Package 'causalweight'

December 1, 2018

Type Package

Title Estimation Methods for Causal Inference Based on Inverse Probability Weighting

Version 0.1.2

Author Hugo Bodory and Martin Huber

Maintainer Hugo Bodory <hugo.bodory@unifr.ch>

Description Various estimation methods for causal inference based on inverse probability weighting. Specifically, the package includes methods for estimating average treatment effects as well as direct and indirect effects in causal mediation analysis. The models refer to the studies of Froelich (2007) <doi:10.1016/j.jeconom.2006.06.004>, Huber (2012) <doi:10.3102/1076998611411917>, Huber (2014) <doi:10.1080/07474938.2013.806197>, Huber (2014) <doi:10.1002/jae.2341>, and Froelich and Huber (2017) <doi:10.1111/rssb.12232>.

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Depends mvtnorm, np

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

Date/Publication 2018-12-01 22:40:05 UTC

R topics documented:

`lateweight` *Local average treatment effect estimation based on inverse probability weighting*

Description

Instrumental variable-based evaluation of local average treatment effects using weighting by the inverse of the instrument propensity score.

Usage

```
lateweight(y, d, z, x, LATT = FALSE, trim = 0.05, logit = FALSE,
  boot = 1999, cluster = NULL)
```

Arguments

`y`	Dependent variable, must not contain missings.
`d`	Treatment, must be binary (either 1 or 0), must not contain missings.
`z`	Instrument for the endogenous treatment, must be binary (either 1 or 0), must not contain missings.
`x`	Confounders of the instrument and outcome, must not contain missings.
`LATT`	If FALSE, the local average treatment effect (LATE) among compliers (whose treatment reacts to the instrument) is estimated. If TRUE, the local average treatment effect on the treated compliers (LATT) is estimated. Default is FALSE.
`trim`	Trimming rule for discarding observations with extreme propensity scores. If `LATT=FALSE`, observations with Pr(Z=1|X)<`trim` or Pr(Z=1|X)>(1-`trim`) are dropped. If `LATT=TRUE`, observations with Pr(Z=1|X)>(1-`trim`) are dropped. Default is 0.05.
`logit`	If FALSE, probit regression is used for propensity score estimation. If TRUE, logit regression is used. Default is FALSE.
`boot`	Number of bootstrap replications for estimating standard errors. Default is 1999.
`cluster`	A cluster ID for block or cluster bootstrapping when units are clustered rather than iid. Must be numerical. Default is NULL (standard bootstrap without clustering).

Details

Estimation of local average treatment effects of a binary endogenous treatment based on a binary instrument that is conditionally valid, implying that all confounders of the instrument and the outcome are observed. Units are weighted by the inverse of their conditional instrument propensities given the observed confounders, which are estimated by probit or logit regression. Standard errors are obtained by bootstrapping the effect.

Value

A lateweight object contains 10 components, `effect`, `se.effect`, `pval.effect`, `first`, `se.first`, `pval.first`, `ITT`, `se.ITT`, `pval.ITT`, and `ntrimmed`:

`effect`: local average treatment effect (LATE) among compliers if `LATT=FALSE` or the local average treatment effect on treated compliers (LATT) if `LATT=TRUE`.

`se.effect`: bootstrap-based standard error of the effect.

`pval.effect`: p-value of the effect.

`first`: first stage estimate of the complier share if `LATT=FALSE` or the first stage estimate among treated if `LATT=TRUE`.

`se.first`: bootstrap-based standard error of the first stage effect.

`pval.first`: p-value of the first stage effect.

`ITT`: intention to treat effect (ITT) of `z` on `y` if `LATT=FALSE` or the ITT among treated if `LATT=TRUE`.

`se.ITT`: bootstrap-based standard error of the ITT.

`pval.ITT`: p-value of the ITT.

`ntrimmed`: number of discarded (trimmed) observations due to extreme propensity score values.

References

Frölich, M. (2007): "Nonparametric IV estimation of local average treatment effects with covariates", Journal of Econometrics, 139, 35-75.

Examples

```
# A little example with simulated data (10000 observations)
n=10000
u=rnorm(n)
x=rnorm(n)
z=(0.25*x+rnorm(n)>0)*1
d=(z+0.25*x+0.25*u+rnorm(n)>0.5)*1
y=0.5*d+0.25*x+u
# The true LATE is equal to 0.5
output=lateweight(y=y,d=d,z=z, x=x, trim=0.05, LATT=FALSE, logit=TRUE, boot=19)
cat("LATE: ",round(c(output$effect),3),", standard error: ",
             round(c(output$se.effect),3), ", p-value: ",
             round(c(output$pval.effect),3))
output$ntrimmed
```

`medlateweight` *Causal mediation analysis with instruments for treatment and mediator based on weighting*

Description

Causal mediation analysis (evaluation of natural direct and indirect effects) with instruments for a binary treatment and a continuous mediator based on weighting as suggested in Frölich and Huber (2017), Theorem 1.

Usage

```
medlateweight(y, d, m, zd, zm, x, trim = 0.1, csquared = FALSE,
  boot = 1999, cminobs = 40, bwreg = NULL, bwm = NULL,
  logit = FALSE, cluster = NULL)
```

Arguments

y	Dependent variable, must not contain missings.
d	Treatment, must be binary (either 1 or 0), must not contain missings.
m	Mediator(s),must be a continuous scalar, must not contain missings.
zd	Instrument for the treatment, must be binary (either 1 or 0), must not contain missings.
zm	Instrument for the mediator, must contain at least one continuous element, may be a scalar or a vector, must not contain missings. If no user-specified bandwidth is provided for the regressors when estimating the conditional cumulative distribution function F(M|Z2,X), i.e. if bwreg=NULL, then zm must be exclusively numeric.
x	Pre-treatment confounders, may be a scalar or a vector, must not contain missings. If no user-specified bandwidth is provided for the regressors when estimating the conditional cumulative distribution function F(M|Z2,X), i.e. if bwreg=NULL, then x must be exclusively numeric.
trim	Trimming rule for discarding observations with extreme weights. Discards observations whose relative weight would exceed the value in trim in the estimation of any of the potential outcomes. Default is 0.1 (i.e. a maximum weight of 10% per observation).
csquared	If TRUE, then not only the control function C, but also its square is used as regressor in any estimated function that conditions on C. Default is FALSE.
boot	Number of bootstrap replications for estimating standard errors. Default is 1999.
cminobs	Minimum number of observations to compute the control function C, see the numerator of equation (7) in Frölich and Huber (2017). A larger value increases boundary bias when estimating the control function for lower values of M, but reduces the variance. Default is 40, but should be adapted to sample size and the number of variables in Z2 and X.
bwreg	Bandwidths for zm and x in the estimation of the conditional cumulative distribution function F(M|Z2,X) based on the np package by Hayfield and Racine (2008). The length of the numeric vector must correspond to the joint number of elements in zm and x and will be used both in the original sample for effect estimation and in bootstrap samples to compute standard errors. If set to NULL, then the rule of thumb is used for bandwidth calculation, see the np package for details. In the latter case, all elements in the regressors must be numeric. Default is NULL.
bwm	Bandwidth for m in the estimation of the conditional cumulative distribution function F(M|Z2,X) based on the np package by Hayfield and Racine (2008). Must be scalar and will be used both in the original sample for effect estimation and in bootstrap samples to compute standard errors. If set to NULL, then the

rule of thumb is used for bandwidth calculation, see the np package for details. Default is NULL.

`logit` If FALSE, probit regression is used for any propensity score estimation. If TRUE, logit regression is used. Default is FALSE.

`cluster` A cluster ID for block or cluster bootstrapping when units are clustered rather than iid. Must be numerical. Default is NULL (standard bootstrap without clustering).

Details

Estimation of causal mechanisms (natural direct and indirect effects) of a binary treatment among treatment compliers based on distinct instruments for the treatment and the mediator. The treatment and its instrument are assumed to be binary, while the mediator and its instrument are assumed to be continuous, see Theorem 1 in Frölich and Huber (2017). The instruments are assumed to be conditionally valid given a set of observed confounders. A control function is used to tackle mediator endogeneity. Standard errors are obtained by bootstrapping the effects.

Value

A medlateweight object contains two components, `results` and `ntrimmed`:

`results`: a 3x7 matrix containing the effect estimates in the first row ("effects"), standard errors in the second row ("se"), and p-values in the third row ("p-value"). The first column provides the total effect, namely the local average treatment effect (LATE) on the compliers. The second and third columns provide the direct effects under treatment and control, respectively ("dir.treat", "dir.control"). The fourth and fifth columns provide the indirect effects under treatment and control, respectively ("indir.treat", "indir.control"). The sixth and seventh columns provide the parametric direct and indirect effect estimates ("dir.para", "indir.para") without intercation terms, respectively. For the parametric estimates, probit or logit specifications are used for the treatment model and OLS specifications for the mediator and outcome models.

`ntrimmed`: number of discarded (trimmed) observations due to large weights.

References

Frölich, M. and Huber, M. (2017): "Direct and indirect treatment effects: Causal chains and mediation analysis with instrumental variables", Journal of the Royal Statistical Society Series B, 79, 1645–1666.

Examples

```
# A little example with simulated data (3000 observations)
## Not run:
n=3000; sigma=matrix(c(1,0.5,0.5,0.5,1,0.5,0.5,0.5,1),3,3)
e=(rmvnorm(n,rep(0,3),sigma))
x=rnorm(n)
zd=(0.5*x+rnorm(n)>0)*1
d=(-1+0.5*x+2*zd+e[,3]>0)
zm=0.5*x+rnorm(n)
m=(0.5*x+2*zm+0.5*d+e[,2])
y=0.5*x+d+m+e[,1]
```

```
# The true direct and indirect effects on compliers are equal to 1 and 0.5, respectively
medlateweight(y,d,m,zd,zm,x,trim=0.1,csquared=FALSE,boot=19,cminobs=40,
              bwreg=NULL,bwm=NULL,logit=FALSE)
## End(Not run)
```

`medweight` *Causal mediation analysis based on inverse probability weighting with optional sample selection correction.*

Description

Causal mediation analysis (evaluation of natural direct and indirect effects) based on weighting by the inverse of treatment propensity scores as suggested in Huber (2014) and Huber and Solovyeva (2018).

Usage

```
medweight(y, d, m, x, w = NULL, s = NULL, z = NULL, selpop = FALSE,
  ATET = FALSE, trim = 0.05, logit = FALSE, boot = 1999,
  cluster = NULL)
```

Arguments

`y`	Dependent variable, must not contain missings.
`d`	Treatment, must be binary (either 1 or 0), must not contain missings.
`m`	Mediator(s), may be a scalar or a vector, must not contain missings.
`x`	Pre-treatment confounders of the treatment, mediator, and/or outcome, must not contain missings.
`w`	Post-treatment confounders of the mediator and the outcome. Default is `NULL`. Must not contain missings.
`s`	Optional selection indicator. Must be one if `y` is observed (non-missing) and zero if `y` is not observed (missing). Default is `NULL`, implying that `y` does not contain any missings. Is ignored if `w` is not `NULL`.
`z`	Optional instrumental variable(s) for selection `s`. If `NULL`, outcome selection based on observables (`x`,`d`,`m`) - known as "missing at random" - is assumed.
`selpop`	Only to be used if both `s` and `z` are defined. If `TRUE`, the effects are estimated for the selected subpopulation with `s=1` only. If `FALSE`, the effects are estimated for the total population.
`ATET`	If FALSE, the average treatment effect (ATE) and the corresponding direct and indirect effects are estimated. If TRUE, the average treatment effect on the treated (ATET) and the corresponding direct and indirect effects are estimated. Default is FALSE.

`trim` Trimming rule for discarding observations with extreme propensity scores. In the absence of post-treatment confounders (w=NULL), observations with Pr(D=1|M,X)<`trim` or Pr(D=1|M,X)>(1-`trim`) are dropped. In the presence of post-treatment confounders (`w` is defined), observations with Pr(D=1|M,W,X)<`trim` or Pr(D=1|M,W,X)>(1-`trim`) are dropped. Default is 0.05. If `s` is defined (only considered if `w` is `NULL`!) and `z` is `NULL`, observations with low selection propensity scores, Pr(S=1|D,M,X)<`trim`, are discarded, too. If `s` and `z` are defined, the treatment propensity scores to be trimmed change to Pr(D=1|M,X,Pr(S=1|D,X,Z)).

`logit` If FALSE, probit regression is used for propensity score estimation. If TRUE, logit regression is used. Default is FALSE.

`boot` Number of bootstrap replications for estimating standard errors. Default is 1999.

`cluster` A cluster ID for block or cluster bootstrapping when units are clustered rather than iid. Must be numerical. Default is NULL (standard bootstrap without clustering).

Details

Estimation of causal mechanisms (natural direct and indirect effects) of a binary treatment under a selection on observables assumption assuming that all confounders of the treatment and the mediator, the treatment and the outcome, or the mediator and the outcome are observed. Units are weighted by the inverse of their conditional treatment propensities given the mediator and/or observed confounders, which are estimated by probit or logit regression. The form of weighting depends on whether the observed confounders are exclusively pre-treatment (`x`), or also contain post-treatment confounders of the mediator and the outcome (`w`). In the latter case, only partial indirect effects (from `d` to `m` to `y`) can be estimated that exclude any causal paths from `d` to `w` to `m` to `y`, see the discussion in Huber (2014). Standard errors are obtained by bootstrapping the effects. In the absence of post-treatment confounders (such that `w` is `NULL`), defining `s` allows correcting for sample selection due to missing outcomes based on the inverse of the conditional selection probability. The latter might either be related to observables, which implies a missing at random assumption, or in addition also to unobservables, if an instrument for sample selection is available. Effects are then estimated for the total population, see Huber and Solovyeva (2018) for further details.

Value

A medweight object contains two components, `results` and `ntrimmed`:

`results`: a 3X5 matrix containing the effect estimates in the first row ("effects"), standard errors in the second row ("se"), and p-values in the third row ("p-value"). The first column provides the total effect, namely the average treatment effect (ATE) if `ATET=FALSE` or the average treatment effect on the treated (ATET) if `ATET=TRUE`. The second and third columns provide the direct effects under treatment and control, respectively ("dir.treat", "dir.control"). See equation (6) if `w=NULL` (no post-treatment confounders) and equation (13) if `w` is defined, respectively, in Huber (2014). If `w=NULL`, the fourth and fifth columns provide the indirect effects under treatment and control, respectively ("indir.treat", "indir.control"), see equation (7) in Huber (2014). If `w` is defined, the fourth and fifth columns provide the partial indirect effects under treatment and control, respectively ("par.in.treat", "par.in.control"), see equation (14) in Huber (2014).

`ntrimmed`: number of discarded (trimmed) observations due to extreme propensity score values.

References

Huber, M. (2014): "Identifying causal mechanisms (primarily) based on inverse probability weighting", Journal of Applied Econometrics, 29, 920-943.

Huber, M. and Solovyeva, A. (2018): "Direct and indirect effects under sample selection and outcome attrition ", SES working paper 496, University of Fribourg.

Examples

```
# A little example with simulated data (10000 observations)
n=10000
x=rnorm(n)
d=(0.25*x+rnorm(n)>0)*1
w=0.2*d+0.25*x+rnorm(n)
m=0.5*w+0.5*d+0.25*x+rnorm(n)
y=0.5*d+m+w+0.25*x+rnorm(n)
# The true direct and partial indirect effects are all equal to 0.5
output=medweight(y=y,d=d,m=m,x=x, w=w, trim=0.05, ATET=FALSE, logit=TRUE, boot=19)
round(output$results,3)
output$ntrimmed
```

`medweightcont` *Causal mediation analysis with a continuous treatment based on weighting by the inverse of generalized propensity scores*

Description

Causal mediation analysis (evaluation of natural direct and indirect effects) of a continuous treatment based on weighting by the inverse of generalized propensity scores as suggested in Hsu, Huber, Lee, and Pipoz (2018).

Usage

```
medweightcont(y, d, m, x, d0, d1, ATET = FALSE, trim = 0.05,
  lognorm = FALSE, bw = NULL, boot = 1999, cluster = NULL)
```

Arguments

`y`	Dependent variable, must not contain missings.
`d`	Continuous treatment, must not contain missings.
`m`	Mediator(s), may be a scalar or a vector, must not contain missings.
`x`	Pre-treatment confounders of the treatment, mediator, and/or outcome, must not contain missings.
`d0`	Value of `d` under non-treatment. Effects are based on pairwise comparisons, i.e. differences in potential outcomes evaluated at `d1` and `d0`.
`d1`	Value of `d` under treatment. Effects are based on pairwise comparisons, i.e. differences in potential outcomes evaluated at `d1` and `d0`.

ATET	If FALSE, the average treatment effect (ATE) and the corresponding direct and indirect effects are estimated. If TRUE, the average treatment effect on the treated (ATET) and the corresponding direct and indirect effects are estimated. Default is FALSE.
trim	Trimming rule for discarding observations with extreme generalized propensity scores. If lognorm=FALSE, observations with f(D=d1|M,X)<trim or f(D=d0|M,X)<trim are dropped, with f denoting the generalized propensity score (or conditional density of treatment). If lognorm=TRUE, then trim corresponds to the share of lowest f(D=d1|M,X) or f(D=d0|M,X), respectively, that are dropped.
lognorm	If FALSE, a linear model with normally distributed errors is assumed for generalized propensity score estimation. If TRUE, a lognormal model is assumed. Default is FALSE.
bw	Bandwith for the second order Epanechnikov kernel functions of the treatment. If set to NULL, the rule of thumb for Epanechnikov kernels is used for bandwidth computation. Default is NULL.
boot	Number of bootstrap replications for estimating standard errors. Default is 1999.
cluster	A cluster ID for block or cluster bootstrapping when units are clustered rather than iid. Must be numerical. Default is NULL (standard bootstrap without clustering).

Details

Estimation of causal mechanisms (natural direct and indirect effects) of a continuous treatment under a selection on observables assumption assuming that all confounders of the treatment and the mediator, the treatment and the outcome, or the mediator and the outcome are observed. Units are weighted by the inverse of their conditional treatment densities (known as generalized propensity scores) given the mediator and/or observed confounders, which are estimated by linear or loglinear regression. Standard errors are obtained by bootstrapping the effects.

Value

A medweightcont object contains two components, results and ntrimmed:

results: a 3X5 matrix containing the effect estimates in the first row ("effects"), standard errors in the second row ("se"), and p-values in the third row ("p-value"). The first column provides the total effect, namely the average treatment effect (ATE) if ATET=FALSE or the average treatment effect on the treated (ATET), i.e. those with D=d1, if ATET=TRUE. The second and third columns provide the direct effects under treatment and control, respectively ("dir.treat", "dir.control"). The fourth and fifth columns provide the indirect effects under treatment and control, respectively ("indir.treat", "indir.control").

ntrimmed: number of discarded (trimmed) observations due to extreme propensity score values.

References

Hsu, Y.-C., Huber, M., Lee, Y.-Y., Pipoz, L.: (2018): "Direct and indirect effects of continuous treatments based on generalized propensity score weighting", SES working paper 495, University of Fribourg.

Examples

```
# A little example with simulated data (10000 observations)
n=10000
x=runif(n=n,min=-1,max=1)
d=0.25*x+runif(n=n,min=-2,max=2)
d=d-min(d)
m=0.5*d+0.25*x+runif(n=n,min=-2,max=2)
y=0.5*d+m+0.25*x+runif(n=n,min=-2,max=2)
# The true direct and indirect effects are all equal to 0.5
output=medweightcont(y,d,m,x, d0=2, d1=3, ATET=FALSE, trim=0.05, lognorm=FALSE, bw=NULL, boot=19)
round(output$results,3)
output$ntrimmed
```

`treatweight` *Treatment evaluation based on inverse probability weighting with optional sample selection correction.*

Description

Treatment evaluation based on inverse probability weighting with optional sample selection correction.

Usage

```
treatweight(y, d, x, s = NULL, z = NULL, selpop = FALSE,
  ATET = FALSE, trim = 0.05, logit = FALSE, boot = 1999,
  cluster = NULL)
```

Arguments

`y`	Dependent variable.
`d`	Treatment, must be binary (either 1 or 0), must not contain missings.
`x`	Confounders of the treatment and outcome, must not contain missings.
`s`	Selection indicator. Must be one if `y` is observed (non-missing) and zero if `y` is not observed (missing). Default is `NULL`, implying that `y` does not contain any missings.
`z`	Optional instrumental variable(s) for selection `s`. If `NULL`, outcome selection based on observables (x,d) - known as "missing at random" - is assumed. If `z` is defined, outcome selection based on unobservables - known as "non-ignorable missingness" - is assumed. Default is `NULL`. If `s` is `NULL`, `z` is ignored.
`selpop`	Only to be used if both `s` and `z` are defined. If `TRUE`, the effect is estimated for the selected subpopulation with s=1 only. If `FALSE`, the effect is estimated for the total population. (note that this relies on somewhat stronger statistical assumptions). Default is `FALSE`. If `s` or `z` is `NULL`, `selpop` is ignored.
`ATET`	If `FALSE`, the average treatment effect (ATE) is estimated. If `TRUE`, the average treatment effect on the treated (ATET) is estimated. Default is `FALSE`.

trim	Trimming rule for discarding observations with extreme propensity scores. If ATET=FALSE, observations with Pr(D=1|X)<trim or Pr(D=1|X)>(1-trim) are dropped. If ATET=TRUE, observations with Pr(D=1|X)>(1-trim) are dropped. If s is defined and z is NULL, observations with extremely low selection propensity scores, Pr(S=1|D,X)<trim, are discarded, too. If s and z are defined, the treatment propensity scores to be trimmed change to Pr(D=1|X,Pr(S=1|D,X,Z)). If in addition selpop is FALSE, observation with Pr(S=1|D,X,Z)<trim are discarded, too. Default for trim is 0.05.
logit	If FALSE, probit regression is used for propensity score estimation. If TRUE, logit regression is used. Default is FALSE.
boot	Number of bootstrap replications for estimating standard errors. Default is 1999.
cluster	A cluster ID for block or cluster bootstrapping when units are clustered rather than iid. Must be numerical. Default is NULL (standard bootstrap without clustering).

Details

Estimation of treatment effects of a binary treatment under a selection on observables assumption assuming that all confounders of the treatment and the outcome are observed. Units are weighted by the inverse of their conditional treatment propensities given the observed confounders, which are estimated by probit or logit regression. Standard errors are obtained by bootstrapping the effect. If s is defined, the procedure allows correcting for sample selectiondue to missing outcomes based on the inverse of the conditional selection probability. The latter might either be related to observables, which implies a missing at random assumption, or in addition also to unobservables, if an instrument for sample selection is available. See Huber (2012, 2014) for further details.

Value

A treatweight object contains six components: effect, se, pval, y1, y0, and ntrimmed.

effect: average treatment effect (ATE) if ATET=FALSE or the average treatment effect on the treated (ATET) if ATET=TRUE.

se: bootstrap-based standard error of the effect.

pval: p-value of the effect.

y1: mean potential outcome under treatment.

y0: mean potential outcome under control.

ntrimmed: number of discarded (trimmed) observations due to extreme propensity score values.

References

Horvitz, D. G., and Thompson, D. J. (1952): "A generalization of sampling without replacement from a finite universe", Journal of the American Statistical Association, 47, 663–685.

Huber, M. (2012): "Identification of average treatment effects in social experiments under alternative forms of attrition", Journal of Educational and Behavioral Statistics, 37 , 443-474.

Huber, M. (2014): "Treatment evaluation in the presence of sample selection", Econometric Reviews, 33, 869-905.

Examples

```
# A little example with simulated data (10000 observations)
n=10000
x=rnorm(n); d=(0.25*x+rnorm(n)>0)*1
y=0.5*d+0.25*x+rnorm(n)
# The true ATE is equal to 0.5
output=treatweight(y=y,d=d,x=x, trim=0.05, ATET=FALSE, logit=TRUE, boot=19)
cat("ATE: ",round(c(output$effect),3),", standard error: ",
    round(c(output$se),3), ", p-value: ",round(c(output$pval),3))
output$ntrimmed
# An example with non-random outcome selection and an instrument for selection
n=10000
sigma=matrix(c(1,0.6,0.6,1),2,2)
e=(2*rmvnorm(n,rep(0,2),sigma))
x=rnorm(n)
d=(0.5*x+rnorm(n)>0)*1
z=rnorm(n)
s=(0.25*x+0.25*d+0.5*z+e[,1]>0)*1
y=d+x+e[,2]; y[s==0]=0
# The true ATE is equal to 1
output=treatweight(y=y,d=d,x=x, s=s, z=z, selpop=FALSE, trim=0.05, ATET=FALSE, logit=TRUE, boot=19)
cat("ATE: ",round(c(output$effect),3),", standard error: ",
    round(c(output$se),3), ", p-value: ",round(c(output$pval),3))
output$ntrimmed
```

Index