

# Package ‘manMetaVAR’

August 2, 2024

**Title** Multivariate Meta-Analysis of Vector Autoregressive Model Coefficients

**Version** 0.9.1

**Description** Research compendium for the manuscript  
Pesigan, I. J. A., et al. (2024).  
Multivariate Meta-Analysis of Vector Autoregressive Model Coefficients.  
<doi:10.0000/0000000000>.

**URL** <https://github.com/jeksterslab/manMetaVAR>,  
<https://jeksterslab.github.io/manMetaVAR/>,  
[https://osf.io/qwnmf/?view\\_only=855be2012b554f05bbc679946845bab8](https://osf.io/qwnmf/?view_only=855be2012b554f05bbc679946845bab8),  
<https://doi.org/10.0000/0000000000>

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

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**Depends** R (>= 3.5.0), OpenMx, fitDTVARMx, metaVAR

**Imports** simStateSpace, mlVAR

**Remotes** jeksterslab/fitDTVARMx, jeksterslab/metaVAR

**Suggests** knitr, rmarkdown, testthat

**RoxygenNote** 7.3.2

**NeedsCompilation** no

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|          |                             |
|----------|-----------------------------|
| Compress | <i>Compress Replication</i> |
|----------|-----------------------------|

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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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**FitDTVARMx***Fit the Model using the fitDTVARMx Package*

---

**Description**

The function fits the model using the [fitDTVARMx](#) package.

**Usage**

```
FitDTVARMx(data)
```

**Arguments**

**data**                      R object. Output of the [GenData\(\)](#) function.

**See Also**

Other Model Fitting Functions: [FitMLVAR\(\)](#)

**Examples**

```
## Not run:
set.seed(42)
data <- GenData(n = 50, time = 100, theta = 0.2)
FitDTVARMx(data)

## End(Not run)
```

---

**FitMetaVARMx***Multivariate Meta-Analysis using the metaVAR Package*

---

**Description**

The function performs multivariate meta-analysis using the [metaVAR](#) package.

**Usage**

```
FitMetaVARMx(fit)
```

**Arguments**

**fit**                      R object. Output of the [FitDTVARMx\(\)](#) function.

### Examples

```
## Not run:
set.seed(42)
data <- GenData(n = 50, time = 100, theta = 0.2)
fit <- FitDTVARMx(data)
FitMetaVARMx(fit)

## End(Not run)
```

---

FitMLVAR

*Fit the Model using the mlVAR Package*

---

### Description

The function fits the model using the [mlVAR](#) package.

### Usage

```
FitMLVAR(data)
```

### Arguments

data                    R object. Output of the [GenData\(\)](#) function.

### See Also

Other Model Fitting Functions: [FitDTVARMx\(\)](#)

### Examples

```
## Not run:
set.seed(42)
data <- GenData(n = 50, time = 100, theta = 0.2)
FitMLVAR(data)

## End(Not run)
```

---

GenData*Simulate Data*

---

**Description**

The function simulates data using the `simStateSpace::SimSSMIVary()` function.

**Usage**

```
GenData(n, time, theta)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>n</code>     | Positive integer. Sample size.           |
| <code>time</code>  | Positive integer. Number of time points. |
| <code>theta</code> | Numeric. Measurement error variance.     |

**Examples**

```
## Not run:  
set.seed(42)  
data <- GenData(n = 50, time = 100, theta = 0.2)  
plot(data)  
  
## End(Not run)
```

---

params*Simulation Parameters*

---

**Description**

Simulation Parameters

**Usage**

```
params
```

**Format**

A dataframe with 25 rows and 3 columns:

**taskid** Simulation Task ID.  
**n** Sample size.  
**time** Number of measurement occasions.

**Author(s)**

Ivan Jacob Agaloos Pesigan

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|     |                               |
|-----|-------------------------------|
| Sim | <i>Simulation Replication</i> |
|-----|-------------------------------|

---

**Description**

Simulation Replication

**Usage**

Sim(taskid, repid, output\_folder, overwrite, integrity, params\_taskid)

**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.

**Value**

The output is saved as an external file in output\_folder.

**Author(s)**

Ivan Jacob Agaloos Pesigan

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|               |  |
|---------------|--|
| SimFitDTVARMx | <i>Simulation Replication - FitDTVARMx</i> |
|---------------|--|

---

**Description**

Simulation Replication - FitDTVARMx

**Usage**

SimFitDTVARMx(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>manCTMed::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

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SimFitMetaVARMx

*Simulation Replication - FitMetaVARMx*

---

**Description**

Simulation Replication - FitMetaVARMx

**Usage**

```
SimFitMetaVARMx(  
  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>manCTMed:::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

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SimFitMLVAR

*Simulation Replication - FitMLVAR*


---

**Description**

Simulation Replication - FitMLVAR

**Usage**

```
SimFitMLVAR(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>manCTMed:::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

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

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**Description**

Simulation File Name

**Usage**

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

**Arguments**

|                            |  |
|----------------------------|--|
| <code>output_type</code>   | Character string. Output type. Valid values include "data", "fit-dynr", "dynr-delta-xmy", "dynr-delta-ymx", "dynr-mc-xmy", and "dynr-mc-ymx" |
| <code>output_folder</code> | Character string. Output folder.   |
| <code>suffix</code>        | Character string. Output of <code>manCTMed:::SimSuffix()</code> .  |

**Value**

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

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SimGenData

---

*Simulation Replication - GenData*


---

## 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>manCTMed:::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

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|         |                                |
|---------|--------------------------------|
| SimProj | <i>Simulation Project Name</i> |
|---------|--------------------------------|

---

**Description**

Simulation Project Name

**Usage**

SimProj()

**Value**

Returns the project name as a character string.

**Author(s)**

Ivan Jacob Agaloos Pesigan

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