

Package ‘HRM’

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Title High-Dimensional Repeated Measures

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Depends R (>= 3.0.0), MASS, matrixcalc, plyr, ggplot2, reshape2

Description Inference for high-dimensional repeated measures in factorial designs.

License GPL-2 | GPL-3

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HRM-package

Inference on low- and high-dimensional multi-group repeated-measures designs with unequal covariance matrices.

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.

Details

Package: HRM
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Author(s)

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References

Happ, M., Harrar, S. W. and Bathke, A. C. (2015), Inference for low- and high-dimensional multi-group repeated measures designs with unequal covariance matrices. *Biom. J.* doi: 10.1002/bimj.201500064

Staffen, W., Strobl, N., Zauner, H., Holler, Y., Dobesberger, J. and Trinka, E. (2014). Combining SPECT and EEG analysis for assessment of disorders with amnesic symptoms to enhance accuracy in early diagnostics. Poster A19 Presented at the 11th Annual Meeting of the Austrian Society of Neurology. 26th-29th March 2014, Salzburg, Austria.

EEG

EEG data of 160 subjects

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:

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.

hrm.plot

Plots profiles of the groups.

Description

Plots profiles of the groups.

Usage

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

Arguments

X	list containing the data matrices of all groups
group	column name of the data frame X specifying the groups
factor1	column name of the data frame X of the first factor variable
subject	column name of the data frame X identifying the subjects
data	column name of the data frame X identifying the measured data
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' in data.frame
hrm.plot(EEG,"group", "dimension", "subject", "value")
```

hrm.test	<i>Test for no main treatment effect, no main time effect, no simple treatment effect and no interaction between treatment and time</i>
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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(n, a, d, X, alpha)
```

Arguments

n	an vector containing the sample sizes of all groups
a	number of groups
d	number of dimensions (time points)
X	list containing the data matrices of all groups
alpha	alpha level used for the test

Value

Returns a data frame consisting of the degrees of freedom, the test value, the critical value and the p-value

Examples

```
# 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))

# test for the main treatment effect and print the p.value
hrm.test(n, a, d, X, 0.05)

```

hrm.test.2	<i>Test for main effects and interaction effects of one or two between-subject factors and one or two within-subject factors</i>
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Description

Test for main effects and interaction effects of one or two between-subject factors and one or two within-subject factors

Usage

```
hrm.test.2(X, alpha = 0.05, group, subgroup, factor1, factor2, subject, data)
```

Arguments

X	list containing the data matrices of all groups
alpha	alpha level used for the test
group	column name of the data frame X specifying the groups
subgroup	column name of the subgroups (crossed with groups)
factor1	column name of the data frame X of within-subject factor
factor2	column name of the second within-subject factor crossed with factor1
subject	column name of the data frame X identifying the subjects
data	column name of the data frame X containing the measurement data

Value

Returns a data frame consisting of the degrees of freedom, the test value, the critical value and the p-value

Examples

```

n=c(45, 22, 57, 36)
X_1 = mvrnorm(n = n[1], mu = rep(0,40), Sigma = diag(40))
X_2 = mvrnorm(n = n[2], mu = rep(0,40), Sigma = diag(40))
X_3 = mvrnorm(n = n[3], mu = rep(0,40), Sigma = diag(40))
X_4 = mvrnorm(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.2(X,0.05,group="group",factor1="variable",
factor2="region",subject="subject",data="value")
```

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