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Author Mohammad Sayari [aut, cre], Akansha Singh [aut], Germaine Uwimpuhwe [aut], Jochen Einbeck [aut]
Maintainer Mohammad Sayari <md.sayari13@gmail.com></md.sayari13@gmail.com>
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crt4armSimData

Simulated 4-Arm Cluster Randomized Trial (CRT) Data

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Description

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A simulated cluster randomised trial dataset containing 10 schools and 1,000 pupils. This is a 4-arm trial design with one control group and three intervention groups.

Usage

crt4armSimData

Format

A data frame with 1,000 rows and 7 variables:

pupils Identifier for each pupil

schools Identifier for each school

interventions Treatment assignment coded as 0 for control and 1–3 for intervention groups

pretest Pre-test scores

gender Binary gender

ethnicity A categorical variable with 3 categories

posttest Post-test scores

Source

Simulated

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crtAddIntervention

Add a New Intervention Group to Clustered Randomized Trial (CRT)

Description

This function adds a new intervention group to an existing CRT dataset. It models post-test outcomes using fixed and random effects estimated from the original data and incorporates user-specified effect size and attrition for the new intervention.

Usage

```
crtAddIntervention(
  originalData,
  ns,
  np,
  es,
  attritionrate,
  outcome,
  interventions,
  schoolsID,
  pupilsID,
  continuous_covariates,
  categorical_covariates)
```

Arguments

originalData A data frame containing the variables including outcome, predictors, the clus-

tering variable, and the intervention for CRT design.

ns The number of schools to assign to the new intervention group.

np The number of pupils per new school.

es The standardized effect size for the new intervention group.

attritionrate The proportion of pupils in the new group to drop due to attrition.

outcome A string specifying the name of the column containing outcome variable (e.g.,

post-test scores).

interventions A string specifying the name of the intervention assignment column.

schoolsID A string specifying the name of the school ID column.

pupilsID A string specifying the name of the pupil ID column.

continuous_covariates

A character vector specifying the names of continuous covariates in the model.

categorical_covariates

A character vector specifying the names of categorical covariates in the model (converted to factors).

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Details

The function performs the following:

- Fits a linear mixed-effects model (lmer) to the original dataset using provided covariates.
- Applies the specified effect size (es) and generates new post-test scores.
- Simulates attrition by removing post-test scores at random.

Value

A data.frame combining the original and new intervention group, including post-test outcomes simulated for the new intervention based on the estimated mixed model.

See Also

1mer from the lme4 package

Examples

```
data(crt4armSimData)
new_crt5armData <- crtAddIntervention(originalData = crt4armSimData, ns = 2,
np = 100, es = 0.3, attritionrate = 0.1, outcome = "posttest", interventions = "interventions",
schoolsID = "schools", pupilsID = "pupils",
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"))
head(new_crt5armData)</pre>
```

crtDataSimulation

Simulate Clustered Randomized Trial (CRT) Data

Description

This function simulates a multiple intervention arms CRT data. The model includes intervention and pre-test scores as covariates.

Usage

```
crtDataSimulation(
    ni,
    nstreated,
    np,
    ns,
    sigma,
    ICC,
    B0,
    es,
    seed,
    attritionrates,
    covariates
)
```

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Arguments

ni The number of intervention groups excluding the control group.

nstreated The number of schools in each group, including the control group. It should be

specified as an integer vector of length ni + 1.

np The number of pupils per school.

The total number of schools.

sigma The standard deviation of the individual-level error.

ICC The intra-class correlation coefficient.

B0 The intercept of the model.

es The standardized effect sizes for each intervention group. It should be specified

as a numeric vector.

seed The random seed for reproducibility.

attritionrates The proportion of attrition for each group, including the control group. It should

be specified as a numeric vector of length ni + 1.

covariates List of covariate specifications. Each element should be a list with the following

fields:

name Character. Name of the covariate.

type Character. Either "continuous" or "categorical".

sd Numeric. Standard deviation (only for continuous covariates).

coefficient Numeric. Coefficient (only for continuous covariates).

levels Character vector. Category levels (only for categorical covariates).

probs Numeric vector. Sampling probabilities (must sum to 1) (categorical only).

reference Character. Reference category (categorical only).

coefficients Named list of numeric values. Coefficients for each non-reference level.

Value

A data. frame containing:

pupils Unique pupil ID

schools School ID

interventions Intervention group (0 = control, 1 to ni for interventions)

covariates Simulated covariates

posttest Simulated posttest scores (NA if attrited)

```
covariates <- list(
  list(name = "pretest", type = "continuous", sd = 1, coefficient = 1.7),
  list(name = "gender", type = "categorical", levels = c("Male", "Female"),
  probs = c(0.3, 0.7), reference = "Male", coefficients = list(B = -0.5)),</pre>
```

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```
list(name = "ethnicity", type = "categorical", levels = c("White", "Black", "Asian"), probs = c(0.3, 0.3, 0.4), reference = "White", coefficients = list(B = 1.02, C = 1.3)) )  

crtdata <- crtDataSimulation(ni = 3, ns = 10, np = 100, nstreated = c(2, 3, 2, 3), sigma = 1, ICC = 0.1, B0 = 1.45, es = c(0.1, 0.2, 0.5), seed = 1234, attritionrates = c(0, 0.1, 0.2, 0.1), covariates = covariates) head(crtdata)
```

futilityAnalysis

Futility Analysis Across Interventions for CRT, MST, or SRT Designs

Description

This function performs a Bayesian futility analysis for each intervention group compared to control, across cluster randomized trials (CRT), multisite trials (MST) or simple randomized trials (SRT).

Usage

```
futilityAnalysis(
  method = c("crt", "mst", "srt"),
  data,
  outcome = "posttest",
  interventions = "interventions",
  Random = "schools",
  Nsim = 10000,
  Threshold = 0.05,
  FutThreshold = 0.8,
  continuous_covariates = NULL,
  categorical_covariates = NULL
)
```

Arguments

method The trial design type: "crt", "mst", or "srt".

data A data frame containing the variables including outcome, predictors, the clus-

tering variable, and the intervention.

outcome The name of the outcome (post-test) variable. interventions A string specifying the intervention variable.

Random The name of the clustering variable (e.g., schools or sites) for CRT and MST

designs.

Nsim Number of MCMC iterations to be performed. A minimum of 10,000 is recom-

mended to ensure convergence.

Threshold The effect size threshold for posterior computation (default = 0.05).

FutThreshold The minimum posterior probability threshold for non-futility (default = 0.8).

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```
continuous_covariates
```

A character vector specifying the names of continuous covariates.

```
categorical_covariates
```

A character vector specifying the names of categorical covariates (converted to factors).

Details

The function loops over each intervention, fits the appropriate Bayesian model (crtBayes, mstBayes, srtBayes), extracts the posterior probability, and determines futility based on the specified probability threshold.

Value

A data.frame with columns:

- Intervention: Intervention group identifier.
- Futility: 1 if considered futile (posterior probability < FutThreshold), 0 otherwise.
- ProbES: Bayesian posterior probabilities that the observed effect size is greater than or equal to a pre-specified threshold

See Also

crtBayes, mstBayes, srtBayes functions from the eefAnalytics package

```
###Futility analysis of cluster randomized trial###
data(crt4armSimData)
futilityAnalysis(method = "crt", data = crt4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000,
Threshold = 0.05, FutThreshold = 0.8,continuous_covariates = c("pretest"),
categorical_covariates = c("gender", "ethnicity"))
###Futility analysis of multisite trial###
data(mst4armSimData)
futilityAnalysis(method = "mst", data = mst4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000,
Threshold = 0.05, FutThreshold = 0.8,continuous_covariates = c("pretest"),
categorical_covariates = c("gender", "ethnicity"))
###Futility analysis of simple randomized trial###
data(srt4armSimData)
futilityAnalysis(method = "srt", data = srt4armSimData, outcome = "posttest",
interventions = "interventions", Nsim = 10000, Threshold = 0.05, FutThreshold = 0.8,
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"))
```

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mst4armSimData

Simulated 4-Arm Multisite Trial (MST) Data

Description

A simulated multisite trial dataset containing 10 schools and 1,000 pupils. This is a 4-arm trial design with one control group and three intervention groups.

Usage

mst4armSimData

Format

A data frame with 1,000 rows and 7 variables:

pupils Identifier for each pupil

schools Identifier for each school

interventions Treatment assignment coded as 0 for control and 1–3 for intervention groups

pretest Pre-test scores

gender Binary gender

ethnicity A categorical variable with 3 categories

posttest Post-test scores

Source

Simulated

 ${\tt mstAddIntervention}$

Add a New Intervention Group to Multisite Trial (MST)

Description

This function adds a new intervention group to an existing Multisite Trial (MST) dataset. It fits a linear mixed-effects model to the original data, then uses its estimates to generate post-test outcomes for the new group, incorporating random intercepts, slopes, and user-defined effect size.

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Usage

```
mstAddIntervention(
  originalData,
  ns,
  np,
  es,
  attritionrate,
  intper,
  outcome,
  interventions,
  schoolsID,
  pupilsID,
  continuous_covariates,
  categorical_covariates
)
```

Arguments

originalData	A data frame containing the variables including outcome, predictors, the clustering variable, and the intervention for MST design.						
ns	The number of schools to assign to the new intervention group.						
np	The number of pupils per new school.						
es	The standardized effect size for the new intervention group.						
attritionrate	The proportion of pupils in the new group to drop due to attrition.						
intper	Proportion of pupils per new school assigned to the Intervention group.						
outcome	A string specifying the name of the column containing outcome variable (e.g., post-test scores).						
interventions	A string specifying the name of the intervention assignment column.						
schoolsID	A string specifying the name of the school ID column.						
pupilsID	A string specifying the name of the pupil ID column.						
continuous_cova	ariates						
	A character vector specifying the names of continuous covariates.						
categorical_covariates							
	A character vector specifying the names of categorical covariates (converted to						

Details

The function:

- Fits a linear mixed-effects model (1mer) with random slopes and intercepts using existing MST data.
- Simulates new schools and pupils, assigning intervention randomly by specified percentage.
- Simulates attrition by removing post-test scores at random.

factors).

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Value

A data. frame containing the combined dataset with the newly added intervention group and simulated outcomes.

See Also

1mer from the lme4 package

Examples

```
data(mst4armSimData)
new_mst5armData <- mstAddIntervention(originalData = mst4armSimData, ns = 2, np = 100, es = 0.3,
intper = 0.5, attritionrate = 0.1, outcome = "posttest", interventions = "interventions",
schoolsID = "schools", pupilsID = "pupils",
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"))
head(new_mst5armData)</pre>
```

mstDataSimulation

Simulate Multisite Trial (MST) Data

Description

This function simulates a multiple intervention arms Multisite Trial (MST) data. The model includes intervention and pre-test scores as covariates.

Usage

```
mstDataSimulation(
    ni,
    tpi,
    np,
    ns,
    sigma,
    sigmab0,
    sigmab1,
    B0,
    es,
    seed,
    attritionrates,
    covariates
)
```

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Arguments

The number of intervention groups excluding the control group.

The proportions (in percent) of total participants assigned to each group, with the first value for the control group. It should be specified as a numeric vector of length ni + 1.

The number of pupils per school.

ns The number of schools.

sigma The standard deviation of the individual-level error.

sigmab0 The standard deviation of random intercepts at the school level.

sigmab1 The standard deviation of random slopes for the intervention effect.

B0 The intercept of the model.

es The standardized effect sizes for each intervention group. It should be specified

as a numeric vector.

seed The random seed for reproducibility.

attritionrates The attrition proportions for each group, including the control group. It should

be specified as a numeric vector of length ni + 1.

covariates List of covariate specifications. Each element should be a list with the following

fields:

name Character. Name of the covariate.

type Character. Either "continuous" or "categorical".

sd Numeric. Standard deviation (only for continuous covariates).

coefficient Numeric. Coefficient (only for continuous covariates).

levels Character vector. Category levels (only for categorical covariates).

probs Numeric vector. Sampling probabilities (must sum to 1) (categorical only).

reference Character. Reference category (categorical only).

coefficients Named list of numeric values. Coefficients for each non-reference level.

Value

A data. frame containing:

pupils Pupil ID

schools School ID

interventions Intervention group assignment (0 = control, 1 to ni = intervention groups)

covariates Simulated covariates

posttest Posttest score (NA if attrited)

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Examples

```
covariates <- list(
  list(name = "pretest", type = "continuous", sd = 1, coefficient = 1.7),
  list(name = "gender", type = "categorical", levels = c("Male", "Female"),
  probs = c(0.3, 0.7), reference = "Male", coefficients = list(B = -0.5)),
  list(name = "ethnicity", type = "categorical", levels = c("White", "Black", "Asian"),
  probs = c(0.3, 0.3, 0.4), reference = "White", coefficients = list(B = 1.02, C = 1.3))
)

mstdata <- mstDataSimulation(ni = 3, ns = 10, np = 100, tpi = c(30, 30, 20, 20),
  sigma = 1, sigmab0 = 0.5, sigmab1 = 0.5, B0 = 1.45,
  es = c(0.2, 0.3, 0.1), seed = 1234, attritionrates = c(0.1, 0.1, 0.1, 0), covariates = covariates)
  head(mstdata)</pre>
```

multiArmAnalysis

Bayesian or Frequentist Analysis with Forest Plot Comparison for Multi-Arm Trial Designs

Description

This function fits Bayesian or frequentist and producing a forest plot across multiple intervention groups for cluster randomized trials (CRT), multisite trials (MST) or simple randomized trials (SRT).

Usage

```
multiArmAnalysis(
 method = "crtBayes",
  data,
 outcome = "posttest",
  interventions = "interventions",
 Random = "schools",
 Nsim = 10000,
  Threshold = 0.05,
  FREQoption = "Default",
  nPerm = NULL,
  nBoot = NULL,
  bootType = NULL,
  continuous_covariates = NULL,
  categorical_covariates = NULL,
 maintitle = NULL,
  xlabel = NULL,
 ylabel = NULL,
  vlinecolor = "black",
  intlabels = NULL,
  intcolors = NULL
)
```

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Arguments

method

The model fitting method. Should be specified as a character string. Choices are:

- "crtBayes": Bayesian analysis of cluster randomised trials using vague priors.
- "crtFREQ": Analysis of cluster randomised trials using a multilevel model under a frequentist setting.
- "mstBayes": Bayesian analysis of multisite randomised trials using vague priors.
- "mstFREQ": Analysis of multisite randomised trials using a multilevel model under a frequentist setting.
- "srtBayes": Bayesian analysis of simple randomised trials using vague priors.
- "srtFREQ": Analysis of simple randomised trials under a frequentist setting.

data A data frame containing the variables including outcome, predictors, the clus-

tering variable, and the intervention.

outcome The name of the outcome (post-test) variable.

interventions A string specifying the intervention variable.

Random The name of the clustering variable (e.g., schools or sites) for CRT and MST

designs.

Nsim Number of MCMC iterations to be performed for Bayesian analysis. A mini-

mum of 10,000 is recommended to ensure convergence.

Threshold The effect size threshold for posterior computation for Bayesian analysis (de-

fault = 0.05).

FREQoption The option for frequentist methods. Choices are "Default", "Permutation", or

"Bootstrap".

nPerm The number of permutations required to generate a permutated p-value.

nBoot The number of bootstraps required to generate bootstrap confidence intervals.

bootType method of bootstrapping including case re-sampling at student level "case(1)", case

re-sampling at school level "case(2)", case re-sampling at both levels "case(1,2)" and residual bootstrapping using "residual". If not provided, default will be case

re-sampling at student level.

continuous_covariates

A character vector specifying the names of continuous covariates.

categorical_covariates

A character vector specifying the names of categorical covariates (converted to

factors).

maintitle main title for the plot.

xlabel Label for the x-axis.

ylabel Label for the y-axis.

vlinecolor Color of the vertical reference line (default = "black").

intlabels Optional custom intervention labels for the plot.

intcolors Optional intervention colors for the plot.

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Details

This function loops through each intervention, fits the requested statistical model, stores the results, and forest plot visualization for easy comparison. It allows flexible customization for plotting aesthetics.

Value

A ggplot object showing intervention effect sizes and their confidence intervals.

See Also

Functions from the **eefAnalytics** package: crtBayes, crtFREQ, mstBayes, mstFREQ, srtBayes, srtFREQ

```
### Bayesian analysis of cluster randomised trials ###
data(crt4armSimData)
multiArmAnalysis(method = "crtBayes", data = crt4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000, Threshold = 0.05,
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
intlabels = c("Intervention A", "Intervention B", "Intervention C"),
maintitle = "Forest plot of comparison of effect sizes", xlabel = "Hedges'g",
ylabel = "Interventions", vlinecolor = "black")
###MLM analysis of multisite trials with residual bootstrap confidence intervals ###
data(mst4armSimData)
multiArmAnalysis(method = "mstFREO", data = mst4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", nBoot = 1000, bootType="residual",
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
intlabels = c("Intervention A", "Intervention B", "Intervention C"),
intcolors = c("Intervention A" = "blue", "Intervention B" = "green", "Intervention C" = "red"),
maintitle = "Forest plot of comparison of effect sizes ", xlabel = "Hedges'g",
ylabel = "Interventions", vlinecolor = "black")
###MLM analysis of multisite trials with permutation p-value###
data(mst4armSimData)
multiArmAnalysis(method = "mstFREQ", data = mst4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", nPerm = 1000,
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
intlabels = c("Intervention A", "Intervention B", "Intervention C"),
intcolors = c("Intervention A" = "blue", "Intervention B" = "green", "Intervention C" = "red"),
maintitle = "Forest plot of comparison of effect sizes",
xlabel = "Hedges'g", ylabel = "Interventions", vlinecolor = "black")
###Bayesian analysis of simple randomised trials###
data(srt4armSimData)
multiArmAnalysis(method = "srtBayes", data = srt4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000, Threshold = 0.05,
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
intlabels = c("Int A", "Int B", "Int C"),
```

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```
intcolors = c("Int A" = "#1F77B4", "Int B" = "#2CA02C", "Int C" = "#D62728"), maintitle = "Forest plot of comparison of effect sizes ", xlabel = "Hedges'g", ylabel = "Interventions", vlinecolor = "black")
```

plotPosteriorProbs

Plot Posterior Probabilities Across Thresholds for CRT, MST, or SRT Designs

Description

This function generates a Bayesian posterior probability plot across multiple thresholds for each intervention group in a clustered randomized trial (CRT), multisite trial (MST), or simple randomized trial (SRT).

Usage

```
plotPosteriorProbs(
 method = c("crt", "mst", "srt"),
  outcome = "posttest",
  interventions = "interventions",
 Random = "schools",
 Nsim = 10000,
  continuous_covariates = NULL,
  categorical_covariates = NULL,
  VerticalLine = NULL,
  VerticalLineColor = "#0000FF",
 HorizontalLine = NULL,
 HorizontalLineColor = "#FF0000",
  threshold_range = c(0, 1),
 maintitle = "Posterior Probabilities Across Thresholds",
 xlabel = "Threshold",
 ylabel = "Posterior Probability",
  intcolors = NULL,
  intlabels = NULL,
  xbreaks = NULL,
 ybreaks = seq(0, 1, by = 0.1)
)
```

Arguments

method The trial design type: "crt", "mst", or "srt".

data A data frame containing the variables including outcome, predictors, the clustering variable, and the intervention.

outcome The name of the outcome (post-test) variable.

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interventions A string specifying the intervention variable.

Random The name of the clustering variable (e.g., schools or sites) for CRT and MST

designs.

Nsim Number of MCMC iterations to be performed. A minimum of 10,000 is recom-

mended to ensure convergence.

continuous_covariates

A character vector specifying the names of continuous covariates.

categorical_covariates

A character vector specifying the names of categorical covariates (converted to

factors).

VerticalLine Optional vertical reference line added at a threshold value. It should be specified

as a numeric value.

VerticalLineColor

The color of the vertical reference line. It should be specified as a character

string (default = "#0000FF").

HorizontalLine Optional posterior probability cutoff for adding a horizontal reference line. It

should be specified as a numeric value.

HorizontalLineColor

The color of the horizontal reference line. It should be specified as a character

string (default = "#FF0000").

threshold_range

The range of thresholds to evaluate. It should be specified as a numeric vector

of length 2 (default = c(0, 1.0)).

maintitle The main title of the plot.

xlabel The label for the x-axis.

ylabel The label for the y-axis.

intcolors Optional intervention colors specified manually. It should be provided as a

named character vector.

intlabels Optional intervention labels to use instead of default names. It should be speci-

fied as a character vector.

xbreaks Tick marks for the x-axis. Must be a numeric vector with values within the

specified threshold_range (default = 0.1).

ybreaks Tick marks for the y-axis. It should be specified as a numeric vector (default =

seq(0, 1, by = 0.1).

Details

The function uses crtBayes(), mstBayes(), or srtBayes() from eefAnalytics package depending on the method.

Value

A ggplot object that displays posterior probabilities across thresholds for each intervention.

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See Also

crtBayes, mstBayes, srtBayes functions from the eefAnalytics package

```
###Plot Posterior Probabilities of cluster randomized trial###
data(crt4armSimData)
plotPosteriorProbs(method = "crt",data = crt4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000,
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
threshold_range = c(0, 0.1), VerticalLine = 0.05, HorizontalLine = 0.8,
VerticalLineColor= "purple", HorizontalLineColor= "black",
intlabels = c("Intervention A", "Intervention B", "Intervention C"),
intcolors = c("Intervention A" = "blue", "Intervention B" = "red",
"Intervention C" = "green"), maintitle= "Posterior probability plot",
xlabel= "Threshold", ylabel= "Posterior probability",
xbreaks= 0.1, ybreaks= seq(0, 1, by = 0.1))
###Plot Posterior Probabilities of multisite trial###
data(mst4armSimData)
plotPosteriorProbs(method = "ms",data = mst4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000,
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
threshold_range = c(0, 0.1), VerticalLine = 0.05, HorizontalLine = 0.8,
VerticalLineColor= "purple", HorizontalLineColor= "black",
intlabels = c("Intervention A", "Intervention B", "Intervention C"),
intcolors = c("Intervention A" = "blue", "Intervention B" = "red",
"Intervention C" = "green"), maintitle= "Posterior probability plot",
xlabel= "Threshold", ylabel= "Posterior probability",
xbreaks = 0.1, ybreaks = seq(0, 1, by = 0.1)
###Futility analysis of simple randomized trial###
data(srt4armSimData)
plotPosteriorProbs(method = "srt",data = srt4armSimData, outcome = "posttest",
interventions = "interventions", Nsim = 10000, threshold_range = c(0, 0.2),
continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"),
VerticalLine = 0.05, HorizontalLine = 0.8, VerticalLineColor= "purple",
\label{localized} \mbox{HorizontalLineColor= "black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black", intlabels = c("Intervention A", "Intervention B", "and the color black"), and the color black black
"Intervention C"), intcolors = c("Intervention A" = "#1F77B4",
"Intervention B" = "#D62728", "Intervention C" = "#2CA02C"),
maintitle= "Posterior probability plot", xlabel= "Threshold",
ylabel= "Posterior probability", xbreaks= 0.1, ybreaks= seq(0, 1, by = 0.1))
```

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Description

Launches a Shiny application that provides an interactive user interface to run the functions provided by the epts package.

Usage

```
runEPTS()
```

Examples

```
if (interactive()) {
  runEPTS()
}
```

srt4armSimData

Simulated 4-Arm Simple Randomized Trial (SRT) Data

Description

A simulated simple randomized trial dataset containing 1,000 individuals. This is a 4-arm trial design with one control group and three intervention groups.

Usage

```
srt4armSimData
```

Format

A data frame with 1,000 rows and 6 variables:

ID Identifier for participants ID

interventions Treatment assignment coded as 0 for control and 1–3 for intervention groups

pretest Pre-test scores

gender Binary gender

ethnicity A categorical variable with 3 categories

posttest Post-test scores

Source

Simulated

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srtAddIntervention	Add a New Intervention Group to Simple Randomized Trial (SRT)
	Data

Description

This function adds a new intervention group to an existing SRT dataset by generating new participant-level data

Usage

```
srtAddIntervention(
  existing_data,
  np,
  es,
  attritionrate,
  outcome,
  interventions,
  id,
  continuous_covariates,
  categorical_covariates)
```

Arguments

existing_data A data frame containing the variables including outcome, predictors, the clus-

tering variable, and the intervention for CRT design.

np The number of new participants to generate for the new intervention group.

es The standardized effect size for the new intervention group.

attritionrate The proportion of pupils in the new group to drop due to attrition.

outcome A string specifying the name of the column containing outcome variable (post-

test scores).

interventions A string specifying the name of the intervention assignment column.

id A string specifying the name of the participant ID column.

continuous_covariates

A character vector specifying the names of continuous covariates.

categorical_covariates

A character vector specifying the names of categorical covariates (converted to factors).

Value

A data. frame combining the original dataset with the newly simulated intervention group.

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Examples

```
data(srt4armSimData)
new_srt5armData <- srtAddIntervention(existing_data = srt4armSimData, np = 100,
es = 0.3, attritionrate = 0.1, outcome = "posttest", interventions = "interventions",
id = "ID", continuous_covariates = c("pretest"), categorical_covariates = c("gender", "ethnicity"))
head(new_srt5armData)</pre>
```

srtDataSimulation

Simulate Simple Randomized Trial (SRT) Data

Description

This function simulates a Simple Randomized Trial (SRT), with multiple intervention arms, pretest and post-test scores, and individual-level attrition. No clustering or hierarchical structure is assumed.

Usage

```
srtDataSimulation(ni, tpi, np, sigma, B0, es, seed, attritionrates, covariates)
```

Arguments

ni	The number of intervention groups excluding the control group.
tpi	The proportions (in percent) assigned to each group, with the first value for the control group followed by the intervention groups. Must sum to 100. It should be specified as a numeric vector of length $ni + 1$.
np	The total number of participants.
sigma	The standard deviation of individual-level error for the post-test score.
В0	The intercept term in the model.
es	The standardized effect sizes for each intervention group. It should be specified as a numeric vector.
seed	The random seed for reproducibility.
attritionrates	The attrition rates for each group, including the control group. It should be specified as a numeric vector of length $ni + 1$.
covariates	List of covariate specifications. Each element should be a list with the following fields:
	name Character. Name of the covariate.
	type Character. Either "continuous" or "categorical".
	sd Numeric. Standard deviation (only for continuous covariates).
	coefficient Numeric. Coefficient (only for continuous covariates).
	levels Character vector. Category levels (only for categorical covariates).

only).

probs Numeric vector. Sampling probabilities (must sum to 1) (categorical

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reference Character. Reference category (categorical only).coefficients Named list of numeric values. Coefficients for each non-reference level.

Value

```
A data.frame containing:

ID Participant ID

interventions Intervention assignment (0 = control, 1 to ni = intervention groups)

covariates Simulated covariates

posttest Posttest score (NA if participant attrited)
```

Examples

```
covariates <- list(
    list(name = "pretest", type = "continuous", sd = 1, coefficient = 1.7),
    list(name = "gender", type = "categorical", levels = c("Male", "Female"),
    probs = c(0.3, 0.7), reference = "Male", coefficients = list(B = -0.5)),
    list(name = "ethnicity", type = "categorical", levels = c("White", "Black", "Asian"),
    probs = c(0.3, 0.3, 0.4), reference = "White", coefficients = list(B = 1.02, C = 1.3))

srtdata <- srtDataSimulation(ni = 3, np = 1000, tpi = c(30, 30, 20, 20),
    sigma = 1, 80 = 1.45, es = c(0.2, 0.3, 0.1), seed = 1234,
    attritionrates = c(0.1, 0.1, 0.1, 0), covariates = covariates)
    head(srtdata)
```

superiorityAnalysis Superiority Analysis Across Interventions for CRT, MST, or SRT Designs

Description

This function performs a Bayesian superiority analysis, comparing each intervention against a reference intervention, across cluster randomized trials (CRT), multisite trials (MST) or simple randomized trials (SRT).

Usage

```
superiorityAnalysis(
  method = c("crt", "mst", "srt"),
  data,
  outcome = "posttest",
  interventions = "interventions",
  Random = "schools",
  Nsim = 10000,
```

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```
Threshold = 0.05,
  refintervention = 1,
  SupThreshold = 0.8,
  continuous_covariates = NULL,
  categorical_covariates = NULL)
```

Arguments

method The trial design type: "crt", "mst", or "srt".

data A data frame containing the variables including outcome, predictors, the clus-

tering variable, and the intervention.

outcome The name of the outcome (post-test) variable.

interventions A string specifying the intervention variable.

Random The name of the clustering variable (e.g., schools or sites) for CRT and MST

designs.

Nsim Number of MCMC iterations to be performed. A minimum of 10,000 is recom-

mended to ensure convergence.

Threshold The effect size threshold for posterior computation (default = 0.05).

refintervention

The value of the intervention used as the reference group (default = 1).

SupThreshold The minimum posterior probability threshold to declare superiority (default =

0.8).

continuous_covariates

A character vector specifying the names of continuous covariates.

categorical_covariates

A character vector specifying the names of categorical covariates (converted to

factors).

Details

The effect size is estimated against a reference intervention, which by default is intervention 1 but can be reassigned to any other intervention, including the control (refintervention = 0).

Value

A data.frame with columns:

- Intervention: Intervention group identifier.
- ProbES: Posterior probability of superiority over the reference intervention.
- Superiority: Label indicating "Superior", "Not Superior", or "Reference".

See Also

crtBayes, mstBayes, srtBayes functions from the eefAnalytics package

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```
###Superiority analysis of cluster randomized trial###
data(crt4armSimData)
superiorityAnalysis(method = "crt", data = crt4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000, refintervention = 2,
Threshold = 0.05, SupThreshold = 0.8, continuous_covariates = c("pretest"),
categorical_covariates = c("gender", "ethnicity"))
###Superiority analysis of multisite trial###
data(mst4armSimData)
superiorityAnalysis(method = "mst", data = mst4armSimData, outcome = "posttest",
interventions = "interventions", Random = "schools", Nsim = 10000, refintervention = 2,
Threshold = 0.05, SupThreshold = 0.8,continuous_covariates = c("pretest"),
categorical_covariates = c("gender", "ethnicity"))
###Superiority analysis of simple randomized trial###
data(srt4armSimData)
superiorityAnalysis(method = "srt", data = srt4armSimData, outcome = "posttest",
interventions = "interventions", Nsim = 10000, refintervention = 2,
Threshold = 0.05, SupThreshold = 0.8, continuous_covariates = c("pretest"),
categorical_covariates = c("gender", "ethnicity"))
```

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```