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
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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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Contents

Compress . . . 2
FitDTVARMx . . . 3
FitMetaVARMx . . . 3
FitMLVAR . . . 4
GenData . . . 5
params . . . 5
Sim . . . 6
SimFitDTVARMx . . . 6
SimFitMetaVARMx . . . 7
SimFitMLVAR . . . 8
SimFN . . . 9
SimGenData . . . 10
SimProj . . . 11

Index **12**

`Compress` *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)

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-snalysis 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

`n`	Positive integer. Sample size.
`time`	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 occassions.

Author(s)

Ivan Jacob Agaloos Pesigan

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)
```

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

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 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.

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-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,
  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)

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

Index

∗ **Compression Functions**
  Compress, 2
∗ **Data Generation Functions**
  GenData, 5
∗ **Meta-Analysis Functions**
  FitMetaVARMx, 3
∗ **Model Fitting Functions**
  FitDTVARMx, 3
  FitMLVAR, 4
∗ **compress**
  Compress, 2
∗ **data**
  params, 5
∗ **fit**
  FitDTVARMx, 3
  FitMLVAR, 4
  SimFitDTVARMx, 6
  SimFitMetaVARMx, 7
  SimFitMLVAR, 8
∗ **gendata**
  GenData, 5
  SimGenData, 10
∗ **manCTMed**
  SimFN, 9
∗ **manMetaVAR**
  Compress, 2
  FitDTVARMx, 3
  FitMetaVARMx, 3
  FitMLVAR, 4
  GenData, 5
  Sim, 6
  SimFitDTVARMx, 6
  SimFitMetaVARMx, 7
  SimFitMLVAR, 8
  SimGenData, 10
  SimProj, 11
∗ **meta**
  FitMetaVARMx, 3
∗ **parameters**
  params, 5
∗ **simulation**
  Sim, 6
  SimFitDTVARMx, 6
  SimFitMetaVARMx, 7
  SimFitMLVAR, 8
  SimFN, 9
  SimGenData, 10
  SimProj, 11

Compress, 2

FitDTVARMx, 3, *4*
fitDTVARMx, *3*
FitDTVARMx(), *3*
FitMetaVARMx, 3
FitMLVAR, *3*, 4

GenData, 5
GenData(), *3, 4*

metaVAR, *3*
mlVAR, *4*

params, 5

Sim, 6
SimFitDTVARMx, 6
SimFitMetaVARMx, 7
SimFitMLVAR, 8
SimFN, 9
SimGenData, 10
SimProj, 11
simStateSpace::SimSSMIVary(), *5*