Package 'genius'

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Title G-Estimation under No-Interaction with Unmeasured Selection

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Description This package implements the MR GENIUS estimator.

Depends R (>= 3.4.1)

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Imports gmm (>= 1.6-1)

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

`genius` *G-Estimation under No-Interaction with Unmeasured Selection*

Description

Implements G-Estimation under No-Interaction with Unmeasured Selection.

Usage

```
genius(Y, A, G, alpha = 0.05, lower = -10, upper = 10)
```

Arguments

Y	A numeric vector of outcomes.
A	A numeric vector of exposures (binary values should be coded in 0/1).
G	A numeric matrix of instruments; each column stores values for one instrument (a numeric vector if only a single instrument is available).
alpha	Significance level for confidence interval (default value=0.05).
lower	The lower end point of the causal effect interval to be searched (default value=-10).
upper	The upper end point of the causal effect interval to be searched (default value=10).

Details

This function implements estimation of causal effect under an additive outcome model. The estimator is given in equations (6) and (12) of Tchetgen Tchetgen et al (2017) for single and multiple instruments, respectively. The term $E(A|G)$ is modelled under the logit and identity links for binary and continuous exposure respectively, with a linear predictor consisting of the main effects of all available instruments.

Value

A "genius" object containing the following items:

beta.est	The point estimate of causal effect of the exposure on the outcome.
beta.var	The corresponding estimated variance.
ci	The corresponding Wald-type confidence interval at specified significance level.
pval	The p-value for two-sided Wald test of null causal effect of the exposure on the outcome.

References

Tchetgen Tchetgen, E., Sun, B. and Walter, S. (2017). The GENIUS Approach to Robust Mendelian Randomization Inference. arXiv e-prints.

Examples

```
# the following packages are needed to simulate data
library("msm")
library("MASS")
expit <- function(x) {
   exp(x)/(1+exp(x))
}

### example with binary exposure, all instruments invalid ###
# true causal effect, beta = 1.0
# Number of instruments, nIV = 10
# Y: vector of outcomes
# A: vector of exposures
# G: matrix of instruments, one column per instrument

nIV=10; N=5000; beta=1;
phi=rep(-0.02,nIV); gamma=rep(-0.15,nIV); alpha=rep(-0.5,nIV);
Gn = mvrnorm(N,rep(0,nIV),diag(rep(1,nIV)))
```

```
G  = (Gn>0)*1;
U= as.vector(phi%*%t(G))+ rtnorm(n=N,mean=0.35,lower=0.2,upper=0.5);
A = rbinom(N,1,expit(as.vector(gamma%*%t(G)))+U-0.35-as.vector(phi%*%t(G)));
Y = as.vector(alpha%*%t(G)) + beta*A + U + rnorm(N);

genius(Y,A,G);

### example with continous exposure, all instruments invalid ###

nIV=10; N=500; beta=1;
phi=rep(-0.5,nIV); gamma=rep(-2,nIV); alpha=rep(-0.5,nIV);
lambda0=1; lambda1=rep(0.5,nIV);
Gn = mvrnorm(N,rep(0,nIV),diag(rep(1,nIV)))

G  = (Gn>0)*1;
U = as.vector(phi%*%t(G))+rnorm(N);
A = as.vector(gamma%*%t(G)) +U + rnorm(N,mean=0,sd=abs(lambda0+as.vector(lambda1%*%t(G))));
Y = as.vector(alpha%*%t(G)) + beta*A + U + rnorm(N);

genius(Y,A,G);
```

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