Package ‘localIV’

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Type Package

Title Estimation of Marginal Treatment Effects using Local Instrumental Variables

Version 0.3.1

Description In the generalized Roy model, the marginal treatment effect (MTE) can be used as a building block for constructing conventional causal parameters such as the average treatment effect (ATE) and the average treatment effect on the treated (ATT). Given a treatment selection equation and an outcome equation, the function mte() estimates the MTE via the semiparametric local instrumental variables method or the normal selection model. The function mte_at() evaluates MTE at different values of the latent resistance u with a given X = x, and the function mte_tilde_at() evaluates MTE projected onto the estimated propensity score. The function ace() estimates population-level average causal effects such as ATE, ATT, or the marginal policy relevant treatment effect.

Depends R (>= 3.3.0)

Imports KernSmooth (>= 2.5.0), mgcv (>= 1.8-19), rlang (>= 0.4.4), sampleSelection (>= 1.2-0), stats

Suggests dplyr, ggplot2, tidyr

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

URL https://github.com/xiangzhou09/localIV

BugReports https://github.com/xiangzhou09/localIV

NeedsCompilation no

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ace

Description

ace estimates Average Causal Effects (ACE) from a fitted MTE model. The estimand can be average treatment effect (ATE), average treatment effect on the treated (ATT), average treatment effect on the untreated (ATU), or the Marginal Policy Relevant Treatment Effect (MPRTE) defined in Zhou and Xie (2019).

Usage

ace(model, estimand = c("ate", "att", "atu", "mprte"), policy = 1)

Arguments

- model: A fitted mte model returned by mte.
- estimand: Type of estimand: "ate", "att", "atu", or "mprte".
- policy: An expression written as a function of p. This is used only when estimand="mprte".

Value

Estimate of ATE, ATT, ATU, or MPRTE

References


Examples

mod <- mte(selection = d ~ x + z, outcome = y ~ x,
data = toydata)

ate <- ace(mod, "ate")
att <- ace(mod, "att")
atu <- ace(mod, "atu")
mprte1 <- ace(mod, "mprte")
mprte2 <- ace(mod, "mprte", policy = p)
mprte3 <- ace(mod, "mprte", policy = 1-p)
mprte4 <- ace(mod, "mprte", policy = I(p<0.25))
c(ate, att, atu, mprte1, mprte2, mprte3, mprte4)

Description

mte fits a MTE model using either the semiparametric local instrumental variables (local IV) method
or the normal selection model (Heckman, Urzua, Vytlacil 2006). The user supplies a formula for
the treatment selection equation, a formula for the outcome equations, and a data frame containing
all variables. The function returns an object of class mte. Observations that contain NA (either in
selection or in outcome) are removed.

Usage

mte(
  selection,
  outcome,
  data = NULL,
  method = c("localIV", "normal"),
  bw = NULL
)

mte_localIV(mf_s, mf_o, bw = NULL)

mte_normal(mf_s, mf_o)

Arguments

selection A formula representing the treatment selection equation.
outcome A formula representing the outcome equations where the left hand side is the
observed outcome and the right hand side includes predictors of both potential
outcomes.
data A data frame, list, or environment containing the variables in the model.
**mte**

- **method**
  How to estimate the model: either "localIV" for the semiparametric local IV method or "normal" for the normal selection model.

- **bw**
  Bandwidth used for the local polynomial regression in the local IV approach. Default is 0.25.

- **mf_s**
  A model frame for the treatment selection equations returned by `model.frame`

- **mf_o**
  A model frame for the outcome equations returned by `model.frame`

**Details**

`mte_localIV` estimates MTE\((x, u)\) using the semiparametric local IV method, and `mte_normal` estimates MTE\((x, u)\) using the normal selection model.

**Value**

An object of class `mte`.

- **coefs**
  A list of coefficient estimates: `gamma` for the treatment selection equation, `beta10` (intercept) and `beta1` (slopes) for the baseline outcome equation, `beta20` (intercept) and `beta2` (slopes) for the treated outcome equation, and `theta1` and `theta2` for the error covariances when `method = "normal"`.

- **ufun**
  A function representing the unobserved component of MTE\((x, u)\).

- **ps**
  Estimated propensity scores.

- **ps_model**
  The propensity score model, an object of class `glm` if `method = "localIV"`, or an object of class `selection` if `method = "normal"`.

- **mf_s**
  The model frame for the treatment selection equation.

- **mf_o**
  The model frame for the outcome equations.

- **complete_row**
  A logical vector indicating whether a row is complete (no missing variables) in the original data.

- **call**
  The matched call.

**References**


**See Also**

- `mte_at` for evaluating MTE at different values of the latent resistance \(u\); `mte_tilde_at` for evaluating MTE projected onto the propensity score; `ace` for estimating average causal effects from a fitted `mte` object.

**Examples**

```r
mod <- mte(selection = d ~ x + z, outcome = y ~ x, data = toydata, bw = 0.25)
summary(mod$ps_model)
hist(mod$ps)
```
mte_vals <- mte_at(u = seq(0.05, 0.95, 0.1), model = mod)
if(require("ggplot2"){)
  ggplot(mte_vals, aes(x = u, y = value)) +
  geom_line(size = 1) +
  xlab("Latent Resistance U") +
  ylab("Estimates of MTE at Mean Values of X") +
  theme_minimal(base_size = 14)
}

mte_at

Evaluate Marginal Treatment Effects from a Fitted MTE Model.

Description

mte_at evaluates marginal treatment effects at different values of the latent resistance `u` with a given `X = x`.

Usage

mte_at(x = NULL, u, model)

Arguments

x Values of the pretreatment covariates at which MTE(x, u) is evaluated. It should be a numeric vector whose length is one less than the number of columns of the design matrix `X` in the outcome model. Default is the sample means.

u A numeric vector. Values of the latent resistance `u` at which MTE(x, u) is evaluated. Note that the estimation involves extrapolation when the specified `u` values lie outside of the support of the propensity score.

model A fitted MTE model returned by `mte`.

Value

mte_at returns a data frame.

u input values of `u`.

x_comp the x-component of the estimated MTE(x, u)

u_comp the u-component of the estimated MTE(x, u)

value estimated values of MTE(x, u)
Examples

```r
mod <- mte(selection = d ~ x + z, outcome = y ~ x, data = toydata)
mte_vals <- mte_at(u = seq(0.05, 0.95, 0.1), model = mod)
if(require("ggplot2")){
  ggplot(mte_vals, aes(x = u, y = value)) +
  geom_line(size = 1) +
  xlab("Latent Resistance U") +
  ylab("Estimates of MTE at Mean Values of X") +
  theme_minimal(base_size = 14)
}
```

**mte_tilde_at**  
*Evaluate Marginal Treatment Effects Projected onto the Propensity Score*

**Description**

`mte_tilde_at` evaluates marginal treatment effects projected onto the estimated propensity score. The projection is done via the function `gam`.

**Usage**

```r
mte_tilde_at(p, u, model, ...)
```

**Arguments**

- `p`  
  A numeric vector. Values of the propensity score at which $\tilde{\text{MTE}}(p, u)$ is evaluated.

- `u`  
  A numeric vector. Values of the latent resistance at which $\tilde{\text{MTE}}(p, u)$ is evaluated.

- `model`  
  A fitted MTE model returned by `mte`.

- `...`  
  Additional parameters passed to `gam`.

**Value**

`mte_tilde_at` returns a list of two elements:

- `df`  
  A data frame containing five columns:
  - `p` input values of `p`.
  - `u` input values of `u`.
  - `p_comp` the p-component of the estimated $\tilde{\text{MTE}}(p, u)$
  - `u_comp` the u-component of the estimated $\tilde{\text{MTE}}(p, u)$
  - `value` estimated values of MTE$(p, u)$

- `proj`  
  Fitted `gam` model for $E[\mu_1(X) - \mu_0(X)|P(Z) = p]$
References


Examples

```r
mod <- mte(selection = d ~ x + z, outcome = y ~ x, data = toydata)

u <- p <- seq(0.05, 0.95, 0.1)
mte_tilde <- mte_tilde_at(p, u, model = mod)

# heatmap showing MTE_tilde(p, u)
if(require("ggplot2")){
  ggplot(mte_tilde$d, aes(x = u, y = p, fill = value)) +
  geom_tile() +
  scale_fill_gradient(name = expression(widetilde(MTE)(p, u)), low = "yellow", high = "blue") +
  xlab("Latent Resistance U") +
  ylab("Propensity Score p(Z)") +
  theme_minimal(base_size = 14)
}

mprte_tilde_df <- subset(mte_tilde$d, p == u)

# heatmap showing MPRTE_tilde(p)
if(require("ggplot2")){
  ggplot(mprte_tilde_df, aes(x = u, y = p, fill = value)) +
  geom_tile() +
  scale_fill_gradient(name = expression(widetilde(MPRTE)(p)), low = "yellow", high = "blue") +
  xlab("Latent Resistance U") +
  ylab("Propensity Score p(Z)") +
  theme_minimal(base_size = 14)
}

# MPRTE_tilde(p) decomposed into the p-component and the u-component
if(require(tidyr) && require(dplyr) && require(ggplot2)){
  mprte_tilde_df %>%
  pivot_longer(cols = c(u_comp, p_comp, value)) %>%
  mutate(name = recode_factor(name,
    `value` = "MPRTE(p)",
    `p_comp` = "p(Z) component",
    `u_comp` = "U component")) %>%
  ggplot(aes(x = p, y = value)) +
  geom_line(aes(linetype = name), size = 1) +
  scale_linetype(name = "") +
  xlab("Propensity Score p(Z)") +
  ylab("Treatment Effect") +
  theme_minimal(base_size = 14) +
  theme(legend.position = "bottom")
}
```
**toydata**

*A Hypothetical Dataset for Illustrative Purpose*

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**Description**

A dataset containing 4 columns: $y$ for a continuous outcome, $d$ for a binary treatment, $x$ for a pretreatment covariate, and $z$ for an excluded instrument.

**Usage**

`toydata`

**Format**

An object of class `data.frame` with 10000 rows and 4 columns.
Index

*Topic datasets
  toydata, 8

ace, 2, 4
expression, 2
gam, 6
glm, 4
model.frame, 4
mte, 2, 3, 5, 6
mte_at, 4, 5
mte_localIV (mte), 3
mte_normal (mte), 3
mte_tilde_at, 4, 6

selection, 4

toydata, 8