ANOVAforMRMCLimitsofAgreement

December 12, 2020

`result.validMRMCVarEstimate.nReader`
Result of simulation study to validate and characterize the MRMC limits of agreement estimates

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Description

Result of simulation study to validate and characterize the MRMC limits of agreement estimates

Usage

```
result.validMRMCVarEstimate.nReader

result.validMRMCVarEstimate.nCase

result.validMRMCVarEstimate.parameter
```

Format

A dataframe with the following columns:

nReader Number of Readers
nCase Number of Cases
alpha_R Reader related parameter
sigma_C Case related parameter
WR_var_MCmean Monte Carlo mean of variance estimation for the WRBM difference score
WR_var_MCvar Monte Carlo variance of variance estimation for the WRBM difference score
True_WR_var Theoretical value for WRBM variance derived from the simulation model
WR_var_relative_bias relative bias for WRBM variance
WR_CV coefficient of variation for WRBM variance
BR_var_MCmean Monte Carlo mean of variance estimation for the BRBM difference score
BR_var_MCvar Monte Carlo variance of variance estimation for the BRBM difference score
True_BR_var Theoretical value for BRBM variance derived from the simulation model
BR_var_relative_bias relative bias for BRBM variance
BR_CV coefficient of variation for BRBM variance

An object of class `data.frame` with 11 rows and 14 columns.

An object of class `data.frame` with 25 rows and 14 columns.

Details

There are three parameter sets for this simulation:

result.validMRMCVarEstimate.nReader Different number of readers $J = 3, 4, ..., 10, K = 100, \alpha_R = 10, \sigma_C^2 = 1$

result.validMRMCVarEstimate.nCase Different number of cases $K = 50, 60, ..., 150, J = 5, \alpha_R = 10, \sigma_C^2 = 1$

result.validMRMCVarEstimate.parameter Different reader and case variabilities $(\alpha_R, \sigma_C^2) \in \{3, 4, 6, 11, 21\} \times \{0.1, 0.2, 0.4, \frac{2}{3}, 1\}, J = 5, K = 100$

In all the parameter sets, $\beta_R = \beta_{\tau R} = 1, \alpha_R = \alpha_{\tau R}, \sigma_C^2 = \sigma_{\tau C}^2$. For each parameter setting, we simulate 1000 trials.

`result.validSimulation.alphaR`

Result of simulation study to verify the simulation is consistent with the derived theoretical values

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Description

Result of simulation study to verify the simulation is consistent with the derived theoretical values

Usage

```
result.validSimulation.alphaR

result.validSimulation.sigmaC
```

Format

A dataframe with the following column:

sigma_C Case related parameter

alpha_R Reader related parameter

WR_mean Monte Carlo mean of the WRBM difference score

WR_var Monte Carlo variance of the WRBM difference score

BR_mean Monte Carlo mean of the BRBM difference score

BR_var Monte Carlo variance of the BRBM difference score

True_WR_var Theoretical value for WRBM variance derived from the simulation model

True_BR_var Theoretical value for BRBM variance derived from the simulation model

WR_var_relative_bias relative bias for WRBM variance

BR_var_relative_bias relative bias for BRBM variance

An object of class `data.frame` with 20 rows and 10 columns.

Details

There are two parameter sets for this simulation:

result.validSimulation.alphaR In this study, we fixed the case-related parameter but change the reader related fixed the case related parameters $\sigma_C^2 = \sigma_{\tau C}^2 = 1$ and allowed the reader related parameter $\alpha_R (= \alpha_{\tau R})$ to range from 2 to 20.

result.validSimulation.sigmaC In this study, we fixed the reader related parameters $\alpha_R = \alpha_{\tau R} = 10$ and allowed the case related parameter $\sigma_C^2 (= \sigma_{\tau C}^2)$ to range from 0.1 to 2, incrementing by 0.1.

In both parameter sets, $\beta_R = \beta_{\tau R} = 1$, so that the reader variability is only affected by α_R. We simulated 100,000 trials with each trial having 4 measurements from 2 readers for a single case under 2 modalities. The Monte Carlo estimates of the variances are the sample variances of the 100,000 independent WRBM and BRBM differences.

`validateMRMCVarEstimation`

Validate and characterize the MRMC limits of agreement estimates

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Description

This function simulates MRMC study with `nReader` readers and `nCase` cases. From the output of `laWRBM.anova` and `laBRBM.anova`, we exact the variance estimations for WRBM and BRBM differences. It outputs the Monte Carlo mean of the variance estimation across all the simulation trials. The relative bias of the Monte Carlo mean comparing to the theoretical value of the variance and the coefficient of variation is also calculated.

Usage

```
validateMRMCVarEstimation(
  nR.list,
  nC.list,
  alpha_R.list,
  sigma_C.list,
  nTrials = 1000
)
```

Arguments

`nR.list`	A r-dimension array for the number of readers in each MRMC study
`nC.list`	A c-dimension array for the number of cases in each MRMC study
`alpha_R.list`	A a-dimension array for the reader related parameter
`sigma_C.list`	A b-dimension array for the case related parameter
`nTrials`	Number of MRMC simulations. Default is 1000

Details

Let $\hat{V}_{BR}^{12}$ denote the estimation of the variance for the BRBM difference for each simulated MRMC study, then the relative bias is defined as $relativeBias\ (\hat{V}_{BR}^{12}) = (\sum \hat{V}_{BR}^{12}/nTrials - V_{BR}^{12})/V_{BR}^{12}$, and the coefficient of variantion is defined as $CV\ (\hat{V}_{BR}^{12}) = sd(\hat{V}_{BR}^{12})/V_{BR}^{12}$, where $sd()$ denote sample standard deviation.

Value

A dataframe with $r * c * a * b$ rows. Each column is as following:

nReader Number of Readers

nCase Number of Cases

alpha_R Reader related parameter

sigma_C Case related parameter

WR_var_MCmean Monte Carlo mean of variance estimation for the WRBM difference score

WR_var_MCvar Monte Carlo variance of variance estimation for the WRBM difference score

True_WR_var Theoretical value for WRBM variance derived from the simulation model

WR_var_relative_bias relative bias for WRBM variance

WR_CV coefficient of variation for WRBM variance

BR_var_MCmean Monte Carlo mean of variance estimation for the BRBM difference score

BR_var_MCvar Monte Carlo variance of variance estimation for the BRBM difference score

True_BR_var Theoretical value for BRBM variance derived from the simulation model

BR_var_relative_bias relative bias for BRBM variance

BR_CV coefficient of variation for BRBM variance

Examples

```
library(iMRMC)
nR.list <- c(5)
nC.list <- c(100)
sigma_C.list <- c(1)
alpha_R.list <- c(10)
#result <- validateMRMCVarEstimation(nR.list, nC.list, alpha_R.list, sigma_C.list)
```

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validateSimulation *Verify the simulation is consistent with the derived theoretical values*

Description

This function simulates independent WRBM and BRBM difference scores and outputs the Monte Carlo mean and variance across the trials for each parameter setting. The relative bias of the Monte Carlo variance comparing to the theoretical value of the variance is also calculated.

Usage

```
validateSimulation(alpha_R.list, sigma_C.list, nTrials = 1e+05)
```

Arguments

alpha_R.list	A a-dimension array for the reader related parameter
sigma_C.list	A b-dimension array for the case related parameter
nTrials	Number of independent trials. Default is 100000

Details

Let $\tilde{V}_{BR}^{12}$ denote the Monte Carlo variance of the BRBM difference, then the relative bias is defined as $relativeBias\ (\tilde{V}_{BR}^{12}) = (\tilde{V}_{BR}^{12} - V_{BR}^{12})/V_{BR}^{12}$.

Value

A dataframe with $a * b$ rows. Each column is as following:

sigma_C Case related parameter

alpha_R Reader related parameter

WR_mean Monte Carlo mean of the WRBM difference score

WR_var Monte Carlo variance of the WRBM difference score

BR_mean Monte Carlo mean of the BRBM difference score

BR_var Monte Carlo variance of the BRBM difference score

True_WR_var Theoretical value for WRBM variance derived from the simulation model

True_BR_var Theoretical value for BRBM variance derived from the simulation model

WR_var_relative_bias relative bias for WRBM variance

BR_var_relative_bias relative bias for BRBM variance

Examples

```
library(iMRMC)
sigma_C.list <- c(1)
alpha_R.list <- c(10)
#result <- validateSimulation(alpha_R.list, sigma_C.list)
```

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