# Package 'manMetaVAR'

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Compress

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Compress Replication

# 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)

FitDTVAR 3

 ${\tt FitDTVAR}$ 

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 GenData() 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)</pre>
```

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)
```

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## **Arguments**

data R object. Output of the GenData() function.

n.chains the number of parallel chains for the model

n.adapt the number of iterations for adaptation. See adapt for details. If n.adapt = 0

then no adaptation takes place.

n.iter 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)</pre>
```

FitMetaVAR

Multivariate Meta-Analysis using the metaVAR Package

# Description

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

## Usage

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

# Arguments

fit R object. Output of the FitDTVARMx() 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(</pre>
```

FitMLVAR 5

```
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)</pre>
```

GenData

Simulate Data

# **Description**

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

# Usage

```
GenData(taskid)
```

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# Arguments

taskid

Positive integer. Task ID.

# Examples

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

Sim 7

Sim	Simulation Replication	

# Description

Simulation Replication

# Usage

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

# Arguments

Positive integer. Task ID. taskid repid Positive integer. Replication ID. Character string. Output folder. output\_folder overwrite Logical. Overwrite existing output in output\_folder. integrity Logical. If integrity = TRUE, check for the output file integrity when overwrite

= FALSE.

Integer. Random seed. seed

# 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)
```

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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

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 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

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 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)

10 SimFitMLVAR

S	imFitMLVAR	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.

## **Details**

This function is executed via the Sim function.

# Value

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

## Author(s)

SimFN 11

|--|

# 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 manCTMed:::.SimSuffix().

#### 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, 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.

SimProj

# **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

 ${\tt SimProj}$ 

Simulation Project Name

# Description

Simulation Project Name

# Usage

SimProj()

## Value

Returns the project name as a character string.

# Author(s)

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