Package ‘localIV’

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Type Package

Title Estimation of Marginal Treatment Effects using Local Instrumental Variables

Version 0.3.0

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

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

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

NeedsCompilation no

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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**

```r
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.
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)
}

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table

| 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**

\[
\text{mte\_at}(x = \text{NULL}, u, \text{model})
\]

**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 \texttt{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)
}
```

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**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 $\tilde{\mathrm{MTE}}(p, u)$ is evaluated.
- `u`: A numeric vector. Values of the latent resistance at which $\tilde{\mathrm{MTE}}(p, u)$ 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 $\tilde{\mathrm{MTE}}(p, u)$
  - `u_comp`: the u-component of the estimated $\tilde{\mathrm{MTE}}(p, u)$
  - `value`: estimated values of $\tilde{\mathrm{MTE}}(p, u)$
- `proj`: Fitted `gam` model for $E[\mu_1(X) - \mu_0(X)|P(Z) = p]$
mte_tilde_at

References


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")
}
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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