Package: ipwErrorY (via r-universe)

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Type Package

Title Inverse Probability Weighted Estimation of Average Treatment
Effect with Misclassified Binary Outcome

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Description An implementation of the correction methods proposed by
Shu and Yi (2017) <doi:10.1177/0962280217743777> for the
inverse probability weighted (IPW) estimation of average
treatment effect (ATE) with misclassified binary outcomes.
Logistic regression model is assumed for treatment model for
all implemented correction methods, and is assumed for the
outcome model for the implemented doubly robust correction
method. Misclassification probability given a true value of the
outcome is assumed to be the same for all individuals.

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ipwErrorY-package	*Inverse Probability Weighted (IPW) Estimation of Average Treatment Effect (ATE) with Misclassified Binary Outcome*

Description

This package is an implementation of the correction methods proposed by Shu and Yi (2017) for the inverse probability weighted (IPW) estimation of average treatment effect (ATE) with misclassified binary outcomes. Logistic regression model is assumed for treatment model for all implemented correction methods, and is assumed for the outcome model for the implemented doubly robust correction method. Misclassification probability given a true value of the outcome is assumed to be the same for all individuals.

Details

The `ipwErrorY` package implements correction methods developed by Shu and Yi (2017) to adjust for misclassification in binary outcomes in the inverse probability weighted estimation of average treatment effect. The function `KnownError` implements the correction method with known outcome misclassification probabilities. The function `EstValidation` implements the optimal linear combination correction method when validation data are available. The function `Est2Replicates` implements the correction method when two independent replicates of the outcome are available. The function `KnownErrorDR` implements the doubly robust correction method with known outcome misclassification probabilities.

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References

Shu D, Yi GY. (2017). Causal inference with measurement error in outcomes: bias analysis and estimation methods. *Statistical Methods in Medical Research* <doi:10.1177/0962280217743777>

Est2Replicates *Estimation of ATE with Two Replicates*

Description

Estimation of average treatment effect when misclassification probabilities are unknown but two independent replicates of the outcome are available

Usage

```
Est2Replicates(data, indA, indYerror, indX,
  constraint = c("sensitivity equals specificity", "known sensitivity",
  "known specificity", "known prevalence"), sensitivity = NULL,
  specificity = NULL, prevalence = NULL, confidence = 0.95)
```

Arguments

data	The dataset to be analyzed in the form of R data frame without missing data
indA	A column name indicating the binary treatment variable
indYerror	A vector of two column names indicating replicates of the binary outcome variable
indX	A vector of column names indicating the covariates included in the treatment model
constraint	The constraint to be used; the default assumes sensitivity equals specificity
sensitivity	The specified sensitivity between 0 and 1 when imposing the constraint that sensitivity is known, and the default is set to be NULL
specificity	The specified specificity between 0 and 1 when imposing the constraint that specificity is known, and the default is set to be NULL
prevalence	The specified prevalence between 0 and 1 when imposing the constraint that prevalence is known, and the default is set to be NULL
confidence	The confidence level between 0 and 1; the default is 0.95 corresponding to a 95 per cent confidence interval

Value

A list of the estimate of average treatment effect, sandwich-variance-based standard error, confidence interval, imposed constraint, and the information on sensitivity and specificity

Examples

```
#create a dataset with sensitivity=0.95 and specificity=0.85
set.seed(100)
X1=rnorm(2000)
A=rbinom(2000,1,1/(1+exp(-0.2-X1)))
Y=rbinom(2000,1,1/(1+exp(-0.2-A-X1)))
```

```
y1=which(Y==1)
y0=which(Y==0)
Yast1=Y
Yast1[y1]=rbinom(length(y1),1,0.95)
Yast1[y0]=rbinom(length(y0),1,0.15)
Yast2=Y
Yast2[y1]=rbinom(length(y1),1,0.95)
Yast2[y0]=rbinom(length(y0),1,0.15)
da=data.frame(A=A,X1=X1,Yast1=Yast1,Yast2=Yast2)
head(da)
#apply the correction method assuming specificity=0.85
Est2Replicates(da,"A",c("Yast1","Yast2"),"X1","known specificity",NULL,0.85,NULL,0.95)
```

EstValidation   *Estimation of ATE with Validation Data*

Description

Estimation of average treatment effect using the optimal linear combination method when misclassification probabilities are unknown but validation data are available

Usage

```
EstValidation(maindata, validationdata, indA, indYerror, indX, indY,
  confidence = 0.95)
```

Arguments

maindata	The non-validation main data in the form of R data frame without missing data
validationdata	The validation data in the form of R data frame without missing data
indA	A column name indicating the binary treatment variable
indYerror	A column name indicating the misclassified binary outcome variable
indX	A vector of column names indicating the covariates included in the treatment model
indY	A column name indicating the true binary outcome variable
confidence	The confidence level between 0 and 1; the default is 0.95 corresponding to a 95 per cent confidence interval

Value

A list of the estimate of average treatment effect, sandwich-variance-based standard error, confidence interval, and the estimated sensitivity and specificity

Examples

```
#create main data and validation data with sensitivity=0.95 and specificity=0.85
set.seed(100)
X1=rnorm(1200)
A=rbinom(1200,1,1/(1+exp(-0.2-X1)))
Y=rbinom(1200,1,1/(1+exp(-0.2-A-X1)))
y1=which(Y==1)
y0=which(Y==0)
Yast=Y
Yast[y1]=rbinom(length(y1),1,0.95)
Yast[y0]=rbinom(length(y0),1,0.15)
mainda=data.frame(A=A,X1=X1,Yast=Yast)
X1=rnorm(800)
A=rbinom(800,1,1/(1+exp(-0.2-X1)))
Y=rbinom(800,1,1/(1+exp(-0.2-A-X1)))
y1=which(Y==1)
y0=which(Y==0)
Yast=Y
Yast[y1]=rbinom(length(y1),1,0.95)
Yast[y0]=rbinom(length(y0),1,0.15)
validationda=data.frame(A=A,X1=X1,Y=Y,Yast=Yast)
head(mainda)
head(validationda)
#apply the optimal linear combination correction method
EstValidation(mainda,validationda,"A","Yast","X1","Y",0.95)
```

KnownError   *Estimation of ATE with Known Error*

Description

Estimation of average treatment effect with known outcome misclassification probabilities, i.e., known sensitivity and specificity

Usage

```
KnownError(data, indA, indYerror, indX, sensitivity, specificity,
  confidence = 0.95)
```

Arguments

data	The dataset to be analyzed in the form of R data frame without missing data
indA	A column name indicating the binary treatment variable
indYerror	A column name indicating the misclassified binary outcome variable
indX	A vector of column names indicating the covariates included in the treatment model
sensitivity	The specified sensitivity between 0 and 1

specificity   The specified specificity between 0 and 1

confidence   The confidence level between 0 and 1; the default is 0.95 corresponding to a 95
                    per cent confidence interval

Value

A list of the estimate of average treatment effect, sandwich-variance-based standard error and confidence interval

Examples

```
#create a dataset with sensitivity=0.95 and specificity=0.85
set.seed(100)
X1=rnorm(2000)
A=rbinom(2000,1,1/(1+exp(-0.2-X1)))
Y=rbinom(2000,1,1/(1+exp(-0.2-A-X1)))
y1=which(Y==1)
y0=which(Y==0)
Yast=Y
Yast[y1]=rbinom(length(y1),1,0.95)
Yast[y0]=rbinom(length(y0),1,0.15)
da=data.frame(X1=X1,A=A,Yast=Yast)
head(da)
#apply the correction method with sensitivity=0.95 and specificity=0.85
KnownError(da,"A","Yast","X1",0.95,0.85,0.95)
```

KnownErrorDR   *Doubly Robust Estimation of ATE with Known Error*

Description

Doubly robust estimation of average treatment effect with known outcome misclassification probabilities, i.e., known sensitivity and specificity

Usage

```
KnownErrorDR(data, indA, indYerror, indXtrt, indXout, sensitivity, specificity,
   sharePara = FALSE, confidence = 0.95)
```

Arguments

data   The dataset to be analyzed in the form of R data frame without missing data

indA   A column name indicating the binary treatment variable

indYerror   A column name indicating the misclassified binary outcome variable

indXtrt   A vector of column names indicating the covariates included in the treatment
                    model

indXout	A vector of column names indicating the covariates included in the outcome model
sensitivity	The specified sensitivity between 0 and 1
specificity	The specified specificity between 0 and 1
sharePara	if the treated and untreated groups share parameters for covariates in the logistic outcome model (i.e., assuming Y~ T+X), then set sharePara=TRUE; if not (i.e., modeling Y~ X for the treated and untreated groups separately), then set sharePara=FALSE. By default, sharePara=FALSE
confidence	The confidence level between 0 and 1; the default is 0.95 corresponding to a 95 per cent confidence interval

Value

A list of the estimate of average treatment effect, sandwich-variance-based standard error and confidence interval

Examples

```
#create a dataset with sensitivity=0.95 and specificity=0.85
set.seed(100)
X=rnorm(2000)
xx=X^2
A=rbinom(2000,1,1/(1+exp(-0.1-X-0.2*xx)))
Y=rbinom(2000,1,1/(1+exp(1-A-0.5*X-xx)))
y1=which(Y==1)
y0=which(Y==0)
Y[y1]=rbinom(length(y1),1,0.95)
Y[y0]=rbinom(length(y0),1,0.15)
Yast=Y
da=data.frame(A=A,X=X,xx=xx,Yast=Yast)
head(da)
#apply the doubly robust correction method with sensitivity=0.95 and specificity=0.85
KnownErrorDR(da,"A","Yast",c("X","xx"),c("X","xx"),0.95,0.85,FALSE,0.95)
```

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