Package 'PTERP'

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Type Package

Title PTE and RP for Optimally-Transformed Surrogate

Version 1.0

Description Evaluates the strength of a surrogate marker by estimating the proportion of treatment effect explained (PTE) and relative power(RP) for the optimally-transformed version of the surrogate. Details available in Wang et al (2022) <arXiv:2209.08414>.

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Imports MASS, mvtnorm, stats, survival

NeedsCompilation no

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Depends R (>= 3.5.0)

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exampledata   *Hypothetical data for example*

Description

Hypothetical data for example

Usage

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

Format

yob the primary outcome

sob the surrogate marker

aob the treatment group indicator where 1 is treatment and 0 is control

Examples

```
data(exampledata)
```

PTERP   *Estimates PTE and RE*

Description

Evaluates the strength of a surrogate marker by estimating the proportion of treatment effect explained (PTE) and relative power(RP) for the optimally-transformed version of the surrogate.

Usage

```
PTERP(data,ncut=c(50,100,150,200,500,1000),n.resam=500)
```

Arguments

data	data
ncut	relative power is calculated at a specific sample size n; this is a numeric vector of sample sizes for which the user wants the relative power, default is c(50,100,150,200,500,1000)
n.resam	number of times to resample, default is 500

Value

A list of:

ptenew.es	Proportion of treatment effect estimate
rp_i1	Estimate of relative power at n=i1 where i1 is the first value given in ncut
rp_i2	Estimate of relative power at n=i2 where i2 is the second value given in ncut, etc.
pte.se	Standard error estimate for the proportion of treatment effect explained
rp.se.i1	Standard error estimate for the relative power at n=i1 where i1 is the first value given in ncut
rp.se.i2	Standard error estimate for the relative power at n=i2 where i2 is the first value given in ncut, etc.

Author(s)

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Examples

```
data(exampledata)

output=PTERP(exampledata,ncut=c(50,100,150,200,500,1000))

#reduce resampling
output=PTERP(exampledata,ncut=c(50,100,150,200,500,1000),n.resam=5)
```

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