Package 'SurrogateRank'

April 9, 2024

Type Package								
Title Rank-Based Test to Evaluate a Surrogate Marker Version 1.0 Description Uses a novel rank-based nonparametric approach to evaluate a surrogate marker in a small sample size setting. Details are described in Parast et al (2024) <doi:10.1093 biomtc="" ujad035="">.</doi:10.1093>								
					License GPL Imports stats NeedsCompilation no Author Layla Parast [aut, cre] Maintainer Layla Parast <pre></pre>			
Repository CRAN								
Date/Publication 2024-04-09 16:40:09 UTC								
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	Calculates the rank-based test statistic for Y and S and the difference, delta							

delta, along with corresponding standard error estimates

Calculates the rank-based test statistic for Y and the rank-based test statistic for S and the difference,

Description

est.power

Usage

```
delta.calculate(full.data = NULL, yone = NULL, yzero = NULL, sone = NULL, szero = NULL)
```

Arguments

full.data	either full.data or yone, yzero, sone, szero must be supplied; if full data is supplied it must be in the following format: one observation per row, Y is in the first column, S is in the second column, treatment group (0 or 1) is in the third column.
yone	primary outcome, Y, in group 1
yzero	primary outcome, Y, in group 0
sone	surrogate marker, S, in group 1
szero	surrogate marker, S, in group 0

Value

u.y	rank-based test statistic for Y
u.s	rank-based test statistic for S
delta	difference, u.y-u.s
sd.u.y	standard error estimate of u.y
sd.u.s	standard error estimate of u.s
sd.delta	standard error estimate of delta

Author(s)

Layla Parast

Examples

```
data(example.data)
delta.calculate(yone = example.data$y1, yzero = example.data$y0, sone = example.data$s1,
szero = example.data$s0)
```

est.power	Estimated power to detect a valid surrogate	
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Description

Calculates the estimated power to detect a valid surrogate given a total sample size and specified alternative

Usage

```
est.power(n.total, rho = 0.8, u.y.alt, delta.alt, power.want.s = 0.7)
```

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Arguments

n. total total sample size in study

rho rank correlation between Y and S in group 0, default is 0.8

u.y.alt specified alternative for u.ydelta.alt specified alternative for u.s

power.want.s desired power for u.s, default is 0.7

Value

estimated power

Author(s)

Layla Parast

Examples

```
est.power(n.total = 50, rho = 0.8, u.y.alt=0.9, delta.alt = 0.1)
```

example.data

Example data

Description

Example data use to illustrate the functions

Usage

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

Format

A list with 4 elements representing 25 observations from a treatment group (group 1) and 25 observations from a control group (group 0):

```
y1 the primary outcome, Y, in group 1
```

y0 the primary outcome, Y, in group 0

s1 the surrogate marker, S, in group 1

s0 the surrogate marker, S, in group 0

Examples

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

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test.surrogate	Tests whether the surrogate is valid
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Description

Calculates the rank-based test statistic for Y and the rank-based test statistic for S and the difference, delta, along with corresponding standard error estimates, then tests whether the surrogate is valid

Usage

```
test.surrogate(full.data = NULL, yone = NULL, yzero = NULL, sone = NULL, szero = NULL, epsilon = NULL, power.want.s = 0.7, u.y.hyp = NULL)
```

Arguments

full.data	either full.data or yone, yzero, sone, szero must be supplied; if full data is supplied it must be in the following format: one observation per row, Y is in the first column, S is in the second column, treatment group (0 or 1) is in the third column.
yone	primary outcome, Y, in group 1
yzero	primary outcome, Y, in group 0
sone	surrogate marker, S, in group 1
szero	surrogate marker, S, in group 0
epsilon	threshold to use for delta, default calculates epsilon as a function of desired power for S
power.want.s	desired power for S, default is 0.7
u.y.hyp	hypothesized value of u.y used in the calculation of epsilon, default uses estimated valued of u.y

Value

u.y	rank-based test statistic for Y
u.s	rank-based test statistic for S
delta	difference, u.y-u.s
sd.u.y	standard error estimate of u.y
sd.u.s	standard error estimate of u.s
sd.delta	standard error estimate of delta
ci.delta	1-sided confidence interval for delta
epsilon.used	the epsilon value used for the test
is.surrogate	logical, TRUE if test indicates S is a good surrogate, FALSE otherwise

Author(s)

Layla Parast

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Examples

```
data(example.data)
test.surrogate(yone = example.data$y1, yzero = example.data$y0, sone = example.data$s1,
szero = example.data$s0)
```

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