Package ‘simMetric’

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Title Metrics (with Uncertainty) for Simulation Studies that Evaluate Statistical Methods

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Description Allows users to quickly apply individual or multiple metrics to evaluate Monte Carlo simulation studies.

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bias

**Calculate the bias**

**Description**

Calculates the bias of the model estimates from the true value and the Monte Carlo standard error for this estimate.

**Usage**

```r
bias(true_value, estimates, get = c("bias", "bias_mcse"), na.rm = FALSE, ...)
```

**Arguments**

- `true_value` The true value which is being estimated.
- `estimates` A numeric vector containing the estimates from the model(s).
- `get` A character vector containing the values returned by the function.
- `na.rm` A logical value indicating whether NA values for `estimates` should be removed before bias calculation.
- `...` Additional arguments to be ignored.

**Value**

A named vector containing the estimate and the Monte Carlo standard error for the bias.

**Examples**

```r
bias(true_value=0, estimates=rnorm(100))
```

---

biasEliminatedCoverage

**Calculate the bias-eliminated coverage**

**Description**

Estimate the bias-eliminated coverage and the Monte Carlo standard error of this estimate given a vector of confidence intervals and the true value.
coverage

Usage

biasEliminatedCoverage(
  estimates,
  ll,
  ul,
  get = c("biasEliminatedCoverage", "biasEliminatedCoverage_mcse"),
  na.rm = FALSE,
  ...
)

Arguments

estimates A numeric vector containing the estimates from the model(s).
ll A numeric vector containing the lower limits of the confidence intervals.
ul A numeric vector containing the upper limits of the confidence intervals.
get A character vector containing the values returned by the function.
na.rm A logical value indicating whether NA values for ll and ul should be removed before coverage estimation.
... Additional arguments to be ignored.

Value

A named vector containing the estimate and the Monte Carlo standard error for the coverage.

Examples

biasEliminatedCoverage(estimates=rnorm(4), ll=c(-1, -1, -1, -1), ul=c(1, 1, 1, -0.5))

coverage

Calculate the coverage

Description

Estimate the coverage and the Monte Carlo standard error of this estimate given a vector of confidence intervals and the true value.

Usage

coverage(
  true_value,
  ll,
  ul,
  get = c("coverage", "coverage_mcse"),
  na.rm = FALSE,
  ...
)
Arguments

true_value  The true value which should be covered by the interval.
ll  A numeric vector containing the lower limits of the confidence intervals.
ul  A numeric vector containing the upper limits of the confidence intervals.
get  A character vector containing the values returned by the function.
na.rm  A logical value indicating whether NA values for ll and ul should be removed before coverage estimation.
...  Additional arguments to be ignored.

Value

A named vector containing the estimate and the Monte Carlo standard error for the coverage.

Examples

coverage(true_value=0, ll=c(-1, -1, -1, -1), ul=c(1, 1, 1, -0.5))

description  Calculate the empirical standard error

Description

Calculates the empirical standard error of the model estimates and its Monte Carlo standard error.

Usage

depSE(estimates, get = c("empSE", "empSE_MCSE"), na.rm = FALSE, ...)

Arguments

estimates  A numeric vector containing the estimates from the model(s).
get  A character vector containing the values returned by the function.
na.rm  A logical value indicating whether NA values for estimates should be removed before depSE calculation.
...  Additional arguments to be ignored.

Value

A named vector containing the estimate and the Monte Carlo standard error for the empirical standard error.

Examples

depSE(estimates=rnorm(100))
**join_metrics**

**Description**
Calculate and join selected evaluation metrics given a data.frame of simulation study results. Provides a fast way to add multiple metrics and their Monte Carlo standard errors.

**Usage**

```r
join_metrics(
  data,  
  id_cols,  
  metrics = c("coverage", "mse", "modSE"),  
  true_value = NULL,  
  ll_col = NULL,  
  ul_col = NULL,  
  estimates_col = NULL,  
  se_col = NULL,  
  p_col = NULL,  
  alpha = 0.05  
)
```

**Arguments**

- **data**: A data.frame that contains results from simulation study and the necessary columns to compute metrics.
- **id_cols**: Column name(s) on which to group data and calculate metrics.
- **metrics**: A vector of metrics to be calculated.
- **true_value**: The true parameter to be estimated.
- **ll_col**: Name of the column that contains the lower limit of the confidence intervals. (Required for calculating coverage.)
- **ul_col**: Name of the column that contains the upper limit of the confidence intervals. (Required for calculating coverage.)
- **estimates_col**: Name of the column that contains the parameter estimates. (Required for calculating bias, empSE, and mse.)
- **se_col**: Name of the column that contains the standard errors. (Required for calculating modSE.)
- **p_col**: Name of the column that contains the p-values. (Required for calculating rejection.)
- **alpha**: The nominal significance level specified. (Required for calculating rejection.)

**Value**

data.frame containing metrics and id_cols

---

**Join metrics**

**Description**

Calculate and join selected evaluation metrics given a data.frame of simulation study results. Provides a fast way to add multiple metrics and their Monte Carlo standard errors.

**Usage**

```r
join_metrics(
  data,  
  id_cols,  
  metrics = c("coverage", "mse", "modSE"),  
  true_value = NULL,  
  ll_col = NULL,  
  ul_col = NULL,  
  estimates_col = NULL,  
  se_col = NULL,  
  p_col = NULL,  
  alpha = 0.05  
)
```

**Arguments**

- **data**: A data.frame that contains results from simulation study and the necessary columns to compute metrics.
- **id_cols**: Column name(s) on which to group data and calculate metrics.
- **metrics**: A vector of metrics to be calculated.
- **true_value**: The true parameter to be estimated.
- **ll_col**: Name of the column that contains the lower limit of the confidence intervals. (Required for calculating coverage.)
- **ul_col**: Name of the column that contains the upper limit of the confidence intervals. (Required for calculating coverage.)
- **estimates_col**: Name of the column that contains the parameter estimates. (Required for calculating bias, empSE, and mse.)
- **se_col**: Name of the column that contains the standard errors. (Required for calculating modSE.)
- **p_col**: Name of the column that contains the p-values. (Required for calculating rejection.)
- **alpha**: The nominal significance level specified. (Required for calculating rejection.)

**Value**

data.frame containing metrics and id_cols
Examples

```r
simulations_df <- data.frame(
  idx=rep(1:10, 100),
  idx2=sample(c("a", "b"), size=1000, replace=TRUE),
  p_value=runif(1000),
  est=rnorm(n=1000),
  conf.ll= rnorm(n=1000, mean=-20),
  conf.ul= rnorm(n=1000, mean=20)
)
res <- join_metrics(
  data=simulations_df,
  id_cols=c("idx", "idx2"),
  metrics=c("rejection", "coverage", "mse"),
  true_value=0,
  ll_col="conf.ll",
  ul_col="conf.ul",
  estimates_col="est",
  p_col="p_value",
)
```

modSE

*Calculates the average model standard error*

Description

Calculates the average model standard error and the Monte Carlo standard error of this estimate.

Usage

```r
modSE(se, get = c("modSE", "modSE_mcse"), na.rm = FALSE, ...)
```

Arguments

- `se` A numeric vector containing the standard errors from the model(s).
- `get` A character vector containing the values returned by the function.
- `na.rm` A logical value indicating whether NA values for `se` should be removed before `modSE` calculation.
- `...` Additional arguments to be ignored.

Value

A named vector containing the estimate and the Monte Carlo standard error for the average model standard error.

Examples

```r
modSE(se=runif(n=20, min=1, max=1.5))
```
Calculate the Mean Squared Error

Description

Calculates the Mean Squared Error of the model estimates from the true value and the Monte Carlo standard error for this estimate.

Usage

```r
mse(true_value, estimates, get = c("mse", "mse_mcse"), na.rm = FALSE, ...)
```

Arguments

- `true_value`: The true value which is being estimated.
- `estimates`: A numeric vector containing the estimates from the model(s).
- `get`: A character vector containing the values returned by the function.
- `na.rm`: A logical value indicating whether NA values for `estimates` should be removed before MSE calculation.
- `...`: Additional arguments to be ignored.

Value

A named vector containing the estimate and the Monte Carlo standard error for the bias.

Examples

```r
mse(true_value=0, estimates=rnorm(100))
```

Calculate the rejection

Description

Calculates the rejection (%) of the model p-values, according to the specified alpha, and the Monte Carlo standard error for this estimate.

Usage

```r
rejection(p, alpha = 0.05, get = c("rejection", "rejectionmcse"), na.rm = FALSE, ...)
```
relativeErrorModSE

Arguments

- `p` P-values from the models.
- `alpha` The nominal significance level specified. The default is 0.05.
- `get` A character vector containing the values returned by the function.
- `na.rm` A logical value indicating whether NA values for `p` should be removed before rejection calculation.
- `...` Additional arguments to be ignored.

Value

A named vector containing the estimate and the Monte Carlo standard error for the rejection.

Examples

```r
rejection(p=runif(200, min=0, max=1))
```

Description

Calculates the relative (%) error in model standard error and the (approximate) Monte Carlo standard error of this estimate.

Usage

```r
relativeErrorModSE(
  se,
  estimates,
  get = c("relativeErrorModSE", "relativeErrorModSE_mcse"),
  na.rm = FALSE,
  ...
)
```

Arguments

- `se` A numeric vector containing the standard errors from the model(s).
- `estimates` A numeric vector containing the estimates from the model(s).
- `get` A character vector containing the values returned by the function.
- `na.rm` A logical value indicating whether NA values for `se` and `estimates` should be removed before `modSE` and `empSE` calculation.
- `...` Additional arguments to be ignored.
**relativePrecision**

**Value**

A named vector containing the estimate and the Monte Carlo standard error for the relative (%) error in model standard error.

**Examples**

```r
tableErrorModSE(se=rnorm(n=1000, mean=10, sd=0.5), estimates=rnorm(n=1000))
```

---

**relativePrecision**

*Calculates the relative (%) increase in precision between two methods*

**Description**

Calculates the relative (%) increase in precision between two competing methods (B vs A). As this metric compares two methods directly, it cannot be used in `join_metrics()`.

**Usage**

```r
relativePrecision(
    estimates_A,
    estimates_B,
    get = c("relativePrecision", "relativePrecision_mcse"),
    na.rm = FALSE
)
```

**Arguments**

- `estimates_A` A numeric vector containing the estimates from model A.
- `estimates_B` A numeric vector containing the estimates from model B.
- `get` A character vector containing the values returned by the function.
- `na.rm` A logical value indicating whether NA values for estimates should be removed before empSE calculation.

**Value**

A named vector containing the estimate and the Monte Carlo standard error for the relative (%) increase in precision of method B versus method A.

**Examples**

```r
relativePrecision(estimates_A=rnorm(n=1000), estimates_B=rnorm(n=1000))
```
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