Package 'semnova'

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Type Package

Title Latent Repeated Measures ANOVA

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Imports lavaan, Matrix, parallel, MASS, stats, methods

Suggests testthat, knitr, rmarkdown

Depends R (>= 3.4.0)

Description Latent repeated measures ANOVA (L-RM-ANOVA) is a structural equation modeling based alternative to traditional repeated measures ANOVA. L-RM-ANOVA extends the latent growth components approach by Mayer et al. (2012) <doi:10.1080/10705511.2012.713242> and introduces latent variables to repeated measures analysis.

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Contents

`anova,lgc-method` *Comparing the fit of LGC objects.*

Description

Comparing the fit of LGC objects.

Usage

```
## S4 method for signature 'lgc'
anova(object, ...)
```

Arguments

`object`	`lgc` object. An `lgc` object to be compared against other `lgc` objects.
`...`	`lgc` object. More `lgc` objects to be compared.

`create_mmodel` *Specifying a measurement model.*

Description

Specifying a measurement model.

Usage

```
create_mmodel(..., list = NULL, lv_scaling = "effect", invariance = NULL)
```

Arguments

`...`	Named arguments each representing a latent variable. The arguments are character vectors containing the variable names the latent variables are measured by.
`list`	List. Each list element represents a latent variable. List elements are character vectors containing the variable names the latent variables are measured by.
`lv_scaling`	Character vector. Defines the strategy for latent variable scaling. Default is `lv_scaling = "effect"`. Possible strategies are: `c("effect", "referent")`.
`invariance`	Not yet implemented.

Value

Object of classe `mmodel`.

Examples

```
mmodel <- create_mmodel(
    A1B1 = "var1",
    A2B1 = "var2",
    A3B1 = "var3",
    A1B2 = "var4",
    A2B2 = "var5",
    A3B2 = "var6",
    lv_scaling = "referent"
)
```

---

lgc *General function to specify a general latent growth components model.*

Description

General function to specify a general latent growth components model.

Usage

```
lgc(
  data,
  mmodel,
  C_matrix,
  hypotheses = NULL,
  covariates = NULL,
  groups = NULL,
  append = NULL,
  verbose = FALSE,
  compound_symmetry = FALSE,
  sphericity = FALSE,
  multiv_tests = c("wilks", "wald"),
  univ_tests = NULL,
  randomization = list(ncores = 1, nsamples = 1000),
  ...
)
```

Arguments

`data`	Dataframe. Data object to be passed to lavaan.
`mmodel`	Object of class `mmodel`. If not provided, manifest variables from the formula object will be used. Otherwise, use `create_mmodel()` to specify measurement model.
`C_matrix`	Contrast matrix. Must be invertible.

hypotheses	List of numeric vectors. Each list element represents a hypothesis. For each hypothesis, the contrasts indicated by the elements of the vectors are tested against zero.
covariates	Not implemented yet.
groups	Not implemented yet.
append	Character. Syntax that is to be appended to lavaan syntax.
verbose	Boolean. Print details during procedure.
compound_symmetry	Boolean. When set to TRUE, compound symmetry is assumed.
sphericity	Boolean or formula. When set to TRUE, sphericity is assumed for all effects.
multiv_tests	Character vector. Multivariate test statistics that are to be computed. Possible statistics are: `c("wilks", "wald")`. Default is `multiv_tests = c("wilks", "wald")`.
univ_tests	Character vector. Univariate test statistics that are to be computed. Possible statistics are: `c("F")`. Default is `univ_tests = NULL`.
randomization	Not yet supported.
...	Additional arguments to be passed to lavaan.

Value

Function returns an lgc object. Use `summary(object)` to print hypotheses. Otherwise use `object@sem_obj` to get access to the underlying lavaan object.

Examples

```
set.seed(323412431)

data("semnova_test_data", package = "semnova")

mmodel <- create_mmodel(
    A1B1 = "var1",
    A2B1 = "var2",
    A3B1 = "var3",
    A1B2 = "var4",
    A2B2 = "var5",
    A3B2 = "var6",
    lv_scaling = "referent"
)

hypotheses <- list(
    Intercept = c(1),
    A         = c(2, 3),
    B         = c(4),
    AB        = c(5, 6)
)

C_matrix <- matrix(
    c(1, 1, 0, 1, 1, 0,
```

```
      1, 0, 1, 1, 0, 1,
      1,-1,-1, 1,-1,-1,
      1, 1, 0,-1,-1, 0,
      1, 0, 1,-1, 0,-1,
      1,-1,-1,-1, 1, 1),
    nrow=6
)

fit_lgc <- lgc(data = semnova_test_data, mmodel, C_matrix, hypotheses)
summary(fit_lgc)
```

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lgc-class *LGC Class.*

Description

LGC Class.

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semnova *Latent repeated-measures ANOVA using the LGC approach*

Description

Function specifies an LGC model. The idata object is used to create the contrast matrix that is passed to the `lgc()` function. Typical hypotheses are specified as well.

Usage

```
semnova(
  formula,
  idesign,
  idata,
  data,
  mmodel = NULL,
  covariates = NULL,
  groups = NULL,
  append = NULL,
  icontrasts = c("contr.poly", "contr.sum"),
  verbose = FALSE,
  compound_symmetry = FALSE,
  sphericity = FALSE,
  multiv_tests = c("wilks", "wald"),
  univ_tests = c("F"),
  randomization = list(ncores = 1, nsamples = 1000),
  ...
)
```

Arguments

formula	Formula.
idesign	Formula. Within-subjects design formula.
idata	Dataframe. The dataframe contains the factorial design.
data	Dataframe. Data object to be passed to lavaan.
mmodel	Object of class mmodel. If not provided, manifest variables from the formula object will be used. Otherwise, use create_mmodel() to specify measurement model.
covariates	Not implemented yet.
groups	Not implemented yet.
append	Character vector. Syntax that is to be appended to lavaan syntax.
icontrasts	Character vector. Use this argument to select the type of contrasts to be used. Default is c("contr.sum", "contr.poly") (not ordered, ordered).
verbose	Boolean. Print details during procedure.
compound_symmetry	Boolean. When set to TRUE, compound symmetry is assumed among dependent variables.
sphericity	Boolean or formula. When set to TRUE, sphericity is assumed for all effects.
multiv_tests	Character vector. Multivariate test statistics that are to be computed. Possible statistics are: c("wilks", "wald"). Default is multiv_tests = c("wilks", "wald").
univ_tests	Character vector. Univariate test statistics that are to be computed. Possible statistics are: c("F"). Default is univ_tests = NULL.
randomization	Not yet supported.
...	Additional arguments to be passed to lavaan.

Value

Function returns an lgc object. Use summary(object) to print hypotheses. Otherwise use object@sem_obj to get access to the underlying lavaan object.

Examples

```
set.seed(323412431)

data("semnova_test_data", package = "semnova")

idata  <- expand.grid(A = c("A1", "A2", "A3"), B = c("B1", "B2"))

mmodel <- create_mmodel(
    A1B1 = "var1",
    A2B1 = "var2",
    A3B1 = "var3",
    A1B2 = "var4",
    A2B2 = "var5",
```

```
    A3B2 = "var6",
    lv_scaling = "referent"
)

fit_semnova <-
    semnova(
        formula = cbind(A1B1, A2B1, A3B1, A1B2, A2B2, A3B2) ~ 1,
        data = semnova_test_data,
        idata = idata,
        idesign = ~ A * B,
        mmodel = mmodel
    )

summary(fit_semnova)
```

`semnova_test_data` *This data set serves for examples and tests.*

Description

This is a simulated data set that 100 observation of six normally distributed variables with mean = 0, variance = 1 and covariance 0.5.

Usage

```
semnova_test_data
```

Format

A data frame with 100 rows and 6 variables:

`summary,lgc-method` *Printing the summary for an LGC object.*

Description

Printing the summary for an LGC object.

Usage

```
## S4 method for signature 'lgc'
summary(object, ...)
```

Arguments

`object`	`lgc` object. The object to get a summary about.
`...`	Additional arguments. Currently none supported.

Index