

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

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

Imports simStateSpace, MASS, mlVAR

Remotes jeksterslab/fitDTVARMx, jeksterslab/metaVAR

Suggests knitr, rmarkdown, testthat

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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

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)  
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)
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)
FitMLVAR(data)

## End(Not run)
```

GenData*Simulate Data*

Description

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

Usage

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

Arguments

<code>n</code>	Positive integer. Sample size.
<code>time</code>	Positive integer. Number of time points.

Examples

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

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

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

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

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

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-dynr", "dynr-delta-xmy", "dynr-delta-ymx", "dynr-mc-xmy", and "dynr-mc-ymx"
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.

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

`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

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