

# Package ‘TippingPoint’

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**Title** Enhanced Tipping Point Displays the Results of Sensitivity Analyses for Missing Data

**Version** 1.1.0

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**Description** Using the idea of “tipping point” (proposed in Gregory Campbell, Gene Pennello and Lilly Yue(2011) <DOI:10.1080/10543406.2011.550094>) to visualize the results of sensitivity analysis for missing data, the package provides a set of functions to list out all the possible combinations of the values of missing data in two treatment arms, calculate corresponding estimated treatment effects and p values and draw a colored heat-map to visualize them. It could deal with randomized experiments with a binary outcome or a continuous outcome. In addition, the package provides a visualized method to compare various imputation methods by adding the rectangles or convex hulls on the basic plot.

**Depends** R (>= 3.0.0)

**Imports** ggplot2 (>= 2.0.0), RColorBrewer, bayesSurv, reshape2

**Suggests** knitr, rmarkdown

**License** GPL-2

**LazyData** true

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**RoxygenNote** 5.0.1

**VignetteBuilder** knitr

**NeedsCompilation** no

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imputedata	<i>Imputation results under different methods</i>
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### Description

Imputation results based on Missing At Random(MAR) and Missing Completely At Random(MCAR) assumption for treatment and control group.

### Usage

imputedata

### Format

Data frame with 500 rows and 8 variables:

- MAR\_T1: Average value of nonrespondents for continuous outcome in treatment group under MAR assumption.
- MAR\_C1: Average value of nonrespondents for continuous outcome in control group under MAR assumption.
- MAR\_T2: Number of success of nonrespondents for binary outcome in treatment group under MAR assumption.
- MAR\_C2: Number of success of nonrespondents for binary outcome in control group under MAR assumption.
- MCAR\_T1: Average value of nonrespondents for continuous outcome in treatment group under MCAR assumption.
- MCAR\_C1: Average value of nonrespondents for continuous outcome in control group under MCAR assumption.
- MCAR\_T2: Number of success of nonrespondents for binary outcome in treatment group under MCAR assumption.
- MCAR\_C2: Number of success of nonrespondents for binary outcome in control group under MCAR assumption.

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tippingdata	<i>An hypothetical dataset used to demonstrate functions.</i>
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**Description**

A hypothetical dataset with continuous and binary outcome.

**Usage**

```
tippingdata
```

**Format**

Data frame with 270 rows and 5 variables:

- continuous: continuous outcome
- binary: binary outcome
- educ: education time(years)
- female: 0=male, 1=female
- treat: 0=control group, 1=treatment group

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TippingPoint	<i>Generic function for Enhanced Tipping Point Displays</i>
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**Description**

Generic function for Enhanced Tipping Point Displays

**Usage**

```
TippingPoint(...)
```

**Arguments**

... Additional arguments, see [TippingPoint.default](#), [TippingPoint.formula](#) for more details.

**References**

1. Liublinska, V. and Rubin, D.B. Enhanced Tipping-Point Displays. In JSM Proceedings, Section on Survey Research Methods, San Diego, CA: American Statistical Association. 3861-3686 (2012).
2. Liublinska, V. & Rubin, D.B. Sensitivity analysis for a partially missing binary outcome in a two-arm randomized clinical trial. *Stat Med* 33, 4170-85 (2014).
3. Liublinska, V. (May, 2013) Sensitivity Analyses in Empirical Studies Plagued with Missing Data. PhD Dissertation, Harvard University, <https://dash.harvard.edu/handle/1/11124841>
4. <https://sites.google.com/site/vliublinska/research>

**See Also**

[TippingPoint.default](#), [TippingPoint.formula](#).

**Examples**

```
TippingPoint(outcome=tippingdata$binary, treat= tippingdata$treat,
  group.infor=TRUE, plot.type = "estimate",ind.values = TRUE,
  impValuesT = NA, impValuesC = NA,
  summary.type = "density", alpha = 0.95, S=1.5, n.grid = 100,
  HistMeanT = c(0.38,0.4), HistMeanC = c(0.2,0.55))
```

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TippingPoint.default *Default method for TippingPoint*

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**Description**

The default method for enhanced tipping point displays.

**Usage**

```
## Default S3 method:
TippingPoint(outcome, treat, group.infor = FALSE,
  plot.type = c("estimate", "p.value", "both"), summary.type = c("density",
  "credible.region", "convex.hull"), alpha = 0.95, HistMeanT = NULL,
  HistMeanC = NULL, ind.values = FALSE, impValuesT = NA,
  impValuesC = NA, impValuesColor = NA, show.points = TRUE,
  point.size = 1, point.shape = 19, S = 3, n.grid = 150, ...)
```

**Arguments**

outcome	A numeric vector of the outcomes, a binary or continuous outcome.
treat	A (non-NA) numeric vector of treatment group.
group.infor	A logical, whether to display the group information.
plot.type	A character, one of "estimate", "p.value" or "both" indicating which one should be represented by a heat-map layer.
summary.type	A character, how to summarize the joint posterior distribution of imputed outcomes for treated and controls, one of "density", "credible.region" or "convex.hull". see <a href="#">geom_density2d</a> , <a href="#">mahalanobis</a> , <a href="#">geom_polygon</a> , <a href="#">credible.region</a> for more details.
alpha	A numeric between 0-1, with alpha of points in Convex hull, 1-alpha removed by Machalanobis distance. It also specifies the probabilities for credible regions used in <a href="#">credible.region</a> , in this case, alpha should be above 0.5 and below 1. The default value is 0.95.
HistMeanT	A numeric vector or NULL, historical values or proportions for the treatment group.

HistMeanC	A numeric vector or NULL, historical values or proportions for the control group.
ind.values	A logical, whether or not to display values in heat-map layer.
impValuesT	NA or imputed values for the treatment group, see <a href="#">imputedata</a> for more details.
impValuesC	NA or imputed values for the control group, see <a href="#">imputedata</a> for more details.
impValuesColor	NA or imputed colors correspond to the columns in impValuesT or impValuesC. The default colors are from <i>Set1</i> in <b>RColorBrewer</b> allowing up to 9. Specify explicitly if need more colors. See <a href="#">display.brewer.all</a> for more colors.
show.points	A logical, whether to show the points for imputed values.
point.size	Size of points for imputed values.
point.shape	Shape of points for imputed values.
S	A integer indicating range of plotting, the default value is 3.
n.grid	A integer, number of points in the grid, only for continuous case, the default is 150.
...	Additional arguments

**See Also**

[TippingPoint](#), [TippingPoint.formula](#).

**Examples**

```
# See more details in vignette using:
# vignette("TippingPoint")
TippingPoint(outcome=tippingdata$binary,treat= tippingdata$treat,
  plot.type = "p.value",ind.values = TRUE,
  impValuesT = imputedata[,c("MAR_T2","MCAR_T2")],
  impValuesC = imputedata[,c("MAR_C2","MCAR_C2")],
  impValuesColor = RColorBrewer::brewer.pal(8,"Accent")[c(4,6)],
  summary.type = "credible.region", alpha = 0.95,
  S=1.5, n.grid = 100, HistMeanT = c(0.38,0.4), HistMeanC = c(0.2,0.55))
```

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TippingPoint.formula    *TippingPoint.formula*

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**Description**

The formula method for enhanced tipping point displays.

**Usage**

```
## S3 method for class 'formula'
TippingPoint(formula, data, ...)
```

**Arguments**

<code>formula</code>	A formula of the form <code>outcome ~ treat</code> .
<code>data</code>	A <code>data.frame</code> containing the variables in the formula.
<code>...</code>	Additional arguments, see details in <a href="#">TippingPoint.default</a> .

**See Also**

[TippingPoint](#), [TippingPoint.default](#).

**Examples**

```
# See more details in vignette using:
# vignette("TippingPoint")
TippingPoint(binary~treat, data=tippingdata,
  plot.type = "both", ind.values = TRUE,
  impValuesT = imputedata[,c("MAR_T2", "MCAR_T2")],
  impValuesC = imputedata[,c("MAR_C2", "MCAR_C2")],
  impValuesColor = c("red", "blue"),
  point.size=0.8, point.shape = 15,
  summary.type = "convex.hull", alpha = 0.95, S=1.5, n.grid = 100,
  HistMeanT = c(0.38, 0.4), HistMeanC = c(0.2, 0.55))
```

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