to make predictions for values of s (lambda) that do not
coef.glmnet coincide with those used in the fitting algorithm. While this is often a good approximation, it can sometimes be a bit coarse. With exact=TRUE, these different values of s are merged (and sorted) with object$lambda, and the model is refit before predictions are made. In this case, it is required to supply the original data x= and y= as additional named arguments to predict() or coef(). The workhorse predict.glmnet() needs to update the model, and so needs the data used to create it. The same is true of weights, offset, penalty.factor, lowerlimits, upperlimits if these were used in the original call. Failure to do so will result in an error.

... This is the mechanism for passing arguments like x= when exact=TRUE; see exact argument.

colx Matrix of new values for x at which predictions are to be made. Must be a matrix; can be sparse as in Matrix package. This argument is not used for type=c("coefficients","nonzero")
type Type of prediction required. Type "link" gives the linear predictors for "binomial", "multinomial", "poisson" or "cox" models; for "gaussian" models it gives the fitted values. Type "response" gives the fitted probabilities for "binomial" or "multinomial", fitted mean for "poisson" and the fitted relative-risk for "cox"; for "gaussian" type "response" is equivalent to type "link". Type "coefficients" computes the coefficients at the requested values for s. Note that for "binomial" models, results are returned only for the class corresponding to the second level of the factor response. Type "class" applies only to "binomial" or "multinomial" models, and produces the class label corresponding to the maximum probability. Type "nonzero" returns a list of the indices of the nonzero coefficients for each value of s.

coloffset If an offset is used in the fit, then one must be supplied for making predictions (except for type="coefficients" or type="nonzero")

colgamma Single value of gamma at which predictions are required, for "relaxed" objects.

Details
The shape of the objects returned are different for "multinomial" objects. This function actually calls NextMethod(), and the appropriate predict method is invoked for each of the three model types. coef(...) is equivalent to predict(type="coefficients",...)

Value
The object returned depends on type.

Author(s)
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Maintainer: Trevor Hastie hastie@stanford.edu

References
cox.fit

Fit a Cox regression model with elastic net regularization for a single value of lambda

Description

Fit a Cox regression model via penalized maximum likelihood for a single value of lambda. Can deal with (start, stop] data and strata, as well as sparse design matrices.

Usage

cox.fit(
  x,
  y, 
  weights, 
  lambda, 
  alpha = 1, 
  offset = rep(0, nobs), 
  thresh = 1e-10, 
  maxit = 1e+05, 
  penalty.factor = rep(1, nvars), 
  exclude = c(), 
  lower.limits = -Inf, 
)
upper.limits = Inf,
warm = NULL,
from.cox.path = FALSE,
save.fit = FALSE,
trace.it = 0
)

Arguments

x       Input matrix, of dimension nobs x nvars; each row is an observation vector. If it is a sparse matrix, it is assumed to be unstandardized. It should have attributes xm and xs, where xm(j) and xs(j) are the centering and scaling factors for variable j respectively. If it is not a sparse matrix, it is assumed that any standardization needed has already been done.

y       Survival response variable, must be a Surv or stratifySurv object.

weights Observation weights. cox.fit does NOT standardize these weights.

lambda   A single value for the lambda hyperparameter.

alpha   See glmnet help file

offset   See glmnet help file

thresh   Convergence threshold for coordinate descent. Each inner coordinate-descent loop continues until the maximum change in the objective after any coefficient update is less than thresh times the null deviance. Default value is 1e-10.

maxit   Maximum number of passes over the data; default is 10^5. (If a warm start object is provided, the number of passes the warm start object performed is included.)

penalty.factor   See glmnet help file

exclude   See glmnet help file

lower.limits   See glmnet help file

upper.limits   See glmnet help file

warm   Either a glmnetfit object or a list (with name beta containing coefficients) which can be used as a warm start. Default is NULL, indicating no warm start. For internal use only.

from.cox.path   Was cox.fit() called from cox.path()? Default is FALSE. This has implications for computation of the penalty factors.

save.fit   Return the warm start object? Default is FALSE.

trace.it   Controls how much information is printed to screen. If trace.it=2, some information about the fitting procedure is printed to the console as the model is being fitted. Default is trace.it=0 (no information printed). (trace.it=1 not used for compatibility with glmnet.path.)

Details

WARNING: Users should not call cox.fit directly. Higher-level functions in this package call cox.fit as a subroutine. If a warm start object is provided, some of the other arguments in the function may be overridden.
cox.fit solves the elastic net problem for a single, user-specified value of lambda. cox.fit works for Cox regression models, including (start, stop] data and strata. It solves the problem using iteratively reweighted least squares (IRLS). For each IRLS iteration, cox.fit makes a quadratic (Newton) approximation of the log-likelihood, then calls elnet.fit to minimize the resulting approximation.

In terms of standardization: cox.fit does not standardize x and weights. penalty.factor is standardized so that they sum up to nvars.

Value

An object with class "coxnet", "glmnetfit" and "glmnet". The list returned contains more keys than that of a "glmnet" object.

a0 Intercept value, NULL for "cox" family.
beta A nvars x 1 matrix of coefficients, stored in sparse matrix format.
df The number of nonzero coefficients.
dim Dimension of coefficient matrix.
lambda Lambda value used.
dev.ratio The fraction of (null) deviance explained. The deviance calculations incorporate weights if present in the model. The deviance is defined to be 2*(loglike_sat - loglike), where loglike_sat is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence dev.ratio=1-dev/nulldev.
nulldev Null deviance (per observation). This is defined to be 2*(loglike_sat-loglike(Null)). The null model refers to the 0 model.
npasses Total passes over the data.
jerr Error flag, for warnings and errors (largely for internal debugging).
offset A logical variable indicating whether an offset was included in the model.
call The call that produced this object.
nobs Number of observations.
warm_fit If save.fit=TRUE, output of C++ routine, used for warm starts. For internal use only.
family Family used for the model, always "cox".
converged A logical variable: was the algorithm judged to have converged?
boundary A logical variable: is the fitted value on the boundary of the attainable values?
obj_function Objective function value at the solution.
Fit a Cox regression model with elastic net regularization for a path of lambda values.

Description

Fit a Cox regression model via penalized maximum likelihood for a path of lambda values. Can deal with (start, stop] data and strata, as well as sparse design matrices.

Usage

```r
cox.path(
  x,
  y,
  weights = NULL,
  offset = NULL,
  alpha = 1,
  nlambda = 100,
  lambda.min.ratio = ifelse(nobs < nvars, 0.01, 1e-04),
  lambda = NULL,
  standardize = TRUE,
  thresh = 1e-10,
  exclude = NULL,
  penalty.factor = rep(1, nvars),
  lower.limits = -Inf,
  upper.limits = Inf,
  maxit = 1e+05,
  trace.it = 0,
  ...
)
```

Arguments

- `x`: See glmnet help file
- `y`: Survival response variable, must be a `Surv` or `stratifySurv` object.
- `weights`: See glmnet help file
- `offset`: See glmnet help file
- `alpha`: See glmnet help file
- `nlambda`: See glmnet help file
- `lambda.min.ratio`: See glmnet help file
- `lambda`: See glmnet help file
- `standardize`: See glmnet help file
thresh Convergence threshold for coordinate descent. Each inner coordinate-descent loop continues until the maximum change in the objective after any coefficient update is less than thresh times the null deviance. Default value is $1e-10$.

exclude See glmnet help file

penalty.factor See glmnet help file

lower.limits See glmnet help file

upper.limits See glmnet help file

maxit See glmnet help file

trace.it Controls how much information is printed to screen. Default is trace.it=0 (no information printed). If trace.it=1, a progress bar is displayed. If trace.it=2, some information about the fitting procedure is printed to the console as the model is being fitted.

... Other arguments passed from glmnet (not used right now).

Details

Sometimes the sequence is truncated before nlambda values of lambda have been used. This happens when cox.path detects that the decrease in deviance is marginal (i.e. we are near a saturated fit).

Value

An object of class "coxnet" and "glmnet".

a0 Intercept value, NULL for "cox" family.

beta A nvars x length(lambda) matrix of coefficients, stored in sparse matrix format.

df The number of nonzero coefficients for each value of lambda.

dim Dimension of coefficient matrix.

lambda The actual sequence of lambda values used. When alpha=0, the largest lambda reported does not quite give the zero coefficients reported (lambda=inf would in principle). Instead, the largest lambda for alpha=0.001 is used, and the sequence of lambda values is derived from this.

dev.ratio The fraction of (null) deviance explained. The deviance calculations incorporate weights if present in the model. The deviance is defined to be $2*(\text{loglike}\_\text{sat} - \text{loglike})$, where loglike\_sat is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence dev.ratio=1-dev/nulldev.

nulldev Null deviance (per observation). This is defined to be $2*(\text{loglike}\_\text{sat} - \text{loglike}(\text{Null}))$. The null model refers to the 0 model.

npasses Total passes over the data summed over all lambda values.

jerr Error flag, for warnings and errors (largely for internal debugging).

offset A logical variable indicating whether an offset was included in the model.

call The call that produced this object.

nobs Number of observations.
Examples

```r
set.seed(2)
nobs <- 100; nvars <- 15
xvec <- rnorm(nobs * nvars)
xvec[sample.int(nobs * nvars, size = 0.4 * nobs * nvars)] <- 0
x <- matrix(xvec, nrow = nobs)
beta <- rnorm(nvars / 3)
fx <- x[, seq(nvars / 3)] %*% beta / 3
ty <- rexp(nobs, exp(fx))
tcens <- rbinom(n = nobs, prob = 0.3, size = 1)
jsurv <- survival::Surv(ty, tcens)
fit1 <- glmnet:::cox.path(x, jsurv)

# works with sparse x matrix
x_sparse <- Matrix::Matrix(x, sparse = TRUE)
fit2 <- glmnet:::cox.path(x_sparse, jsurv)

# example with (start, stop] data
set.seed(2)
start_time <- runif(100, min = 0, max = 5)
stop_time <- start_time + runif(100, min = 0.1, max = 3)
status <- rbinom(n = nobs, prob = 0.3, size = 1)
jsurv_ss <- survival::Surv(start_time, stop_time, status)
fit3 <- glmnet:::cox.path(x, jsurv_ss)

# example with strata
jsurv_ss2 <- stratifySurv(jsurv_ss, rep(1:2, each = 50))
fit4 <- glmnet:::cox.path(x, jsurv_ss2)
```

**CoxExample**

*Synthetic dataset with right-censored survival response*

**Description**

Randomly generated data for Cox regression example.

**Usage**

```r
data(CoxExample)
```

**Format**

List containing the following elements:

- **x** 1,000 by 30 matrix of numeric values.
- **y** 1,000 by 2 matrix with column names "time" and "status". The first column consists of positive numbers representing time to event, while the second column represents the status indicator (0=right-censored, 1=observed).
Compute gradient for Cox model

Description

Compute the gradient of the log partial likelihood at a particular fit for Cox model.

Usage

```
coxgrad(eta, y, w, std.weights = TRUE, diag.hessian = FALSE)
```

Arguments

- `eta`: Fit vector (usually from glmnet at a particular lambda).
- `y`: Survival response variable, must be a `Surv` or `stratifySurv` object.
- `w`: Observation weights (default is all equal to 1).
- `std.weights`: If TRUE (default), observation weights are standardized to sum to 1.
- `diag.hessian`: If TRUE, compute the diagonal of the Hessian of the log partial likelihood as well. Default is FALSE.

Details

Compute a gradient vector at the fitted vector for the log partial likelihood. This is like a residual vector, and useful for manual screening of predictors for glmnet in applications where \( p \) is very large (as in GWAS). Uses the Breslow approach to ties.

This function is essentially a wrapper: it checks whether the response provided is right-censored or \([\text{start}, \text{stop}]\) survival data, and calls the appropriate internal routine.

Value

A single gradient vector the same length as `eta`. If `diag.hessian`=TRUE, the diagonal of the Hessian is included as an attribute "diag_hessian".

See Also

`coxnet.deviance`

Examples

```
set.seed(1)
eta <- rnorm(10)
time <- runif(10, min = 1, max = 10)
d <- ifelse(rnorm(10) > 0, 1, 0)
y <- survival::Surv(time, d)
coxgrad(eta, y)
```

# return diagonal of Hessian as well
coxnet.deviance

Compute deviance for Cox model

Description

Compute the deviance (-2 log partial likelihood) for Cox model.

Usage

```r
coxnet.deviance(  
  pred = NULL,  
  y,  
  x = NULL,  
  offset = NULL,  
  weights = NULL,  
  std.weights = TRUE,  
  beta = NULL  
)
```

Arguments

- **pred**: Fit vector or matrix (usually from glmnet at a particular lambda or a sequence of lambdas).
- **y**: Survival response variable, must be a Surv or stratifySurv object.
- **x**: Optional x matrix, to be supplied if pred = NULL.
- **offset**: Optional offset vector.
- **weights**: Observation weights (default is all equal to 1).
- **std.weights**: If TRUE (default), observation weights are standardized to sum to 1.
- **beta**: Optional coefficient vector/matrix, to be supplied if pred = NULL.
Details

Computes the deviance for a single set of predictions, or for a matrix of predictions. The user can either supply the predictions directly through the pred option, or by supplying the x matrix and beta coefficients. Uses the Breslow approach to ties.

The function first checks if pred is passed: if so, it is used as the predictions. If pred is not passed but x and beta are passed, then these values are used to compute the predictions. If neither x nor beta are passed, then the predictions are all taken to be 0.

coxnet.deviance() is a wrapper: it calls the appropriate internal routine based on whether the response is right-censored data or (start, stop] survival data.

Value

A vector of deviances, one for each column of predictions.

See Also

coxgrad

Examples

```r
set.seed(1)
eta <- rnorm(10)
time <- runif(10, min = 1, max = 10)
d <- ifelse(rnorm(10) > 0, 1, 0)
y <- survival::Surv(time, d)
coxnet.deviance(pred = eta, y = y)

# if pred not provided, it is set to zero vector
coxnet.deviance(y = y)

# example with x and beta
x <- matrix(rnorm(10 * 3), nrow = 10)
beta <- matrix(1:3, ncol = 1)
coxnet.deviance(y = y, x = x, beta = beta)

# example with (start, stop] data
y2 <- survival::Surv(time, time + runif(10), d)
coxnet.deviance(pred = eta, y = y2)

# example with strata
y2 <- stratifySurv(y, rep(1:2, length.out = 10))
coxnet.deviance(pred = eta, y = y2)
```
cox_obj_function

Elastic net objective function value for Cox regression model

Description

Returns the elastic net objective function value for Cox regression model.

Usage

```r
cox_obj_function(y, pred, weights, lambda, alpha, coefficients, vp)
```

Arguments

- `y`: Survival response variable, must be a `Surv` or `stratifySurv` object.
- `pred`: Model's predictions for `y`.
- `weights`: Observation weights.
- `lambda`: A single value for the lambda hyperparameter.
- `alpha`: The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$.
- `coefficients`: The model's coefficients.
- `vp`: Penalty factors for each of the coefficients.

---

cv.glmnet

Cross-validation for glmnet

Description

Does k-fold cross-validation for glmnet, produces a plot, and returns a value for lambda (and gamma if `relax=TRUE`)

Usage

```r
cv.glmnet(
  x,
  y,
  weights = NULL,
  offset = NULL,
  lambda = NULL,
  type.measure = c("default", "mse", "deviance", "class", "auc", "mae", "C"),
  nfolds = 10,
  foldid = NULL,
  alignment = c("lambda", "fraction"),
  grouped = TRUE,
  keep = FALSE,
)```
parallel = FALSE,
gamma = c(0, 0.25, 0.5, 0.75, 1),
relax = FALSE,
trace.it = 0,
...
)

Arguments

x x matrix as in glmnet.

y response y as in glmnet.

weights Observation weights; defaults to 1 per observation

offset Offset vector (matrix) as in glmnet

lambda Optional user-supplied lambda sequence; default is NULL, and glmnet chooses its own sequence. Note that this is done for the full model (master sequence), and separately for each fold. The fits are then alligned using the master sequence (see the allignment argument for additional details). Adapting lambda for each fold leads to better convergence. When lambda is supplied, the same sequence is used everywhere, but in some GLMs can lead to convergence issues.

type.measure loss to use for cross-validation. Currently five options, not all available for all models. The default is type.measure="deviance", which uses squared-error for gaussian models (a.k.a type.measure="mse" there), deviance for logistic and poisson regression, and partial-likelihood for the Cox model. type.measure="class" applies to binomial and multinomial logistic regression only, and gives misclassification error. type.measure="auc" is for two-class logistic regression only, and gives area under the ROC curve. type.measure="mse" or type.measure="mae" (mean absolute error) can be used by all models except the "cox"; they measure the deviation from the fitted mean to the response. type.measure="C" is Harrel's concordance measure, only available for cox models.

nfolds number of folds - default is 10. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is nfolds=3

foldid an optional vector of values between 1 and nfolds identifying what fold each observation is in. If supplied, nfolds can be missing.

alignment This is an experimental argument, designed to fix the problems users were having with CV, with possible values "lambda" (the default) else "fraction". With "lambda" the lambda values from the master fit (on all the data) are used to line up the predictions from each of the folds. In some cases this can give strange values, since the effective lambda values in each fold could be quite different. With "fraction" we line up the predictions in each fold according to the fraction of progress along the regularization. If in the call a lambda argument is also provided, alignment="fraction" is ignored (with a warning).

grouped This is an experimental argument, with default TRUE, and can be ignored by most users. For all models except the "cox", this refers to computing nfolds separate statistics, and then using their mean and estimated standard error to describe the CV curve. If grouped=FALSE, an error matrix is built up at the observation level
cv.glmnet

from the predictions from the nfolds fits, and then summarized (does not apply to type.measure="auc"). For the "cox" family, grouped=TRUE obtains the CV partial likelihood for the Kth fold by subtraction; by subtracting the log partial likelihood evaluated on the full dataset from that evaluated on the (K-1)/K dataset. This makes more efficient use of risk sets. With grouped=FALSE the log partial likelihood is computed only on the Kth fold.

keep

If keep=TRUE, a prevalidated array is returned containing fitted values for each observation and each value of lambda. This means these fits are computed with this observation and the rest of its fold omitted. The foldid vector is also returned. Default is keep=FALSE. If relax=TRUE, then a list of such arrays is returned, one for each value of 'gamma'. Note: if the value 'gamma=1' is omitted, this case is included in the list since it corresponds to the original 'glmnet' fit.

parallel

If TRUE, use parallel foreach to fit each fold. Must register parallel before hand, such as doMC or others. See the example below.

gamma

The values of the parameter for mixing the relaxed fit with the regularized fit, between 0 and 1; default is gamma = c(0, 0.25, 0.5, 0.75, 1)

relax

If TRUE, then CV is done with respect to the mixing parameter gamma as well as lambda. Default is relax=FALSE.

trace.it

If trace.it=1, then progress bars are displayed; useful for big models that take a long time to fit. Limited tracing if parallel=TRUE.

... Other arguments that can be passed to glmnet.

Details

The function runs glmnet nfolds+1 times; the first to get the lambda sequence, and then the remainder to compute the fit with each of the folds omitted. The error is accumulated, and the average error and standard deviation over the folds is computed. Note that cv.glmnet does NOT search for values for alpha. A specific value should be supplied, else alpha=1 is assumed by default. If users would like to cross-validate alpha as well, they should call cv.glmnet with a pre-computed vector foldid, and then use this same fold vector in separate calls to cv.glmnet with different values of alpha. Note also that the results of cv.glmnet are random, since the folds are selected at random. Users can reduce this randomness by running cv.glmnet many times, and averaging the error curves.

If relax=TRUE then the values of gamma are used to mix the fits. If \( \eta \) is the fit for lasso/elastic net, and \( \eta_R \) is the relaxed fit (with unpenalized coefficients), then a relaxed fit mixed by \( \gamma \) is

\[
\eta(\gamma) = (1 - \gamma)\eta_R + \gamma \eta.
\]

There is practically no extra cost for having a lot of values for gamma. However, 5 seems sufficient for most purposes. CV then selects both gamma and lambda.

Value

an object of class "cv.glmnet" is returned, which is a list with the ingredients of the cross-validation fit. If the object was created with relax=TRUE then this class has a prefix class of "cv.relaxed".
lambda the values of lambda used in the fits.
cvm The mean cross-validated error - a vector of length length(lambda).
cvsd estimate of standard error of cvm.
cvup upper curve = cvm+cvsd.
cvlo lower curve = cvm-cvsd.
nzero number of non-zero coefficients at each lambda.
name a text string indicating type of measure (for plotting purposes).
glmnet.fit a fitted glmnet object for the full data.
lambda.min value of lambda that gives minimum cvm.
lambda.1se largest value of lambda such that error is within 1 standard error of the minimum.
fit.preval if keep=TRUE, this is the array of prevalidated fits. Some entries can be NA, if that and subsequent values of lambda are not reached for that fold
foldid if keep=TRUE, the fold assignments used
index a one column matrix with the indices of lambda.min and lambda.1se in the sequence of coefficients, fits etc.
relaxed if relax=TRUE, this additional item has the CV info for each of the mixed fits. In particular it also selects lambda, gamma pairs corresponding to the 1se rule, as well as the minimum error. It also has a component index, a two-column matrix which contains the lambda and gamma indices corresponding to the "min" and "1se" solutions.

Author(s)
Jerome Friedman, Trevor Hastie and Rob Tibshirani
Noah Simon helped develop the 'coxnet' function.
Jeffrey Wong and B. Narasimhan helped with the parallel option
Maintainer: Trevor Hastie <hastie@stanford.edu>

References

See Also
glmnet and plot, predict, and coef methods for "cv.glmnet" and "cv.relaxed" objects.
Examples

```r
cv.glmnet

set.seed(1010)
n = 1000
p = 100
ncz = trunc(p/10)
x = matrix(rnorm(n * p), n, p)
beta = rnorm(ncz)
fx = x[, seq(ncz)] %*% beta
eps = rnorm(n) * 5
y = drop(fx + eps)
px = exp(fx)
px = px/(1 + px)
ly = rbinom(n = length(px), prob = px, size = 1)
set.seed(1011)
cvob1 = cv.glmnet(x, y)
plot(cvob1)
coef(cvob1)
predict(cvob1, newx = x[1:5, ], s = "lambda.min")
title("Gaussian Family", line = 2.5)
set.seed(1011)
cvob1a = cv.glmnet(x, y, type.measure = "mae")
plot(cvob1a)
title("Gaussian Family", line = 2.5)
set.seed(1011)
par(mfrow = c(2, 2), mar = c(4.5, 4.5, 4, 1))
cvob2 = cv.glmnet(x, ly, family = "binomial")
plot(cvob2)
title("Binomial Family", line = 2.5)
frame()
set.seed(1011)
cvob3 = cv.glmnet(x, ly, family = "binomial", type.measure = "class")
plot(cvob3)
title("Binomial Family", line = 2.5)
## Not run:
cvob1r = cv.glmnet(x, y, relax = TRUE)
plot(cvob1r)
predict(cvob1r, newx = x[, 1:5])
set.seed(1011)
cvob3a = cv.glmnet(x, ly, family = "binomial", type.measure = "auc")
plot(cvob3a)
title("Binomial Family", line = 2.5)
set.seed(1011)
mu = exp(fx/10)
y = rpois(n, mu)
cvob4 = cv.glmnet(x, y, family = "poisson")
plot(cvob4)
title("Poisson Family", line = 2.5)

# Multinomial
n = 500
p = 30
```

nzc = trunc(p/10)
x = matrix(rnorm(n * p), n, p)
beta3 = matrix(rnorm(30), 10, 3)
beta3 = rbind(beta3, matrix(0, p - 10, 3))
f3 = x %*% beta3
p3 = exp(f3)
p3 = p3/apply(p3, 1, sum)
g3 = glmnet:::rmult(p3)
set.seed(10101)
cvfit = cv.glmnet(x, g3, family = "multinomial")
plot(cvfit)
title("Multinomial Family", line = 2.5)
# Cox
beta = rnorm(nzc)
fx = x[, seq(nzc)] %*% beta/3
hx = exp(fx)
ty = rexp(n, hx)
tcens = rbinom(n = n, prob = 0.3, size = 1)  # censoring indicator
y = cbind(time = ty, status = 1 - tcens)  # y=Surv(ty,1-tcens) with library(survival)
foldid = sample(rep(seq(10), length = n))
fit1_cv = cv.glmnet(x, y, family = "cox", foldid = foldid)
plot(fit1_cv)
title("Cox Family", line = 2.5)
# Parallel
require(doMC)
registerDoMC(cores = 4)
x = matrix(rnorm(1e+05 * 100), 1e+05, 100)
y = rnorm(1e+05)
system.time(cv.glmnet(x, y))
system.time(cv.glmnet(x, y, parallel = TRUE))

## End(Not run)

deviance.glmnet

Extract the deviance from a glmnet object

Description

Compute the deviance sequence from the glmnet object

Usage

## S3 method for class 'glmnet'
deviance(object, ...)

Arguments

object fitted glmnet object
...
additional print arguments
Details

A glmnet object has components dev.ratio and nulldev. The former is the fraction of (null) deviance explained. The deviance calculations incorporate weights if present in the model. The deviance is defined to be 2*(loglike_sat - loglike), where loglike_sat is the log-likelihood for the saturated model (a model with a free parameter per observation). Null deviance is defined to be 2*(loglike_sat -loglike(Null)); The NULL model refers to the intercept model, except for the Cox, where it is the 0 model. Hence dev.ratio=1-deviance/nulldev, and this deviance method returns (1-dev.ratio)*nulldev.

Value

(1-dev.ratio)*nulldev

Author(s)

Jerome Friedman, Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

References


See Also

glmnet, predict, print, and coef methods.

Examples

```r
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
fit1 = glmnet(x, y)
deviance(fit1)
```

---

## dev_function

**Elastic net deviance value**

### Description

Returns the elastic net deviance value.

### Usage

```
dev_function(y, mu, weights, family)
```
elnet.fit

Solve weighted least squares (WLS) problem for a single lambda value

Arguments

- **y**: Quantitative response variable.
- **mu**: Model's predictions for y.
- **weights**: Observation weights.
- **family**: A description of the error distribution and link function to be used in the model. This is the result of a call to a family function.

Description

Solves the weighted least squares (WLS) problem for a single lambda value. Internal function that users should not call directly.

Usage

```r
elnet.fit(
  x,
  y,
  weights,
  lambda,
  alpha = 1,
  intercept = TRUE,
  thresh = 1e-07,
  maxit = 1e+05,
  penalty.factor = rep(1, nvars),
  exclude = c(),
  lower.limits = -Inf,
  upper.limits = Inf,
  warm = NULL,
  from.glmnet.fit = FALSE,
  save.fit = FALSE
)
```

Arguments

- **x**: Input matrix, of dimension nobs x nvars; each row is an observation vector. If it is a sparse matrix, it is assumed to be unstandardized. It should have attributes `xm` and `xs`, where `xm(j)` and `xs(j)` are the centering and scaling factors for variable j respectively. If it is not a sparse matrix, it is assumed that any standardization needed has already been done.
- **y**: Quantitative response variable.
- **weights**: Observation weights. `elnet.fit` does NOT standardize these weights.
- **lambda**: A single value for the lambda hyperparameter.
alpha

The elasticnet mixing parameter, with 0 ≤ α ≤ 1. The penalty is defined as

\[(1 - \alpha)/2 ||\beta||^2 + \alpha ||\beta||_1.\]

alpha=1 is the lasso penalty, and alpha=0 the ridge penalty.

intercept

Should intercept be fitted (default=TRUE) or set to zero (FALSE)?

thresh

Convergence threshold for coordinate descent. Each inner coordinate-descent loop continues until the maximum change in the objective after any coefficient update is less than thresh times the null deviance. Default value is 1e-7.

maxit

Maximum number of passes over the data; default is 10^5. (If a warm start object is provided, the number of passes the warm start object performed is included.)

penalty.factor

Separate penalty factors can be applied to each coefficient. This is a number that multiplies lambda to allow differential shrinkage. Can be 0 for some variables, which implies no shrinkage, and that variable is always included in the model. Default is 1 for all variables (and implicitly infinity for variables listed in exclude). Note: the penalty factors are internally rescaled to sum to nvars.

exclude

Indices of variables to be excluded from the model. Default is none. Equivalent to an infinite penalty factor.

lower.limits

Vector of lower limits for each coefficient; default -Inf. Each of these must be non-positive. Can be presented as a single value (which will then be replicated), else a vector of length nvars.

upper.limits

Vector of upper limits for each coefficient; default Inf. See lower.limits.

warm

Either a glmnetfit object or a list (with names beta and a0 containing coefficients and intercept respectively) which can be used as a warm start. Default is NULL, indicating no warm start. For internal use only.

from.glmnet.fit

Was elnet.fit() called from glmnet.fit()? Default is FALSE. This has implications for computation of the penalty factors.

save.fit

Return the warm start object? Default is FALSE.

details

WARNING: Users should not call elnet.fit directly. Higher-level functions in this package call elnet.fit as a subroutine. If a warm start object is provided, some of the other arguments in the function may be overriden.

elnet.fit is essentially a wrapper around a C++ subroutine which minimizes

\[
1/2 \sum w_i(y_i - X_i^T \beta)^2 + \sum \lambda \gamma_j [(1 - \alpha)/2 \beta^2 + \alpha |\beta|],
\]

over \(\beta\), where \(\gamma_j\) is the relative penalty factor on the jth variable. If intercept = TRUE, then the term in the first sum is \(w_i(y_i - \beta_0 - X_i^T \beta)^2\), and we are minimizing over both \(\beta_0\) and \(\beta\).

None of the inputs are standardized except for penalty.factor, which is standardized so that they sum up to nvars.
Value

An object with class "glmnetfit" and "glmnet". The list returned has the same keys as that of a glmnet object, except that it might have an additional warm_fit key.

- \(a0\) Intercept value.
- \(\text{beta}\) A nvars x 1 matrix of coefficients, stored in sparse matrix format.
- \(\text{df}\) The number of nonzero coefficients.
- \(\text{dim}\) Dimension of coefficient matrix.
- \(\text{lambda}\) Lambda value used.
- \(\text{dev.ratio}\) The fraction of (null) deviance explained. The deviance calculations incorporate weights if present in the model. The deviance is defined to be \(2*(\text{loglike_sat} - \text{loglike})\), where \(\text{loglike_sat}\) is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence \(\text{dev.ratio}=1-\text{dev/nulldev}\).
- \(\text{nulldev}\) Null deviance (per observation). This is defined to be \(2*(\text{loglike_sat} - \text{loglike(Null)})\). The null model refers to the intercept model.
- \(\text{npasses}\) Total passes over the data.
- \(\text{jerr}\) Error flag, for warnings and errors (largely for internal debugging).
- \(\text{offset}\) Always FALSE, since offsets do not appear in the WLS problem. Included for compatibility with glmnet output.
- \(\text{call}\) The call that produced this object.
- \(\text{nobs}\) Number of observations.
- \(\text{warm_fit}\) If \(\text{save.fit}=\text{TRUE}\), output of C++ routine, used for warm starts. For internal use only.

Description

Helps to find ties in death times of data.

Usage

\[
\text{fid}(x, \text{index})
\]

Arguments

- \(x\) Sorted vector of death times.
- \(\text{index}\) Vector of indices for the death times.
get_cox_lambda_max

Value

A list with two arguments.

index_first A vector of indices for the first observation at each death time as they appear in the sorted list.

index_ties If there are no ties at all, this is NULL. If not, this is a list with length equal to the number of unique times with ties. For each time with ties, index_ties gives the indices of the observations with a death at that time.

Examples

# Example with no ties
glmnet:::fid(c(1, 4, 5, 6), 1:5)

# Example with ties
glmnet:::fid(c(1, 1, 1, 2, 3, 3, 4, 4, 4), 1:9)

get_cox_lambda_max

Get lambda max for Cox regression model

Description

Return the lambda max value for Cox regression model, used for computing initial lambda values. For internal use only.

Usage

get_cox_lambda_max(
  x,
  y,
  alpha,
  weights = rep(1, nrow(x)),
  offset = rep(0, nrow(x)),
  exclude = c(),
  vp = rep(1, ncol(x))
)

Arguments

x Input matrix, of dimension nobs x nvars; each row is an observation vector. If it is a sparse matrix, it is assumed to be unstandardized. It should have attributes xm and xs, where xm(j) and xs(j) are the centering and scaling factors for variable j respectively. If it is not a sparse matrix, it is assumed to be standardized.

y Survival response variable, must be a Surv or stratifySurv object.

alpha The elasticnet mixing parameter, with 0 ≤ α ≤ 1.

weights Observation weights.
get_start

offset      Offset for the model. Default is a zero vector of length nrow(y).
exclude    Indices of variables to be excluded from the model.
vp          Separate penalty factors can be applied to each coefficient.

Details

This function is called by cox.path for the value of lambda max.

When x is not sparse, it is expected to already be centered and scaled. When x is sparse, the function
will get its attributes xm and xs for its centering and scaling factors. The value of lambda_max
changes depending on whether x is centered and scaled or not, so we need xm and xs to get the
correct value.

get_etas

Helper function to get etas (linear predictions)

Description

Given x, coefficients and intercept, return linear predictions. Wrapper that works with both regular
and sparse x. Only works for single set of coefficients and intercept.

Usage

get_etas(x, beta, a0)

Arguments

x          Input matrix, of dimension nobs x nvars; each row is an observation vector. If it
           is a sparse matrix, it is assumed to be unstandardized. It should have attributes xm
           and xs, where xm(j) and xs(j) are the centering and scaling factors for variable
           j respectively. If it is not a sparse matrix, it is assumed to be standardized.
beta       Feature coefficients.
a0          Intercept.

get_start

Get null deviance, starting mu and lambda max

Description

Return the null deviance, starting mu and lambda max values for initialization. For internal use
only.
Usage

```r
get_start(
  x,
  y,
  weights,
  family,
  intercept,
  is.offset,
  offset,
  exclude,
  vp,
  alpha
)
```

Arguments

- **x**: Input matrix, of dimension `nobs x nvars`; each row is an observation vector. If it is a sparse matrix, it is assumed to be unstandardized. It should have attributes `xm` and `xs`, where `xm(j)` and `xs(j)` are the centering and scaling factors for variable `j` respectively. If it is not a sparse matrix, it is assumed to be standardized.

- **y**: Quantitative response variable.

- **weights**: Observation weights.

- **family**: A description of the error distribution and link function to be used in the model. This is the result of a call to a family function. (See `family` for details on family functions.)

- **intercept**: Does the model we are fitting have an intercept term or not?

- **is.offset**: Is the model being fit with an offset or not?

- **offset**: Offset for the model. If `is.offset=FALSE`, this should be a zero vector of the same length as `y`.

- **exclude**: Indices of variables to be excluded from the model.

- **vp**: Separate penalty factors can be applied to each coefficient.

- **alpha**: The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$.

Details

This function is called by `glmnet.path` for null deviance, starting `mu` and `lambda` max values. It is also called by `glmnet.fit` when used without warmstart, but they only use the null deviance and starting `mu` values.

When `x` is not sparse, it is expected to already be centered and scaled. When `x` is sparse, the function will get its attributes `xm` and `xs` for its centering and scaling factors.

Note that whether `x` is centered & scaled or not, the values of `mu` and `nulldev` don’t change. However, the value of `lambda_max` does change, and we need `xm` and `xs` to get the correct value.
glmnet

fit a GLM with lasso or elasticnet regularization

Description

Fit a generalized linear model via penalized maximum likelihood. The regularization path is computed for the lasso or elasticnet penalty at a grid of values for the regularization parameter lambda. Can deal with all shapes of data, including very large sparse data matrices. Fits linear, logistic and multinomial, poisson, and Cox regression models.

Usage

glmnet(
  x,
  y,
  family = c("gaussian", "binomial", "poisson", "multinomial", "cox", "mgaussian"),
  weights = NULL,
  offset = NULL,
  alpha = 1,
  nlambda = 100,
  lambda.min.ratio = ifelse(nobs < nvars, 0.01, 1e-04),
  lambda = NULL,
  standardize = TRUE,
  intercept = TRUE,
  thresh = 1e-07,
  dfmax = nvars + 1,
  pmax = min(dfmax * 2 + 20, nvars),
  exclude = NULL,
  penalty.factor = rep(1, nvars),
  lower.limits = -Inf,
  upper.limits = Inf,
  maxit = 1e+05,
  type.gaussian = ifelse(nvars < 500, "covariance", "naive"),
  type.logistic = c("Newton", "modified.Newton"),
  standardize.response = FALSE,
  type.multinomial = c("ungrouped", "grouped"),
  relax = FALSE,
  trace.it = 0,
  ...
)

relax.glmnet(fit, x, ..., maxp = n - 3, path = FALSE, check.args = TRUE)

Arguments

x input matrix, of dimension nobs x nvars; each row is an observation vector. Can be in sparse matrix format (inherit from class "sparseMatrix" as in package
`glmnet` 35

Matrix. Requirement: `nvars > 1`; in other words, `x` should have 2 or more columns.

`y` response variable. Quantitative for `family = "gaussian"`, or `family = "poisson"` (non-negative counts). For `family = "binomial"` should be either a factor with two levels, or a two-column matrix of counts or proportions (the second column is treated as the target class; for a factor, the last level in alphabetical order is the target class). For `family = "multinomial"`, can be a `nc >= 2` level factor, or a matrix with `nc` columns of counts or proportions. For either "binomial" or "multinomial", if `y` is presented as a vector, it will be coerced into a factor. For `family = "cox"`, preferably a `Surv` object from the survival package: see Details section for more information. For `family = "mgaussian"`, `y` is a matrix of quantitative responses.

`family` Either a character string representing one of the built-in families, or else a `glm()` family object. For more information, see Details section below or the documentation for response type (above).

`weights` observation weights. Can be total counts if responses are proportion matrices. Default is 1 for each observation.

`offset` A vector of length `nobs` that is included in the linear predictor (a `nobs x nc` matrix for the "multinomial" family). Useful for the "poisson" family (e.g. log of exposure time), or for refining a model by starting at a current fit. Default is `NULL`. If supplied, then values must also be supplied to the `predict` function.

`alpha` The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$. The penalty is defined as

$$
(1 - \alpha)/2||\beta||^2_2 + \alpha||\beta||_1.
$$

`alpha = 1` is the lasso penalty, and `alpha = 0` the ridge penalty.

`nlambda` The number of lambda values - default is 100.

`lambda.min.ratio` Smallest value for lambda, as a fraction of `lambda.max`, the (data derived) entry value (i.e. the smallest value for which all coefficients are zero). The default depends on the sample size `nobs` relative to the number of variables `nvars`. If `nobs > nvars`, the default is 0.0001, close to zero. If `nobs < nvars`, the default is 0.01. A very small value of `lambda.min.ratio` will lead to a saturated fit in the `nobs < nvars` case. This is undefined for "binomial" and "multinomial" models, and `glmnet` will exit gracefully when the percentage deviance explained is almost 1.

`lambda` A user supplied lambda sequence. Typical usage is to have the program compute its own lambda sequence based on `nlambda` and `lambda.min.ratio`. Supplying a value of `lambda` overrides this. WARNING: use with care. Avoid supplying a single value for `lambda` (for predictions after CV use `predict()` instead). Supply instead a decreasing sequence of lambda values. `glmnet` relies on its warms starts for speed, and its often faster to fit a whole path than compute a single fit.

`standardize` Logical flag for x variable standardization, prior to fitting the model sequence. The coefficients are always returned on the original scale. Default is `standardize = TRUE`. If variables are in the same units already, you might not wish to standardize. See details below for `y` standardization with `family = "gaussian"`. 


intercept Should intercept(s) be fitted (default=TRUE) or set to zero (FALSE)

thresh Convergence threshold for coordinate descent. Each inner coordinate-descent
loop continues until the maximum change in the objective after any coefficient
update is less than thresh times the null deviance. Defaults value is 1E-7.

dfmax Limit the maximum number of variables in the model. Useful for very large
nvars, if a partial path is desired.

pmax Limit the maximum number of variables ever to be nonzero

exclude Indices of variables to be excluded from the model. Default is none. Equivalent
to an infinite penalty factor for the variables excluded (next item). Users can
supply instead an exclude function that generates the list of indices. This function
is most generally defined as function(x, y, weights, ...), and is called
inside glmnet to generate the indices for excluded variables. The ... argument
is required, the others are optional. This is useful for filtering wide data, and
works correctly with cv.glmnet. See the vignette 'Introduction' for examples.

penalty.factor Separate penalty factors can be applied to each coefficient. This is a number
that multiplies lambda to allow differential shrinkage. Can be 0 for some vari-
ables, which implies no shrinkage, and that variable is always included in the
model. Default is 1 for all variables (and implicitly infinity for variables listed
in exclude). Note: the penalty factors are internally rescaled to sum to nvars,
and the lambda sequence will reflect this change.

lower.limits Vector of lower limits for each coefficient; default -Inf. Each of these must be
non-positive. Can be presented as a single value (which will then be replicated),
else a vector of length nvars

upper.limits Vector of upper limits for each coefficient; default Inf. See lower.limits

maxit Maximum number of passes over the data for all lambda values; default is 10^5.

type.gaussian Two algorithm types are supported for (only) family="gaussian". The de-
default when nvar<500 is type.gaussian="covariance", and saves all inner-
products ever computed. This can be much faster than type.gaussian="naive",
which loops through nobs every time an inner-product is computed. The latter
can be far more efficient for nvar >> nobs situations, or when nvar > 500.

type.logistic If "Newton" then the exact hessian is used (default), while "modified.Newton"
uses an upper-bound on the hessian, and can be faster.

standardize.response This is for the family="mgaussian" family, and allows the user to standardize
the response variables

type.multinomial If "grouped" then a grouped lasso penalty is used on the multinomial coeffi-
cients for a variable. This ensures they are all in our out together. The default is
"ungrouped"

relax If TRUE then for each active set in the path of solutions, the model is refit without
any regularization. See details for more information. This argument is new,
and users may experience convergence issues with small datasets, especially
with non-gaussian families. Limiting the value of 'maxp' can alleviate these
issues in some cases.
trace.it  If trace.it=1, then a progress bar is displayed; useful for big models that take a long time to fit.

... Additional argument used in relax.glmnet. These include some of the original arguments to 'glmnet', and each must be named if used.

fit  For relax.glmnet a fitted 'glmnet' object

maxp  a limit on how many relaxed coefficients are allowed. Default is 'n-3', where 'n' is the sample size. This may not be sufficient for non-gaussian families, in which case users should supply a smaller value. This argument can be supplied directly to 'glmnet'.

path  Since glmnet does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with relaxed fits. With path=TRUE, each relaxed fit on a particular set of variables is computed pathwise using the original sequence of lambda values (with a zero attached to the end). Not needed for Gaussian models, and should not be used unless needed, since will lead to longer compute times. Default is path=FALSE. appropriate subset of variables

check.args  Should relax.glmnet make sure that all the data dependent arguments used in creating 'fit' have been resupplied. Default is 'TRUE'.

Details

The sequence of models implied by lambda is fit by coordinate descent. For family="gaussian" this is the lasso sequence if alpha=1, else it is the elasticnet sequence.

The objective function for "gaussian" is

$$\frac{1}{2} \text{RSS/}nobs + \lambda \text{* penalty},$$

and for the other models it is

$$-\text{loglik/}nobs + \lambda \text{* penalty}.$$  

Note also that for "gaussian", glmnet standardizes y to have unit variance (using 1/n rather than 1/(n-1) formula) before computing its lambda sequence (and then unstandardizes the resulting coefficients); if you wish to reproduce/compare results with other software, best to supply a standardized y. The coefficients for any predictor variables with zero variance are set to zero for all values of lambda.

Details on family option:

From version 4.0 onwards, glmnet supports both the original built-in families, as well as any family object as used by stats:glm(). This opens the door to a wide variety of additional models. For example family=binomial(link=cloglog) or family=negative.binomial(theta=1.5) (from the MASS library). Note that the code runs faster for the built-in families. The built in families are specified via a character string. For all families, the object produced is a lasso or elasticnet regularization path for fitting the generalized linear regression paths, by maximizing the appropriate penalized log-likelihood (partial likelihood for the "cox" model). Sometimes the sequence is truncated before nlambda values of lambda have been used, because of instabilities in the inverse link functions near a saturated fit. glmnet(...,family="binomial") fits a traditional logistic regression model for the log-odds. glmnet(...,family="multinomial") fits a symmetric multinomial model, where each class is represented by a linear model (on the
log-scale). The penalties take care of redundancies. A two-class "multinomial" model will produce the same fit as the corresponding "binomial" model, except the pair of coefficient matrices will be equal in magnitude and opposite in sign, and half the "binomial" values. Two useful additional families are the family="mgaussian" family and the type.multinomial="grouped" option for multinomial fitting. The former allows a multi-response gaussian model to be fit, using a "group -lasso" penalty on the coefficients for each variable. Tying the responses together like this is called "multi-task" learning in some domains. The grouped multinomial allows the same penalty for the family="multinomial" model, which is also multi-responsed. For both of these the penalty on the coefficient vector for variable j is

$$(1 - \alpha)/2||\beta_j||^2 + \alpha||\beta_j||_2.$$  

When $\alpha=1$ this is a group-lasso penalty, and otherwise it mixes with quadratic just like elasticnet. A small detail in the Cox model: if death times are tied with censored times, we assume the censored times occurred just before the death times in computing the Breslow approximation; if users prefer the usual convention of after, they can add a small number to all censoring times to achieve this effect.

**Details on response for family="cox":**

For Cox models, the response should preferably be a Surv object, created by the Surv() function in survival package. For right-censored data, this object should have type "right", and for (start, stop] data, it should have type "counting". To fit stratified Cox models, strata should be added to the response via the stratifySurv() function before passing the response to glmnet(). (For backward compatibility, right-censored data can also be passed as a two-column matrix with columns named 'time' and 'status'. The latter is a binary variable, with '1' indicating death, and '0' indicating right censored.)

**Details on relax option:**

If relax=TRUE a duplicate sequence of models is produced, where each active set in the elasticnet path is refit without regularization. The result of this is a matching "glmnet" object which is stored on the original object in a component named "relaxed", and is part of the glmnet output. Generally users will not call relax.glmnet directly, unless the original 'glmnet' object took a long time to fit. But if they do, they must supply the fit, and all the original arguments used to create that fit. They can limit the length of the relaxed path via 'maxp'.

**Value**

An object with S3 class "glmnet","*". where "*" is "elnet", "lognet", "multnet", "fishnet" (poisson), "coxnet" or "mrelnet" for the various types of models. If the model was created with relax=TRUE then this class has a prefix class of "relaxed".

call

the call that produced this object

a0

Intercept sequence of length length(lambda)

beta

For "elnet", "lognet", "fishnet" and "coxnet" models, a nvars x length(lambda) matrix of coefficients, stored in sparse column format ("CsparseMatrix"). For "multnet" and "mgaussian", a list of nc such matrices, one for each class.

lambda

The actual sequence of lambda values used. When alpha=0, the largest lambda reported does not quite give the zero coefficients reported (lambda=inf would in principle). Instead, the largest lambda for alpha=0.001 is used, and the sequence of lambda values is derived from this.
dev.ratio  The fraction of (null) deviance explained (for "elnet", this is the R-square). The deviance calculations incorporate weights if present in the model. The deviance is defined to be 2*(loglike_sat - loglike), where loglike_sat is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence dev.ratio=1-dev/nulldev.

nulldev  Null deviance (per observation). This is defined to be 2*(loglike_sat - loglike(Null)); The NULL model refers to the intercept model, except for the Cox, where it is the 0 model.

df  The number of nonzero coefficients for each value of lambda. For "multnet", this is the number of variables with a nonzero coefficient for any class.

dfmat  For "multnet" and "mrelnet" only. A matrix consisting of the number of nonzero coefficients per class

dim  dimension of coefficient matrix (ices)

nobs  number of observations

npasses  total passes over the data summed over all lambda values

offset  a logical variable indicating whether an offset was included in the model

jerr  error flag, for warnings and errors (largely for internal debugging).

relaxed  If relax=TRUE, this additional item is another glmnet object with different values for beta and dev.ratio

Author(s)
Jerome Friedman, Trevor Hastie, Balasubramanian Narasimhan, Noah Simon, Kenneth Tay and Rob Tibshirani
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References
Glmnet webpage with four vignettes: https://glmnet.stanford.edu.

See Also
print, predict, coef and plot methods, and the cv.glmnet function.
Examples

# Gaussian
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
fit1 = glmnet(x, y)
print(fit1)
coef(fit1, s = 0.01)  # extract coefficients at a single value of lambda
predict(fit1, newx = x[1:10, ], s = c(0.01, 0.005))  # make predictions

# Relaxed
fit1r = glmnet(x, y, relax = TRUE)  # can be used with any model

# multivariate gaussian
y = matrix(rnorm(100 * 3), 100, 3)
fit1m = glmnet(x, y, family = "mgaussian")
plot(fit1m, type.coef = "2norm")

# binomial
g2 = sample(c(0,1), 100, replace = TRUE)
fit2 = glmnet(x, g2, family = "binomial")
fit2n = glmnet(x, g2, family = binomial(link=cloglog))
fit2r = glmnet(x,g2, family = "binomial", relax=TRUE)
fit2rp = glmnet(x,g2, family = "binomial", relax=TRUE, path=TRUE)

# multinomial
g4 = sample(1:4, 100, replace = TRUE)
fit3 = glmnet(x, g4, family = "multinomial")
fit3a = glmnet(x, g4, family = "multinomial", type.multinomial = "grouped")

# poisson
N = 500
p = 20
nz = 5
x = matrix(rnorm(N * p), N, p)
beta = rnorm(nz)
f = x[, seq(nz)] %*% beta
mu = exp(f)
y = rpois(N, mu)
fit = glmnet(x, y, family = "poisson")
plot(fit)
pfit = predict(fit, x, s = 0.001, type = "response")
plot(pfit, y)

# Cox
set.seed(10101)
N = 1000
p = 30
nz = p/3
x = matrix(rnorm(N * p), N, p)
b = rnorm(nz)
fx = x[, seq(nz)] %*% beta/3
hx = exp(fx)
ty = rexp(N, hx)
tcens = rbinom(n = N, prob = 0.3, size = 1)  # censoring indicator
y = cbind(time = ty, status = 1 - tcens)  # y=Surv(ty,1-tcens) with library(survival)
fit = glmnet(x, y, family = "cox")
plot(fit)

# Cox example with (start, stop] data
set.seed(2)
nobs <- 100; nvars <- 15
xvec <- rnorm(nobs * nvars)
xvec[sample.int(nobs * nvars, size = 0.4 * nobs * nvars)] <- 0
x <- matrix(xvec, nrow = nobs)
start_time <- runif(100, min = 0, max = 5)
stop_time <- start_time + runif(100, min = 0.1, max = 3)
status <- rbinom(n = nobs, prob = 0.3, size = 1)
jsurv_ss <- survival::Surv(start_time, stop_time, status)
fit <- glmnet(x, jsurv_ss, family = "cox")

# Cox example with strata
jsurv_ss2 <- stratifySurv(jsurv_ss, rep(1:2, each = 50))
fit <- glmnet(x, jsurv_ss2, family = "cox")

# Sparse
n = 10000
p = 200
nzc = trunc(p/10)
x = matrix(rnorm(n * p), n, p)
iz = sample(1:(n * p), size = n * p * 0.85, replace = FALSE)
x[iz] = 0
sx = Matrix(x, sparse = TRUE)
inherits(sx, "sparseMatrix")  #confirm that it is sparse
beta = rnorm(nzc)
fx = x[, seq(nzc)] %*% beta
eps = rnorm(n)
y = fx + eps
px = exp(fx)
px = px/(1 + px)
ly = rbinom(n = length(px), prob = px, size = 1)
system.time(fit1 <- glmnet(sx, y))
system.time(fit2n <- glmnet(x, y))

---

glmnet.control  internal glmnet parameters

**Description**

View and/or change the factory default parameters in glmnet
Usage

glmnet.control(
  fdev = 1e-05,
  devmax = 0.999,
  eps = 1e-06,
  big = 9.9e+35,
  mnlam = 5,
  pmin = 1e-09,
  exmx = 250,
  prec = 1e-10,
  mxit = 100,
  itrace = 0,
  epsnr = 1e-06,
  mxitnr = 25,
  factory = FALSE
)

Arguments

fdev minimum fractional change in deviance for stopping path; factory default = 1.0e-5
devmax maximum fraction of explained deviance for stopping path; factory default = 0.999
eps minimum value of lambda.min.ratio (see glmnet); factory default = 1.0e-6
big large floating point number; factory default = 9.9e35. Inf in definition of upper.limit is set to big
mnlam minimum number of path points (lambda values) allowed; factory default = 5
pmin minimum probability for any class. factory default = 1.0e-9. Note that this implies a pmax of 1-pmin.
exmx maximum allowed exponent. factory default = 250.0
prec convergence threshold for multi response bounds adjustment solution. factory default = 1.0e-10
mxit maximum iterations for multiresponse bounds adjustment solution. factory default = 100
itrace If 1 then progress bar is displayed when running glmnet and cv.glmnet. factory default = 0
epsnr convergence threshold for glmnet.fit. factory default = 1.0e-6
mxitnr maximum iterations for the irLS loop in glmnet.fit. factory default = 25
factory If TRUE, reset all the parameters to the factory default; default is FALSE

Details

If called with no arguments, glmnet.control() returns a list with the current settings of these parameters. Any arguments included in the call sets those parameters to the new values, and then silently returns. The values set are persistent for the duration of the R session.
Value

A list with named elements as in the argument list

Author(s)

Jerome Friedman, Kenneth Tay, Trevor Hastie
Maintainer: Trevor Hastie <hastie@stanford.edu>

See Also

glmnet

Examples

```r
glmnet.control(fdev = 0)  # continue along path even though not much changes
glmnet.control()  # view current settings
glmnet.control(factory = TRUE)  # reset all the parameters to their default
```

# glmnet.fit

## Fit a GLM with elastic net regularization for a single value of lambda

### Description

Fit a generalized linear model via penalized maximum likelihood for a single value of lambda. Can deal with any GLM family.

### Usage

```r
glmnet.fit(
  x,
  y,
  weights,
  lambda,
  alpha = 1,
  offset = rep(0, nobs),
  family = gaussian(),
  intercept = TRUE,
  thresh = 1e-10,
  maxit = 1e+05,
  penalty.factor = rep(1, nvars),
  exclude = c(),
  lower.limits = -Inf,
  upper.limits = Inf,
  warm = NULL,
  from.glmnet.path = FALSE,
)```

save.fit = FALSE,
trace.it = 0
)

**Arguments**

- **x**: Input matrix, of dimension \( n_{\text{obs}} \times n_{\text{vars}} \); each row is an observation vector. If it is a sparse matrix, it is assumed to be unstandardized. It should have attributes \( \text{xm} \) and \( \text{xs} \), where \( \text{xm}(j) \) and \( \text{xs}(j) \) are the centering and scaling factors for variable \( j \) respectively. If it is not a sparse matrix, it is assumed that any standardization needed has already been done.

- **y**: Quantitative response variable.

- **weights**: Observation weights. `glmnet.fit` does NOT standardize these weights.

- **lambda**: A single value for the \( \lambda \) hyperparameter.

- **alpha**: The elasticnet mixing parameter, with \( 0 \leq \alpha \leq 1 \). The penalty is defined as

\[
(1 - \alpha) / 2 ||\beta||^2_2 + \alpha ||\beta||_1.
\]

\( \alpha=1 \) is the lasso penalty, and \( \alpha=0 \) the ridge penalty.

- **offset**: A vector of length \( n_{\text{obs}} \) that is included in the linear predictor. Useful for the "poisson" family (e.g. log of exposure time), or for refining a model by starting at a current fit. Default is NULL. If supplied, then values must also be supplied to the `predict` function.

- **family**: A description of the error distribution and link function to be used in the model. This is the result of a call to a family function. Default is `gaussian()`. (See `family` for details on family functions.)

- **intercept**: Should intercept be fitted (default=TRUE) or set to zero (FALSE)?

- **thresh**: Convergence threshold for coordinate descent. Each inner coordinate-descent loop continues until the maximum change in the objective after any coefficient update is less than thresh times the null deviance. Default value is \( 1\times10^{-10} \).

- **maxit**: Maximum number of passes over the data; default is \( 10^5 \). (If a warm start object is provided, the number of passes the warm start object performed is included.)

- **penalty.factor**: Separate penalty factors can be applied to each coefficient. This is a number that multiplies \( \lambda \) to allow differential shrinkage. Can be 0 for some variables, which implies no shrinkage, and that variable is always included in the model. Default is 1 for all variables (and implicitly infinity for variables listed in `exclude`). Note: the penalty factors are internally rescaled to sum to \( n_{\text{vars}} \).

- **exclude**: Indices of variables to be excluded from the model. Default is none. Equivalent to an infinite penalty factor.

- **lower.limits**: Vector of lower limits for each coefficient; default \(-\text{Inf}\). Each of these must be non-positive. Can be presented as a single value (which will then be replicated), else a vector of length \( n_{\text{vars}} \).

- **upper.limits**: Vector of upper limits for each coefficient; default \( \text{Inf} \). See `lower.limits`.
glmnet.fit

warm
Either a glmnetfit object or a list (with names beta and a0 containing coefficients and intercept respectively) which can be used as a warm start. Default is NULL, indicating no warm start. For internal use only.

from.glmnet.path
Was glmnet.fit() called from glmnet.path()? Default is FALSE. This has implications for computation of the penalty factors.

save.fit
Return the warm start object? Default is FALSE.

trace.it
Controls how much information is printed to screen. If trace.it=2, some information about the fitting procedure is printed to the console as the model is being fitted. Default is trace.it=0 (no information printed). (trace.it=1 not used for compatibility with glmnet.path.)

Details

WARNING: Users should not call glmnet.fit directly. Higher-level functions in this package call glmnet.fit as a subroutine. If a warm start object is provided, some of the other arguments in the function may be overriden.

glmnet.fit solves the elastic net problem for a single, user-specified value of lambda. glmnet.fit works for any GLM family. It solves the problem using iteratively reweighted least squares (IRLS). For each IRLS iteration, glmnet.fit makes a quadratic (Newton) approximation of the log-likelihood, then calls elnet.fit to minimize the resulting approximation.

In terms of standardization: glmnet.fit does not standardize x and weights. penalty.factor is standardized so that they sum up to nvars.

Value

An object with class "glmnetfit" and "glmnet". The list returned contains more keys than that of a "glmnet" object.

a0
Intercept value.

beta
A nvars x 1 matrix of coefficients, stored in sparse matrix format.

df
The number of nonzero coefficients.

dim
Dimension of coefficient matrix.

lambda
Lambda value used.

dev.ratio
The fraction of (null) deviance explained. The deviance calculations incorporate weights if present in the model. The deviance is defined to be 2*(loglike_sat - loglike), where loglike_sat is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence dev.ratio=1-dev/nulldev.

nulldev
Null deviance (per observation). This is defined to be 2*(loglike_sat -loglike(Null)). The null model refers to the intercept model.

npasses
Total passes over the data.

jerr
Error flag, for warnings and errors (largely for internal debugging).

offset
A logical variable indicating whether an offset was included in the model.

call
The call that produced this object.

nobs
Number of observations.
warm_fit If save.fit=TRUE, output of C++ routine, used for warm starts. For internal use only.
family Family used for the model.
converged A logical variable: was the algorithm judged to have converged?
boundary A logical variable: is the fitted value on the boundary of the attainable values?
obj_function Objective function value at the solution.

---

**glmnet.measures**

*Display the names of the measures used in CV for different "glmnet" families*

---

**Description**

Produces a list of names of measures

**Usage**

```r
glmnet.measures(
  family = c("all", "gaussian", "binomial", "poisson", "multinomial", "cox", "mgaussian", "GLM")
)
```

**Arguments**

- `family` If a "glmnet" family is supplied, a list of the names of measures available for that family are produced. Default is "all", in which case the names of measures for all families are produced.

**Details**

Try it and see. A very simple function to provide information

**Author(s)**

Trevor Hastie
Maintainer: Trevor Hastie <hastie@stanford.edu>

**See Also**

cv.glmnet and assess.glmnet.
glmnet.path  

**Fit a GLM with elastic net regularization for a path of lambda values**

**Description**

Fit a generalized linear model via penalized maximum likelihood for a path of lambda values. Can deal with any GLM family.

**Usage**

```r
glmnet.path(
  x,
  y,
  weights = NULL,
  lambda = NULL,
  nlambdas = 100,
  lambda.min.ratio = ifelse(nobs < nvars, 0.01, 1e-04),
  alpha = 1,
  offset = NULL,
  family = gaussian(),
  standardize = TRUE,
  intercept = TRUE,
  thresh = 1e-10,
  maxit = 1e+05,
  penalty.factor = rep(1, nvars),
  exclude = integer(0),
  lower.limits = -Inf,
  upper.limits = Inf,
  trace.it = 0
)
```

**Arguments**

- `x`  
  Input matrix, of dimension `nobs x nvars`; each row is an observation vector. Can be a sparse matrix.

- `y`  
  Quantitative response variable.

- `weights`  
  Observation weights. Default is 1 for each observation.

- `lambda`  
  A user supplied lambda sequence. Typical usage is to have the program compute its own lambda sequence based on `nlambdas` and `lambda.min.ratio`. Supplying a value of lambda overrides this.

- `nlambdas`  
  The number of lambda values, default is 100.

- `lambda.min.ratio`  
  Smallest value for lambda as a fraction of lambda.max, the (data derived) entry value (i.e. the smallest value for which all coefficients are zero). The default depends on the sample size `nobs` relative to the number of variables `nvars`. If `nobs >= nvars`, the default is 0.0001, close to zero. If `nobs < nvars`, the default
is 0.01. A very small value of lambda.min.ratio will lead to a saturated fit in the nobs < nvars case. This is undefined for some families of models, and the function will exit gracefully when the percentage deviance explained is almost 1.

**alpha**
The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$. The penalty is defined as 

$$(1 - \alpha)/2||\beta||_2^2 + \alpha||\beta||_1.$$ 

alpha=1 is the lasso penalty, and alpha=0 the ridge penalty.

**offset**
A vector of length nobs that is included in the linear predictor. Useful for the "poisson" family (e.g. log of exposure time), or for refining a model by starting at a current fit. Default is NULL. If supplied, then values must also be supplied to the predict function.

**family**
A description of the error distribution and link function to be used in the model. This is the result of a call to a family function. Default is gaussian(). (See family for details on family functions.)

**standardize**
Logical flag for x variable standardization, prior to fitting the model sequence. The coefficients are always returned on the original scale. Default is standardize=TRUE. If variables are in the same units already, you might not wish to standardize.

**intercept**
Should intercept be fitted (default=TRUE) or set to zero (FALSE)?

**thresh**
Convergence threshold for coordinate descent. Each inner coordinate-descent loop continues until the maximum change in the objective after any coefficient update is less than thresh times the null deviance. Default value is 1e-10.

**maxit**
Maximum number of passes over the data; default is 10^5.

**penalty.factor**
Separate penalty factors can be applied to each coefficient. This is a number that multiplies lambda to allow differential shrinkage. Can be 0 for some variables, which implies no shrinkage, and that variable is always included in the model. Default is 1 for all variables (and implicitly infinity for variables listed in exclude). Note: the penalty factors are internally rescaled to sum to nvars.

**exclude**
Indices of variables to be excluded from the model. Default is none. Equivalent to an infinite penalty factor.

**lower.limits**
Vector of lower limits for each coefficient; default -Inf. Each of these must be non-positive. Can be presented as a single value (which will then be replicated), else a vector of length nvars.

**upper.limits**
Vector of upper limits for each coefficient; default Inf. See lower.limits.

**trace.it**
Controls how much information is printed to screen. Default is trace.it=0 (no information printed). If trace.it=1, a progress bar is displayed. If trace.it=2, some information about the fitting procedure is printed to the console as the model is being fitted.

**Details**

`glmnet.path` solves the elastic net problem for a path of lambda values. It generalizes `glmnet::glmnet` in that it works for any GLM family.

Sometimes the sequence is truncated before nlambda values of lambda have been used. This happens when `glmnet.path` detects that the decrease in deviance is marginal (i.e. we are near a saturated fit).
Value

An object with class "glmnetfit" and "glmnet".

a0
Intercept sequence of length length(lambda).

beta
A nvars x length(lambda) matrix of coefficients, stored in sparse matrix format.

df
The number of nonzero coefficients for each value of lambda.

dim
Dimension of coefficient matrix.

lambda
The actual sequence of lambda values used. When alpha=0, the largest lambda reported does not quite give the zero coefficients reported (lambda=inf would in principle). Instead, the largest lambda for alpha=0.001 is used, and the sequence of lambda values is derived from this.

dev.ratio
The fraction of (null) deviance explained. The deviance calculations incorporate weights if present in the model. The deviance is defined to be 2*(loglike_sat - loglike), where loglike_sat is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence dev.ratio=1-dev/nulldev.

nulldev
Null deviance (per observation). This is defined to be 2*(loglike_sat -loglike(Null)). The null model refers to the intercept model.
npasses
Total passes over the data summed over all lambda values.
jerr
Error flag, for warnings and errors (largely for internal debugging).

offset
A logical variable indicating whether an offset was included in the model.
call
The call that produced this object.
family
Family used for the model.
nobs
Number of observations.

Examples

set.seed(1)
x <- matrix(rnorm(100 * 20), nrow = 100)
y <- ifelse(rnorm(100) > 0, 1, 0)

# binomial with probit link
fit1 <- glmnet:::glmnet.path(x, y, family = binomial(link = "probit"))

makeX

convert a data frame to a data matrix with one-hot encoding

Description

Converts a data frame to a data matrix suitable for input to glmnet. Factors are converted to dummy matrices via "one-hot" encoding. Options deal with missing values and sparsity.

Usage

makeX(train, test = NULL, na.impute = FALSE, sparse = FALSE, ...)
Arguments

train  Required argument. A dataframe consisting of vectors, matrices and factors

test   Optional argument. A dataframe matching 'train' for use as testing data

na.impute Logical, default FALSE. If TRUE, missing values for any column in the resultant 'x' matrix are replaced by the means of the nonmissing values derived from 'train'

sparse Logical, default FALSE. If TRUE then the returned matrix(es) are converted to matrices of class "CsparseMatrix". Useful if some factors have a large number of levels, resulting in very big matrices, mostly zero

Details

The main function is to convert factors to dummy matrices via "one-hot" encoding. Having the 'train' and 'test' data present is useful if some factor levels are missing in either. Since a factor with k levels leads to a submatrix with 1/k entries zero, with large k the sparse=TRUE option can be helpful; a large matrix will be returned, but stored in sparse matrix format. Finally, the function can deal with missing data. The current version has the option to replace missing observations with the mean from the training data. For dummy submatrices, these are the mean proportions at each level.

Value

If only 'train' was provided, the function returns a matrix 'x'. If missing values were imputed, this matrix has an attribute containing its column means (before imputation). If 'test' was provided as well, a list with two components is returned: 'x' and 'xtest'.

Author(s)

Trevor Hastie
Maintainer: Trevor Hastie hastie@stanford.edu

See Also

glmnet

Examples

```
set.seed(101)
### Single data frame
X = matrix(rnorm(20), 10, 2)
X3 = sample(letters[1:3], 10, replace = TRUE)
X4 = sample(LETTERS[1:3], 10, replace = TRUE)
df = data.frame(X, X3, X4)
makeX(df)
makeX(df, sparse = TRUE)

### Single data frame with missing values
Xn = X
```
MultiGaussianExample  

Synthetic dataset with multiple Gaussian responses

Description

Randomly generated data for multi-response Gaussian regression example.

Usage

data(MultiGaussianExample)
**Format**

List containing the following elements:

- x 100 by 20 matrix of numeric values.
- y 100 by 4 matrix of numeric values, each column representing one response vector.

---

**MultinomialExample**  
*Synthetic dataset with multinomial response*

---

**Description**

Randomly generated data for multinomial regression example.

**Usage**

```r
data(MultinomialExample)
```

---

**Format**

List containing the following elements:

- x 500 by 30 matrix of numeric values.
- y Numeric vector of length 500 containing 142 ones, 174 twos and 184 threes.

---

**mycoxph**  
*Helper function to fit coxph model for survfit.coxnet*

---

**Description**

This function constructs the coxph call needed to run the "hack" of coxph with 0 iterations. It's a separate function as we have to deal with function options like strata, offset and observation weights.

**Usage**

```r
mycoxph(object, s, ...)
```

**Arguments**

- **object**  
  A class coxnet object.

- **s**  
  The value of the penalty parameter lambda at which the survival curve is required.

- **...**  
  The same ... that was passed to survfit.coxnet.
mycoxpred  

*Helper function to amend ... for new data in survfit.coxnet*

**Description**

This function amends the function arguments passed to survfit.coxnet via ... if new data was passed to survfit.coxnet. It’s a separate function as we have to deal with function options like newstrata and newoffset.

**Usage**

```
mycoxpred(object, s, ...)
```

**Arguments**

- `object`  
  A class coxnet object.
- `s`  
  The response for the fitted model.
- `...`  
  The same ... that was passed to survfit.coxnet.

---

```
n.a.replace  

Replace the missing entries in a matrix columnwise with the entries in a supplied vector
```

**Description**

Missing entries in any given column of the matrix are replaced by the column means or the values in a supplied vector.

**Usage**

```
n.a.replace(x, m = rowSums(x, na.rm = TRUE))
```

**Arguments**

- `x`  
  A matrix with potentially missing values, and also potentially in sparse matrix format (i.e. inherits from "sparseMatrix")
- `m`  
  Optional argument. A vector of values used to replace the missing entries, columnwise. If missing, the column means of ’x’ are used

**Details**

This is a simple imputation scheme. This function is called by makeX if the na.impute=TRUE option is used, but of course can be used on its own. If ’x’ is sparse, the result is sparse, and the replacements are done so as to maintain sparsity.
Value

A version of 'x' is returned with the missing values replaced.

Author(s)

Trevor Hastie
Maintainer: Trevor Hastie hastie@stanford.edu

See Also

makeX and glmnet

Examples

```r
set.seed(101)
### Single data frame
X = matrix(rnorm(20), 10, 2)
X[3, 1] = NA
X[5, 2] = NA
X3 = sample(letters[1:3], 10, replace = TRUE)
X3[6] = NA
X4 = sample(LETTERS[1:3], 10, replace = TRUE)
X4[9] = NA
dfn = data.frame(X, X3, X4)

x = makeX(dfn)
m = rowSums(x, na.rm = TRUE)
na.replace(x, m)

x = makeX(dfn, sparse = TRUE)
nan.replace(x, m)
```

---

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>obj_function</td>
<td>Elastic net objective function value</td>
</tr>
</tbody>
</table>

Description

Returns the elastic net objective function value.

Usage

```r
obj_function(y, mu, weights, family, lambda, alpha, coefficients, vp)
```
Arguments

\begin{itemize}
  \item \textit{y} \quad \text{Quantitative response variable.}
  \item \textit{mu} \quad \text{Model’s predictions for } y.
  \item \textit{weights} \quad \text{Observation weights.}
  \item \textit{family} \quad \text{A description of the error distribution and link function to be used in the model. This is the result of a call to a family function.}
  \item \textit{lambda} \quad \text{A single value for the lambda hyperparameter.}
  \item \textit{alpha} \quad \text{The elasticnet mixing parameter, with } 0 \leq \alpha \leq 1.
  \item \textit{coefficients} \quad \text{The model’s coefficients (excluding intercept).}
  \item \textit{vp} \quad \text{Penalty factors for each of the coefficients.}
\end{itemize}

\begin{tabular}{ll}
\textbf{pen\_function} & \textit{Elastic net penalty value} \\
\end{tabular}

Description

Returns the elastic net penalty value without the lambda factor.

Usage

\begin{verbatim}
pen_function(coefficients, alpha = 1, vp = 1)
\end{verbatim}

Arguments

\begin{itemize}
  \item \textit{coefficients} \quad \text{The model’s coefficients (excluding intercept).}
  \item \textit{alpha} \quad \text{The elasticnet mixing parameter, with } 0 \leq \alpha \leq 1.
  \item \textit{vp} \quad \text{Penalty factors for each of the coefficients.}
\end{itemize}

Details

The penalty is defined as

\[(1 - \alpha)/2 \sum vp_j \beta_j^2 + \alpha \sum vp_j |\beta|.

Note the omission of the multiplicative lambda factor.
plot.cv.glmnet

Plots the cross-validation curve produced by cv.glmnet

Description

Plots the cross-validation curve, and upper and lower standard deviation curves, as a function of
the lambda values used. If the object has class "cv.relaxed" a different plot is produced, showing
both lambda and gamma

Usage

## S3 method for class 'cv.glmnet'
plot(x, sign.lambda = 1, ...)

## S3 method for class 'cv.relaxed'
plot(x, se.bands = TRUE, ...)

Arguments

x         fitted "cv.glmnet" object
sign.lambda Either plot against log(lambda) (default) or its negative if sign.lambda=-1.
...        Other graphical parameters to plot
se.bands  Should shading be produced to show standard-error bands; default is TRUE

Details

A plot is produced, and nothing is returned.

Author(s)

Jerome Friedman, Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

References

Models via Coordinate Descent

See Also

glmnet and cv.glmnet.
Examples

```r
set.seed(1010)
n = 1000
p = 100
nzc = trunc(p/10)
x = matrix(rnorm(n * p), n, p)
beta = rnorm(nzc)
fx = (x[, seq(nzc)] %*% beta)
eps = rnorm(n) * 5
y = drop(fx + eps)
px = exp(fx)
px = px/(1 + px)
ly = rbinom(n = length(px), prob = px, size = 1)
cvob1 = cv.glmnet(x, y)
plot(cvob1)
title("Gaussian Family", line = 2.5)
cvob1r = cv.glmnet(x, y, relax = TRUE)
plot(cvob1r)
frame()
set.seed(1011)
par(mfrow = c(2, 2), mar = c(4.5, 4.5, 4, 1))
cvob2 = cv.glmnet(x, ly, family = "binomial")
plot(cvob2)
title("Binomial Family", line = 2.5)
## set.seed(1011)
## cvob3 = cv.glmnet(x, ly, family = "binomial", type = "class")
## plot(cvob3)
## title("Binomial Family", line = 2.5)
```

Description

Produces a coefficient profile plot of the coefficient paths for a fitted "glmnet" object.

Usage

```r
## S3 method for class 'glmnet'
plot(x, xvar = c("norm", "lambda", "dev"), label = FALSE, ...)

## S3 method for class 'mrelnet'
plot(
  x,
  xvar = c("norm", "lambda", "dev"),
  label = FALSE,
  type.coef = c("coef", "2norm"),
```
## S3 method for class 'multnet'
plot(
  x,
  xvar = c("norm", "lambda", "dev"),
  label = FALSE,
  type.coef = c("coef", "2norm"),
  ...
)

## S3 method for class 'relaxed'
plot(x, xvar = c("lambda", "dev"), label = FALSE, gamma = 1, ...)

### Arguments

- **x**: fitted "glmnet" model
- **xvar**: What is on the X-axis. "norm" plots against the L1-norm of the coefficients, "lambda" against the log-lambda sequence, and "dev" against the percent deviance explained.
- **label**: If TRUE, label the curves with variable sequence numbers.
- **...**: Other graphical parameters to plot
- **type.coef**: If type.coef="2norm" then a single curve per variable, else if type.coef="coef", a coefficient plot per response
- **gamma**: Value of the mixing parameter for a "relaxed" fit

### Details

A coefficient profile plot is produced. If x is a multinomial model, a coefficient plot is produced for each class.

### Author(s)

Jerome Friedman, Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

### References


### See Also

glmnet, print, predict and coef methods.
Examples

```r
x = matrix(rnorm(100*20), 100, 20)
y = rnorm(100)
g2 = sample(1:2, 100, replace = TRUE)
g4 = sample(1:4, 100, replace = TRUE)
fit1 = glmnet(x, y)
plot(fit1)
plot(fit1, xvar = "lambda", label = TRUE)
fit3 = glmnet(x, g4, family = "multinomial")
plot(fit3, pch = 19)
```

PoissonExample

**Synthetic dataset with count response**

Description

Randomly generated data for Poisson regression example.

Usage

data(PoissonExample)

Format

List containing the following elements:

- `x` 500 by 20 matrix of numeric values.
- `y` Numeric vector of length 500 consisting of non-negative integers.

predict.cv.glmnet

**make predictions from a "cv.glmnet" object.**

Description

This function makes predictions from a cross-validated glmnet model, using the stored "glmnet.fit" object, and the optimal value chosen for lambda (and gamma for a 'relaxed' fit.

Usage

```r
## S3 method for class 'cv.glmnet'
predict(object, newx, s = c("lambda.1se", "lambda.min"), ...)
```

```r
## S3 method for class 'cv.relaxed'
predict(
  object,
  newx,
```
\begin{verbatim}
s = c("lambda.1se", "lambda.min"),
gamma = c("gamma.1se", "gamma.min"),
...
\end{verbatim}

**Arguments**

- **object**
  Fitted "cv.glmnet" or "cv.relaxed" object.

- **newx**
  Matrix of new values for \( x \) at which predictions are to be made. Must be a matrix; can be sparse as in \texttt{Matrix} package. See documentation for \texttt{predict.glmnet}.

- **s**
  Value(s) of the penalty parameter \( \lambda \) at which predictions are required. Default is the value \( s="\lambda.1se" \) stored on the CV object. Alternatively \( s="\lambda.\min" \) can be used. If \( s \) is numeric, it is taken as the value(s) of \( \lambda \) to be used. (For historical reasons we use the symbol 's' rather than 'lambda' to reference this parameter)

- **gamma**
  Value (single) of \( \gamma \) at which predictions are to be made

**Details**

This function makes it easier to use the results of cross-validation to make a prediction.

**Value**

The object returned depends on the \ldots argument which is passed on to the \texttt{predict} method for \texttt{glmnet} objects.

**Author(s)**

Jerome Friedman, Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

**References**


**See Also**

\texttt{glmnet}, \texttt{and print}, \texttt{and coef} methods, and \texttt{cv.glmnet}.
Examples

```r
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
cv.fit = cv.glmnet(x, y)
predict(cv.fit, newx = x[1:5, ])
coef(cv.fit)
coef(cv.fit, s = "lambda.min")
predict(cv.fit, newx = x[1:5, ], s = c(0.001, 0.002))
cv.fitr = cv.glmnet(x, y, relax = TRUE)
predict(cv.fit, newx = x[1:5, ])
coef(cv.fit)
coef(cv.fit, s = "lambda.min", gamma = "gamma.min")
predict(cv.fit, newx = x[1:5, ], s = c(0.001, 0.002), gamma = "gamma.min")
```

predict.glmnetfit

Get predictions from a `glmnetfit` fit object

Description

Gives fitted values, linear predictors, coefficients and number of non-zero coefficients from a fitted `glmnetfit` object.

Usage

```r
## S3 method for class 'glmnetfit'
predict(
  object,
  newx,
  s = NULL,
  type = c("link", "response", "coefficients", "nonzero"),
  exact = FALSE,
  newoffset,
  ...
)
```

Arguments

- `object`: Fitted "glmnetfit" object.
- `newx`: Matrix of new values for `x` at which predictions are to be made. Must be a matrix. This argument is not used for `type = c("coefficients","nonzero")`.
- `s`: Value(s) of the penalty parameter lambda at which predictions are required. Default is the entire sequence used to create the model.
- `type`: Type of prediction required. Type "link" gives the linear predictors (eta scale); Type "response" gives the fitted values (mu scale). Type "coefficients" computes the coefficients at the requested values for `s`. Type "nonzero" returns a list of the indices of the nonzero coefficients for each value of `s`.
This argument is relevant only when predictions are made at values of $\mathbf{s}$ (lambda) different from those used in the fitting of the original model. If `exact=FALSE` (default), then the predict function uses linear interpolation to make predictions for values of $\mathbf{s}$ (lambda) that do not coincide with those used in the fitting algorithm. While this is often a good approximation, it can sometimes be a bit coarse. With `exact=TRUE`, these different values of $\mathbf{s}$ are merged (and sorted) with `object$lambda`, and the model is refit before predictions are made. In this case, it is required to supply the original data `x=` and `y=` as additional named arguments to predict() or coef(). The workhorse `predict.glmnet()` needs to update the model, and so needs the data used to create it. The same is true of weights, offset, penalty.factor, lower.limits, upper.limits if these were used in the original call. Failure to do so will result in an error.

If an offset is used in the fit, then one must be supplied for making predictions (except for type="coefficients" or type="nonzero").

This is the mechanism for passing arguments like `x=` when `exact=TRUE`; see `exact` argument.

The object returned depends on type.

---

**Description**

Print a summary of the results of cross-validation for a glmnet model.

**Usage**

```r
## S3 method for class 'cv.glmnet'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

- `x` fitted `cv.glmnet` object
- `digits` significant digits in printout
- `...` additional print arguments

**Details**

A summary of the cross-validated fit is produced, slightly different for a 'cv.relaxed' object than for a 'cv.glmnet' object. Note that a 'cv.relaxed' object inherits from class 'cv.glmnet', so by directly invoking `print.cv.glmnet(object)` will print the summary as if `relax=TRUE` had not been used.
print.glmnet

Author(s)
Jerome Friedman, Trevor Hastie and Rob Tibshirani
Maintainer: Trevor Hastie hastie@stanford.edu

References

See Also
glmnet, predict and coef methods.

Examples

```r
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
fit1 = cv.glmnet(x, y)
print(fit1)
fit1r = cv.glmnet(x, y, relax = TRUE)
print(fit1r)
## print.cv.glmnet(fit1r) ## CHECK WITH TREVOR
```

---

print.glmnet  

Print a summary of the glmnet path at each step along the path.

Usage

```r
# S3 method for class 'glmnet'
print(x, digits = max(3,getOption("digits") - 3), ...)
```

Arguments

- `x`: fitted glmnet object
- `digits`: significant digits in printout
- `...`: additional print arguments

Description

Print a summary of the glmnet path at each step along the path.
The call that produced the object \( x \) is printed, followed by a three-column matrix with columns \( \text{Df} \), \%Dev and \( \text{Lambda} \). The \( \text{Df} \) column is the number of nonzero coefficients (\( \text{Df} \) is a reasonable name only for lasso fits). \%Dev is the percent deviance explained (relative to the null deviance). In the case of a 'relaxed' fit, an additional column is inserted, \%Dev \( \text{R} \) which gives the percent deviance explained by the relaxed model. For a "bigGlm" model, a simpler summary is printed.

The matrix above is silently returned

References


See Also

\texttt{glmnet}, \texttt{predict} and \texttt{coef} methods.

Examples

```r
x = matrix(rnorm(100 * 20), 100, 20)
y = rnorm(100)
fit1 = glmnet(x, y)
print(fit1)
```
response.coxnet  

Make response for coxnet

Description
Internal function to make the response y passed to glmnet suitable for coxnet (i.e. glmnet with family = "cox"). Sanity checks are performed here too.

Usage
response.coxnet(y)

Arguments
y  

Response variable. Either a class "Surv" object or a two-column matrix with columns named 'time' and 'status'.

Details
If y is a class "Surv" object, this function returns y with no changes. If y is a two-column matrix with columns named 'time' and 'status', it is converted into a "Surv" object.

Value
A class "Surv" object.

rmult  

Generate multinomial samples from a probability matrix

Description
Generate multinomial samples

Usage
rmult(p)

Arguments
p  

matrix of probabilities, with number of columns the number of classes

Details
Simple function that calls the rmultinom function. It generates a class label for each row of its input matrix of class probabilities.
Value

a vector of class memberships

Author(s)

Trevor Hastie
Maintainer: Trevor Hastie hastie@stanford.edu

---

SparseExample

**Synthetic dataset with sparse design matrix**

Description

Randomly generated data for Gaussian regression example with the design matrix \( x \) being in sparse matrix format.

Usage

data(SparseExample)

Format

List containing the following elements:

- \( x \) 100 by 20 matrix of numeric values. \( x \) is in sparse matrix format, having class "dgCMatrix".
- \( y \) Numeric vector of length 100.

---

stratifySurv

**Add strata to a Surv object**

Description

Helper function to add strata as an attribute to a Surv object. The output of this function can be used as the response in `glmnet()` for fitting stratified Cox models.

Usage

stratifySurv(y, strata = rep(1, length(y)))

Arguments

- \( y \) A Surv object.
- \( strata \) A vector of length equal to the number of observations in \( y \), indicating strata membership. Default is all belong to same strata.
Details

When fitting a stratified Cox model with glmnet(), strata should be added to a Surv response with this helper function. Note that it is not sufficient to add strata as an attribute to the Surv response manually: if the result does not have class stratifySurv, subsetting of the response will not work properly.

Value

An object of class stratifySurv (in addition to all the classes y belonged to).

Examples

```r
y <- survival::Surv(1:10, rep(0:1, length.out = 10))
strata <- rep(1:3, length.out = 10)
y2 <- stratifySurv(y, strata) # returns stratifySurv object
```

Description

Computes the predicted survivor function for a Cox proportional hazards model with elastic net penalty.

Usage

```r
## S3 method for class 'coxnet'
survfit(formula, s = NULL, ...)
```

Arguments

- `formula`: A class coxnet object.
- `s`: Value(s) of the penalty parameter lambda at which the survival curve is required. Default is the entire sequence used to create the model. However, it is recommended that survfit.coxnet is called for a single penalty parameter.
- `...`: This is the mechanism for passing additional arguments like (i) x= and y= for the x and y used to fit the model, (ii) weights= and offset= when the model was fit with these options, (iii) arguments for new data (newx, newoffset, newstrata), and (iv) arguments to be passed to survfit.coxph().

Details

To be consistent with other functions in glmnet, if s is not specified, survival curves are returned for the entire lambda sequence. This is not recommended usage: it is best to call survfit.coxnet with a single value of the penalty parameter for the s option.
Value

If s is a single value, an object of class "survfitcox" and "survfit" containing one or more survival curves. Otherwise, a list of such objects, one element for each value in s. Methods defined for survfit objects are print, summary and plot.

Examples

```r
set.seed(2)
nobs <- 100; nvars <- 15
xvec <- rnorm(nobs * nvars)
xvec[sample.int(nobs * nvars, size = 0.4 * nobs * nvars)] <- 0
x <- matrix(xvec, nrow = nobs)
beta <- rnorm(nvars / 3)
fx <- x[, seq(nvars / 3)] %*% beta / 3
ty <- rexp(nobs, exp(fx))
tcens <- rbinom(n = nobs, prob = 0.3, size = 1)
y <- survival::Surv(ty, tcens)
fit1 <- glmnet(x, y, family = "cox")

# survfit object for Cox model where lambda = 0.1
sf1 <- survival::survfit(fit1, s = 0.1, x = x, y = y)
plot(sf1)

# example with new data
sf2 <- survival::survfit(fit1, s = 0.1, x = x, y = y, newx = x[1:3, ])
plot(sf2)

# example with strata
y2 <- stratifySurv(y, rep(1:2, length.out = nobs))
fit2 <- glmnet(x, y2, family = "cox")
sf3 <- survival::survfit(fit2, s = 0.1, x = x, y = y2)
sf4 <- survival::survfit(fit2, s = 0.1, x = x, y = y2,
                         newx = x[1:3, ], newstrata = c(1, 1, 1))
```

---

**survfit.cv.glmnet**

*Compute a survival curve from a cv.glmnet object*

**Description**

Computes the predicted survivor function for a Cox proportional hazards model with elastic net penalty from a cross-validated glmnet model.

**Usage**

```r
## S3 method for class 'cv.glmnet'
survfit(formula, s = c("lambda.1se", "lambda.min"), ...)
```
use.cox.path

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>formula</td>
<td>A class cv.glmnet object. The object should have been fit with family = &quot;cox&quot;.</td>
</tr>
<tr>
<td>s</td>
<td>Value(s) of the penalty parameter lambda at which predictions are required. Default is the value s=&quot;lambda.1se&quot; stored on the CV object. Alternatively s=&quot;lambda.min&quot; can be used. If s is numeric, it is taken as the value(s) of lambda to be used.</td>
</tr>
<tr>
<td>...</td>
<td>Other arguments to be passed to survfit.coxnet.</td>
</tr>
</tbody>
</table>

Details

This function makes it easier to use the results of cross-validation to compute a survival curve.

Value

If s is a single value, an object of class "survfitcox" and "survfit" containing one or more survival curves. Otherwise, a list of such objects, one element for each value in s. Methods defined for survfit objects are print, summary and plot.

Examples

```r
set.seed(2)
nobs <- 100; nvars <- 15
xvec <- rnorm(nobs * nvars)
x <- matrix(xvec, nrow = nobs)
beta <- rnorm(nvars / 3)
fx <- x[, seq(nvars / 3)] %*% beta / 3
ty <- rexp(nobs, exp(fx))
tcens <- rbinom(n = nobs, prob = 0.3, size = 1)
y <- survival::Surv(ty, tcens)
cvfit <- cv.glmnet(x, y, family = "cox")
# default: s = "lambda.1se"
survival::survfit(cvfit, x = x, y = y)

# s = "lambda.min"
survival::survfit(cvfit, s = "lambda.min", x = x, y = y)
```

Description

Helper function to check if glmnet should call cox.path().

Usage

```
use.cox.path(x, y)
```
Arguments

x  Design matrix.
y  Response variable.

Details

For family="cox", we only call the original coxnet() function if (i) x is not sparse, (ii) y is right-censored data, and (iii) we are not fitting a stratified Cox model. This function also throws an error if y has a "strata" attribute but is not of type "stratifySurv".

Value

TRUE if cox.path() should be called, FALSE otherwise.

weighted_mean_sd

Helper function to compute weighted mean and standard deviation

Description

Helper function to compute weighted mean and standard deviation. Deals gracefully whether x is sparse matrix or not.

Usage

weighted_mean_sd(x, weights = rep(1, nrow(x)))

Arguments

x  Observation matrix.
weights  Optional weight vector.

Value

A list with components.

mean  vector of weighted means of columns of x
sd  vector of weighted standard deviations of columns of x
## Index

* **Cox**  
  Cindex, 8  
  coxgrad, 18  
  coxnet.deviance, 19

* **classification**  
  assess.glmmnet, 4

* **cross-validation**  
  Cindex, 8

* **datasets**  
  beta_CVX, 6

* **data**  
  BinomialExample, 8  
  CoxExample, 17  
  MultiGaussianExample, 51  
  MultinomialExample, 52  
  PoissonExample, 59  
  QuickStartExample, 64  
  SparseExample, 66

* **models**  
  assess.glmmnet, 4  
  bigGlm, 7  
  Cindex, 8  
  coef.glmmnet, 10  
  cv.glmmnet, 21  
  deviance.glmmnet, 26  
  glmmnet, 34  
  glmmnet-package, 3  
  glmmnet.control, 41  
  glmmnet.measures, 46  
  makeX, 49  
  na.replace, 53  
  plot.cv.glmmnet, 56  
  plot.glmmnet, 57  
  predict.cv.glmmnet, 59  
  print.cv.glmmnet, 62  
  print.glmmnet, 63

* **model**  
  coxgrad, 18  
  coxnet.deviance, 19

* **package**  
  glmnet-package, 3

* **regression**  
  bigGlm, 7  
  coef.glmmnet, 10  
  cv.glmmnet, 21  
  deviance.glmmnet, 26  
  glmmnet, 34  
  glmmnet-package, 3  
  glmmnet.control, 41  
  plot.cv.glmmnet, 56  
  plot.glmmnet, 57  
  predict.cv.glmmnet, 59  
  print.cv.glmmnet, 62  
  print.glmmnet, 63

  assess.glmmnet, 4  
  beta_CVX, 6  
  bigGlm, 7  
  BinomialExample, 8

  Cindex, 8  
  coef.cv.glmmnet (predict.cv.glmmnet), 59  
  coef.cv.relaxed (predict.cv.glmmnet), 59  
  coef.glmmnet, 10  
  coef.relaxed (coef.glmmnet), 10  
  confusion.glmmnet (assess.glmmnet), 4  
  cox.fit, 12  
  cox.path, 15  
  cox_obj_function, 21  
  CoxExample, 17  
  coxgrad, 18  
  coxnet.deviance, 19  
  cv.glmmnet, 21

  dev_function, 27  
  deviance.glmmnet, 26  
  elnet.fit, 28
family, 33, 44, 48

fid, 30

get_cox_lambda_max, 31
get_eta, 32
get_start, 32

glmnet, 34

glmnet-package, 3

glmnet.control, 41

glmnet.fit, 43

glmnet.measures, 46

glmnet.path, 47

makeX, 49

MultiGaussianExample, 51

MultinomialExample, 52

mycoxph, 52

mycoxpred, 53

na.replace, 53

obj_function, 54

pen_function, 55

plot.cv.glmnet, 56

plot.cv.relaxed (plot.cv.glmnet), 56

plot.glmnet, 57

plot.mrelnet (plot.glmnet), 57

plot.multnet (plot.glmnet), 57

plot.relaxed (plot.glmnet), 57

PoissonExample, 59

predict.coxnet (coef.glmnet), 10

predict.cv.glmnet, 59

predict.cv.relaxed (predict.cv.glmnet), 59

predict.elnet (coef.glmnet), 10

predict.fishnet (coef.glmnet), 10

predict.glmnet (coef.glmnet), 10

predict.glmnetfit, 61

predict.lognet (coef.glmnet), 10

predict.mrelnet (coef.glmnet), 10

predict.multnet (coef.glmnet), 10

predict.relaxed (coef.glmnet), 10

print.bigGlm (print.glmnet), 63

print.cv.glmnet, 62

print.cv.relaxed (print.cv.glmnet), 62

print.glmnet, 63

print.relaxed (print.glmnet), 63

QuickStartExample, 64

relax.glmnet (glmnet), 34

response.coxnet, 65

rmult, 65

roc.glmnet (assess.glmnet), 4

SparseExample, 66

stratifySurv, 66

survfit.coxnet, 67

survfit.cv.glmnet, 68

use.cox.path, 69

weighted_mean_sd, 70

x (beta_CVX), 6

y (beta_CVX), 6