Package ‘experiment’
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Title R Package for Designing and Analyzing Randomized Experiments
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Depends boot, MASS, R (>= 2.4.0)
Description Provides various statistical methods for designing and analyzing randomized experiments. One functionality of the package is the implementation of randomized-block and matched-pair designs based on possibly multivariate pre-treatment covariates. The package also provides the tools to analyze various randomized experiments including cluster randomized experiments, two-stage randomized experiments, randomized experiments with noncompliance, and randomized experiments with missing data.
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R topics documented:

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ATEbounds

Bounding the Average Treatment Effect when some of the Outcome Data are Missing

Description

This function computes the sharp bounds on the average treatment effect when some of the outcome data are missing. The confidence intervals for the bounds are also computed.

Usage

ATEbounds(
  formula,
  data = parent.frame(),
  maxY = NULL,
  minY = NULL,
  alpha = 0.05,
  n.reps = 0,
  strata = NULL,
  ratio = NULL,
  survey = NULL,
  ...
)

Arguments

formula A formula of the form Y ~ X where Y is the name of the outcome variable and X is the name of the (randomized) treatment variable. X should be a factor variable but its value can take more than two levels. The missing values for Y should be coded as NA.
data A data frame containing the relevant variables.
maxY A scalar. The maximum value of the outcome variable. The default is the maximum sample value.
minY A scalar. The minimum value of the outcome variable. The default is the minimum sample value.

alpha A positive scalar that is less than or equal to 0.5. This will determine the \((1-\alpha)\) level of confidence intervals. The default is 0.05.

n.reps A positive integer. The number of bootstrap replicates used for the construction of confidence intervals via B-method of Berran (1988). If it equals zero, the confidence intervals will not be constructed.

strata The variable name indicating strata. If this is specified, the quantities of interest will be first calculated within each strata and then aggregated. The default is NULL.

ratio A \(J \times M\) matrix of probabilities where \(J\) is the number of strata and \(M\) is the number of treatment and control groups. Each element of the matrix specifies the probability of a unit falling into that category. The default is NULL in which case the sample estimates of these probabilities are used for computation.

survey The variable name for survey weights. The default is NULL.

... The variable name for other arguments passed to other functions.

Details

For the details of the method implemented by this function, see the references.

Value

A list of class ATEbounds which contains the following items:

call The matched call.
Y The outcome variable.
D The treatment variable.
bounds The point estimates of the sharp bounds on the average treatment effect.
bounds.Y The point estimates of the sharp bounds on the outcome variable within each treatment/control group.
bmethod.ci The B-method confidence interval of the bounds on the average treatment effect.
bonf.ci The Bonferroni confidence interval of the bounds on the average treatment effect.
bonf.ci.Y The Bonferroni confidence interval of the bounds on the outcome variable within each treatment/control group.
bmethod.ci.Y The B-method confidence interval of the bounds on the outcome variable within each treatment/control group.
maxY The maximum value of the outcome variable used in the computation.
minY The minimum value of the outcome variable used in the computation.
nobs The number of observations.
nobs.Y The number of observations within each treatment/control group.
ratio The probability of treatment assignment (within each strata if strata is specified) used in the computation.
Author(s)

Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Edu>, https://imai.fas.harvard.edu;

References


ATEcluster

Estimation of the Average Treatment Effects in Cluster-Randomized Experiments

Description

This function estimates various average treatment effect in cluster-randomized experiments without using pre-treatment covariates. The treatment variable is assumed to be binary. Currently, only the matched-pair design is allowed. The details of the methods for this design are given in Imai, King, and Nall (2007).

Usage

ATEcluster(
  Y,
  Z,
  grp,
  data = parent.frame(),
  match = NULL,
  weights = NULL,
  fpc = TRUE
)

Arguments

Y
  The outcome variable of interest.

Z
  The (randomized) cluster-level treatment variable. This variable should be binary. Two units in the same cluster should have the same value.

grp
  A variable indicating clusters of units. Two units in the same cluster should have the same value.
data A data frame containing the relevant variables.
match A variable indicating matched-pairs of clusters. Two units in the same matched-pair of clusters should have the same value. The default is NULL (i.e., no matching).
weights A variable indicating the population cluster sizes, which will be used to construct weights for each pair of clusters. Two units in the same cluster should have the same value. The default is NULL, in which case sample cluster sizes will be used for constructing weights.
fpc A logical variable indicating whether or not finite population correction should be used for estimating the lower bound of CACE variance. This is relevant only when weights are specified.

Value
A list of class ATEcluster which contains the following items:
call The matched call.
n The total number of units.
n1 The total number of units in the treatment group.
n0 The total number of units in the control group.
Y The outcome variable.
Y1bar The cluster-specific (unweighted) average value of the observed outcome for the treatment group.
Y0bar The cluster-specific (unweighted) average value of the observed outcome for the control group.
Y1var The cluster-specific sample variance of the observed outcome for the treatment group.
Y0var The cluster-specific sample variance of the observed outcome for the control group.
Z The treatment variable.
grp The cluster-indicator variable.
match The matched-pair indicator variable.
weights The weight variable in its original form.
est The estimated average treatment effect based on the arithmetic mean weights.
var The estimated variance of the average treatment effect estimator based on the arithmetic mean weights. This uses the variance formula provided in Imai, King, and Nall (2007).
var.lb The estimated sharp lower bound of the cluster average treatment effect estimator using the arithmetic mean weights.
est.dk The estimated average treatment effect based on the harmonic mean weights.
var.dk The estimated variance of the average treatment effect estimator based on the harmonic mean weights. This uses the variance formula provided in Donner and Klar (1993).
The estimated variance of the average treatment effect estimator based on the harmonic mean weights. This uses the variance formula provided in Imai, King, and Nall (2007).

de eff
The estimated relative efficiency of the matched-pair design over the completely randomized design (the ratio of two estimated variances).
m
The number of pairs in the matched-pair design.
N1
The population cluster sizes for the treatment group.
N0
The population cluster sizes for the control group.
w1
Cluster-specific weights for the treatment group.
w0
Cluster-specific weights for the control group.
w
Pair-specific normalized arithmetic mean weights. These weights sum up to the total number of units in the sample, i.e., n.
w.dk
Pair-specific normalized harmonic mean weights. These weights sum up to the total number of units in the sample, i.e., n.
diff
Within-pair differences if the matched-pair design is analyzed. This equals the difference between \( Y_{1\text{bar}} \) and \( Y_{0\text{bar}} \).

Author(s)
Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Edu>, https://imai.fas.harvard.edu;

References

<table>
<thead>
<tr>
<th>ATEnocov</th>
<th>Estimation of the Average Treatment Effect in Randomized Experiments</th>
</tr>
</thead>
</table>

Description

This function computes the standard “difference-in-means” estimate of the average treatment effect in randomized experiments without using pre-treatment covariates. The treatment variable is assumed to be binary. Currently, the two designs are allowed: complete randomized design and matched-pair design.

Usage

ATEnocov(Y, Z, data = parent.frame(), match = NULL)
**ATOPnoassumption**

**Arguments**

- **Y**: The outcome variable of interest.
- **Z**: The (randomized) treatment variable. This variable should be binary.
- **data**: A data frame containing the relevant variables.
- **match**: A variable indicating matched-pairs. The two units in the same matched-pair should have the same value.

**Value**

A list of class ATEnocov which contains the following items:

- **call**: The matched call.
- **Y**: The outcome variable.
- **Z**: The treatment variable.
- **match**: The matched-pair indicator variable.
- **ATEest**: The estimated average treatment effect.
- **ATE.var**: The estimated variance of the average treatment effect estimator.
- **diff**: Within-pair differences if the matched-pair design is analyzed.

**Author(s)**

Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Edu>, https://imai.fas.harvard.edu;

**References**


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**Description**

This function computes the no assumption bounds on the average treatment effect among always-observed pairs (ATOP) when some of the outcome data are missing. The confidence intervals for the ATOP are also computed.

**Usage**

ATOPnoassumption(Ya, Yb, Ra, Rb, Ta, Tb, l, u, alpha, rep)
Arguments

Ya A vector of the outcomes of the first unit in the matched pairs. The missing values for Ya should be coded as NA.
Yb A vector of the outcomes of the second unit in the matched pairs. The missing values for Yb should be coded as NA.
Ra A vector of the missing data indicators of the first unit in the matched pairs.
Rb A vector of the missing data indicators of the second unit in the matched pairs.
Ta A vector of the treatment conditions of the first unit in the matched pairs.
Tb A vector of the treatment conditions of the second unit in the matched pairs.
l The lower limit of the outcome.
u The upper limit of the outcome.
alpha A positive scalar that is less than or equal to 0.5. This will determine the (1-alpha) level of confidence intervals. The default is 0.05.
rep The number of repetitions for bootstrapping.

Details

For the details of the method implemented by this function, see the references.

Value

A list of class ATOPnoassumption which contains the following items:

LB The lower bound for the ATOP.
UB The upper bound for the ATOP.
LB.CI The lower limit of the confidence interval for the ATOP.
UB.CI The upper limit of the confidence interval for the ATOP.

Author(s)

Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Edu>, https://imai.fas.harvard.edu; Zhichao Jiang, Department of Politics, Princeton University <zhichaoj@princeton.edu>.

References


Examples

data(seguro)
attach(seguro)
ATOPnoassumption(Ya,Yb,Ra,Rb,Ta,Tb,l=0,u=1,alpha=0.05,rep=100)
Description

This function computes the bounds on the average treatment effect among always-observed pairs (ATOP) with pre-specified sensitivity parameters when some of the outcome data are missing. The sensitivity parameters characterizes the degree of the within-pair similarity and the dependence between the potential missing indicators and the treatment. The confidence intervals for the ATOP are also computed.

Usage

\texttt{ATOPobs(Ya, Yb, Ra, Rb, Ta, Tb, gamma, kappa1, kappa0, l, u, alpha, rep)}

Arguments

- \texttt{Ya}: A vector of the outcomes of the first unit in the matched pairs. The missing values for \texttt{Ya} should be coded as \texttt{NA}.
- \texttt{Yb}: A vector of the outcomes of the second unit in the matched pairs. The missing values for \texttt{Yb} should be coded as \texttt{NA}.
- \texttt{Ra}: A vector of the missing data indicators of the first unit in the matched pairs.
- \texttt{Rb}: A vector of the missing data indicators of the second unit in the matched pairs.
- \texttt{Ta}: A vector of the treatment conditions of the first unit in the matched pairs.
- \texttt{Tb}: A vector of the treatment conditions of the second unit in the matched pairs.
- \texttt{gamma}: The sensitivity parameter which characterizes the degree of the within-pair similarity.
- \texttt{kappa1}: The sensitivity parameter which characterizes the dependence between \texttt{R}(1) and \texttt{T}.
- \texttt{kappa0}: The sensitivity parameter which characterizes the dependence between \texttt{R}(0) and \texttt{T}.
- \texttt{l}: The lower limit of the outcome.
- \texttt{u}: The upper limit of the outcome.
- \texttt{alpha}: A positive scalar that is less than or equal to 0.5. This will determine the (1-\texttt{alpha}) level of confidence intervals. The default is 0.05.
- \texttt{rep}: The number of repetitions for bootstrapping.

Details

For the details of the method implemented by this function, see the references.
Value

A list of class ATOPsens which contains the following items:

- **LB**: The lower bound for the ATOP.
- **UB**: The upper bound for the ATOP.
- **LB.CI**: The lower limit of the confidence interval for the ATOP.
- **UB.CI**: The upper limit of the confidence interval for the ATOP.

Author(s)

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References


Examples

```r
data(seguro)
attach(seguro)
ATOPsens(Ya,Yb,Ra,Rb,Ta,Tb,gamma=0.95,l=0,u=1,alpha=0.05,rep=100)
```

Description

This function computes the bounds on the average treatment effect among always-observed pairs (ATOP) with pre-specified sensitivity parameters when some of the outcome data are missing. The sensitivity parameter characterizes the degree of the within-pair similarity. The confidence intervals for the ATOP are also computed.

Usage

```r
ATOPsens(Ya, Yb, Ra, Rb, Ta, Tb, gamma, l, u, alpha, rep)
```
Arguments

Ya  A vector of the outcomes of the first unit in the matched pairs. The missing values for Ya should be coded as NA.
Yb  A vector of the outcomes of the second unit in the matched pairs. The missing values for Yb should be coded as NA.
Ra  A vector of the missing data indicators of the first unit in the matched pairs.
Rb  A vector of the missing data indicators of the second unit in the matched pairs.
Ta  A vector of the treatment conditions of the first unit in the matched pairs.
Tb  A vector of the treatment conditions of the second unit in the matched pairs.
gamma  The sensitivity parameter which characterizes the degree of the within-pair similarity.
l  The lower limit of the outcome.
u  The upper limit of the outcome.
alpha  A positive scalar that is less than or equal to 0.5. This will determine the (1-alpha) level of confidence intervals. The default is 0.05.
rep  The number of repetitions for bootstrapping.

Details

For the details of the method implemented by this function, see the references.

Value

A list of class ATOPsens which contains the following items:

LB  The lower bound for the ATOP.
UB  The upper bound for the ATOP.
LB.CI  The lower limit of the confidence interval for the ATOP.
UB.CI  The upper limit of the confidence interval for the ATOP.

Author(s)

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References


Examples

data(seguro)
attach(seguro)
ATOPobs(Ya,Yb,Ra,Rb,Ta,Tb,gamma=0.95,kappa1=1,kappa0=1,l=0,u=1,alpha=0.05,rep=100)
AUPEC

Estimation of the unnormalized Area Under Prescription Evaluation Curve (AUPEC) in Completely Randomized Experiments

Description

This function estimates AUPEC. The details of the methods for this design are given in Imai and Li (2019).

Usage

AUPEC(T, tau, Y)

Arguments

T The unit-level binary treatment receipt variable.

tau The unit-level continuous score for treatment assignment. We assume those that have tau<0 should not have treatment. Conditional Average Treatment Effect is one possible measure.

Y The outcome variable of interest.

Value

A list that contains the following items:

aupec The estimated Area Under Prescription Evaluation Curve

sd The estimated standard deviation of AUPEC.

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, http://mlli.mit.edu;

References

Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

Description

This function estimates various complier average causal effect in cluster-randomized experiments without using pre-treatment covariates when unit-level noncompliance exists. Both the encouragement and treatment variables are assumed to be binary. Currently, only the matched-pair design is allowed. The details of the methods for this design are given in Imai, King, and Nall (2007).

Usage

```r
CACEcluster( 
  Y, 
  D, 
  Z, 
  grp, 
  data = parent.frame(), 
  match = NULL, 
  weights = NULL, 
  ...
)
```

Arguments

- **Y**: The outcome variable of interest.
- **D**: The unit-level treatment receipt variable. This variable should be binary but can differ across units within each cluster.
- **Z**: The (randomized) cluster-level encouragement variable. This variable should be binary. Two units in the same cluster should have the same value.
- **grp**: A variable indicating clusters of units. Two units in the same cluster should have the same value.
- **data**: A data frame containing the relevant variables.
- **match**: A variable indicating matched-pairs of clusters. Two units in the same matched-pair of clusters should have the same value. The default is NULL (i.e., no matching).
- **weights**: A variable indicating the population cluster sizes, which will be used to construct weights for each pair of clusters. Two units in the same cluster should have the same value. The default is NULL, in which case sample cluster sizes will be used for constructing weights.
- **...**: Optional arguments passed to ATEcluster, which is called internally.
Value

A list of class `CACEcluster` which contains the following items:

- `call`: The matched call.
- `ITTY`: The output object from `ATEcluster` which is used to estimate the ITT effect of the encouragement on the outcome variable.
- `ITTD`: The output object from `ATEcluster` which is used to estimate the ITT effect of the encouragement on the treatment receipt variable.
- `n1`: The total number of units in the treatment group.
- `n0`: The total number of units in the control group.
- `Z`: The treatment variable.
- `est`: The estimated complier average causal effect.
- `var`: The estimated variance of the complier average causal effect estimator.
- `cov`: The estimated covariance between two ITT estimator.
- `m`: The number of pairs in the matched-pair design.
- `N1`: The population cluster sizes for the treatment group.
- `N0`: The population cluster sizes for the control group.
- `w`: Pair-specific normalized arithmetic mean weights. These weights sum up to the total number of units in the sample, i.e., n.

Author(s)

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References


Description

This function computes the point estimates and variance estimates of the complier average direct effect (CADE) and the complier average spillover effect (CASE). The estimators calculated using this function are either individual weighted or cluster-weighted. The point estimates and variances of ITT effects are also included.

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`CADErand`  
*Randomization-based method for the complier average direct effect and the complier average spillover effect*
Usage

CADErand(data, individual = 1)

Arguments

data A data frame containing the relevant variables. The names for the variables should be: “Z” for the treatment assignment, “D” for the actual received treatment, “Y” for the outcome, “A” for the treatment assignment mechanism and “id” for the cluster ID. The variable for the cluster ID should be a factor.

individual A binary variable with TRUE for individual-weighted estimators and FALSE for cluster-weighted estimators.

Details

For the details of the method implemented by this function, see the references.

Value

A list of class CADErand and which contains the following items:

CADE1 The point estimate of CADE(1).
CADE0 The point estimate of CADE(0).
CADE1 The point estimate of CASE(1).
CASE0 The point estimate of CASE(0).
var.CADE1 The variance estimate of CADE(1).
var.CADE0 The variance estimate of CADE(0).
var.CASE1 The variance estimate of CASE(1).
var.CASE0 The variance estimate of CASE(0).
DEY1 The point estimate of DEY(1).
DEY0 The point estimate of DEY(0).
DED1 The point estimate of DED(1).
DED0 The point estimate of DED(0).
var.DEY1 The variance estimate of DEY(1).
var.DEY0 The variance estimate of DEY(0).
var.DED1 The variance estimate of DED(1).
var.DED0 The variance estimate of DED(0).
SEY1 The point estimate of SEY(1).
SEY0 The point estimate of SEY(0).
SED1 The point estimate of SED(1).
SED0 The point estimate of SED(0).
var.SEY1 The variance estimate of SEY(1).
var.SEY0 The variance estimate of SEY(0).
var.SED1 The variance estimate of SED(1).
var.SED0 The variance estimate of SED(0).
**Author(s)**

Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Edu>, [https://imai.fas.harvard.edu](https://imai.fas.harvard.edu); Zhichao Jiang, Department of Politics, Princeton University <zhichaoj@princeton.edu>.

**References**


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**CADEreg**

*Regression-based method for the complier average direct effect*

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**Description**

This function computes the point estimates of the complier average direct effect (CADE) and four different variance estimates: the HC2 variance, the cluster-robust variance, the cluster-robust HC2 variance and the variance proposed in the reference. The estimators calculated using this function are cluster-weighted, i.e., the weights are equal for each cluster. To obtain the individual-weighted estimators, please multiply the received treatment and the outcome by \( n_j J/N \), where \( n_j \) is the number of individuals in cluster \( j \), \( J \) is the number of clusters and \( N \) is the total number of individuals.

**Usage**

CADEreg(data)

**Arguments**

- **data**: A data frame containing the relevant variables. The names for the variables should be: “Z” for the treatment assignment, “D” for the actual received treatment, “Y” for the outcome, “A” for the treatment assignment mechanism and “id” for the cluster ID. The variable for the cluster id should be a factor.

**Details**

For the details of the method implemented by this function, see the references.

**Value**

A list of class CADEreg which contains the following items:

- **CADE1**: The point estimate of CADE(1).
- **CADE0**: The point estimate of CADE(0).
- **var1.clu**: The cluster-robust variance of CADE(1).
- **var0.clu**: The cluster-robust variance of CADE(0).
NoncompLI

var1.clu.hc2 The cluster-robust HC2 variance of CADE(1).
var0.clu.hc2 The cluster-robust HC2 variance of CADE(0).
var1.hc2 The HC2 variance of CADE(1).
var0.hc2 The HC2 variance of CADE(0).
var1.ind The individual-robust variance of CADE(1).
var0.ind The individual-robust variance of CADE(0).
var1.reg The proposed variance of CADE(1).
var0.reg The proposed variance of CADE(0).

Author(s)
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References

NoncompLI Bayesian Analysis of Randomized Experiments with Noncompliance and Missing Outcomes Under the Assumption of Latent Ignorability

Description
This function estimates the average causal effects for randomized experiments with noncompliance and missing outcomes under the assumption of latent ignorability (Frangakis and Rubin, 1999). The models are based on Bayesian generalized linear models and are fitted using the Markov chain Monte Carlo algorithms. Various types of the outcome variables can be analyzed to estimate the Intention-to-Treat effect and Complier Average Causal Effect.

Usage
NoncompLI(
  formulae,
  Z,
  D,
  data = parent.frame(),
  n.draws = 5000,
  param = TRUE,
  in.sample = FALSE,
  model.c = "probit",
  model.o = "probit",
)
model.r = "probit",
tune.c = 0.01,
tune.o = 0.01,
tune.r = 0.01,
tune.v = 0.01,
p.mean.c = 0,
p.mean.o = 0,
p.mean.r = 0,
p.prec.c = 0.001,
p.prec.o = 0.001,
p.prec.r = 0.001,
p.df.o = 10,
p.scale.o = 1,
p.shape.o = 1,
mda.probit = TRUE,
coef.start.c = 0,
coef.start.o = 0,
tau.start.o = NULL,
coef.start.r = 0,
var.start.o = 1,
burnin = 0,
thin = 0,
verbose = TRUE
}

Arguments

formulae A list of formulae where the first formula specifies the (pre-treatment) covariates in the outcome model (the latent compliance covariate will be added automatically), the second formula specifies the compliance model, and the third formula defines the covariate specification for the model for missing-data mechanism (the latent compliance covariate will be added automatically). For the outcome model, the formula should take the two-sided standard R formula where the outcome variable is specified in the left hand side of the formula which is then separated by ~ from the covariate equation in the right hand side, e.g., y ~ x1 + x2. For the compliance and missing-data mechanism models, the one-sided formula should be used where the left hand side is left unspecified, e.g., ~ x1 + x2.

Z A randomized encouragement variable, which should be a binary variable in the specified data frame.

D A treatment variable, which should be a binary variable in the specified data frame.

data A data frame which contains the variables that appear in the model formulae (formulae), the encouragement variable (Z), and the treatment variable (D).

n.draws The number of MCMC draws. The default is 5000.

param A logical variable indicating whether the Monte Carlo draws of the model parameters should be saved in the output object. The default is TRUE.
in.sample
A logical variable indicating whether or not the sample average causal effect should be calculated using the observed potential outcome for each unit. If it is set to FALSE, then the population average causal effect will be calculated. The default is FALSE.

model.c
The model for compliance. Either logit or probit model is allowed. The default is probit.

model.o
The model for outcome. The following five models are allowed: logit, probit, oprobit (ordered probit regression), gaussian (gaussian regression), negbin (negative binomial regression), and twopart (two part model where the first part is the probit regression for $Pr(Y > 0|X)$ and the second part models $p(log(Y)|X, Y > 0)$ using the gaussian regression). The default is probit.

model.r
The model for (non)response. Either logit or probit model is allowed. The default is probit.

tune.c
Tuning constants for fitting the compliance model. These positive constants are used to tune the (random-walk) Metropolis-Hastings algorithm to fit the logit model. Use either a scalar or a vector of constants whose length equals that of the coefficient vector. The default is 0.01.

tune.o
Tuning constants for fitting the outcome model. These positive constants are used to tune the (random-walk) Metropolis-Hastings algorithm to fit logit, ordered probit, and negative binomial models. Use either a scalar or a vector of constants whose length equals that of the coefficient vector for logit and negative binomial models. For the ordered probit model, use either a scalar or a vector of constants whose length equals that of cut-point parameters to be estimated. The default is 0.01.

tune.r
Tuning constants for fitting the (non)response model. These positive constants are used to tune the (random-walk) Metropolis-Hastings algorithm to fit the logit model. Use either a scalar or a vector of constants whose length equals that of the coefficient vector. The default is 0.01.

tune.v
A scalar tuning constant for fitting the variance component of the negative binomial (outcome) model. The default is 0.01.

p.mean.c
Prior mean for the compliance model. It should be either a scalar or a vector of appropriate length. The default is 0.

p.mean.o
Prior mean for the outcome model. It should be either a scalar or a vector of appropriate length. The default is 0.

p.mean.r
Prior mean for the (non)response model. It should be either a scalar or a vector of appropriate length. The default is 0.

p.prec.c
Prior precision for the compliance model. It should be either a positive scalar or a positive semi-definite matrix of appropriate size. The default is 0.001.

p.prec.o
Prior precision for the outcome model. It should be either a positive scalar or a positive semi-definite matrix of appropriate size. The default is 0.001.

p.prec.r
Prior precision for the (non)response model. It should be either a positive scalar or a positive semi-definite matrix of appropriate size. The default is 0.001.

p.df.o
A positive integer. Prior degrees of freedom parameter for the inverse chisquare distribution in the gaussian and twopart (outcome) models. The default is 10.
NoncompLI

p.scale.o  A positive scalar. Prior scale parameter for the inverse chisquare distribution (for
the variance) in the gaussian and twopart (outcome) models. For the negative
binomial (outcome) model, this is used for the scale parameter of the inverse
gamma distribution. The default is 1.

p.shape.o  A positive scalar. Prior shape for the inverse chisquare distribution in the nega-
tive binomial (outcome) model. The default is 1.

mda.probit  A logical variable indicating whether to use marginal data augmentation for pro-
bit models. The default is TRUE.

coef.start.c  Starting values for coefficients of the compliance model. It should be either a
scalar or a vector of appropriate length. The default is 0.

coef.start.o  Starting values for coefficients of the outcome model. It should be either a scalar
or a vector of appropriate length. The default is 0.

tau.start.o  Starting values for thresholds of the ordered probit (outcome) model. If it is
set to NULL, then the starting values will be a sequence starting from 0 and then
incrementing by 0.1. The default is NULL.

coef.start.r  Starting values for coefficients of the (non)response model. It should be either a
scalar or a vector of appropriate length. The default is 0.

var.start.o  A positive scalar starting value for the variance of the gaussian, negative bino-
mial, and twopart (outcome) models. The default is 1.

burnin  The number of initial burnins for the Markov chain. The default is 0.

thin  The size of thinning interval for the Markov chain. The default is 0.

verbose  A logical variable indicating whether additional progress reports should be pr-
ited while running the code. The default is TRUE.

Details
For the details of the model being fitted, see the references. Note that when always-takers exist
we fit either two logistic or two probit models by first modeling whether a unit is a complier or a
noncomplier, and then modeling whether a unit is an always-taker or a never-taker for those who
are classified as non-compliers.

Value
An object of class NoncompLI which contains the following elements as a list:

call  The matched call.
Y  The outcome variable.
D  The treatment variable.
Z  The (randomized) encouragement variable.
R  The response indicator variable for Y.
A  The indicator variable for (known) always-takers, i.e., the control units who
received the treatment.
C  The indicator variable for (known) compliers, i.e., the encouraged units who
received the treatment when there is no always-takers.
The matrix of covariates used for the outcome model.

The matrix of covariates used for the compliance model.

The matrix of covariates used for the (non)response model.

The number of MCMC draws.

The Monte carlo draws of quantities of interest from their posterior distributions. Quantities of interest include ITT (intention-to-treat) effect, CACE (complier average causal effect), Y\(\bar{\text{r}}\)C (The mean outcome value under the treatment for compliers), Y\(\bar{\theta}\)barC (The mean outcome value under the control for compliers), Y\(\bar{\text{r}}\)barN (The mean outcome value for never-takers), Y\(\bar{\text{r}}\)barA (The mean outcome value for always-takers), p\(\bar{\text{C}}\) (The proportion of compliers), p\(\bar{\text{N}}\) (The proportion of never-takers), p\(\bar{\text{A}}\) (The proportion of always-takers)

If param is set to TRUE, the following elements are also included:

The Monte carlo draws of coefficients of the outcome model from their posterior distribution.

If model = "twopart", this element contains the Monte carlo draws of coefficients of the outcome model for \(p(\log(Y)|X, Y > 0)\) from their posterior distribution.

The Monte carlo draws of coefficients of the compliance model from their posterior distribution.

If always-takers exist, then this element contains the Monte carlo draws of coefficients of the compliance model for always-takers from their posterior distribution.

The Monte carlo draws of coefficients of the (non)response model from their posterior distribution.

The Monte carlo draws of the variance parameter for the gaussian, negative binomial, and twopart (outcome) models.

Author(s)
Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Ed>, https://imai.fas.harvard.edu;

References


### Description

This function estimates the Population Average Prescription Difference with a budget constraint. The details of the methods for this design are given in Imai and Li (2019).

### Usage

\[ \text{PAPD}(T, \text{Thatfp}, \text{Thatgp}, Y, \text{plim}) \]

### Arguments

- **T**: The unit-level binary treatment receipt variable.
- **Thatfp**: The unit-level binary treatment that would have been assigned by the first individualized treatment rule.
- **Thatgp**: The unit-level binary treatment that would have been assigned by the second individualized treatment rule.
- **Y**: The outcome variable of interest.
- **plim**: The maximum percentage of population that can be treated under the budget constraint. Should be a decimal between 0 and 1.

### Value

A list that contains the following items:

- **papd**: The estimated Population Average Prescription Difference
- **sd**: The estimated standard deviation of PAPD.

### Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>, [http://mlli.mit.edu](http://mlli.mit.edu);

### References

Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

Estimation of the Population Average Prescription Effect in Completely Randomized Experiments

Description

This function estimates the Population Average Prescription Effect with and without a budget constraint. The details of the methods for this design are given in Imai and Li (2019).

Usage

\text{PAPE}(T, \text{That}, Y, \text{plim} = \text{NA})

Arguments

- \text{T} \quad \text{The unit-level binary treatment receipt variable.}
- \text{That} \quad \text{The unit-level binary treatment that would have been assigned by the individualized treatment rule.}
- \text{Y} \quad \text{The outcome variable of interest.}
- \text{plim} \quad \text{The maximum percentage of population that can be treated under the budget constraint. Should be a decimal between 0 and 1. Default is NA which assumes no budget constraint.}

Value

A list that contains the following items:

- pape \quad \text{The estimated Population Average Prescription Effect.}
- sd \quad \text{The estimated standard deviation of PAPE.}

Author(s)

Michael Lingzhi Li, Operations Research Center, Massachusetts Institute of Technology <mlli@mit.edu>,
http://mlli.mit.edu;

References

Imai and Li (2019). “Experimental Evaluation of Individualized Treatment Rules”,

This function can be used to randomize the treatment assignment for randomized experiments. In addition to the complete randomization, it implements randomized-block and matched-pair designs.

**Usage**

```r
call = randomize(data, group = c("Treat", "Control"), ratio = NULL, indx = NULL, block = NULL, n.block = NULL, match = NULL, complete = TRUE)
```

**Arguments**

data: A data frame containing the observations to which the treatments are randomly assigned.
group: A numerical or character vector indicating the treatment/control groups. The length of the vector equals the total number of such groups. The default specifies two groups called “Treat” and “Control”.
ratio: An optional numerical vector which specifies the proportion of the treatment/control groups within the sample. The length of the vector should equal the number of groups. The default is the equal allocation.
indx: An optional variable name in the data frame to be used as the names of the observations. If not specified, the row names of the data frame will be used so long as they are available. If the row names are not available, the integer sequence starting from 1 will be used.
block: An optional variable name in the data frame or a formula to be used as the blocking variables for randomized-block designs. If a variable name is specified, then the unique values of that variable will form blocks unless n.block is specified (see below). If a formula is specified, it will be evaluated using data and then blocking will be based on the mahalanobis distance of the resulting model matrix. In this case, users may want to specify n.block to avoid creating blocks that have too few observations.
n.block: An optional scalar specifying the number of blocks to be created for randomized block designs. If unspecified, the unique values of the blocking variable will define blocks. If specified, the blocks of roughly equal size will be created based on the quantile of the blocking variable.
match

An optional variable name in the data frame or a formula to be used as the matching variables for matched-pair designs. This input is applicable only to the case where there are two groups. Pairs of observations will be formed based on the similar values of the matching variable. If a formula is specified, the mahalanobis distance of the resulting model matrix will be used.

complete

logical. If it equals TRUE (default), then complete randomization will be performed (within each block if randomized block designs are used). Otherwise, simple randomization will be implemented. For matched-pair designs, complete has to equal TRUE.

Details

Randomized-block designs refer to the complete randomization of the treatment within the pre-specified blocks which contain multiple observations. Matched-pair designs refer to the randomization of the binary treatment variable within the pre-specified pair of observations.

Value

A list of class randomize which contains the following items:

call

the matched call.
treatment

The vector of randomized treatments.
data

The data frame that was used to conduct the randomization.
block

The blocking variable that was used to implement randomized-block designs.
match

The matching variable that was used to implement matched-pair designs.
block.id

The variable indicating which observations belong to which blocks in randomized-block designs.
match.id

The variable indicating which observations belong to which pairs in matched-pair designs.

Author(s)

Kosuke Imai, Department of Government and Department of Statistics, Harvard University <imai@Harvard.Edu>, https://imai.fas.harvard.edu;

seguro

Data from the Mexican universal health insurance program, Seguro Popular.

Description

This data set contains the outcome, missing indicator and the treatment for the application in Kosuke Imai and Zhichao Jiang (2018).

Usage

seguro
Format

A data frame with 14,902 rows and 6 variables:

- Ya: Satisfaction for the first unit in the matched pairs
- Yb: Satisfaction for the second unit in the matched pairs
- Ra: Missing indicator for the first unit in the matched pairs
- Rb: Missing indicator for the second unit in the matched pairs
- Ta: Treatment assignment for the first unit in the matched pairs
- Tb: Treatment assignment for the second unit in the matched pairs

Examples

```r
data(seguro)
```
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