

# Package ‘CMFsurrogate’

October 12, 2022

**Type** Package

**Title** Calibrated Model Fusion Approach to Combine Surrogate Markers

**Version** 1.0

**Date** 2022-09-22

**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)>.

**License** GPL

**Imports** splines, MASS, stats

**NeedsCompilation** no

**Author** Xuan Wang [aut],  
Layla Parast [cre]

**Maintainer** Layla Parast <[parast@austin.utexas.edu](mailto:parast@austin.utexas.edu)>

**Depends** R (>= 3.5.0)

**Repository** CRAN

**Date/Publication** 2022-09-23 15:20:05 UTC

## R topics documented:

<code>example.data</code> . . . . .	2
<code>gen.bootstrap.weights</code> . . . . .	2
<code>pte.estimate.multiple</code> . . . . .	3
<code>resam</code> . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

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](#)