# 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,
```

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https://jeksterslab.github.io/manMetaVAR/,
```

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BugReports https://github.com/jeksterslab/manMetaVAR/issues

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Imports simStateSpace, mlVAR

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NeedsCompilation no

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2 Compress

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 ${\it Compress Replication}$ 

## Description

Compress Replication

## Usage

Index

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)

FitDTVARMx 3

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)</pre>
```

 ${\tt FitMetaVARMx}$ 

Multivariate Meta-Analysis using the metaVAR Package

## Description

The function performs multivariate meta-snalysis using the metaVAR package.

## Usage

```
FitMetaVARMx(fit)
```

#### **Arguments**

fit

R object. Output of the FitDTVARMx() function.

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#### **Examples**

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

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)</pre>
```

GenData 5

GenData

Simulate Data

#### **Description**

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

#### Usage

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

### **Arguments**

n Positive integer. Sample size.

time Positive integer. Number of time points. theta Numeric. Measurement error variance.

## **Examples**

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

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 occassions.

## Author(s)

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Sim

Simulation Replication

## **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

SimFitDTVARMx

Simulation Replication - FitDTVARMx

#### Description

Simulation Replication - FitDTVARMx

#### Usage

SimFitDTVARMx(taskid, repid, output\_folder, seed, suffix, overwrite, integrity)

SimFitMetaVARMx 7

#### **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

 ${\tt SimFitMetaVARMx}$ 

Simulation Replication - FitMetaVARMx

#### **Description**

Simulation Replication - FitMetaVARMx

## Usage

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

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#### **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

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 manCTMed:::.SimSuffix().

overwrite Logical. Overwrite existing output in output\_folder.

integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

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#### **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

Simulation File Name

#### **Description**

Simulation File Name

#### Usage

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

## Arguments

```
output_type Character string. Output type. Valid values include "data", "fit-dynr", "dynr-delta-xmy", "dynr-mc-xmy", and "dynr-mc-ymx"

output_folder Character string. Output folder.

suffix Character string. Output of manCTMed:::.SimSuffix().
```

#### 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 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)

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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)

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