# Package 'manMCMedMiss'

January 10, 2023

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<b>Title</b> Monte Carlo Confidence Intervals for the Indirect Effect with Missing Data
Version 0.9.2
<b>Description</b> Research compendium for the manuscript  Monte Carlo Confidence Intervals for the Indirect Effect with Missing Data containing scripts used in the simulation study and other supplementary materials.
<pre>URL https://github.com/jeksterslab/manMCMedMiss,</pre>
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BugReports https://github.com/jeksterslab/manMCMedMiss/issues
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Author Ivan Jacob Agaloos Pesigan [aut, cre, cph] ( <a href="https://orcid.org/0000-0003-4818-8420">https://orcid.org/0000-0003-4818-8420</a> ), Shu Fai Cheung [ctb] ( <a href="https://orcid.org/0000-0002-9871-9448">https://orcid.org/0000-0002-9871-9448</a> )
Maintainer Ivan Jacob Agaloos Pesigan <r.jeksterslab@gmail.com></r.jeksterslab@gmail.com>
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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)

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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

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  $m^{\mathrm{th}}$  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  $V_{\mathrm{within}}$ .

ariv Average relative increase in variance ARIV.

**m** Number of imputations M.

**k** Number of parameters k.

**nu1** Numerator degrees of freedom  $\nu_1$  for  $D_1$ .

**nu2** Denominator degrees of freedom  $\nu_2$  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.  $\tau'$ , that is, the slope for Y regressed on X, adjusting for M. beta Numeric.  $\beta$ , 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()
```

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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  $V_{\mathrm{between}}$ .

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
)
```

28 NBML

# **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**  $\tau'$ , that is, the path from X to Y, adjusting for M.

**beta**  $\beta$ , that is, the path from M to Y.

**alpha**  $\alpha$ , 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**  $\tau'$ , that is, the path from X to Y, adjusting for M.

**beta**  $\beta$ , that is, the path from M to Y.

**alpha**  $\alpha$ , 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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