

# 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. (In Preparation).  
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/uenr7/>, <https://doi.org/10.0000/0000000000>

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

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## Contents

Compress . . . . .	2
FitDTVAR . . . . .	3

FitJAGS . . . . .	3
FitMetaVAR . . . . .	4
FitMLVAR . . . . .	5
GenData . . . . .	6
params . . . . .	6
Sim . . . . .	7
SimFitDTVAR . . . . .	8
SimFitJAGS . . . . .	9
SimFitMetaVAR . . . . .	10
SimFitMLVAR . . . . .	11
SimFN . . . . .	12
SimGenData . . . . .	12
SimProj . . . . .	13
<b>Index</b>	<b>14</b>

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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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**FitDTVAR***Fit the Model using the fitDTVARMx Package*

---

**Description**

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

**Usage**

```
FitDTVAR(data, ncores = NULL)
```

**Arguments**

data	R object. Output of the <a href="#">GenData()</a> function.
ncores	Positive integer. Number of cores to use.

**See Also**

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

**Examples**

```
## Not run:
set.seed(42)
data <- GenData(taskid = 1)
fit <- FitDTVAR(
  data = data,
  ncores = parallel::detectCores()
)
summary(fit)

## End(Not run)
```

---

**FitJAGS***Fit the Model using JAGS*

---

**Description**

The function fits the model using JAGS.

**Usage**

```
FitJAGS(
  data,
  n_chains = 8,
  n_adapt = 10000,
  n_iter = 1e+05,
  thin = 20,
  ess_crit = 1000,
  max_iter = 10000,
  seed = NULL
)
```

**Arguments**

<code>data</code>	R object. Output of the <a href="#">GenData()</a> function.
<code>n_chains</code>	The number of parallel chains for the model.
<code>n_adapt</code>	The number of iterations for adaptation.
<code>n_iter</code>	Number of iterations to monitor.
<code>thin</code>	Thinning interval for monitors.
<code>ess_crit</code>	Positive integer. Effective sample size criteria.
<code>max_iter</code>	Positive integer. Maximum number of reruns to get effective sample size.
<code>seed</code>	Integer. Random seed.

**See Also**

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

**Examples**

```
## Not run:
set.seed(42)
data <- GenData(taskid = 1)
fit <- FitJAGS(data = data)
summary(fit)

## End(Not run)
```

**Description**

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

**Usage**

```
FitMetaVAR(fit, ncores = NULL)
```

**Arguments**

fit	R object. Output of the <a href="#">FitDTVARmX()</a> function.
ncores	Positive integer. Number of cores to use.

**Examples**

```
## Not run:
set.seed(42)
data <- GenData(taskid = 1)
fit <- FitDTVAR(
  data = data,
  ncores = parallel::detectCores()
)
pooled <- FitMetaVAR(
  fit = fit,
  ncores = parallel::detectCores()
)
summary(pooled)

## End(Not run)
```

---

FitMLVAR

*Fit the Model using the mlVAR Package*

---

**Description**

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

**Usage**

```
FitMLVAR(data, ncores = NULL)
```

**Arguments**

data	R object. Output of the <a href="#">GenData()</a> function.
ncores	Positive integer. Number of cores to use.

**See Also**

Other Model Fitting Functions: [FitDTVAR\(\)](#), [FitJAGS\(\)](#)

**Examples**

```
## Not run:
set.seed(42)
data <- GenData(taskid = 1)
fit <- FitMLVAR(data = data)
summary(fit)

## End(Not run)
```

---

GenData

*Simulate Data*


---

**Description**

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

**Usage**

```
GenData(taskid)
```

**Arguments**

taskid                      Positive integer. Task ID.

**Examples**

```
## Not run:
set.seed(42)
data <- GenData(taskid = 1)

## 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,  
  seed,  
  n_chains,  
  n_adapt,  
  n_iter,  
  thin,  
  ess_crit,  
  max_iter  
)
```

**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.
- seed** Integer. Random seed.
- n\_chains** The number of parallel chains for the model.

n_adapt	The number of iterations for adaptation.
n_iter	Number of iterations to monitor.
thin	Thinning interval for monitors.
ess_crit	Positive integer. Effective sample size critria.
max_iter	Positive integer. Maximum number of reruns to get effective sample size.

**Value**

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

**Author(s)**

Ivan Jacob Agaloos Pesigan

---

SimFitDTVAR

*Simulation Replication - FitDTVAR*

---

**Description**

Simulation Replication - FitDTVAR

**Usage**

```
SimFitDTVAR(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 manCTMed:::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)**

Ivan Jacob Agaloos Pesigan



**Description**

Simulation Replication - FitJAGS

**Usage**

```
SimFitJAGS(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  n_chains,
  n_adapt,
  n_iter,
  thin,
  ess_crit,
  max_iter
)
```

**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> .
n_chains	The number of parallel chains for the model.
n_adapt	The number of iterations for adaptation.
n_iter	Number of iterations to monitor.
thin	Thinning interval for monitors.
ess_crit	Positive integer. Effective sample size criteria.
max_iter	Positive integer. Maximum number of reruns to get effective sample size.

**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

---

SimFitMetaVAR

*Simulation Replication - FitMetaVAR*


---

**Description**

Simulation Replication - FitMetaVAR

**Usage**

```
SimFitMetaVAR(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 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

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`SimFitMLVAR`*Simulation Replication - FitMLVAR*

---

**Description**

Simulation Replication - FitMLVAR

**Usage**

```
SimFitMLVAR(taskid, repid, output_folder, seed, suffix, overwrite, integrity)
```

**Arguments**

<code>taskid</code>	Positive integer. Task ID.
<code>repid</code>	Positive integer. Replication ID.
<code>output_folder</code>	Character string. Output folder.
<code>seed</code>	Integer. Random seed.
<code>suffix</code>	Character string. Output of <code>manCTMed::SimSuffix()</code> .
<code>overwrite</code>	Logical. Overwrite existing output in <code>output_folder</code> .
<code>integrity</code>	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**

output_type	Character string. Output type. Valid values include "data", "fit-dt-var-mx", "fit-meta-var-mx", "fit-ml-var", and "fit-jags".
output_folder	Character string. Output folder.
suffix	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	<i>Simulation Replication - GenData</i>
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**Description**

Simulation Replication - GenData

**Usage**

```
SimGenData(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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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

# Index

- \* **Compression Functions**
  - Compress, [2](#)
- \* **Data Generation Functions**
  - GenData, [6](#)
- \* **Meta-Analysis Functions**
  - FitMetaVAR, [4](#)
- \* **Model Fitting Functions**
  - FitDTVAR, [3](#)
  - FitJAGS, [3](#)
  - FitMLVAR, [5](#)
- \* **compress**
  - Compress, [2](#)
- \* **data**
  - params, [6](#)
- \* **fit**
  - FitDTVAR, [3](#)
  - FitJAGS, [3](#)
  - FitMLVAR, [5](#)
  - SimFitDTVAR, [8](#)
  - SimFitJAGS, [9](#)
  - SimFitMetaVAR, [10](#)
  - SimFitMLVAR, [11](#)
- \* **gendata**
  - GenData, [6](#)
  - SimGenData, [12](#)
- \* **manCTMed**
  - SimFN, [12](#)
- \* **manMetaVAR**
  - Compress, [2](#)
  - FitDTVAR, [3](#)
  - FitJAGS, [3](#)
  - FitMetaVAR, [4](#)
  - FitMLVAR, [5](#)
  - GenData, [6](#)
  - Sim, [7](#)
  - SimFitDTVAR, [8](#)
  - SimFitJAGS, [9](#)
  - SimFitMetaVAR, [10](#)
  - SimFitMLVAR, [11](#)
- SimGenData, [12](#)
  - SimProj, [13](#)
- \* **meta**
  - FitMetaVAR, [4](#)
- \* **parameters**
  - params, [6](#)
- \* **simulation**
  - Sim, [7](#)
  - SimFitDTVAR, [8](#)
  - SimFitJAGS, [9](#)
  - SimFitMetaVAR, [10](#)
  - SimFitMLVAR, [11](#)
  - SimFN, [12](#)
  - SimGenData, [12](#)
  - SimProj, [13](#)
- Compress, [2](#)
- FitDTVAR, [3, 4, 5](#)
- fitDTVARMx, [3](#)
- FitDTVARMx(), [5](#)
- FitJAGS, [3, 3, 5](#)
- FitMetaVAR, [4](#)
- FitMLVAR, [3, 4, 5](#)
- GenData, [6](#)
- GenData(), [3–5](#)
- metaVAR, [4](#)
- mlVAR, [5](#)
- params, [6](#)
- Sim, [7](#)
- SimFitDTVAR, [8](#)
- SimFitJAGS, [9](#)
- SimFitMetaVAR, [10](#)
- SimFitMLVAR, [11](#)
- SimFN, [12](#)
- SimGenData, [12](#)
- SimProj, [13](#)
- simStateSpace::SimSSMIVary(), [6](#)