Package: cohetsurr (via r-universe)

March 6, 2025

Type Package

Title Assessing Complex Heterogeneity in Surrogacy

Version 1.1

Date 2025-03-05

Description Provides functions to assess and test for complex heterogeneity in the utility of a surrogate marker with respect to multiple baseline covariates, using both a parametric model and a semiparametric two-step model. More details are available in: Knowlton, R., Tian, L., & Parast, L. (2025). ``A General Framework to Assess Complex Heterogeneity in the Strength of a Surrogate Marker,'' Statistics in Medicine, 44(5), e70001 <doi:10.1002/sim.70001>. A tutorial for this package can be found at <`https://laylaparast.com/home/cohetsurr.html`>.

License GPL

Imports stats, matrixStats, mvtnorm

NeedsCompilation no

Author Rebecca Knowlton [aut], Layla Parast [aut, cre]

Maintainer Layla Parast <`parast@austin.utexas.edu`>

Date/Publication 2025-03-06 00:00:13 UTC

Repository https://laylaparast.r-universe.dev

RemoteUrl https://github.com/cran/cohetsurr

RemoteRef HEAD

RemoteSha 6b2137c5294cab7c52f64acc18913fe1c2837c4c

Contents

`complex.heterogeneity` *Estimates the proportion of treatment effect explained by the surrogate marker as a function of multiple baseline covariates.*

Description

Assesses complex heterogeneity in the utility of a surrogate marker by estimating the proportion of treatment effect explained by the surrogate marker as a function of multiple baseline covariates. Optionally, tests for evidence of heterogeneity overall and flags regions where the proportion of treatment effect explained is above a given threshold.

Usage

```
complex.heterogeneity(y, s, a, W.mat, type = "model", variance = FALSE,
test = FALSE, W.grid = NULL, grid.size = 4, threshold = NULL)
```

Arguments

`y`	y, the outcome
`s`	s, the surrogate marker
`a`	a, the treatment assignment with 1 indicating the treatment group and 0 indicating the control group
`W.mat`	matrix of baseline covariate observations, where the first column is W1, second columns is W2, and so on.
`type`	options are "model", "two step", or "both"; specifies the estimation method that should be used for the proportion of treatment effect explained
`variance`	TRUE or FALSE, if variance/standard error estimates are wanted
`test`	TRUE or FALSE, if test for heterogeneity is wanted
`W.grid`	grid for the baseline covariates W where estimation will be provided
`grid.size`	number of measures for each baseline covariate to include in the estimation grid, if one is not provided by the user directly
`threshold`	threshold to flag regions where the estimated proportion of the treatment effect explained is at least that high

Value

A list is returned:

`return.grid`	grid of estimates for the overall treatment effect, the residual treatment effect, and the proportion of treatment effect explained as a function of the baseline covariates, W. Includes variance estimates and regions flagged above the threshold, if specified by the user.
`pval`	p-value(s) from the F test and the two step omnibus test for heterogeneity, depending on type argument

Author(s)

Rebecca Knowlton

References

Knowlton, R., Tian, L., & Parast, L. (2025). A General Framework to Assess Complex Heterogeneity in the Strength of a Surrogate Marker. Statistics in Medicine, 44(5), e70001

Examples

```
data(exampledata)
names(exampledata)
complex.heterogeneity(y = exampledata$y,
                      s = exampledata$s,
                      a = exampledata$a,
                      W.mat = matrix(cbind(exampledata$w1, exampledata$w2), ncol = 2),
                      type = "model",
               W.grid = matrix(cbind(exampledata$w1.grid, exampledata$w2.grid),ncol=2))
#computationally intensive

  complex.heterogeneity(y = exampledata$y,
                        s = exampledata$s,
                        a = exampledata$a,
                        W.mat = matrix(cbind(exampledata$w1,
                        exampledata$w2), ncol = 2),
                        type = "both",
                        variance = TRUE,
                        test = TRUE,
                        W.grid = matrix(cbind(exampledata$w1.grid,
                        exampledata$w2.grid), ncol = 2),
                        threshold = 0.75)
```

`exampledata` *Example data*

Description

Example data

Usage

```
data("exampledata")
```

Format

A list with 7 elements representing 1000 observations from a treatment group and 1000 observations from a control group, and a grid of baseline covariate values at which to calculate estimates:

`y`	the outcome
`s`	the surrogate marker
`a`	the treatment assignment, where 1 indicates treatment and 0 indicates control
`w1`	the first baseline covariate of interest
`w2`	the second baseline covariate of interest
`w1.grid`	the grid of first baseline covariate values to provide estimates for
`w2.grid`	the grid of second baseline covariate values to provide estimates for

Examples

```
data(exampledata)
names(exampledata)
```

Index