

Package: simMetric (via r-universe)

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

Version 0.1.1

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

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bias	<i>Calculate the bias</i>
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Description

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

Usage

```
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

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

biasEliminatedCoverage	<i>Calculate the bias-eliminated coverage</i>
------------------------	---

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.

Usage

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

Arguments

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

<code>coverage</code>	<i>Calculate the coverage</i>
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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

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

<code>empSE</code>	<i>Calculate the empirical standard error</i>
--------------------	---

Description

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

Usage

```
empSE(estimates, get = c("empSE", "empSE_mcse"), na.rm = FALSE, ...)
```

Arguments

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

Value

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

Examples

```
empSE(estimates=rnorm(100))
```

join_metrics	<i>Join metrics</i>
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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

```
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

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

Value

`data.frame` containing metrics and `id_cols`

Examples

```

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

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

Arguments

<code>se</code>	A numeric vector containing the standard errors from the model(s).
<code>get</code>	A character vector containing the values returned by the function.
<code>na.rm</code>	A logical value indicating whether NA values for <code>se</code> should be removed before <code>modSE</code> calculation.
<code>...</code>	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

```
modSE(se=runif(n=20, min=1, max=1.5))
```

mse	<i>Calculate the Mean Squared Error</i>
-----	---

Description

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

Usage

```
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

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

rejection	<i>Calculate the rejection</i>
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Description

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

Usage

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

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

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

relativeErrorModSE	<i>Calculates the relative (%) error in model standard error</i>
--------------------	--

Description

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

Usage

```
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.

Value

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

Examples

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

relativePrecision	<i>Calculates the relative (%) increase in precision between two methods</i>
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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

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

Arguments

<code>estimates_A</code>	A numeric vector containing the estimates from model A.
<code>estimates_B</code>	A numeric vector containing the estimates from model B.
<code>get</code>	A character vector containing the values returned by the function.
<code>na.rm</code>	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

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

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