

Package ‘CMFsurrogate’

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Type Package

Title Calibrated Model Fusion Approach to Combine Surrogate Markers

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Description Uses a calibrated model fusion approach to optimally combine multiple surrogate markers. Specifically, two initial estimates of optimal composite scores of the markers are obtained; the optimal calibrated combination of the two estimated scores is then constructed which ensures both validity of the final combined score and optimality with respect to the proportion of treatment effect explained (PTE) by the final combined score. The primary function, `pte.estimate.multiple()`, estimates the PTE of the identified combination of multiple surrogate markers. Details are described in Wang et al (2022) <[doi:10.1111/biom.13677](https://doi.org/10.1111/biom.13677)>. A tutorial for the package is available at <<https://www.laylaparast.com/cmfsurrogate>> and a Shiny App is available at <<https://parastlab.shinyapps.io/CMFsurrogateApp/>>.

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Imports splines, MASS, stats, utils

NeedsCompilation no

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Contents

example.data	2
gen.bootstrap.weights	2
pte.estimate.multiple	3
resam	4

Index	5
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example.data

Example data

Description

Example data

Usage

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

Format

A list with 3 elements:

sob the surrogate markers

yob the primary outcome

aob the treatment indicator

Examples

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

gen.bootstrap.weights *Generate bootstrap sample*

Description

Generate bootstrap sample

Usage

```
gen.bootstrap.weights(n, num.perturb = 500)
```

Arguments

n sample size

num.perturb number of replicates/resamples

Value

matrix with n rows and num.perturb columns of indices

pte.estimate.multiple *Estimates the proportion of treatment effect explained by the optimal combination of multiple surrogate markers using a calibrated model fusion approach*

Description

Estimates the proportion of treatment effect explained by the optimal combination of multiple surrogate markers using a calibrated model fusion approach

Usage

```
pte.estimate.multiple(sob, yob, aob, var = TRUE, rep = 500)
```

Arguments

sob	surrogates
yob	primary outcome, y
aob	treatment indicator
var	TRUE or FALSE, if variance/SE of PTE is being requested
rep	if var is TRUE, number of resampled draws to use for bootstrap

Value

pte.es	Estimate of the proportion of treatment effect explained (PTE)
pte.se	if var = TRUE, estimate of the standard error of the PTE

References

Wang, X., Parast, L., Han, L., Tian, L., & Cai, T. (2022). Robust approach to combining multiple markers to improve surrogacy. *Biometrics*, In press.

Examples

```
data(example.data)
out=pte.estimate.multiple(sob=example.data$sob, yob=example.data$yob,
aob=example.data$aob, var = FALSE)
out
```

resam

Estimates quantities using resampled data

Description

Estimates quantities using resampled data

Usage

```
resam(index, yob, sob, aob, n)
```

Arguments

index	index
yob	y
sob	surrogates
aob	treatment
n	n

Value

Outputs parametric estimate, additive linear estimate, and convex combination estimate

Index

`example.data`, [2](#)

`gen.bootstrap.weights`, [2](#)

`pte.estimate.multiple`, [3](#)

`resam`, [4](#)