Package 'nparLD'

October 14, 2026

Type Package

Title Nonparametric Analysis of Longitudinal Data in Factorial Experiments

Version 2.3.3

Description Provides nonparametric procedures for the analysis of longitudinal data in factorial experiments. The package implements hypothesis tests on marginal distribution functions and unweighted relative marginal effects. It supports arbitrary crossed factorial designs with longitudinal or repeated-measures factors, missing observations, dependent replicates, rank- and pseudo-rank-based inference, Wald-type and ANOVA-type statistics, multiple contrast tests, and simultaneous confidence intervals.

URL https://github.com/FrankKonietschke/nparLD

BugReports https://github.com/FrankKonietschke/nparLD/issues

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports MASS, Matrix, ggplot2, mvtnorm, multcomp, rlang

Config/roxygen2/version 8.1.0

Suggests knitr, rmarkdown, spelling, testthat (>= 3.0.0)

Config/testthat/edition 3

Depends R (>= 3.5)

VignetteBuilder knitr

Language en-US

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-10-14 06:50:09 UTC

Contents

amylase . . . 3
ATS . . . 4
brdu . . . 4
contrastMatrix . . . 5
covariance . . . 5
dental . . . 6
edema . . . 7
effects.nparld_fit . . . 8
factorInfo . . . 8
MCTP . . . 9
nparLD . . . 9
panic . . . 14
panic2 . . . 15
permTest . . . 16
plasma . . . 17
plot.nparld_fit . . . 18
plot.nparld_mctp . . . 19
print.nparld_covarianceinfo . . . 21
print.nparld_factorinfo . . . 21
print.nparld_fit . . . 22
print.nparld_mctp . . . 23
print.nparld_permtest . . . 23
print.nparld_test_table . . . 24
print.summary.nparld_fit . . . 24
rat . . . 25
respiration . . . 26
shoulder . . . 27
summary.nparld_fit . . . 28
tree . . . 29
WTS . . . 30

Index **31**

amylase *Alpha-amylase saliva study*

Description

Measurements of alpha-amylase levels in saliva from healthy volunteers. The study illustrates a two-factor longitudinal design with two repeated measures factors.

Usage

```
amylase
```

Format

A data frame with variables:

resp Alpha-amylase measurement.

time1 First repeated-measures factor.

time2 Second repeated-measures factor.

subject Subject identifier.

Examples

```
data(amylase)

fit <- nparLD(resp ~ time1 * time2,
              data = amylase,
              subject = "subject",
              effect = "weighted",
              hypothesis = "H0F")
fit

# Dunnett-type contrasts for the levels of time2
fit <- nparLD(resp ~ time1 * time2,
              data = amylase,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("time2", "Dunnett"),
              Factor.Information = TRUE)
fit
plot(fit)
plot(MCTP(fit))
```

ATS *Extract ANOVA-type test results*

Description

Extracts the ANOVA-type statistic table from a fitted nparLD model.

Usage

```
ATS(object, ...)
```

Arguments

object	An object of class "nparld_fit".
...	Further arguments.

Value

A matrix or data frame containing ANOVA-type test statistics.

brdu *BrdU incorporation in fibroblasts*

Description

BrdU incorporation in fibroblast cultures measured under four dose conditions. For each culture and dose condition, three replicate measurements are available. The data set is provided in long format and can be used to illustrate dependent replicate measurements in nparLD().

Usage

```
brdu
```

Format

A data frame with 60 rows and 4 variables:

resp BrdU incorporation response.

dose Dose condition, with levels 0, 0.1, 1, and 10.

culture Culture identifier. This is the independent experimental unit.

replicate Replicate identifier within each culture-dose condition.

Details

The original variables were CultureNo, Replic, Dose, and Brdu. In the package data set, the variables were renamed to culture, replicate, dose, and resp for consistency with the examples.

Examples

```
data(brdu)

fit <- nparLD(
  resp ~ dose,
  data = brdu,
  subject = "culture",
  replicate = "replicate",
  hypothesis = "H0p",
  cell.weights = "subjects"
)

fit
```

`contrastMatrix` *Extract contrast matrix*

Description

Extracts the contrast matrix from a multiple contrast test procedure.

Usage

```
contrastMatrix(object, ...)
```

Arguments

`object`	An object of class `"nparld_mctp"` or `"nparld_fit"`.
`...`	Further arguments.

Value

A contrast matrix.

`covariance` *Extract covariance matrix*

Description

Extracts the estimated covariance matrix of the relative effect estimator from a fitted nparLD model.

Usage

```
covariance(object, ...)
```

Arguments

object	An object of class "nparld_fit".
...	Further arguments.

Value

A covariance matrix.

---

dental *Dental growth study*

Description

Measurements of distances between the center of the pituitary and the pterygomaxillary fissure in boys. The data illustrate a one-factor longitudinal design.

Usage

```
dental
```

Format

A data frame with variables:

resp Distance measurement in millimeters.

time Age at measurement.

subject Subject identifier.

Examples

```
data(dental)

dental$time <- factor(dental$time)


fit <- nparLD(resp ~ time,
              data = dental,
              subject = "subject",
              hypothesis = "H0F")
fit



fit <- nparLD(resp ~ time,
              data = dental,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("time", "Tukey"))
```

```
fit
plot(fit)
plot(MCTP(fit))
```

---

edema *Postoperative edema study*

Description

Skin-temperature measurements from patients after hand surgery. The study compares treatment groups and includes two repeated-measures factors.

Usage

```
edema
```

Format

A data frame with variables:

resp Skin temperature measurement.

time1 Hand factor.

time2 Day factor.

group Treatment group.

subject Subject identifier.

Examples

```
data(edema)


fit <- nparLD(resp ~ group * time1 * time2,
              data = edema,
              subject = "subject",
              hypothesis = "H0F")
fit



fit <- nparLD(resp ~ group * time1 * time2,
              data = edema,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group", "Tukey"),
              Factor.Information = TRUE)
fit
```

```
plot(fit)
plot(MCTP(fit))
```

`effects.nparld_fit` *Extract estimated relative effects*

Description

Extracts the estimated relative effects table from a fitted nparLD model.

Usage

```
## S3 method for class 'nparld_fit'
effects(object, ...)
```

Arguments

`object`	An object of class `"nparld_fit"`.
`...`	Further arguments.

Value

A data frame containing estimated relative effects.

`factorInfo` *Extract factor-specific information*

Description

Extracts factor-specific relative effects from a fitted nparLD model.

Usage

```
factorInfo(object, ...)
```

Arguments

`object`	An object of class `"nparld_fit"`.
`...`	Further arguments.

Value

An object of class `"nparld_factorinfo"`.

MCTP *Extract multiple contrast test results*

Description

Extracts the multiple contrast test procedure from a fitted nparLD model.

Usage

```
MCTP(object, ...)
```

Arguments

object	An object of class "nparld_fit".
...	Further arguments.

Value

An object of class "nparld_mctp".

nparLD *Nonparametric analysis of longitudinal data*

Description

Performs nonparametric inference for longitudinal or repeated-measures data from crossed factorial experiments. The function can be used to test hypotheses in marginal distribution functions or hypotheses in unweighted relative marginal effects. It allows crossed whole-plot and sub-plot factors, missing values, and dependent replicate measurements.

Usage

```
nparLD(
  formula,
  data,
  subject,
  replicate = NULL,
  cell.weights = c("subjects", "observations"),
  effect = c("unweighted", "weighted"),
  hypothesis = c("H0F", "H0p"),
  contrast = NULL,
  sci.method = c("fisher", "multi.t"),
  Factor.Information = FALSE,
  CI.method = c("logit", "normal"),
  alpha = 0.05,
```

```
  covariance = FALSE,
  perm.test = FALSE,
  B = 1000
)
```

Arguments

formula	A model formula of the form response ~ factors. Factors on the right-hand side may contain crossed whole-plot and subplot factors and their interactions.
data	A data frame containing the response, subject variable, design factors, and optionally a replicate variable.
subject	Character string specifying the subject identifier.
replicate	Optional character string specifying the replicate identifier. Replicates can be dependent within subject-condition cells.
cell.weights	Character string specifying how dependent replicates are weighted. Use "subjects" for subject-level cell weighting and "observations" for observation-level cell weighting. For dependent replicates under hypothesis = "H0F", cell.weights = "subjects" averages rank scores within subject-condition cells before covariance estimation, whereas cell.weights = "observations" uses the sums of the observed rank scores within subject-condition cells and therefore gives more weight to subjects with more observed replicate measurements.The default is "subjects".
effect	Character string specifying whether weighted or unweighted relative effects are used. Use "weighted" for effects based on ordinary ranks and a sample-size weighted reference distribution. Use "unweighted" for effects based on pseudo-ranks and an equally weighted factorial-cell reference distribution. Weighted effects depend on the sample-size allocation and are mainly descriptive. Unweighted effects are the inferential target for hypothesis = "H0p". In balanced designs, both effect definitions coincide. The default is effect = "unweighted".
hypothesis	Character string specifying the hypothesis type. Use "H0F" for hypotheses in marginal distribution functions and "H0p" for hypotheses in unweighted relative marginal effects. The latter permits unequal variances or higher-order distributional differences under the null hypothesis and is related to the nonparametric Behrens-Fisher problem.
contrast	Optional list specifying a factor or interaction term for simultaneous inference. A one-element specification such as list("time") uses the standard hypothesis matrix for the selected model term, that is, the same contrast structure underlying the WTS and ATS for that term. A two-element specification such as list("time", "Tukey") or list("time", "Dunnett") applies the named multiple contrast procedure to the marginal relative effects of the selected term. A numeric vector or matrix may be supplied as the second element for user-defined contrasts.
sci.method	Character string specifying the method for simultaneous confidence intervals. Available choices are "fisher" and "multi.t". The default is "fisher".

`Factor.Information`
: Logical. If `TRUE`, factor-specific relative effects, standard errors, and confidence intervals are returned. These summaries can also be displayed with `plot(fit, term = ...)`.

`CI.method`
: Character string specifying the method for confidence intervals for relative effects. Available choices are `"logit"` and `"normal"`. The default is `"logit"`.

`alpha`
: Significance level for tests and confidence intervals. The default is `alpha = 0.05`.

`covariance`
: Logical. If `TRUE`, the estimated covariance matrix used for the selected hypothesis is included in the output. The default is `FALSE`.

`perm.test`
: Logical. Should the paired two-time-point permutation test be used when applicable? This option is only available for paired designs with two time points.

`B`
: Number of permutation samples used for the paired permutation test.

Details

The function provides rank- and pseudo-rank-based procedures for factorial longitudinal data. The argument `hypothesis = "H0F"` specifies hypotheses in marginal distribution functions. These hypotheses compare the complete marginal distributions and are tested by rank-based procedures.

The argument `hypothesis = "H0p"` specifies hypotheses in unweighted relative marginal effects. These effects describe the relative position of each marginal distribution with respect to a common unweighted reference distribution and are particularly useful for effect interpretation, multiple contrast procedures, simultaneous confidence intervals, and graphical summaries.

The `contrast` argument computes a multiple contrast test along with simultaneous confidence intervals for the selected model terms. A one-element specification such as `list("time")` uses the same hypothesis matrix as the global test procedures (Wald- and ANOVA-type statistics) for the selected term. This provides simultaneous inference for the components of the corresponding global null hypothesis. A two-element specification such as `list("time", "Tukey")` or `list("time", "Dunnett")` first forms the marginal relative effects for the selected term and then applies the requested multiple contrast procedure. Thus, `list("time", "Tukey")` gives pairwise comparisons of the marginal time effects, whereas `list("time", "Dunnett")` compares the marginal time effects with the first time point. User-defined contrast vectors or matrices can be supplied as the second list element.

Missing observations are allowed. Incomplete subject-condition cells contribute where observations are available, and covariance estimation is based on the independent subject-level units. Dependent replicate measurements can be specified using the `replicate` argument. For hypotheses in relative marginal effects, `cell.weights = "subjects"` targets a typical subject-condition cell, whereas `cell.weights = "observations"` targets a typical replicate observation. For hypotheses in marginal distribution functions, dependent replicates are handled by averaging rank or pseudo-rank scores within subject-condition cells. In case of bivariate data (e.g., before and after measurements), the function implements a studentized permutation test for testing either `hypothesis = "H0F"` or `hypothesis = "H0p"`.

Value

An object of class `"nparld_fit"`. The object is a list containing the results of the nonparametric longitudinal analysis. The main components are:

- `Design`: character string describing the detected longitudinal factorial design.
- `wholeplots`: names of the whole-plot factors.
- `subplots`: names of the subplot or repeated-measures factors.
- `text.ranks`: character string describing the type of ranks used.
- `text.hypotheses`: character string describing the type of hypotheses tested.
- `N.info`: information on the number of subjects and observations.
- `effects`: a data frame with estimated relative effects. This includes the factor-level combinations, the number of contributing subjects and observations, the number of missing observations, the mean rank or pseudo-rank score, the estimated relative effect, and its standard error. For `hypothesis = "H0p"`, confidence limits are also returned.
- `factor.info`: optional factor-specific relative effects, standard errors, and confidence limits for main effects and interactions, returned when `Factor.Information = TRUE`. These summaries can be displayed with `plot(fit, term = ...)`.
- `WTS`: Wald-type test statistics, degrees of freedom, and p-values for the tested main effects and interactions.
- `ATS`: ANOVA-type test statistics, denominator degrees of freedom, and p-values for the tested main effects and interactions.
- `MCTP`: multiple contrast test results, returned when `contrast` is specified. These include the selected factor or interaction, the simultaneous confidence interval method, the global multiple contrast test, local contrast estimates with standard errors, simultaneous confidence limits, test statistics, p-values, degrees of freedom, and the corresponding contrast matrix.
- `covariance.info`: estimated covariance matrix used for the selected hypothesis, returned when `covariance = TRUE`.
- `perm`: permutation test results, returned when a permutation test is requested and applicable.
- `hypothesis`: the type of hypothesis tested, either `"H0F"` for hypotheses in marginal distribution functions or `"H0p"` for hypotheses in unweighted relative marginal effects.
- `CI.method`: method used for confidence intervals.
- `.internal`: internal objects used for computation and advanced post-processing.

Some components may be `NULL` depending on the selected hypothesis, contrast specification, and output options.

References

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Rubarth, K., Pauly, M., & Konietschke, F. (2022). Ranking procedures for repeated measures designs with missing data: estimation, testing and asymptotic theory. Statistical Methods in Medical Research, 31(1), 105-118.

Rubarth, K., Sattler, P., Zimmermann, H. G., & Konietschke, F. (2021). Estimation and testing of Wilcoxon–Mann–Whitney effects in factorial clustered data designs. Symmetry, 14(2), 244.

Examples

```
## One repeated-measures factor: dental data
data(dental)

fit_dental <- nparLD(
  resp ~ time,
  data = dental,
  subject = "subject",
  hypothesis = "H0p"
)

fit_dental

## Crossed factorial longitudinal design: shoulder data
data(shoulder)


fit_shoulder <- nparLD(
  resp ~ group1 * group2 * time,
  data = shoulder,
  subject = "subject",
  hypothesis = "H0p"
)

fit_shoulder


## Multiple contrast procedure for an interaction


fit_contrast <- nparLD(
  resp ~ group1 * group2 * time,
  data = shoulder,
  subject = "subject",
  hypothesis = "H0p",
  contrast = list("group1:time")
```

```
)

MCTP(fit_contrast)
print(MCTP(fit_contrast), show.matrix = TRUE)


## Missing response values

dat_miss <- dental
dat_miss$resp[c(2, 7, 12)] <- NA

fit_miss <- nparLD(
  resp ~ time,
  data = dat_miss,
  subject = "subject",
  hypothesis = "H0p"
)

fit_miss


## Dependent replicate measurements: BrdU data
data(brdu)


fit_brdu <- nparLD(
  resp ~ dose,
  data = brdu,
  subject = "culture",
  replicate = "replicate",
  hypothesis = "H0p",
  cell.weights = "subjects"
)

fit_brdu



## Graphical displays
plot(fit_dental)
plot(fit_shoulder)
plot(MCTP(fit_contrast))
```

---

panic *Panic disorder study I*

Description

Clinical Global Impression scores from patients with panic disorder and agoraphobia. The data illustrate a one-factor longitudinal design with ordinal responses.

Usage

```
panic
```

Format

A data frame with variables:

resp Clinical Global Impression score.

time Visit or week of assessment.

subject Patient identifier.

Examples

```
data(panic)


fit <- nparLD(resp ~ time,
              data = panic,
              subject = "subject",
              hypothesis = "H0F", contrast =list("time", "Dunnett"))
fit



fit <- nparLD(resp ~ time,
              data = panic,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("time", "Dunnett"))
fit
plot(fit)
plot(MCTP(fit))
```

---

panic2 *Panic disorder study II*

Description

Panic and agoraphobia scores from patients with panic disorder, with or without agoraphobia. The data illustrate a factorial longitudinal design with one whole-plot factor and one repeated-measures factor.

Usage

```
panic2
```

Format

A data frame with variables:

resp Panic and agoraphobia score.

time Visit or week of assessment.

group Agoraphobia group.

subject Patient identifier.

Examples

```
data(panic2)


fit <- nparLD(resp ~ group * time,
              data = panic2,
              subject = "subject",
              hypothesis = "H0F", effect="unweighted")
fit



fit <- nparLD(resp ~ group * time,
              data = panic2,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group:time"),
              Factor.Information = TRUE,
              covariance=TRUE)
fit
plot(fit)
plot(MCTP(fit))
```

---

permTest *Extract permutation test results*

Description

Extracts permutation test results from a fitted nparLD model.

Usage

```
permTest(object, ...)

## S3 method for class 'nparld_fit'
permTest(object, table = FALSE, ...)
```

Arguments

object	An object of class "nparld_fit".
...	Further arguments passed to methods.
table	Logical. If TRUE, return only the permutation test table.

Value

A permutation test object.

---

plasma *Plasma-renin activity study*

Description

Plasma-renin activity measurements from a randomized study of healthy non-smokers. The data illustrate a factorial longitudinal design with one whole-plot factor and one repeated-measures factor.

Usage

```
plasma
```

Format

A data frame with variables:

resp Plasma-renin activity measurement.

time Measurement time.

group Drug group.

subject Subject identifier.

Examples

```
data(plasma)


fit <- nparLD(resp ~ group * time,
              data = plasma,
              subject = "subject",
              hypothesis = "H0F", effect="weighted")
fit
```

```
fit <- nparLD(resp ~ group * time,
              data = plasma,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group", "Tukey"))
fit
plot(fit)
plot(MCTP(fit))
```

`plot.nparld_fit` *Plot nparLD results*

Description

Displays graphical summaries of estimated relative effects from an `nparLD()` fit.

Usage

```
## S3 method for class 'nparld_fit'
plot(
  x,
  term = NULL,
  xlab = NULL,
  ylab = "Relative effect",
  main = NULL,
  legend.title = NULL,
  ref.line = 0.5,
  ref.lty = "dashed",
  ref.col = "grey40",
  ...
)
```

Arguments

`x`	An object of class `"nparld_fit"`.
`term`	Optional character vector specifying one or more model terms for which factor-specific relative effects and confidence intervals should be plotted. The requested terms require `Factor.Information = TRUE` in the original call to `nparLD()`. If `term = NULL`, the cell-level relative effects in `x$effects` are plotted.
`xlab`	Optional x-axis label.
`ylab`	Optional y-axis label. The default is `"Relative effect"`.
`main`	Optional plot title.

legend.title	Optional legend title.
ref.line	Optional horizontal reference line. The default is 0.5.
ref.lty	Line type for the reference line.
ref.col	Colour of the reference line.
...	Further arguments.

Details

If term is not supplied, estimated relative effects and confidence intervals are plotted for the full factorial design. If term is supplied, factor-specific relative effects and confidence intervals are plotted for the selected main effect or interaction. Term-specific plots require that the model was fitted with Factor.Information = TRUE.

The default plot displays the estimated cell-level relative effects. If term is supplied, the plot displays factor-specific relative effects and confidence intervals for the selected main effects or interactions. This requires that the model was fitted with Factor.Information = TRUE. The horizontal reference line at 0.5 indicates no tendency relative to the reference distribution. Values above 0.5 indicate a tendency toward larger responses, whereas values below 0.5 indicate a tendency toward smaller responses.

Examples

```
data(shoulder)

fit <- nparLD(
  resp ~ group1 * group2 * time,
  data = shoulder,
  subject = "subject",
  hypothesis = "H0p",
  Factor.Information = TRUE
)

## Cell-level relative effects
plot(fit)

## Factor-specific relative effects and confidence intervals
plot(fit, term = "time")
plot(fit, term = "group1:time")
```

---

plot.nparld_mctp *Plot nparLD multiple contrast results*

Description

Displays simultaneous confidence intervals for local contrasts from a multiple contrast test procedure. The plot shows the contrast estimates together with their simultaneous confidence limits and a vertical reference line at zero. Intervals excluding zero are highlighted by default.

Usage

```
## S3 method for class 'nparld_mctp'
plot(
  x,
  xlab = "Contrast effect",
  ylab = "",
  main = NULL,
  ref.line = 0,
  ref.lty = 2,
  ref.col = "gray50",
  pch = 19,
  lwd = 2,
  col = NULL,
  ...
)
```

Arguments

x	An object of class "nparld_mctp".
xlab	Label for the x-axis. The default is "Contrast effect".
ylab	Label for the y-axis. The default is an empty label.
main	Optional plot title.
ref.line	Optional vertical reference line. The default is 0.
ref.lty	Line type for the reference line.
ref.col	Colour of the reference line.
pch	Plotting character.
lwd	Line width.
col	Optional colors for confidence intervals and point estimates. If NULL, intervals excluding zero are shown in red and intervals including zero are shown in black.
...	Further graphical arguments.

Details

Displays simultaneous confidence intervals for the local contrast results returned by the multiple contrast test procedure. The vertical reference line at zero indicates the null value for contrast effects.

Examples

```
data(shoulder)

fit <- nparLD(
  resp ~ group1 * group2 * time,
  data = shoulder,
  subject = "subject",
  hypothesis = "H0p",
```

```
  contrast = list("time", "Dunnett")
)

plot(MCTP(fit))
```

`print.nparld_covarianceinfo`

Print nparLD covariance matrix

Description

Displays the estimated covariance matrix of the relative effect estimator.

Usage

```
## S3 method for class 'nparld_covarianceinfo'
print(x, digits = 4, ...)
```

Arguments

`x`	An object of class `"nparld_covarianceinfo"`.
`digits`	Number of digits used for printing numerical results.
`...`	Further arguments.

Details

The printed matrix is the estimated covariance matrix used for the selected hypothesis. It is returned when `covariance = TRUE`.

`print.nparld_factorinfo`

Print nparLD factor information

Description

Prints factor-specific relative effects, standard errors, and confidence limits for the main effects and interactions of an `nparLD()` fit. Factor information is returned when the model is fitted with `Factor.Information = TRUE` and can also be displayed graphically with `plot(fit, term = ...)`.

Usage

```
## S3 method for class 'nparld_factorinfo'
print(x, digits = 4, ...)
```

Arguments

x	An object of class "nparld_factorinfo".
digits	Number of digits used for printing numerical results.
...	Further arguments.

Details

Factor information consists of term-specific relative effects, standard errors, and confidence limits for main effects and interactions. These summaries are returned when Factor.Information = TRUE and can be visualized with plot(fit, term = ...).

---

print.nparld_fit *Print an nparLD fit*

Description

Prints a concise overview of a fitted nparLD() model.

Usage

```
## S3 method for class 'nparld_fit'
print(x, digits = 4, ...)
```

Arguments

x	An object of class "nparld_fit".
digits	Number of digits used for printed numerical results.
...	Further arguments.

Details

The print method provides a compact summary of the fitted model, including the detected design, whole-plot and subplot factors, number of subjects, hypothesis type, ranking method, and, for effect-based inference, the confidence interval method.

The inferential output is intentionally restricted to the ANOVA-type statistic (ATS) in order to keep the standard print output concise. More detailed results, including estimated relative effects, factor-specific summaries, Wald-type statistics, multiple contrast procedures, and permutation-test results when available, are provided by summary(). Individual result components can also be extracted using the corresponding accessor functions.

If a multiple contrast procedure was requested during model fitting, the print method indicates that the corresponding results are available through MCTP().

print.nparld_mctp *Print nparLD multiple contrast results*

Description

Prints the global and local results of a multiple contrast test procedure. The local results include contrast estimates, standard errors, simultaneous confidence limits, test statistics, adjusted p-values, and degrees of freedom. The contrast matrix can optionally be displayed with `show.matrix = TRUE`.

Usage

```
## S3 method for class 'nparld_mctp'
print(x, digits = 4, show.matrix = FALSE, ...)
```

Arguments

`x`	An object of class `"nparld_mctp"`.
`digits`	Number of digits used for printing numerical results.
`show.matrix`	Logical. If `TRUE`, print the contrast matrix used in the multiple contrast procedure.
`...`	Further arguments.

Details

The method prints the global multiple contrast test and the local contrast results, including estimates, standard errors, simultaneous confidence limits, test statistics, adjusted p-values, and degrees of freedom. The contrast matrix can be displayed with `show.matrix = TRUE` or extracted with `contrastMatrix()`.

print.nparld_permtest *Print nparLD permutation test results*

Description

Print nparLD permutation test results

Usage

```
## S3 method for class 'nparld_permtest'
print(x, digits = 4, ...)
```

Arguments

`x`	An object of class `"nparld_permtest"`.
`digits`	Number of digits used for printing numerical results.
`...`	Further arguments.

print.nparld_test_table *Print nparLD test table*

Description

Print nparLD test table

Usage

```
## S3 method for class 'nparld_test_table'
print(x, digits = 4, ...)
```

Arguments

x	An object of class "nparld_test_table".
digits	Number of digits used for printing numerical results.
...	Further arguments.

print.summary.nparld_fit *Print summary of an nparLD fit*

Description

Prints the detailed summary of a fitted nparLD() model.

Usage

```
## S3 method for class 'summary.nparld_fit'
print(x, digits = 4, ...)
```

Arguments

x	An object of class "summary.nparld_fit".
digits	Number of digits used for printing numerical results.
...	Further arguments.

Details

The summary print method provides a detailed representation of the fitted model. It displays design information, hypothesis and ranking information, estimated relative effects, factor-specific effect summaries when available, and the global Wald-type and ANOVA-type statistics.

If additional inferential procedures were requested during model fitting, multiple contrast results and permutation-test results are also printed. Large auxiliary components, such as covariance matrices, are not printed automatically and can be obtained through the corresponding accessor functions.

This method is intentionally more detailed than `print.nparld_fit()`, which provides a concise overview of the fitted model and the ANOVA-type statistic.

Value

The summary object is returned invisibly.

---

rat *Rat growth study*

Description

Body-weight measurements from rats observed over a five-week period. The data illustrate longitudinal growth curves in several treatment groups.

Usage

```
rat
```

Format

A data frame with variables:

resp Body weight in grams.

time Week of measurement.

group Treatment group.

subject Rat identifier.

Examples

```
data(rat)

fit <- nparLD(resp ~ group * time,
              data = rat,
              subject = "subject",
              hypothesis = "H0F")
fit
```

```
fit <- nparLD(resp ~ group * time,
              data = rat,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group:time"))
fit
plot(fit)
plot(MCTP(fit))
```

`respiration` *Respiratory disorder study*

Description

Ordinal health-status measurements from patients with a respiratory disorder. The data include study center, treatment group, and repeated visits.

Usage

```
respiration
```

Format

A data frame with variables:

resp Ordinal health-status response.

time Visit number.

center Study center.

treatment Treatment group.

patient Patient identifier.

Examples

```
data(respiration)

fit <- nparLD(resp ~ center * treatment * time,
              data = respiration,
              subject = "patient",
              hypothesis = "H0F")
fit
```

```
fit <- nparLD(resp ~ center * treatment * time,
              data = respiration,
              subject = "patient",
              hypothesis = "H0p",
              contrast = list("treatment", "Tukey"))
fit
plot(fit)
plot(MCTP(fit))
```

---

shoulder *Shoulder tip pain study*

Description

Shoulder pain scores from patients after laparoscopic abdominal surgery. The study includes treatment group, gender group, and repeated pain measurements.

Usage

```
shoulder
```

Format

A data frame with variables:

resp Shoulder pain score.

time Measurement occasion.

group1 Treatment group.

group2 Gender group.

subject Patient identifier.

Examples

```
data(shoulder)
```

```
fit <- nparLD(resp ~ group1 * group2 * time,
              data = shoulder,
              subject = "subject",
              hypothesis = "H0F")
fit
```

```
fit <- nparLD(resp ~ group1 * group2 * time,
              data = shoulder,
```

```
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group1:time"),
              Factor.Information=TRUE)
fit
plot(fit)
plot(MCTP(fit))
```

`summary.nparld_fit` *Summarize an nparLD fit*

Description

Produces a detailed summary of a fitted `nparLD()` model.

Usage

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

Arguments

`object`	An object of class `"nparld_fit"`.
`...`	Further arguments passed to or from other methods.

Details

The summary method collects the principal results of the fitted model into a structured object and provides the detailed counterpart to the concise `print()` method.

The summary includes information on the detected design, whole-plot and subplot factors, number of subjects, hypothesis type, ranking method, and, for effect-based inference, the confidence interval method. It also contains estimated relative effects, factor-specific effect summaries when available, Wald-type and ANOVA-type statistics, multiple contrast results when requested, and permutation-test results when available.

The returned object can be printed using the corresponding `print.summary.nparld_fit()` method or inspected programmatically. Large auxiliary components, such as covariance matrices, are not included in the printed summary and can be obtained through the corresponding accessor functions.

Value

An object of class `"summary.nparld_fit"` containing the detailed results of the fitted model.

tree *Vitality of treetops*

Description

Repeated vitality scores of treetops from three experimental areas. The data illustrate an ordinal longitudinal response in several groups.

Usage

```
tree
```

Format

A data frame with variables:

resp Vitality score.

time Year or measurement occasion.

group Experimental area.

subject Tree identifier.

Examples

```
data(tree)


fit <- nparLD(resp ~ group * time,
              data = tree,
              subject = "subject",
              hypothesis = "H0F")
fit




fit <- nparLD(resp ~ group * time,
              data = tree,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group:time"))
fit
plot(fit)
plot(MCTP(fit))
```

WTS *Extract Wald-type test results*

Description

Extracts the Wald-type statistic table from a fitted nparLD model.

Usage

```
WTS(object, ...)
```

Arguments

object	An object of class "nparld_fit".
...	Further arguments.

Value

A matrix or data frame containing Wald-type test statistics.

Index

∗ **datasets**
  amylase, 3
  brdu, 4
  dental, 6
  edema, 7
  panic, 14
  panic2, 15
  plasma, 17
  rat, 25
  respiration, 26
  shoulder, 27
  tree, 29

amylase, 3
ATS, 4

brdu, 4

contrastMatrix, 5
covariance, 5

dental, 6

edema, 7
effects.nparld_fit, 8

factorInfo, 8

MCTP, 9

nparLD, 9

panic, 14
panic2, 15
permTest, 16
plasma, 17
plot.nparld_fit, 18
plot.nparld_mctp, 19
print.nparld_covarianceinfo, 21
print.nparld_factorinfo, 21
print.nparld_fit, 22
print.nparld_mctp, 23
print.nparld_permtest, 23
print.nparld_test_table, 24
print.summary.nparld_fit, 24

rat, 25
respiration, 26

shoulder, 27
summary.nparld_fit, 28

tree, 29

WTS, 30