

Package ‘IUPS’

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Type Package

Title Incorporating Uncertainties in Propensity Scores

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Depends R (>= 2.14), R2jags, Matching, boot

SystemRequirements JAGS (>= 3.3.0)

Description This package includes functions to incorporate
uncertainties in estimated propensity scores and provide
adjusted standard errors for making valid causal inference.

License GPL-3

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bpsm

*Bayesian Propensity Score Matching***Description**

A function includes both Bayesian and non-Bayesian methods to incorporate uncertainties in estimated propensity scores and to provide adjusted standard errors for propensity score matching estimators.

Usage

```
bpsm(Y, t, X, estimand = "ATE", method = "AI", M = 1, L = 1, K = 10000, S = 1000)
```

Arguments

Y	A vector containing the outcome variable.
t	A vector containing the treatment indicator.
X	A matrix containing the covariates.
estimand	A character string for the estimand. The default is "ATE", average treatment effects. The other option is "ATT", average treatment effects on the treated.
method	A character string for the method to adjust standard errors. The default is "AI", which uses the methods proposed by Abadie and Imbens (2011). "BPSM" invokes the Bayesian methods developed by An (2010). "Both" use both methods.
M	Number of matches requested.
L	Number of within-group matches requested for the AI method.
K	Numbers of iterations. Only needed for BPSM.
S	Number of posterior samples. Only needed for BPSM.

Details

Estimated propensity scores are used to match treated units with untreated units. The function includes two methods to take into account the uncertainties in the estimated propensity scores and to provide adjusted standard errors. The AI method is computationally more efficient but may produce negative standard errors in some cases. In contrast, the BPSM method always provides positive standard errors but requires longer computational time to converge, especially when the sample size is large.

Value

estimates	The estimated treatment effects and their adjusted standard errors. Phat shows the results with unadjusted standard errors. AI shows the results with adjusted standard errors based on the AI method. BP* shows the results with adjusted standard errors based on the Bayesian method.
estimand	A character string indicting the estimand requested.

time	The time elapsed for the computation.
sims	The number of iterations requested for the Bayesian computation, K
posterior	The posterior sample distribution of the treatment effects. BPSM uses the posterior standard deviation to approximate the standard error.

Note

The latest version of the Abadie and Imbens paper may be found at <http://www.hks.harvard.edu/fs/aabadie/pscore.pdf>. To use BPSM, first install JAGS to the local computer. JAGS is available at <http://mcmc-jags.sourceforge.net/>. Some parts of the code is still preliminary. So use at your own risk.

Author(s)

Weihua An, Huizi Xu, and Zhida Zheng, Indiana University Bloomington.

References

An, Weihua. 2010. "Bayesian Propensity Score Estimators: Incorporating Uncertainties In Propensity Scores Into Causal Inference." *Sociological Methodology* 40: 151-189. http://mypage.iu.edu/~weihuaan/Documents/2010_BPSE.pdf.

Abadie, Alberto and Guido W. Imbens. 2011. "Matching On the Estimated Propensity Score." *Working Paper*. http://mypage.iu.edu/~weihuaan/Documents/pscore_2011.pdf.

See Also

[bpsr](#), [modelpsm](#), [modelpsr](#), [Match](#), [sortps](#)

Examples

```
library(boot)

a = 2; b = c(1, -2, 5); N = 500
x1 <- runif(N, 0, 1)
x2 <- runif(N, 0, 1)
X <- as.matrix(cbind(rep(1, N), x1, x2))
p <- inv.logit( X %*% b )
t <- rbinom(N, 1, p)
e <- rnorm(N, 0, 1)
Y <- 5 * t + a * ( x1 + x2 ) + e
bpsm( Y, t, X, method = "AI", estimand = "ATE" )
```

Description

A function uses Bayesian methods to incorporate uncertainties in estimated propensity scores and provide adjusted standard errors for propensity score regressions.

Usage

```
bpsr(Y, t, X, K = 10000, S = 1000)
```

Arguments

Y	A vector containing the outcome variable.
t	A vector containing the treatment indicator.
X	A matrix containing the covariates.
K	Numbers of iterations.
S	Number of posterior samples.

Details

Estimated propensity scores are used as an additional covariate in the main outcome model to control for selection or to provide better control for the nonlinear effects of covariates. The function `bpsr` takes into account the uncertainties in estimating the propensity scores and adjusts the standard errors accordingly.

Value

estimates	The estimated treatment effects and their adjusted standard errors. Phat shows the results with unadjusted standard errors. BPSR shows the results with adjusted standard errors using the Bayesian method.
time	The time elapsed for the computation.
sims	The number of iterations requested for the Bayesian computation, K
posterior	The posterior sample distribution of the treatment effects. The function <code>bpsr</code> uses the posterior standard deviation to approximate the standard error.

Note

To use `bpsr`, first install JAGS to the local computer. JAGS is available at <http://mcmc-jags.sourceforge.net/>.

Author(s)

Weihua An, Huizi Xu, and Zhida Zheng, Indiana University Bloomington.

References

An, Weihua. 2010. "Bayesian Propensity Score Estimators: Incorporating Uncertainties In Propensity Scores Into Causal Inference." *Sociological Methodology* 40: 151-189. http://mypage.iu.edu/~weihuaan/Documents/2010_BPSE.pdf.

See Also

[bpsm](#), [modelpsm](#), [modelpsr](#), [Match](#), [sortps](#)

Examples

```
## Not run:
library(boot)

a = 2; b = c(1, -2, 5); N = 500
x1 <- runif(N, 0, 1)
x2 <- runif(N, 0, 1)
X <- cbind(rep(1, N), x1, x2)
p <- inv.logit( X %*% b )
t <- rbinom(N, 1, p)
e <- rnorm(N, 0, 1)
Y <- 5 * t + a * ( x1 + x2 ) + e
bpsr(Y, t, X )

## End(Not run)
```

modelpsm

modelpsm

Description

The JAGS model to feed in BPSM. It is an internal function called by BPSM.

Usage

```
modelpsm()
```

Author(s)

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See Also

[bpsm](#), [bpsr](#), [modelpsr](#), [Match](#), [sortps](#)

 modelpsr

modelpsr

Description

The JAGS model to feed in BPSR. It is an internal function called by BPSR.

Usage

```
modelpsr()
```

Author(s)

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See Also

[bpsm](#), [bpsr](#), [modelpsm](#), [Match](#), [sortps](#)

 sortps

Sorting Propensity Scores

Description

An internal function called by BPSM to sort propensity scores and match units with close propensity scores in the same treatment condition.

Usage

```
sortps(D, N, N1, p2, L, Data)
```

Arguments

D	Number of covariates including the intercept.
N	Number of units.
N1	Number of treated units.
p2	Estimated propensity scores.
L	Number of within-group matches requested for the AI method.
Data	A matrix containing Y, t, and X.

Details

The function generates the above arguments from the inputted data and returns IDs of the matched units with close propensity scores in the same treatment condition.

sortps

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See Also

[bpsm](#), [bpsr](#), [modelpsm](#), [modelpsr](#), [Match](#)

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