

# Package ‘shorm’

April 29, 2026

**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>>.

**License** GPL-3

**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

**Date/Publication** 2026-04-29 08:20:02 UTC

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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 examine its uncertainty and obtain a more robust conclusion, we may wish to repeat 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 SHARP 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.
niter	An integer for the number of iterations in SHARP test procedure

**Value**

A dataframe of test results from all repetitions. 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)
```

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**SharpScatter***Function to visualize SHARP test results*

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**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_label 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)
```

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SHARptest

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


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**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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