Package: MatchGATE (via r-universe)

September 6, 2024

Title Estimate Group Average Treatment Effects with Matching

Version 0.0.10

Description Two novel matching-based methods for estimating group average treatment effects (GATEs). The match_y1y0() and match_y1y0_bc() functions are used for imputing the potential outcomes based on matching and bias-corrected matching techniques, respectively. The EstGATE() function is employed to estimate the GATE after imputing the potential outcomes.

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Encoding UTF-8

RoxygenNote 7.3.1

Imports locpol, stats

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-04-08 15:10:05 UTC

Contents

`EstGATE` *Estimating Group Average Treatment Effects*

Description

When imputed values for Y^1 and Y^0 are available for each individual, we can use `EstGATE` to estimate the group average treatment effects (GATE) defined by

$$GATE(z) = E[Y^1 - Y^0|Z = z]$$

for some for possible values z of Z.

Usage

```
EstGATE(Y1_Y0, Z, Zeval, h)
```

Arguments

`Y1_Y0`	A vector in which each element is a treatment effect for each individual.
`Z`	A subvector of the covariates `X`, which is used to define the subgroup of interest.
`Zeval`	Vector of evaluation points of `Z`.
`h`	A smoothing parameter, bandwidth.

Value

The value of the corresponding GATE at different evaluation points.

Examples

```
set.seed(691)
n <- 2000
X1 <- runif(n, -0.5,0.5)
X2 <- rnorm(n, sd = 0.5)
X = cbind(X1, X2)
A = sample(c(0,1), n, TRUE)
Y0 <- X2 + X1*X2/2 + rnorm(n, sd = 0.25)
Y1 <- A * (2*X1^2) + X2 + X1*X2/2 + rnorm(n, sd = 0.25)
Y <- A * Y1 + (1-A)*Y0
res.match <- match_y1y0(X, A, Y, K = 5)
y1_y0 <- res.match$Y1 - res.match$Y0
Z <- X1
Zeval = seq(min(Z), max(Z), len = 101)
h <- 0.5 * n^(-1/5)
res <- EstGATE(Y1_Y0 = y1_y0, Z, Zeval, h = h)
plot(x = Zeval, y = 2*Zeval^2,
     type = "l", xlim = c(-0.6, 0.5),
     main = "Estimated value vs. true value",
     xlab = "Zeval", ylab = "GATE",
```

```
     col = "DeepPink", lwd = "2")
lines(x = res$Zeval, y = res$GATE,
      col="DarkTurquoise", lwd = "2")
legend('bottomleft', c("Estimated GATE","True GATE"),
       col=c("DarkTurquoise","DeepPink"),
       text.col=c("DarkTurquoise","DeepPink"), cex = 0.8)
```

`match_y1y0` *Imputing Missing Potential Outcomes with Matching*

Description

Impute missing potential outcomes for each individual with matching.

Usage

```
match_y1y0(X, A, Y, K = 5, method = "euclidean")
```

Arguments

`X`	A matrix representing covariates, where each row represents the value of a different covariates for an individual.
`A`	A vector representing the treatment received by each individual.
`Y`	A vector representing the observed outcome for each individual.
`K`	When imputing missing potential outcomes, the average number of similar individuals are taken based on covariates similarity.
`method`	The distance measure to be used. It is a argument embed in `dist` function.

Details

Here are the implementation details for the imputation processes. Denote $\hat{Y}_i^0$ and $\hat{Y}_i^1$ as the imputed potential outcomes for individual i. Without loss of generality, if $A_i = 0$, then $\hat{Y}_i^0 = Y_i$, and $\hat{Y}_i^1$ is the average of outcomes for the K units that are the most similar to the individual i, i.e.,

$$\hat{Y}_i^0 = \frac{1}{K} \sum_{j \in \mathcal{J}_K(i)} Y_j,$$

where $\mathcal{J}_K(i)$ represents the set of K matched individuals with $A_i = 1$, that are the closest to the individual i in terms of covariates similarity, and vice versa.

Value

Returns a matrix of completed matches, where each row is the imputed (Y^1, Y^0) for each individual.

Examples

```
n <- 100
p <- 2
X <- matrix(rnorm(n*p), ncol = p)
A <- sample(c(0,1), n, TRUE)
Y <- A * (2*X[,1]) + X[,2]^2 + rnorm(n)
match_y1y0(X = X, A = A, Y = Y, K =5)
```

`match_y1y0_bc` *Imputing Missing Potential Outcomes with Bias-Corrected Matching*

Description

Impute missing potential outcomes for each individual with bias-corrected matching.

Usage

```
match_y1y0_bc(X, A, Y, miu1.hat, miu0.hat, K = 5, method = "euclidean")
```

Arguments

`X`	A matrix representing covariates, where each row represents the value of a different covariates for an individual.
`A`	A vector representing the treatment received by each individual.
`Y`	A vector representing the observed outcome for each individual.
`miu1.hat`	The estimated outcome regression function for Y^1.
`miu0.hat`	The estimated outcome regression function for Y^0.
`K`	When imputing missing potential outcomes, the average number of similar individuals are taken based on covariates similarity.
`method`	The distance measure to be used. It is a argument embed in `dist` function.

Details

Here are the implementation details for the imputation processes. Denote $\hat{Y}_i^0$ and $\hat{Y}_i^1$ as the imputed potential outcomes for individual i. For example, if $A_i = 0$, then $\hat{Y}_i^0 = Y_i^0$. However, for obtaining $\hat{Y}_i^1$, we require to introduce an outcome regression function $\mu_1(X)$ for Y^1. Let $\hat{\mu}_1(X)$ be the fitted value of $\mu_1(X)$, then $\hat{Y}_i^1$ is defined as follows,

$$\hat{Y}_i^1 = \frac{1}{K} \sum_{j \in \mathcal{J}_K(i)} \{Y_j + \hat{\mu}_1(X_i) - \hat{\mu}_1(X_j)\},$$

where $\mathcal{J}_K(i)$ represents the set of K matched individuals with $A_i = 1$, that are the closest to the individual i in terms of covariates similarity, and vice versa.

Value

Returns a matrix of completed matches, where each row is the imputed (Y^1, Y^0) for each individual.

Examples

```
n = 100
X1 <- runif(n, -0.5,0.5)
X2 <- sample(c(0,1,2), n, TRUE)
X = cbind(X1, X2)
A = sample(c(0,1), n, TRUE)
Y = A * (2*X1) + X1 + X2^2 + rnorm(n)
miu1_hat <- cbind(1,X) %*% as.matrix(lm(Y ~ X, subset = A==1)$coef)
miu0_hat <- cbind(1,X) %*% as.matrix(lm(Y ~ X, subset = A==0)$coef)
match_y1y0_bc(X = X, A = A, Y = Y, miu1.hat = miu1_hat,
              miu0.hat = miu0_hat, K = 5)
```

Index