Package 'CausalModels'

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Type Package

Title Causal Inference Modeling for Estimation of Causal Effects

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Description Provides an array of statistical models common in causal inference such as
standardization, IP weighting, propensity matching, outcome regression, and doubly-robust
estimators. Estimates of the average treatment effects from each model are given with the
standard error and a 95% Wald confidence interval (Hernan, Robins (2020) <https:
//miguelhernan.org/whatifbook/>).

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URL https://github.com/ander428/CausalModels

BugReports https://github.com/ander428/CausalModels/issues

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doubly_robust   *Doubly Robust Model*

Description

`doubly_robust` trains both an outcome model and a propensity model to generate predictions for
the outcome and probability of treatment respectively. By default, the model uses standardization
and propensity_scores to form a doubly-robust model between standardization and IP weighting.
Alternatively, any outcome and treatment models can be provided instead, but must be compatible
with the predict generic function in R. Since many propensity models may not predict probabili-
ties without additional arguments into the predict function, the predictions themselves can be given
for both the outcome and propensity scores.

Usage

```
doubly_robust(
  data,
  out.mod = NULL,
  p.mod = NULL,
  f = NA,
  family = gaussian(),
  simple = pkg.env$simple,
  scores = NA,
  p.f = NA,
  p.simple = pkg.env$simple,
  p.family = binomial(),
  p.scores = NA,
  n.boot = 50,
  ...
)
```

Arguments

data	a data frame containing the variables in the model. This should be the same data used in init_params.
out.mod	(optional) a regression model that predicts the outcome. NOTE: the model given must be compatible with the predict generic function.
p.mod	(optional) a propensity model that predicts the probability of treatment. NOTE: the model given must be compatible with the predict generic function.

f	(optional) an object of class "formula" that overrides the default parameter
family	the family to be used in the general linear model. By default, this is set to [gaussian]().
simple	a boolean indicator to build default formula with interactions. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false.
scores	(optional) use calculated outcome estimates.
p.f	(optional) an object of class "formula" that overrides the default formula for the denominator of the IP weighting function.
p.simple	a boolean indicator to build default formula with interactions for the propensity models. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false. NOTE: if this is changed, the coefficient for treatment may not accurately represent the average causal effect.
p.family	the family to be used in the underlying propensity model. By default, this is set to [binomial]().
p.scores	(optional) use calculated propensity scores.
n.boot	an integer value that indicates number of bootstrap iterations to calculate standard error.
...	additional arguments that may be passed to the underlying [glm]() model.

Value

doubly_robust returns an object of [class]() "doubly_robust".

The functions print, summary, and predict can be used to interact with the underlying glm model.

An object of class "doubly_robust" is a list containing the following:

out.call	the matched call of the outcome model.
p.call	the matched call of the propensity model.
out.model	the underlying outcome model.
p.model	the underlying propensity model.
y_hat	the estimated outcome values.
p.scores	the estimated propensity scores.
ATE	the estimated average treatment effect (risk difference).
ATE.summary	a data frame containing the ATE, SE, and 95% CI of the ATE.
data	the data frame used to train the model.

Examples

```
library(causaldata)
data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
```

```
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)

# model using all defaults
model <- doubly_robust(data = nhefs.nmv)
summary(model)

# use alternative outcome model
out.mod <- propensity_matching(data = nhefs.nmv)
db.model <- doubly_robust(
  out.mod = out.mod,
  data = nhefs.nmv
)
db.model

# give calculated outcome predictions and give formula for propensity scores
db.model <- doubly_robust(
  scores = predict(out.mod),
  p.f = qsmk ~ sex + race + age,
  data = nhefs.nmv
)
db.model
```

---

gestimation   *One Parameter G-Estimation of Structural Nested Mean Models*

Description

'gestimation' uses the `propensity_scores` function to generate inverse probability weights. The weights can either be standardized weights or non-standardized weights. A grid search is done on α to construct the best β coefficient in the structural nested mean model. Alternatively, a linear mean model can be used for a closed form estimator.

Usage

```
gestimation(
  data,
  grid,
  ids = list(),
  f = NA,
  family = binomial(),
  simple = pkg.env$simple,
```

```
    p.f = NA,
    p.simple = pkg.env$simple,
    p.family = binomial(),
    p.scores = NA,
    SW = TRUE,
    n.boot = 100,
    type = "one.grid",
    ...
)
```

Arguments

data	a data frame containing the variables in the model. This should be the same data used in [init_params](#).
grid	a list of possible β values that will be used in the grid search.
ids	(optional) see documentation for [geeglm](#). By default rownames of the data will be used.
f	(optional) an object of class "formula" that overrides the default parameter. NOTE: for g-estimation this should be a propensity formula.
family	the family to be used in the general linear model. By default, this is set to [gaussian](#).
simple	(optional) a boolean indicator to build default formula with interactions for the g-estimation model. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false. NOTE: β will be appended to the end of the formula
p.f	(optional) an object of class "formula" that overrides the default formula for the denominator of the IP weighting function.
p.simple	(optional) a boolean indicator to build default formula with interactions for the propensity models. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false. NOTE: if this is changed, the coefficient for treatment may not accurately represent the average causal effect.
p.family	the family to be used in the underlying propensity model. By default, this is set to [binomial](#).
p.scores	(optional) use calculated propensity scores for the weights. If using standardized weights, the numerator will still be modeled.
SW	a boolean indicator to indicate the use of standardized weights. By default, this is set to true.
n.boot	(optional) an integer value that indicates number of bootstrap iterations to calculate standard error. If no value is given, the standard error from the underlying linear model will be used. NOTE: when type is 'one.grid' bootstrapping is not performed. By default, this is set to 100.
type	the type of g-estimation to perform. It must be one of "one.grid" or "one.linear" for a one parameter grid and linear mean model estimation respectively.
...	additional arguments that may be passed to the underlying model.

Value

gestimation returns an object of [class](#) "gestimation".

The functions print, summary, and predict can be used to interact with the underlying glm or geeglm model.

An object of class "gestimation" is a list containing the following:

call	the matched call.
formula	the formula used in the model.
model	the underlying glm model. If the model performed a grid search, this will be renamed 'best.model'
weights	the estimated IP weights.
type	returns the value used for the 'type' parameter.
ATE	the estimated average treatment effect (risk difference).
ATE.summary	a data frame containing the ATE, SE, and 95% CI of the ATE.

Examples

```
library(causaldata)
data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)

gest.model <- gestimation(nhefs.nmv, type = "one.linear", n.boot = 150)
gest.model$ATE.summary
```

---

init_params	*Initialize CausalModels Package*

Description

This function is required to be run first before any other function can run. This will set within the package the global outcome, treatment, and covariate functions for each model to use.

Usage

```
init_params(outcome, treatment, covariates, data, simple = FALSE)
```

Arguments

`outcome`	the outcome variable of interest (must be continuous).
`treatment`	the treatment with the causal effect of interest on the outcome.
`covariates`	a list/vector of covariate names to be use for confounding adjustment.
`data`	a data frame containing the variables in the model.
`simple`	a boolean indicator to build default formula with interactions. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false.

Value

No return value. Called for parameter initialization.

---

ipweighting	*Parametric IP Weighting*

Description

'ipweighting' uses the `propensity_scores` function to generate inverse probability weights. The weights can either be standardized weights or non-standardized weights. The weights are used to train a general linear model whose coefficient for treatment represents the average treatment effect on the additive scale.

Usage

```
ipweighting(
  data,
  f = NA,
  family = gaussian(),
  p.f = NA,
  p.simple = pkg.env$simple,
  p.family = binomial(),
  p.scores = NA,
  SW = TRUE,
  n.boot = 0,
  ...
)
```

Arguments

`data`	a data frame containing the variables in the model. This should be the same data used in `init_params`.
`f`	(optional) an object of class "formula" that overrides the default parameter
`family`	the family to be used in the general linear model. By default, this is set to `gaussian`.

p.f	(optional) an object of class "formula" that overrides the default formula for the denominator of the IP weighting function.
p.simple	a boolean indicator to build default formula with interactions for the propensity models. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false. NOTE: if this is changed, the coefficient for treatment may not accurately represent the average causal effect.
p.family	the family to be used in the underlying propensity model. By default, this is set to [binomial].
p.scores	(optional) use calculated propensity scores for the weights. If using standardized weights, the numerator will still be modeled.
SW	a boolean indicator to indicate the use of standardized weights. By default, this is set to true.
n.boot	(optional) an integer value that indicates number of bootstrap iterations to calculate standard error. If no value is given, the standard error from the underlying linear model will be used.
...	additional arguments that may be passed to the underlying [glm] model.

Value

ipweighting returns an object of [class] "ipweighting".

The functions print, summary, and predict can be used to interact with the underlying glm model.

An object of class "ipweighting" is a list containing the following:

call	the matched call.
formula	the formula used in the model.
model	the underlying glm model.
weights	the estimated IP weights.
ATE	the estimated average treatment effect (risk difference).
ATE.summary	a data frame containing the ATE, SE, and 95% CI of the ATE.

Examples

```
library(causaldata)
data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)
```

```
# model using all defaults
model <- ipweighting(data = nhefs.nmv)
summary(model)

# Model using calculated propensity scores and manual outcome formula
p.scores <- propensity_scores(nhefs.nmv)$p.scores
model <- ipweighting(wt82_71 ~ qsmk, p.scores = p.scores, data = nhefs.nmv)
summary(model)
```

---

iv_est   *Standard Instrumental Variable Estimator*

Description

'iv_est' calculates the standard IV estimand using the conditional means on a given instrumental variable.

Usage

```
iv_est(IV, data, n.boot = 50)
```

Arguments

IV   the instrumental variable to be used in the conditional means. Must be a factor
                with no more than 2 levels. It is assumed the second level is the positive level,
                i.e., the binary equivalent of the second factor level should be 1 and the first
                should be 0.

data   a data frame containing the variables in the model. This should be the same data
                used in init_params.

n.boot   an integer value that indicates number of bootstrap iterations to calculate stan-
                dard error.

Value

iv_est returns a data frame containing the standard IV estimate, standard error, and Wald 95

Examples

```
library(causaldata)
data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)
```

```
nhefs.iv <- nhefs[which(!is.na(nhefs$wt82) & !is.na(nhefs$price82)), ]
nhefs.iv$highprice <- as.factor(ifelse(nhefs.iv$price82 >= 1.5, 1, 0))
nhefs.iv$qsmk <- as.factor(nhefs.iv$qsmk)
init_params(wt82_71, qsmk,
            covariates = confounders,
            data = nhefs.iv)

iv_est("highprice", nhefs.iv)
```

---

outcome_regression   *Outcome Regression*

Description

'outcome_regression' builds a linear model using all covariates. The treatment effects are stratified within the levels of the covariates. The model will automatically provide all discrete covariates in a contrast matrix. To view estimated change in treatment effect from continuous variables, a list called `contrasts`, needs to be given with specific values to estimate. A vector of values can be given for any particular continuous variable.

Usage

```
outcome_regression(
  data,
  f = NA,
  simple = pkg.env$simple,
  family = gaussian(),
  contrasts = list(),
  ...
)
```

Arguments

data	a data frame containing the variables in the model. This should be the same data used in [init_params]().
f	(optional) an object of class "formula" that overrides the default parameter
simple	a boolean indicator to build default formula with interactions. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false.
family	the family to be used in the general linear model. By default, this is set to [gaussian](). NOTE: if this is changed, the assumptions about the model output may be incorrect and may not provide accurate treatment effects.
contrasts	a list of continuous covariates and values in the model to be included in the contrast matrix (e.g. `list(age = c(18, 25, 40), weight = c(90, 159))`).
...	additional arguments that may be passed to the underlying [glht]() model.

Value

outcome_regression returns an object of class "outcome_regression"

The functions print, summary, and predict can be used to interact with the underlying glht model.

An object of class "outcome_regression" is a list containing the following:

call	the matched call.
formula	the formula used in the model.
model	the underlying glht model.
ATE	a data frame containing the ATE, SE, and 95% CI of the ATE.
ATE.summary	a more detailed summary of the ATE estimations from glht.

Examples

```
library(causaldata)
library(multcomp)

data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)

out.mod <- outcome_regression(nhefs.nmv, contrasts = list(
  age = c(21, 55),
  smokeintensity = c(5, 20, 40)
))
print(out.mod)
summary(out.mod)
head(data.frame(preds = predict(out.mod)))
```

---

propensity_matching   *Propensity Matching*

Description

'propensity_matching' uses either stratification or standardization to model an outcome conditional on the propensity scores. In stratification, the model will break the propensity scores into groups and output a glht model based off a contrast matrix which estimates the change in average causal effect within groups of propensity scores. In standardization, the model will output a standardization model that conditions on the propensity strata rather than the covariates. The model can also predict the expected outcome.

Usage

```
propensity_matching(
  data,
  f = NA,
  simple = pkg.env$simple,
  p.scores = NA,
  p.simple = pkg.env$simple,
  type = "strata",
  grp.width = 0.1,
  quant = TRUE,
  ...
)
```

Arguments

data	a data frame containing the variables in the model. This should be the same data used in init_params.
f	(optional) an object of class "formula" that overrides the default parameter
simple	a boolean indicator to build default formula with interactions. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false.
p.scores	(optional) use calculated propensity scores for matching. Otherwise, propensity scores will be automatically modeled.
p.simple	a boolean indicator to build default formula with interactions for the propensity models. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false.
type	a string representing the type of propensity model to be used. By default, the function will stratify. Standardization with propensity scores may also be used. The value given for type must be in c("strata", "stdm").
grp.width	a decimal value to specify the range to stratify the propensity scores. If option quant is set to true, this will represent the spread of percentiles. If false, it will represent the spread of raw values of propensity scores. Must be a decimal between 0 and 1. By default, this is set to 0.1. This option is ignored for standardization.
quant	a boolean indicator to specify the type of stratification. If true (default), the model will stratify by percentiles. If false, the scores will be grouped by a range of their raw values. This option is ignored for standardization.

... additional arguments that may be passed to the underlying `propensity_scores` function.

Value

`propensity_matching` returns an object of `class` "propensity_matching"

The functions `print`, `summary`, and `predict` can be used to interact with the underlying `glht` or `standardization` model.

An object of class "propensity_matching" is a list containing the following:

`call`	the matched call.
`formula`	the formula used in the model.
`model`	either the underlying `glht` or `standardization` model.
`p.scores`	the estimated propensity scores
`ATE`	a data frame containing the ATE, SE, and 95% CI of the ATE.
`ATE.summary`	either a data frame containing the `glht` or `standardization` summary.

Examples

```
library(causaldata)
library(multcomp)

data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)

pm.model <- propensity_matching(nhefs.nmv)
pm.model$ATE.summary
summary(pm.model)
head(data.frame(preds = predict(pm.model)))
```

---

propensity_scores   *Propensity Scores*

Description

'propensity_scores' builds a logistic regression with the target as the treatment variable and the covariates as the independent variables.

Usage

```
propensity_scores(
  data,
  f = NA,
  simple = pkg.env$simple,
  family = binomial(),
  ...
)
```

Arguments

data	a data frame containing the variables in the model. This should be the same data used in `init_params`.
f	(optional) an object of class "formula" that overrides the default parameter
simple	a boolean indicator to build default formula with interactions. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false.
family	the family to be used in the general linear model. By default, this is set to `binomial` NOTE: if this is changed, the outcome of the model may not be the probabilities and the results will not be valid.
...	additional arguments that may be passed to the underlying `glm` model.

Value

propensity_scores returns an object of `class` "propensity_scores"

The functions `print`, `summary`, and `predict` can be used to interact with the underlying glm model.

An object of class "propensity_scores" is a list containing the following:

call	the matched call.
formula	the formula used in the model.
model	the underlying glm model.
p.scores	the estimated propensity scores.

Examples

```
library(causaldata)
data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)

p.score <- propensity_scores(nhefs.nmv)
p.score
```

---

standardization   *Parametric Standardization*

Description

'standardization' uses a standard [glm](#) linear model to perform parametric standardization by adjusting bias through including all confounders as covariates. The model will calculate during training both the risk difference and the risk ratio. Both can be accessed from the model as well as estimates of the counterfactuals of treatment.

Usage

```
standardization(
  data,
  f = NA,
  family = gaussian(),
  simple = pkg.env$simple,
  n.boot = 50,
  ...
)
```

Arguments

data	a data frame containing the variables in the model. This should be the same data used in [init_params](#).
f	(optional) an object of class "formula" that overrides the default parameter
family	the family to be used in the general linear model. By default, this is set to [gaussian](#).

simple	a boolean indicator to build default formula with interactions. If true, interactions will be excluded. If false, interactions will be included. By default, simple is set to false. NOTE: if this is changed, the coefficient for treatment may not accurately represent the average causal effect.
n.boot	an integer value that indicates number of bootstrap iterations to calculate standard error.
...	additional arguments that may be passed to the underlying [glm](#) model.

Value

standardization returns an object of [class](#) "standardization".

The functions print, summary, and predict can be used to interact with the underlying glm model.

An object of class "standardization" is a list containing the following:

call	the matched call.
formula	the formula used in the model.
model	the underlying glm model.
ATE	a data frame containing estimates of the treatment effect of the observed, counterfactuals, and risk metrics.
ATE.summary	a data frame containing the ATE, SE, and 95% CI of the ATE.

Examples

```
library(causaldata)

data(nhefs)
nhefs.nmv <- nhefs[which(!is.na(nhefs$wt82)), ]
nhefs.nmv$qsmk <- as.factor(nhefs.nmv$qsmk)

confounders <- c(
  "sex", "race", "age", "education", "smokeintensity",
  "smokeyrs", "exercise", "active", "wt71"
)

init_params(wt82_71, qsmk,
  covariates = confounders,
  data = nhefs.nmv
)

# model using all defaults
model <- standardization(data = nhefs.nmv)
print(model)
summary(model)
print(model$ATE.summary)
print(model$ATE.summary$Estimate[[2]] -
  model$ATE.summary$Estimate[[3]]) # manually calculate risk difference
```

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