

# Package: glmnet (via r-universe)

November 14, 2024

**Type** Package

**Title** Lasso and Elastic-Net Regularized Generalized Linear Models

**Version** 4.1-8

**Date** 2023-08-19

**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](https://doi.org/10.18637/jss.v033.i01) and [doi:10.18637/jss.v039.i05](https://doi.org/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](https://doi.org/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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**RemoteSha** 625f6ca6e3132ce730563ce34233c37f347754c8

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glmnet-package	<i>Elastic net model paths for some generalized linear models</i>
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## 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](mailto:hastie@stanford.edu)

## References

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent (2010)*, *Journal of Statistical Software*, Vol. 33(1), 1-22, doi:10.18637/jss.v033.i01.

Simon, N., Friedman, J., Hastie, T. and Tibshirani, R. (2011) *Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent*, *Journal of Statistical Software*, Vol. 39(5), 1-13, doi:10.18637/jss.v039.i05.

Tibshirani, Robert, Bien, J., Friedman, J., Hastie, T., Simon, N., Taylor, J. and Tibshirani, Ryan. (2012) *Strong Rules for Discarding Predictors in Lasso-type Problems*, *JRSSB*, Vol. 74(2), 245-266, <https://arxiv.org/abs/1011.2234>.

Hastie, T., Tibshirani, Robert and Tibshirani, Ryan (2020) *Best Subset, Forward Stepwise or Lasso? Analysis and Recommendations Based on Extensive Comparisons*, *Statist. Sc.* Vol. 35(4), 579-592, <https://arxiv.org/abs/1707.08692>.

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

## Examples

```
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

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

```

)

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 be 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](mailto: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]]
```

---

beta\_CVX

*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.

## 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

<code>x</code>	input matrix
<code>...</code>	Most other arguments to <code>glmnet</code> that make sense
<code>path</code>	Since <code>glmnet</code> does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with unpenalized fits. With <code>path=TRUE</code> , 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 <code>path=FALSE</code> .

## 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**

```
# 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	<i>Synthetic dataset with binary response</i>
-----------------	---

---

**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	<i>compute C index for a Cox model</i>
--------	--

---

**Description**

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

**Usage**

```
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](mailto:hastie@stanford.edu)

**References**

Harrel Jr, F. E. and Lee, K. L. and Mark, D. B. (1996) *Tutorial in biostatistics: multivariable prognostic models: issues in developing models, evaluating assumptions and adequacy, and measuring and reducing error*, *Statistics in Medicine*, 15, pages 361–387.

**See Also**

cv.glmnet

**Examples**

```
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) <i>different</i> 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 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, lower.limits, upper.limits 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; seeexact argument.

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

Jerome Friedman, Trevor Hastie and Rob Tibshirani  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### References

- Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent (2010)*, *Journal of Statistical Software*, Vol. 33(1), 1-22, doi:10.18637/jss.v033.i01.
- Simon, N., Friedman, J., Hastie, T. and Tibshirani, R. (2011) *Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent*, *Journal of Statistical Software*, Vol. 39(5), 1-13, doi:10.18637/jss.v039.i05.
- Glmnet webpage with four vignettes, <https://glmnet.stanford.edu>.

### See Also

glmnet, and print, and coef methods, and cv.glmnet.

**Examples**

```

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")
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)

```

---

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 $x_s$ , where $x_m(j)$ and $x_s(j)$ 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.
<code>y</code>	Survival response variable, must be a <code>Surv</code> or <code>stratifySurv</code> object.
<code>weights</code>	Observation weights. <code>cox.fit</code> does NOT standardize these weights.
<code>lambda</code>	A single value for the lambda hyperparameter.
<code>alpha</code>	See <code>glmnet</code> help file
<code>offset</code>	See <code>glmnet</code> help file
<code>thresh</code>	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 <code>thresh</code> times the null deviance. Default value is $1e-10$ .
<code>maxit</code>	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.)
<code>penalty.factor</code>	See <code>glmnet</code> help file
<code>exclude</code>	See <code>glmnet</code> help file
<code>lower.limits</code>	See <code>glmnet</code> help file
<code>upper.limits</code>	See <code>glmnet</code> help file
<code>warm</code>	Either a <code>glmnetfit</code> object or a list (with name <code>beta</code> containing coefficients) which can be used as a warm start. Default is <code>NULL</code> , indicating no warm start. For internal use only.
<code>from.cox.path</code>	Was <code>cox.fit()</code> called from <code>cox.path()</code> ? Default is <code>FALSE</code> . This has implications for computation of the penalty factors.
<code>save.fit</code>	Return the warm start object? Default is <code>FALSE</code> .
<code>trace.it</code>	Controls how much information is printed to screen. If <code>trace.it=2</code> , some information about the fitting procedure is printed to the console as the model is being fitted. Default is <code>trace.it=0</code> (no information printed). ( <code>trace.it=1</code> not used for compatibility with <code>glmnet.path</code> .)

## 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 $nvars \times 1$ 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 $2*(\text{loglike\_sat} - \text{loglike})$ , where <code>loglike_sat</code> is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence <code>dev.ratio=1-dev/nulldev</code> .
nulldev	Null deviance (per observation). This is defined to be $2*(\text{loglike\_sat} - \text{loglike}(\text{Null}))$ . 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 <code>save_fit=TRUE</code> , 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.

---

cox.path	<i>Fit a Cox regression model with elastic net regularization for a path of lambda values</i>
----------	---

---

**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**

```

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".

<code>a0</code>	Intercept value, NULL for "cox" family.
<code>beta</code>	A <code>nvars x length(lambda)</code> matrix of coefficients, stored in sparse matrix format.
<code>df</code>	The number of nonzero coefficients for each value of <code>lambda</code> .
<code>dim</code>	Dimension of coefficient matrix.
<code>lambda</code>	The actual sequence of <code>lambda</code> values used. When <code>alpha=0</code> , the largest <code>lambda</code> reported does not quite give the zero coefficients reported ( <code>lambda=inf</code> would in principle). Instead, the largest <code>lambda</code> for <code>alpha=0.001</code> is used, and the sequence of <code>lambda</code> values is derived from this.
<code>dev.ratio</code>	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 <code>loglike_sat</code> is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence <code>dev.ratio=1-dev/nulldev</code> .
<code>nulldev</code>	Null deviance (per observation). This is defined to be $2*(\text{loglike\_sat} - \text{loglike}(\text{Null}))$ . The null model refers to the 0 model.
<code>npasses</code>	Total passes over the data summed over all <code>lambda</code> values.
<code>jerr</code>	Error flag, for warnings and errors (largely for internal debugging).
<code>offset</code>	A logical variable indicating whether an offset was included in the model.
<code>call</code>	The call that produced this object.
<code>nobs</code>	Number of observations.

**Examples**

```
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

```
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).

---

coxgrad

*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**

<code>eta</code>	Fit vector (usually from <code>glmnet</code> at a particular <code>lambda</code> ).
<code>y</code>	Survival response variable, must be a <code>Surv</code> or <code>stratifySurv</code> object.
<code>w</code>	Observation weights (default is all equal to 1).
<code>std.weights</code>	If TRUE (default), observation weights are standardized to sum to 1.
<code>diag.hessian</code>	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 (start, 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
coxgrad(eta, y, diag.hessian = TRUE)

# example with (start, stop] data
y2 <- survival::Surv(time, time + runif(10), d)
coxgrad(eta, y2)

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

---

coxnet.deviance	<i>Compute deviance for Cox model</i>
-----------------	---------------------------------------

---

## Description

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

## Usage

```
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**

```
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**

```
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

```
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 aligned using the master sequence (see the alignment 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.

n folds	number of folds - default is 10. Although n folds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is n folds=3
foldid	an optional vector of values between 1 and n folds identifying what fold each observation is in. If supplied, n folds 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 n folds 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 from the predictions from the n folds fits, and then summarized (does not apply to <code>type.measure="auc"</code> ). For the "cox" family, grouped=TRUE obtains the CV partial likelihood for the Kth fold by <i>subtraction</i> ; by subtracting the log partial likelihood evaluated on the full dataset from that evaluated on the 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 <i>prevalidated</i> 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 <code>gamma = c(0, 0.25, 0.5, 0.75, 1)</code>
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 <code>trace.it=1</code> , then progress bars are displayed; useful for big models that take a long time to fit. Limited tracing if <code>parallel=TRUE</code>
...	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`".

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

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent (2010)*, *Journal of Statistical Software*, Vol. 33(1), 1-22, doi:[10.18637/jss.v033.i01](https://doi.org/10.18637/jss.v033.i01).  
 Simon, N., Friedman, J., Hastie, T. and Tibshirani, R. (2011) *Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent*, *Journal of Statistical Software*, Vol. 39(5), 1-13, doi:[10.18637/jss.v039.i05](https://doi.org/10.18637/jss.v039.i05).

**See Also**

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

**Examples**

```
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)
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  $2 * (\text{loglike\_sat} - \text{loglike})$ , 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  $2 * (\text{loglike\_sat} - \text{loglike}(\text{Null}))$ ; The NULL model refers to the intercept model, except for the Cox, where it is the 0 model. Hence  $\text{dev.ratio} = 1 - \text{deviance} / \text{nulldev}$ , and this deviance method returns  $(1 - \text{dev.ratio}) * \text{nulldev}$ .

## Value

$(1 - \text{dev.ratio}) * \text{nulldev}$

## Author(s)

Jerome Friedman, Trevor Hastie and Rob Tibshirani  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

## References

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent*

## See Also

`glmnet`, `predict`, `print`, and `coef` methods.

**Examples**

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

---

dev_function	<i>Elastic net deviance value</i>
--------------	-----------------------------------

---

**Description**

Returns the elastic net deviance value.

**Usage**

```
dev_function(y, mu, weights, family)
```

**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.

---

e1net.fit	<i>Solve weighted least squares (WLS) problem for a single lambda value</i>
-----------	---

---

**Description**

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

**Usage**

```
e1net.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 $0 \leq \alpha \leq 1$ . The penalty is defined as $(1 - \alpha)/2 \ \beta\ _2^2 + \alpha \ \beta\ _1.$ <p>alpha=1 is the lasso penalty, and alpha=0 the ridge penalty.</p>
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 `e1net.fit` directly. Higher-level functions in this package call `e1net.fit` as a subroutine. If a warm start object is provided, some of the other arguments in the function may be overridden.

`e1net.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  $j$ th 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.

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

---

fid	<i>Helper function for Cox deviance and gradient</i>
-----	--

---

**Description**

Helps to find ties in death times of data.

**Usage**

```
fid(x, index)
```

**Arguments**

x	Sorted vector of death times.
index	Vector of indices for the death times.

**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	<i>Get lambda max for Cox regression model</i>
--------------------	--

---

**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 $0 \leq \alpha \leq 1$ .
weights	Observation weights.
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\_eta

*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_eta(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**

```
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 <a href="#">family</a> 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 <code>is.offset=FALSE</code> , this should be a zero vector of the same length as <code>y</code> .
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	<i>fit a GLM with lasso or elasticnet regularization</i>
--------	--

---

### 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 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 <div style="text-align: center; margin: 10px 0;"> <math display="block">(1 - \alpha)/2 \ \beta\ _2^2 + \alpha \ \beta\ _1.</math> </div> <p>alpha=1 is the lasso penalty, and alpha=0 the ridge penalty.</p>   |
| 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.

<code>lambda</code>	A user supplied <code>lambda</code> sequence. Typical usage is to have the program compute its own <code>lambda</code> sequence based on <code>nlambda</code> and <code>lambda.min.ratio</code> . Supplying a value of <code>lambda</code> overrides this. <b>WARNING:</b> use with care. Avoid supplying a single value for <code>lambda</code> (for predictions after CV use <code>predict()</code> instead). Supply instead a decreasing sequence of <code>lambda</code> values. <code>glmnet</code> relies on its warm starts for speed, and its often faster to fit a whole path than compute a single fit.
<code>standardize</code>	Logical flag for <code>x</code> variable standardization, prior to fitting the model sequence. The coefficients are always returned on the original scale. Default is <code>standardize=TRUE</code> . If variables are in the same units already, you might not wish to standardize. See details below for <code>y</code> standardization with <code>family="gaussian"</code> .
<code>intercept</code>	Should intercept(s) be fitted (default= <code>TRUE</code> ) or set to zero ( <code>FALSE</code> )
<code>thresh</code>	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 <code>thresh</code> times the null deviance. Defaults value is <code>1E-7</code> .
<code>dfmax</code>	Limit the maximum number of variables in the model. Useful for very large <code>nvars</code> , if a partial path is desired.
<code>pmax</code>	Limit the maximum number of variables ever to be nonzero
<code>exclude</code>	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 <code>exclude</code> function that generates the list of indices. This function is most generally defined as <code>function(x, y, weights, ...)</code> , and is called inside <code>glmnet</code> to generate the indices for excluded variables. The <code>...</code> argument is required, the others are optional. This is useful for filtering wide data, and works correctly with <code>cv.glmnet</code> . See the vignette 'Introduction' for examples.
<code>penalty.factor</code>	Separate penalty factors can be applied to each coefficient. This is a number that multiplies <code>lambda</code> 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 <code>exclude</code> ). Also, any <code>penalty.factor</code> that is set to <code>inf</code> is converted to an <code>exclude</code> , and then internally reset to 1. Note: the penalty factors are internally rescaled to sum to <code>nvars</code> , and the <code>lambda</code> sequence will reflect this change.
<code>lower.limits</code>	Vector of lower limits for each coefficient; default <code>-Inf</code> . Each of these must be non-positive. Can be presented as a single value (which will then be replicated), else a vector of length <code>nvars</code>
<code>upper.limits</code>	Vector of upper limits for each coefficient; default <code>Inf</code> . See <code>lower.limits</code>
<code>maxit</code>	Maximum number of passes over the data for all <code>lambda</code> values; default is <code>10^5</code> .
<code>type.gaussian</code>	Two algorithm types are supported for (only) <code>family="gaussian"</code> . The default when <code>nvar &lt; 500</code> is <code>type.gaussian="covariance"</code> , and saves all inner-products ever computed. This can be much faster than <code>type.gaussian="naive"</code> ,

	which loops through nobs every time an inner-product is computed. The latter can be far more efficient for $nvar \gg nobs$ situations, or when $nvar > 500$ .
<code>type.logistic</code>	If "Newton" then the exact hessian is used (default), while "modified.Newton" uses an upper-bound on the hessian, and can be faster.
<code>standardize.response</code>	This is for the <code>family="mgaussian"</code> family, and allows the user to standardize the response variables
<code>type.multinomial</code>	If "grouped" then a grouped lasso penalty is used on the multinomial coefficients for a variable. This ensures they are all in our out together. The default is "ungrouped"
<code>relax</code>	If TRUE then for each <i>active set</i> in the path of solutions, the model is refit without any regularization. See <code>details</code> 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.
<code>trace.it</code>	If <code>trace.it=1</code> , then a progress bar is displayed; useful for big models that take a long time to fit.
<code>...</code>	Additional argument used in <code>relax.glmnet</code> . These include some of the original arguments to 'glmnet', and each must be named if used.
<code>fit</code>	For <code>relax.glmnet</code> a fitted 'glmnet' object
<code>maxp</code>	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'.
<code>path</code>	Since <code>glmnet</code> does not do stepsize optimization, the Newton algorithm can get stuck and not converge, especially with relaxed fits. With <code>path=TRUE</code> , 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 <code>path=FALSE</code> . appropriate subset of variables
<code>check.args</code>	Should <code>relax.glmnet</code> 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

$$1/2RSS/nobs + \lambda * penalty,$$

and for the other models it is

$$-loglik/nobs + \lambda * penalty.$$

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-responses. For both of these the penalty on the coefficient vector for variable `j` is

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

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 <i>any</i> 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

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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
nzc = 5
x = matrix(rnorm(N * p), N, p)
beta = rnorm(nzc)
f = x[, seq(nzc)] %*% 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
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")
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,
  mxitr = 100,
  itrace = 0,
  epsnr = 1e-06,
  mxitrn = 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

<code>mxit</code>	maximum iterations for multiresponse bounds adjustment solution. factory default = 100
<code>itrace</code>	If 1 then progress bar is displayed when running <code>glmnet</code> and <code>cv.glmnet</code> . factory default = 0
<code>epsnr</code>	convergence threshold for <code>glmnet.fit</code> . factory default = 1.0e-6
<code>mxitr</code>	maximum iterations for the IRLS loop in <code>glmnet.fit</code> . factory default = 25
<code>factory</code>	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

```
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**

```

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 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. 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 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 <a href="#">family</a> 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 $1e-10$ .
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	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 $-\text{Inf}$ . Each of these must be non-positive. Can be presented as a single value (which will then be replicated), else a vector of length nvars.
upper.limits	Vector of upper limits for each coefficient; default $\text{Inf}$ . 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.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 overridden.

`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 $2*(\text{loglike\_sat} - \text{loglike})$ , where <code>loglike_sat</code> is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence <code>dev.ratio=1-dev/nulldev</code> .
nulldev	Null deviance (per observation). This is defined to be $2*(\text{loglike\_sat} - \text{loglike}(\text{Null}))$ . 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 <code>save_fit=TRUE</code> , 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.

---

<code>glmnet.measures</code>	<i>Display the names of the measures used in CV for different "glmnet" families</i>
------------------------------	---

---

### Description

Produces a list of names of measures

### Usage

```
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**

```
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**

<code>x</code>	Input matrix, of dimension <code>nobs</code> x <code>nvars</code> ; each row is an observation vector. Can be a sparse matrix.
<code>y</code>	Quantitative response variable.
<code>weights</code>	Observation weights. Default is 1 for each observation.
<code>lambda</code>	A user supplied lambda sequence. Typical usage is to have the program compute its own lambda sequence based on <code>nlambda</code> and <code>lambda.min.ratio</code> . Supplying a value of lambda overrides this.
<code>nlambda</code>	The number of lambda values, default is 100.
<code>lambda.min.ratio</code>	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 <code>nobs</code> relative to the number of variables <code>nvars</code> . If <code>nobs</code> >= <code>nvars</code> , the default is 0.0001, close to zero. If <code>nobs</code> < <code>nvars</code> , the default is 0.01. A very small value of <code>lambda.min.ratio</code> will lead to a saturated fit in the <code>nobs</code> < <code>nvars</code> case. This is undefined for some families of models, and the function will exit gracefully when the percentage deviance explained is almost 1.
<code>alpha</code>	The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$ . The penalty is defined as $(1 - \alpha)/2 \ \beta\ _2^2 + \alpha \ \beta\ _1.$ <p><code>alpha=1</code> is the lasso penalty, and <code>alpha=0</code> the ridge penalty.</p>
<code>offset</code>	A vector of length <code>nobs</code> 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 <code>predict</code> function.
<code>family</code>	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 <code>gaussian()</code> . (See <a href="#">family</a> for details on family functions.)
<code>standardize</code>	Logical flag for x variable standardization, prior to fitting the model sequence. The coefficients are always returned on the original scale. Default is <code>standardize=TRUE</code> . If variables are in the same units already, you might not wish to standardize.
<code>intercept</code>	Should intercept be fitted (default=TRUE) or set to zero (FALSE)?
<code>thresh</code>	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 <code>thresh</code> times the null deviance. Default value is $1e-10$ .
<code>maxit</code>	Maximum number of passes over the data; default is $10^5$ .
<code>penalty.factor</code>	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 <code>exclude</code> ). Note: the penalty factors are internally rescaled to sum to <code>nvars</code> .
<code>exclude</code>	Indices of variables to be excluded from the model. Default is none. Equivalent to an infinite penalty factor.

<code>lower.limits</code>	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 <code>nvars</code> .
<code>upper.limits</code>	Vector of upper limits for each coefficient; default $\text{Inf}$ . See <code>lower.limits</code> .
<code>trace.it</code>	Controls how much information is printed to screen. Default is <code>trace.it=0</code> (no information printed). If <code>trace.it=1</code> , a progress bar is displayed. If <code>trace.it=2</code> , 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".

<code>a0</code>	Intercept sequence of length <code>length(lambda)</code> .
<code>beta</code>	A <code>nvars x length(lambda)</code> matrix of coefficients, stored in sparse matrix format.
<code>df</code>	The number of nonzero coefficients for each value of lambda.
<code>dim</code>	Dimension of coefficient matrix.
<code>lambda</code>	The actual sequence of lambda values used. When <code>alpha=0</code> , the largest lambda reported does not quite give the zero coefficients reported ( <code>lambda=inf</code> would in principle). Instead, the largest lambda for <code>alpha=0.001</code> is used, and the sequence of lambda values is derived from this.
<code>dev.ratio</code>	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 <code>loglike_sat</code> is the log-likelihood for the saturated model (a model with a free parameter per observation). Hence <code>dev.ratio=1-dev/nulldev</code> .
<code>nulldev</code>	Null deviance (per observation). This is defined to be $2*(\text{loglike\_sat} - \text{loglike}(\text{Null}))$ . The null model refers to the intercept model.
<code>npasses</code>	Total passes over the data summed over all lambda values.
<code>jerr</code>	Error flag, for warnings and errors (largely for internal debugging).
<code>offset</code>	A logical variable indicating whether an offset was included in the model.
<code>call</code>	The call that produced this object.
<code>family</code>	Family used for the model.
<code>nobs</code>	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	<i>convert a data frame to a data matrix with one-hot encoding</i>
-------	--

---

**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**

<code>train</code>	Required argument. A dataframe consisting of vectors, matrices and factors
<code>test</code>	Optional argument. A dataframe matching 'train' for use as testing data
<code>na.impute</code>	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'
<code>sparse</code>	Logical, default FALSE. If TRUE then the returned matrice(s) are converted to matrices of class "CsparseMatrix". Useful if some factors have a large number of levels, resulting in very big matrices, mostly zero
<code>...</code>	additional arguments, currently unused

**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](mailto: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 freame with missing values
Xn = X
Xn[3, 1] = NA
Xn[5, 2] = NA
X3n = X3
X3n[6] = NA
X4n = X4
X4n[9] = NA
dfn = data.frame(Xn, X3n, X4n)

makeX(dfn)
makeX(dfn, sparse = TRUE)
makeX(dfn, na.impute = TRUE)
makeX(dfn, na.impute = TRUE, sparse = TRUE)

### Test data as well
X = matrix(rnorm(10), 5, 2)
X3 = sample(letters[1:3], 5, replace = TRUE)
X4 = sample(LETTERS[1:3], 5, replace = TRUE)
dft = data.frame(X, X3, X4)

makeX(df, dft)
makeX(df, dft, sparse = TRUE)

### Missing data in test as well
Xn = X
Xn[3, 1] = NA
Xn[5, 2] = NA
X3n = X3
X3n[1] = NA
X4n = X4
X4n[2] = NA
dfn = data.frame(Xn, X3n, X4n)
```

```
makeX(dfn, dftn)
makeX(dfn, dftn, sparse = TRUE)
makeX(dfn, dftn, na.impute = TRUE)
makeX(dfn, dftn, sparse = TRUE, na.impute = TRUE)
```

---

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**

```
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

```
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.

---

na.replace	<i>Replace the missing entries in a matrix columnwise with the entries in a supplied vector</i>
------------	---

---

### Description

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

### Usage

```
na.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](mailto:hastie@stanford.edu)

### See Also

makeX and glmnet

### Examples

```
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)
na.replace(x, m)
```

---

obj\_function

*Elastic net objective function value*

---

### Description

Returns the elastic net objective function value.

### Usage

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

### 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.
lambda	A single value for the lambda hyperparameter.
alpha	The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$ .
coefficients	The model's coefficients (excluding intercept).
vp	Penalty factors for each of the coefficients.

---

pen_function	<i>Elastic net penalty value</i>
--------------	----------------------------------

---

**Description**

Returns the elastic net penalty value without the lambda factor.

**Usage**

```
pen_function(coefficients, alpha = 1, vp = 1)
```

**Arguments**

coefficients	The model's coefficients (excluding intercept).
alpha	The elasticnet mixing parameter, with $0 \leq \alpha \leq 1$ .
vp	Penalty factors for each of the coefficients.

**Details**

The penalty is defined as

$$(1 - \alpha)/2 \sum v p_j \beta_j^2 + \alpha \sum v p_j |\beta_j|.$$

Note the omission of the multiplicative lambda factor.

---

plot.cv.glmnet	<i>plot the cross-validation curve produced by cv.glmnet</i>
----------------	--

---

**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](mailto:hastie@stanford.edu)

**References**

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent*

**See Also**

glmnet and cv.glmnet.

**Examples**

```

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)

```

---

plot.glmnet                      *plot coefficients from a "glmnet" object*

---

### Description

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

### Usage

```
## 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](mailto:hastie@stanford.edu)

**References**

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent*

**See Also**

glmnet, and print, predict and coef methods.

**Examples**

```
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

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

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

## 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 Matrix package. See documentation for 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)
...	Not used. Other arguments to predict.
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 ... argument which is passed on to the predict method for glmnet objects.

**Author(s)**

Jerome Friedman, Trevor Hastie and Rob Tibshirani  
 Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

**References**

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent* (2010), *Journal of Statistical Software*, Vol. 33(1), 1-22, [doi:10.18637/jss.v033.i01](https://doi.org/10.18637/jss.v033.i01).

Simon, N., Friedman, J., Hastie, T. and Tibshirani, R. (2011) *Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent*, *Journal of Statistical Software*, Vol. 39(5), 1-13, [doi:10.18637/jss.v039.i05](https://doi.org/10.18637/jss.v039.i05).

Hastie, T., Tibshirani, Robert and Tibshirani, Ryan (2020) *Best Subset, Forward Stepwise or Lasso? Analysis and Recommendations Based on Extensive Comparisons*, *Statist. Sc.* Vol. 35(4), 579-592, <https://arxiv.org/abs/1707.08692>.

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

**See Also**

glmnet, and print, and coef methods, and cv.glmnet.

**Examples**

```
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.fitr, newx = x[1:5, ])
coef(cv.fitr)
coef(cv.fitr, s = "lambda.min", gamma = "gamma.min")
predict(cv.fitr, 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**

```
## 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.
exact	This argument is relevant only when predictions are made at values of s (lambda) <i>different</i> 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 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 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.
newoffset	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.

**Value**

The object returned depends on type.

---

print.cv.glmnet      *print a cross-validated glmnet object*

---

### Description

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

### Usage

```
## 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.

### Author(s)

Jerome Friedman, Trevor Hastie and Rob Tibshirani  
Maintainer: Trevor Hastie [hastie@stanford.edu](mailto:hastie@stanford.edu)

### References

Friedman, J., Hastie, T. and Tibshirani, R. (2008) *Regularization Paths for Generalized Linear Models via Coordinate Descent*  
<https://arxiv.org/abs/1707.08692>  
Hastie, T., Tibshirani, Robert, Tibshirani, Ryan (2019) *Extended Comparisons of Best Subset Selection, Forward Stepwise Selection, and the Lasso*

### See Also

glmnet, predict and coef methods.

**Examples**

```
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 glmnet object
```

---

**Description**

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

**Usage**

```
## 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

**Details**

The call that produced the object x is printed, followed by a three-column matrix with columns Df, %Dev and Lambda. The Df column is the number of nonzero coefficients (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 R which gives the percent deviance explained by the relaxed model. For a "bigGlm" model, a simpler summary is printed.

**Value**

The matrix above is silently returned

**References**

Friedman, J., Hastie, T. and Tibshirani, R. (2008). Regularization Paths for Generalized Linear Models via Coordinate Descent

**See Also**

glmnet, predict and coef methods.

## Examples

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

---

QuickStartExample	<i>Synthetic dataset with Gaussian response</i>
-------------------	---

---

## Description

Randomly generated data for Gaussian regression example.

## Usage

```
data(QuickStartExample)
```

## Format

List containing the following elements:

**x** 100 by 20 matrix of numeric values.

**y** Numeric vector of length 100.

---

response.coxnet	<i>Make response for coxnet</i>
-----------------	---------------------------------

---

## 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	<i>Generate multinomial samples from a probability matrix</i>
-------	---

---

**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](mailto:hastie@stanford.edu)

---

SparseExample	<i>Synthetic dataset with sparse design matrix</i>
---------------	--

---

**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	<i>Add strata to a Surv object</i>
--------------	------------------------------------

---

### 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

```
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
```

---

survfit.coxnet	<i>Compute a survival curve from a coxnet object</i>
----------------	--

---

### Description

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

**Usage**

```
## 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 <code>survfit.coxnet</code> is called for a single penalty parameter.
...	This is the mechanism for passing additional arguments like (i) <code>x=</code> and <code>y=</code> for the <code>x</code> and <code>y</code> used to fit the model, (ii) <code>weights=</code> and <code>offset=</code> when the model was fit with these options, (iii) arguments for new data ( <code>newx</code> , <code>newoffset</code> , <code>newstrata</code> ), and (iv) arguments to be passed to <code>survfit.coxph()</code> .

**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**

```
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

```

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

```

### Arguments

formula	A class cv.glmnet object. The object should have been fit with family="cox".
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.
...	Other arguments to be passed to survfit.coxnet.

### 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

```

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)

```

---

use.cox.path

*Check if glmnet should call cox.path*


---

### 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`

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