

# Package ‘HRM’

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**Title** High-Dimensional Repeated Measures

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**LazyData** true

**Depends** R (>= 3.4.0), MASS, matrixcalc, plyr, ggplot2

**Imports** xtable, reshape2, tcltk, data.table, doBy, mvtnorm, Rcpp (>= 0.12.16), pseudorank (>= 0.3.8)

**Suggests** RGtk2 (>= 2.8.0), cairoDevice, testthat

**LinkingTo** Rcpp

**SystemRequirements** C++11

**Description** Methods for testing main and interaction effects in possibly high-dimensional parametric or nonparametric repeated measures in factorial designs for univariate or multivariate data.

The observations of the subjects are assumed to be multivariate normal if using the parametric test. The nonparametric version tests with regard to nonparametric relative effects (based on pseudo-ranks).

It is possible to use up to 2 whole- and 3 subplot factors.

**License** GPL-2 | GPL-3

**RoxygenNote** 7.0.2

**URL** <http://github.com/happma/HRM>

**BugReports** <http://github.com/happma/HRM/issues>

**NeedsCompilation** yes

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HRM-package	<i>Inference on low- and high-dimensional multi-group repeated-measures designs with unequal covariance matrices.</i>
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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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 Type: Package  
 Version: 1.0.2  
 Date: 2018-10-16  
 License: GPL-2 | GPL-3

### Author(s)

Maintainer: martin.happ@aon.at

### References

- Happ, M., Harrar, S. W. and Bathke, A. C. (2016), Inference for low- and high-dimensional multi-group repeated measures designs with unequal covariance matrices. *Biom. J.*, 58: 810-830. doi: 10.1002/bimj.201500064
- Happ, M., Harrar, S. W. and Bathke, A. C. (2017), High-dimensional Repeated Measures. *Journal of Statistical Theory and Practice*. doi: 10.1080/15598608.2017.1307792
- Staffen, W., Strobl, N., Zauner, H., Hoeller, 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.

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`confint.HRM`*Function to calculate confidence intervals*

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### Description

Function to calculate simultaneous, asymptotic (1-alpha) confidence intervals for an object of class 'HRM'.

### Usage

```
## S3 method for class 'HRM'  
confint(object, parm, level = 0.95, ...)
```

### Arguments

<code>object</code>	an object from class 'HRM' returned from the function <code>hrm_test</code>
<code>parm</code>	currently ignored; all possible confidence intervals are calculated
<code>level</code>	confidence level (FWER) used for calculating the intervals
<code>...</code>	Further arguments passed to 'hrm_test' will be ignored

### Value

Returns a data.frame with mean and 1-alpha confidence interval for each factor combination

### Examples

```
# hrm.test with a data.frame using a 'formula' object  
  
# using the EEG dataset  
?EEG  
  
## Not run:  
# z <- hrm_test(value ~ group*region*variable, subject = "subject", data = EEG)  
# confint(z)  
## End(Not run)
```

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 EEG

*EEG data of 160 subjects*


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### Description

A dataset containing EEG data (Staffen et al., 2014) of 160 subjects, 4 variables are measured at ten different locations.

### Usage

```
data(EEG)
```

### Format

A data frame with 6400 rows and 7 variables.

### Details

The columns are as follows:

- 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.

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 hrm\_GUI

*Graphical User Interface for Testing Multi-Factor High-Dimensional Repeated Measures*


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### 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\_test

*Test for Multi-Factor High-Dimensional Repeated Measures***Description**

Performing main and interaction effects of up to three whole- or subplot-factors. In total, a maximum of four factors can be used. There are two different S3 methods available. The first method requires a list of matrices in the wide table format. The second method requires a data.frame in the long table format.

**Usage**

```
hrm_test(data, ...)

## S3 method for class 'list'
hrm_test(data, alpha = 0.05, ...)

## S3 method for class 'data.frame'
hrm_test(
  data,
  formula,
  alpha = 0.05,
  subject,
  variable = NULL,
  nonparametric = FALSE,
  np.correction = NA,
  character.only = FALSE,
  ...
)
```

**Arguments**

data	Either a data.frame (one observation per row) or a list with matrices (one subject per row) for all groups containing the data
...	Further arguments passed to 'hrm_test' will be ignored
alpha	alpha level used for calculating the critical value for the test
formula	A model formula object. The left hand side contains the response variable and the right hand side contains the whole- and subplot factors.
subject	column name within the data frame X identifying the subjects
variable	if not 'NULL' then multivariate tests are applied. We assume that for each factor level of 'variable', we observe several repeated measurements. Currently only supports designs with 1 whole- and one sub-plot factor.

nonparametric Logical variable indicating whether the nonparametric version of the test statistic should be used

np.correction Logical variable indicating whether a small sample size correction for the non-parametric test should be used (TRUE) or not (FALSE). By using NA, np.correction is used automatically in an high-dimensional setting.

character.only a logical indicating whether subject can be assumed to be a character string

### Value

Returns an object from class HRM containing

result A dataframe 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.

data The data.frame or list containing the data.

### Examples

```
## hrm_test with a list of matrices

# 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(mvnorm(n[1],mu_1, sigma_1), mvnorm(n[2],mu_2, sigma_2))
X=lapply(X, as.matrix)

hrm_test(data=X, alpha=0.05)

## hrm.test with a data.frame using a 'formula' object

# using the EEG dataset
?EEG

# Univariate Approach
hrm_test(value ~ group*region*variable, subject = "subject", data = EEG)

# Multivariate Approach: testing effects for each variable
```

```
hrm_test(value~group*region, subject=subject, variable=variable, data = EEG)
```

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plot.HRM *Plotting Profile Curves*

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### Description

Plotting profile curves for up to one whole- or subplot-factor

### Usage

```
## S3 method for class 'HRM'
plot(x, xlab = "time", ylab = "mean", legend = TRUE, legend.title = "", ...)
```

### Arguments

x	An object of class 'HRM' from the function 'hrm_test'
xlab	label of the x-axis of the plot
ylab	label of the y-axis of the plot
legend	logical indicating if a legend should be plotted
legend.title	title of the legend
...	Further arguments passed to the 'plot' function

### Examples

```
data(EEG)
head(EEG)

# plots profiles according to groups with
# subplot-factor called dimension

# first create an HRM object
object_hrm <- hrm_test(value ~ group*dimension, subject = "subject", data = EEG)

# plot the HRM object, here we use the additional argument 'theme_bw()' for ggplot2
plot(object_hrm, legend = TRUE, legend.title = "Group", ... = theme_bw() )

# same plot without a legend
# note that 'theme_bw' overwrites the standard legend properties of plot.HRM
plot(object_hrm, ... = theme_bw() +
  theme(legend.title = element_blank(), legend.position="none") )
```

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