

# Package ‘glmpath’

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**Title** L1 Regularization Path for Generalized Linear Models and Cox Proportional Hazards Model

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**Description** A path-following algorithm for L1 regularized generalized linear models and Cox proportional hazards model

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bootstrap.path	<i>Generates a set of bootstrap coefficients for glmpath or coxpath</i>
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### Description

This function generates a set of bootstrap coefficients for glmpath or coxpath. For each bootstrap run, the regularization parameter may be determined based on either aic or bic.

### Usage

```
bootstrap.path(x, y, data, B, index = NULL,
               path = c("glmpath", "coxpath"),
               method = c("aic", "bic"), trace = FALSE, ...)
```

### Arguments

x	matrix of features
y	response
data	a list of data components. If path=glmpath, data consists of x: a matrix of features and y: response. data is not needed if x and y are input separately. If path=coxpath, data must be provided, including x: a matrix of features, time: the survival time, and status: censor status with 1 if died and 0 if censored.
B	number of bootstrap runs
index	matrix (B rows, ncol(x) columns) of bootstrap sample indices. Each row is a vector of indices for a bootstrap run. If index=NULL, the indices are randomly chosen.
path	Bootstrap coefficients for either glmpath or coxpath are computed. Default is path=glmpath.
method	For each bootstrap run, the regularization parameter is determined based on either aic or bic. Default is aic.
trace	If TRUE, the number of bootstrap runs is printed out.
...	other options for glmpath or coxpath

### Details

Fitting glmpath or coxpath gives a series of solution sets with a varying size of the active set. Once we select an appropriate value of the regularization parameter, and thus a set of coefficients, we may then validate the chosen coefficients through bootstrap analysis. plot.bootstrap summarizes the bootstrap results by generating the histograms or the pair scatter plots of the bootstrap coefficients.

### Value

bootstrap.path returns a bootpath object, which is a matrix (B by ncol(x)) of bootstrap coefficients. Coefficients computed from the whole data are stored as an attribute coefficients.

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Bradley Efron and Robert Tibshirani (1993) *An Introduction to the Bootstrap* CHAPMAN & HALL/CRC, Boca Raton.

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

coxpath, glmpath, plot.bootstrap

**Examples**

```
data(heart.data)
attach(heart.data)
bootstrap.a <- bootstrap.path(x, y, B=5, method="bic")
detach(heart.data)
data(lung.data)
attach(lung.data)
bootstrap.b <- bootstrap.path(data=lung.data, B=5, path="coxpath")
detach(lung.data)
```

---

coxpath

*Fits the entire L1 regularization path for Cox proportional hazards model*

---

**Description**

This algorithm uses predictor-corrector method to compute the entire regularization path for Cox proportional hazards model with L1 penalty.

**Usage**

```
coxpath(data, nopenalty.subset = NULL, method = c("breslow", "efron"),
        lambda2 = 1e-5, max.steps = 10 * min(n, m), max.norm = 100 * m,
        min.lambda = (if (m >= n) 1e-3 else 0), max.vars = Inf,
        max.arclength = Inf, frac.arclength = 1, add.newvars = 1,
        bshoot.threshold = 0.1, relax.lambda = 1e-7,
        approx.Gram = FALSE, standardize = TRUE,
        eps = .Machine$double.eps, trace = FALSE)
```

**Arguments**

<code>data</code>	a list consisting of <code>x</code> : a matrix of features, <code>time</code> : the survival time, and <code>status</code> : censor status with 1 if died and 0 if censored.
<code>nopenalty.subset</code>	a set of indices for the predictors that are not subject to the L1 penalty
<code>method</code>	approximation method for tied survival times. Approximations derived by Breslow (1974) and Efron (1977) are available. Default is <code>breslow</code> .
<code>lambda2</code>	regularization parameter for the L2 norm of the coefficients. Default is $1e-5$ .
<code>max.steps</code>	an optional bound for the number of steps to be taken. Default is $10 * \min\{\text{nrow}(x), \text{ncol}(x)\}$ .
<code>max.norm</code>	an optional bound for the L1 norm of the coefficients. Default is $100 * \text{ncol}(x)$ .
<code>min.lambda</code>	an optional (lower) bound for the size of $\lambda$ . When $\text{ncol}(x)$ is relatively large, the coefficient estimates are prone to numerical precision errors at extremely small $\lambda$ . In such cases, early stopping is recommended. Default is 0 for $\text{ncol}(x) < \text{nrow}(x)$ cases and $1e-3$ otherwise.
<code>max.vars</code>	an optional bound for the number of active variables. Default is <code>Inf</code> .
<code>max.arclength</code>	an optional bound for arc length (L1 norm) of a step. If <code>max.arclength</code> is extremely small, an exact nonlinear path is produced. Default is <code>Inf</code> .
<code>frac.arclength</code>	Under the default setting, the next step size is computed so that the active set changes right at the next value of $\lambda$ . When <code>frac.arclength</code> is assigned some fraction between 0 and 1, the step size is decreased by the factor of <code>frac.arclength</code> in arc length. If <code>frac.arclength=0.2</code> , the step length is adjusted so that the active set would change after five smaller steps. Either <code>max.arclength</code> or <code>frac.arclength</code> can be used to force the path to be more accurate. Default is 1.
<code>add.newvars</code>	<code>add.newvars</code> candidate variables (that are currently not in the active set) are used in the corrector step as potential active variables. Default is 1.
<code>bshoot.threshold</code>	If the absolute value of a coefficient is larger than <code>bshoot.threshold</code> at the first corrector step it becomes nonzero (therefore when $\lambda$ is considered to have been decreased too far), $\lambda$ is increased again. i.e. A backward distance in $\lambda$ that makes the coefficient zero is computed. Default is 0.1.
<code>relax.lambda</code>	A variable joins the active set if $ l'(\beta)  > \lambda * (1 - \text{relax.lambda})$ . Default is $1e-7$ . If no variable joins the active set even after many (>20) steps, the user should increase <code>relax.lambda</code> to $1e-6$ or $1e-5$ , but not more than that. This adjustment is sometimes needed because of the numerical precision/error propagation problems. In general, the paths are less accurate with relaxed $\lambda$ .
<code>approx.Gram</code>	If <code>TRUE</code> , an approximated Gram matrix is used in predictor steps; each step takes less number of computations, but the total number of steps usually increases. This might be useful when the number of features is large.
<code>standardize</code>	If <code>TRUE</code> , predictors are standardized to have a unit variance.
<code>eps</code>	an effective zero
<code>trace</code>	If <code>TRUE</code> , the algorithm prints out its progress.

## Details

This algorithm implements the predictor-corrector method to determine the entire path of the coefficient estimates as the amount of regularization varies; it computes a series of solution sets, each time estimating the coefficients with less regularization, based on the previous estimate. The coefficients are estimated with no error at the knots, and the values are connected, thereby making the paths piecewise linear.

## Value

A coxpath object is returned.

lambda	vector of $\lambda$ values for which the exact coefficients are computed
lambda2	$\lambda_2$ used
step.length	vector of step lengths in $\lambda$
corr	matrix of $l'(\beta)$ values (derivatives of the log-partial-likelihood)
new.df	vector of degrees of freedom (to be used in the plot function)
df	vector of degrees of freedom at each step
loglik	vector of log-partial-likelihood computed at each step
aic	vector of AIC values
bic	vector of BIC values
b.predictor	matrix of coefficient estimates from the predictor steps
b.corrector	matrix of coefficient estimates from the corrector steps
new.A	vector of boolean values indicating the steps at which the active set changed (to be used in the plot/predict functions)
actions	actions taken at each step
meanx	means of the columns of x
sdx	standard deviations of the columns of x
xnames	column names of x
method	method used
nopenalty.subset	nopenalty.subset used
standardize	TRUE if the predictors were standardized before fitting

## Author(s)

Mee Young Park and Trevor Hastie

## References

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

## See Also

cv.coxpath, plot.coxpath, predict.coxpath, summary.coxpath

## Examples

```
data(lung.data)
attach(lung.data)
fit.a <- coxpath(lung.data)
fit.b <- coxpath(lung.data, method="efron")
detach(lung.data)
```

---

cv.coxpath	<i>Computes cross-validated (minus) log-partial-likelihoods for coxpath</i>
------------	---

---

## Description

This function computes cross-validated (minus) log-partial-likelihoods for coxpath.

## Usage

```
cv.coxpath(data, method = c("breslow", "efron"), nfold = 5,
            fraction = seq(0, 1, length = 100),
            mode = c("norm", "lambda"), plot.it = TRUE, se = TRUE, ...)
```

## Arguments

data	a list consisting of x: a matrix of features, time: the survival time, and status: censor status with 1 if died and 0 if censored.
method	approximation method for tied survival times. Approximations derived by Breslow (1974) and Efron (1977) are available. Default is breslow.
nfold	number of folds to be used in cross-validation. Default is nfold=5.
fraction	the fraction of L1 norm or $\log(\lambda)$ with respect to their maximum values at which the CV errors are computed. Default is <code>seq(0, 1, length=100)</code> .
mode	If mode=norm, cross-validation is run at certain values of L1 norm. If mode=lambda, cross-validation is run at certain values of $\log(\lambda)$ . Default is norm.
plot.it	If TRUE, CV curve is plotted.
se	If TRUE, standard errors are plotted.
...	other options for coxpath

## Author(s)

Mee Young Park and Trevor Hastie

## References

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

coxpath, plot.coxpath, predict.coxpath

**Examples**

```
data(lung.data)
attach(lung.data)
cv <- cv.coxpath(lung.data)
detach(lung.data)
```

---

cv.glmpath	<i>Computes cross-validated (minus) log-likelihoods or prediction errors for glmpath</i>
------------	--

---

**Description**

This function computes cross-validated (minus) log-likelihoods or prediction errors for glmpath.

**Usage**

```
cv.glmpath(x, y, data, family = binomial, weight = rep(1, n),
           offset = rep(0, n), nfold = 10,
           fraction = seq(0, 1, length = 100),
           type = c("loglik", "response"), mode = c("norm", "lambda"),
           plot.it = TRUE, se = TRUE, ...)
```

**Arguments**

x	matrix of features
y	response
data	a list consisting of x: a matrix of features and y: response. data is not needed if above x and y are input separately.
family	name of a family function that represents the distribution of y to be used in the model. It must be binomial, gaussian, or poisson. For each one, the canonical link function is used; logit for binomial, identity for gaussian, and log for poisson distribution. Default is binomial.
weight	an optional vector of weights for observations
offset	an optional vector of offset. If a column of x is used as offset, the corresponding column must be excluded from x.
nfold	number of folds to be used in cross-validation. Default is nfold=10.
fraction	the fraction of L1 norm or $\log(\lambda)$ with respect to their maximum values at which the CV errors are computed. Default is seq(0, 1, length=100).
type	If type=loglik, cross-validated minus log-likelihoods are computed. If type=response, cross-validated prediction errors are computed. Default is loglik.

<code>mode</code>	If <code>mode=norm</code> , cross-validation is run at certain values of L1 norm. If <code>mode=lambda</code> , cross-validation is run at certain values of $\log(\lambda)$ . Default is <code>norm</code> .
<code>plot.it</code>	If TRUE, CV curve is plotted.
<code>se</code>	If TRUE, standard errors are plotted.
<code>...</code>	other options for <code>glmpath</code>

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

`glmpath`, `plot.glmpath`, `predict.glmpath`

**Examples**

```
data(heart.data)
attach(heart.data)
cv.a <- cv.glmpath(x, y, family=binomial)
cv.b <- cv.glmpath(x, y, family=binomial, type="response")
detach(heart.data)
```

---

`glmpath`

*Fits the entire L1 regularization path for generalized linear models*

---

**Description**

This algorithm uses predictor-corrector method to compute the entire regularization path for generalized linear models with L1 penalty.

**Usage**

```
glmpath(x, y, data, nopenalty.subset = NULL, family = binomial,
        weight = rep(1, n), offset = rep(0, n), lambda2 = 1e-5,
        max.steps = 10 * min(n, m), max.norm = 100 * m,
        min.lambda = (if (m >= n) 1e-6 else 0), max.vars = Inf,
        max.arclength = Inf, frac.arclength = 1, add.newvars = 1,
        bshoot.threshold = 0.1, relax.lambda = 1e-8,
        standardize = TRUE, eps = .Machine$double.eps,
        trace = FALSE)
```



**Arguments**

<code>x</code>	matrix of features
<code>y</code>	response
<code>data</code>	a list consisting of <code>x</code> : a matrix of features and <code>y</code> : response. <code>data</code> is not needed if <code>x</code> and <code>y</code> are input separately.
<code>nopenalty.subset</code>	a set of indices for the predictors that are not subject to the L1 penalty
<code>family</code>	name of a family function that represents the distribution of <code>y</code> to be used in the model. It must be <code>binomial</code> , <code>gaussian</code> , or <code>poisson</code> . For each one, the canonical link function is used; <code>logit</code> for binomial, <code>identity</code> for gaussian, and <code>log</code> for poisson distribution. Default is <code>binomial</code> .
<code>weight</code>	an optional vector of weights for observations
<code>offset</code>	an optional vector of offset. If a column of <code>x</code> is used as offset, the corresponding column must be removed from <code>x</code> .
<code>lambda2</code>	regularization parameter for the L2 norm of the coefficients. Default is $1e-5$ .
<code>max.steps</code>	an optional bound for the number of steps to be taken. Default is $10 * \min\{\text{nrow}(x), \text{ncol}(x)\}$ .
<code>max.norm</code>	an optional bound for the L1 norm of the coefficients. Default is $100 * \text{ncol}(x)$ .
<code>min.lambda</code>	an optional (lower) bound for the size of $\lambda$ . Default is $0$ for $\text{ncol}(x) < \text{nrow}(x)$ cases and $1e-6$ otherwise.
<code>max.vars</code>	an optional bound for the number of active variables. Default is <code>Inf</code> .
<code>max.arclength</code>	an optional bound for arc length (L1 norm) of a step. If <code>max.arclength</code> is extremely small, an exact nonlinear path is produced. Default is <code>Inf</code> .
<code>frac.arclength</code>	Under the default setting, the next step size is computed so that the active set changes right at the next value of $\lambda$ . When <code>frac.arclength</code> is assigned some fraction between $0$ and $1$ , the step size is decreased by the factor of <code>frac.arclength</code> in arc length. If <code>frac.arclength</code> = $0.2$ , the step length is adjusted so that the active set would change after five smaller steps. Either <code>max.arclength</code> or <code>frac.arclength</code> can be used to force the path to be more accurate. Default is $1$ .
<code>add.newvars</code>	<code>add.newvars</code> candidate variables (that are currently not in the active set) are used in the corrector step as potential active variables. Default is $1$ .
<code>bshoot.threshold</code>	If the absolute value of a coefficient is larger than <code>bshoot.threshold</code> at the first corrector step it becomes nonzero (therefore when $\lambda$ is considered to have been decreased too far), $\lambda$ is increased again. i.e. A backward distance in $\lambda$ that makes the coefficient zero is computed. Default is $0.1$ .
<code>relax.lambda</code>	A variable joins the active set if $ l'(\beta)  > \lambda * (1 - \text{relax.lambda})$ . Default is $1e-8$ . If no variable joins the active set even after many ( $>20$ ) steps, the user should increase <code>relax.lambda</code> to $1e-7$ or $1e-6$ , but not more than that. This adjustment is sometimes needed because of the numerical precision/error propagation problems. In general, the paths are less accurate with relaxed $\lambda$ .
<code>standardize</code>	If <code>TRUE</code> , predictors are standardized to have a unit variance.
<code>eps</code>	an effective zero
<code>trace</code>	If <code>TRUE</code> , the algorithm prints out its progress.

## Details

This algorithm implements the predictor-corrector method to determine the entire path of the coefficient estimates as the amount of regularization varies; it computes a series of solution sets, each time estimating the coefficients with less regularization, based on the previous estimate. The coefficients are estimated with no error at the knots, and the values are connected, thereby making the paths piecewise linear.

## Value

A glmpath object is returned.

lambda	vector of $\lambda$ values for which the exact coefficients are computed
lambda2	$\lambda_2$ used
step.length	vector of step lengths in $\lambda$
corr	matrix of $l'(\beta)$ values (derivatives of the log-likelihood)
new.df	vector of degrees of freedom (to be used in the plot function)
df	vector of degrees of freedom at each step
deviance	vector of deviance computed at each step
aic	vector of AIC values
bic	vector of BIC values
b.predictor	matrix of coefficient estimates from the predictor steps
b.corrector	matrix of coefficient estimates from the corrector steps
new.A	vector of boolean values indicating the steps at which the active set changed (to be used in the plot/predict functions)
actions	actions taken at each step
meanx	means of the columns of x
sdx	standard deviations of the columns of x
xnames	column names of x
family	family used
weight	weights used
offset	offset used
nopenalty.subset	nopenalty.subset used
standardize	TRUE if the predictors were standardized before fitting

## Author(s)

Mee Young Park and Trevor Hastie

## References

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

cv.glmpath, plot.glmpath, predict.glmpath, summary.glmpath

**Examples**

```
data(heart.data)
attach(heart.data)
fit.a <- glmpath(x, y, family=binomial)
fit.b <- glmpath(x, y, family=gaussian)
detach(heart.data)
```

---

heart.data

*Dataset for glmpath*


---

**Description**

*South African Heart Disease dataset* used to test glmpath algorithm

**Usage**

```
data(heart.data)
```

**Format**

A dataset with 462 observations on 9 variables and a binary response.

**x** x contains 9 columns of the following variables: sbp (systolic blood pressure); tobacco (cumulative tobacco); ldl (low density lipoprotein cholesterol); adiposity; famhist (family history of heart disease); typea (type-A behavior); obesity; alcohol (current alcohol consumption); age (age at onset)

**y** response, coronary heart disease

**References**

Hastie, T., Tibshirani, R., and Friedman, J. (2001) *Elements of Statistical Learning; Data Mining, Inference, and Prediction* Springer-Verlag, New York.

**Examples**

```
data(heart.data)
attach(heart.data)
fit <- glmpath(x, y, family=binomial)
detach(heart.data)
```

---

lung.data

Dataset for coxpath

---

### Description

*Lung cancer dataset* used to test coxpath algorithm

### Usage

```
data(lung.data)
```

### Format

A dataset consisting of 137 observations with their survival time, censor status as well as 6 features.

**x** x contains 6 columns of the following variables: trt (1=standard treatment, and 2=test); celltype (1=squamous, 2=smallcell, 3=adeno, and 4=large); karno (Karnofsky performance score); diagtime (months from diagnosis to randomization); age (in years); prior (prior therapy 0=no, and 1=yes)

**time** survival time

**status** censor status

### References

Kalbfleisch, J. and Prentice, R. (2002) *The Statistical Analysis of Failure Time Data* J. Wiley, Hoboken, N.J.

### Examples

```
data(lung.data)
attach(lung.data)
fit <- coxpath(lung.data)
detach(lung.data)
```

---

plot.bootpath

Generates the histograms or the pairwise scatter plots of the bootstrap coefficients computed from bootstrap.path

---

### Description

This function takes a bootpath object from bootstrap.path and generates the histograms or the pairwise scatter plots of the bootstrap coefficients.

**Usage**

```
## S3 method for class 'bootpath'
plot(x, type = c("histogram", "pairplot"),
     mfrow = NULL, mar = NULL, ...)
```

**Arguments**

x	a bootpath object from bootstrap.path.
type	If type=histogram, the histograms of bootstrap coefficients for individual features are generated. The red vertical bar indicates the coefficient computed using the whole data. The thick bar at zero indicates the frequency of the zero coefficients. If type=pairplot, the pairwise scatter plots of the bootstrap coefficients are generated. The red solid dot indicates the pair of coefficients computed using the whole data. Default is histogram.
mfrow	determines the numbers of rows and columns of the histograms on a page. 2 rows are generated as a default.
mar	margin relative to the current font size
...	other options for the plot

**Details**

Fitting glmpath or coxpath gives a series of solution sets with a varying size of the active set. Once we select an appropriate value of the regularization parameter, and, thus a set of coefficients, we may then validate the chosen coefficients through a bootstrap analysis. plot.bootstrap summarizes the bootstrap results by generating the histograms or the pairwise scatter plots of the bootstrap coefficients.

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Bradley Efron and Robert Tibshirani (1993) *An Introduction to the Bootstrap* CHAPMAN & HALL/CRC, Boca Raton.

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

bootstrap.path, coxpath, glmpath

**Examples**

```
data(heart.data)
attach(heart.data)
bootstrap.a <- bootstrap.path(x, y, B=5)
plot(bootstrap.a)
```

```
plot(bootstrap.a, type="pairplot")
detach(heart.data)
```

---

plot.coxpath

*Plots the regularization path computed from coxpath*


---

## Description

This function takes a coxpath object and visualizes the regularization path. The horizontal axis can be norm, lambda or step. The vertical axis can be coefficients, aic or bic.

## Usage

```
## S3 method for class 'coxpath'
plot(x, xvar = c("norm", "lambda", "step"),
     type = c("coefficients", "aic", "bic"),
     plot.all.steps = FALSE, xlimit = NULL, predictor = FALSE,
     omit.zero = TRUE, breaks = TRUE, mar = NULL, main = NULL,
     eps = .Machine$double.eps, ...)
```

## Arguments

x	a coxpath object
xvar	horizontal axis. xvar=norm plots against the L1 norm of the coefficients (to which L1 norm penalty was applied); xvar=lambda plots against $\lambda$ ; and xvar=step plots against the number of steps taken. Default is norm.
type	type of the plot, or the vertical axis. Default is coefficients.
plot.all.steps	If TRUE, all the steps taken along the path are marked on the plot. If FALSE, which is the default, only the steps at which the active set changed are shown on the plot.
xlim	When the user wants to visualize a (beginning) sub-part of the plot, xlim sets an upper limit to the L1 norm or the number of steps, or a lower limit to $\lambda$ .
predictor	If TRUE and type=coefficients, the predictor step estimates are connected with dotted lines. If FALSE, only the corrector step estimates are connected with solid lines.
omit.zero	If TRUE, the predictors that were never in the active set are omitted.
breaks	If TRUE, vertical lines are drawn at the points where the active set changes and numbered with the degrees of freedom.
mar	margin relative to the current font size
main	title of the plot
eps	an effective zero
...	other options for the plot

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

cv.coxpath, coxpath, predict.coxpath

**Examples**

```
data(lung.data)
attach(lung.data)
fit <- coxpath(lung.data)
par(mfrow=c(3,2))
plot(fit)
plot(fit,xvar="lambda")
plot(fit,xvar="step")
plot(fit,xvar="step",xlimit=8)
plot(fit,type="aic")
plot(fit,type="bic")
detach(lung.data)
```

---

plot.glmpath

---

*Plots the regularization path computed from glmpath*


---

**Description**

This function takes a glmpath object and visualizes the regularization path. The horizontal axis can be norm, lambda or step. The vertical axis can be coefficients, aic or bic.

**Usage**

```
## S3 method for class 'glmpath'
plot(x, xvar = c("norm", "lambda", "step"),
     type = c("coefficients", "aic", "bic"),
     plot.all.steps = FALSE, xlimit = NULL, predictor = FALSE,
     omit.zero = TRUE, breaks = TRUE, mar = NULL,
     eps = .Machine$double.eps, main = NULL, ...)
```

**Arguments**

<code>x</code>	a glmpath object
<code>xvar</code>	horizontal axis. <code>xvar=norm</code> plots against the L1 norm of the coefficients (to which L1 norm penalty was applied); <code>xvar=lambda</code> plots against $\lambda$ ; and <code>xvar=step</code> plots against the number of steps taken. Default is <code>norm</code> .
<code>type</code>	type of the plot, or the vertical axis. Default is <code>coefficients</code> .
<code>plot.all.steps</code>	If TRUE, all the steps taken along the path are marked on the plot. If FALSE, which is the default, only the steps at which the active set changed are shown on the plot.
<code>xlimit</code>	When the user wants to visualize a (beginning) sub-part of the plot, <code>xlimit</code> sets an upper limit to the L1 norm or the number of steps, or a lower limit to $\lambda$ .
<code>predictor</code>	If TRUE and <code>type=coefficients</code> , the predictor step estimates are connected with dotted lines. If FALSE, only the corrector step estimates are connected with solid lines.
<code>omit.zero</code>	If TRUE and <code>type=coefficients</code> , the predictors that were never in the active set are omitted.
<code>breaks</code>	If TRUE, vertical lines are drawn at the points where the active set changes and numbered with the degrees of freedom.
<code>mar</code>	margin relative to the current font size
<code>eps</code>	an effective zero
<code>main</code>	title of the plot
<code>...</code>	other options for the plot

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

`cv.glmpath`, `glmpath`, `predict.glmpath`

**Examples**

```
data(heart.data)
attach(heart.data)
fit <- glmpath(x, y, family=binomial)
par(mfrow=c(3,2))
plot(fit)
plot(fit,xvar="lambda")
plot(fit,xvar="step")
plot(fit,xvar="step",xlim=8)
```



```
plot(fit,type="aic")
plot(fit,type="bic")
detach(heart.data)
```

---

predict.coxpath	<i>Makes predictions at particular points along the fitted coxpath</i>
-----------------	--

---

## Description

This function makes predictions at particular points along the fitted coxpath. The coefficients, log-partial-likelihood, linear predictor or the risk can be computed. A coxph object can be returned at one particular value of  $\lambda$ .

## Usage

```
## S3 method for class 'coxpath'
predict(object, data, s, type = c("coefficients", "loglik",
  "lp", "risk", "coxph"), mode = c("step",
  "norm.fraction", "norm", "lambda.fraction", "lambda"),
  eps = .Machine$double.eps, ...)
```

## Arguments

object	a coxpath object
data	a list containing x, time, and status, with which the predictions are made. If type=lp or type=risk, then x is required. If type=loglik or type=coxph, then x, time, and status are required.
s	the values of mode at which the predictions are made. If type=coxph, only the first element of s is used. If s is missing, then the steps at which the active set changed are used, and thus, mode is automatically switched to step.
type	If type=coefficients, the coefficients are returned; if type=loglik, log-partial-likelihoods are returned; if type=lp, linear predictors ( $x'\beta$ ) are returned; if type=risk, risks ( $e^{x'\beta}$ ) are returned; and if type=coxph, a coxph object (as in <b>survival</b> package) at the first element of s is returned. (i.e. the components of a coxph object such as coefficients, variance, and the test statistics are adjusted to the shrinkage corresponding to s. A coxph object can be further used as an argument to the functions in <b>survival</b> package.) Default is coefficients. The coefficients for the initial input variables are returned (rather than the standardized coefficients).
mode	what mode=s refers to. If mode=step, s is the number of steps taken; if mode=norm.fraction, s is the fraction of the L1 norm of the standardized coefficients (with respect to the largest norm); if mode=norm, s is the L1 norm of the standardized coefficients; if mode=lambda.fraction, s is the fraction of $\log(\lambda)$ ; and if mode=lambda, s is $\lambda$ . Default is step.
eps	an effective zero
...	other options for the prediction

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

cv.coxpath, coxpath, plot.coxpath

**Examples**

```
data(lung.data)
attach(lung.data)
fit <- coxpath(lung.data)
pred.a <- predict(fit, x, s = seq(0, 1, length=10),
                  mode = "norm.fraction")
library(survival)
pred.b <- predict(fit, lung.data, s = 0.5, type = "coxph",
                  mode = "lambda.fraction")
pred.s <- survfit(pred.b)
plot(pred.s)
detach(lung.data)
```

---

predict.glmpath

*Makes predictions at particular points along the fitted glmpath*

---

**Description**

This function makes predictions at particular points along the fitted glmpath. The linear predictor, estimated response, log-likelihood, or the coefficients can be computed.

**Usage**

```
## S3 method for class 'glmpath'
predict(object, newx, newy, s, type = c("link", "response",
    "loglik", "coefficients"), mode = c("step",
    "norm.fraction", "norm", "lambda.fraction", "lambda"),
    weight = NULL, offset = NULL,
    eps = .Machine$double.eps, ...)
```

**Arguments**

object	a glmpath object
newx	a matrix of features at which the predictions are made. If type=link, type=response, or type=loglik, newx is required.
newy	a vector of responses corresponding to newx. If type=loglik, newy is required.
s	the values of mode at which the predictions are made. If s is missing, then the steps at which the active set changed are used, and thus, mode is automatically switched to step.
type	If type=link, the linear predictors are returned; if type=response, the estimated responses are returned; if type=loglik, the log-likelihoods are returned, and if type=coefficients, the coefficients are returned. The coefficients for the initial input variables are returned (rather than the standardized coefficients). Default is link.
mode	what mode=s refers to. If mode=step, s is the number of steps taken; if mode=norm.fraction, s is the fraction of the L1 norm of the standardized coefficients (with respect to the largest norm); if mode=norm, s is the L1 norm of the standardized coefficients; if mode=lambda.fraction, s is the fraction of $\log(\lambda)$ ; and if mode=lambda, s is $\lambda$ . Default is step.
weight	an optional vector of weights for observations. weight is effective only if type=loglik.
offset	If offset was used in object, offset must be provided for prediction, unless type=coefficients.
eps	an effective zero
...	other options for the prediction

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

cv.glmpath, glmpath, plot.glmpath

**Examples**

```
data(heart.data)
attach(heart.data)
fit <- glmpath(x, y, family=binomial)
pred <- predict(fit, x, s = seq(0, 1, length=10), mode="norm.fraction")
detach(heart.data)
```

---

summary.coxpath	<i>Produces an anova-type summary for a coxpath object</i>
-----------------	--

---

## Description

This function produces an anova-type summary for a coxpath object.

## Usage

```
## S3 method for class 'coxpath'  
summary(object, ...)
```

## Arguments

object	a coxpath object
...	additional arguments

## Details

An anova type of summary is returned, including Df, Log-partial-likelihood, AIC, and BIC values for the steps where the active set changed.

## Value

A data.frame is returned, with the following components at transition points:

Df	degrees of freedom at each step
Log.p.lik	log-partial-likelihood at each step
AIC	AIC value at each step
BIC	BIC value at each step

## Author(s)

Mee Young Park and Trevor Hastie

## References

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

## See Also

coxpath, plot.coxpath, print.coxpath

**Examples**

```
data(lung.data)
attach(lung.data)
fit <- coxpath(lung.data)
summary(fit)
detach(lung.data)
```

---

`summary.glmpath`*Produces an anova-type summary for a glmpath object*

---

**Description**

This function produces an anova-type summary for a glmpath object.

**Usage**

```
## S3 method for class 'glmpath'
summary(object, ...)
```

**Arguments**

<code>object</code>	a glmpath object
<code>...</code>	additional arguments

**Details**

An anova type of summary is returned, including Df, Deviance, AIC, and BIC values for the steps where the active set changed.

**Value**

A data.frame is returned, with the following components at transition points:

Df	degrees of freedom at each step
Deviance	deviance computed at each step
AIC	AIC value at each step
BIC	BIC value at each step

**Author(s)**

Mee Young Park and Trevor Hastie

**References**

Mee Young Park and Trevor Hastie (2007) L1 regularization path algorithm for generalized linear models. *J. R. Statist. Soc. B*, 69, 659-677.

**See Also**

`glmpath`, `plot.glmpath`, `print.glmpath`

**Examples**

```
data(heart.data)
attach(heart.data)
fit <- glmpath(x, y)
summary(fit)
detach(heart.data)
```

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