

# Package ‘manMCMedMiss’

January 3, 2023

**Title** Monte Carlo Confidence Intervals for the Indirect Effect with Missing Data

**Version** 0.9.2

**Description** 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.

**URL** <https://github.com/jeksterslab/manMCMedMiss>,  
<https://jeksterslab.github.io/manMCMedMiss/>

**BugReports** <https://github.com/jeksterslab/manMCMedMiss/issues>

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**Depends** R (>= 3.5.0)

**Imports** stats, ggplot2, MASS, mice, party

**Suggests** knitr, rmarkdown, testthat, DT, microbenchmark, semmcci

**RoxygenNote** 7.2.3

**NeedsCompilation** no

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AmputeData	<i>Ampute Data</i>
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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 <code>patterns = NULL</code> , the default value is all possible missing data patterns for a data set with 3 columns.

Value

Returns a dataframe.

Author(s)

Ivan Jacob Agaloos Pesigan

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\(\)](#)

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Check	<i>Check Replication</i>
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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)

Ivan Jacob Agaloos Pesigan

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CheckAmputeData	<i>Check Replication - SimAmputeData</i>
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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

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CheckFitModelMI

*Check Replication - SimFitModelMI*

---

**Description**

Check Replication - SimFitModelMI

**Usage**

```
CheckFitModelMI(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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckFitModelML	<i>Check Replication - SimFitModelML</i>
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**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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckGenData	<i>Check Replication - SimGenData</i>
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**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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckImputeData

*Check Replication - SimImputeData*

---

**Description**

Check Replication - SimImputeData

**Usage**

```
CheckImputeData(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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckJointSigMI	<i>Check Replication - SimJointSigMI</i>
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**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)**

Ivan Jacob Agaloos Pesigan

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CheckJointSigML	<i>Check Replication - SimJointSigML</i>
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**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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckMCMI

*Check Replication - SimMCMI*

---

**Description**

Check Replication - SimMCMI

**Usage**

```
CheckMCMI(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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckMCML	<i>Check Replication - SimMCML</i>
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**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)**

Ivan Jacob Agaloos Pesigan

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CheckMINB	<i>Check Replication - SimMINB</i>
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**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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckNBMI

*Check Replication - SimNBMI*

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**Description**

Check Replication - SimNBMI

**Usage**

```
CheckNBMI(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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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CheckNBML	<i>Check Replication - SimNBML</i>
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**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)**

Ivan Jacob Agaloos Pesigan

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CheckStackedMINB	<i>Check Replication - SimStackedMINB</i>
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**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 <code>manMCMedMiss:::SimSuffix()</code> .

**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

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Compress

*Compress Replication*

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**Description**

Compress Replication

**Usage**

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

**Arguments**

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

**Value**

The output is saved as an external file in `output_folder`.

**Author(s)**

Ivan Jacob Agaloos Pesigan

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elliott2007	<i>Intervention on Healthy Dietary Behavior Via Knowledge of Healthy Dietary Behavior</i>
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### 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

elliott2007

### 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

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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 <code>results()</code> .
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 <code>mech = "COMPLETE"</code> , <code>prop</code> 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 <code>n = NULL</code> , use all sample sizes.

**Value**

Returns a `ggplot2` plot object.

**Author(s)**

Ivan Jacob Agaloos Pesigan

**See Also**

Other Figure Functions: [FigScatterPlot\(\)](#)

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FigScatterPlot	<i>Scatter Plot of Type I Error Rate, Statistical Power, and Miss Rate</i>
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---

## 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 <code>results()</code> .
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 <code>mech = "COMPLETE"</code> , <code>prop</code> 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 <code>n = NULL</code> , use all sample sizes.

## Value

Returns a `ggplot2` plot object.

## Author(s)

Ivan Jacob Agaloos Pesigan

## See Also

Other Figure Functions: [FigBoxPlot\(\)](#)



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FitModelIndirect	<i>Fit the Simple Mediation Model using Normal Theory Maximum Likelihood (Indirect Effect)</i>
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**Description**

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

**Usage**

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

**Arguments**

data_complete	Numeric matrix. Output of the GenData function or a three-column data set with complete data.
consistent	Logical. If consistent = TRUE, use the consistent estimate of the covariance matrix (maximum likelihood estimator). If consistent = FALSE, use the unbiased 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	<i>Fit the Simple Mediation Model using Multiple Imputation</i>
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---

**Description**

Fit the Simple Mediation Model using Multiple Imputation

**Usage**

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

**Arguments**

<code>data_mi</code>	List of numeric matrices. Output of the <code>ImputeData</code> function or a list of three-column data sets with imputed data.
<code>mplus_bin</code>	Character string. Path of Mplus binary.

**Details**

Let

$M = \text{Number of imputations,}$  and

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

The vector of pooled coefficients/parameter estimates is given by

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

The covariance within imputations is given by

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

where  $\text{Var}(\hat{\theta}_m)$  is the parameter covariance matrix for the  $m^{\text{th}}$  imputation. The covariance between imputations is given by

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

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

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

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  $\mathbf{V}_{\text{total}}$ .

**vcov\_tilde** Adjusted total covariance matrix  $\tilde{\mathbf{V}}_{\text{total}}$ .

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

**vcov\_within** Covariance within imputations  $\mathbf{V}_{\text{within}}$ .

**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](https://doi.org/10.1080/01621459.1991.10475152)

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

## See Also

Other Model Fitting Functions: [FitModelIndirect\(\)](#), [FitModelML\(\)](#)

---

FitModelML	<i>Fit the Simple Mediation Model using Normal Theory Maximum Likelihood</i>
------------	--

---

## 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.

**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).

**sabik** 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

*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\(\)](#)

---

ImputeData

*Impute Data*


---

**Description**

Generates m complete data sets using multiple imputation.

**Usage**

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

**Arguments**

data_missing	Numeric matrix. Output of the AmputeData function or a three-column data set 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

**Usage**

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

**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\(\)](#)

---

JointSigML	<i>Joint Significance Test for the Indirect Effect using Normal Theory Maximum Likelihood</i>
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---

**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)**

Ivan Jacob Agaloos Pesigan

**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**

<code>fit_mi</code>	Object. Output of the <code>FitModelMI</code> function.
<code>R</code>	Positive integer. Number of Monte Carlo replications.
<code>alpha</code>	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	<i>Monte Carlo Confidence Intervals for the Indirect Effect using Normal Theory Maximum Likelihood</i>
------	--

---

**Description**

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

**Usage**

```
MCML(fit_ml, R = 2000L, 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: [MCMCI\(\)](#), [MINB\(\)](#), [NBMI\(\)](#), [NBML\(\)](#), [NBStackedMI\(\)](#)

---

MINB	<i>Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Multiple Imputation (NB nested within MI or MI(NB))</i>
------	---

---

**Description**

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

**Usage**

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

**Arguments**

<code>data_mi</code>	List of numeric matrices. Output of the <code>ImputeData</code> function or a list of three-column data sets with imputed data.
<code>B</code>	Positive integer. Number of bootstrap samples.
<code>alpha</code>	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](https://doi.org/10.1080/00273171.2013.816235)

**See Also**

Other Confidence Interval Functions: [MCMCI\(\)](#), [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))

**Usage**

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

Arguments

data_missing	Numeric matrix. Output of the <code>AmputeData</code> function or a three-column data set with missing data.
data_mi	List of numeric matrices. Output of the <code>ImputeData</code> function or a list of three-column data sets with imputed data.
B	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	<i>Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Normal Theory Maximum Likelihood (ML nested within NB or NB(ML))</i>
------	--

---

Description

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

Usage

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

**Arguments**

<code>data</code>	Numeric matrix. Output of the <code>GenData</code> or <code>AmputeData</code> functions.
<code>B</code>	Positive integer. Number of bootstrap samples.
<code>mplus_bin</code>	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	<i>Nonparametric Bootstrap Confidence Intervals for the Indirect Effect using Multiple Imputation (NB using Stacked MI)</i>
-------------	---

---

**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**

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

**Value**

Nonparametric bootstrap percentile confidence intervals.

**Author(s)**

Ivan Jacob Agaloos Pesigan

See Also

Other Confidence Interval Functions: [MCMI\(\)](#), [MCML\(\)](#), [MINB\(\)](#), [NBMI\(\)](#), [NBML\(\)](#)

---

params	<i>Simulation Parameters</i>
--------	------------------------------

---

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  $\sigma^2_{\varepsilon_M}$ .
- sigmasqepsilony** Error variance  $\sigma^2_{\varepsilon_Y}$ .
- alphabeta**  $\alpha\beta$ , that is, the indirect effect of  $X$  on  $Y$  via  $M$ .

Author(s)

Ivan Jacob Agaloos Pesigan

---

results	<i>Simulation Results</i>
---------	---------------------------

---

Description

Simulation Results

Usage

results

**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.

**sigmasqepsilnm** 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  $M$ .

**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)**

Ivan Jacob Agaloos Pesigan

---

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

---

SimAmputeData

*Simulation Replication - AmputeData*

---

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .

**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



---

SimFitModelMI*Simulation Replication - FitModelMI*

---

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

---

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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

---

SimFN	<i>Simulation File Name</i>
-------	-----------------------------

---

**Description**

Simulation File Name

**Usage**

SimFN(data\_type, output\_type, output\_folder, suffix)

**Arguments**

- |               |   |
|---------------|---|
| data_type     | Character string. Input data type. Valid values include "complete-00", "mar-30", "mar-20", "mar-10", "mcar-30", "mcar-20", and "mcar-10"                            |
| output_type   | Character string. Output type. Valid values include "data", "fit-mi", "fit-ml", "mc-mi", "mc-ml", "mi-nb", "nb-mi", "nb-ml", "sig-mi", "sig-ml", and "stackedmi-nb" |
| output_folder | Character string. Output folder.  |
| suffix        | Character string. Output of manMCMedMiss:::SimSuffix().   |

**Value**

Returns a character string file name with the output\_folder in the OS-specific format.

---

SimGenData	<i>Simulation Replication - GenData</i>
------------	---

---

**Description**

Simulation Replication - GenData

**Usage**

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

**Arguments**

taskid	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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .

**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

**Usage**

```
SimImputeData(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  m,
  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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

**Usage**

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

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

**Usage**

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

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

**Usage**

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

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

**Usage**

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



**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

**Usage**

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

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

---

SimNBMI

*Simulation Replication - NBMI*

---

**Description**

Simulation Replication - NBMI

**Usage**

```
SimNBMI(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  B,
  m,
  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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
B	Positive integer. Number of bootstrap samples.
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

---

SimNBML

*Simulation Replication - NBML*

---

**Description**

Simulation Replication - NBML

**Usage**

```
SimNBML(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  B,
  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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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

**Usage**

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

**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 <code>manMCMedMiss:::SimSuffix()</code> .
overwrite	Logical. Overwrite existing output in <code>output_folder</code> .
integrity	Logical. If <code>integrity = TRUE</code> , check for the output file integrity when <code>overwrite = FALSE</code> .
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)**

Ivan Jacob Agaloos Pesigan

---

Sum	<i>Summarize Simulations</i>
-----	------------------------------

---

**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	<i>Bind Results</i>
---------	---------------------

---

**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.

**Value**

Returns a dataframe of results and parameters.

**Author(s)**

Ivan Jacob Agaloos Pesigan

---

SumHit

*Extract Zero Hit and Theta Hit from Summary Output*

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**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

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SumJointSigMI

*Summarize Simulations - SimJointSigMI*

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**Description**

Summarize Simulations - SimJointSigMI

**Usage**

```
SumJointSigMI(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

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SumJointSigML	<i>Summarize Simulations - SimJointSigML</i>
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**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)**

Ivan Jacob Agaloos Pesigan



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SumMCMI	<i>Summarize Simulations - SimMCMI</i>
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**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

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SumMCML	<i>Summarize Simulations - SimMCML</i>
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**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.

**Details**

This function is executed via the Sum function.

**Value**

Returns a numeric matrix.

**Author(s)**

Ivan Jacob Agaloos Pesigan

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SumMINB	<i>Summarize Simulations - SimMINB</i>
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**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)**

Ivan Jacob Agaloos Pesigan

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SumNBMI	<i>Summarize Simulations - SimNBMI</i>
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**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

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SumNBML	<i>Summarize Simulations - SimNBML</i>
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**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.

**Details**

This function is executed via the Sum function.

**Value**

Returns a numeric matrix.

**Author(s)**

Ivan Jacob Agaloos Pesigan

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SumNBStackedMI	<i>Summarize Simulations - SimNBStackedMI</i>
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**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)**

Ivan Jacob Agaloos Pesigan

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TabDescribe	<i>Descriptive Statistics of Type I Error Rate, Statistical Power, and Miss Rate</i>
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**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

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Tree	<i>Conditional Inference Tree</i>
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**Description**

Conditional Inference Tree

**Usage**

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

**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.
maxdepth	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)**

Ivan Jacob Agaloos Pesigan

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