

# Package ‘manMetaVAR’

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**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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**Imports** simStateSpace, mlVAR

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

**Suggests** knitr, rmarkdown, testthat

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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*

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**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)
```

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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>
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**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>
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**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

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*Simulation Replication - GenData*


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## 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`*Simulation Project Name*

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**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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