Package 'MANOVA.RM'

Type Package

Title Resampling-Based Analysis of Multivariate Data and Repeated
Measures Designs

Version 0.5.3

Date 2022-01-18

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Depends R (>= 3.4.0)

Description Implemented are various tests for semi-parametric repeated measures
and general MANOVA designs that do neither assume multivariate normality nor
covariance homogeneity, i.e., the procedures are applicable for a wide range
of general multivariate factorial designs. In addition to asymptotic inference
methods, novel bootstrap and permutation approaches are implemented as well. These pro-
vide more
accurate results in case of small to moderate sample sizes. Furthermore, post-hoc
comparisons are provided for the multivariate analyses.
Friedrich, S., Konietschke, F. and Pauly, M. (2019) <doi:10.32614/RJ-2019-051>.

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Imports plyr (>= 1.8.4), MASS (>= 7.3-51), Matrix (>= 1.2-17), magic
(>= 1.5-9), plotrix (>= 3.5-12), parallel, methods, ellipse,
multcomp, data.table (>= 1.12.6)

LazyData TRUE

Suggests RGtk2 (>= 2.20.31), knitr, rmarkdown, HSAUR3, tidyr(>=
1.0.0), ggplot2, GFD, testthat

Encoding UTF-8

RoxygenNote 7.1.2

VignetteBuilder knitr, rmarkdown

URL https://github.com/smn74/MANOVA.RM

BugReports https://github.com/smn74/MANOVA.RM/issues

NeedsCompilation no

R **topics documented:**

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conf.reg	*The conf.reg() function calculates confidence regions for contrasts in multivariate factorial designs. In the two-dimensional case, confidence ellipsoids can be plotted via the generic* plot() *function.*

Description

The conf.reg() function calculates confidence regions for contrasts in multivariate factorial designs. In the two-dimensional case, confidence ellipsoids can be plotted via the generic plot() function.

Usage

```
conf.reg(object, nullhypo)
```

Arguments

object	A MANOVA object.
nullhypo	In scenarios with more than one factor, the null hypothesis, i.e., the contrast of interest must be specified.

Value

A `confreg` object containing the following components:

center	The center of the confidence ellipsoid.
scale	The scaling factors for the axis of the confidence ellipsoid calculated as $\sqrt{\lambda * c/N}$, where λ are the eigenvalues, c denotes the bootstrap quantile and N is the total sample size. See Friedrich and Pauly (2018) for details.
eigenvectors	The corresponding eigenvectors, which determine the axes of the ellipsoid.

References

Friedrich, S., and Pauly, M. (2018). MATS: Inference for potentially singular and heteroscedastic MANOVA. Journal of Multivariate Analysis, 165, 166-179.

Examples

```
data(EEG)
EEG_mod <- MANOVA(resp ~ sex * diagnosis,
                    data = EEG, subject = "id", resampling = "paramBS",
                    alpha = 0.05, iter = 10, CPU = 1)
conf.reg(EEG_mod, nullhypo = "sex")
```

EEG	*EEG Measurements in Patients with Alzheimer's Disease (long format)*

Description

At the Department of Neurology, University Clinic of Salzburg, 160 patients were diagnosed with either AD, MCI, or SCC, based on neuropsychological diagnostics. This data set contains z-scores for brain rate and Hjorth complexity, each measured at frontal, temporal and central electrode positions and averaged across hemispheres. In addition to standardization, complexity values were multiplied by -1 in order to make them more easily comparable to brain rate values: For brain rate we know that the values decrease with age and pathology, while Hjorth complexity values are known to increase with age and pathology. The three between-subjects factors considered were sex (men vs. women), diagnosis (AD vs. MCI vs. SCC), and age ($<$ 70 vs. $>=$ 70 years). Additionally, the within-subjects factors region (frontal, temporal, central) and feature (brain rate, complexity) structure the response vector.

Usage

```
data(EEG)
```

Format

A data frame with 960 rows and 7 variables:

resp EEG measurements

sex sex of the patient

age age of the patient, coded as 0 for less than 70 years and 1 for $>= 70$ years

diagnosis neuropsychological diagnosis, AD for Alzheimer's Disease, MCI for mild cognitive impairment or SCC for subjective cognitive complaints without clinically significant deficits

region brain region of the EEG measurements, one of "temporal", "frontal" and "central"

feature feature of the EEG measurements, either "brainrate" or "complexity"

id Subject id

Source

Bathke, A., Friedrich, S., Konietschke, F., Pauly, M., Staffen, W., Strobl, N. and Hoeller, Y. (2018). Testing Mean Differences among Groups: Multivariate and Repeated Measures Analysis with Minimal Assumptions. Multivariate Behavioral Research. Doi: 10.1080/00273171.2018.1446320.

Examples

```
 library(ggplot2)
ggplot(EEG, aes(x=sex, y=resp)) + geom_point(alpha=0.5) + facet_grid(region+feature~diagnosis) +
    stat_summary(fun.y = mean, fun.ymin = min, fun.ymax = max, colour = "red")
```

EEGwide   *EEG Measurements in Patients with Alzheimer's Disease (wide format)*

Description

At the Department of Neurology, University Clinic of Salzburg, 160 patients were diagnosed with either AD, MCI, or SCC, based on neuropsychological diagnostics. This data set contains z-scores for brain rate and Hjorth complexity, each measured at frontal, temporal and central electrode positions and averaged across hemispheres. In addition to standardization, complexity values were multiplied by -1 in order to make them more easily comparable to brain rate values: For brain rate we know that the values decrease with age and pathology, while Hjorth complexity values are known to increase with age and pathology. The three between-subjects factors considered were sex (men vs. women), diagnosis (AD vs. MCI vs. SCC), and age (< 70 vs. $>= 70$ years). Additionally, the within-subjects factors region (frontal, temporal, central) and feature (brain rate, complexity) structure the response vector.

Usage

```
data(EEGwide)
```

Format

A data frame with 160 rows and 9 variables:

brainrate_temporal EEG measurements for brainrate in temporal regions

brainrate_frontal EEG measurements for brainrate in frontal regions

brainrate_central EEG measurements for brainrate in central regions

complexity_temporal EEG measurements for complexity in temporal regions

complexity_frontal EEG measurements for complexity in frontal regions

complexity_central EEG measurements for complexity in central regions

sex sex of the patient

age age of the patient

diagnosis neuropsychological diagnosis, AD for Alzheimer's Disease, MCI for mild cognitive impairment or SCC for subjective cognitive complaints without clinically significant deficits

AgeGroup categorized age, coded as 0 for less than 70 years and 1 for $>= 70$ years

Details

Note that this data set contains exactly the same data as the data set 'EEG', only the format is different. The transformation between the different formats can be achieved using, e.g., the tidyr package.

Source

Bathke, A., Friedrich, S., Konietschke, F., Pauly, M., Staffen, W., Strobl, N. and Hoeller, Y. (2018). Testing Mean Differences among Groups: Multivariate and Repeated Measures Analysis with Minimal Assumptions. Multivariate Behavioral Research. Doi: 10.1080/00273171.2018.1446320.

@examples library("ggplot2") qplot(data = EEGwide, diagnosis)

GUI.MANOVA   *A graphical user interface for the MANOVA() function*

Description

This function provides a graphical user interface for calculating statistical tests for multivariate data.

Usage

```
GUI.MANOVA()
```

Details

The function produces a GUI for the calculation of the test statistics. Data can be loaded via the "load data" button. The formula, number of resampling iterations (default: 10,000) and the significance level alpha (default: 0.05) need to be specified. Furthermore, the column name specifying the subjects in the data needs to be provided. For the resampling methods, the user can choose between a parametric bootstrap approach (see e.g. Konietschke et al. (2015)) and a Wild bootstrap using Rademacher weights (see e.g. Bathke et al. (2018)).

GUI.MANOVAwide   *A graphical user interface for the MANOVA.wide() function*

Description

This function provides a graphical user interface for calculating statistical tests for multivariate data.

Usage

```
GUI.MANOVAwide()
```

Details

The function produces a GUI for the calculation of the test statistics. Data can be loaded via the "load data" button. The formula, number of resampling iterations (default: 10,000) and the significance level alpha (default: 0.05) need to be specified. For the resampling methods, the user can choose between a parametric bootstrap approach (see e.g. Konietschke et al. (2015)) and a Wild bootstrap using Rademacher weights (see e.g. Bathke et al. (2018)).

GUI.RM   *A graphical user interface for the RM() function*

Description

This function provides a graphical user interface for calculating statistical tests in repeated measures designs.

Usage

```
GUI.RM()
```

Details

The function produces a GUI for the calculation of the test statistics and for plotting. Data can be loaded via the "load data" button. The formula, number of resampling iterations (default: 10,000) and the significance level alpha (default: 0.05) need to be specified. Furthermore, the number of sub-plot factors and the column name specifying the subjects in the data need to be provided. For the resampling methods, the user can choose between a permutation approach (Friedrich et al. (2017)), a parametric bootstrap approach (Konietschke et al. (2015)) and a Wild bootstrap using Rademacher weights (Bathke et al. (2018)). If the plot option is chosen, an additional window opens containing information on the plots.

| MANOVA | *Tests for Multivariate Data in Semi-Parametric Factorial Designs* |

Description

The MANOVA function calculates the Wald-type statistic (WTS) and a modified ANOVA-type statistic (MATS) as well as resampling versions of these test statistics for semi-parametric multivariate data.

Usage

```
MANOVA(
  formula,
  data,
  subject,
  iter = 10000,
  alpha = 0.05,
  resampling = "paramBS",
  para = FALSE,
  CPU,
  seed,
  nested.levels.unique = FALSE,
  dec = 3
)
```

Arguments

formula	A model [formula](#) object. The left hand side contains the response variable and the right hand side contains the factor variables of interest.
data	A data.frame, list or environment containing the variables in formula. Data must be in long format and must not contain missing values.
subject	The column name of the subjects in the data.
iter	The number of iterations used for calculating the resampled statistic. The default option is 10,000.
alpha	A number specifying the significance level; the default is 0.05.
resampling	The resampling method to be used, one of "paramBS" (parametric bootstrap approach) and "WildBS" (wild bootstrap approach with Rademacher weights).
para	If parallel computing should be used. Default is FALSE.
CPU	The number of cores used for parallel computing. If not specified, cores are detected via [detectCores](#).
seed	A random seed for the resampling procedure. If omitted, no reproducible seed is set.

nested.levels.unique

>A logical specifying whether the levels of the nested factor(s) are labeled uniquely or not. Default is FALSE, i.e., the levels of the nested factor are the same for each level of the main factor. For an example and more explanations see the GFD package and the corresponding vignette.

dec   Number of decimals the results should be rounded to. Default is 3.

Details

The MANOVA() function provides the Wald-type statistic (WTS) as well as the modified ANOVA-type statistic (MATS) for multivariate designs with metric data as described in Konietschke et al. (2015) and Friedrich and Pauly (2018), respectively. The MATS is invariant under scale transformations of the components and applicable to designs with singular covariance matrices. Both tests are applicable for non-normal error terms, different sample sizes and/or heteroscedastic variances. They are implemented for designs with an arbitrary number of crossed factors or for nested designs. In addition to the asymptotic p-values, the function also provides p-values based on resampling approaches.

Value

A MANOVA object containing the following components:

Descriptive   Some descriptive statistics of the data for all factor level combinations. Displayed are the number of individuals per factor level combination and the vector of means (one column per dimension).

Covariance   The estimated covariance matrix.

WTS   The value of the WTS along with degrees of freedom of the central chi-square distribution and p-value.

MATS   The value of the MATS.

resampling   p-values for the test statistic based on the chosen resampling approach.

NOTE

The number of resampling iterations has been set to 10 in the examples due to run time restrictions on CRAN. Usually it is recommended to use at least 1000 iterations. For more information and detailed examples also refer to the package vignette.

References

Friedrich, S., Konietschke, F., and Pauly, M. (2019). Resampling-Based Analysis of Multivariate Data and Repeated Measures Designs with the R Package MANOVA.RM. The R Journal, 11(2), 380-400.

Konietschke, F., Bathke, A. C., Harrar, S. W. and Pauly, M. (2015). Parametric and nonparametric bootstrap methods for general MANOVA. Journal of Multivariate Analysis, 140, 291-301.

Friedrich, S., Brunner, E. and Pauly, M. (2017). Permuting longitudinal data in spite of the dependencies. Journal of Multivariate Analysis, 153, 255-265.

Bathke, A., Friedrich, S., Konietschke, F., Pauly, M., Staffen, W., Strobl, N. and Hoeller, Y. (2018). Testing Mean Differences among Groups: Multivariate and Repeated Measures Analysis with Minimal Assumptions. Multivariate Behavioral Research, 53(3), 348-359, Doi: 10.1080/00273171.2018.1446320.

Friedrich, S., Konietschke, F., Pauly, M. (2017). GFD - An R-package for the Analysis of General Factorial Designs. Journal of Statistical Software, 79(1), 1-18.

Friedrich, S., and Pauly, M. (2018). MATS: Inference for potentially singular and heteroscedastic MANOVA. Journal of Multivariate Analysis, 165, 166-179.

See Also

[RM](#)

Examples

```
data(EEG)
EEG_mod <- MANOVA(resp ~ sex * diagnosis,
                  data = EEG, subject = "id", resampling = "paramBS",
                  alpha = 0.05, iter = 10)
summary(EEG_mod)
```

MANOVA.wide   *Tests for Multivariate Data in Semi-Parametric Factorial Designs*

Description

The MANOVA.wide function calculates the Wald-type statistic (WTS) and a modified ANOVA-type statistic (MATS) as well as resampling versions of these test statistics for semi-parametric multivariate data provided in wide format.

Usage

```
MANOVA.wide(
  formula,
  data,
  iter = 10000,
  alpha = 0.05,
  resampling = "paramBS",
  para = FALSE,
  CPU,
  seed,
  nested.levels.unique = FALSE,
  dec = 3,
  ...
)
```

Arguments

formula	A model [formula](#) object. The left hand side contains the matrix of response variables and the right hand side contains the factor variables of interest.
data	A data.frame, list or environment containing the variables in formula. Data must be in wide format. Note: Lines containing missing values will be removed.
iter	The number of iterations used for calculating the resampled statistic. The default option is 10,000.
alpha	A number specifying the significance level; the default is 0.05.
resampling	The resampling method to be used, one of "paramBS" (parametric bootstrap approach) and "WildBS" (wild bootstrap approach with Rademacher weights). The Wild Bootstrap is calculated for all test statistics.
para	If parallel computing should be used. Default is FALSE.
CPU	The number of cores used for parallel computing. If not specified, cores are detected via [detectCores](#).
seed	A random seed for the resampling procedure. If omitted, no reproducible seed is set.
nested.levels.unique	
	A logical specifying whether the levels of the nested factor(s) are labeled uniquely or not. Default is FALSE, i.e., the levels of the nested factor are the same for each level of the main factor. For an example and more explanations see the GFD package and the corresponding vignette.
dec	Number of decimals the results should be rounded to. Default is 3.
...	Not used yet.

Value

See [MANOVA](#)

NOTE

The number of resampling iterations has been set to 100 in the examples due to run time restrictions on CRAN. Usually it is recommended to use at least 1000 iterations.

See Also

[MANOVA](#)

Examples

```
#Example on producing plastic film from Krzanowski (1998, p. 381), see \code{\link{manova.summary}}
tear <- c(6.5, 6.2, 5.8, 6.5, 6.5, 6.9, 7.2, 6.9, 6.1, 6.3,
          6.7, 6.6, 7.2, 7.1, 6.8, 7.1, 7.0, 7.2, 7.5, 7.6)
gloss <- c(9.5, 9.9, 9.6, 9.6, 9.2, 9.1, 10.0, 9.9, 9.5, 9.4,
           9.1, 9.3, 8.3, 8.4, 8.5, 9.2, 8.8, 9.7, 10.1, 9.2)
opacity <- c(4.4, 6.4, 3.0, 4.1, 0.8, 5.7, 2.0, 3.9, 1.9, 5.7,
             2.8, 4.1, 3.8, 1.6, 3.4, 8.4, 5.2, 6.9, 2.7, 1.9)
rate     <- gl(2,10, labels = c("Low", "High"))
```

```
additive <- gl(2, 5, length = 20, labels = c("Low", "High"))
example <- data.frame(tear, gloss, opacity, rate, additive)
fit <- MANOVA.wide(cbind(tear, gloss, opacity) ~ rate * additive,
data = example, iter = 1000)
summary(fit)
```

MANOVARM	*MANOVA.RM: A package for calculating test statistics and their resampling versions for heteroscedastic semi-parametric multivariate data or repeated measures designs.*

Description

The MANOVA.RM package provides three important functions: MANOVA(), RM() and multRM() which will be explained in detail below.

MANOVA and MANOVA.wide function

The MANOVA() and MANOVA.wide() functions provide the Wald-type statistic (WTS) as well as a modified ANOVA-type statistic (MATS) as in Friedrich and Pauly (2018) for multivariate designs with metric data as described in Konietschke et al. (2015). These are applicable for non-normal error terms, different sample sizes and/or heteroscedastic variances. The MATS can even handle designs involving singular covariance matrices. The tests are implemented for designs with an arbitrary number of crossed factors or for nested designs. In addition to the asymptotic p-values, they also provide p-values based on resampling approaches (parametric or wild bootstrap). The difference between the two functions is the format of the data: For MANOVA(), the data needs to be in long format, while MANOVA.wide() is for data in wide format. For further details, see `MANOVA` and `MANOVA.wide`.

RM function

The RM() function provides the Wald-type statistic (WTS) as well as the ANOVA-type statistic (ATS) for repeated measures designs with metric data as described in Friedrich et al. (2017). These are even applicable for non-normal error terms and/or heteroscedastic variances. It is implemented for designs with an arbitrary number of whole-plot and sub-plot factors and allows for different sample sizes. In addition to the asymptotic p-values, it also provides p-values based on resampling approaches (Permutation, parametric bootstrap, Wild bootstrap). For further details, see `RM`.

multRM function

The multRM() function is a combination of the procedures above suited for multivariate repeated measures designs. It provides the WTS and the MATS along with p-values based on a parametric or a wild bootstrap approach.

References

Friedrich, S., Konietschke, F., and Pauly, M. (2019). Resampling-Based Analysis of Multivariate Data and Repeated Measures Designs with the R Package MANOVA.RM. The R Journal, 11(2), 380-400.

Konietschke, F., Bathke, A. C., Harrar, S. W. and Pauly, M. (2015). Parametric and nonparametric bootstrap methods for general MANOVA. Journal of Multivariate Analysis, 140, 291-301.

Friedrich, S., Brunner, E. and Pauly, M. (2017). Permuting longitudinal data in spite of the dependencies. Journal of Multivariate Analysis, 153, 255-265.

Friedrich, S., Konietschke, F., Pauly, M. (2016). GFD - An R-package for the Analysis of General Factorial Designs. Journal of Statistical Software, 79(1), 1-18.

Bathke, A., Friedrich, S., Konietschke, F., Pauly, M., Staffen, W., Strobl, N. and Hoeller, Y. (2018). Testing Mean Differences among Groups: Multivariate and Repeated Measures Analysis with Minimal Assumptions. Multivariate Behavioral Research. Doi: 10.1080/00273171.2018.1446320.

Friedrich, S., and Pauly, M. (2018). MATS: Inference for potentially singular and heteroscedastic MANOVA. Journal of Multivariate Analysis, 165, 166-179.

---

multRM	*Tests for Repeated Measures in Multivariate Semi-Parametric Factorial Designs*

Description

The multRM() function calculates the Wald-type statistic (WTS) and the modified ANOVA-type statistic (MATS) as well as resampling versions of these test statistics for multivariate semi-parametric repeated measures designs.

Usage

```
multRM(
  formula,
  data,
  subject,
  within,
  iter = 10000,
  alpha = 0.05,
  resampling = "paramBS",
  para = FALSE,
  CPU,
  seed,
  dec = 3
)
```

Arguments

formula	A model formula object. The left hand side contains the matrix of response variables (using cbind()) and the right hand side contains the factor variables of interest. The within-subject factors must be specified last in the formula, e.g. cbind(outcome1,outcome2) ~ between1 * between2 * within1 * within2.
data	A data.frame, list or environment containing the variables in formula. Data must be in long format and must not contain missing values.
subject	The column name of the subjects in the data. NOTE: Subjects within different groups of between-subject factors must have individual labels, see Details for more explanation.
within	Specifies the within-subject factor(s) in the formula.
iter	The number of iterations used for calculating the resampled statistic. The default option is 10,000.
alpha	A number specifying the significance level; the default is 0.05.
resampling	The resampling method to be used, one of "paramBS" (parametric bootstrap approach) and "WildBS" (wild bootstrap approach with Rademacher weights).
para	If parallel computing should be used. Default is FALSE.
CPU	The number of cores used for parallel computing. If not specified, cores are detected via detectCores.
seed	A random seed for the resampling procedure. If omitted, no reproducible seed is set.
dec	Number of decimals the results should be rounded to. Default is 3.

Details

The multRM() function provides the Wald-type statistic as well as the modified ANOVA-type statistic (Friedrich and Pauly, 2018) for repeated measures designs with multivariate metric outcomes. These methods are even applicable for non-normal error terms and/or heteroscedastic variances. Implemented are designs with an arbitrary number of between-subject (whole-plot) and within-subject (sub-plot) factors and the methods allow for different sample sizes. In addition to the asymptotic p-values, p-values based on resampling approaches are provided. NOTE: The within-subject factors need to be specified in the function call (within =).

If subjects in different groups of the between-subject factor have the same id, they will not be identified as different subjects and thus it is erroneously assumed that their measurements belong to one subject. See [RM](RM) for more explanations and an example.

Value

A MANOVA object containing the following components:

Descriptive	Some descriptive statistics of the data for all factor level combinations. Displayed are the number of individuals per factor level combination and the vector of means (one column per dimension).
Covariance	The estimated covariance matrix.

WTS	The value of the WTS along with degrees of freedom of the central chi-square distribution and p-value.
MATS	The value of the MATS.
resampling	p-values for the test statistic based on the chosen resampling approach.

References

Friedrich, S., Brunner, E. and Pauly, M. (2017). Permuting longitudinal data in spite of the dependencies. Journal of Multivariate Analysis, 153, 255-265.

Bathke, A., Friedrich, S., Konietschke, F., Pauly, M., Staffen, W., Strobl, N. and Hoeller, Y. (2018). Testing Mean Differences among Groups: Multivariate and Repeated Measures Analysis with Minimal Assumptions. Multivariate Behavioral Research, 53(3), 348-359, Doi: 10.1080/00273171.2018.1446320.

Friedrich, S., Konietschke, F., Pauly, M. (2017). GFD - An R-package for the Analysis of General Factorial Designs. Journal of Statistical Software, 79(1), 1-18.

Friedrich, S., and Pauly, M. (2018). MATS: Inference for potentially singular and heteroscedastic MANOVA. Journal of Multivariate Analysis, 165, 166-179.

See Also

RM, MANOVA

Examples

```
## Not run:
data(EEG)
library(tidyr)
eeg <- spread(EEG, feature, resp)
fit <- multRM(cbind(brainrate, complexity) ~ sex * region, data = eeg,
              subject = "id", within = "region")
summary(fit)

## End(Not run)
```

---

o2cons   *Oxygen Consumption of Leukocytes*

Description

A dataset containing measurements on the oxygen consumption of leukocytes in the presence and absence of inactivated staphylococci.

Usage

```
data(o2cons)
```

Format

A data frame with 144 rows and 5 variables:

O2 oxygen consumption of leukocytes in μl

Staphylococci whether or not inactivated staphylococci were added, 1 denotes yes, 0 no

Time the measurements were taken after 6, 12 and 18 minutes

Group the treatment group, either P for Placebo or V for Verum

Subject the subject id

Source

Friedrich, S., Brunner, E. & Pauly, M. (2017). Permuting longitudinal data in spite of the dependencies. Journal of Multivariate Analysis, 153, 255-265.

Examples

```
 library(ggplot2)
ggplot(o2cons, aes(x=Group, y=O2)) + geom_point(alpha=0.5) + facet_grid(Staphylococci~Time) +
 stat_summary(fun.y = mean, fun.ymin = min, fun.ymax = max, colour = "red")
```

---

plot.RM	*Plot function for an RM object*

Description

Generic plot function for RM objects: Returns a plot of the mean values along with confidence intervals for a specified RM-model.

Usage

```
## S3 method for class 'RM'
plot(x, leg = TRUE, ...)
```

Arguments

x	An object of class RM
leg	Logical: Should a legend be plotted?
...	Additional parameters to be passed to plot()

---

print.MANOVA   *Display MANOVA object*

Description

Returns a short summary of the results (test statistics with p-values)

Usage

```
## S3 method for class 'MANOVA'
print(x, ...)
```

Arguments

x   A MANOVA object

...   Additional parameters (currently not used)

---

print.RM   *Display an RM object*

Description

Returns a short summary of the results (test statistics with p-values)

Usage

```
## S3 method for class 'RM'
print(x, ...)
```

Arguments

x   An RM object

...   Additional parameters (currently not used)

RM   *Tests for Repeated Measures in Semi-Parametric Factorial Designs*

Description

The RM() function calculates the Wald-type statistic (WTS), the ANOVA-type statistic (ATS) as well as resampling versions of these test statistics for semi-parametric repeated measures designs.

Usage

```
RM(
  formula,
  data,
  subject,
  within,
  no.subf,
  iter = 10000,
  alpha = 0.05,
  resampling = "Perm",
  para = FALSE,
  CPU,
  seed,
  CI.method = "t-quantile",
  dec = 3
)
```

Arguments

formula	A model [formula](#) object. The left hand side contains the response variable and the right hand side contains the factor variables of interest. The within-subject factor(s) must be the last factor(s) in the formula, e.g. outcome ~ between1 * between2 * within1 * within2.
data	A data.frame, list or environment containing the variables in formula. Data must be in long format and must not contain missing values.
subject	The column name of the subjects in the data. NOTE: Subjects within different groups of between-subject factors must have individual labels, see Details for more explanation.
within	Specifies the within-subject factor(s) in the formula. Either this or no.subf must be specified.
no.subf	The number of within-subject factors in the data. Must be specified if within is omitted.
iter	The number of iterations used for calculating the resampled statistic. The default option is 10,000.
alpha	A number specifying the significance level; the default is 0.05.

resampling	The resampling method to be used, one of "Perm" (randomly permute all observations), "paramBS" (parametric bootstrap approach) and "WildBS" (wild bootstrap approach with Rademacher weights). Except for the Wild Bootstrap, all methods are applied to the WTS only.
para	If parallel computing should be used. Default is FALSE.
CPU	The number of cores used for parallel computing. If not specified, cores are detected via `detectCores`.
seed	A random seed for the resampling procedure. If omitted, no reproducible seed is set.
CI.method	The method for calculating the quantiles used for the confidence intervals, either "t-quantile" (the default) or "resampling" (the quantile of the resampled WTS).
dec	Number of decimals the results should be rounded to. Default is 3.

Details

The RM() function provides the Wald-type statistic as well as the ANOVA-type statistic for repeated measures designs with metric data as described in Friedrich et al. (2017). These are even applicable for non-normal error terms and/or heteroscedastic variances. It is implemented for designs with an arbitrary number of between-subject (whole-plot) and within-subject (sub-plot) factors and allows for different sample sizes. In addition to the asymptotic p-values, it also provides p-values based on resampling approaches. NOTE: The number of within-subject factors or their labels need to be specified in the function call. If only one factor is present, it is assumed that this is a within-subject factor (e.g. time).

If subjects in different groups of the between-subject factor have the same id, they will not be identified as different subjects and thus it is erroneously assumed that their measurements belong to one subject. Example: Consider a study with one between-subject factor "treatment" with levels verum and placebo and one within-subject factor "time" (4 measurements). If subjects in the placebo group are labeled 1-20 and subjects in the verum group have the same labels, the program erroneously assumes 20 individuals with 8 measurements each instead of 40 individuals with 4 measurements each.

Value

An RM object containing the following components:

Descriptive	Some descriptive statistics of the data for all factor level combinations. Displayed are the number of individuals per factor level combination, the mean and 100*(1-alpha)% confidence intervals (based on t-quantiles).
Covariance	The estimated covariance matrix.
WTS	The value of the WTS along with degrees of freedom of the central chi-square distribution and corresponding p-value.
ATS	The value of the ATS, degrees of freedom of the central F distribution and the corresponding p-value.
resampling	p-values for the test statistics based on the chosen resampling approach.

References

Friedrich, S., Konietschke, F., and Pauly, M. (2019). Resampling-Based Analysis of Multivariate Data and Repeated Measures Designs with the R Package MANOVA.RM. The R Journal, 11(2), 380-400.

Friedrich, S., Brunner, E. and Pauly, M. (2017). Permuting longitudinal data in spite of the dependencies. Journal of Multivariate Analysis, 153, 255-265.

Bathke, A., Friedrich, S., Konietschke, F., Pauly, M., Staffen, W., Strobl, N. and Hoeller, Y. (2018). Testing Mean Differences among Groups: Multivariate and Repeated Measures Analysis with Minimal Assumptions. Multivariate Behavioral Research, 53(3), 348-359, Doi: 10.1080/00273171.2018.1446320.

Friedrich, S., Konietschke, F., Pauly, M. (2017). GFD - An R-package for the Analysis of General Factorial Designs. Journal of Statistical Software, 79(1), 1-18.

See Also

GFD, nparLD, MANOVA

Examples

```
data(o2cons)
## Not run:
oxy <- RM(O2 ~ Group * Staphylococci * Time, data = o2cons,
            subject = "Subject", no.subf = 2, iter = 1000,
            resampling = "Perm")
summary(oxy)
plot(oxy, factor = "Group")

# For more details including the output of the examples also refer to the
# package vignette.

# using the EEG data, consider additional within-subjects factors 'brain region'
# and 'feature'
data(EEG)
EEG_model <- RM(resp ~ sex * diagnosis * feature * region,
                data = EEG, subject = "id", within = c("feature", "region"),
                resampling = "WildBS",
                iter = 1000,  alpha = 0.01, seed = 987, dec = 2)
summary(EEG_model)

## End(Not run)
```

---

simCI	*Multivariate post-hoc comparisons and simultaneous confidence intervals for contrasts in multivariate factorial designs*

Description

Multivariate post-hoc comparisons and simultaneous confidence intervals for contrasts in multivariate factorial designs

Usage

```
simCI(
  object,
  contrast,
  contmat = NULL,
  type = NULL,
  base = 1,
  interaction = TRUE,
  factor = NA,
  silent = FALSE,
  ...
)
```

Arguments

object	A MANOVA object.
contrast	The contrast matrix of interest, can either be "pairwise" or "user-defined".
contmat	If contrast = "user-defined", the contrast matrix must be specified here. Note that its rows must sum to zero.
type	If contrast is "pairwise", the type of the pairwise comparison must be specified here. Calculation is based on the contrMat function in package multcomp, see the corresponding help page for details on the types of contrasts available.
base	An integer specifying which group is considered the baseline group for Dunnett contrasts, see contrMat.
interaction	Logical. If interaction = FALSE in models with more than one factor, the factor of interest for the post-hoc analysis must be specified. Default is TRUE, which means post-hoc tests are performed for all factor level combinations.
factor	Only needed if interaction = FALSE. Specifies the factor for which post-hoc analysis are requested.
silent	Set to TRUE to suppress output.
...	Not used yet.

Details

The simCI() function computes the multivariate p-values for the chosen contrast of the multivariate mean vector based on the bootstrap version of the sum statistic. Details on this test can be found in Friedrich and Pauly (2018). Furthermore, confidence intervals for summary effects (i.e., averaged over each dimension), also based on the bootstrap version of the sum statistic, are returned as well.

Value

Multivariate p-values and simultaneous confidence intervals for the chosen contrasts.

References

Friedrich, S., and Pauly, M. (2018). MATS: Inference for potentially singular and heteroscedastic MANOVA. Journal of Multivariate Analysis, 165, 166-179.

See Also

[contrMat](#)

---

summary.MANOVA *Summarizing a MANOVA object*

Description

Returns a summary of the results including mean vectors and sample sizes for all groups as well as test statistics with degrees of freedom and p-values

Usage

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

Arguments

object   A MANOVA object

...   Additional parameters (currently not used)

---

summary.RM *Summarizing an RM object*

Description

Returns a summary of the results including mean values, variances and sample sizes for all groups as well as test statistics with degrees of freedom and p-values

Usage

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

Arguments

object   An RM object

...   Additional parameters (currently not used)

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