Package ‘glmnet’

February 19, 2015

Type Package
Title Lasso and elastic-net regularized generalized linear models
Version 1.9-8
Date 2014-5-23
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Depends Matrix (>= 1.0-6), utils
Suggests survival, foreach
Description Extremely efficient procedures for fitting the entire lasso or elastic-net regularization path for linear regression, logistic and multinomial regression models, poisson regression and the Cox model. Two recent additions are the multireponse gaussian, and the grouped multinomial. The algorithm uses cyclical coordinate descent in a path-wise fashion, as described in the paper listed below.
License GPL-2
URL http://www.jstatsoft.org/v33/i01/.
NeedsCompilation yes
Repository CRAN
Date/Publication 2014-05-24 22:49:45

R topics documented:

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glmnet-package

Elastic net model paths for some generalized linear models

Description

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

Details

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

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

Author(s)

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

References

http://www.jstatsoft.org/v33/i01/
http://www.jstatsoft.org/v39/i05/
Glmnet Vignette http://www.stanford.edu/~hastie/glmmnet/glmmnet_alpha.html
cv.glmmnet

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)

---

cv.glmmnet

Cross-validation for glmnet

Description

Does k-fold cross-validation for glmnet, produces a plot, and returns a value for lambda

Usage

cv.glmmnet(x, y, weights, offset, lambda, type.measure, nfolds, foldid, grouped, keep, parallel, ...)

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
nfolds number of folds - default is 10. Although nfolds can be as large as the sample size (leave-one-out CV), it is not recommended for large datasets. Smallest value allowable is nfolds=3
foldid an optional vector of values between 1 and nfold identifying what fold each observation is in. If supplied, nfold can be missing.
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.

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

`keep` If `keep=TRUE`, a *prevalidated* array is returned containing fitted values for each observation and each value of `lambda`. This means these fits are computed with this observation and the rest of its fold omitted. The `foldid` vector is also returned. Default is `keep=FALSE`

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

... Other arguments that can be passed to glmnet

### Details

The function runs `glmnet` `nfold`s+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.

### Value

An object of class "cv.glmnet" is returned, which is a list with the ingredients of the cross-validation fit.

- `lambda` the values of `lambda` used in the fits.
- `cvm` The mean cross-validated error - a vector of length `length(lambda)`.
- `cvsd` estimate of standard error of `cvm`.
- `cvup` upper curve = `cvm+cvsd`.
- `cvlo` lower curve = `cvm-cvsd`.
- `nzero` number of non-zero coefficients at each `lambda`.
- `name` a text string indicating type of measure (for plotting purposes).
- `glmnet.fit` a fitted glmnet object for the full data.
lambda.min  value of lambda that gives minimum cvm.
lambda.1se  largest value of lambda such that error is within 1 standard error of the minimum.
fit.preval  if keep=TRUE, this is the array of prevalidated fits. Some entries can be NA, if that and subsequent values of lambda are not reached for that fold
foldid  if keep=TRUE, the fold assignments used

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
http://www.jstatsoft.org/v33/i01/
http://www.jstatsoft.org/v39/i05/

See Also
glmnet and plot, predict, and coef methods for "cv.glmnet" object.

Examples
set.seed(1010)
n=1000; p=100
ncr=trunc(p/10)
x=matrix(rnorm(n*p),n,p)
beta=rnorm(ncr)
fx= x[, seq(ncr)] %% 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)
cvobi=cv.glmnet(x,y)
plot(cvobi)
coef(cvobi)
predict(cvobi,newx=x[1:5], s="lambda.min")
title("Gaussian Family", line=2.5)
set.seed(1011)
cvobla=cv.glmnet(x,y,type.measure="mae")
plot(cvobla)
```r
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, y, family="binomial")
plot(cvob2)
title("Binomial Family", line=2.5)
frame()
set.seed(1011)
cvob3=cv.glmnet(x, y, family="binomial", type.measure="class")
plot(cvob3)
title("Binomial Family", line=2.5)
set.seed(1011)
cvob3a=cv.glmnet(x, y, 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=cbind(beta3, matrix(0, p-10, 3))
f3=x%*% beta3
p3=exp(f3)
p3=p3/apply(p3, 1, sum)
g3=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=exp(x, hx)
tcens=rbinom(n=n, prob=.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)
## Not run:
# Parallel
require(doMC)
registerDoMC(cores=4)
x=matrix(rnorm(1e5 * 100), 1e5, 100)
y=rnorm(1e5)
system.time(cv.glmnet(x, y))
```
deviance.glmnet

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**

```r
## 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 $2 \times (\text{loglike}_{\text{sat}} - \text{loglike})$, where $\text{loglike}_{\text{sat}}$ is the log-likelihood for the saturated model (a model with a free parameter per observation). Null deviance is defined to be $2 \times (\text{loglike}_{\text{sat}} - \text{loglike}(\text{Null}))$; 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 $(1-\text{dev.ratio}) \times \text{nulldev}$.

**Value**

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

**Author(s)**

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**References**


**See Also**

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

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

---

glmnet

**fit a GLM with lasso or elasticnet regularization**

Description

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

Usage

```r
glmnet(x, y, family = c("gaussian", "binomial", "poisson", "multinomial", "cox", "mgaussian"),
weights, offset = NULL, alpha = 1, nlambda = 100,
lambda.min.ratio = ifelse(nobs < nvars, 0.01, 0.0001), lambda = NULL,
standardize = TRUE, intercept = TRUE, thresh = 1e-07,
dfmax = nvars + 1,
pmax = min(dfmax * 2 + 20, nvars), exclude, penalty.factor = rep(1, nvars),
lower.limits = -Inf, upper.limits = Inf, maxit = 100000,
type.gaussian = ifelse(nvars < 500, "covariance", "naive"),
type.logistic = c("Newton", "modified.Newton"),
standardize.response = FALSE, type.multinomial = c("ungrouped", "grouped"))
```

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; not yet available for family="cox")
- `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 nclass>2 level factor, or a matrix with nclass columns of counts or proportions. For family="cox", y should be 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. The function Surv() in package survival produces such a matrix. For family="mgaussian", y is a matrix of quantitative responses.
- `family`: Response type (see above)
- `weights`: observation weights. Can be total counts if responses are proportion matrices. Default is 1 for each observation
offset

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

alpha

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

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

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

nlambda

The number of lambda values - default is 100.

lambda.min.ratio

Smallest value for lambda, as a fraction of lambda.max, the (data derived) entry value (i.e. the smallest value for which all coefficients are zero). The default depends on the sample size `nobs` relative to the number of variables `nvars`.

If `nobs > nvars`, the default is 0.0001, close to zero. If `nobs < nvars`, the default is 0.01. A very small value of lambda.min.ratio will lead to a saturated fit in the `nobs < nvars` case. This is undefined for "binomial" and "multinomial" models, and glmnet will exit gracefully when the percentage deviance explained is almost 1.

lambda

A user supplied lambda sequence. Typical usage is to have the program compute its own lambda sequence based on `nlambda` and `lambda.min.ratio`. Supplying a value of lambda overrides this. WARNING: use with care. Do not supply a single value for lambda (for predictions after CV use `predict()` instead). Supply instead a decreasing sequence of lambda values. glmnet relies on its warms starts for speed, and its often faster to fit a whole path than compute a single fit.

standardize

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

intercept

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

thresh

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

dfmax

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

pmax

Limit the maximum number of variables ever to be nonzero

exclude

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

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

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

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

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

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

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

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

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. For the other families, this 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. Note that the objective function for "gaussian" is

\[
1/2\text{RSS}/nobs + \lambda \times \text{penalty},
\]

and for the other models it is

\[
-\text{loglik}/nobs + \lambda \times \text{penalty}.
\]

Note also that for "gaussian", glmnet standardizes \(y\) to have unit variance 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 latest two features in glmnet 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-responded. 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 elastic-net.

Value

An object with S3 class "glmnet","*", where "*" is "elnet","lognet","multnet","fishnet" (poisson), "coxnet" or "mrelnet" for the various types of models.

call the call that produced this object

alpha

A vector of length 1.

Beta

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

lambda

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

dev.ratio

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

nulldev

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

df

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

dfmat

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

dim

dimension of coefficient matrix (ices)

nobs

number of observations

npasses

total passes over the data summed over all lambda values

offset

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

jerr

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

Author(s)

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References


http://www.jstatsoft.org/v33/i01/
http://www.jstatsoft.org/v39/i05/

Glmnet Vignette http://www.stanford.edu/~hastie/glmnet/glmnet_alpha.html

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

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

# binomial
g2=sample(1:2,100,replace=TRUE)
fit2=glmnet(x,g2,family="binomial")

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

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

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

# Sparse
n=10000;p=200
nzcl= trunc(p/10)
x=matrix(rnorm(n*p),n,p)
iz=sample(l:(n*p),size=n*p*.85,replace=FALSE)
x[iz]=0
sx=Matrix(x,sparse=TRUE)
inherits(sx,"sparseMatrix")#confirm that it is sparse
beta=rnorm(nzcl)
fx=x[,seq(nzcl)]%*%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(fit2<-glmnet(x,y))

---

### glmnet.control

**internal glmnet parameters**

**Description**

View and/or change the factory default parameters in glmnet

**Usage**

```r
glmnet.control(fdev=1.0e-5, devmax=0.999, eps=1.0e-6, big=9.9e35, mnlam=5, pmin=1.0e-9, exmx=250.0, prec=1e-10, mexit=100, 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
plot.cv.glmnet

big       large floating point number; factory default = 9.9e35. Inf in definition of upper.limit is set to big
mnlam    minimum number of path points (lambda values) allowed; factory default = 5
pmin      minimum probability for any class. factory default = 1.0e-9. Note that this implies a pmax of 1-pmin.
exmx      maximum allowed exponent. factory default = 250.0
prec      convergence threshold for multi response bounds adjustment solution. factory default = 1.0e-10
mxit      maximum iterations for multiresponse bounds adjustment solution. factory default = 100
factory   If TRUE, reset all the parameters to the factory default; default is FALSE

Details

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

Value

A list with named elements as in the argument list

Author(s)

Jerome Friedman, Trevor Hastie
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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

plot.cv.glmnet          plot the cross-validation curve produced by cv.glmnet

Description

Plots the cross-validation curve, and upper and lower standard deviation curves, as a function of the lambda values used.
plot.cv.glmnet

Usage

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

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

Details

A plot is produced, and nothing is returned.

Author(s)

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References


See Also

glmnet and cv.glmnet.

Examples

```r
set.seed(1010)
n=1000;p=100
ncz=trunc(p/10)
x=matrix(rnorm(n*p),n,p)
beta=rnorm(ncz)
fz=x[,seq(ncz)] %*% beta
eps=rnorm(n)*5
y=drop(fz+eps)
pz=exp(fz)
pz=pz/(1+pz)
ly=rbinom(n=length(pz),prob=pz,size=1)
cvob1=cv.glmnet(x,y)
plot(cvob1)
title("Gaussian Family",line=2.5)
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)
```
plot.glmnet

Description

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

Usage

```r
set.seed(1011)
cvobb3=cv.glmnet(x,ly,family="binomial",type="class")
plot(cvobb3)
title("Binomial Family",line=2.5)
```

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.
- **type.coef**: If type.coef="2norm" then a single curve per variable, else if type.coef="coef", a coefficient plot per response
- **...**: Other graphical parameters to plot

Details

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

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References

predict.cv.glmnet

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)

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.

Usage

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

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

Arguments

object  Fitted "cv.glmnet" 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.

...  Not used. Other arguments to predict.

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)

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References

http://www.jstatsoft.org/v33/i01/

See Also

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

Examples

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

---

**predict.glmnet**

*make predictions from a "glmnet" object.*

Description

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

Usage

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

Arguments

- **object**: Fitted "glmnet" model 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. 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 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 \( s \).
- **exact**: If `exact=TRUE`, and predictions are to made at values of \( s \) not included in the original fit, these values of \( s \) are merged with `object$lambda`, and the model is refit before predictions are made. If `exact=FALSE` (default), then the predict function uses linear interpolation to make predictions for values of \( s \) that do not coincide with those used in the fitting algorithm. Note that `exact=TRUE` is fragile when used inside a nested sequence of function calls. `predict.glmnet()` needs to update the model, and expects the data used to create it to be around.
- **offset**: If an offset is used in the fit, then one must be supplied for making predictions (except for `type="coefficients"` or `type="nonzero"`)
- **...**: Not used. Other arguments to predict.

Details

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

Value

The object returned depends on type.

Author(s)

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References

http://www.jstatsoft.org/v33/i01/

http://www.jstatsoft.org/v39/i05/

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)
f1 = glmnet(x,y)
predict(fit1,newx=x[1:5,],s=c(0.01,0.005))
predict(fit1,type="coef")
f2 = glmnet(x,g2,family="binomial")
predict(fit2,type="response",newx=x[2:5,])
predict(fit2,type="nonzero")
f3 = glmnet(x,g4,family="multinomial")
predict(fit3,newx=x[1:3],type="response",s=0.01)

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).

Value
The matrix above is silently returned.

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References

See Also
glmnet, predict and coef methods.

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