

ANOVA for MRMCLimitsofAgreement

December 11, 2020

validateMRMCVarEstimation

Validate and characterize the MRMC limits of agreement estimates

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

<code>nR.list</code>	A r -dimension array for the number of readers in each MRMC study
<code>nC.list</code>	A c -dimension array for the number of cases in each MRMC study
<code>alpha_R.list</code>	A a -dimension array for the reader related parameter
<code>sigma_C.list</code>	A b -dimension array for the case related parameter
<code>nTrials</code>	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 variation 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(3,4,5)
nC.list <- c(100)
sigma_C.list <- c(1)
alpha_R.list <- c(10)
result <- validateMRMCVarEstimation(alpha_R.list, sigma_C.list)
```

validateSimulation	<i>Verify the simulation is consistent with the derived theoretical values</i>
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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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