Package 'manMCMedMiss'

January 9, 2023

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Description

The function generates a data set with missing values for data generated by GenData using the multivariate amputation approach. See mice::ampute() for more details.

Usage

```
AmputeData(data_complete, mech = "MAR", prop = 0.3, patterns = NULL)
```

Arguments

data_complete Numeric matrix. Output of the GenData function or a three-column data set with

complete data.

mech Missing data mechanism.

prop Proportion of missing data.

patterns Numeric matrix consisting of zeroes and ones. Each row in the matrix represents

a missing data pattern where 0 indicates a missing observation. If patterns = NULL, the default value is all possible missing data patterns for a data set with 3

columns.

Value

Returns a dataframe.

Author(s)

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References

Schouten, R. M., Lugtig, P. and Vink, G. (2018). Generating missing values for simulation purposes: A multivariate amputation procedure. *Journal of Statistical Computation and Simulation*, 88(15), 1909–1930. doi:10.1080/00949655.2018.1491577

See Also

Other Data Generation Functions: GenData(), ImputeData()

Check

Check Replication

Description

Check Replication

Usage

```
Check(taskids, repids, output_folder, nbmi)
```

Arguments

taskids Vector of taskids. repids Vector of repids.

output_folder Character string. Output folder.

nbmi Logical. If nbmi = TRUE, include MINB, NBMI, and StackedMINB.

Value

Returns file names of replications that need to be run.

Author(s)

CheckAmputeData 5

CheckAmputeData Check Replication - SimAmputeData

Description

Check Replication - SimAmputeData

Usage

CheckAmputeData(taskid, repid, output_folder, suffix)

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

 $Check \ \textit{Replication - SimFitModelMI} \\$

Description

Check Replication - SimFitModelMI

```
CheckFitModelMI(taskid, repid, output_folder, suffix)
```

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Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

CheckFitModelML Check Replication - SimFitModelML

Description

Check Replication - SimFitModelML

Usage

```
CheckFitModelML(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

CheckGenData 7

CheckGenData Check Replication - SimGenData

Description

Check Replication - SimGenData

Usage

CheckGenData(taskid, repid, output_folder, suffix)

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

 $Check \ Impute Data \\ Check \ Replication - Sim Impute Data$

Description

Check Replication - SimImputeData

Usage

CheckImputeData(taskid, repid, output_folder, suffix)

8 CheckJointSigMI

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

CheckJointSigMI Check Replication - SimJointSigMI

Description

Check Replication - SimJointSigMI

Usage

```
CheckJointSigMI(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

CheckJointSigML 9

CheckJointSigML

Check Replication - SimJointSigML

Description

Check Replication - SimJointSigML

Usage

```
CheckJointSigML(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

CheckMCMI

Check Replication - SimMCMI

Description

Check Replication - SimMCMI

```
CheckMCMI(taskid, repid, output_folder, suffix)
```

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Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

Check Replication - SimMCML

Description

Check Replication - SimMCML

Usage

```
CheckMCML(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

CheckMINB 11

CheckMINB

Check Replication - SimMINB

Description

Check Replication - SimMINB

Usage

```
CheckMINB(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

CheckNBMI

Check Replication - SimNBMI

Description

Check Replication - SimNBMI

```
CheckNBMI(taskid, repid, output_folder, suffix)
```

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Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

Check Replication - SimNBML

Description

Check Replication - SimNBML

Usage

```
CheckNBML(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

CheckStackedMINB 13

CheckStackedMINB Check Replication - SimStackedMINB

Description

Check Replication - SimStackedMINB

Usage

```
CheckStackedMINB(taskid, repid, output_folder, suffix)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Details

This function is executed via the Check function.

Value

Returns file names of replications that need to be run.

Author(s)

Ivan Jacob Agaloos Pesigan

Compress Replication

Description

Compress Replication

output_folder

Usage

```
Compress(taskid, repid, output_folder)
```

Arguments

taskid Positive integer. Task ID.
repid Positive integer. Replication ID.

Character string. Output folder.

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Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

elliot2007

Intervention on Healthy Dietary Behavior Via Knowledge of Healthy Dietary Behavior

Description

A study by Elliot and others (2007) on the effects of an intervention on healthy dietary behavior mediated by knowledge of healthy dietary behavior. This data was used as an empirical example in Yuan and MacKinnon (2009) and Wu and Jia (2013).

Usage

elliot2007

Format

A data frame with 354 cases and 3 variables:

- **x** Intervention group membership.
- **m** Knowledge of healthy dietary behavior (knowledge post-intervention minus knowledge pre-intervention).
- y Healthy dietary behavior (behavior post-intervention minus behavior pre-intervention).

Source

https://odin.mdacc.tmc.edu/~yyuan/Software/Mediation/Bayesian/CodeRelease/BayesianMediation/firefighters.txt

References

Elliot, D. L., Goldberg, L., Kuehl, K. S., Moe, E. L., Breger, R. K., & Pickering, M. A. (2007). The PHLAME (Promoting Healthy Lifestyles: Alternative Models' Effects) firefighter study: Outcomes of two models of behavior change. *Journal of occupational and environmental medicine*, 49(2), 204–213. doi:10.1097/JOM.0b013e3180329a8d

Wu, W., & Jia, F. (2013). A new procedure to test mediation with missing data through nonparametric bootstrapping and multiple imputation, *Multivariate Behavioral Research*, 48(5), 663-691. doi:10.1080/00273171.2013.816235

Yuan, Y., & MacKinnon, D. P. (2009). Bayesian mediation analysis. *Psychological methods*, *14*(4), 301–322. doi:10.1037/a0016972

FigBoxPlot 15

FigBoxPlot	Box Plot of Type I Error Rate, Statistical Power, and Miss Rate

Description

Box Plot of Type I Error Rate, Statistical Power, and Miss Rate

Usage

```
FigBoxPlot(results, type, mech, prop, n = NULL)
```

Arguments

results	Data frame. The package data frame results().
type	Character string. Type of results to plot. Valid values are "type1", "power", and "miss" for Type I error rate, statistical power, and miss rate, respectively.
mech	Character string. Missing data mechanism. Valid values are "COMPLETE", "MAR", and "MCAR".
prop	Numeric. Proportion of missing data. Valid values are .1, .2, .3. Note that if $mech = "COMPLETE"$, prop will be set to 0.
n	Vector of positive integers. Sample size. Valid values are 50, 75, 100, 150, 200, 250, 500, and 1000. If n = NULL, use all sample sizes.

Value

Returns a ggplot2 plot object.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Figure Functions: FigScatterPlot()

FigScatterPlot

FigScatterPlot	Scatter Plot of Type I Error Rate, Statistical Power, and Miss Rate

Description

Scatter Plot of Type I Error Rate, Statistical Power, and Miss Rate

Usage

```
FigScatterPlot(results, type, mech, prop, n = NULL)
```

Arguments

results	Data frame. The package data frame results().
type	Character string. Type of results to plot. Valid values are "type1", "power", and "miss" for Type I error rate, statistical power, and miss rate, respectively.
mech	Character string. Missing data mechanism. Valid values are "COMPLETE", "MAR", and "MCAR".
prop	Numeric. Proportion of missing data. Valid values are .1, .2, .3. Note that if $mech = "COMPLETE"$, prop will be set to 0.
n	Vector of positive integers. Sample size. Valid values are 50, 75, 100, 150, 200, 250, 500, and 1000. If n = NULL, use all sample sizes.

Value

Returns a ggplot2 plot object.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Figure Functions: FigBoxPlot()

FitModelIndirect 17

FitModelIndirect	Fit the Simple Mediation Model using Normal Theory Maximum Like-
	lihood (Indirect Effect)

Description

Fit the Simple Mediation Model using Normal Theory Maximum Likelihood (Indirect Effect)

Usage

```
FitModelIndirect(data_complete, consistent = TRUE)
```

Arguments

complete data.

consistent Logical. If consistent = TRUE, use the consistent estimate of the covariance

matrix (maximum likelihood estimator). If consistent = FALSE, use the unbi-

ased estimate of the covariance matrix.

Value

Returns the indirect effect.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Model Fitting Functions: FitModelMI(), FitModelML()

FitModelMI	Fit the Simple Mediation Model using Multiple Imputation

Description

Fit the Simple Mediation Model using Multiple Imputation

```
FitModelMI(data_mi, mplus_bin)
```

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Arguments

data_mi List of numeric matrices. Output of the ImputeData function or a list of three-

column data sets with imputed data.

mplus_bin Character string. Path of Mplus binary.

Details

Let

$$M =$$
Number of imputations, and

$$m = \{1, 2, \cdots, M\}.$$

The vector of pooled coefficients/parameter estimates is given by

$$\bar{\boldsymbol{\theta}} = M^{-1} \sum_{m=1}^{M} \hat{\boldsymbol{\theta}}_{m}.$$

The covariance within imputations is given by

$$\mathbf{V}_{\text{within}} = M^{-1} \sum_{m=1}^{M} \text{Var} \left(\hat{\boldsymbol{\theta}}_{m} \right)$$

where $\operatorname{Var}\left(\hat{\boldsymbol{\theta}}_{m}\right)$ is the parameter covariance matrix for the m^{th} imputation. The covariance between imputations is given by

$$\mathbf{V}_{\text{between}} = (M-1)^{-1} \sum_{m=1}^{M} \left(\hat{\boldsymbol{\theta}}_{m} - \bar{\boldsymbol{\theta}} \right) \left(\hat{\boldsymbol{\theta}}_{m} - \bar{\boldsymbol{\theta}} \right)'.$$

The total covariance matrix is given by

$$\mathbf{V}_{\text{total}} = \mathbf{V}_{\text{within}} + \mathbf{V}_{\text{between}} + M^{-1}\mathbf{V}_{\text{between}}.$$

The adjusted total covariance matrix is given by

$$\tilde{\mathbf{V}}_{\text{total}} = (1 + \text{ARIV}) \, \mathbf{V}_{\text{within}}$$

where

$$\mathrm{ARIV} = k^{-1} \left[\left(1 + M^{-1} \right) \mathrm{tr} \left(\mathbf{V}_{\mathrm{between}} \mathbf{V}_{\mathrm{within}}^{-1} \right) \right]$$

and k is the number of parameters.

Value

Returns a list with the following elements:

coef Vector of pooled coefficients/parameter estimates $\bar{\theta}$.

vcov Total covariance matrix $V_{\rm total}$.

vcov_tilde Adjusted total covariance matrix $\tilde{\mathbf{V}}_{\mathrm{total}}$.

 \mathbf{vcov} _between Covariance between imputations $\mathbf{V}_{\mathrm{between}}$.

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 $vcov_within$ Covariance within imputations V_{within} .

ariv Average relative increase in variance ARIV.

m Number of imputations M.

k Number of parameters k.

nu1 Numerator degrees of freedom ν_1 for D_1 .

nu2 Denominator degrees of freedom ν_2 for D_1 .

d1 D_1 test statistic.

Author(s)

Ivan Jacob Agaloos Pesigan

References

Li, K. H., Raghunathan, T. E., & Rubin, D. B. (1991). Large-sample significance levels from multiply imputed data using moment-based statistics and an F reference distribution. *Journal of the American Statistical Association*, 86 (416), 1065–1073. doi:10.1080/01621459.1991.10475152

Rubin, D. B. (1987). *Multiple imputation for nonresponse in surveys*. John Wiley & Sons, Inc. doi:10.1002/9780470316696

See Also

Other Model Fitting Functions: FitModelIndirect(), FitModelML()

FitModelML	Fit the Simple Mediation Model using Normal Theory Maximum Likelihood

Description

Fit the Simple Mediation Model using Normal Theory Maximum Likelihood

Usage

```
FitModelML(data, mplus_bin)
```

Arguments

data Numeric matrix. Output of the GenData or AmputeData functions.

mplus_bin Character string. Path of Mplus binary.

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Value

```
Returns a list with the following elements:
```

fit Model fit.

coef Coefficients/parameter estimates

vcov Sampling variance-covariance matrix.

output Mplus output.

Values in fit.

free_parameters Number of free parameters

h0_loglikelihood H0 loglikelihood.

h1_loglikelihood H1 loglikelihood.

aic Akaike information criterion (AIC).

bic Bayesian information criterion (BIC).

sabic Sample-size adjusted BIC (SABIC).

chisq Chi-square value.

chisq_df Chi-square degrees of freedom.

chisq_p Chi-square p-value.

cfi Comparative fit index (CFI).

tli Tucker-Lewis index (TLI).

rmsea Root mean square error of approximation (RMSEA) estimate.

rmsea_low Root mean square error of approximation (RMSEA) lower limit confidence interval.

rmsea_up Root mean square error of approximation (RMSEA) upper limit confidence interval.

rmsea_p Root mean square error of approximation (RMSEA) probability.

srmr Standardized root mean square residual (SRMR).

condition_number Condition number for the information matrix (ratio of smallest to largest eigenvalue).

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Model Fitting Functions: FitModelIndirect(), FitModelMI()

GenData 21

GenData

Generate Data

Description

Let the simple mediation model be defined by the equations

$$Y = \delta_Y + \tau' X + \beta M + \varepsilon_Y,$$

and

$$M = \delta_M + \alpha X + \varepsilon_M.$$

The function generates data from the multivariate normal distribution using the model-implied mean vector and covariance matrix of the simple mediation model. See MASS::mvrnorm() for more details.

Usage

```
GenData(n = 100L, tauprime = 0, beta = 0.5, alpha = 0.5, mu = 0, sigmasq = 1)
```

Arguments

n	Positive integer.	Sample size.
---	-------------------	--------------

tauprime Numeric. τ' , that is, the slope for Y regressed on X, adjusting for M. beta Numeric. β , that is, the slope for Y regressed on M, adjusting for X.

alpha Numeric vector. Significance level.

mu Numeric. Common mean for X,M, and Y, that is, $\mu_X=\mu_M=\mu_Y.$ sigmasq Numeric. Common variance for X,M, and Y, that is, $\sigma_X^2=\sigma_M^2=\sigma_Y^2.$

Value

Returns a matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

References

MacKinnon, D. P. (2008). *Introduction to statistical mediation analysis*. Lawrence Erlbaum Associates.

See Also

Other Data Generation Functions: AmputeData(), ImputeData()

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ImputeData

Impute Data

Description

Generates m complete data sets using multiple imputation.

Usage

```
ImputeData(data_missing, m, mplus_bin)
```

Arguments

with missing data.

m Positive integer. Number of imputations.mplus_bin Character string. Path of Mplus binary.

Value

Returns a list of complete data sets.

Author(s)

Ivan Jacob Agaloos Pesigan

References

```
Asparouhov, T., & Muthen, B. (2022). Multiple imputation with Mplus. Retrieved from http://www.statmodel.com/download/Imputations7.pdf
```

See Also

Other Data Generation Functions: AmputeData(), GenData()

JointSigMI Joint Significance Test for the Indirect Effect using Multiple Imputation

Description

Joint Significance Test for the Indirect Effect using Multiple Imputation

```
JointSigMI(fit_mi, alpha = c(0.05, 0.01, 0.001))
```

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Arguments

fit_mi Object. Output of the FitModelMI function.

alpha Numeric vector. Significance level.

Value

Returns a list with the following elements:

vcov Joint significance test based on the total covariance matrix.

vcov_tilde Joint significance test based on the adjusted total covariance matrix.

Note the 1 corresponds to a significant result and 0 otherwise. The output vector's name corresponds to the alpha level.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Significance Test Functions: JointSigML()

Joint Significance Test for the Indirect Effect using Normal Theory

Maximum Likelihood

Description

Joint Significance Test for the Indirect Effect using Normal Theory Maximum Likelihood

Usage

```
JointSigML(fit_ml, alpha = c(0.05, 0.01, 0.001))
```

Arguments

fit_ml Object. Output of the FitModelML function.

alpha Numeric vector. Significance level.

Value

Note the 1 corresponds to a significant result and 0 otherwise. The output vector's name corresponds to the alpha level.

Author(s)

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See Also

Other Significance Test Functions: JointSigMI()

MCMI Monte Carlo Confidence Intervals for the Indirect Effect using Multiple Imputation

Description

Monte Carlo Confidence Intervals for the Indirect Effect using Multiple Imputation

Usage

```
MCMI(fit_mi, R = 20000L, alpha = c(0.05, 0.01, 0.001))
```

Arguments

fit_mi Object. Output of the FitModelMI function.

R Positive integer. Number of Monte Carlo replications.

alpha Numeric vector. Significance level.

Value

Returns a list with the following elements:

vcov Monte Carlo confidence intervals based on the total covariance matrix.

vcov_tilde Monte Carlo confidence intervals based on the adjusted total covariance matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

```
Other Confidence Interval Functions: MCML(), MINB(), NBMI(), NBML(), NBStackedMI()
```

MCML 25

MCML	Monte Carlo Confidence Intervals for the Indirect Effect using Normal Theory Maximum Likelihood
	тнеот у тахітат Ексиноой

Description

Monte Carlo Confidence Intervals for the Indirect Effect using Normal Theory Maximum Likelihood

Usage

```
MCML(fit_ml, R = 20000L, alpha = c(0.05, 0.01, 0.001))
```

Arguments

fit_ml Object. Output of the FitModelML function.

R Positive integer. Number of Monte Carlo replications.

alpha Numeric vector. Significance level.

Value

Monte Carlo confidence intervals.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Confidence Interval Functions: MCMI(), MINB(), NBMI(), NBML(), NBStackedMI()

MICombine	Combine	Parameter	Estimates	Vector	and	Sampling	Variance-
	Covarian	ce Matrix Es	timated fron	n Multip	le Imp	outations	

Description

Combine Parameter Estimates Vector and Sampling Variance-Covariance Matrix Estimated from Multiple Imputations

```
MICombine(param_vec, var_mat)
```

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Arguments

param_vec List of vectors of paramater estimates.

var_mat List of matrices of sampling variances and covariances.

Value

Returns a list with the following elements:

m Number of imputations M.

k Number of parameters k.

estimates Vector of pooled coefficients/parameter estimates $\bar{\theta}$.

within Covariance within imputations $V_{\rm within}$.

between Covariance between imputations V_{between} .

total Total covariance matrix $V_{\rm total}$.

total_adjusted Adjusted total covariance matrix $\tilde{\mathbf{V}}_{\mathrm{total}}$.

ariv Average relative increase in variance ARIV.

Author(s)

Ivan Jacob Agaloos Pesigan

References

Li, K. H., Raghunathan, T. E., & Rubin, D. B. (1991). Large-sample significance levels from multiply imputed data using moment-based statistics and an F reference distribution. *Journal of the American Statistical Association*, 86 (416), 1065–1073. doi:10.1080/01621459.1991.10475152

Rubin, D. B. (1987). *Multiple imputation for nonresponse in surveys*. John Wiley & Sons, Inc. doi:10.1002/9780470316696

MINB	Nonparametric Bootstrap Confidence Intervals for the Indirect Effect
	using Multiple Imputation (NB nested within MI or MI(NB))

Description

Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Multiple Imputation (NB nested within MI or MI(NB))

```
MINB(data_mi, B = 5000L, alpha = c(0.05, 0.01, 0.001))
```

NBMI 27

Arguments

data_mi	List of numeric matrices. Output of the ImputeData function or a list of three-column data sets with imputed data.
В	Positive integer. Number of bootstrap samples.
alpha	Numeric vector. Significance level.

Value

Nonparametric bootstrap percentile confidence intervals.

Author(s)

Ivan Jacob Agaloos Pesigan

References

Wu, Wei., & Jia, F. (2012). A new procedure to test mediation with missing data through nonparametric bootstrapping and multiple imputation. *Multivariate Behavioral Research*, 48(5), 663–691. doi:10.1080/00273171.2013.816235

See Also

Other Confidence Interval Functions: MCMI(), MCML(), NBMI(), NBML(), NBStackedMI()

NBMI Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Multiple Imputation (MI nested within NB or NB(MI))

Description

Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Multiple Imputation (MI nested within NB or NB(MI))

```
NBMI(
   data_missing,
   data_mi,
   B = 5000L,
   m = 100L,
   alpha = c(0.05, 0.01, 0.001),
   mplus_bin
)
```

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Arguments

data_missing	Numeric matrix. Output of the AmputeData function or a three-column data set with missing data.
data_mi	List of numeric matrices. Output of the ImputeData function or a list of three-column data sets with imputed data.
В	Positive integer. Number of bootstrap samples.
m	Positive integer. Number of imputations.
alpha	Numeric vector. Significance level.
mplus_bin	Character string. Path of Mplus binary.

Value

Nonparametric bootstrap percentile confidence intervals.

Author(s)

Ivan Jacob Agaloos Pesigan

References

Zhang, Z., & Wang, L. (2012). Methods for mediation analysis with missing data. *Psychometrika*, 78(1), 154–184. doi:10.1007/s1133601293015

Zhang, Z., Wang, L., & Tong, X. (2015). Mediation analysis with missing data through multiple imputation and bootstrap. *Quantitative psychology research* (pp. 341–355). Springer International Publishing. doi:10.1007/9783319199771_24

See Also

Other Confidence Interval Functions: MCMI(), MCML(), MINB(), NBML(), NBStackedMI()

NBML	Nonparametric Bootstrap Confidence Intervals for the Indirect Effect
	using Normal Theory Maximum Likelihood (ML nested within NB or
	NB(ML))

Description

Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Normal Theory Maximum Likelihood (ML nested within NB or NB(ML))

```
NBML(data, B = 5000L, mplus_bin)
```

NBStackedMI 29

Arguments

data Numeric matrix. Output of the GenData or AmputeData functions.

B Positive integer. Number of bootstrap samples.

mplus_bin Character string. Path of Mplus binary.

Value

Nonparametric bootstrap confidence intervals. bc corresponds to bias-corrected and pc corresponds to percentile confidence intervals.

Author(s)

Ivan Jacob Agaloos Pesigan

See Also

Other Confidence Interval Functions: MCMI(), MCML(), MINB(), NBMI(), NBStackedMI()

NBStackedMI	Nonparametric Bootstrap Confidence Intervals for the Indirect Effect
	using Multiple Imputation (NB using Stacked MI)

Description

Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Multiple Imputation (NB using Stacked MI)

Usage

```
NBStackedMI(data_mi, B = 5000L, alpha = c(0.05, 0.01, 0.001))
```

Arguments

data_mi List of numeric matrices. Output of the ImputeData function or a list of three-

column data sets with imputed data.

B Positive integer. Number of bootstrap samples.

alpha Numeric vector. Significance level.

Value

Nonparametric bootstrap percentile confidence intervals.

Author(s)

30 results

See Also

Other Confidence Interval Functions: MCMI(), MCML(), MINB(), NBMI(), NBML()

params

Simulation Parameters

Description

Simulation Parameters

Usage

params

Format

A dataframe with 472 rows and 7 columns:

taskid Simulation Task ID.

tauprime τ' , that is, the path from X to Y, adjusting for M.

beta β , that is, the path from M to Y.

alpha α , that is, the path from X to M.

n Sample size.

sigmasqepsilonm Error variance $\sigma_{\varepsilon_M}^2$.

sigmasqepsilony Error variance $\sigma_{\varepsilon_Y}^2$.

alphabeta $\alpha\beta$, that is, the indirect effect of X on Y via M.

Author(s)

Ivan Jacob Agaloos Pesigan

results

Simulation Results

Description

Simulation Results

Usage

results

results 31

Format

A dataframe with 24,544 rows and 13 columns:

zero_hit The proportion of replications where the confidence intervals contained zero.

theta_hit The proportion of replications where the confidence intervals contained the population $\alpha\beta$.

replications Simulation replications.

taskid Simulation Task ID.

tauprime τ' , that is, the path from X to Y, adjusting for M.

beta β , that is, the path from M to Y.

alpha α , that is, the path from X to M.

n Sample size.

sigmasqepsilonm Error variance $\sigma_{\varepsilon_M}^2$.

sigmasqepsilony Error variance $\sigma_{\varepsilon_{\nu}}^2$.

alphabeta $\alpha\beta$, that is, the indirect effect of X on Y via M.

mechanism Missing data mechanism. "COMPLETE" for complete data, "MCAR" for missing completely at random, and "MAR" for missing at random.

proportion Proportion of missing data (.0, .1, .2, .3).

method Method used.

type1 Type I error rate.

power Statistical power.

miss Miss rate.

The methods are as follows:

MC.COMPLETE for Monte Carlo method with maximum likelihood estimates for complete data.

MC.FIML for Monte Carlo method with full information maximum likelihood estimates.

MC.MI for Monte Carlo method with multiple imputation estimates.

MC.MI.ADJ for Monte Carlo method with adjusted multiple imputation estimates.

NBBC.COMPLETE for bias-corrected nonparametric bootstrap with maximum likelihood estimates for complete data.

NBBC.FIML for full maximum likelihood nested within bias-corrected nonparametric bootstrap.

NBPC.COMPLETE for percentile nonparametric bootstrap with full maximum likelihood estimates for complete.

NBPC.FIML for full maximum likelihood nested within percentile nonparametric bootstrap.

SIG.COMPLETE for joint-significant test for complete data.

SIG.FIML for the joint-significant test with full maximum likelihood estimates.

SIG.MI for joint-significant test with multiple imputation estimates.

SIG.MI.ADJ for the joint-significant test with adjusted multiple imputation estimates.

Author(s)

32 Sim

Sim Simulation Replication

Description

Simulation Replication

Usage

```
Sim(
  taskid,
  repid,
  output_folder,
  overwrite,
  integrity,
  params_taskid,
  alpha,
  m,
  R,
  B,
  mplus_bin,
  nbmi
)
```

Arguments

taskid Positive integer. Task ID. Positive integer. Replication ID. repid output_folder Character string. Output folder. Logical. Overwrite existing output in output_folder. overwrite Logical. If integrity = TRUE, check for the output file integrity when overwrite integrity = FALSE. params_taskid Data frame with a single row. Simulation parameters for a specific taskid. Numeric vector. Significance level. alpha Positive integer. Number of imputations. m R Positive integer. Number of Monte Carlo replications. В Positive integer. Number of bootstrap samples. mplus_bin Character string. Path of Mplus binary. Logical. If nbmi = TRUE, include MINB, NBMI, and StackedMINB. nbmi

Value

The output is saved as an external file in output_folder.

SimAmputeData 33

Author(s)

Ivan Jacob Agaloos Pesigan

Description

Simulation Replication - AmputeData

Usage

SimAmputeData(taskid, repid, output_folder, seed, suffix, overwrite, integrity)

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

34 SimFitModelMI

SimFitModelMI

 $Simulation \ Replication \ - \ Fit Model MI$

Description

Simulation Replication - FitModelMI

Usage

```
SimFitModelMI(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  mplus_bin
)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

mplus_bin Character string. Path of Mplus binary.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

SimFitModelML 35

SimFitModelML Simulation Replication - FitModelML

Description

Simulation Replication - FitModelML

Usage

```
SimFitModelML(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  mplus_bin
)
```

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

mplus_bin Character string. Path of Mplus binary.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

36 SimGenData

SimFN

Simulation File Name

Description

Simulation File Name

Usage

```
SimFN(data_type, output_type, output_folder, suffix)
```

Arguments

Value

Returns a character string file name with the output_folder in the OS-specific format.

SimGenData

Simulation Replication - GenData

Description

Simulation Replication - GenData

```
SimGenData(
  taskid,
  repid,
  output_folder,
  params_taskid,
  seed,
  suffix,
  overwrite,
  integrity
)
```

SimImputeData 37

Arguments

repid Positive integer. Task ID.

repid Positive integer. Replication ID.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

Sut 11x Character suring. Output of manneneuritss....simsut 11x().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimImputeData Simulation Replication - ImputeData

Description

Simulation Replication - ImputeData

```
SimImputeData(
   taskid,
   repid,
   output_folder,
   seed,
   suffix,
   overwrite,
   integrity,
   m,
   mplus_bin
)
```

38 SimJointSigMI

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID.

output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

m Positive integer. Number of imputations.mplus_bin Character string. Path of Mplus binary.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimJointSigMI Simulation Replication - JointSigMI

Description

Simulation Replication - JointSigMI

```
SimJointSigMI(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  alpha
)
```

SimJointSigML 39

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID.

output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

alpha Numeric vector. Significance level.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimJointSigML

Simulation Replication - JointSigML

Description

Simulation Replication - JointSigML

```
SimJointSigML(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  alpha
)
```

40 SimMCMI

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

alpha Numeric vector. Significance level.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimMCMI

Simulation Replication - MCMI

Description

Simulation Replication - MCMI

```
SimMCMI(
   taskid,
   repid,
   output_folder,
   seed,
   suffix,
   overwrite,
   integrity,
   R,
   alpha
)
```

SimMCML 41

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

R Positive integer. Number of Monte Carlo replications.

alpha Numeric vector. Significance level.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimMCML

Simulation Replication - MCML

Description

Simulation Replication - MCML

```
SimMCML(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  R,
  alpha
)
```

42 SimMINB

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

R Positive integer. Number of Monte Carlo replications.

alpha Numeric vector. Significance level.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimMINB

Simulation Replication - MINB

Description

Simulation Replication - MINB

```
SimMINB(
   taskid,
   repid,
   output_folder,
   seed,
   suffix,
   overwrite,
   integrity,
   B,
   alpha
)
```

SimNBMI 43

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID.

output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMis.

 $suffix \qquad \qquad Character\ string.\ Output\ of\ manMCMedMiss:::.SimSuffix().$

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

B Positive integer. Number of bootstrap samples.

alpha Numeric vector. Significance level.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

Simulation Replication - NBMI

Description

SimNBMI

Simulation Replication - NBMI

```
SimNBMI(
   taskid,
   repid,
   output_folder,
   seed,
   suffix,
   overwrite,
   integrity,
   B,
   m,
   mplus_bin
)
```

44 SimNBML

Arguments

Positive integer. Task ID. taskid Positive integer. Replication ID. repid output_folder Character string. Output folder. seed Integer. Random seed. suffix Character string. Output of manMCMedMiss:::.SimSuffix(). overwrite Logical. Overwrite existing output in output_folder. Logical. If integrity = TRUE, check for the output file integrity when overwrite integrity = FALSE. В Positive integer. Number of bootstrap samples. Positive integer. Number of imputations.

Character string. Path of Mplus binary.

Details

mplus_bin

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimNBML Simulation Replication - NBML

Description

Simulation Replication - NBML

```
SimNBML(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  B,
  mplus_bin
)
```

SimNBStackedMI 45

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

B Positive integer. Number of bootstrap samples.

mplus_bin Character string. Path of Mplus binary.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimNBStackedMI

Simulation Replication - NBStackedMI

Description

Simulation Replication - NBStackedMI

```
SimNBStackedMI(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  B,
  alpha
)
```

46 SimProj

Arguments

taskid Positive integer. Task ID.

repid Positive integer. Replication ID. output_folder Character string. Output folder.

seed Integer. Random seed.

suffix Character string. Output of manMCMedMiss:::.SimSuffix().

overwrite Logical. Overwrite existing output in output_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

B Positive integer. Number of bootstrap samples.

alpha Numeric vector. Significance level.

Details

This function is executed via the Sim function.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimProj Simulation Project Name

Description

Simulation Project Name

Usage

SimProj()

Value

Returns the project name as a character string.

Author(s)

Sum 47

Sum Summarize Simulations

Description

Summarize Simulations

Usage

```
Sum(taskid, reps, output_folder, params_taskid, nbmi)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

nbmi Logical. If nbmi = TRUE, include MINB, NBMI, and StackedMINB.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SumBind Bind Results

Description

Bind Results

Usage

```
SumBind(tasks, output_folder, data_raw_folder, params)
```

Arguments

tasks Positive integer. Number of simulations tasks or cases.

output_folder Character string. Output folder.

data_raw_folder

Character string. data-raw folder in the project directory.

params Data frame. Simulation parameters for all simulation tasks or cases.

48 SumJointSigMI

Value

Returns a dataframe of results and parameters.

Author(s)

Ivan Jacob Agaloos Pesigan

SumHit

Extract Zero Hit and Theta Hit from Summary Output

Description

Extract Zero Hit and Theta Hit from Summary Output

Usage

```
SumHit(summary_output, params_taskid)
```

Arguments

```
summary_output Numeric matrix. Output of Sum* functions.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.
```

Value

Returns a dataframe of results and parameters.

Author(s)

Ivan Jacob Agaloos Pesigan

SumJointSigMI

Summarize Simulations - SimJointSigMI

Description

Summarize Simulations - SimJointSigMI

```
SumJointSigMI(taskid, reps, output_folder, params_taskid)
```

SumJointSigML 49

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

SumJointSigML Summarize Simulations - SimJointSigML

Description

Summarize Simulations - SimJointSigML

Usage

```
SumJointSigML(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

50 SumMCML

Summarize Simulations - SimMCMI

Description

Summarize Simulations - SimMCMI

Usage

```
SumMCMI(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

SumMCML Summarize Simulations - SimMCML

Description

Summarize Simulations - SimMCML

Usage

```
SumMCML(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

SumMINB 51

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

SumMINB

Summarize Simulations - SimMINB

Description

Summarize Simulations - SimMINB

Usage

```
SumMINB(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

52 SumNBML

SumNBMI Summarize Simulations - SimNBMI

Description

Summarize Simulations - SimNBMI

Usage

```
SumNBMI(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

SumNBML Summarize Simulations - SimNBML

Description

Summarize Simulations - SimNBML

Usage

```
SumNBML(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

SumNBStackedMI 53

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

Ivan Jacob Agaloos Pesigan

SumNBStackedMI

Summarize Simulations - SimNBStackedMI

Description

Summarize Simulations - SimNBStackedMI

Usage

```
SumNBStackedMI(taskid, reps, output_folder, params_taskid)
```

Arguments

taskid Positive integer. Task ID.

reps Positive integer. Number of replications.

output_folder Character string. Output folder.

params_taskid Data frame with a single row. Simulation parameters for a specific taskid.

Details

This function is executed via the Sum function.

Value

Returns a numeric matrix.

Author(s)

54 Tree

TabDescribe Descriptive Statistics of Type I Error Rate, Statistical Power, and M. Rate

Description

Descriptive Statistics of Type I Error Rate, Statistical Power, and Miss Rate

Usage

```
TabDescribe(results, type, mech, prop, n = NULL)
```

Arguments

results	Data frame. The package data frame results().
type	Character string. Type of results to plot. Valid values are "type1", "power", and "miss" for Type I error rate, statistical power, and miss rate, respectively.
mech	Character string. Missing data mechanism. Valid values are "COMPLETE", "MAR", and "MCAR".
prop	Numeric. Proportion of missing data. Valid values are .1, .2, .3. Note that if $mech = "COMPLETE"$, prop will be set to 0.
n	Vector of positive integers. Sample size. Valid values are 50, 75, 100, 150, 200, 250, 500, and 1000. If n = NULL, use all sample sizes.

Value

Returns a table of means (M), standard deviations (SD), and row counts (N).

Author(s)

Ivan Jacob Agaloos Pesigan

Tree	Conditional Inference Tree	

Description

Conditional Inference Tree

```
Tree(results, type, alpha = 1e-04, maxdepth = 0, dichotomize = TRUE)
```

Tree 55

Arguments

results Data frame. The package data frame results().

type Character string. Type of results to plot. Valid values are "type1", "power",

and "miss" for Type I error rate, statistical power, and miss rate, respectively.

alpha Significance level used for splitting.

maximum depth of the tree. The default maxdepth = 0 means that no restrictions

are applied to tree sizes.

dichotomize Logical. Dichotomize the outcome variable into robust = TRUE and robust =

FALSE.

Value

Returns the result of party::ctree().

Author(s)

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