Package 'hetsurr'

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Type Package

Title Assessing Heterogeneity in the Utility of a Surrogate Marker

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Description Provides a function to assess and test for heterogeneity in the utility of a surrogate marker with respect to a baseline covariate. The main function can be used for either a continuous or discrete baseline covariate. More details will be available in the future in: Parast, L., Cai, T., Tian L (2021). ``Testing for Heterogeneity in the Utility of a Surrogate Marker.'' Biometrics, In press.

License GPL

Imports stats, Rsurrogate, graphics

NeedsCompilation no

Depends R (>= 3.5.0)

R topics documented:

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example.data   *Example data*

Description

Example data

Usage

```
data("example.data")
```

Format

A list with 6 elements representing 2000 observations from a treatment group and 1500 observations from a control group:

y1 the primary outcome in the treatment group

y0 the primary outcome in the control group

s1 the surrogate marker in the treatment group

s0 the surrogate marker in the control group

w1 the baseline covariate of interest in the treatment group

w0 the baseline covariate of interest in the control group

Examples

```
data(example.data)
names(example.data)
```

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hetsurr.fun   *Assess and test for heterogeneity in the utility of a surrogate*

Description

This function assesses and tests for heterogeneity in the utility of a surrogate with respect to a continuous or discrete baseline covariate. The method is nonparametric and focuses on estimation of the proportion of the treatment effect that is explained by the surrogate marker. Inference information is provided including a confidence band for the proportion and results from formal testing for heterogeneity. When the baseline covariate is continuous, two tests are performed - an omnibus test and a trend test; when the baseline covariate is discrete, only one test is performed - an omnibus test.

Usage

```
hetsurr.fun(y1, y0, s1, s0, w1, w0, wf.grd = NULL, h0 = NULL, h1 = NULL, h2 = NULL,
h3 = NULL, h4 = NULL, var.want = FALSE, type = "cont", test.want = FALSE, c.adj = 1)
```

Arguments

y1	the primary outcome in the treatment group
y0	the primary outcome in the control group
s1	the surrogate marker in the treatment group
s0	the surrogate marker in the control group
w1	the baseline covariate of interest in the treatment group
w0	the baseline covariate of interest in the control group
wf.grd	the grid of the baseline covariate where estimates are wanted; if this is not specified, this will bet set equal to 50 equally spaced points between the 10th and 90th percentile of the union of w1 and w0 values (if continuous) or the set of unique categories (if discrete)
h0	bandwidth; if not specific, this is set to a value of appropriate order

h1	bandwidth; if not specific, this is set to a value of appropriate order
h2	bandwidth; if not specific, this is set to a value of appropriate order
h3	bandwidth; if not specific, this is set to a value of appropriate order
h4	bandwidth; if not specific, this is set to a value of appropriate order
var.want	TRUE or FALSE; indicates whether variance estimate are wanted, default is FALSE
type	"cont" or "discrete"; indicates the form of the baseline covariate w, default is "cont"
test.want	TRUE or FALSE; indicates whether testing results are wanted, default is FALSE
c.adj	a multiplicative adjustment for the bandwidth; default is 1

Details

This function calculates the treatment effect, Delta, the residual treatment effect, Delta_S, and the proportion of treatment effect explained R_S, as a function of the baseline covariate (if continuous) or stratified by category (if discrete). The estimation approach is nonparametric. Variance estimates can be requested including a confidence band for R_S. Results from formal testing for heterogeneity can also be requested. When the baseline covariate is continuous, two tests are performed - an omnibus test and a trend test; when the baseline covariate is discrete, only one test is performed - an omnibus test.

Value

w.values	values of the baseline covariate at which estimates are provided
delta.w	estimated treatment effect, Delta, at each w value
delta.w.s	estimated residual treatment effect, Delta_S, at each w value
R.w.s	estimated proportion of treatment effect explained, R_S, at each w value
se.delta.w	estimated standard error of Delta
se.delta.w.s	estimated standard error of Delta.S
se.R.w.s	estimated standard error of R.S
conf.delta.w.lower	
	lower bound of the confidence intervals for Delta
conf.delta.w.upper	
	upper bound of the confidence intervals for Delta
conf.delta.w.s.lower	
	lower bound of the confidence intervals for Delta.S
conf.delta.w.s.upper	
	upper bound of the confidence intervals for Delta.S
conf.R.w.s.lower	
	lower bound of the confidence intervals for R.S
conf.R.w.s.upper	
	upper bound of the confidence intervals for R.S
band.R.w.s.lower	
	lower bound of the confidence band for R.S
band.R.w.s.upper	
	upper bound of the confidence band for R.S
omnibus.test.statistic	
	test statistic from omnibus test; for a continuous baseline covariate only

omnibus.p.value

> p-value from omnibus test, testing for evidence of heterogeneity; for a continuous baseline covariate only

trend.test.statistic

> test statistic from the trend test; for a continuous baseline covariate only

trend.p.value   p-value from trend test, testing for evidence of heterogeneity; for a continuous baseline covariate only

test.statistic p-value from the test testing for evidence of heterogeneity; for a discrete baseline covariate only

p.value   p-value from the test testing for evidence of heterogeneity; for a discrete baseline covariate only

Author(s)

Layla Parast

References

Parast, L., Cai, T., Tian L (2021). Testing for Heterogeneity in the Utility of a Surrogate Marker. Biometrics, In press.

Examples

```
data(example.data)
names(example.data)
#computationally intensive

het.ob = hetsurr.fun(y1=example.data$y1, y0=example.data$y0, s1=example.data$s1,
s0=example.data$s0, w1=example.data$w1, w0=example.data$w0, wf.grd = seq(0.25, 1.75,
length=50), var.want =FALSE, type = "cont")
het.ob = hetsurr.fun(y1=example.data$y1, y0=example.data$y0, s1=example.data$s1,
s0=example.data$s0, w1=example.data$w1, w0=example.data$w0, wf.grd = seq(0.25, 1.75,
length=50), var.want =TRUE,  test.want = TRUE, type = "cont")

#reducing dimension of example data to provide a computationally faster example
het.ob = hetsurr.fun(y1=example.data$y1[1:500], y0=example.data$y0[1:500],
s1=example.data$s1[1:500], s0=example.data$s0[1:500], w1=example.data$w1[1:500],
w0=example.data$w0[1:500], wf.grd = seq(0.25, 1.75, length=5), var.want =FALSE,
type = "cont")
```

---

hetsurr.plot   *Constructs plots of the treatment effect, residual treatment effect, and proportion explained as a function of the continuous baseline covariate*

Description

Constructs plots of the treatment effect, residual treatment effect, and proportion explained as a function of the continuous baseline covariate

Usage

```
hetsurr.plot(hetsurr.results, xlab.name = "Baseline Covariate", placement = "bottomleft")
```

Arguments

hetsurr.results

    This is a list produced by the hetsurr.fun function.

xlab.name   This is the label for the x-axis; default is "Baseline Covariate".

placement   This is the placement for the legend; default is "bottomleft".

Value

Produces a plot with 3 panels.

Author(s)

Layla Parast

References

Parast, L., Cai, T., Tian L (2021). Testing for Heterogeneity in the Utility of a Surrogate Marker. Biometrics, In press.

Examples

```
data(example.data)
names(example.data)
#computationally intensive

het.ob = hetsurr.fun(y1=example.data$y1, y0=example.data$y0, s1=example.data$s1,
s0=example.data$s0, w1=example.data$w1, w0=example.data$w0, wf.grd = seq(0.25, 1.75,
length=50), var.want =TRUE,  test.want = TRUE, type = "cont")
hetsurr.plot(het.ob)

#reducing dimension of example data to provide a computationally faster example
het.ob = hetsurr.fun(y1=example.data$y1[1:300], y0=example.data$y0[1:300],
s1=example.data$s1[1:300], s0=example.data$s0[1:300], w1=example.data$w1[1:300],
w0=example.data$w0[1:300], wf.grd = seq(0.25, 1.75, length=5), var.want =TRUE,
test.want = TRUE, type = "cont")
hetsurr.plot(het.ob)
```

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