

Package ‘hdnom’

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Type Package

Title Benchmarking and Visualization Toolkit for Penalized Cox Models

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Description Creates nomogram visualizations for penalized Cox regression models, with the support of reproducible survival model building, validation, calibration, and comparison for high-dimensional data.

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LazyData TRUE

URL <https://nanx.me/hdnom/>, <https://github.com/nanxstats/hdnom>

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<code>as_nomogram</code>	<i>Construct nomogram objects for high-dimensional Cox models</i>
--------------------------	---

Description

Construct nomograms objects for high-dimensional Cox models

Usage

```
as_nomogram(
  object,
  x,
  time,
  event,
  pred.at = NULL,
  fun.at = NULL,
  funlabel = NULL
)
```

Arguments

<code>object</code>	Model object fitted by <code>'hdnom::fit_*</code> ()' functions.
<code>x</code>	Matrix of training data used for fitting the model.
<code>time</code>	Survival time. Must be of the same length with the number of rows as <code>x</code> .
<code>event</code>	Status indicator, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as <code>x</code> .
<code>pred.at</code>	Time point at which to plot nomogram prediction axis.
<code>fun.at</code>	Function values to label on axis.
<code>funlabel</code>	Label for fun axis.

Note

The nomogram visualizes the model under the automatically selected "optimal" hyperparameters (e.g. lambda, alpha, gamma).

Examples

```
data(smart)
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)

nom <- as_nomogram(
  fit, x, time, event, pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

print(nom)
plot(nom)
```

calibrate

Calibrate high-dimensional Cox models

Description

Calibrate high-dimensional Cox models

Usage

```
calibrate(
  x,
  time,
  event,
  model.type = c("lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad",
    "snet"),
  alpha,
  lambda,
  pen.factor = NULL,
  gamma,
  lambda1,
  lambda2,
  method = c("fitting", "bootstrap", "cv", "repeated.cv"),
  boot.times = NULL,
  nfolds = NULL,
  rep.times = NULL,
  pred.at,
  ngroup = 5,
  seed = 1001,
  trace = TRUE
)
```

Arguments

x	Matrix of training data used for fitting the model; on which to run the calibration.
time	Survival time. Must be of the same length with the number of rows as x.
event	Status indicator, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as x.
model.type	Model type to calibrate. Could be one of "lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad", or "snet".
alpha	Value of the elastic-net mixing parameter alpha for enet, aenet, mnet, and snet models. For lasso, alasso, mcp, and scad models, please set alpha = 1. alpha=1: lasso (l1) penalty; alpha=0: ridge (l2) penalty. Note that for mnet and snet models, alpha can be set to very close to 0 but not 0 exactly.
lambda	Value of the penalty parameter lambda to use in the model fits on the resampled data. From the Cox model you have built.
pen.factor	Penalty factors to apply to each coefficient. From the built <i>adaptive lasso</i> or <i>adaptive elastic-net</i> model.
gamma	Value of the model parameter gamma for MCP/SCAD/Mnet/Snet models.
lambda1	Value of the penalty parameter lambda1 for fused lasso model.
lambda2	Value of the penalty parameter lambda2 for fused lasso model.
method	Calibration method. Options including "fitting", "bootstrap", "cv", and "repeated.cv".
boot.times	Number of repetitions for bootstrap.
nfolds	Number of folds for cross-validation and repeated cross-validation.
rep.times	Number of repeated times for repeated cross-validation.
pred.at	Time point at which calibration should take place.
ngroup	Number of groups to be formed for calibration.
seed	A random seed for resampling.
trace	Logical. Output the calibration progress or not. Default is TRUE.

Examples

```

data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

# Fit Cox model with lasso penalty
fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)

# Model calibration by fitting the original data directly
cal.fitting <- calibrate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,

```

```

    method = "fitting",
    pred.at = 365 * 9, ngroup = 5,
    seed = 1010
  )

# Model calibration by 5-fold cross-validation
cal.cv <- calibrate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,
  method = "cv", nfolds = 5,
  pred.at = 365 * 9, ngroup = 5,
  seed = 1010
)

print(cal.fitting)
summary(cal.fitting)
plot(cal.fitting)

print(cal.cv)
summary(cal.cv)
plot(cal.cv)

# # Test fused lasso, SCAD, and Mnet models
# data(smart)
# x = as.matrix(smart[, -c(1, 2)])[1:500, ]
# time = smart$TEVENT[1:500]
# event = smart$EVENT[1:500]
# y = survival::Surv(time, event)
#
# set.seed(1010)
# cal.fitting = calibrate(
#   x, time, event, model.type = "flasso",
#   lambda1 = 5, lambda2 = 2,
#   method = "fitting",
#   pred.at = 365 * 9, ngroup = 5,
#   seed = 1010)
#
# cal.boot = calibrate(
#   x, time, event, model.type = "scad",
#   gamma = 3.7, alpha = 1, lambda = 0.03,
#   method = "bootstrap", boot.times = 10,
#   pred.at = 365 * 9, ngroup = 5,
#   seed = 1010)
#
# cal.cv = calibrate(
#   x, time, event, model.type = "mnet",
#   gamma = 3, alpha = 0.3, lambda = 0.03,
#   method = "cv", nfolds = 5,
#   pred.at = 365 * 9, ngroup = 5,
#   seed = 1010)
#
# cal.repcv = calibrate(

```

```
# x, time, event, model.type = "flasso",
# lambda1 = 5, lambda2 = 2,
# method = "repeated.cv", nfolds = 5, rep.times = 3,
# pred.at = 365 * 9, ngroup = 5,
# seed = 1010)
#
# print(cal.fitting)
# summary(cal.fitting)
# plot(cal.fitting)
#
# print(cal.boot)
# summary(cal.boot)
# plot(cal.boot)
#
# print(cal.cv)
# summary(cal.cv)
# plot(cal.cv)
#
# print(cal.repcv)
# summary(cal.repcv)
# plot(cal.repcv)
```

calibrate_external *Externally calibrate high-dimensional Cox models*

Description

Externally calibrate high-dimensional Cox models

Usage

```
calibrate_external(
  object,
  x,
  time,
  event,
  x_new,
  time_new,
  event_new,
  pred.at,
  ngroup = 5
)
```

Arguments

object	Model object fitted by <code>hdnom::fit_*</code> .
x	Matrix of training data used for fitting the model.
time	Survival time of the training data. Must be of the same length with the number of rows as x.

event	Status indicator of the training data, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as x.
x_new	Matrix of predictors for the external validation data.
time_new	Survival time of the external validation data. Must be of the same length with the number of rows as x_new.
event_new	Status indicator of the external validation data, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as x_new.
pred.at	Time point at which external calibration should take place.
ngroup	Number of groups to be formed for external calibration.

Examples

```

library("survival")

# Load imputed SMART data
data(smart)
# Use the first 1000 samples as training data
# (the data used for internal validation)
x <- as.matrix(smart[, -c(1, 2)])[1:1000, ]
time <- smart$TEVENT[1:1000]
event <- smart$EVENT[1:1000]

# Take the next 1000 samples as external calibration data
# In practice, usually use data collected in other studies
x_new <- as.matrix(smart[, -c(1, 2)])[1001:2000, ]
time_new <- smart$TEVENT[1001:2000]
event_new <- smart$EVENT[1001:2000]

# Fit Cox model with lasso penalty
fit <- fit_lasso(
  x, Surv(time, event),
  nfolds = 5, rule = "lambda.1se", seed = 11
)

# External calibration
cal.ext <- calibrate_external(
  fit, x, time, event,
  x_new, time_new, event_new,
  pred.at = 365 * 5, ngroup = 5
)

print(cal.ext)
summary(cal.ext)
plot(cal.ext, xlim = c(0.6, 1), ylim = c(0.6, 1))
# # Test fused lasso, MCP, and Snet models
# data(smart)
# # Use first 500 samples as training data
# # (the data used for internal validation)
# x <- as.matrix(smart[, -c(1, 2)])[1:500, ]
# time <- smart$TEVENT[1:500]
# event <- smart$EVENT[1:500]

```



```
#
# # Take 1000 samples as external validation data.
# # In practice, usually use data collected in other studies.
# x_new <- as.matrix(smart[, -c(1, 2)])[1001:2000, ]
# time_new <- smart$TEVENT[1001:2000]
# event_new <- smart$EVENT[1001:2000]
#
# fllassofit <- fit_fllasso(x, survival::Surv(time, event), nfolds = 5, seed = 11)
# scadfit <- fit_mcp(x, survival::Surv(time, event), nfolds = 5, seed = 11)
# mnetfit <- fit_snet(x, survival::Surv(time, event), nfolds = 5, seed = 11)
#
# cal.ext1 <- calibrate_external(
#   fllassofit, x, time, event,
#   x_new, time_new, event_new,
#   pred.at = 365 * 5, ngroup = 5)
#
# cal.ext2 <- calibrate_external(
#   scadfit, x, time, event,
#   x_new, time_new, event_new,
#   pred.at = 365 * 5, ngroup = 5)
#
# cal.ext3 <- calibrate_external(
#   mnetfit, x, time, event,
#   x_new, time_new, event_new,
#   pred.at = 365 * 5, ngroup = 5)
#
# print(cal.ext1)
# summary(cal.ext1)
# plot(cal.ext1)
#
# print(cal.ext2)
# summary(cal.ext2)
# plot(cal.ext2)
#
# print(cal.ext3)
# summary(cal.ext3)
# plot(cal.ext3)
```

compare_by_calibrate *Compare high-dimensional Cox models by model calibration*

Description

Compare high-dimensional Cox models by model calibration

Usage

```
compare_by_calibrate(
  x,
  time,
```

```

event,
model.type = c("lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad",
  "snet"),
method = c("fitting", "bootstrap", "cv", "repeated.cv"),
boot.times = NULL,
nfolds = NULL,
rep.times = NULL,
pred.at,
ngroup = 5,
seed = 1001,
trace = TRUE
)

```

Arguments

<code>x</code>	Matrix of training data used for fitting the model; on which to run the calibration.
<code>time</code>	Survival time. Must be of the same length with the number of rows as <code>x</code> .
<code>event</code>	Status indicator, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as <code>x</code> .
<code>model.type</code>	Model types to compare. Could be at least two of "lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad", or "snet".
<code>method</code>	Calibration method. Could be "bootstrap", "cv", or "repeated.cv".
<code>boot.times</code>	Number of repetitions for bootstrap.
<code>nfolds</code>	Number of folds for cross-validation and repeated cross-validation.
<code>rep.times</code>	Number of repeated times for repeated cross-validation.
<code>pred.at</code>	Time point at which calibration should take place.
<code>ngroup</code>	Number of groups to be formed for calibration.
<code>seed</code>	A random seed for cross-validation fold division.
<code>trace</code>	Logical. Output the calibration progress or not. Default is TRUE.

Examples

```

data(smart)
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$EVENT

# Compare lasso and adaptive lasso by 5-fold cross-validation
cmp.cal.cv <- compare_by_calibrate(
  x, time, event,
  model.type = c("lasso", "alasso"),
  method = "fitting",
  pred.at = 365 * 9, ngroup = 5, seed = 1001
)

print(cmp.cal.cv)
summary(cmp.cal.cv)
plot(cmp.cal.cv)

```

compare_by_validate *Compare high-dimensional Cox models by model validation*

Description

Compare high-dimensional Cox models by model validation

Usage

```
compare_by_validate(
  x,
  time,
  event,
  model.type = c("lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad",
    "snet"),
  method = c("bootstrap", "cv", "repeated.cv"),
  boot.times = NULL,
  nfolds = NULL,
  rep.times = NULL,
  tauc.type = c("CD", "SZ", "UNO"),
  tauc.time,
  seed = 1001,
  trace = TRUE
)
```

Arguments

x	Matrix of training data used for fitting the model; on which to run the validation.
time	Survival time. Must be of the same length with the number of rows as x.
event	Status indicator, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as x.
model.type	Model types to compare. Could be at least two of "lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad", or "snet".
method	Validation method. Could be "bootstrap", "cv", or "repeated.cv".
boot.times	Number of repetitions for bootstrap.
nfolds	Number of folds for cross-validation and repeated cross-validation.
rep.times	Number of repeated times for repeated cross-validation.
tauc.type	Type of time-dependent AUC. Including "CD" proposed by Chambless and Diao (2006)., "SZ" proposed by Song and Zhou (2008)., "UNO" proposed by Uno et al. (2007).
tauc.time	Numeric vector. Time points at which to evaluate the time-dependent AUC.
seed	A random seed for cross-validation fold division.
trace	Logical. Output the validation progress or not. Default is TRUE.

References

Chambless, L. E. and G. Diao (2006). Estimation of time-dependent area under the ROC curve for long-term risk prediction. *Statistics in Medicine* 25, 3474–3486.

Song, X. and X.-H. Zhou (2008). A semiparametric approach for the covariate specific ROC curve with survival outcome. *Statistica Sinica* 18, 947–965.

Uno, H., T. Cai, L. Tian, and L. J. Wei (2007). Evaluating prediction rules for t-year survivors with censored regression models. *Journal of the American Statistical Association* 102, 527–537.

Examples

```
data(smart)
x <- as.matrix(smart[, -c(1, 2)])[1:1000, ]
time <- smart$TEVENT[1:1000]
event <- smart$EVENT[1:1000]

# Compare lasso and adaptive lasso by 5-fold cross-validation
cmp.val.cv <- compare_by_validate(
  x, time, event,
  model.type = c("lasso", "alasso"),
  method = "cv", nfolds = 5, tauc.type = "UNO",
  tauc.time = seq(0.25, 2, 0.25) * 365, seed = 1001
)

print(cmp.val.cv)
summary(cmp.val.cv)
plot(cmp.val.cv)
plot(cmp.val.cv, interval = TRUE)
```

fit_aenet

Model selection for high-dimensional Cox models with adaptive elastic-net penalty

Description

Automatic model selection for high-dimensional Cox models with adaptive elastic-net penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_aenet(
  x,
  y,
  nfolds = 5L,
  alphas = seq(0.05, 0.95, 0.05),
  rule = c("lambda.min", "lambda.1se"),
  seed = c(1001, 1002),
  parallel = FALSE
)
```

Arguments

x	Data matrix.
y	Response matrix made with Surv .
nfolds	Fold numbers of cross-validation.
alphas	Alphas to tune in cv.glmnet .
rule	Model selection criterion, "lambda.min" or "lambda.1se". See cv.glmnet for details.
seed	Two random seeds for cross-validation fold division in two estimation steps.
parallel	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the <code>doParallel</code> package and run <code>registerDoParallel()</code> with the number of CPU cores before calling this function.

Examples

```

data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

# To enable parallel parameter tuning, first run:
# library("doParallel")
# registerDoParallel(detectCores())
# then set fit_aenet(..., parallel = TRUE).

fit <- fit_aenet(
  x, y,
  nfolds = 3, alphas = c(0.3, 0.7),
  rule = "lambda.1se", seed = c(5, 7)
)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)

```

fit_lasso

Model selection for high-dimensional Cox models with adaptive lasso penalty

Description

Automatic model selection for high-dimensional Cox models with adaptive lasso penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_lasso(
  x,
  y,
  nfolds = 5L,
  rule = c("lambda.min", "lambda.1se"),
  seed = c(1001, 1002)
)
```

Arguments

x	Data matrix.
y	Response matrix made by Surv .
nfolds	Fold numbers of cross-validation.
rule	Model selection criterion, "lambda.min" or "lambda.1se". See cv.glmnet for details.
seed	Two random seeds for cross-validation fold division in two estimation steps.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

fit <- fit_lasso(x, y, nfolds = 3, rule = "lambda.1se", seed = c(7, 11))

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)
```

fit_enet

Model selection for high-dimensional Cox models with elastic-net penalty

Description

Automatic model selection for high-dimensional Cox models with elastic-net penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_enet(
  x,
  y,
  nfolds = 5L,
  alphas = seq(0.05, 0.95, 0.05),
  rule = c("lambda.min", "lambda.1se"),
  seed = 1001,
  parallel = FALSE
)
```

Arguments

x	Data matrix.
y	Response matrix made by Surv .
nfolds	Fold numbers of cross-validation.
alphas	Alphas to tune in cv.glmnet .
rule	Model selection criterion, "lambda.min" or "lambda.1se". See cv.glmnet for details.
seed	A random seed for cross-validation fold division.
parallel	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the doParallel package and run registerDoParallel() with the number of CPU cores before calling this function.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

# To enable parallel parameter tuning, first run:
# library("doParallel")
# registerDoParallel(detectCores())
# then set fit_enet(..., parallel = TRUE).

fit <- fit_enet(
  x, y,
  nfolds = 3, alphas = c(0.3, 0.7),
  rule = "lambda.1se", seed = 11
)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)
```

```
plot(nom)
```

fit_lasso	<i>Model selection for high-dimensional Cox models with fused lasso penalty</i>
-----------	---

Description

Automatic model selection for high-dimensional Cox models with fused lasso penalty, evaluated by cross-validated likelihood.

Usage

```
fit_lasso(
  x,
  y,
  nfolds = 5L,
  lambda1 = c(0.001, 0.05, 0.5, 1, 5),
  lambda2 = c(0.001, 0.01, 0.5),
  maxiter = 25,
  epsilon = 0.001,
  seed = 1001,
  trace = FALSE,
  parallel = FALSE,
  ...
)
```

Arguments

x	Data matrix.
y	Response matrix made by Surv .
nfolds	Fold numbers of cross-validation.
lambda1	Vector of lambda1 candidates. Default is 0.001, 0.05, 0.5, 1, 5.
lambda2	Vector of lambda2 candidates. Default is 0.001, 0.01, 0.5.
maxiter	The maximum number of iterations allowed. Default is 25.
epsilon	The convergence criterion. Default is 1e-3.
seed	A random seed for cross-validation fold division.
trace	Output the cross-validation parameter tuning progress or not. Default is FALSE.
parallel	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the <code>doParallel</code> package and run <code>registerDoParallel()</code> with the number of CPU cores before calling this function.
...	other parameters to cv1 and penalized .

Note

The cross-validation procedure used in this function is the *approximated cross-validation* provided by the penalized package. Be careful dealing with the results since they might be more optimistic than a traditional CV procedure. This cross-validation method is more suitable for datasets with larger number of observations, and a higher number of cross-validation folds.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])[1:120, ]
time <- smart$TEVENT[1:120]
event <- smart$EVENT[1:120]
y <- survival::Surv(time, event)

fit <- fit_flasso(
  x, y,
  lambda1 = c(1, 10), lambda2 = c(0.01),
  nfolds = 3, seed = 11
)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)
```

fit_lasso

Model selection for high-dimensional Cox models with lasso penalty

Description

Automatic model selection for high-dimensional Cox models with lasso penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_lasso(x, y, nfolds = 5L, rule = c("lambda.min", "lambda.1se"), seed = 1001)
```

Arguments

x	Data matrix.
y	Response matrix made by Surv .
nfolds	Fold numbers of cross-validation.
rule	Model selection criterion, "lambda.min" or "lambda.1se". See cv.glmnet for details.
seed	A random seed for cross-validation fold division.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)
```

fit_mcp

Model selection for high-dimensional Cox models with MCP penalty

Description

Automatic model selection for high-dimensional Cox models with MCP penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_mcp(
  x,
  y,
  nfolds = 5L,
  gammas = c(1.01, 1.7, 3, 100),
  eps = 1e-04,
  max.iter = 10000L,
  seed = 1001,
  trace = FALSE,
  parallel = FALSE
)
```

Arguments

x	Data matrix.
y	Response matrix made by Surv .
nfolds	Fold numbers of cross-validation.
gammas	Gammas to tune in cv.ncvsurv .
eps	Convergence threshold.

max.iter	Maximum number of iterations.
seed	A random seed for cross-validation fold division.
trace	Output the cross-validation parameter tuning progress or not. Default is FALSE.
parallel	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the doParallel package and run registerDoParallel() with the number of CPU cores before calling this function.

Examples

```

data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$Eevent
event <- smart$Eevent
y <- survival::Surv(time, event)

fit <- fit_mcp(x, y, nfolds = 3, gammas = c(2.1, 3), seed = 1001)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)

```

fit_mnet

Model selection for high-dimensional Cox models with Mnet penalty

Description

Automatic model selection for high-dimensional Cox models with Mnet penalty, evaluated by penalized partial-likelihood.

Usage

```

fit_mnet(
  x,
  y,
  nfolds = 5L,
  gammas = c(1.01, 1.7, 3, 100),
  alphas = seq(0.05, 0.95, 0.05),
  eps = 1e-04,
  max.iter = 10000L,
  seed = 1001,
  trace = FALSE,
  parallel = FALSE
)

```

Arguments

<code>x</code>	Data matrix.
<code>y</code>	Response matrix made by <code>Surv</code> .
<code>nfolds</code>	Fold numbers of cross-validation.
<code>gammas</code>	Gammas to tune in <code>cv.ncvsurv</code> .
<code>alphas</code>	Alphas to tune in <code>cv.ncvsurv</code> .
<code>eps</code>	Convergence threshold.
<code>max.iter</code>	Maximum number of iterations.
<code>seed</code>	A random seed for cross-validation fold division.
<code>trace</code>	Output the cross-validation parameter tuning progress or not. Default is FALSE.
<code>parallel</code>	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the <code>doParallel</code> package and run <code>registerDoParallel()</code> with the number of CPU cores before calling this function.

Examples

```

data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$EVENT
y <- survival::Surv(time, event)

fit <- fit_mnet(
  x, y,
  nfolds = 3,
  gammas = 3, alphas = c(0.3, 0.6, 0.9),
  max.iter = 15000, seed = 1010
)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)

```

fit_scad

Model selection for high-dimensional Cox models with SCAD penalty

Description

Automatic model selection for high-dimensional Cox models with SCAD penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_scad(
  x,
  y,
  nfolds = 5L,
  gammas = c(2.01, 2.3, 3.7, 200),
  eps = 1e-04,
  max.iter = 10000L,
  seed = 1001,
  trace = FALSE,
  parallel = FALSE
)
```

Arguments

x	Data matrix.
y	Response matrix made by Surv .
nfolds	Fold numbers of cross-validation.
gammas	Gammas to tune in cv.ncvsurv .
eps	Convergence threshold.
max.iter	Maximum number of iterations.
seed	A random seed for cross-validation fold division.
trace	Output the cross-validation parameter tuning progress or not. Default is FALSE.
parallel	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the <code>doParallel</code> package and run <code>registerDoParallel()</code> with the number of CPU cores before calling this function.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$EVENT
y <- survival::Surv(time, event)

fit <- fit_scad(
  x, y,
  nfolds = 3, gammas = c(3.7, 5),
  max.iter = 15000, seed = 1010
)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)
```

```
plot(nom)
```

```
fit_snet
```

Model selection for high-dimensional Cox models with Snet penalty

Description

Automatic model selection for high-dimensional Cox models with Snet penalty, evaluated by penalized partial-likelihood.

Usage

```
fit_snet(
  x,
  y,
  nfolds = 5L,
  gammas = c(2.01, 2.3, 3.7, 200),
  alphas = seq(0.05, 0.95, 0.05),
  eps = 1e-04,
  max.iter = 10000L,
  seed = 1001,
  trace = FALSE,
  parallel = FALSE
)
```

Arguments

<code>x</code>	Data matrix.
<code>y</code>	Response matrix made by Surv .
<code>nfolds</code>	Fold numbers of cross-validation.
<code>gammas</code>	Gammas to tune in cv.ncvsurv .
<code>alphas</code>	Alphas to tune in cv.ncvsurv .
<code>eps</code>	Convergence threshold.
<code>max.iter</code>	Maximum number of iterations.
<code>seed</code>	A random seed for cross-validation fold division.
<code>trace</code>	Output the cross-validation parameter tuning progress or not. Default is FALSE.
<code>parallel</code>	Logical. Enable parallel parameter tuning or not, default is FALSE. To enable parallel tuning, load the <code>doParallel</code> package and run <code>registerDoParallel()</code> with the number of CPU cores before calling this function.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$EVENT
y <- survival::Surv(time, event)

fit <- fit_snet(
  x, y,
  nfolds = 3,
  gammas = 3.7, alphas = c(0.3, 0.8),
  max.iter = 15000, seed = 1010
)

nom <- as_nomogram(
  fit, x, time, event,
  pred.at = 365 * 2,
  funlabel = "2-Year Overall Survival Probability"
)

plot(nom)
```

glmnet_basesurv

Breslow baseline hazard estimator for glmnet objects

Description

Derived from `peperr::basesurv` and `gbm::basehaz.gbm`.

Usage

```
glmnet_basesurv(time, event, lp, times.eval = NULL, centered = FALSE)
```

Arguments

<code>time</code>	Survival time
<code>event</code>	Status indicator
<code>lp</code>	Linear predictors
<code>times.eval</code>	Survival time to evaluate
<code>centered</code>	Should we center the survival curve? See basehaz for details.

Value

list containing cumulative base hazard

Examples

NULL

glmnet_survcurve	<i>Survival curve prediction for glmnet objects</i>
------------------	---

Description

Derived from c060::predictProb.coxnet

Usage

```
glmnet_survcurve(object, time, event, x, survtime)
```

Arguments

object	glmnet model object
time	Survival time
event	Status indicator
x	Predictor matrix
survtime	Survival time to evaluate

Value

list containing predicted survival probabilities and linear predictors for all samples

Examples

NULL

infer_variable_type	<i>Extract information of selected variables from high-dimensional Cox models</i>
---------------------	---

Description

Extract the names and type of selected variables from fitted high-dimensional Cox models.

Usage

```
infer_variable_type(object, x)
```

Arguments

object	Model object.
x	Data matrix used to fit the model.

Value

A list containing the index, name, type and range of the selected variables.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)
infer_variable_type(fit, x)
```

kmpplot	<i>Kaplan-Meier plot with number at risk table for internal calibration and external calibration results</i>
---------	--

Description

Kaplan-Meier plot with number at risk table for internal calibration and external calibration results

Usage

```
kmpplot(
  object,
  group.name = NULL,
  time.at = NULL,
  col.pal = c("JCO", "Lancet", "NPG", "AAAS")
)
```

Arguments

object	An object returned by <code>calibrate</code> or <code>calibrate_external</code> .
group.name	Risk group labels. Default is Group 1, Group 2, ..., Group k.
time.at	Time points to evaluate the number at risk.
col.pal	Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".

Examples

```
data("smart")
# Use the first 1000 samples as training data
# (the data used for internal validation)
x <- as.matrix(smart[, -c(1, 2)])[1:1000, ]
time <- smart$TEVENT[1:1000]
event <- smart$Eevent[1:1000]
```

```

# Take the next 1000 samples as external calibration data
# In practice, usually use data collected in other studies
x_new <- as.matrix(smart[, -c(1, 2)])[1001:2000, ]
time_new <- smart$EVEENT[1001:2000]
event_new <- smart$EVEENT[1001:2000]

# Fit Cox model with lasso penalty
fit <- fit_lasso(x, survival::Surv(time, event), nfolds = 5, rule = "lambda.1se", seed = 11)

# Internal calibration
cal.int <- calibrate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,
  method = "cv", nfolds = 5,
  pred.at = 365 * 9, ngroup = 3
)

kmplot(
  cal.int,
  group.name = c("High risk", "Medium risk", "Low risk"),
  time.at = 1:6 * 365
)

# External calibration
cal.ext <- calibrate_external(
  fit, x, time, event,
  x_new, time_new, event_new,
  pred.at = 365 * 5, ngroup = 3
)

kmplot(
  cal.ext,
  group.name = c("High risk", "Medium risk", "Low risk"),
  time.at = 1:6 * 365
)

```

logrank_test

Log-rank test for internal calibration and external calibration results

Description

Log-rank test for internal calibration and external calibration results

Usage

```
logrank_test(object)
```

Arguments

object An object returned by `calibrate` or `calibrate_external`.

Examples

```
data("smart")
# Use the first 1000 samples as training data
# (the data used for internal validation)
x <- as.matrix(smart[, -c(1, 2)])[1:1000, ]
time <- smart$TEVENT[1:1000]
event <- smart$EVENT[1:1000]

# Take the next 1000 samples as external calibration data
# In practice, usually use data collected in other studies
x_new <- as.matrix(smart[, -c(1, 2)])[1001:2000, ]
time_new <- smart$TEVENT[1001:2000]
event_new <- smart$EVENT[1001:2000]

# Fit Cox model with lasso penalty
fit <- fit_lasso(
  x, survival::Surv(time, event),
  nfolds = 5, rule = "lambda.1se", seed = 11
)

# Internal calibration
cal.int <- calibrate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,
  method = "cv", nfolds = 5,
  pred.at = 365 * 9, ngroup = 3
)

logrank_test(cal.int)

# External calibration
cal.ext <- calibrate_external(
  fit, x, time, event,
  x_new, time_new, event_new,
  pred.at = 365 * 5, ngroup = 3
)

logrank_test(cal.ext)
```

Description

Derived from `peperr::basesurv` and `gbm::basehaz.gbm`.

Usage

```
ncvreg_basesurv(time, event, lp, times.eval = NULL, centered = FALSE)
```

Arguments

time	Survival time
event	Status indicator
lp	Linear predictors
times.eval	Survival time to evaluate
centered	Should we center the survival curve? See basehaz for details.

Value

list containing cumulative base hazard

Examples

```
NULL
```

ncvreg_survcurve	<i>Survival curve prediction for ncvreg objects</i>
------------------	---

Description

Derived from `c060::predictProb.coxnet`

Usage

```
ncvreg_survcurve(object, time, event, x, survtime)
```

Arguments

object	ncvreg model object
time	Survival time
event	Status indicator
x	Predictor matrix
survtime	Survival time to evaluate

Value

list containing predicted survival probabilities and linear predictors for all samples

Examples

```
NULL
```

penalized_basesurv *Breslow baseline hazard estimator for penfit objects*

Description

Derived from `peperr::basesurv` and `gbm::basehaz.gbm`.

Usage

```
penalized_basesurv(time, event, lp, times.eval = NULL, centered = FALSE)
```

Arguments

<code>time</code>	Survival time
<code>event</code>	Status indicator
<code>lp</code>	Linear predictors
<code>times.eval</code>	Survival time to evaluate
<code>centered</code>	Should we center the survival curve? See basehaz for details.

Value

list containing cumulative base hazard

Examples

```
NULL
```

penalized_survcurve *Survival curve prediction for penfit objects*

Description

Derived from `c060::predictProb.coxnet`

Usage

```
penalized_survcurve(object, time, event, x, survtime)
```

Arguments

<code>object</code>	penalized model object
<code>time</code>	Survival time
<code>event</code>	Status indicator
<code>x</code>	Predictor matrix
<code>survtime</code>	Survival time to evaluate

Value

list containing predicted survival probabilities and linear predictors for all samples

Examples

NULL

plot.hdnom.calibrate *Plot calibration results*

Description

Plot calibration results

Usage

```
## S3 method for class 'hdnom.calibrate'
plot(
  x,
  xlim = c(0, 1),
  ylim = c(0, 1),
  col.pal = c("JCO", "Lancet", "NPG", "AAAS"),
  ...
)
```

Arguments

x	An object returned by <code>calibrate</code> .
xlim	x axis limits of the plot.
ylim	y axis limits of the plot.
col.pal	Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".
...	Other parameters for plot.

Examples

NULL

`plot.hdnom.calibrate.external`*Plot external calibration results*

Description

Plot external calibration results

Usage

```
## S3 method for class 'hdnom.calibrate.external'
plot(
  x,
  xlim = c(0, 1),
  ylim = c(0, 1),
  col.pal = c("JCO", "Lancet", "NPG", "AAAS"),
  ...
)
```

Arguments

<code>x</code>	An object returned by calibrate_external .
<code>xlim</code>	x axis limits of the plot.
<code>ylim</code>	y axis limits of the plot.
<code>col.pal</code>	Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".
<code>...</code>	Other parameters for plot.

Examples

```
NULL
```

`plot.hdnom.compare.calibrate`*Plot model comparison by calibration results*

Description

Plot model comparison by calibration results

Usage

```
## S3 method for class 'hdnom.compare.calibrate'
plot(
  x,
  xlim = c(0, 1),
  ylim = c(0, 1),
  col.pal = c("JCO", "Lancet", "NPG", "AAAS"),
  ...
)
```

Arguments

x	An object returned by <code>compare_by_calibrate</code> .
xlim	x axis limits of the plot.
ylim	y axis limits of the plot.
col.pal	Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".
...	Other parameters (not used).

Examples

```
NULL
```

```
plot.hdnom.compare.validate
```

Plot model comparison by validation results

Description

Plot model comparison by validation results

Usage

```
## S3 method for class 'hdnom.compare.validate'
plot(
  x,
  interval = FALSE,
  col.pal = c("JCO", "Lancet", "NPG", "AAAS"),
  ylim = NULL,
  ...
)
```


Arguments

- x An object returned by [compare_by_validate](#).
- interval Show maximum, minimum, 0.25, and 0.75 quantiles of time-dependent AUC as ribbons? Default is FALSE.
- col.pal Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".
- ylim Range of y coordinates. For example, c(0.5, 1).
- ... Other parameters (not used).

Examples

NULL

plot.hdnom.nomogram *Plot nomogram objects*

Description

Plot nomogram objects

Usage

```
## S3 method for class 'hdnom.nomogram'  
plot(x, ...)
```

Arguments

- x An object returned by [as_nomogram](#).
- ... Other parameters.

Examples

NULL

```
plot.hdnom.validate    Plot optimism-corrected time-dependent discrimination curves for validation
```

Description

Plot optimism-corrected time-dependent discrimination curves for validation

Usage

```
## S3 method for class 'hdnom.validate'
plot(x, col.pal = c("JCO", "Lancet", "NPG", "AAAS"), ylim = NULL, ...)
```

Arguments

x	An object returned by validate .
col.pal	Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".
ylim	Range of y coordinates. For example, c(0.5, 1).
...	Other parameters (not used).

Examples

```
NULL
```

```
plot.hdnom.validate.external
    Plot time-dependent discrimination curves for external validation
```

Description

Plot time-dependent discrimination curves for external validation

Usage

```
## S3 method for class 'hdnom.validate.external'
plot(x, col.pal = c("JCO", "Lancet", "NPG", "AAAS"), ylim = NULL, ...)
```

Arguments

x	An object returned by validate_external .
col.pal	Color palette to use. Possible values are "JCO", "Lancet", "NPG", and "AAAS". Default is "JCO".
ylim	Range of y coordinates. For example, c(0.5, 1).
...	Other parameters (not used).

Examples

```
NULL
```

```
predict.hdnom.model    Make predictions from high-dimensional Cox models
```

Description

Predict overall survival probability at certain time points from fitted Cox models.

Usage

```
## S3 method for class 'hdnom.model'
predict(object, x, y, newx, pred.at, ...)
```

Arguments

object	Model object.
x	Data matrix used to fit the model.
y	Response matrix made with Surv .
newx	Matrix (with named columns) of new values for x at which predictions are to be made.
pred.at	Time point at which prediction should take place.
...	Other parameters (not used).

Value

A `nrow(newx) x length(pred.at)` matrix containing overall survival probability.

Examples

```
data("smart")
x <- as.matrix(smart[, -c(1, 2)])
time <- smart$TEVENT
event <- smart$Eevent
y <- survival::Surv(time, event)

fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)
predict(fit, x, y, newx = x[101:105, ], pred.at = 1:10 * 365)
```

```
print.hdnom.calibrate Print calibration results
```

Description

Print calibration results

Usage

```
## S3 method for class 'hdnom.calibrate'  
print(x, ...)
```

Arguments

x	An object returned by calibrate .
...	Other parameters (not used).

Examples

```
NULL
```

```
print.hdnom.calibrate.external  
Print external calibration results
```

Description

Print external calibration results

Usage

```
## S3 method for class 'hdnom.calibrate.external'  
print(x, ...)
```

Arguments

x	An object returned by calibrate_external .
...	Other parameters (not used).

Examples

```
NULL
```

```
print.hdnom.compare.calibrate
```

Print model comparison by calibration results

Description

Print model comparison by calibration results

Usage

```
## S3 method for class 'hdnom.compare.calibrate'  
print(x, ...)
```

Arguments

x	An object returned by compare_by_calibrate .
...	Other parameters (not used).

Examples

```
NULL
```

```
print.hdnom.compare.validate
```

Print model comparison by validation results

Description

Print model comparison by validation results

Usage

```
## S3 method for class 'hdnom.compare.validate'  
print(x, ...)
```

Arguments

x	An object returned by compare_by_validate .
...	Other parameters (not used).

Examples

```
NULL
```

print.hdnom.model *Print high-dimensional Cox model objects*

Description

Print high-dimensional Cox model objects

Usage

```
## S3 method for class 'hdnom.model'  
print(x, ...)
```

Arguments

x	Model object.
...	Other parameters (not used).

Examples

```
data("smart")  
x <- as.matrix(smart[, -c(1, 2)])  
time <- smart$TEVENT  
event <- smart$Eevent  
y <- survival::Surv(time, event)  
  
fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)  
print(fit)
```

print.hdnom.nomogram *Print nomograms objects*

Description

Print nomograms objects

Usage

```
## S3 method for class 'hdnom.nomogram'  
print(x, ...)
```

Arguments

x	An object returned by as_nomogram .
...	Other parameters.

Examples

```
NULL
```

`print.hdnom.validate` *Print validation results*

Description

Print validation results

Usage

```
## S3 method for class 'hdnom.validate'  
print(x, ...)
```

Arguments

`x` An object returned by `validate`.
`...` Other parameters (not used).

Examples

NULL

`print.hdnom.validate.external`
Print external validation results

Description

Print external validation results

Usage

```
## S3 method for class 'hdnom.validate.external'  
print(x, ...)
```

Arguments

`x` An object returned by `validate_external`.
`...` Other parameters (not used).

Examples

NULL

smart

Imputed SMART study data

Description

Imputed SMART study data (no missing values).

Usage

data(smart)

Format

A numeric matrix with 3873 samples, and 29 variables (27 variables + time variable + event variable):

- Demographics
 - SEX - gender
 - AGE - age in years
- Classical risk factors
 - SMOKING - smoking (never, former, current)
 - PACKYRS - in years
 - ALCOHOL - alcohol use (never, former, current)
 - BMI - Body mass index, in kg/m²
 - DIABETES
- Blood pressure
 - SYSTH - Systolic, by hand, in mm Hg
 - SYSTBP - Systolic, automatic, in mm Hg
 - DIASTH - Diastolic, by hand, in mm Hg
 - DIASTBP - Diastolic, automatic, in mm Hg
- Lipid levels
 - CHOL - Total cholesterol, in mmol/L
 - HDL - High-density lipoprotein cholesterol, in mmol/L
 - LDL - Low-density lipoprotein cholesterol, in mmol/L
 - TRIG - Triglycerides, in mmol/L
- Previous symptomatic atherosclerosis
 - CEREBRAL - Cerebral
 - CARDIAC - Coronary
 - PERIPH - Peripheral
 - AAA - Abdominal aortic aneurysm
- Markers of atherosclerosis
 - HOMOC - Homocysteine, in μ mol/L

- GLUT - Glutamine, in $\mu\text{mol/L}$
- CREAT - Creatinine clearance, in mL/min
- ALBUMIN - Albumin (no, micro, macro)
- IMT - Intima media thickness, in mm
- STENOSIS - Carotid artery stenosis > 50%

Note

See `data-raw/smart.R` for the code to generate this data.

References

Steyerberg, E. W. (2008). Clinical prediction models: a practical approach to development, validation, and updating. Springer Science & Business Media.

Examples

```
data(smarto)
dim(smarto)
```

smarto	<i>Original SMART study data</i>
--------	----------------------------------

Description

Original SMART study data (with missing values) from Steyerberg et, al. 2008.

Usage

```
data(smarto)
```

Format

A numeric matrix with 3873 samples, and 29 variables (27 variables + time variable + event variable):

- Demographics
 - SEX - gender
 - AGE - age in years
- Classical risk factors
 - SMOKING - smoking (never, former, current)
 - PACKYRS - in years
 - ALCOHOL - alcohol use (never, former, current)
 - BMI - Body mass index, in kg/m^2
 - DIABETES
- Blood pressure

- SYSTH - Systolic, by hand, in mm Hg
- SYSTBP - Systolic, automatic, in mm Hg
- DIASTH - Diastolic, by hand, in mm Hg
- DIASTBP - Diastolic, automatic, in mm Hg
- Lipid levels
 - CHOL - Total cholesterol, in mmol/L
 - HDL - High-density lipoprotein cholesterol, in mmol/L
 - LDL - Low-density lipoprotein cholesterol, in mmol/L
 - TRIG - Triglycerides, in mmol/L
- Previous symptomatic atherosclerosis
 - CEREBRAL - Cerebral
 - CARDIAC - Coronary
 - PERIPH - Peripheral
 - AAA - Abdominal aortic aneurysm
- Markers of atherosclerosis
 - HOMOC - Homocysteine, in $\mu\text{mol/L}$
 - GLUT - Glutamine, in $\mu\text{mol/L}$
 - CREAT - Creatinine clearance, in mL/min
 - ALBUMIN - Albumin (no, micro, macro)
 - IMT - Intima media thickness, in mm
 - STENOSIS - Carotid artery stenosis > 50%

References

Steyerberg, E. W. (2008). Clinical prediction models: a practical approach to development, validation, and updating. Springer Science & Business Media.

Examples

```
data(smarto)
dim(smarto)
```

```
summary.hdnom.calibrate
```

Summary of calibration results

Description

Summary of calibration results

Usage

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

Arguments

object An object returned by [calibrate](#).
... Other parameters (not used).

Examples

NULL

summary.hdnom.calibrate.external
Summary of external calibration results

Description

Summary of external calibration results

Usage

```
## S3 method for class 'hdnom.calibrate.external'  
summary(object, ...)
```

Arguments

object An object returned by [calibrate_external](#).
... Other parameters (not used).

Examples

NULL

summary.hdnom.compare.calibrate
Summary of model comparison by calibration results

Description

Summary of model comparison by calibration results

Usage

```
## S3 method for class 'hdnom.compare.calibrate'  
summary(object, ...)
```

Arguments

object An object returned by [compare_by_calibrate](#).
 ... Other parameters (not used).

Examples

NULL

summary.hdnom.compare.validate

Summary of model comparison by validation results

Description

Summary of model comparison by validation results

Usage

```
## S3 method for class 'hdnom.compare.validate'
summary(object, silent = FALSE, ...)
```

Arguments

object An object [compare_by_validate](#).
 silent Print summary table header or not, default is FALSE.
 ... Other parameters (not used).

Examples

NULL

summary.hdnom.validate

Summary of validation results

Description

Summary of validation results

Usage

```
## S3 method for class 'hdnom.validate'
summary(object, silent = FALSE, ...)
```

Arguments

object	A validate object.
silent	Print summary table header or not, default is FALSE.
...	Other parameters (not used).

Examples

```
NULL
```

```
summary.hdnom.validate.external
      Summary of external validation results
```

Description

Summary of external validation results

Usage

```
## S3 method for class 'hdnom.validate.external'
summary(object, silent = FALSE, ...)
```

Arguments

object	An object returned by validate_external .
silent	Print summary table header or not, default is FALSE.
...	Other parameters (not used).

Examples

```
NULL
```

```
theme_hdnom      Plot theme (ggplot2) for hdnom
```

Description

Plot theme (ggplot2) for hdnom

Usage

```
theme_hdnom(base_size = 14)
```

Arguments

base_size	base font size
-----------	----------------

 validate

Validate high-dimensional Cox models with time-dependent AUC

Description

Validate high-dimensional Cox models with time-dependent AUC

Usage

```
validate(
  x,
  time,
  event,
  model.type = c("lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad",
    "snet"),
  alpha,
  lambda,
  pen.factor = NULL,
  gamma,
  lambda1,
  lambda2,
  method = c("bootstrap", "cv", "repeated.cv"),
  boot.times = NULL,
  nfolds = NULL,
  rep.times = NULL,
  tauc.type = c("CD", "SZ", "UNO"),
  tauc.time,
  seed = 1001,
  trace = TRUE
)
```

Arguments

<code>x</code>	Matrix of training data used for fitting the model; on which to run the validation.
<code>time</code>	Survival time. Must be of the same length with the number of rows as <code>x</code> .
<code>event</code>	Status indicator, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as <code>x</code> .
<code>model.type</code>	Model type to validate. Could be one of "lasso", "alasso", "flasso", "enet", "aenet", "mcp", "mnet", "scad", or "snet".
<code>alpha</code>	Value of the elastic-net mixing parameter <code>alpha</code> for <code>enet</code> , <code>aenet</code> , <code>mnet</code> , and <code>snet</code> models. For <code>lasso</code> , <code>alasso</code> , <code>mcp</code> , and <code>scad</code> models, please set <code>alpha = 1</code> . <code>alpha=1</code> : lasso (l1) penalty; <code>alpha=0</code> : ridge (l2) penalty. Note that for <code>mnet</code> and <code>snet</code> models, <code>alpha</code> can be set to very close to 0 but not 0 exactly.
<code>lambda</code>	Value of the penalty parameter <code>lambda</code> to use in the model fits on the resampled data. From the fitted Cox model.

pen.factor	Penalty factors to apply to each coefficient. From the fitted <i>adaptive lasso</i> or <i>adaptive elastic-net</i> model.
gamma	Value of the model parameter gamma for MCP/SCAD/Mnet/Snet models.
lambda1	Value of the penalty parameter lambda1 for fused lasso model.
lambda2	Value of the penalty parameter lambda2 for fused lasso model.
method	Validation method. Could be "bootstrap", "cv", or "repeated.cv".
boot.times	Number of repetitions for bootstrap.
nfolds	Number of folds for cross-validation and repeated cross-validation.
rep.times	Number of repeated times for repeated cross-validation.
tauc.type	Type of time-dependent AUC. Including "CD" proposed by Chambless and Diao (2006), "SZ" proposed by Song and Zhou (2008), "UNO" proposed by Uno et al. (2007).
tauc.time	Numeric vector. Time points at which to evaluate the time-dependent AUC.
seed	A random seed for resampling.
trace	Logical. Output the validation progress or not. Default is TRUE.

References

Chambless, L. E. and G. Diao (2006). Estimation of time-dependent area under the ROC curve for long-term risk prediction. *Statistics in Medicine* 25, 3474–3486.

Song, X. and X.-H. Zhou (2008). A semiparametric approach for the covariate specific ROC curve with survival outcome. *Statistica Sinica* 18, 947–965.

Uno, H., T. Cai, L. Tian, and L. J. Wei (2007). Evaluating prediction rules for t-year survivors with censored regression models. *Journal of the American Statistical Association* 102, 527–537.

Examples

```
data(smart)
x <- as.matrix(smart[, -c(1, 2)])[1:500, ]
time <- smart$TEVENT[1:500]
event <- smart$EVENT[1:500]
y <- survival::Surv(time, event)

fit <- fit_lasso(x, y, nfolds = 5, rule = "lambda.1se", seed = 11)

# Model validation by bootstrap with time-dependent AUC
# Normally boot.times should be set to 200 or more,
# we set it to 3 here only to save example running time.
val.boot <- validate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,
  method = "bootstrap", boot.times = 3,
  tauc.type = "UNO", tauc.time = seq(0.25, 2, 0.25) * 365,
  seed = 1010
)
```

```

# Model validation by 5-fold cross-validation with time-dependent AUC
val.cv <- validate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,
  method = "cv", nfolds = 5,
  tauc.type = "UNO", tauc.time = seq(0.25, 2, 0.25) * 365,
  seed = 1010
)

# Model validation by repeated cross-validation with time-dependent AUC
val.repcv <- validate(
  x, time, event,
  model.type = "lasso",
  alpha = 1, lambda = fit$lambda,
  method = "repeated.cv", nfolds = 5, rep.times = 3,
  tauc.type = "UNO", tauc.time = seq(0.25, 2, 0.25) * 365,
  seed = 1010
)

# bootstrap-based discrimination curves has a very narrow band
print(val.boot)
summary(val.boot)
plot(val.boot)

# k-fold cv provides a more strict evaluation than bootstrap
print(val.cv)
summary(val.cv)
plot(val.cv)

# repeated cv provides similar results as k-fold cv
# but more robust than k-fold cv
print(val.repcv)
summary(val.repcv)
plot(val.repcv)
# # Test fused lasso, SCAD, and Mnet models
#
# data(smart)
# x = as.matrix(smart[, -c(1, 2)])[1:500,]
# time = smart$TEVENT[1:500]
# event = smart$EVENT[1:500]
# y = survival::Surv(time, event)
#
# set.seed(1010)
# val.boot = validate(
#   x, time, event, model.type = "flasso",
#   lambda1 = 5, lambda2 = 2,
#   method = "bootstrap", boot.times = 10,
#   tauc.type = "UNO", tauc.time = seq(0.25, 2, 0.25) * 365,
#   seed = 1010)
#
# val.cv = validate(

```



```
# x, time, event, model.type = "scad",
# gamma = 3.7, alpha = 1, lambda = 0.05,
# method = "cv", nfolds = 5,
# tauc.type = "UNO", tauc.time = seq(0.25, 2, 0.25) * 365,
# seed = 1010)
#
# val.repcv = validate(
# x, time, event, model.type = "mnet",
# gamma = 3, alpha = 0.3, lambda = 0.05,
# method = "repeated.cv", nfolds = 5, rep.times = 3,
# tauc.type = "UNO", tauc.time = seq(0.25, 2, 0.25) * 365,
# seed = 1010)
#
# print(val.boot)
# summary(val.boot)
# plot(val.boot)
#
# print(val.cv)
# summary(val.cv)
# plot(val.cv)
#
# print(val.repcv)
# summary(val.repcv)
# plot(val.repcv)
```

validate_external	<i>Externally validate high-dimensional Cox models with time-dependent AUC</i>
-------------------	--

Description

Externally validate high-dimensional Cox models with time-dependent AUC

Usage

```
validate_external(
  object,
  x,
  time,
  event,
  x_new,
  time_new,
  event_new,
  tauc.type = c("CD", "SZ", "UNO"),
  tauc.time
)
```

Arguments

object	Model object fitted by <code>hdnom::fit_*</code> .
x	Matrix of training data used for fitting the model.
time	Survival time of the training data. Must be of the same length with the number of rows as x.
event	Status indicator of the training data, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as x.
x_new	Matrix of predictors for the external validation data.
time_new	Survival time of the external validation data. Must be of the same length with the number of rows as x_new.
event_new	Status indicator of the external validation data, normally 0 = alive, 1 = dead. Must be of the same length with the number of rows as x_new.
tauc.type	Type of time-dependent AUC. Including "CD" proposed by Chambless and Diao (2006), "SZ" proposed by Song and Zhou (2008), "UNO" proposed by Uno et al. (2007).
tauc.time	Numeric vector. Time points at which to evaluate the time-dependent AUC.

References

Chambless, L. E. and G. Diao (2006). Estimation of time-dependent area under the ROC curve for long-term risk prediction. *Statistics in Medicine* 25, 3474–3486.

Song, X. and X.-H. Zhou (2008). A semiparametric approach for the covariate specific ROC curve with survival outcome. *Statistica Sinica* 18, 947–965.

Uno, H., T. Cai, L. Tian, and L. J. Wei (2007). Evaluating prediction rules for t-year survivors with censored regression models. *Journal of the American Statistical Association* 102, 527–537.

Examples

```
data(smart)
# Use the first 1000 samples as training data
# (the data used for internal validation)
x <- as.matrix(smart[, -c(1, 2)])[1:1000, ]
time <- smart$TEVENT[1:1000]
event <- smart$EVENT[1:1000]

# Take the next 1000 samples as external validation data
# In practice, usually use data collected in other studies
x_new <- as.matrix(smart[, -c(1, 2)])[1001:2000, ]
time_new <- smart$TEVENT[1001:2000]
event_new <- smart$EVENT[1001:2000]

# Fit Cox model with lasso penalty
fit <- fit_lasso(
  x, survival::Surv(time, event),
  nfolds = 5, rule = "lambda.1se", seed = 11
)
```

```

# External validation with time-dependent AUC
val.ext <- validate_external(
  fit, x, time, event,
  x_new, time_new, event_new,
  tauc.type = "UNO",
  tauc.time = seq(0.25, 2, 0.25) * 365
)

print(val.ext)
summary(val.ext)
plot(val.ext)

# # Test fused lasso, MCP, and Snet models
# data(smart)
# # Use first 600 samples as training data
# # (the data used for internal validation)
# x <- as.matrix(smart[, -c(1, 2)])[1:600, ]
# time <- smart$TEVENT[1:600]
# event <- smart$EVENT[1:600]
#
# # Take 500 samples as external validation data.
# # In practice, usually use data collected in other studies.
# x_new <- as.matrix(smart[, -c(1, 2)])[1001:1500, ]
# time_new <- smart$TEVENT[1001:1500]
# event_new <- smart$EVENT[1001:1500]
#
# fllassofit <- fit_fllasso(x, survival::Surv(time, event), nfolds = 5, seed = 11)
# scadfit <- fit_mcp(x, survival::Surv(time, event), nfolds = 5, seed = 11)
# mnetfit <- fit_snet(x, survival::Surv(time, event), nfolds = 5, seed = 11)
#
# val.ext1 <- validate_external(
#   fllassofit, x, time, event,
#   x_new, time_new, event_new,
#   tauc.type = "UNO",
#   tauc.time = seq(0.25, 2, 0.25) * 365)
#
# val.ext2 <- validate_external(
#   scadfit, x, time, event,
#   x_new, time_new, event_new,
#   tauc.type = "CD",
#   tauc.time = seq(0.25, 2, 0.25) * 365)
#
# val.ext3 <- validate_external(
#   mnetfit, x, time, event,
#   x_new, time_new, event_new,
#   tauc.type = "SZ",
#   tauc.time = seq(0.25, 2, 0.25) * 365)
#
# print(val.ext1)
# summary(val.ext1)
# plot(val.ext1)
#
# print(val.ext2)

```

```
# summary(val.ext2)
# plot(val.ext2)
#
# print(val.ext3)
# summary(val.ext3)
# plot(val.ext3)
```

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