Package ‘targeted’

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Type Package

Title Targeted Inference

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Description Various methods for targeted and semiparametric inference including augmented inverse probability weighted estimators for missing data and causal inference (Bang and Robins (2005) <doi:10.1111/j.1541-0420.2005.00377.x>) and estimators for risk differences and relative risks (Richardson et al. (2017) <doi:10.1080/01621459.2016.1192546>).

Depends R (>= 4.0), lava (>= 1.7.0)

Imports data.table, digest, futile.logger, future.apply, optimx, progressr, methods, mets, R6, Rcpp (>= 1.0.0), survival

Suggests grf, mgcv, testthat (>= 0.11), rmarkdown, scatterplot3d, SuperLearner (>= 2.0-28), knitr

BugReports https://github.com/kkholst/targeted/issues

License Apache License (== 2.0)

LinkingTo Rcpp, RcppArmadillo

LazyLoad yes

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R topics documented:

`targeted-package` *Targeted inference*

Description

Methods for targeted and semiparametric inference including augmented inverse probability weighted estimators for missing data and causal inference.

Author(s)

Klaus K. Holst (Maintainer) klaus@holst.it

Examples

```
example(riskreg)
example(cate)
example(ate)
example(calibration)
```

ate *AIPW estimator for Average Treatement Effect*

Description

Augmented Inverse Probability Weighting estimator for the Average (Causal) Treatment Effect.

Usage

```
ate(
  formula,
  data = parent.frame(),
  weights,
  binary = TRUE,
  nuisance = NULL,
  propensity = nuisance,
  all,
  missing = FALSE,
  labels = NULL,
  ...
)
```

Arguments

`formula`	Formula (see details below)
`data`	data.frame
`weights`	optional frequency weights
`binary`	Binary response (default TRUE)
`nuisance`	outcome regression formula
`propensity`	propensity model formula
`all`	If TRUE all standard errors are calculated (default TRUE when exposure only has two levels)
`missing`	If TRUE a missing data (AIPW) estimator is returned
`labels`	Optional treatment labels
`...`	Additional arguments to lower level functions

Details

The formula may either be specified as: response ~ treatment | nuisance-formula | propensity-formula

For example: `ate(y~a | x+z+a | x*z, data=...)`

Alternatively, as a list: `ate(list(y~a, ~x+z, ~x*z), data=...)`

Or using the nuisance (and propensity argument): `ate(y~a, nuisance=~x+z, ...)`

Value

An object of class 'ate.targeted' is returned. See targeted-class for more details about this class and its generic functions.

Author(s)

Klaus K. Holst

Examples

```
m <- lvm(y ~ a+x, a~x)
distribution(m,~ a+y) <- binomial.lvm()
d <- sim(m,1e3,seed=1)

a <- ate(y ~ a, nuisance=~x, data=d)
summary(a)

# Multiple treatments
m <- lvm(y ~ a+x, a~x)
distribution(m,~ y) <- binomial.lvm()
m <- ordinal(m, K=4, ~a)
transform(m, ~a) <- factor
d <- sim(m, 1e4, seed=1)
(a <- ate(y~a|a*x|x, data=d))

# Comparison with randomized experiment
m0 <- cancel(m, a~x)
d0 <- sim(m0,2e5)
lm(y~a-1,d0)

# Choosing a different contrast for the association measures
summary(a, contrast=c(2,4))
```

---

calibration *Calibration (training)*

Description

Calibration for multiclassication methods

Usage

```
calibration(
  pr,
  cl,
  weights = NULL,
  threshold = 10,
  method = "bin",
  breaks = nclass.Sturges,
```

```
  df = 3,
  ...
)
```

Arguments

`pr`	matrix with probabilities for each class
`cl`	class variable
`weights`	counts
`threshold`	do not calibrate if less then 'threshold' events
`method`	either 'isotonic' (pava), 'logistic', 'mspline' (monotone spline), 'bin' (local constant)
`breaks`	optional number of bins (only for method 'bin')
`df`	degrees of freedom (only for spline methods)
`...`	additional arguments to lower level functions

Details

...

Value

An object of class 'calibration' is returned. See calibration-class for more details about this class and its generic functions.

Author(s)

Klaus K. Holst

Examples

```
sim1 <- function(n, beta=c(-3, rep(.5,10)), rho=.5) {
 p <- length(beta)-1
 xx <- lava::rmvn0(n,sigma=diag(nrow=p)*(1-rho)+rho)
 y <- rbinom(n, 1, lava::expit(cbind(1,xx)%*%beta))
 d <- data.frame(y=y, xx)
 names(d) <- c("y",paste0("x",1:p))
 return(d)
}

set.seed(1)
beta <- c(-2,rep(1,10))
d <- sim1(1e4, beta=beta)
a1 <- NB(y ~ ., data=d)
a2 <- glm(y ~ ., data=d, family=binomial)
## a3 <- randomForest(factor(y) ~ ., data=d, family=binomial)

d0 <- sim1(1e5, beta=beta)
p1 <- predict(a1, newdata=d0)
```

```
p2 <- predict(a2, newdata=d0, type="response")
## p3 <- predict(a3, newdata=d0, type="prob")

c2 <- calibration(p2, d0$y, method="isotonic")
c1 <- calibration(p1, d0$y, breaks=100)
if (interactive()) {
  plot(c1)
  plot(c2,col="red",add=TRUE)
  abline(a=0,b=1)##'
  with(c1$xy[[1]], points(pred,freq,type="b", col="red"))
}

set.seed(1)
beta <- c(-2,rep(1,10))
dd <- lava::csplit(sim1(6e4, beta=beta), k=3)
mod <- NB(y ~ ., data=dd[[1]])
p1 <- predict(mod, newdata=dd[[2]])
cal <- calibration(p1, dd[[2]]$y)
p2 <- predict(mod, newdata=dd[[3]])
pp <- predict(c1, p2)
cc <- calibration(pp, dd[[3]]$y)
if (interactive()) {##'
  plot(cal)
  plot(cc, add=TRUE, col="blue")
}
```

`calibration-class` *calibration class object*

Description

The functions `calibration` returns an object of the class `calibration`.

An object of class '`calibration`' is a list with at least the following components:

stepfun estimated step-functions (see `stepfun`) for each class

classes the unique classes

model model/method type (string)

xy list of data.frame's with predictions (pr) and estimated probabilities of success (only for 'bin' method)

Value

objects of the S3 class '`calibration`'

S3 generics

The following S3 generic functions are available for an object of class `targeted`:

- `predict`Apply calibration to new data.
- `plot`Plot the calibration curves (reliability plot).
- `print`Basic print method.

See Also

`calibration`, `calibrate`

Examples

```
## See example(calibration) for examples
```

`cate` *Conditional Average Treatment Effect estimation*

Description

Conditional Average Treatment Effect estimation via Double Machine Learning

Usage

```
cate(
  treatment,
  response_model,
  propensity_model,
  contrast = c(1, 0),
  data,
  nfolds = 5,
  type = "dml1",
  ...
)
```

Arguments

`treatment`	formula specifying treatment and variables to condition on
`response_model`	SL object
`propensity_model`	SL object
`contrast`	treatment contrast (default 1 vs 0)
`data`	data.frame
`nfolds`	Number of folds
`type`	'dml1' or 'dml2'
`...`	additional arguments to SuperLearner

Value

cate.targeted object

Author(s)

Klaus Kähler Holst

Examples

```
sim1 <- function(n=1e4,
                 seed=NULL,
                 return_model=FALSE, ...) {
suppressPackageStartupMessages(require("lava"))
if (!is.null(seed)) set.seed(seed)
m <- lava::lvm()
regression(m, ~a) <- function(z1,z2,z3,z4,z5)
         cos(z1)+sin(z1*z2)+z3+z4+z5^2
regression(m, ~u) <- function(a,z1,z2,z3,z4,z5)
        (z1+z2+z3)*a + z1+z2+z3 + a
distribution(m, ~a) <- binomial.lvm()
if (return_model) return(m)
lava::sim(m, n, p=par)
}

d <- sim1(200)
if (require("SuperLearner",quietly=TRUE)) {
  e <- cate(a ~ z1+z2+z3, response=u~., data=d)
  e
}
```

`cross_validated-class` *cross_validated class object*

Description

The functions `cv` returns an object of the type `cross_validated`.

An object of class '`cross_validated`' is a list with at least the following components:

cv An array with the model score(s) evaluated for each fold, repetition, and model. estimates (see `estimate.default`)

names Names (character vector) of the models

rep number of repetitions of the CV

folds Number of folds of the CV

Value

objects of the S3 class '`cross_validated`'

S3 generics

The following S3 generic functions are available for an object of class `cross_validated`:

- `coef`Extract average model scores from the cross-validation procedure.
- `print`Basic print method.
- `summary`Summary of the cross-validation procedure.'

See Also

`cv`

Examples

```
## See example(cv) for examples
```

`crr` *Conditional Relative Risk estimation*

Description

Conditional Relative Risk estimation via Double Machine Learning

Usage

```
crr(
  treatment,
  response_model,
  propensity_model,
  importance_model,
  contrast = c(1, 0),
  data,
  nfolds = 5,
  type = "dml1",
  ...
)
```

Arguments

`treatment`	formula specifying treatment and variables to condition on
`response_model`	SL object (outcome/response model)
`propensity_model`	SL object (treatment/propensity model)
`importance_model`	SL object (conditional expectation of outcome model on variables conditioned on in treatment argument)
`contrast`	treatment contrast (default 1 vs 0)

data	data.frame
nfolds	Number of folds
type	'dml1' or 'dml2'
...	additional arguments to SuperLearner

Value

cate.targeted object

Author(s)

Klaus Kähler Holst & Andreas Nordland

Examples

```
sim1 <- function(n=1e4,
                 seed=NULL,
                 return_model=FALSE, ...) {
  suppressPackageStartupMessages(require("lava"))
  if (!is.null(seed)) set.seed(seed)
  m <- lava::lvm()
  distribution(m, ~x) <- gaussian.lvm()
  distribution(m, ~v) <- gaussian.lvm(mean = 5)
  distribution(m, ~a) <- binomial.lvm("logit")
  regression(m, "a") <- function(v, x){.2*v + x}
  distribution(m, "y") <- gaussian.lvm()
  regression(m, "y") <- function(a, v, x){v+x+a*x+a*v*v}
  if (return_model) return(m)
  lava::sim(m, n = n)
}

d <- sim1(n = 1e3, seed = 1)
if (require("SuperLearner",quietly=TRUE)) {
  e <- crr(data=d,
           type = "dml2",
           treatment = a ~ v,
           response_model = y~ a*(x + v + I(v^2)),
           importance_model = SL(D_ ~ v + I(v^2)),
           nfolds = 2)
  summary(e) # the true parameters are c(1,1)
}
```

cv *Cross-validation*

Description

Generic cross-validation function

Usage

```
cv(
  models,
  data,
  response = NULL,
  K = 5,
  rep = 1,
  weights = NULL,
  modelscore,
  seed = NULL,
  shared = NULL,
  args.pred = NULL,
  ...
)
```

Arguments

`models`	List of fitting functions
`data`	data.frame or matrix
`response`	Response variable (vector or name of column in `data`).##'
`K`	Number of folds (default 5. K=0 splits in 1:n/2, n/2:n with last part used for testing)
`rep`	Number of repetitions (default 1)
`weights`	Optional frequency weights
`modelscore`	Model scoring metric (default: RMSE / Brier score). Must be a function with arguments: response, prediction, weights, ...
`seed`	Random seed (argument parsed to future_Apply::future_lapply)
`shared`	Function applied to each fold with results send to each model
`args.pred`	Optional arguments to prediction function (see details below)
`...`	Additional arguments parsed to models in models

Details

models should be list of objects of class ml_model. Alternatively, each element of models should be a list with a fitting function and a prediction function.

The `reponse` argument can optionally be a named list where the name is then used as the name of the response argument in models. Similarly, if data is a named list with a single data.frame/matrix then this name will be used as the name of the data/design matrix argument in models.

Value

An object of class '`cross_validated`' is returned. See `cross_validated-class` for more details about this class and its generic functions.

Author(s)

Klaus K. Holst

Examples

```
f0 <- function(data,...) lm(...,data=data)
f1 <- function(data,...) lm(Sepal.Length~Species,data=data)
f2 <- function(data,...) lm(Sepal.Length~Species+Petal.Length,data=data)
x <- cv(list(m0=f0,m1=f1,m2=f2),rep=10, data=iris, formula=Sepal.Length~.)
x
```

`design` *Extract design matrix*

Description

Extract design matrix from data.frame and formula

Usage

```
design(formula, data, intercept = FALSE, rm_envir = FALSE, ...)
```

Arguments

`formula`	formula
`data`	data.frame
`intercept`	If FALSE (default) an intercept is not included
`rm_envir`	Remove environment
`...`	additional arguments (e.g, specials such weights, offsets, subset)

Value

An object of class 'design'

Author(s)

Klaus Kähler Holst

`expand.list` *Create a list from all combination of input variables*

Description

Similar to `expand.grid` function, this function creates all combinations of the input arguments but returns the result as a list.

Usage

```
expand.list(...)
```

Arguments

`...` input variables

Value

list

Author(s)

Klaus Kähler Holst

Examples

```
expand.list(x=2:4, z=c("a","b"))
```

`ml_model` *R6 class for prediction models*

Description

R6 class for prediction models

R6 class for prediction models

Details

Provides standardized estimation and prediction methods

Public fields

`info` Optional information/name of the model

`formals` List with formal arguments of estimation and prediction functions

`formula` Formula specifying response and design matrix

Active bindings

`fit` Active binding returning estimated model object

Methods

Public methods:

- `ml_model$new()`
- `ml_model$estimate()`
- `ml_model$predict()`
- `ml_model$update()`
- `ml_model$print()`
- `ml_model$response()`
- `ml_model$design()`
- `ml_model$clone()`

Method `new()`**:** Create a new prediction model object

Usage:

```
ml_model$new(
  formula = NULL,
  fit,
  pred = predict,
  pred.args = NULL,
  info = NULL,
  specials,
  response.arg = "y",
  x.arg = "x",
  ...
)
```

Arguments:

`formula` formula specifying outcome and design matrix

`fit` function for fitting the model (must be a function response, 'y', and design matrix, 'x'. Alternatively, a function with a single 'formula' argument)

`pred` prediction function (must be a function of model object, 'fit', and new design matrix, 'newdata')

`pred.args` optional arguments to prediction function

`info` optional description of the model

`specials` optional additional terms (weights, offset, id, subset, ...) passed to 'fit'

`response.arg` name of response argument

`x.arg` name of design matrix argument

`...` optional arguments to fitting function

Method `estimate()`**:** Estimation method

Usage:

```
ml_model$estimate(data, ..., store = TRUE)
```

Arguments:

`data` data.frame

`...` Additional arguments to estimation method

`store` Logical determining if estimated model should be stored inside the class.

Method `predict()`: Prediction method

Usage:

```
ml_model$predict(newdata, ..., fit = NULL)
```

Arguments:

`newdata` data.frame

`...` Additional arguments to prediction method

`fit` Optional model fit object

Method `update()`: Update formula

Usage:

```
ml_model$update(formula, ...)
```

Arguments:

`formula` formula

`...` Additional arguments to lower level functions

Method `print()`: Print method

Usage:

```
ml_model$print(...)
```

Arguments:

`...` Additional arguments to lower level functions

Method `response()`: Extract response from data

Usage:

```
ml_model$response(data)
```

Arguments:

`data` data.frame

Method `design()`: Extract design matrix (features) from data

Usage:

```
ml_model$design(data)
```

Arguments:

`data` data.frame

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
ml_model$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Author(s)

Klaus Kähler Holst

Examples

```
data(iris)
rf <- function(formula, ...)
ml_model$new(formula, info="grf::probability_forest",
             fit=function(x,y, ...) grf::probability_forest(X=x, Y=y, ...),
             pred=function(fit, newdata) predict(fit, newdata)$predictions, ...)

args <- expand.list(num.trees=c(100,200), mtry=1:3,
                    formula=c(Species ~ ., Species ~ Sepal.Length + Sepal.Width))
models <- lapply(args, function(par) do.call(rf, par))

x <- models[[1]]$clone()
x$estimate(iris)
predict(x, newdata=head(iris))

 # Reduce Ex. timing
a <- targeted::cv(models, data=iris)
cbind(coef(a), attr(args, "table"))
```

NB *Naive Bayes*

Description

Naive Bayes Classifier

Usage

```
NB(
  formula,
  data,
  weights = NULL,
  kernel = FALSE,
  laplace.smooth = 0,
  prior = NULL,
  ...
)
```

Arguments

formula	Formula with syntax: response ~ predictors | weights
data	data.frame
weights	optional frequency weights

`kernel`	If TRUE a kernel estimator is used for numeric predictors (otherwise a gaussian model is used)
`laplace.smooth`	Laplace smoothing
`prior`	optional prior probabilities (default estimated from data)
`...`	additional arguments to lower level functions

Value

An object of class 'NB' is returned. See NB-class for more details about this class and its generic functions.

Author(s)

Klaus K. Holst

Examples

```
data(iris)
m2 <- NB(Species ~ Sepal.Width + Petal.Length, data=iris)
pr2 <- predict(m2, newdata=iris)
```

NB-class *NB class object*

Description

The functions NB returns an object of the type NB.

An object of class 'NB' is a list with at least the following components:

prior Matrix with prior probabilities, i.e. marginal class probabilities Pr(class)

pcond list of matrices with conditional probabilities of the features given the classes (one list element per class), Pr(x|class)

classes Names (character vector) of the classes

xvar number of repetitions of the CV

xmodel Number of folds of the CV

model Number of folds of the CV

Value

objects of the S3 class 'NB'

S3 generics

The following S3 generic functions are available for an object of class NB:

- `predict`Predict class probabilities for new features data.
- `print`Basic print method.

See Also

NB, NB2

Examples

```
## See example(NB) for examples
```

---

pava *Pooled Adjacent Violators Algorithm*

Description

Pooled Adjacent Violators Algorithm

Usage

```
pava(y, x = numeric(0), weights = numeric(0))
```

Arguments

y	response variable
x	(optional) predictor vector (otherwise y is assumed to be a priori sorted according to relevant predictor)
weights	weights (optional) weights

Value

List with index (idx) of jump points and values (value) at each jump point.

Author(s)

Klaus K. Holst

Examples

```
x <- runif(5e3, -5, 5)
pr <- lava::expit(-1 + x)
y <- rbinom(length(pr), 1, pr)
pv <- pava(y, x)
plot(pr ~ x, cex=0.3)
with(pv, lines(sort(x)[index], value, col="red", type="s"))
```

`predict.density` *Prediction for kernel density estimates*

Description

Kernel density estimator predictions

Usage

```
## S3 method for class 'density'
predict(object, xnew, ...)
```

Arguments

`object`	density object
`xnew`	New data on which to make predictions for
`...`	additional arguments to lower level functions

Author(s)

Klaus K. Holst

`predict.NB` *Predictions for Naive Bayes Classifier*

Description

Naive Bayes Classifier predictions

Usage

```
## S3 method for class 'NB'
predict(object, newdata, expectation = NULL, threshold = c(0.001, 0.001), ...)
```

Arguments

`object`	density object
`newdata`	new data on which to make predictions
`expectation`	Variable to calculate conditional expectation wrt probabilities from NB classifier
`threshold`	Threshold parameters. First element defines the threshold on the probabilities and the second element the value to set those truncated probabilities to.
`...`	Additional arguments to lower level functions

Author(s)

Klaus K. Holst

RATE *Responder Average Treatment Effect*

Description

Estimation of the Average Treatment Effect among Responders

Usage

```
RATE(
  response,
  post.treatment,
  treatment,
  data,
  family = gaussian(),
  M = 5,
  pr.treatment,
  treatment.level,
  SL.args.response = list(family = gaussian(), SL.library = c("SL.mean", "SL.glm")),
  SL.args.post.treatment = list(family = binomial(), SL.library = c("SL.mean", "SL.glm")),
  preprocess = NULL,
  efficient = TRUE,
  ...
)
```

Arguments

`response`	Response formula (e.g, Y~D*A)
`post.treatment`	Post treatment marker formula (e.g., D~W)
`treatment`	Treatment formula (e.g, A~1)
`data`	data.frame
`family`	Exponential family for response (default gaussian)
`M`	Number of folds in cross-fitting (M=1 is no cross-fitting)
`pr.treatment`	(optional) Randomization probability of treatment.
`treatment.level`	Treatment level in binary treatment (default 1)
`SL.args.response`	Arguments to SuperLearner for the response model
`SL.args.post.treatment`	Arguments to SuperLearner for the post treatment indicator
`preprocess`	(optional) Data preprocessing function
`efficient`	If TRUE, the estimate will be efficient. If FALSE, the estimate will be a simple plug-in estimate.
`...`	Additional arguments to lower level functions

Value

estimate object

Author(s)

Andreas Nordland, Klaus K. Holst

`RATE.surv` *Responder Average Treatment Effect*

Description

Estimation of the Average Treatment Effect among Responders for Survival Outcomes

Usage

```
RATE.surv(
  response,
  post.treatment,
  treatment,
  censoring,
  tau,
  data,
  M = 5,
  pr.treatment,
  call.response,
  args.response = list(),
 SL.args.post.treatment = list(family = binomial(), SL.library = c("SL.mean", "SL.glm")),
  call.censoring,
  args.censoring = list(),
  preprocess = NULL,
  ...
)
```

Arguments

`response`	Response formula (e.g., Surv(time, event) ~ D + W).
`post.treatment`	Post treatment marker formula (e.g., D ~ W).
`treatment`	Treatment formula (e.g., A ~ 1).
`censoring`	Censoring formula (e.g., Surv(time, event == 0) ~ D + A + W)).
`tau`	Time-point of interest, see Details.
`data`	data.frame.
`M`	Number of folds in cross-fitting (M=1 is no cross-fitting).
`pr.treatment`	(optional) Randomization probability of treatment.

`call.response` Model call for the response model (e.g. "mets::phreg").

`args.response` Additional arguments to the response model.

`SL.args.post.treatment` Additional arguments to SuperLearner for the post treatment indicator model.

`call.censoring` Similar to call.response.

`args.censoring` Similar to args.response.

`preprocess` (optional) Data pre-processing function.

`...` Additional arguments to lower level data pre-processing functions.

Details

Estimation of

$$\frac{P(T \leq \tau|A=1) - P(T \leq \tau|A=1)}{E[D|A=1]}$$

under right censoring based on plug-in estimates of $P(T \leq \tau|A=a)$ and $E[D|A=1]$.

An efficient one-step estimator of $P(T \leq \tau|A=a)$ is constructed using the efficient influence function

$$\frac{I\{A=a\}}{P(A=a)}\Big(\frac{\Delta}{S^c_0(\tilde{T}|X)}I\{\tilde{T} \leq \tau\}+\int_0^\tau \frac{S_0(u|X)-S_0(\tau|X)}{S_0(u|X)S^c_0(u|X)}dM^c_0(u|X))\Big)+\Big(1-\frac{I\{A=a\}}{P(A=a)}\Big)F_0(\tau|A=a,W)-P(T \leq \tau|A$$

An efficient one-step estimator of $E[D|A=1]$ is constructed using the efficient influence function

$$\frac{A}{P(A=1)}\left(D-E[D|A=1,W]\right)+E[D|A=1,W]-E[D|A=1].$$

Value

estimate object

Author(s)

Andreas Nordland, Klaus K. Holst

`riskreg` *Risk regression*

Description

Risk regression with binary exposure and nuisance model for the odds-product.

Let A be the binary exposure, V the set of covariates, and Y the binary response variable, and define $p_a(v) = P(Y=1 \mid A=a, V=v), a \in \{0,1\}$.

The **target parameter** is either the *relative risk*

$$\mathrm{RR}(v) = \frac{p_1(v)}{p_0(v)}$$

or the *risk difference*

$$\mathrm{RD}(v) = p_1(v) - p_0(v)$$

We assume a target parameter model given by either

$$\log\{RR(v)\} = \alpha^t v$$

or

$$\operatorname{arctanh}\{RD(v)\} = \alpha^t v$$

and similarly a working linear **nuisance model** for the *odds-product*

$$\phi(v) = \log\left(\frac{p_0(v)p_1(v)}{(1-p_0(v))(1-p_1(v))}\right) = \beta^t v$$

.

A **propensity model** for $E(A = 1|V)$ is also fitted using a logistic regression working model

$$\operatorname{logit}\{E(A = 1 \mid V = v)\} = \gamma^t v.$$

If both the odds-product model and the propensity model are correct the estimator is efficient. Further, the estimator is consistent in the union model, i.e., the estimator is double-robust in the sense that only one of the two models needs to be correctly specified to get a consistent estimate.

Usage

```
riskreg(
  formula,
  target = NULL,
  nuisance = NULL,
  propensity = nuisance,
  data,
  weights,
  type = "rr",
  optimal = TRUE,
  std.err = TRUE,
  start = NULL,
  mle = FALSE,
  ...
)
```

Arguments

`formula`	formula (see details below)
`target`	(optional) target model (formula)
`nuisance`	nuisance model (formula)
`propensity`	propensity model (formula)
`data`	data.frame
`weights`	optional weights

type	type of association measure (rd og rr)
optimal	If TRUE optimal weights are calculated
std.err	If TRUE standard errors are calculated
start	optional starting values
mle	Semi-parametric (double-robust) estimate or MLE (TRUE gives MLE)
...	additional arguments to unconstrained optimization routine (nlminb)

Details

The 'formula' argument should be given as `response ~ exposure | target-formula | nuisance-formula` or `response ~ exposure | target | nuisance | propensity`

E.g., `riskreg(y ~ a | 1 | x+z | x+z, data=...)`

Alternatively, the model can specifed using the target, nuisance and propensity arguments: `riskreg(y ~ a, target=~1, nuisance=~x+z, ...)`

The `riskreg_fit` function can be used with matrix inputs rather than formulas.

Value

An object of class '`riskreg.targeted`' is returned. See `targeted-class` for more details about this class and its generic functions.

Author(s)

Klaus K. Holst

References

Richardson, T. S., Robins, J. M., & Wang, L. (2017). On modeling and estimation for the relative risk and risk difference. Journal of the American Statistical Association, 112(519), 1121–1130. http://dx.doi.org/10.1080/01621459.2016.1192546

Examples

```
m <- lvm(a[-2] ~ x,
        lp.target[1] ~ 1,
        lp.nuisance[-1] ~ 2*x)
distribution(m,~a) <- binomial.lvm("logit")
m <- binomial.rr(m, "y","a","lp.target","lp.nuisance")
d <- sim(m,5e2,seed=1)

I <- model.matrix(~1, d)
X <- model.matrix(~1+x, d)
with(d, riskreg_mle(y, a, I, X, type="rr"))

with(d, riskreg_fit(y, a, nuisance=X, propensity=I, type="rr"))
riskreg(y ~ a | 1 | x ,  data=d, type="rr")

## Model with same design matrix for nuisance and propensity model:
```

```
with(d, riskreg_fit(y, a, nuisance=X, type="rr"))

a <- riskreg(y ~ a, nuisance=~x,  data=d, type="rr")
a

riskreg(y ~ a, nuisance=~x,  data=d, type="rr", mle=TRUE)
```

---

scoring *Predictive model scoring*

Description

Predictive model scoring

Usage

```
scoring(
  response,
  ...,
  type = "quantitative",
  metrics = NULL,
  weights = NULL,
  names = NULL,
  messages = 1
)
```

Arguments

`response`	Observed response
`...`	model predictions (continuous predictions or class probabilities (matrices))
`type`	continuous or categorical response (the latter is automatically chosen if response is a factor, otherwise a continuous response is assumed)
`metrics`	which metrics to report
`weights`	optional frequency weights
`names`	optional names of models coments (given as ..., alternatively these can be named arguments)
`messages`	controls amount of messages/warnings (0: none)

Value

Numeric matrix of dimension m x p, where m is the number of different models and p is the number of model metrics

Examples

```
data(iris)
set.seed(1)
dat <- csplit(iris,2)
g1 <- NB(Species ~ Sepal.Width + Petal.Length, data=dat[[1]])
g2 <- NB(Species ~ Sepal.Width, data=dat[[1]])
pr1 <- predict(g1, newdata=dat[[2]], wide=TRUE)
pr2 <- predict(g2, newdata=dat[[2]], wide=TRUE)
table(colnames(pr1)[apply(pr1,1,which.max)], dat[[2]]$Species)
table(colnames(pr2)[apply(pr2,1,which.max)], dat[[2]]$Species)
scoring(dat[[2]]$Species, pr1=pr1, pr2=pr2)
## quantitative response:
scoring(response=1:10, prediction=rnorm(1:10))
```

SL *SuperLearner wrapper for ml_model*

Description

SuperLearner wrapper for ml_model

Usage

```
SL(
  formula = ~.,
  ...,
  SL.library = c("SL.mean", "SL.glm"),
  binomial = FALSE,
  data = NULL
)
```

Arguments

formula	Model design
...	Additional arguments for SuperLearner::SuperLearner
SL.library	character vector of prediction algorithms
binomial	boolean specifying binomial or gaussian family (default FALSE)
data	Optional data.frame

Value

ml_model object

Author(s)

Klaus Kähler Holst

`softmax` *Softmax transformation*

Description

Softmax transformation

Usage

```
softmax(x, log = FALSE, ref = TRUE, ...)
```

Arguments

`x`	Input matrix (e.g., linear predictors of multinomial logistic model)
`log`	Return on log-scale (default FALSE)
`ref`	Add reference level (add 0 column to x)
`...`	Additional arguments to lower level functions

Value

Numeric matrix of dimension n x p, where `n= nrow(x)` and `p = ncol(x) + (ref==TRUE)`

`solve_ode` *Solve ODE*

Description

Solve ODE with Runge-Kutta method (RK4)

Usage

```
solve_ode(ode_ptr, input, init, par = 0)
```

Arguments

`ode_ptr`	pointer (externalptr) to C++ function
`input`	Input matrix. 1st column specifies the time points
`init`	Initial conditions
`par`	Parameters defining the ODE (parsed to ode_ptr)

Details

The external point should be created with the function `targeted::specify_ode`.

Value

Matrix with solution

Author(s)

Klaus Kähler Holst

See Also

specify_ode

Examples

```
example(specify_ode)
```

---

specify_ode — *Specify Ordinary Differential Equation (ODE)*

Description

Define compiled code for ordinary differential equation.

Usage

```
specify_ode(code, fname = NULL, pname = c("dy", "x", "y", "p"))
```

Arguments

code	string with the body of the function definition (see details)
fname	Optional name of the exported C++ function
pname	Vector of variable names (results, inputs, states, parameters)

Details

The model (code) should be specified as the body of of C++ function. The following variables are defined bye default (see the argument pname)

- dyVector with derivatives, i.e. the rhs of the ODE (the result).
- xVector with the first element being the time, and the following elements additional exogenous input variables,
- yVector with the dependent variable
- pParameter vector

$y'(t) = f_p(x(t), y(t))$ All variables are treated as Armadillo (http://arma.sourceforge.net/) vectors/matrices.

As an example consider the *Lorenz Equations* $\frac{dx_t}{dt} = \sigma(y_t - x_t)$ $\frac{dy_t}{dt} = x_t(\rho - z_t) - y_t$ $\frac{dz_t}{dt} = x_t y_t - \beta z_t$

We can specify this model as `ode <- 'dy(0) = p(0)*(y(1)-y(0)); dy(1) = y(0)*(p(1)-y(2)); dy(2) = y(0)*y(1)-p(2)*y(2);' dy <- specify_ode(ode)`

As an example of model with exogenous inputs consider the following ODE: $y'(t) = \beta_0 + \beta_1 y(t) + \beta_2 y(t)x(t) + \beta_3 x(t) \cdot t$ This could be specified as `mod <- 'double t = x(0); dy = p(0) + p(1)*y + p(2)*x(1)*y + p(3)*x(1)*t;' dy <- specify_ode(mod)`##'

Value

pointer (externalptr) to C++ function

Author(s)

Klaus Kähler Holst

See Also

solve_ode

`targeted-class` *targeted class object*

Description

The functions `riskreg` and `ate` returns an object of the type `targeted`.

An object of class '`targeted`' is a list with at least the following components:

estimate An `estimate` object with the target parameter estimates (see `estimate.default`)

opt Object returned from the applied optimization routine

npar number of parameters of the model (target and nuisance)

type String describing the model

Value

objects of the S3 class '`targeted`'

S3 generics

The following S3 generic functions are available for an object of class `targeted`:

- `coef`Extract target coefficients of the estimated model.
- `vcov`Extract the variance-covariance matrix of the target parameters.
- `IC`Extract the estimated influence function.
- `print`Print estimates of the target parameters.
- `summary`Extract information on both target parameters and estimated nuisance model.'

See Also

riskreg, ate

Examples

```
## See example(riskreg) for examples
```

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