Package 'nparLD'

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Type Package

Title Nonparametric Analysis of Longitudinal Data in Factorial Experiments

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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.

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Author Frank Konietschke [aut, cre],
Kimihiro Noguchi [ctb] (Original package author),
Mahbub Latif [ctb] (Original package author),
Karthinathan Thangavelu [ctb] (Original package author),
Yulia R. Gel [ctb] (Original package author),
Edgar Brunner [ctb]

Maintainer Frank Konietschke <frank.konietschke@charite.de>

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Contents

`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(fit$MCTP)
```

---

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

```
## Not run:
data(brdu)

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

fit

## End(Not run)
```

`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)

## Not run:
fit <- nparLD(resp ~ time,
              data = dental,
              subject = "subject",
              hypothesis = "H0F")
```

```
fit

## End(Not run)

## Not run:
fit <- nparLD(resp ~ time,
              data = dental,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("time", "Tukey"))
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

---

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)

## Not run:
fit <- nparLD(resp ~ group * time1 * time2,
              data = edema,
              subject = "subject",
              hypothesis = "H0F")
```

```
fit

## End(Not run)

## Not run:
fit <- nparLD(resp ~ group * time1 * time2,
              data = edema,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group", "Tukey"),
              Factor.Information = TRUE)
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

---

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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Brunner, E., Konietschke, F., Pauly, M., Puri, M. L. (2017). Rank-based procedures in factorial designs: Hypotheses about non-parametric treatment effects. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 79(5), 1463-1485.

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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)

## Not run:
fit_shoulder <- nparLD(
  resp ~ group1 * group2 * time,
  data = shoulder,
  subject = "subject",
  hypothesis = "H0p"
)

fit_shoulder

## End(Not run)

## Multiple contrast procedure for an interaction

## Not run:
fit_contrast <- nparLD(
  resp ~ group1 * group2 * time,
  data = shoulder,
  subject = "subject",
  hypothesis = "H0p",
  contrast = list("group1:time")
)

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

## End(Not run)

## Missing response values
```

```
## Not run:
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

## End(Not run)

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

## Not run:
fit_brdu <- nparLD(
  resp ~ dose,
  data = brdu,
  subject = "culture",
  replicate = "replicate",
  hypothesis = "H0p",
  cell.weights = "subjects"
)

fit_brdu

## End(Not run)

## Not run:
## Graphical displays
plot(fit_dental)
plot(fit_shoulder)
plot(fit_contrast$MCTP)

## End(Not run)
```

`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)

## Not run:
fit <- nparLD(resp ~ time,
              data = panic,
              subject = "subject",
              hypothesis = "H0F", contrast =list("time", "Dunnett"))
fit

## End(Not run)

## Not run:
fit <- nparLD(resp ~ time,
              data = panic,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("time", "Dunnett"))
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

---

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)

## Not run:
fit <- nparLD(resp ~ group * time,
              data = panic2,
              subject = "subject",
              hypothesis = "H0F", effect="unweighted")
fit

## End(Not run)

## Not run:
fit <- nparLD(resp ~ group * time,
              data = panic2,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group:time"),
              Factor.Information = TRUE,
              covariance=TRUE)
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

---

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)

## Not run:
fit <- nparLD(resp ~ group * time,
              data = plasma,
              subject = "subject",
              hypothesis = "H0F", effect="weighted")
fit

## End(Not run)

## Not run:
fit <- nparLD(resp ~ group * time,
              data = plasma,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group", "Tukey"))
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

`plot.nparld_fit` *Plot nparLD results*

Description

Displays graphical summaries of estimated relative effects from an `nparLD()` fit. By default, the method plots the cell-level relative effects stored in `x$effects`. If `term` is supplied, it plots factor-specific relative effects and confidence intervals for selected main effects or interactions. Term-specific plots require that the model was fitted with `Factor.Information = TRUE`.

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

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(fit$MCTP)
```

---

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 nparLD fit*

Description

Prints the main results of a fitted `nparLD()` model, including the detected design, hypothesis type, ranking method, estimated relative effects, and global WTS and ATS results. Optional components such as factor-specific information, multiple contrast results, covariance matrices, and permutation tests are displayed when available.

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 displays the detected design, sample size information, hypothesis type, ranking method, estimated relative effects, and global WTS and ATS results. Optional components are printed when available, including factor-specific information, multiple contrast results, covariance matrices, and permutation test results.

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 is stored in x$Contrast.Matrix and is printed only when show.matrix = TRUE.

---

print.summary.nparld_fit

Print summary of an nparLD fit

Description

Prints the main components of a summarized nparLD() fit, including design information, hypothesis type, estimated relative effects, and global WTS and ATS results. Optional components such as factor-specific information, multiple contrast results, covariance matrices, and permutation tests are displayed when available.

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.

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

```
## Not run:
data(rat)

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

## End(Not run)

## Not run:
fit <- nparLD(resp ~ group * time,
              data = rat,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group:time"))
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

`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

```
## Not run:
data(respiration)

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

## End(Not run)

## Not run:
fit <- nparLD(resp ~ center * treatment * time,
              data = respiration,
              subject = "patient",
              hypothesis = "H0p",
              contrast = list("treatment", "Tukey"))
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

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)

## Not run:
fit <- nparLD(resp ~ group1 * group2 * time,
              data = shoulder,
              subject = "subject",
              hypothesis = "H0F")
fit

## End(Not run)

## Not run:
fit <- nparLD(resp ~ group1 * group2 * time,
              data = shoulder,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group1:time"),
              Factor.Information=TRUE)
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

summary.nparld_fit *Summarize an nparLD fit*

Description

Extracts the main components of a fitted nparLD() object into a structured summary object. The summary is useful for inspecting, printing, or programmatically accessing the main results without working directly with all internal components of the fitted object.

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 returns a structured list containing the main components of the fitted object. In contrast to print(), which is mainly intended for console display, summary() is useful for storing or extracting the main results programmatically.

Value

An object of class "summary.nparld_fit" containing selected components 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)

## Not run:
fit <- nparLD(resp ~ group * time,
              data = tree,
              subject = "subject",
              hypothesis = "H0F")
fit

## End(Not run)


## Not run:
fit <- nparLD(resp ~ group * time,
              data = tree,
              subject = "subject",
              hypothesis = "H0p",
              contrast = list("group:time"))
fit
plot(fit)
plot(fit$MCTP)

## End(Not run)
```

Index