

Package

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Title Computing Bounds for Harm Rate
Version 0.1
Description This package can help calculating bounds for the harm rate from the treatment to the outcome, and it can check whether the individual surrogate paradox exist.
Depends R (>= 3.4)
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ACCORD_eye	<i>ACCORD eye study data</i>
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Description

The ACCORD Eye study aimed at determining the effect of intensive glycemia on the risk of development or the progression of diabetic retinopathy.

Usage

ACCORD_eye

Format

A data frame with with 2596 rows and 3 columns:

Treatment Equals to 1 if the patient receives intensive treatment, and 0 indicated the patient received standard treatment.

Surrogate Equals to 1 if the glycated hemoglobin level was smaller than 6% at one year follow up and 0 otherwise.

Outcome Equals to 1 if progression of diabetic retinopathy was observed at the fourth year and 0 otherwise.

Source

The original data is from National Institutes of Health (NIH) (<https://biolincc.nhlbi.nih.gov/studies/accord/>)

boot_HRbound	<i>Bootstrap Harm Rate Bound</i>
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Description

Calculate bootstrap confidence interval for the bound of harm rate from the treatment to the outcome.

Usage

```
boot_HRbound(Tr, S, Y, c1 = 0, c3 = 1, n, conf.level = 0.95)
```

Arguments

Tr	Treatment variable, a vector taking value 1 or 0.
S	Surrogate variable, a vector taking value 1 or 0.
Y	Outcome variable, a vector taking value 1 or 0.
c1	Harm rate from the treatment to the surrogate, which takes value between 0 and 1.
c3	The upper bound for the proportion of the individuals that do not conform to causal necessity.
n	Number of bootstrap samples. A positive integer.
conf.level	Confidence level of the interval.

Details

This function computes the bootstrap confidence interval for the sharp bound of harm rate from the treatment to the surrogate.

Value

Calculate confidence interval for the bound of the harm rate from the treatment to the outcome.

Examples

```
boot_HRbound(Tr = ACCORD_eye[, 1], S = ACCORD_eye[, 2], Y = ACCORD_eye[, 3], n = 1000)
```

HRbound	<i>Harm Rate Bounds</i>
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Description

Calculate the bounds of harm rate from the treatment to the outcome.

Usage

```
HRbound(Tr, S, Y, c1 = 0, c3 = 1)
```

Arguments

Tr	Treatment variable, a vector taking value 1 or 0.
S	Surrogate variable, a vector taking value 1 or 0.
Y	Outcome variable, a vector taking value 1 or 0.
c1	Harm rate from the treatment to the surrogate, which takes value between 0 and 1.
c3	The upper bound for the proportion of the individuals that do not conform to causal necessity.

Details

This function calculates the lower and upper sharp bounds of harm rate from the treatment to the surrogate, using the method proposed in Ma et al.

Value

Lower and upper bound of the harm rate from the treatment to the outcome.

References

Ma, L., Yin, Y., Liu, L. and Geng, Z. On the Individual Surrogate Paradox. Submitted

Examples

```
HRbound(Tr = ACCORD_eyel[, 1], S = ACCORD_eyel[, 2], Y = ACCORD_eyel[, 3])
```

ISP	<i>Individual Surrogate Paradox</i>
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Description

Check whether individual surrogate paradox manifests by calculating the bound of harm rate from the treatment to the outcome.

Usage

```
ISP(Tr, S, Y, c1, c3 = 1)
```

Arguments

Tr	Treatment variable, a vector taking value 1 or 0.
S	Surrogate variable, a vector taking value 1 or 0.
Y	Outcome variable, a vector taking value 1 or 0.
c1	Harm rate from the treatment to the surrogate, which takes value between 0 and 1.
c3	The upper bound for the proportion of the individuals that do not conform to causal necessity.

Details

This function calculates the sharp bounds of harm rate from the treatment to the surrogate, and determine whether individual surrogate paradox exists using the method proposed in Ma et al.

Value

Lower and upper bound of the harm rate from the treatment to the outcome, and whether the individual surrogate paradox manifests.

References

Ma, L., Yin, Y., Liu, L. and Geng, Z. On the Individual Surrogate Paradox. Submitted

Examples

```
ISP(Tr = ACCORD_eye[, 1], S = ACCORD_eye[, 2], Y = ACCORD_eye[, 3], c1 = 0.5)
```

`plot_bound`*Plot Harm Rate Bounds*

Description

Present a plot for the bounds of harm rate from the treatment to the outcome.

Usage

```
plot_bound(Tr, S, Y, c3 = 1)
```

Arguments

Tr	Treatment variable, a vector taking value 1 or 0.
S	Surrogate variable, a vector taking value 1 or 0.
Y	Outcome variable, a vector taking value 1 or 0.
c3	The upper bound for the propotion of the individuals that do not conform to causal necessity.

Details

This function plots the lower and upper sharp bounds of harm rate from the treatment to the surrogate when c1 varies.

Value

Lower and upper bound of the harm rate from the treatment to the outcome, and whether the individual surrogate paradox manifests.

References

Ma, L., Yin, Y., Liu, L. and Geng, Z. On the Individual Surrogate Paradox. Submitted

Examples

```
plot_bound(Tr = ACCORD_eye[, 1], S = ACCORD_eye[, 2], Y = ACCORD_eye[, 3], c3 = 0)
```

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