Package ‘mfcurve’

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Type Package

Title Multi-Factor Curve Analysis for Grouped Data in 'R'

Version 1.0.2

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Description Implements multi-factor curve analysis for grouped data in 'R', replicating and extending the functionality of the the 'Stata' ado 'mfcurve' (Krähmer, 2023) <`https://ideas.repec.org/c/boc/bocode/s459224.html`>.

Related to the idea of specification curve analysis (Simonsohn, Simmons, and Nelson, 2020) <doi:10.1038/s41562-020-0912-z>.

Includes data preprocessing, statistical testing, and visualization of results with confidence intervals.

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.2

Imports dplyr, stats, plotly, tidyr, tidyselect, magrittr, rlang

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

VignetteBuilder knitr

URL `https://github.com/XAM12/mfcurve_R`

BugReports `https://github.com/XAM12/mfcurve_R/issues`

NeedsCompilation no

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Contents

`mfcurve` *Wrapper for mfcurve preprocessing and plotting*

Description

Calls `mfcurve_preprocessing()` and `mfcurve_plotting()` in sequence to generate a two-panel interactive mfcurve plot.

Usage

```
mfcurve(
  data,
  outcome,
  factors,
  test = "mean",
  alpha = 0.05,
  showTitle = TRUE,
  SaveProcessedData = FALSE,
  mode = "collapsed",
  rounding = 2,
  plotOrigin = FALSE,
  CI = TRUE,
  showGrandMean = TRUE,
  showSigStars = TRUE
)
```

Arguments

`data`	A data frame containing the variables.
`outcome`	Name of the numeric outcome variable (string).
`factors`	Character vector of factor variable names for grouping.
`test`	Reference for t-tests: "mean", "zero", or "leave-one-out". Passed to preprocessing. Default is "mean".
`alpha`	Significance level for t-tests and confidence intervals. Default is 0.05.
`showTitle`	Logical. Show the plot title? Default is TRUE.
`SaveProcessedData`	Logical. If TRUE, writes group-level statistics to the session temporary directory (`tempdir()`) as timestamped files: `group_stats_*.csv` and `group_stats_*.rds`. Default is FALSE.
`mode`	Factor labeling mode: "collapsed" (default) or "expanded".
`rounding`	Number of digits to round outcome statistics. Default is 2.
`plotOrigin`	Logical. Force axes to include 0? Default is FALSE.
`CI`	Logical. Display confidence intervals? Default is TRUE.
`showGrandMean`	Logical. Show the grand mean line? Default is TRUE.
`showSigStars`	Logical. Show markers for significant values? Default is TRUE.

Details

`mfcurve()` plots the mean of an outcome variable across all combinations of multiple grouping factors, producing a two-panel interactive plot.

The upper panel shows group means (and confidence intervals, if requested); the lower panel marks which factor levels are present in each group. In the lower panel, factor labels can be displayed in two modes:

- In **collapsed** mode, each factor occupies only one row. Factor levels are differentiated by marker color.
- In **expanded** mode, each factor is split into its levels (dummy-coded), with levels listed below each other. Markers indicate whether a specific factor level is present or absent in the group.

While collapsed mode saves space when many factors or levels are present, expanded mode may be more intuitive (especially for readers familiar with specification curves).

`mfcurve()` allows optional significance testing (t-tests). Group-level statistics can be saved if needed.

Value

Invisibly returns the plotly object representing the two-panel plot. If `SaveProcessedData = TRUE`, also writes `group_stats` to CSV and RDS in `tempdir()` and prints the file paths.

See Also

`mfcurve_preprocessing`, `mfcurve_plotting`

Examples

```
# Simulate data for a 3 x 2 experimental design: 3 treatments (A, B, C), 2 doses (low, high)
set.seed(123)
df <- data.frame(
  treatment = sample(c("A", "B", "C"), 1000, replace = TRUE),
  dose      = sample(c("low", "high"), 1000, replace = TRUE)
)

# Generate self-rated health (scale 1-10) with small group differences
df$self_rated_health <- 6 +
  ifelse(df$treatment == "B", 0.5, ifelse(df$treatment == "C", -0.5, 0)) +
  ifelse(df$dose == "high", 0.3, 0) +
  rnorm(1000, 0, 1.5)

# Restrict health scores to valid range
df$self_rated_health <- pmin(pmax(df$self_rated_health, 1), 10)

# Create mfcurve plot
mfcurve(
  data = df,
  outcome = "self_rated_health",
  factors = c("treatment", "dose"),
  test = "mean"
```

```
)
```

`mfcurve_plotting` *Create a two-panel mfcurve plot from processed statistics*

Description

Generates an interactive two-panel plot showing group means (with optional confidence intervals) and corresponding factor combinations.

Usage

```
mfcurve_plotting(
  group_stats_vis,
  lower_data,
  grand_mean,
  outcome,
  factors,
  level,
  rounding = 2,
  showTitle = TRUE,
  plotOrigin = FALSE,
  CI = TRUE,
  mode = "collapsed",
  showGrandMean = TRUE,
  showSigStars = TRUE
)
```

Arguments

`group_stats_vis`	Data frame containing group-level summary statistics.
`lower_data`	Data frame defining the factor structure for the lower panel.
`grand_mean`	Numeric. The overall mean of the outcome variable.
`outcome`	Name of the outcome variable (string).
`factors`	Character vector of factor variable names.
`level`	Level for confidence intervals (e.g., 0.95).
`rounding`	Number of digits to round outcome values. Default is 2.
`showTitle`	Logical. Show the plot title? Default is TRUE.
`plotOrigin`	Logical. Force axes to include 0? Default is FALSE.
`CI`	Logical. Display confidence intervals? Default is TRUE.
`mode`	Labeling mode for the lower panel: "collapsed" (default) or "expanded".
`showGrandMean`	Logical. Show the grand mean overall groups. Default is TRUE.
`showSigStars`	Logical. Flag significant results. Default is TRUE.

Value

A plotly object (invisible).

`mfcurve_preprocessing` *Preprocess data and compute group statistics*

Description

Prepares the data and computes descriptive statistics and t-tests for groups defined by combinations of categorical factors.

Usage

```
mfcurve_preprocessing(data, outcome, factors, alpha = 0.05, test = "mean")
```

Arguments

`data`	Data frame containing the variables.
`outcome`	Name of the numeric outcome variable (string).
`factors`	Character vector of factor variable names for grouping.
`alpha`	Significance level for the t-tests and confidence intervals. Default is 0.05.
`test`	Reference for t-tests: "mean" (grand mean), "leave-one-out" (mean of all other groups), or "zero" (testing against 0).

Value

A list with:

group_stats Data frame with computed statistics and CI bounds.

group_stats_vis Visualization-ready version with rounded values.

lower_data Data for the lower panel (without y positions).

grand_mean Overall mean of the outcome variable.

level Confidence level used.

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