Package ‘shorm’

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Title Detect the Shape of Dose-Response Curves

Version 0.1.3

Description Provides functions for hormesis screening by classifying the shapes of dose-response curves based on semiparametric tests. The shapes are indications of different potential toxicology effect. It also offers a scalable visualization scheme to present testing conclusions for large-scale dataset with a large number of dose-response curves. For more information, see Jin et al. (2026) <`https://github.com/YinglJin-0203/shorm/blob/main/Manuscripts/BotanicalHormesisTestingFinalDraft.docx`>.

Encoding UTF-8

RoxygenNote 7.3.3

Imports SRMERS, ggplot2, scales, dplyr

Collate 'RepeatSHARP.R' 'SHARPtest.R' 'SharpScatter.R'

URL `https://github.com/YinglJin-0203/shorm`

NeedsCompilation no

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Repository CRAN

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`RepeatSHARP` *Implement SHARP test repeatedly on a dose-response curve*

Description

The SHARP shape detection test relies on a underlying random generation process, which may lead to ambiguous test results. To examin its uncertainty and obtain a more robust conclusion, we may with to repet the test on the same data.

Usage

```
RepeatSHARP(df, nRep, mixed = FALSE, xName, yName, rName, niter = 1000)
```

Arguments

`df`	Dose-response curve data in a table format. Dose and responses should be two separate columns with numeric values.
`nRep`	Number of repetitions of SHAPR test. Integer.
`mixed`	Logical indicator (TRUE for FALSE) for whether or not to use the mixed-model-based test.
`xName`	The column name for dose. Character string.
`yName`	The column name for response. Character string.
`rName`	The column name for random effect. Only used if mixed = TRUE. Character string.git a
`niter`	An integer for the number of iterations in SHARP test procedure

Value

A dataframe of test results from all repititions. Each row is one single test with four p values after Holm adjustment.

Examples

```
# Simulate dose-response data
x <- seq(0, 1, length.out = 48)
y <- 2*sqrt(x)+rnorm(48)
y[17:32] <- y[17:32]+0.5
y[33:48] <- y[33:48]+1
curve <- data.frame(x, y)
curve$rep <- rep(1:3, each = 16)

# Fixed-model based test
RepeatSHARP(curve, nRep = 10, xName = "x", yName = "y", niter = 10)

# Mixed-model based test
RepeatSHARP(curve, nRep = 10, mixed = TRUE, xName = "x", yName = "y", rName = "rep", niter = 10)
```

`SharpScatter` *Function to visualize SHARP test results*

Description

Function to visualize SHARP test results

Usage

```
SharpScatter(
  pinc,
  pdec,
  pconc,
  pconv,
  alpha = 0.05,
  scale = TRUE,
  label = NULL,
  size_point = 2,
  size_label = 5,
  ...
)
```

Arguments

`pinc`, `pdec`, `pconc`, `pconv`	SHARP test p-values corresponding to increasing, decreasing, concave and convex
`alpha`	significance threshold. alpha=NULL corresponding to no significance threshold
`scale`	if the axis should be scale so that the significant threshold is placed in the center
`label`	labels of the point to visualize. label=NULL means no labeling.
`size_point`, `size_label`	the size of points and label. size_lable is used when label is not NULL.
`...`	additional parameters passed to ggplot

Details

The shape scatter plot represents the four p-values (corresponding to four shape types) of SHARP test on a 2D space. it can not only visualize the conclusions of the test, but also the confidence level of the test. The plot surface is divided into two parts along two perpendicular directions, corresponding to two opposite shapes. The coordinates of points are derived from p-values such that:

- Inconclusive shapes are placed in the center area within the significance thresholds ($p > 0.05$)
- Significant shapes are placed in the edge area out of the significance thresholds ($p < 0.05$)
- The closer points are to the significance thresholds, the more ambiguous shape conclusion is

Value

The plotted ggplot object

Examples

```
# Simulate dose-response data
x <- seq(0, 1, length.out = 48)
y <- 2*sqrt(x)+rnorm(48)
y[17:32] <- y[17:32]+0.5
y[33:48] <- y[33:48]+1
curve <- data.frame(x, y)
curve$rep <- rep(1:3, each = 16)

# Fixed-model based test
sharpt <- SHARPtest(curve, xName = "x", yName = "y", niter = 100)

# Plot the graph
SharpScatter(sharpt[1], sharpt[2], sharpt[3], sharpt[4], niter = 100)
```

`SHARPtest` *Implement SHARP test once on a dose-response curve*

Description

Implement SHARP test once on a dose-response curve

Usage

```
SHARPtest(df, mixed = FALSE, xName, yName, rName, niter = 1000)
```

Arguments

`df`	Dose-response curve data in a table format. Dose and responses should be two separate columns with numeric values.
`mixed`	Logical indicator (TRUE for FALSE) for whether or not to use the mixed-model-based test.
`xName`	The column name for dose. Character string.
`yName`	The column name for response. Character string.
`rName`	The column name for random effect. Only used if mixed = TRUE. Character string.
`niter`	An integer for the number of iterations in SHARP test procedure.

Value

A vector of four p values after Holm adjustment, indicating the significance of four different shapes types.

Examples

```
# Simulate dose-response data
x <- seq(0, 1, length.out = 48)
y <- 2*sqrt(x)+rnorm(48)
y[17:32] <- y[17:32]+0.5
y[33:48] <- y[33:48]+1
curve <- data.frame(x, y)
curve$rep <- rep(1:3, each = 16)

# Fixed-model based test
SHARPtest(curve, xName = "x", yName = "y", niter = 100)

# Mixed-model based test
SHARPtest(curve, mixed = TRUE, xName = "x", yName = "y", rName = "rep", niter = 100)
```

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