

Package: localIV (via r-universe)

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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 ($\geq 3.3.0$)

Imports KernSmooth ($\geq 2.5.0$), mgcv ($\geq 1.8-19$), rlang ($\geq 0.4.4$), sampleSelection ($\geq 1.2-0$), 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>

Repository <https://xiangzhou09.r-universe.dev>

RemoteUrl <https://github.com/xiangzhou09/localiv>

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 ace

Estimating Average Causal Effects from a Fitted MTE Model.

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 <code>mte</code> .
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

Heckman, James J., Sergio Urzua, and Edward Vytlacil. 2006. "[Understanding Instrumental Variables in Models with Essential Heterogeneity](#)." *The Review of Economics and Statistics* 88:389-432.

Zhou, Xiang and Yu Xie. 2019. "[Marginal Treatment Effects from A Propensity Score Perspective](#)." *Journal of Political Economy*, 127(6): 3070-3084.

Zhou, Xiang and Yu Xie. 2020. "[Heterogeneous Treatment Effects in the Presence of Self-selection: a Propensity Score Perspective](#)." *Sociological Methodology*.

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)

```

mte

Fitting a Marginal Treatment Effects (MTE) Model.

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.

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 <code>model.frame</code>
mf_o	A model frame for the outcome equations returned by <code>model.frame</code>

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: <code>gamma</code> for the treatment selection equation, <code>beta10</code> (intercept) and <code>beta1</code> (slopes) for the baseline outcome equation, <code>beta20</code> (intercept) and <code>beta2</code> (slopes) for the treated outcome equation, and <code>theta1</code> and <code>theta2</code> for the error covariances when <code>method = "normal"</code> .
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 <code>glm</code> if <code>method = "localIV"</code> , or an object of class <code>selection</code> if <code>method = "normal"</code> .
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

Heckman, James J., Sergio Urzua, and Edward Vytlacil. 2006. "Understanding Instrumental Variables in Models with Essential Heterogeneity." *The Review of Economics and Statistics* 88:389-432.

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

```
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

```

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	<i>Evaluate Marginal Treatment Effects Projected onto the Propensity Score</i>
--------------	--

Description

mte_tilde_at evaluates marginal treatment effects projected onto the estimated propensity score. The projection is done via the function [gam](#).

Usage

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

Arguments

p	A numeric vector. Values of the propensity score at which $\widehat{MTE}(p, u)$ is evaluated.
u	A numeric vector. Values of the latent resistance at which $\widehat{MTE}(p, u)$ 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: <ul style="list-style-type: none"> • p input values of p. • u input values of u. • p_comp the p-component of the estimated $\widehat{MTE}(p, u)$ • u_comp the u-component of the estimated $\widehat{MTE}(p, u)$ • value estimated values of $\widehat{MTE}(p, u)$
proj	Fitted gam model for $E[\mu_1(X) - \mu_0(X) P(Z) = p]$

References

Zhou, Xiang and Yu Xie. 2019. "[Marginal Treatment Effects from A Propensity Score Perspective.](#)" *Journal of Political Economy*, 127(6): 3070-3084.

Zhou, Xiang and Yu Xie. 2020. "[Heterogeneous Treatment Effects in the Presence of Self-selection: a Propensity Score Perspective.](#)" *Sociological Methodology*.

Examples

```
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$df, 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$df, 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*

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.

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