

# Package ‘pboost’

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**Title** Profile Boosting Framework for Parametric Models

**Version** 0.2.1

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**Description** A profile boosting framework for feature selection in parametric models.

It offers a unified interface pboost() and several wrapped models, including linear model, generalized linear models, quantile regression, Cox proportional hazards model, beta regression.

An S3 interface EBIC() is provided as the stopping rule for the profile boosting by default.

**Imports** stats, Matrix, MASS, betareg, quantreg, survival, Formula

**License** GPL (>= 3)

**Encoding** UTF-8

**URL** <https://github.com/paradoxical-rhapsody/pboost>

**BugReports** <https://github.com/paradoxical-rhapsody/pboost/issues>

**RoxygenNote** 7.3.3

**Depends** R (>= 4.1.0)

**NeedsCompilation** no

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## Description

The Extended BIC possesses the selection consistency in high-dimensional model.

It can be called by the fitted model that has standard `logLik` method to access the attributes `nobs` and `df`, such as `lm`, `glm`.

## Usage

```
EBIC(object, p, p.keep, ...)

## S3 method for class 'betareg'
EBIC(object, p, p.keep, ...)

## S3 method for class 'coxph'
EBIC(object, p, p.keep, ...)

## S3 method for class 'glm'
EBIC(object, p, p.keep, ...)

## S3 method for class 'lm'
EBIC(object, p, p.keep, ...)

## S3 method for class 'rq'
EBIC(object, p, p.keep, ...)
```

## Arguments

<code>object</code>	Fitted model object.
<code>p</code>	Total number of candidate features, which is available in <code>pboost</code> .
<code>p.keep</code>	Number of features that are pre-specified to be kept in model.
<code>...</code>	Additional parameters, which is available in <code>pboost</code> .

## Details

The extended BIC (EBIC) is defined as

$$\text{EBIC}(\text{obj}) = \text{BIC}(\text{obj}) + 2 * r * \log(\text{choose}(p - |\text{p.keep}|, df - |\text{p.keep}|)).$$

## Value

A function to obtain the EBIC value of a fitted object.

## References

- Jiahua Chen and Zehua Chen (2008). Extended Bayesian information criteria for model selection with large model spaces. *Biometrika*, 95(3):759–771. doi:[10.1093/biomet/asn034](https://doi.org/10.1093/biomet/asn034)
- Jiahua Chen and Zehua Chen (2012). Extended BIC for small-n-large-p sparse GLM. *Statistical Sinica*, 22(2):555–574. doi:[10.5705/ss.2010.216](https://doi.org/10.5705/ss.2010.216)

## See Also

[plm](#), [pglm](#), [pcoxph](#), [prq](#), [pbetareg](#).

**pbetareg**

*Profile Boosting for Beta Regression*

## Description

**pbetareg** inherits the usage of [betareg::betareg](#).

## Usage

```
pbetareg(
  formula,
  data,
  subset,
  na.action,
  weights,
  offset,
  link = c("logit", "probit", "cloglog", "cauchit", "log", "loglog"),
  link.phi = NULL,
  type = c("ML", "BC", "BR"),
  dist = NULL,
  nu = NULL,
  control = betareg.control(...),
  model = TRUE,
  y = TRUE,
  x = FALSE,
  ...,
  stopFun = EBIC,
  keep = NULL,
  maxK = NULL,
  verbose = FALSE
)
```

## Arguments

formula	See <a href="#">pboost</a> .
data	See <a href="#">pboost</a> .

subset	Parameters passed to <code>betareg::betareg</code> .
na.action	Parameters passed to <code>betareg::betareg</code> .
weights	Parameters passed to <code>betareg::betareg</code> .
offset	Parameters passed to <code>betareg::betareg</code> .
link	Parameters passed to <code>betareg::betareg</code> .
link.phi	Parameters passed to <code>betareg::betareg</code> .
type	Parameters passed to <code>betareg::betareg</code> .
dist	Parameters passed to <code>betareg::betareg</code> .
nu	Parameters passed to <code>betareg::betareg</code> .
control	Parameters passed to <code>betareg::betareg</code> .
model	Parameters passed to <code>betareg::betareg</code> .
y	Parameters passed to <code>betareg::betareg</code> .
x	Parameters passed to <code>betareg::betareg</code> .
...	Parameters passed to <code>betareg::betareg</code> .
stopFun	Parameters passed to <code>pboost</code> .
keep	Parameters passed to <code>pboost</code> .
maxK	Parameters passed to <code>pboost</code> .
verbose	Parameters passed to <code>pboost</code> .

**Value**

An `betareg` model object fitted on the selected features.

**Examples**

```
library(betareg)
set.seed(2025)
n <- 300
p <- 100
x <- matrix(runif(n*p), n)
mu <- runif(n)
phi <- 1.0

shape1 <- mu * phi
shape2 <- (1-mu) * phi
y <- rbeta(n, shape1, shape2)
DF <- data.frame(y, x)

pbetareg(y ~ ., DF, verbose=TRUE)
```

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<b>pboost</b>	<i>Profile Boosting Framework</i>
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## Description

`pboost` is the generic workhorse function of profile boosting framework for parametric regression.

## Usage

```
pboost(
  formula,
  data,
  fitFun,
  scoreFun,
  stopFun,
  ...,
  keep = NULL,
  maxK = NULL,
  verbose = FALSE
)
```

## Arguments

<code>formula</code>	An object of class <code>formula</code> of the form <code>LHS ~ RHS</code> , where the right-hand side ( <code>RHS</code> ) specifies the candidate features for the linear predictor $\eta = \sum_j \beta_j x_j$ . The following restrictions and recommendations apply: <ul style="list-style-type: none"> <li>• All variables appearing on the RHS must be numeric in the supplied data</li> <li>• For computational efficiency, each term on the RHS must correspond to a single column in the resulting model matrix. Supported expressions include main effects (<code>x1</code>), interactions (<code>x1:x2</code>), and simple transformations (<code>log(x1)</code>, <code>I(x1^2)</code>, etc.). Complex terms that expand into multiple columns—such as <code>poly(x, degree)</code>, <code>bs(x)</code>, or <code>ns(x)</code>—are <b>not supported</b>.</li> <li>• Offset terms should not be included in the formula. Instead, provide them via the dedicated <code>offset</code> argument of <code>fitFun</code>.</li> </ul>
<code>data</code>	An data frame containing the variables in the model.
<code>fitFun</code>	Function to fit the empirical risk function in the form <code>fitFun(formula, data, ...)</code> .
<code>scoreFun</code>	Function to compute the derivative of empirical risk function in the form <code>scoreFun(object)</code> , where <code>object</code> is returned by <code>fitFun</code> . <code>scoreFun</code> should return a vector with the same length of <code>y</code> in <code>data</code> .
<code>stopFun</code>	Stopping rule for profile boosting, which has the form <code>stopFun(object)</code> to evaluate the performance of model object returned by <code>fitFun</code> , such as <code>EBIC</code> or <code>BIC</code> .
<code>...</code>	Additional arguments to be passed to <code>fitFun</code> .

keep	Initial set of features that are included in model fitting. <b>If keep is specified, it should also be fully included in the RHS of formula.</b>
maxK	Maximal number of identified features. If maxK is specified, it will suppress stopFun, saying that the profile boosting continues until the procedure identifies maxK features. The pre-specified features in keep are counted toward maxK.
verbose	Print the procedure path?

**Value**

Model object fitted on the selected features.

**Examples**

```
set.seed(2025)
n <- 200
p <- 300
x <- matrix(rnorm(n*p), n)
eta <- drop(x[, 1:3] %*% runif(3, 1.0, 1.5))
y <- rbinom(n, 1, 1/(1+exp(-eta)))
DF <- data.frame(y, x)

scoreLogistic <- function(object) {
  eta.hat <- object[["linear.predictors"]]
  return(object[["y"]] - 1/(1+exp(-eta.hat)))
}

( result <- pboost(y~, DF, glm, scoreLogistic, EBIC, family="binomial") )

attr(terms(formula(result), data=DF), "term.labels")
```

**Description**

Profile boosting for Cox model.

**Usage**

```
pcoxph(
  formula,
  data,
  weights,
  subset,
  na.action,
  init,
  control,
```

```
ties = c("efron", "breslow", "exact"),
singular.ok = TRUE,
robust,
model = FALSE,
x = FALSE,
y = TRUE,
tt,
method = ties,
id,
cluster,
istate,
statedata,
nocenter = c(-1, 0, 1),
...,
stopFun = EBIC,
keep = NULL,
maxK = NULL,
verbose = FALSE
)
```

## Arguments

formula	See <a href="#">pboost</a> .
data	See <a href="#">pboost</a> .
weights	Parameters passed to <a href="#">survival::coxph</a> .
subset	Parameters passed to <a href="#">survival::coxph</a> .
na.action	Parameters passed to <a href="#">survival::coxph</a> .
init	Parameters passed to <a href="#">survival::coxph</a> .
control	Parameters passed to <a href="#">survival::coxph</a> .
ties	Parameters passed to <a href="#">survival::coxph</a> .
singular.ok	Parameters passed to <a href="#">survival::coxph</a> .
robust	Parameters passed to <a href="#">survival::coxph</a> .
model	Parameters passed to <a href="#">survival::coxph</a> .
x	Parameters passed to <a href="#">survival::coxph</a> .
y	Parameters passed to <a href="#">survival::coxph</a> .
tt	Parameters passed to <a href="#">survival::coxph</a> .
method	Parameters passed to <a href="#">survival::coxph</a> .
id	Parameters passed to <a href="#">survival::coxph</a> .
cluster	Parameters passed to <a href="#">survival::coxph</a> .
istate	Parameters passed to <a href="#">survival::coxph</a> .
statedata	Parameters passed to <a href="#">survival::coxph</a> .
nocenter	Parameters passed to <a href="#">survival::coxph</a> .
...	Parameters passed to <a href="#">survival::coxph</a> .

<code>stopFun</code>	Parameters passed to <code>pboost</code> .
<code>keep</code>	Parameters passed to <code>pboost</code> .
<code>maxK</code>	Parameters passed to <code>pboost</code> .
<code>verbose</code>	Parameters passed to <code>pboost</code> .

**Value**

An `coxph` model object fitted on the selected features.

**Examples**

```
library(survival)
set.seed(2025)
n <- 300
p <- 200

DF <- data.frame(
  time = rpois(n, 5),
  status = rbinom(n, 1, 0.3),
  matrix(rnorm(n*p), n)
)

pcoxph(Surv(time, status) ~ ., DF, verbose=TRUE)
```

**Description**

Profile boosting for Gaussian graphical model.

**Usage**

```
pggm(
  S,
  nObs,
  maxK = floor(min(nObs - 1, NROW(S) - 1, 50)),
  digits = 8,
  verbose = FALSE
)
```

**Arguments**

<code>S</code>	Covariance matrix.
<code>nObs</code>	Number of observations.
<code>maxK</code>	Maximum number of identified edges.
<code>digits</code>	Integer indicating the number of decimal places or significant digits to be used.
<code>verbose</code>	Print the procedure path?

**Value**

Index set of identified features.

**Examples**

```
library(MASS)
library(Matrix)

set.seed(2025)
n <- 1000
p <- 10

Omega <- Diagonal(p)
diag(Omega[1:4, 2:5]) <- diag(Omega[2:5, 1:4]) <- 0.5
Sigma <- chol2inv(chol(Omega))
X <- mvrnorm(n, rep(0, p), Sigma, empirical=TRUE)
S <- cov(X)
system.time( egg <- pggm(S, n) )
```

pglm

*Profile Boosting for Generalized Linear Models.*
**Description**

`pglm` inherits the usage of the built-in function `glm`.

**Usage**

```
pglm(
  formula,
  family = gaussian,
  data,
  weights,
  subset,
  na.action,
  start = NULL,
  etastart,
  mustart,
  offset,
  control = list(...),
  model = TRUE,
  method = "glm.fit",
  x = FALSE,
  y = TRUE,
  singular.ok = TRUE,
  contrasts = NULL,
  ...,
```

```

stopFun = EBIC,
keep = NULL,
maxK = NULL,
verbose = FALSE
)

```

### Arguments

formula	See <a href="#">pboost</a> .
family	Parameters passed to <a href="#">glm</a> .
data	See <a href="#">pboost</a> .
weights	Parameters passed to <a href="#">glm</a> .
subset	Parameters passed to <a href="#">glm</a> .
na.action	Parameters passed to <a href="#">glm</a> .
start	Parameters passed to <a href="#">glm</a> .
etastart	Parameters passed to <a href="#">glm</a> .
mustart	Parameters passed to <a href="#">glm</a> .
offset	Parameters passed to <a href="#">glm</a> .
control	Parameters passed to <a href="#">glm</a> .
model	Parameters passed to <a href="#">glm</a> .
method	Parameters passed to <a href="#">glm</a> .
x	Parameters passed to <a href="#">glm</a> .
y	Parameters passed to <a href="#">glm</a> .
singular.ok	Parameters passed to <a href="#">glm</a> .
contrasts	Parameters passed to <a href="#">glm</a> .
...	Parameters passed to <a href="#">glm</a> .
stopFun	Parameters passed to <a href="#">pboost</a> .
keep	Parameters passed to <a href="#">pboost</a> .
maxK	Parameters passed to <a href="#">pboost</a> .
verbose	Parameters passed to <a href="#">pboost</a> .

### Value

An [glm](#) model object fitted on the selected features.

### References

Zengchao Xu, Shan Luo and Zehua Chen (2022). Partial profile score feature selection in high-dimensional generalized linear interaction models. *Statistics and Its Interface*. [doi:10.4310/SII-706](#)

## Examples

```

set.seed(2025)
n <- 300
p <- 200
x <- matrix(rnorm(n*p), n)

eta <- drop( x[, 1:3] %*% runif(3, 1.0, 1.5) )
y <- rbinom(n, 1, 1/(1+exp(-eta)))
DF <- data.frame(y, x)

pglm(y ~ ., "binomial", DF, verbose=TRUE)
pglm(y ~ ., "binomial", DF, stopFun=EBIC, verbose=TRUE)

scoreLogistic <- function(object) {
  eta.hat <- object[["linear.predictors"]]
  return(object[["y"]] - 1/(1+exp(-eta.hat)))
}
pboost(y ~ ., DF, glm, scoreLogistic, EBIC, family="binomial", verbose=TRUE)

```

**plm***Profile Boosting for Linear Models.*

## Description

**plm** inherits the usage of the built-in function **lm**.

## Usage

```

plm(
  formula,
  data,
  subset,
  weights,
  na.action,
  method = "qr",
  model = TRUE,
  x = FALSE,
  y = FALSE,
  qr = TRUE,
  singular.ok = TRUE,
  contrasts = NULL,
  offset,
  ...,
  stopFun = EBIC,
  keep = NULL,
  maxK = NULL,
  verbose = FALSE
)

```

## Arguments

<code>formula</code>	See <a href="#">pboost</a> .
<code>data</code>	See <a href="#">pboost</a> .
<code>subset</code>	Parameters passed to <a href="#">lm</a> .
<code>weights</code>	Parameters passed to <a href="#">lm</a> .
<code>na.action</code>	Parameters passed to <a href="#">lm</a> .
<code>method</code>	Parameters passed to <a href="#">lm</a> .
<code>model</code>	Parameters passed to <a href="#">lm</a> .
<code>x</code>	Parameters passed to <a href="#">lm</a> .
<code>y</code>	Parameters passed to <a href="#">lm</a> .
<code>qr</code>	Parameters passed to <a href="#">lm</a> .
<code>singular.ok</code>	Parameters passed to <a href="#">lm</a> .
<code>contrasts</code>	Parameters passed to <a href="#">lm</a> .
<code>offset</code>	Parameters passed to <a href="#">lm</a> .
<code>...</code>	Parameters passed to <a href="#">lm</a> .
<code>stopFun</code>	Parameters passed to <a href="#">pboost</a> .
<code>keep</code>	Parameters passed to <a href="#">pboost</a> .
<code>maxK</code>	Parameters passed to <a href="#">pboost</a> .
<code>verbose</code>	Parameters passed to <a href="#">pboost</a> .

## Details

`plm` is an equivalent implementation to the sequential lasso method proposed by Luo and Chen(2014, doi:[10.1080/01621459.2013.877275](https://doi.org/10.1080/01621459.2013.877275)).

## Value

An `lm` model object fitted on the selected features.

## References

- Zengchao Xu, Shan Luo and Zehua Chen (2022). Partial profile score feature selection in high-dimensional generalized linear interaction models. *Statistics and Its Interface*. doi:[10.4310/SII.2021.706](https://doi.org/10.4310/SII.2021.706)
- Shan Luo and Zehua Chen (2014). A Sequential Lasso Method for Feature Selection with Ultra-High Dimensional Feature Space. *Journal of the American Statistical Association*, 109(507):223–232. doi:[10.1080/01621459.2013.877275](https://doi.org/10.1080/01621459.2013.877275)

## Examples

```
set.seed(2025)
n <- 300
p <- 200
x <- matrix(rnorm(n*p), n)

eta <- drop( x[, 1:3] %*% runif(3, 1.0, 1.5) )
y <- eta + rnorm(n, sd=sd(eta))
DF <- data.frame(y, x)

plm(y ~ ., DF, verbose=TRUE)
plm(y ~ ., DF, stopFun=BIC, verbose=TRUE)
pboost(y ~ ., DF, lm, residuals, EBIC, verbose=TRUE)
```

prq

*Profile Boosting for Quantile Regression*

## Description

`prq` inherits the usage of the function `quantreg::rq`.

## Usage

```
prq(
  formula,
  tau = 0.5,
  data,
  subset,
  weights,
  na.action,
  method = "br",
  model = TRUE,
  contrasts = NULL,
  ...,
  stopFun = EBIC,
  keep = NULL,
  maxK = NULL,
  verbose = FALSE
)
```

## Arguments

formula	See <code>pboost</code> .
tau	Parameters passed to <code>quantreg::rq</code> .
data	See <code>pboost</code> .
subset	Parameters passed to <code>quantreg::rq</code> .

<code>weights</code>	Parameters passed to <code>quantreg::rq</code> .
<code>na.action</code>	Parameters passed to <code>quantreg::rq</code> .
<code>method</code>	Parameters passed to <code>quantreg::rq</code> .
<code>model</code>	Parameters passed to <code>quantreg::rq</code> .
<code>contrasts</code>	Parameters passed to <code>quantreg::rq</code> .
<code>...</code>	Parameters passed to <code>quantreg::rq</code> .
<code>stopFun</code>	Parameters passed to <code>pboost</code> .
<code>keep</code>	Parameters passed to <code>pboost</code> .
<code>maxK</code>	Parameters passed to <code>pboost</code> .
<code>verbose</code>	Parameters passed to <code>pboost</code> .

**Value**

An `rq` model object fitted on the selected features.

**Examples**

```
library(quantreg)
set.seed(2025)
n <- 300
p <- 200
x <- matrix(rnorm(n*p), n)

eta <- drop( x[, 1:3] %*% runif(3, 1.0, 1.5) )
y <- eta + (1.0 + x[, 3]) * rnorm(n)
DF <- data.frame(y, x)

tau <- 0.5
prq(y ~ ., tau, DF, verbose=TRUE)

BIC <- function(obj) AIC(obj, k=-1)
prq(y ~ ., tau, DF, stopFun=BIC, verbose=TRUE)

scorerq <- function(object) {
  return(ifelse(object[["y"]] < fitted(object), tau - 1, tau))
}
pboost(y ~ ., DF, rq, scorerq, EBIC, tau=tau, verbose=TRUE)
```

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