Package 'SMARTbayesR'

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Type Package

Title Bayesian Set of Best Dynamic Treatment Regimes and Sample Size in SMARTs

Version 1.0.2

Description Permits determination of a set of optimal dynamic treatment regimes and sample size for a SMART design in the Bayesian setting. Please see Artman (2020) <arXiv:2008.02341>.

Depends R (>= 4.0.0), stats

License GPL-3

Encoding UTF-8

Suggests knitr, rmarkdown (>= 2.1), data.table

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LogOR *Log-Odds Ratios for Embedded Dynamic Treatment Regimes*

Description

Computes the embedded dynamic treatment regime specific log odds ratios.

Usage

```
LogOR(
  response_prob = c(0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8),
  stage_one_trt_one_response_prob = 0.6,
  stage_one_trt_two_response_prob = 0.3,
  design = "general"
)
```

Arguments

response_prob	the probability of response for each of embedded treatment sequences. In the case of the design 1 SMART, there are 6 and for the general design there are 8.
stage_one_trt_one_response_prob	the probability of response to stage-1 treatment given initial treatment one.
stage_one_trt_two_response_prob	the probability of response to stage-1 treatment given initial treatment two.
design	which SMART design: design-1 or general.

Value

The embedded dynamic treatment regime specific log-OR.

MCBUpperLimits *Simultaneous Upper Credible Intervals*

Description

Compute simultaneous upper credible intervals from draws of embedded dynamic treatment regime probabilities given by the function argument “thetadraws”.

Usage

```
MCBUpperLimits(thetadraws, alpha = 0.05, design = "design-1")
```

Arguments

thetadraws	draws of the embedded dynamic treatment regimes.
alpha	the type I error rate (probability of excluding the true best EDTR).
design	specifies to which SMART design to apply function: either design-1 or general.

Value

Upper 1-alpha level simultaneous credible interval limits for each of the embedded dynamic treatment regimes.

Examples

```
dat <- SimDesign1(sample_size=250,
                  response_prob = c(0.5,0.9,0.3,0.7,0.5,0.8),
                  stage_one_trt_one_response_prob = 0.7,
                  stage_one_trt_two_response_prob = 0.4)

x <- PosteriorTrtSeqProb(niter = 1000, dat, design = "design-1")

thetadraws <- PosteriorEDTRProbs(x, design = "design-1")

MCBUpperLimits(thetadraws,
               alpha = 0.05,
               design = "design-1")
```

PosteriorEDTRProbs *Convert Treatment Sequence Draws into Dynamic Treatment Regime Draws*

Description

Apply Robin's G-computation formula to compute the embedded dynamic treatment regime draws from the marginal draws.

If design is "design-1", then compute for Design 1 SMART with 6 embedded treatment sequences and 4 embedded dynamic treatment regimes.

If design is "general", then compute for General SMART with 8 embedded treatment sequences and 8 embedded dynamic treatment regimes.

Usage

```
PosteriorEDTRProbs(x, design = "design-1")
```

Arguments

x	A data frame consisting of draws from the posterior of the end of study response probabilities of each treatment sequence and of stage-1 response probabilities for each stage-1 treatment
design	Which SMART design to compute the posterior draws for: "design-1" or "general".

Details

For the General SMART design, x should have columns p_1, p_2, p_3, p_4, p_5, p_6, p_7, p_8, s1, and s2.

For the Design-1 SMART, x should have columns p_1, p_2, p_3, p_4, p_5, p_6, s1, and s2. These are the posterior draws of the response probabilities for each treatment sequence and stage-1 response probability draws.

s1 contains the draws of the stage-1 response probability for the first treatment and s2 is analogous for the second treatment.

Value

Matrix of EDTR specific posterior response probability draws at the end of the study There will be 4 columns for design-1 and 8 columns for design General, each corresponding to an EDTR. The number of rows will be the same as that of x.

Examples

```
dat <- SimDesign1(sample_size=250,
                  response_prob = c(0.5,0.9,0.3,0.7,0.5,0.8),
                  stage_one_trt_one_response_prob = 0.7,
                  stage_one_trt_two_response_prob = 0.4)

x <- PosteriorTrtSeqProb(niter = 1000, dat, design = "design-1")

PosteriorEDTRProbs(x, design = "design-1")
```

PosteriorTrtSeqProb *Treatment Sequence Response Probabilties from Dataset*

Description

Draws from the posterior of the treatment sequence response probabilities.

Usage

```
PosteriorTrtSeqProb(niter, dat, design = "design-1")
```

Arguments

niter	the number of posterior draws.
dat	a data frame (see Details).
design	an indicator of which SMART design, design-1 or general.

Details

dat should contain the following columns:

y, the end of study binary response indicator

a1, the stage-1 treatment assignment indicator

s, the end of stage-1 binary response indicator

Additionally, for design-1 it should contain a2, the stage-2 treatment assignment indicator

For the general design, it should contain

a2r, stage-2 treatment assignment for responders to stage-1 treatment.

a2nr, stage-2 treatment assignment for non-responders to stage-1 treatment.

Value

Posterior draws of the probability of response at the end of the study for each embedded treatment sequence and the posterior draws of the probability of response at the end of stage-1 for each stage-1 treatment.

Examples

```
dat <- SimDesign1(sample_size=250,
                              response_prob = c(0.5,0.9,0.3,0.7,0.5,0.8),
                              stage_one_trt_one_response_prob = 0.7,
                              stage_one_trt_two_response_prob = 0.4)

PosteriorTrtSeqProb(niter = 1000, dat, design = "design-1")
```

PowerBayesian *Power Computation when Planning a SMART*

Description

This function computes the power for a sequential multiple assignment randomized trial (SMART) of one of two designs: "design-1" or "general".

Usage

```
PowerBayesian(
  design = "design-1",
  sample_size = 100,
  response_prob = c(0.5, 0.9, 0.3, 0.7, 0.5, 0.8),
  stage_one_trt_one_response_prob = 0.7,
  stage_one_trt_two_response_prob = 0.5,
  rejection_indices = 2:3,
  alpha = 0.05
)
```

Arguments

design	specifies for which SMART design to calculate the power: design-1 or general.
sample_size	the total SMART study sample size.
response_prob	a vector of probabilities of response for each of embedded treatment sequences. In the case of design 1, there are 6 and for general design there are 8.
stage_one_trt_one_response_prob	the probability of response to stage-1 treatment for first initial treatment.
stage_one_trt_two_response_prob	the probability of response to stage-1 treatment for second initial treatment.
rejection_indices	a vector of indices of which embedded dynamic treatment regimes to exclude in power calculation.
alpha	type I error rate (probability of excluding optimal embedded dynamic treatment regime)

Value

The power to exclude embedded dynamic treatment regimes specified by rejection_indices from the set of best.

Examples

```
PowerBayesian(
  design = "design-1",
  sample_size = 100,
  response_prob = c(0.5, 0.9, 0.3, 0.7, 0.5, 0.8),
  stage_one_trt_one_response_prob = 0.7,
  stage_one_trt_two_response_prob = 0.5,
  rejection_indices = 1:2
)

PowerBayesian(
  design = "general",
  sample_size = 250,
```

```
  response_prob = c(0.5, 0.9, 0.7, 0.2, 0.3, 0.8, 0.4, 0.7),
  stage_one_trt_one_response_prob = 0.7,
  stage_one_trt_two_response_prob = 0.5,
  rejection_indices = c(1, 2, 4, 5, 6)
)
```

SimDesign1 *Simulate a SMART with Design 1*

Description

This function simulates a SMART with Design 1.

Usage

```
SimDesign1(
  sample_size = 250,
  response_prob = c(0.5, 0.5, 0.5, 0.8, 0.7, 0.5),
  stage_one_trt_one_response_prob = 0.7,
  stage_one_trt_two_response_prob = 0.4
)
```

Arguments

sample_size	the total sample size
response_prob	a vector of probabilities of response for each of the 6 embedded treatment sequences.
stage_one_trt_one_response_prob	the probability of response to first stage-1 treatment.
stage_one_trt_two_response_prob	the probability of response to second stage-1 treatment.

Value

a data frame with treatment response indicators for each stage of treatment, a1 and a2, end of stage-1 response indicator s, and final outcome y.

Examples

```
dat <- SimDesign1(sample_size=250,
                            response_prob = c(0.5,0.9,0.3,0.7,0.5,0.8),
                            stage_one_trt_one_response_prob = 0.7,
                            stage_one_trt_two_response_prob = 0.4)
```

SMARTbayesR *SMARTbayesR: A package for Bayesian computation of optimal dynamic treatment regimes and sample size determination*

Description

The SMARTbayesR package allows computation of a set of optimal embedded dynamic treatment regimes for a SMART. Furthermore, it allows power to be calculated for sample size determination.

Details

Five of the important functions are as follows: PosteriorTrtSeqProb, PosteriorEDTRProbs, MCBUpperLimits, LogOR, and PowerBayesian.

SMARTbayesR functions

PosteriorTrtSeqProb draws from the posterior of the probabilities of response for each treatment sequence and stage-1 response probabilities.

PosteriorEDTRProbs converts treatment sequence end of study response probabilities, stage-1 response probabilities into end of study DTR response probabilities.

MCBUpperLimits calculates simultaneous credible intervals which determines the set of optimal DTRs.

LogOR computes the log-OR between each embedded dynamic treatment regime and the best.

PowerBayesian computes the power in a SMART to exlude DTRs inferior to the best by a specified amount.

Please see Artman (2020) <arXiv:2008.02341> for details about the methodology.

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