

Package ‘TippingPoint’

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

Version 1.2.0

Author Shengjie Zhang <zhangshengjie@mrbc-nccd.com>, Xikun Han <hanxikun2017@gmail.com> and Victoria Liublinska <vliublin@g.harvard.edu>

Maintainer Xikun Han <hanxikun2017@gmail.com>

Description Using the idea of “tipping point” (proposed in Gregory Campbell, Gene Pennello and Lilly Yue(2011) <[DOI:10.1080/10543406.2011.550094](https://doi.org/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 missing values in two treatment arms, calculate corresponding estimated treatment effects and p values, and draw a colored heat-map. 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, reshape2

Suggests knitr, rmarkdown, bayesSurv

URL <https://github.com/XikunHan/TippingPoint>

License GPL-2

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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.

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

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))
```

TippingPoint.default *Default method for TippingPoint*

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 geom_density2d , mahalanobis , geom_polygon , credible.region 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 credible.region , 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 imputedata for more details.
impValuesC	NA or imputed values for the control group, see imputedata 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 RColorBrewer allowing up to 9. Specify explicitly if need more colors. See display.brewer.all 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))
```

TippingPoint.formula *TippingPoint.formula*

Description

The formula method for enhanced tipping point displays.

Usage

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

Arguments

formula	A formula of the form outcome ~ treat.
data	A data.frame containing the variables in the formula.
...	Additional arguments, see details in TippingPoint.default .

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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