

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

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Author Ivan Jacob Agaloos Pesigan [aut, cre, cph] (ORCID:
<<https://orcid.org/0000-0003-4818-8420>>)

Maintainer Ivan Jacob Agaloos Pesigan <r.jeksterslab@gmail.com>

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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

FitDTVAR*Fit the Model using the fitDTVARMx Package*

Description

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

Usage

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

Arguments

<code>data</code>	R object. Output of the GenData() function.
<code>ncores</code>	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 = 4, n.adapt = 2000, n.iter = 10000)
```

Arguments

<code>data</code>	R object. Output of the GenData() function.
<code>n.chains</code>	the number of parallel chains for the model
<code>n.adapt</code>	the number of iterations for adaptation. See adapt for details. If <code>n.adapt = 0</code> then no adaptation takes place.
<code>n.iter</code>	number of iterations to monitor

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)
```

FitMetaVAR

Multivariate Meta-Analysis using the metaVAR Package

Description

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

Usage

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

Arguments

<code>fit</code>	R object. Output of the FitDTVARmX() function.
<code>ncores</code>	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)
```

Arguments

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

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

Sim	<i>Simulation Replication</i>
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Description

Simulation Replication

Usage

```
Sim(taskid, repid, output_folder, overwrite, integrity, seed)
```

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.

Value

The output is saved as an external file in output_folder.

Author(s)

Ivan Jacob Agaloos Pesigan

SimFitDTVAR	<i>Simulation Replication - FitDTVAR</i>
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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 <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

SimFitJAGS

Simulation Replication - FitJAGS

Description

Simulation Replication - FitJAGS

Usage

```
SimFitJAGS(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

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

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	<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

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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