Package ‘HRM’
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Title High-Dimensional Repeated Measures
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Description Methods for testing main and interaction effects in possibly high-dimensional repeated measures in factorial designs. The observations of the subjects are assumed to be multivariate normal. It is possible to use up to 2 whole- and 3 subplot factors.
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Description

Tests for main and simple treatment effects, time effects, as well as treatment by time interactions in possibly high-dimensional multi-group repeated measures designs. The groups are allowed to have different variance-covariance matrices but the observations must follow a multivariate normal distribution.

Details

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Version: 0.7.1
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Author(s)

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References


Description

A dataset containing EEG data (Staffen et al., 2014) of 160 subjects, 4 variables are measured at ten different locations. The columns are as follows:
hrm.GUI

Usage

data(EEG)

Format

A data frame with 6400 rows and 7 variables.

Details

• group. Diagnostic group of the subject: Alzheimer’s Disease (AD), Mild Cognitive Impairment (MCI), Subject Cognitive Complaints (SCC+, SCC-).

• value. Measured data of a subject at a specific variable and region.

• sex. Sex of the subject: Male (M) or Female (W).

• subject. A unique identification of a subject.

• variable. The variables measured are activity, complexity, mobility and brain rate coded from 1 to 4.

• region. Frontal left/right, central left/right, temporal left/right, occipital left/right, parietal left/right coded as 1 to 10.

• dimension. Mixing variable and region together, levels range from 1 to 40.

Graphical User Interface for the Function ‘hrm_test’.

Description

Graphical User Interface (R Package RGtk2 needed) for the Function ‘hrm_test’: Test for main effects and interaction effects of one or two between-subject factors and one, two or three within-subject factors (at most four factors can be used).

Usage

hrm.GUI()

Value

The results can be saved as LaTeX Code or as plain text. Additionally a plot of the group profiles can be saved when using one whole- and one subplot factor.
hrm.plot

Plots profiles of the groups.

Description

Plots profiles of the groups in case of one whole- and one subplot-factor.

Usage

hrm.plot(data, group, factor1, subject, response, xlab = "dimension", ylab = "means")

Arguments

data A data.frame containing the data
group column name within the data frame data specifying the groups
factor1 column name within the data frame data specifying the first subplot-factor
subject column name within the data frame X identifying the subjects
response column name within the data frame X containing the response variable
xlab label of the x-axis of the plot
ylab label of the y-axis of the plot

Value

Plots profiles of the groups.

Examples

data(EEG)
head(EEG)

# plots profiles according to groups with
# subplot-factor called dimension
hrm.plot(EEG,"group", "dimension", "subject", "value")
hrm.test.dataframe

hrm.test.dataframe  Test for main effects and interaction effects.

Description
Test for main effects and interaction effects of one or two between-subject factors and one, two or three within-subject factors (at most four factors can be used).

Usage
hrm.test.dataframe(data, alpha = 0.05, group, subgroup, factor1, factor2, factor3, subject, response)

Arguments
- data: A data.frame containing the data
- alpha: alpha level used for the test
- group: column name within the data frame data specifying the groups
- subgroup: column name within the data frame data specifying the subgroups (crossed with groups)
- factor1: column name within the data frame data specifying the first subplot-factor
- factor2: column name within the data frame data specifying the second subplot-factor
- factor3: column name within the data frame data specifying the third subplot-factor
- subject: column name within the data frame X identifying the subjects
- response: column name within the data frame X containing the response variable

Value
Returns an object from class HRM containing
- result: A data frame with the results from the hypotheses tests.
- alpha: The type-I error rate which was used.
- subject: The column name identifying the subjects.
- factors: A list containing the whole- and subplot factors.

Examples
n=c(45, 22, 57, 36)
X_1 = mvnorm(n = n[1], mu = rep(0,40), Sigma = diag(40))
X_2 = mvnorm(n = n[2], mu = rep(0,40), Sigma = diag(40))
X_3 = mvnorm(n = n[3], mu = rep(0,40), Sigma = diag(40))
X_4 = mvnorm(n = n[4], mu = rep(0,40), Sigma = diag(40))
X_1 = c(t(as.matrix(X_1)))
X_1 = data.frame(group = "SCC+", value = X_1)
X_2 = c(t(as.matrix(X_2)))
X_2 = data.frame(group= "SCC", value = X_2)

X_3 = c(t(as.matrix(X_3)))
X_3 = data.frame(group = "MCI", value = X_3)

X_4 = c(t(as.matrix(X_4)))
X_4 = data.frame(group = "AD", value = X_4)

X = rbind(X_1, X_2, X_3, X_4)
X$subject = gl(160, 40)
X$variable = as.factor(rep(gl(4, 10),160))
X$region = as.factor(rep(rep(1:10,4),160))
X$subgroup = as.factor(rep(gl(2, 40),80))
X$group = as.factor(X$group)

hrm.test.dataframe(data=X, alpha=0.05, group="group", factor1="variable",
factor2="region", subject="subject", response="value")

---

**hrm.test.matrix**

*Test for main and interaction effects.*

**Description**

Test for no main treatment effect, no main time effect, no simple treatment effect and no interaction between treatment and time

**Usage**

hrm.test.matrix(data, alpha = 0.05)

**Arguments**

- **data**
  - A list containing the data matrices of all groups. The rows are the independent subjects, these observations are assumed to be multivariate normally distributed. The columns of all matrices need to be in the same order.

- **alpha**
  - alpha level used for the test

**Value**

Returns an object from class HRM containing

- **result**
  - A dataframe with the results from the hypotheses tests.

- **alpha**
  - The type-I error rate which was used.

- **subject**
  - The column name identifying the subjects.

- **factors**
  - A list containing the whole- and subplot factors.
Examples

```r
# number patients per group
n = c(10,10)
# number of groups
a=2
# number of variables
d=40

# defining the list consisting of the samples from each group
mu_1 = mu_2 = rep(0,d)
# autoregressive covariance matrix
sigma_1 = diag(d)
for(k in 1:d) for(l in 1:d) sigma_1[k,l] = 1/(1-0.5^2)*0.5^abs(k-l))
sigma_2 = 1.5*sigma_1
X = list(mvrnorm(n[1],mu_1, sigma_1), mvrnorm(n[2],mu_2, sigma_2))
X=lapply(X, as.matrix)
# test for the main treatment effect and print the p.value
hrm.test.matrix(data=X, alpha=0.05)
```

hrm_test  

`hrm_test`  

Test for main effects and interaction effects.

Description

Test for main effects and interaction effects of one or two between-subject factors and one, two or three within-subject factors (at most four factors can be used).

Usage

```
hrm_test(formula, data, alpha = 0.05, subject)
```

Arguments

- **formula**: A model formula object. The left hand side contains the response variable and the right hand side contains the whole- and subplot factors.
- **data**: A data.frame containing the data. The columns containing the factor variables need to have the type 'factor'. One column is needed to indentify the subjects.
- **alpha**: alpha level used for the test
- **subject**: column name within the data frame X identifying the subjects

Value

Returns an object from class HRM containing

- **result**: A dat frame with the results from the hypotheses tests.
- **formula**: The formula object which was used.
- **alpha**: The type-I error rate which was used.
- **subject**: The column name identifying the subjects.
- **factors**: A list containing the whole- and subplot factors.
Examples

data(EEG)

hrm_test(value ~ group*region+variable+variable:region-group,
        data = EEG, alpha=0.05, subject="subject")
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