

# Package: PTERP (via r-universe)

October 13, 2024

**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>](https://arxiv.org/abs/2209.08414).

**License** GPL

**Imports** MASS, mvtnorm, stats, survival

**NeedsCompilation** no

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

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

**Depends** R (>= 3.5.0)

**Date/Publication** 2022-10-10 17:10:02 UTC

**Repository** <https://laylaparast.r-universe.dev>

**RemoteUrl** <https://github.com/cran/PTERP>

**RemoteRef** HEAD

**RemoteSha** 4bed5f2828ac22efb29cc4bbee716b7a94cb2ba9

## Contents

exampledata . . . . .	2
PTERP . . . . .	2
<b>Index</b>	<b>4</b>

---

exampledata	<i>Hypothetical data for example</i>
-------------	--------------------------------------

---

**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	<i>Estimates PTE and RE</i>
-------	-----------------------------

---

**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:

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

**Author(s)**

Xuan Wang

**Examples**

```
data(exampladata)

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

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

# Index

exampledata, [2](#)

PTERP, [2](#)