

Package ‘eefAnalytics’

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Title Analysing Education Trials

Description Provides tools for analysing education trials. Making different methods accessible in a single place is essential for sensitivity analysis of education trials, particularly the implication of the different methods in analysing simple randomised trials, cluster randomised trials and multisite trials.

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R topics documented:

caceCRTBoot	2
caceMSTBoot	3
caceSRTBoot	5
ComparePlot	6
crtData	7
crtFREQ	8
mlmBayes	10
mstData	12
mstFREQ	12
plot.eefAnalytics	14
srtFREQ	18

Index	21
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caceCRTBoot	<i>Complier Average Causal Effect (CACE) Analysis of Cluster Randomised Education Trials using Multilevel Model.</i>
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Description

caceCRTBoot performs exploratory CACE analysis of cluster randomised education trials.

Usage

```
caceCRTBoot(formula, random, intervention, compliance, nBoot, data)
```

Arguments

formula	the model to be analysed. It is of the form $y \sim x_1 + x_2 + \dots$. Where y is the outcome variable and X s are the predictors.
random	a string variable specifying the "clustering variable" as contained in the data. See example below
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
compliance	a string variable specifying the "compliance variable" as contained in the data. The data must be in percentages ranging from 0 - 100.
nBoot	number of bootstraps required to generate bootstrap confidence interval. Default is NULL.
data	data frame containing the data to be analysed.

Value

S3 object; a list consisting of

- CACE. Estimates of CACE adjusted effect sizes based on pre-specified thresholds. Only produced for threshold with at least 50
- Compliers. Percentage of pupils that achieved a pre-specified threshold of compliance.

Examples

```
if(interactive()){

data(crtData)

##### weighted ITT #####
caceOutput<- caceCRTBoot(Posttest~ Prettest+ Intervention,
random="School",intervention="Intervention",
compliance = "Percentage_Attendance",nBoot=1000,data=crtData)

cace <- caceOutput$CACE
cace
```

```
Complier <- caceOutput$Compliers
Complier

### visualising CACE effect size

plot(caceOutput)
}
```

caceMSTBoot

CACE Analysis of Multisite Randomised Education Trials.

Description

caceMSTBoot performs exploratory CACE analysis of multisite randomised education trials.

Usage

```
caceMSTBoot(formula, random, intervention, compliance, nBoot, data)
```

Arguments

formula	the model to be analysed. It is of the form $y \sim x_1+x_2+\dots$. Where y is the outcome variable and X s are the predictors.
random	a string variable specifying the "clustering variable" as contained in the data. See example below
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
compliance	a string variable specifying the "compliance variable" as contained in the data. The data must be in percentages ranging from 0 - 100.
nBoot	number of bootstraps required to generate bootstrap confidence interval. Default is NULL.
data	data frame containing the data to be analysed.

Value

S3 object; a list consisting of

- CACE. Estimates of CACE adjusted effect sizes based on pre-specified thresholds. Only produced for threshold with at least 50
- Compliers. Percentage of pupils that achieved a pre-specified threshold of compliance.

Examples

```

if(interactive()){

data(mstData)

#####
## MLM analysis of multisite trials + 1.96SE ##
#####

output1 <- mstFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",data=mstData)

### Fixed effects
beta <- output1$Beta
beta

### Effect size
ES1 <- output1$ES
ES1

## Covariance matrix
covParm <- output1$covParm
covParm

### plot random effects for schools

plot(output1)

#####
## MLM analysis of multisite trials      ##
## with bootstrap confidence intervals    ##
#####

output2 <- mstFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",nBoot=1000,data=mstData)

tp <- output2$Bootstrap
### Effect size

ES2 <- output2$ES
ES2

### plot bootstrapped values

plot(output2, group=1)

#####
## MLM analysis of mutltisite trials with permutation p-value##
#####

output3 <- mstFREQ(Posttest~ Intervention+Prettest,random="School",

```

```

intervention="Intervention",nPerm=1000,data=mstData)

ES3 <- output3$ES
ES3

#### plot permutated values

plot(output3, group=1)
}

```

caceSRTBoot

CACE Analysis of Simple Randomised Education Trials.

Description

caceSRTBoot performs exploraty CACE analysis of simple randomised education trials.

Usage

```
caceSRTBoot(formula, intervention, compliance, nBoot, data)
```

Arguments

formula	the model to be analysed. It is of the form $y \sim x_1+x_2+\dots$. Where y is the outcome variable and Xs are the predictors.
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
compliance	a string variable specifying the "compliance variable" as contained in the data. The data must be in percentages ranging from 0 - 100.
nBoot	number of non-parametric bootstraps. Default is NULL.
data	data frame containing the data to be analysed.

Value

S3 mcpi object; a list consisting of

- CACE. Estimates of CACE adjusted effect sizes based on pre-specified thresholds. Only produced for threshold with atleast 50
- Compliers Percentage of pupils that achieved a pre-specified threshold of compliance.

Examples

```

if(interactive()){

data(mstData)
##### weighted ITT #####
caceOutput3<- caceSRTBoot(Posttest~ Prettest+ Intervention,
intervention="Intervention",

```

```

compliance = "Percentage_Attendance", nBoot=1000, data=mstData)

cace <- caceOutput3$CACE
cace

Complier <- caceOutput3$Compliers
Complier

### visualising CACE effect size

plot(caceOutput3)
}

```

ComparePlot

A plot function to compare diferent eefAnalytics S3 objects from the eefAnalytics package.

Description

A forest plot comparing the different eefAnalytics results.

Usage

```
ComparePlot(eefAnalyticsList, group = NULL, modelNames = NULL)
```

Arguments

eefAnalyticsList	A list of eefAnalytics S3 objects from eefAnalytics package.
group	a value indicating which intervention to plot. This must not be greater than the number of intervention excluding the control group. For a two arm trial, the maximum value is 1 and a maximum value of 2 for three arm trial.
modelNames	a string factor containing the names of model to compare

Details

ComparePlot produces a forest plot which compares the effect size and the associated confidence interval from the different model. For a multilevel model, it shows effect size based on residual variance and total variance.

Value

Returns a forest plot to compare the different models

Examples

```

if(interactive()){

data(mstData)
#####
##### SRT #####
#####

outputSRT <- srtFREQ(Posttest~ Intervention + Prettest,
                    intervention = "Intervention", data = mstData)

outputSRTBoot <- srtFREQ(Posttest~ Intervention + Prettest,
                       intervention = "Intervention",nBoot=1000, data = mstData)

#####
##### MST #####
#####

outputMST <- mstFREQ(Posttest~ Intervention + Prettest,
                    random = "School", intervention = "Intervention", data = mstData)

outputMSTBoot <- mstFREQ(Posttest~ Intervention + Prettest,
                        random = "School", intervention = "Intervention",
                        nBoot = 1000, data = mstData)

#####
##### Bayesian #####
#####

outputMSTbayes <- mlmBayes(Posttest~ Intervention + Prettest,
                          random = "School", intervention = "Intervention",
                          nSim = 10000, data = mstData)

## comparing different results

ComparePlot(list(outputSRT,outputSRTBoot,outputMST,outputMSTBoot,outputMSTbayes),
            modelNames =c("ols", "olsBoot","MLM","MLMBoot","MLMbayes"),group=1)

}

```

crtData

*Cluster randomised trial data.***Description**

A cluster randomised trial dataset containing 22 schools.

Format

A data frame with 265 rows and 5 variables

Details

- Posttest. posttest scores
- Prettest. prettest scores
- Intervention. indicator for intervention groups
- Intervention2. a simulated indicator for intervention groups three arm trial coded as 1 for intervention group and 0 for control group.
- Compliance. percentage of sessions attended by pupils
- School. numeric school identifier

crtFREQ	<i>Analysis of Cluster Randomised Education Trials using Multilevel Model.</i>
---------	--

Description

crtFREQ performs Analysis of cluster randomised education trial using multilevel model under the frequentist framework.

Usage

```
crtFREQ(formula, random, intervention, nPerm = NULL, nBoot = NULL, data)
```

Arguments

formula	the model to be analysed. It is of the form $y \sim x_1 + x_2 + \dots$. Where y is the outcome variable and X_s are the predictors.
random	a string variable specifying the "clustering variable" as contained in the data. See example below
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
nPerm	number of permutations required to generate permuted p-value. Default is NULL.
nBoot	number of bootstraps required to generate bootstrap confidence interval. Default is NULL.
data	data frame containing the data to be analysed.

Value

S3 object; a list consisting of

- Beta. Estimates and confidence intervals for predictors specified in the model.
- ES. Hedges' g effect size for the intervention(s). If nBoot is not specified, the confidence intervals are 95
- covParm. Vector of variance decomposition into between cluster variance (Schools) and within cluster variance (Pupils). It also contains the intral-cluster correlation (ICC).
- SchEffects. Random intercepts for clusters, e.g schools.
- Perm. A "nPerm x w" matrix containing permuted effect sizes using residual variance and total variance. "w" denotes number of intervention. "w=1" for two arm trial and "w=2" for three arm trial excluding the control group. It is produced only when nPerm is specified.
- Bootstrap. A "w x nBoot" matrix containing the bootstrapped effect sizes using residual variance (Within) and total variance (Total). "w=1" for two arm trial and "w=2" for three arm trial excluding the control group. It is only produced when nBoot is specified.

Examples

```

if(interactive()){

data(crtData)

#####
## MLM analysis of cluster randomised trials + 1.96SE ##
#####

output1 <- crtFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",data=crtData)

### Fixed effects
beta <- output1$Beta
beta

### Effect size
ES1 <- output1$ES
ES1

## Covariance matrix
covParm <- output1$covParm
covParm

### plot random effects for schools

plot(output1)

#####
## MLM analysis of cluster randomised trials ##
## with bootstrap confidence intervals ##
#####

```

```

output2 <- crtFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",nBoot=1000,data=crtData)

### Effect size

ES2 <- output2$ES
ES2

### plot bootstrapped values

plot(output2, group=1)

#####
## MLM analysis of cluster randomised trials with permutation p-value##
#####

output3 <- crtFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",nPerm=1000,data=crtData)

### Effect size

ES3 <- output3$ES
ES3

### plot permutated values

plot(output3, group=1)
}

```

mlmBayes

Bayesia multilevel analysis of randomised educatuon trials using vague priors.

Description

mlmBayes performs analysis of randomised education trials using multilevel model under Bayesian framework assuming vague priors.

Usage

```
mlmBayes(formula, random, intervention, nSim, data)
```

Arguments

formula the model to be analysed. It is of the form $y \sim x_1+x_2+\dots$. Where y is the outcome variable and X_s are the predictors.

random	a string variable specifying the "clustering variable" as contained in the data. See example below
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
nSim	number of MCMC iterations. A minimum of 10,000 is recommended.
data	data frame containing the data to be analysed.

Value

S3 object; a list consisting of

- Beta. Estimates and confidence intervals for predictors specified in the model.
- ES. Hedges' g effect size for the intervention(s). If nBoot is not specified, the confidence intervals are 95
- covParm. Vector of variance decomposition into between cluster variance (Schools) and within cluster variance (Pupils). It also contains the intral-cluster correlation (ICC).
- SchEffects. Random intercepts for clusters, e.g schools.
- ProbES. A matrix containing the probability of observing effect size greater than a pre-specified threshold.

Examples

```
if(interactive()){
  data(crtData)

#####
## Bayesian analysis of cluster randomised trials ##
#####

output <- mlmBayes(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",nSim=10000,data=crtData)

### Fixed effects
beta <- output$Beta
beta

### Effect size
ES1 <- output$ES
ES1

## Covariance matrix
covParm <- output$covParm
covParm

### plot random effects for schools

plot(output)
```

```
### plot posterior probability of an effect size to be bigger than a pre-specified threshold
plot(output,group=1)
}
```

mstData	<i>Multisite trial data.</i>
---------	------------------------------

Description

A multisite trial dataset containing 54 schools.

Format

A data frame with 210 rows and 5 variables

Details

- Posttest. posttest scores
- Prettest. prettest scores
- Intervention. indicator for intervention groups in two arm trial
- Intervention2. a simulated indicator for intervention groups three arm trial
- Compliance. percentage of sessions attended by pupils coded as 1 for intervention group and 0 for control group.
- Compliance. percentage of sessions attended by pupils
- School. numeric school identifier

mstFREQ	<i>Analysis of Multisite Randomised Education Trials using Multilevel Model.</i>
---------	--

Description

mstFREQ performs analysis of multisite randomised education trial using multilevel model within the frequentist framework.

Usage

```
mstFREQ(formula, random, intervention, nPerm = NULL, data, nBoot = NULL)
```

Arguments

formula	the model to be analysed. It is of the form $y \sim x_1+x_2+\dots$. Where y is the outcome variable and X_s are the predictors.
random	a string variable specifying the "clustering variable" as contained in the data. See example below
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
nPerm	number of permutations required to generate permuted p-value. Default is NULL.
data	data frame containing the data to be analysed.
nBoot	number of bootstraps required to generate bootstrap confidence interval. Default is NULL.

Value

S3 object; a list consisting of

- Beta. Estimates and confidence intervals for predictors specified in the model.
- ES. Hedges' g effect size for the intervention(s). If nBoot is not specified, the confidence intervals are 95
- covParm. Vector of variance decomposition into between cluster variance (Schools), clustering by intervention interaction (Intervention:School) and within cluster variance (Pupils). It also contains the intral-cluster correlation (ICC).
- SchEffects. Random intercepts for clusters, e.g schools.
- Perm. A "nPerm x w" matrix containing permuted effect sizes using residual variance and total variance. "w" denotes number of intervention. "w=1" for two arm trial and "w=2" for three arm trial excluding the control group. It is produced only when nPerm is specified.
- Bootstrap. A "w x nBoot" matrix containing the bootstrapped effect sizes using residual variance (Within) and total variance (Total). "w=1" for two arm trial and "w=2" for three arm trial excluding the control group. It is only produced when nBoot is specified.

Examples

```
if(interactive()){

data(mstData)

#####
## MLM analysis of multisite trials + 1.96SE ##
#####

output1 <- mstFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",data=mstData)

### Fixed effects
beta <- output1$Beta
```

```

beta

### Effect size
ES1 <- output1$ES
ES1

## Covariance matrix
covParm <- output1$covParm
covParm

### plot random effects for schools

plot(output1)

#####
## MLM analysis of multisite trials      ##
## with bootstrap confidence intervals    ##
#####

output2 <- mstFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",nBoot=1000,data=mstData)

tp <- output2$Bootstrap
### Effect size

ES2 <- output2$ES
ES2

### plot bootstrapped values

plot(output2, group=1)

#####
## MLM analysis of mutltisite trials with permutation p-value##
#####

output3 <- mstFREQ(Posttest~ Intervention+Prettest,random="School",
intervention="Intervention",nPerm=1000,data=mstData)

ES3 <- output3$ES
ES3

#### plot permutated values

plot(output3, group=1)
}

```

Description

plots different figures based on output from eefAnalytics package.

Usage

```
## S3 method for class 'eefAnalytics'
plot(x, group = NULL, ...)
```

Arguments

x	an output object from the eefAnalytics package.
group	a value indicating which intervention to plot. This must not be greater than the number of intervention excluding the control group. For a two arm trial, the maximum value is 1 and a maximum value of 2 for three arm trial.
...	arguments passed to <code>plot.default</code>

Details

Plot produces graphical visualisation depending on which model is fitted:

- For `srtFREQ()`, plot can only be used when `nBoot` or `nPerm` is specified to visualise the distribution of bootstrapped or permuted values.
- For `crtFREQ()` or `mstFREQ`, plot shows the distribution of random intercepts when `group=NULL`. It produces histogram of permuted or bootstrapped values when `group` is specified and either `nBoot` or `nPerm` is also specified.
- For `mlmBayes()`, plot produces the distribution of random intercepts when `group = NULL`. It produces the probability of effect size to be greater than a pre-specified threshold when `group` is specified.
- Lastly, plot produces forest plots to compare CACE estimated for different level of compliance when `caceSRTBoot()` or `caceCRTBoot()` or `caceMSTBoot()` is used.

Value

Returns relevant plots for each model.

Examples

```
if(interactive()){

#### read data
data(mstData)
data(crtData)

#####
##### SRT #####
#####

##### Bootstrapped
```

```

outputSRTBoot <- srtFREQ(Posttest~ Intervention + Prettest,
                        intervention = "Intervention",nBoot=1000, data = mstData)
plot(outputSRTBoot,group=1)

##### Permutation
outputSRTPerm <- srtFREQ(Posttest~ Intervention + Prettest,
                        intervention = "Intervention",nPerm=1000, data = mstData)

plot(outputSRTPerm,group=1)

#####
##### MST #####
#####

#### Random intercepts
outputMST <- mstFREQ(Posttest~ Intervention + Prettest,
                    random = "School", intervention = "Intervention", data = mstData)
plot(outputMST)

#### Bootstrapped
outputMSTBoot <- mstFREQ(Posttest~ Intervention + Prettest,
                        random = "School", intervention = "Intervention",
                        nBoot = 1000, data = mstData)

plot(outputMSTBoot)
plot(outputMSTBoot,group=1)

#### Permutation
outputMSTPerm <- mstFREQ(Posttest~ Intervention + Prettest,
                        random = "School", intervention = "Intervention",
                        nPerm = 1000, data = mstData)

plot(outputMSTPerm)
plot(outputMSTPerm,group=1)

#####
##### Bayesian #####
#####

outputMSTbayes <- mlmBayes(Posttest~ Intervention + Prettest,
                          random = "School", intervention = "Intervention",
                          nSim = 10000, data = mstData)

## Random intercepts
plot(outputMSTbayes)

## Probability of effect size greater than a precified threshold
plot(outputMSTbayes,group=1)

```



```
plot(outputCRTCase)
}
```

srtFREQ	<i>Analysis of Simple Randomised Education Trial using Linear Regression Model.</i>
---------	---

Description

srtFREQ performs analysis of educational trials under the assumption of independent errors among pupils. This can also be used with schools as fixed effects.

Usage

```
srtFREQ(formula, intervention, nBoot = NULL, nPerm = NULL, data)
```

Arguments

formula	the model to be analysed. It is of the form $y \sim x_1 + x_2 + \dots$. Where y is the outcome variable and X_s are the predictors.
intervention	a string variable specifying the "intervention variable" as appeared in the formula. See example below
nBoot	number of bootstraps required to generate bootstrap confidence interval. Default is NULL.
nPerm	number of permutations required to generate permuted p-value. Default is NULL.
data	data frame containing the data to be analysed.

Value

S3 object; a list consisting of

- Beta. Estimates and confidence intervals for the predictors specified in the model.
- ES. Hedges' g effect size for the intervention(s). If nBoot is not specified, the confidence intervals are 95
- sigma2. Residual variance.
- Perm. A vector containing permuted effect sizes under null hypothesis. It is produced only if nPerm is specified.
- Bootstrap. A vector containing bootstrapped effect sizes. It is produced only if nBoot is specified.

Examples

```

if(interactive()){

data(mstData)

#####
## Analysis of simple randomised trials using Hedges Effect Size ##
#####

output1 <- srtFREQ(Posttest~ Intervention+Prettest,
intervention="Intervention",data=mstData )
ES1 <- output1$ES
ES1

#####
## Analysis of simple randomised trials using Hedges Effect Size ##
## with Permutation p-value ##
#####

output2 <- srtFREQ(Posttest~ Intervention+Prettest,
intervention="Intervention",nPerm=1000,data=mstData )

ES2 <- output2$ES
ES2

#### plot permutated values

plot(output2, group=1)

#####
## Analysis of simple randomised trials using Hedges Effect Size ##
## with non-parametric bootstrap confidence intervals ##
#####

output3 <- srtFREQ(Posttest~ Intervention+Prettest,
intervention="Intervention",nBoot=1000,data=mstData)

ES3 <- output3$ES
ES3

### plot bootstrapped values

plot(output3, group=1)

#####
## Analysis of simple randomised trials using Hedges' effect size ##
## with schools as fixed effects ##
#####

```

```

output4 <- srtFREQ(Posttest~ Intervention+Prettest+as.factor(School),
intervention="Intervention",data=mstData )

ES4 <- output4$ES
ES4

#####
## Analysis of simple randomised trials using Hedges' effect size ##
## with schools as fixed effects and with permutation p-value    ##
#####

output5 <- srtFREQ(Posttest~ Intervention+Prettest+as.factor(School),
intervention="Intervention",nPerm=1000,data=mstData )

ES5 <- output5$ES
ES5

#### plot permuted values

plot(output5, group=1)

#####
## Analysis of simple randomised trials using Hedges' effect size ##
## with schools as fixed effects and with permutation p-value    ##
#####

output6 <- srtFREQ(Posttest~ Intervention+Prettest+as.factor(School),
intervention="Intervention",nBoot=1000,data=mstData)

ES6 <- output6$ES
ES6

### plot bootstrapped values

plot(output6, group=1)
}

```

Index

`caceCRTBoot`, [2](#)

`caceMSTBoot`, [3](#)

`caceSRTBoot`, [5](#)

`ComparePlot`, [6](#)

`crtData`, [7](#)

`crtFREQ`, [8](#)

`m1mBayes`, [10](#)

`mstData`, [12](#)

`mstFREQ`, [12](#)

`plot.default`, [15](#)

`plot.eefAnalytics`, [14](#)

`srtFREQ`, [18](#)