Package ‘caratREG’

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Type Package

Title Regression Analysis Methods for Covariate-Adaptive Randomized Trials

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Author Fuyi Tu [aut, cre], Wei Ma [aut, ths], Hanzhong Liu [aut, ths]

Maintainer Fuyi Tu <fuyi.tu@ruc.edu.cn>

Description
This package implements all of the regression methods considered in Ma et al. (2020) for estimating and inferring the treatment effect under covariate-adaptive randomization.

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Imports dplyr (>= 1.0.0), MASS, stats

RoxygenNote 7.1.1

NeedsCompilation no

R topics documented:

`caratREG-package` *Regression Analysis Methods for Covariate-Adaptive Randomized Trials*

Description

This package implements all of the regression methods considered in Ma et al. (2020) for estimating and inferring the treatment effect under covariate-adaptive randomization.

Details

Index of help topics:

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caratREG-package        Regression Analysis Methods for
                        Covariate-Adaptive Randomized Trials
tau.adj                 Regression without interaction
tau.diff                Difference in means
tau.interact            Regression with interaction
```

Author(s)

Fuyi Tu [aut, cre], Wei Ma [aut, ths], Hanzhong Liu [aut, ths]

Maintainer: Fuyi Tu <fuyi.tu@ruc.edu.cn>

References

Ma, W., Tu, F., & Liu, H. (2020). *Regression analysis for covariate-adaptive randomization: A robust and efficient inference perspective*. arXiv preprint arXiv:2009.02287.

`tau.adj` *Regression without interaction*

Description

Estimating and inferring the treatment effect based on regression without interaction.

Usage

```
tau.adj(A, B, Y, X = NULL, pi, q, conf.level = 0.95)
```

Arguments

`A`	a numeric vector of treatment assignments. Its length should be the same as the number of subjects.
`B`	a numeric vector of stratum labels. Its length should be the same as the number of subjects.
`Y`	a numeric vector of observed outcomes. Its length should be the same as the number of subjects.
`X`	an (optional) numeric design matrix containing additional covariates used in the regression.
`pi`	a numeric value for the target treatment proportion in each stratum.
`q`	a numeric value indicating the balance level of covariate-adaptive randomizations. Detailed information can be found in Section 2, Ma et al.(2020).
`conf.level`	confidence level of the interval. Default is 0.95.

Details

Estimating and inferring the treatment effect based on regression without interaction. It implements the methods as described in Sections 3.2 and 4.2, Ma et al. (2020).

Value

A list of class "htest" containing the following components:

statistic	the value of the t-statistic.
p.value	the p-value for the test
conf.int	a confidence interval under chosen level conf.level for the difference in treatment effect between treatment group and control group.
estimate	estimated treatment effect difference between treatment group and control group.
method	a character string indicating what type of regression was performed.

References

Ma, W., Tu, F., & Liu, H. (2020). *Regression analysis for covariate-adaptive randomization: A robust and efficient inference perspective*. arXiv preprint arXiv:2009.02287.

Examples

```
n <- 1000
pi <- 0.5
q <- pi*(1-pi)
alphavec <- c(5,8,3,12)
m2e<-function(x){
 6*exp(x)*x*(1-x)
}
mu0 <- alphavec[2]*3.6-alphavec[1]*2-alphavec[4]*integrate(m2e,lower = 0,upper = 1)$value
mu1 <- 0
X1 <- rgamma(n,2)
X2 <- sample(c(1,2,3),n,replace = TRUE, prob = c(0.3,0.6,0.1))
X3 <- rpois(n,3)
X4 <- rbeta(n,2,2)
X1_S <- rep(1,n)
X1_S[which(X1 >= 2.5)] <- 2
profile <- cbind(X1_S, X2)
strata <- unique(cbind(X1_S,X2))
B <- numeric(n)
for(i in 1:nrow(strata)){
 B[which(profile[,1] == strata[i,1] & profile[,2] == strata[i,2])] = i
}
X <- cbind(X1,X3)
A <- sample(c(0,1),n,replace=TRUE,prob=c(1-pi,pi))
Y0 <- mu0+alphavec[1]*X1+log(alphavec[3]*X1*log(X3+1)+1)+alphavec[4]*exp(X4)+rnorm(n,sd = 2)
Y1 <- mu1+alphavec[2]*X2^2+log(alphavec[3]*X1*log(X3+1)+1)+rnorm(n,sd = 1)
Y <- Y0*(1-A)+Y1*A
tau.adj(A, B, Y, X, pi, q)
```

---

tau.diff — *Difference in means*

Description

Estimating and inferring the treatment effect based on difference in means.

Usage

```
tau.diff(A, B, Y, X = NULL, pi, q, conf.level = 0.95)
```

Arguments

A	a numeric vector of treatment assignments. Its length should be the same as the number of subjects.
B	a numeric vector of stratum labels. Its length should be the same as the number of subjects.
Y	a numeric vector of observed outcomes. Its length should be the same as the number of subjects.
X	an (optional) numeric design matrix containing additional covariates used in the regression.
pi	a numeric value for the target treatment proportion in each stratum.
q	a numeric value indicating the balance level of covariate-adaptive randomizations. Detailed information can be found in Section 2, Ma et al.(2020).
conf.level	confidence level of the interval. Default is 0.95.

Details

Estimating and inferring the treatment effect based on difference in means. It implements the methods as described in Sections 3.1 and 4.1, Ma et al. (2020).

Value

A list of class `"htest"` containing the following components:

statistic	the value of the t-statistic.
p.value	the p-value for the test
conf.int	a confidence interval under chosen level `conf.level` for the difference in treatment effect between treatment group and control group.
estimate	estimated treatment effect difference between treatment group and control group.
method	a character string indicating what type of regression was performed.

References

Ma, W., Tu, F., & Liu, H. (2020). *Regression analysis for covariate-adaptive randomization: A robust and efficient inference perspective*. arXiv preprint arXiv:2009.02287.

Examples

```
n <- 1000
pi <- 0.5
q <- pi*(1-pi)
alphavec <- c(5,8,3,12)
m2e<-function(x){
 6*exp(x)*x*(1-x)
}
mu0 <- alphavec[2]*3.6-alphavec[1]*2-alphavec[4]*integrate(m2e,lower = 0,upper = 1)$value
mu1 <- 0
X1 <- rgamma(n,2)
```

```
X2 <- sample(c(1,2,3),n,replace = TRUE, prob = c(0.3,0.6,0.1))
X3 <- rpois(n,3)
X4 <- rbeta(n,2,2)
X1_S <- rep(1,n)
X1_S[which(X1 >= 2.5)] <- 2
profile <- cbind(X1_S, X2)
strata <- unique(cbind(X1_S,X2))
B <- numeric(n)
for(i in 1:nrow(strata)){
 B[which(profile[,1] == strata[i,1] & profile[,2] == strata[i,2])] = i
}
X <- cbind(X1,X3)
A <- sample(c(0,1),n,replace=TRUE,prob=c(1-pi,pi))
Y0 <- mu0+alphavec[1]*X1+log(alphavec[3]*X1*log(X3+1)+1)+alphavec[4]*exp(X4)+rnorm(n,sd = 2)
Y1 <- mu1+alphavec[2]*X2^2+log(alphavec[3]*X1*log(X3+1)+1)+rnorm(n,sd = 1)
Y <- Y0*(1-A)+Y1*A
tau.diff(A, B, Y, X, pi, q)
```

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tau.interact *Regression with interaction*

Description

Estimating and inferring the treatment effect based on regression with interaction.

Usage

```
tau.interact(A, B, Y, X = NULL, pi, q, conf.level = 0.95)
```

Arguments

A	a numeric vector of treatment assignments. Its length should be the same as the number of subjects.
B	a numeric vector of stratum labels. Its length should be the same as the number of subjects.
Y	a numeric vector of observed outcomes. Its length should be the same as the number of subjects.
X	an (optional) numeric design matrix containing additional covariates used in the regression.
pi	a numeric value for the target treatment proportion in each stratum.
q	a numeric value indicating the balance level of covariate-adaptive randomizations. Detailed information can be found in Section 2, Ma et al.(2020).
conf.level	confidence level of the interval. Default is 0.95.

Details

Estimating and inferring the treatment effect based on regression with interaction. It implements the methods as described in Sections 3.3 and 4.3, Ma et al. (2020).

Value

A list of class "htest" containing the following components:

statistic	the value of the t-statistic.
p.value	the p-value for the test
conf.int	a confidence interval under chosen level conf.level for the difference in treatment effect between treatment group and control group.
estimate	estimated treatment effect difference between treatment group and control group.
method	a character string indicating what type of regression was performed.

References

Ma, W., Tu, F., & Liu, H. (2020). *Regression analysis for covariate-adaptive randomization: A robust and efficient inference perspective*. arXiv preprint arXiv:2009.02287.

Examples

```
n <- 1000
pi <- 0.5
q <- pi*(1-pi)
alphavec <- c(5,8,3,12)
m2e<-function(x){
 6*exp(x)*x*(1-x)
}
mu0 <- alphavec[2]*3.6-alphavec[1]*2-alphavec[4]*integrate(m2e,lower = 0,upper = 1)$value
mu1 <- 0
X1 <- rgamma(n,2)
X2 <- sample(c(1,2,3),n,replace = TRUE, prob = c(0.3,0.6,0.1))
X3 <- rpois(n,3)
X4 <- rbeta(n,2,2)
X1_S <- rep(1,n)
X1_S[which(X1 >= 2.5)] <- 2
profile <- cbind(X1_S, X2)
strata <- unique(cbind(X1_S,X2))
B <- numeric(n)
for(i in 1:nrow(strata)){
 B[which(profile[,1] == strata[i,1] & profile[,2] == strata[i,2])] = i
}
X <- cbind(X1,X3)
A <- sample(c(0,1),n,replace=TRUE,prob=c(1-pi,pi))
Y0 <- mu0+alphavec[1]*X1+log(alphavec[3]*X1*log(X3+1)+1)+alphavec[4]*exp(X4)+rnorm(n,sd = 2)
Y1 <- mu1+alphavec[2]*X2^2+log(alphavec[3]*X1*log(X3+1)+1)+rnorm(n,sd = 1)
Y <- Y0*(1-A)+Y1*A
tau.diff(A, B, Y, X, pi, q)
```

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