Package 'manMetaVAR'

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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)

FitDTVAR 3

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.

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Usage

```
FitJAGS(
    data,
    n_chains = 4,
    n_adapt = 1000,
    n_iter = 1000,
    thin = 1,
    ess_crit = 200,
    max_iter = 1L,
    seed = NULL
)
```

Arguments

data R object. Output of the GenData() function. The number of parallel chains for the model. n_chains 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 critria. Positive integer. Maximum number of reruns to get effective sample size. max_iter Integer. Random seed. 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)</pre>
```

FitMetaVAR

Multivariate Meta-Analysis using the metaVAR Package

Description

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

FitMLVAR 5

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)</pre>
```

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()
```

6 params

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)
```

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

plot.manmetavar_data 7

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

Description

Plot Method for an Object of Class manmetavar_data

Usage

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

Arguments

x Object of class manmetavar_data.

... additional arguments.

Author(s)

Ivan Jacob Agaloos Pesigan

Sim

Simulation Replication

Description

Simulation Replication

Sim

Usage

```
Sim(
  taskid,
  repid,
  output_folder,
  overwrite,
  integrity,
  seed,
  n_chains,
  n_adapt,
  n_iter,
  thin,
  ess_crit,
  max_iter,
  run_jags
)
```

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 critria. |
| max_iter | Positive integer. Maximum number of reruns to get effective sample size. |
| run_jags | Logical. If run_jags = TRUE, run JAGS model. |
| | |

Value

The output is saved as an external file in output_folder.

Author(s)

SimFitDTVAR 9

|--|

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 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 SimFitJAGS

 ${\tt SimFitJAGS}$

 ${\it Simulation Replication - Fit JAGS}$

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

| 41 -2 -1 | De West Conserve Text ID |
|---------------|---|
| 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. |
| 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 critria. |
| max_iter | Positive integer. Maximum number of reruns to get effective sample size. |

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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)

12 SimFitMLVAR

| 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)

SimFN 13

| | 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-dt-var-mx",

"fit-meta-var-mx", "fit-ml-var", and "fit-jags".

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.

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

```
summary.manmetavar_data
```

 ${\it Summary Method for \ an \ Object \ of \ Class \ } {\it manmetavar_data}$

Description

Summary Method for an Object of Class manmetavar_data

Usage

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

Arguments

object Object of class manmetavar_data.
... additional arguments.

Author(s)

Ivan Jacob Agaloos Pesigan

```
summary.manmetavar_fitdtvar
```

Summary Method for an Object of Class manmetavar_fitdtvar

Description

Summary Method for an Object of Class manmetavar_fitdtvar

Usage

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

Arguments

```
object Object of class manmetavar_fitdtvar.
... additional arguments.
```

Author(s)

Ivan Jacob Agaloos Pesigan

```
summary.manmetavar_fitjags
```

Summary Method for an Object of Class manmetavar_fitjags

Description

Summary Method for an Object of Class manmetavar_fitjags

Usage

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

Arguments

```
objectObject of class manmetavar_fitjags.additional arguments.
```

Author(s)

```
summary.manmetavar_fitmetavar
```

Summary Method for an Object of Class manmetavar_fitmetavar

Description

Summary Method for an Object of Class manmetavar_fitmetavar

Usage

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

Arguments

```
object Object of class manmetavar_fitmetavar.
... additional arguments.
```

Author(s)

Ivan Jacob Agaloos Pesigan

```
summary.manmetavar_fitmlvar
```

Summary Method for an Object of Class manmetavar_fitmlvar

Description

Summary Method for an Object of Class manmetavar_fitmlvar

Usage

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

Arguments

```
object Object of class manmetavar_fitmlvar.
... additional arguments.
```

Author(s)

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