

Package ‘manMetaVAR’

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Title Multivariate Meta-Analysis of Vector Autoregressive Model
Coefficients

Version 0.9.1

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

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Contents

Compress	2
FitDTVAR	3

FitJAGS	3
FitMetaVAR	4
FitMLVAR	5
GenData	6
params	6
plot.gendata	7
Sim	7
SimFitDTVVAR	9
SimFitJAGS	10
SimFitMetaVAR	11
SimFitMLVAR	12
SimFN	13
SimGenData	13
SimProj	14
summary.fitjags	14
summary.gendata	15
Index	16

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 = 1000,  
  n_iter = 10000,  
  thin = 1,  
  ess_crit = 1000,  
  max_iter = 1000,  
  seed = NULL  
)
```

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.
n_iter	Number of iterations to monitor.
thin	Thinning interval for monitors.
ess_crit	Positive integer. Effective sample size criteria.
max_iter	Positive integer. Maximum number of reruns to get effective sample size.
seed	Integer. Random seed.

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)
```

Description

The function performs multivariate meta-analysis 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(
  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, 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: [FitDTVAR\(\)](#), [FitJAGS\(\)](#)

Examples

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

## End(Not run)
```

GenData	<i>Simulate Data</i>
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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	<i>Simulation Parameters</i>
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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

plot.gendata	<i>Plot Method for an Object of Class gendata</i>
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Description

Plot Method for an Object of Class gendata

Usage

```
## S3 method for class 'gendata'  
plot(x, ...)
```

Arguments

- x** Object of class gendata.
- ...** additional arguments.

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,  
  n_chains,  
  n_adapt,  
  n_iter,  
  thin,  
  ess_crit,  
  max_iter  
)
```

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.
n_chains	The number of parallel chains for the model.
n_adapt	The number of iterations for adaptation.
n_iter	Number of iterations to monitor.
thin	Thinning interval for monitors.
ess_crit	Positive integer. Effective sample size criteria.
max_iter	Positive integer. Maximum number of reruns to get effective sample size.

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)
```

Arguments

<code>taskid</code>	Positive integer. Task ID.
<code>repid</code>	Positive integer. Replication ID.
<code>output_folder</code>	Character string. Output folder.
<code>seed</code>	Integer. Random seed.
<code>suffix</code>	Character string. Output of <code>manCTMed::SimSuffix()</code> .
<code>overwrite</code>	Logical. Overwrite existing output in <code>output_folder</code> .
<code>integrity</code>	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

Description

Simulation Replication - FitJAGS

Usage

```

SimFitJAGS(
  taskid,
  repid,
  output_folder,
  seed,
  suffix,
  overwrite,
  integrity,
  n_chains,
  n_adapt,
  n_iter,
  thin,
  ess_crit,
  max_iter
)

```

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> .
n_chains	The number of parallel chains for the model.
n_adapt	The number of iterations for adaptation.
n_iter	Number of iterations to monitor.
thin	Thinning interval for monitors.
ess_crit	Positive integer. Effective sample size criteria.
max_iter	Positive integer. Maximum number of reruns to get effective sample size.

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-dt-var-mx", "fit-meta-var-mx", "fit-ml-var", and "fit-jags".
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	<i>Simulation Project Name</i>
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Description

Simulation Project Name

Usage

SimProj()

Value

Returns the project name as a character string.

Author(s)

Ivan Jacob Agaloos Pesigan

summary.fitjags	<i>Summary Method for an Object of Class fitjags</i>
-----------------	--

Description

Summary Method for an Object of Class fitjags

Usage

```
## S3 method for class 'fitjags'  
summary(object, ...)
```

Arguments

object	Object of class fitjags.
...	additional arguments.

Author(s)

Ivan Jacob Agaloos Pesigan

summary.gendata

Summary Method for an Object of Class gendata

Description

Summary Method for an Object of Class gendata

Usage

```
## S3 method for class 'gendata'  
summary(object, ...)
```

Arguments

object	Object of class gendata.
...	additional arguments.

Author(s)

Ivan Jacob Agaloos Pesigan

Index

- * **Compression Functions**
 - Compress, [2](#)
- * **Data Generation Functions**
 - GenData, [6](#)
- * **Meta-Analysis Functions**
 - FitMetaVAR, [4](#)
- * **Model Fitting Functions**
 - FitDTVAR, [3](#)
 - FitJAGS, [3](#)
 - FitMLVAR, [5](#)
- * **compress**
 - Compress, [2](#)
- * **data**
 - params, [6](#)
- * **fit**
 - FitDTVAR, [3](#)
 - FitJAGS, [3](#)
 - FitMLVAR, [5](#)
 - SimFitDTVAR, [9](#)
 - SimFitJAGS, [10](#)
 - SimFitMetaVAR, [11](#)
 - SimFitMLVAR, [12](#)
- * **gendata**
 - GenData, [6](#)
 - SimGenData, [13](#)
- * **manCTMed**
 - SimFN, [13](#)
- * **manMetaVAR**
 - Compress, [2](#)
 - FitDTVAR, [3](#)
 - FitJAGS, [3](#)
 - FitMetaVAR, [4](#)
 - FitMLVAR, [5](#)
 - GenData, [6](#)
 - Sim, [7](#)
 - SimFitDTVAR, [9](#)
 - SimFitJAGS, [10](#)
 - SimFitMetaVAR, [11](#)
 - SimFitMLVAR, [12](#)
- SimGenData, [13](#)
- SimProj, [14](#)
- * **meta**
 - FitMetaVAR, [4](#)
- * **methods**
 - plot.gendata, [7](#)
 - summary.fitjags, [14](#)
 - summary.gendata, [15](#)
- * **parameters**
 - params, [6](#)
- * **simulation**
 - Sim, [7](#)
 - SimFitDTVAR, [9](#)
 - SimFitJAGS, [10](#)
 - SimFitMetaVAR, [11](#)
 - SimFitMLVAR, [12](#)
 - SimFN, [13](#)
 - SimGenData, [13](#)
 - SimProj, [14](#)
- Compress, [2](#)
- FitDTVAR, [3](#), [4](#), [5](#)
- fitDTVARMx, [3](#)
- FitDTVARMx(), [5](#)
- FitJAGS, [3](#), [3](#), [5](#)
- FitMetaVAR, [4](#)
- FitMLVAR, [3](#), [4](#), [5](#)
- GenData, [6](#)
- GenData(), [3–5](#)
- metaVAR, [4](#)
- mlVAR, [5](#)
- params, [6](#)
- plot.gendata, [7](#)
- Sim, [7](#)
- SimFitDTVAR, [9](#)
- SimFitJAGS, [10](#)

SimFitMetaVAR, [11](#)
SimFitMLVAR, [12](#)
SimFN, [13](#)
SimGenData, [13](#)
SimProj, [14](#)
simStateSpace::SimSSMIVary(), [6](#)
summary.fitjags, [14](#)
summary.gendata, [15](#)