Package ‘baskexact’

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R topics documented:

adjust_lambda .......................................................... 2
basket_test ............................................................ 3
check_mon_between .................................................. 5
check_mon_within ..................................................... 6
Adjust Lambda

Description
Finds the value for lambda such that the family wise error rate is protected at level alpha.

Usage
```
adjust_lambda(
  design,
  alpha = 0.025,
  theta1 = NULL,
  n,
  epsilon,
  tau,
  logbase,
  prune,
  prec_digits,
  ...
)
```

Arguments
- **design**: An object of class Basket created by `setupBasket`.
- **alpha**: The one-sided significance level.
theta1: Probabilities under the alternative hypothesis. If length(theta1) == 1, then this is a common probability for all baskets. If is.null(theta1) then the type 1 error rate under the global null hypothesis is computed.

n: The sample size per basket.

epsilon: A tuning parameter that determines the amount of borrowing. See details for more information.

tau: A tuning parameter that determines how similar the baskets have to be that borrowing occurs. See details for more information.

logbase: A tuning parameter that determines which logarithm base is used to compute the Jensen-Shannon divergence. See details for more information.

prune: Whether baskets with a number of responses below the critical pooled value should be pruned before the final analysis.

prec_digits: Number of decimal places that are considered when adjusting lambda

...: Further arguments.

Details

adjust_alpha finds the greatest value with prec_digits for lambda which controls the family wise error rate at level alpha (one-sided). A combination of the uniroot function followed by a grid search is used to find the correct value for lambda.

This method is implemented for the class OneStageBasket.

Value

The greatest value with prec_digits decimal places for lambda which controls the family wise error rate at level alpha (one-sided) and the exact family wise error rate for this value of lambda.

Methods (by class)

- OneStageBasket: Adjust lambda for a single-stage design.

Examples

design <- setupOneStageBasket(k = 3, shape1 = 1, shape2 = 1, theta0 = 0.2)
adjust_lambda(design = design, alpha = 0.025, n = 15, epsilon = 1, tau = 0,
logbase = 2, prune = FALSE, prec_digits = 4)
Usage

basket_test(design, n, r, lambda, epsilon, tau, logbase = 2, prune, ...)

## S4 method for signature 'OneStageBasket'
basket_test(design, n, r, lambda, epsilon, tau, logbase = 2, prune, ...)

Arguments

design An object of class Basket created by setupBasket.
n The sample size per basket.
r The vector of observed responses.
lambda The posterior probability threshold. See details for more information.
epsilon A tuning parameter that determines the amount of borrowing. See details for more information.
tau A tuning parameter that determines how similar the baskets have to be that borrowing occurs. See details for more information.
logbase A tuning parameter that determines which logarithm base is used to compute the Jensen-Shannon divergence. See details for more information.
prune Whether baskets with a number of responses below the critical pooled value should be pruned before the final analysis.
... Further arguments.

Value

A list, including matrices of the weights that are used for borrowing, posterior distribution parameters for all baskets without and with borrowing, as well as the posterior probabilities for all baskets without and with borrowing.

Methods (by class)

- OneStageBasket: Testing for a single-stage basket design.

Examples

design <- setupOneStageBasket(k = 3, shape1 = 1, shape2 = 1, theta0 = 0.2)
basket_test(design = design, n = 24, r = c(5, 9, 10), lambda = 0.99,
            epsilon = 1, tau = 0, logbase = 2, prune = FALSE)
Check Between-Trial Monotonicity

Description

Checks whether the between-trial monotonicity condition holds.

Usage

check_mon_between(
  design,
  n,
  lambda,
  epsilon,
  tau,
  logbase = 2,
  prune,
  details,
  ...
)

## S4 method for signature 'OneStageBasket'
check_mon_between(
  design,
  n,
  lambda,
  epsilon,
  tau,
  logbase = 2,
  prune,
  details,
  ...
)

Arguments

design An object of class Basket created by setupBasket.
n The sample size per basket.
lambda The posterior probability threshold. See details for more information.
epsilon A tuning parameter that determines the amount of borrowing. See details for more information.
tau A tuning parameter that determines how similar the baskets have to be that borrowing occurs. See details for more information.
logbase A tuning parameter that determines which logarithm base is used to compute the Jensen-Shannon divergence. See details for more information.
\textbf{prune} \hspace{2cm} Whether baskets with a number of responses below the critical pooled value should be pruned before the final analysis.

\textbf{details} \hspace{2cm} Whether the cases where the monotonicity condition is violated should be returned, in case there are any.

... \hspace{2cm} Further arguments.

**Details**

check\_mon\_between checks whether the between-trial monotonicity condition holds. For a single-stage design with equal prior distributions and equal sample sizes for each basket this condition states that there are no cases where at least one null hypothesis is rejected when there is a case with an equal or higher number of responses in each basket for which no null hypothesis is rejected.

If \texttt{prune = TRUE} then the baskets with an observed number of baskets smaller than the pooled critical value are not borrowed from. The pooled critical value is the smallest integer \( c \) for which all null hypotheses can be rejected if the number of responses is exactly \( c \) for all baskets.

This method is implemented for the class \texttt{OneStageBasket}.

\section*{Value}

If \texttt{details = FALSE} then only a logical value is returned. If \texttt{details = TRUE} then if there are any cases where the between-trial monotonicity condition is violated, a list of these cases and their results are returned.

\section*{Methods (by class)}

- \texttt{OneStageBasket}: Between-trial monotonicity condition for a single-stage design.

\section*{Examples}

\begin{verbatim}
  design <- setupOneStageBasket(k = 4, shape1 = 1, shape2 = 1, theta0 = 0.2)
  check_mon_between(design = design, n = 24, lambda = 0.99, epsilon = 3,
                    tau = 0, prune = FALSE, details = TRUE)
\end{verbatim}
Usage

check_mon_within(
  design,
  n,
  lambda,
  epsilon,
  tau,
  logbase = 2,
  prune,
  details,
  ...
)

## S4 method for signature 'OneStageBasket'
check_mon_within(
  design,
  n,
  lambda,
  epsilon,
  tau,
  logbase = 2,
  prune,
  details,
  ...
)

Arguments

design An object of class Basket created by setupBasket.
n The sample size per basket.
lambda The posterior probability threshold. See details for more information.
epsilon A tuning parameter that determines the amount of borrowing. See details for more information.
tau A tuning parameter that determines how similar the baskets have to be that borrowing occurs. See details for more information.
logbase A tuning parameter that determines which logarithm base is used to compute the Jensen-Shannon divergence. See details for more information.
prune Whether baskets with a number of responses below the critical pooled value should be pruned before the final analysis.
details Whether the cases where the monotonicity condition is violated should be returned, in case there are any.
...
Further arguments.

Details

check_mon_within checks whether the within-trial monotonicity condition holds. For a single-stage design with equal prior distributions and equal sample sizes for each basket this condition
OneStageBasket-class

states that there are no cases where the null hypothesis of a basket is rejected when there is at least one other basket with more observed responses for which the null hypothesis cannot be rejected.

If prune = TRUE then the baskets with an observed number of baskets smaller than the pooled critical value are not borrowed from. The pooled critical value is the smallest integer c for which all null hypotheses can be rejected if the number of responses is exactly c for all baskets.

This method is implemented for the class OneStageBasket.

Value

If details = FALSE then only a logical value is returned. If details = TRUE then if there are any cases where the within-trial monotonicity condition is violated, a list of these cases and their results are returned.

Methods (by class)

- OneStageBasket: Within-trial monotonicity condition for a single-stage design.

Examples

design <- setupOneStageBasket(k = 4, shape1 = 1, shape2 = 1, theta0 = 0.2)
check_mon_within(design = design, n = 24, lambda = 0.99, epsilon = 0.5,
    tau = 0, prune = FALSE, details = TRUE)

Description

OneStageBasket is an S4 class. An object of this class contains the most important design features of a single-stage basket trial.

Details

This class implements a single-stage basket trial based on the design proposed by Fujikawa et al. In this design, at first separate posterior distributions are calculated for each basket based on a beta-binomial model. Information is then borrowed between baskets by calculating weights that reflect the similarity between the basket and computing posterior distributions for each basket where the parameters of the beta posterior are calculated as a weighted sum of the individual posterior distributions. The weight between two baskets i and j is found as (1 - JSD(i, j)*)^epsilon where JSD(i, j) is the Jensen-Shannon divergence between basket i and j. A small value of epsilon results in stronger borrowing also across baskets with heterogeneous results. If epsilon is large then information is only borrowed between baskets with similar results. If a weight is smaller than tau it is set to 0, which results in no borrowing. If for a basket the posterior probability that \( \theta > \theta_0 \) is greater than lambda, then the null hypothesis is rejected.

Currently only common prior distributions and a common null hypothesis are supported.
Slots

k  The number of baskets.
shape1 First common shape parameter of the beta prior.
shape2 Second common shape parameter of the beta prior.
theta0 A common probability under the null hypothesis.

References


Description

Computes the exact power for a basket trial.

Usage

pow(
  design, 
  theta1, 
  n, 
  lambda, 
  epsilon, 
  tau, 
  logbase = 2, 
  prune = FALSE, 
  results = c("ewp", "group"), 
  ...
)

## S4 method for signature 'OneStageBasket'
pow(
  design, 
  theta1, 
  n, 
  lambda, 
  epsilon, 
  tau, 
  logbase = 2, 
  prune = FALSE, 
  results = c("ewp", "group"), 
  ...
)
Arguments

- **design**: An object of class `Basket` created by `setupBasket`.
- **theta1**: Probabilities under the alternative hypothesis. If `length(theta1) == 1`, then this is a common probability for all baskets.
- **n**: The sample size per basket.
- **lambda**: The posterior probability threshold. See details for more information.
- **epsilon**: A tuning parameter that determines the amount of borrowing. See details for more information.
- **tau**: A tuning parameter that determines how similar the baskets have to be that borrowing occurs. See details for more information.
- **logbase**: A tuning parameter that determines which logarithm base is used to compute the Jensen-Shannon divergence. See details for more information.
- **prune**: Whether baskets with a number of responses below the critical pooled value should be pruned before the final analysis.
- **results**: Whether only the experimentwise power (option `ewp`) or also the rejection probabilities per group (option `group`) should be returned.
- **...** Further arguments.

Details

`pow` computes the exact experimentwise power and the exact rejection probabilities per group. The experimentwise power is the probability to reject at least one null hypothesis for a basket with \(\theta_1 > \theta_0\). The rejection probabilities correspond to the type 1 error rate for baskets with \(\theta_1 = \theta_0\) and to the power for baskets with \(\theta_1 > \theta_0\).

If `prune = TRUE` then the baskets with an observed number of baskets smaller than the pooled critical value are not borrowed from. The pooled critical value is the smallest integer \(c\) for which all null hypotheses can be rejected if the number of responses is exactly \(c\) for all baskets.

This method is implemented for the class `OneStageBasket`.

Value

If `results = "ewp"` then the experimentwise power is returned as a numeric value. If `results = "group"` then a list with the rejection probabilities per group and the experimentwise power is returned. For baskets with \(\theta_1 = \theta_0\) the rejection probabilities corresponds to the type 1 error rate, for baskets with \(\theta_1 > \theta_0\) the rejection probabilities corresponds to the power.

Methods (by class)

- `OneStageBasket`: Power for a single-stage basket design.

Examples

```r
design <- setupOneStageBasket(k = 3, theta0 = 0.2)
pow(design, theta1 = c(0.2, 0.5, 0.5), n = 15, lambda = 0.99, epsilon = 2, tau = 0)
```
setupOneStageBasket  

**Setup OneStageBasket**

**Description**

Creates an object of class `OneStageBasket`.

**Usage**

```r
setupOneStageBasket(k, shape1 = 1, shape2 = 1, theta0)
```

**Arguments**

- `k`: The number of baskets.
- `shape1`: First common shape parameter of the beta prior.
- `shape2`: Second common shape parameter of the beta prior.
- `theta0`: A common probability under the null hypothesis.

**Details**

A `OneStageBasket` object contains the most important design features of a basket trial. Currently only common prior distributions and a common null hypothesis are supported.

**Value**

An S4 object of class `OneStageBasket`.

**Examples**

```r
design <- setupOneStageBasket(k = 3, theta0 = 0.2)
```

---

**toer**  

**Type 1 Error Rate**

**Description**

Computes the exact family wise type 1 error rate of a basket trial.
Usage

toer(
  design, theta1 = NULL, n, lambda, epsilon, tau, logbase = 2, prune = FALSE, results = c("fwer", "group"), ...
)

## S4 method for signature 'OneStageBasket'

\[ \text{toer}( \text{design}, \theta_1 = \text{NULL}, n, \lambda, \epsilon, \tau, \logbase = 2, \text{prune} = \text{FALSE}, \text{results} = \text{c("fwer", "group")}, \ldots) \]

Arguments

design An object of class Basket created by setupBasket.
theta1 Probabilities under the alternative hypothesis. If length(\theta_1) == 1, then this is a common probability for all baskets. If is.null(\theta_1) then the type I error rate under the global null hypothesis is computed.
n The sample size per basket.
lambda The posterior probability threshold. See details for more information.
epsilon A tuning parameter that determines the amount of borrowing. See details for more information.
tau A tuning parameter that determines how similar the baskets have to be that borrowing occurs. See details for more information.
logbase A tuning parameter that determines which logarithm base is used to compute the Jensen-Shannon divergence. See details for more information.
prune Whether baskets with a number of responses below the critical pooled value should be pruned before the final analysis.
results Whether only the family wise error rate (option "fwer") or also the rejection probabilities per group (option "group") should be returned.

... Further arguments.
toer computes the exact family wise type 1 error rate and the exact rejection probabilities per group. The family wise type 1 error rate is the probability to reject at least one null hypothesis for a basket with $\theta_1 = \theta_0$. If all $\theta_1 > \theta_0$ then the family wise type 1 error rate under the global null hypothesis is computed. The rejection probabilities correspond to the type 1 error rate for baskets with $\theta_1 = \theta_0$ and to the power for baskets with $\theta_1 > \theta_0$.

If `prune = TRUE` then the baskets with an observed number of baskets smaller than the pooled critical value are not borrowed from. The pooled critical value is the smallest integer $c$ for which all null hypotheses can be rejected if the number of responses is exactly $c$ for all baskets.

This method is implemented for the class `OneStageBasket`.

**Value**

If `results = "fwer"` then the family wise type 1 error rate is returned as a numeric value. If `results = "group"` then a list with the rejection probabilities per group and the family wise type 1 error rate is returned. If all $\theta_1 > \theta_0$ then the family wise type 1 error rate is calculated under the global null hypothesis. For baskets with $\theta_1 = \theta_0$ the rejection probabilities correspond to the type 1 error rate, for baskets with $\theta_1 > \theta_0$ the rejection probabilities corresponds to the power.

**Methods (by class)**

- `OneStageBasket`: Type 1 error rate for a single-stage basket design.

**Examples**

```r
design <- setupOneStageBasket(k = 3, theta0 = 0.2)
toer(design, n = 15, lambda = 0.99, epsilon = 2, tau = 0)
```
Index

adjust_lambda, 2
adjust_lambda, OneStageBasket-method
  (adjust_lambda), 2

basket_test, 3
basket_test, OneStageBasket-method
  (basket_test), 3

check_mon_between, 5
check_mon_between, OneStageBasket-method
  (check_mon_between), 5
check_mon_within, 6
check_mon_within, OneStageBasket-method
  (check_mon_within), 6

OneStageBasket, 3, 6, 8, 10, 11, 13
OneStageBasket (OneStageBasket-class), 8
OneStageBasket-class, 8

pow, 9
pow, OneStageBasket-method (pow), 9

setupOneStageBasket, 11

toer, 11
toer, OneStageBasket-method (toer), 11