Package 'SenSpe'

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Title Estimating Specificity at Controlled Sensitivity, or Vice Versa

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Depends R (>= 2.8.0)

Suggests knitr, rmarkdown

VignetteBuilder knitr

Description Perform biomarker evaluation and comparison in terms of specificity at a controlled sensitivity level, or sensitivity at a controlled specificity level. Point estimation and exact bootstrap of Huang, Parakati, Patil, and Sanda (2023) <doi:10.5705/ss.202021.0020> for the one- and two-biomarker problems are implemented.

License GPL (>= 2)

NeedsCompilation yes

Repository CRAN

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R topics documented:

snsp1m *Estimating specificity (or sensitivity) at a controlled sensitivity (or specificity) level*

Description

Point estimation and exact bootstrap-based inference

Usage

```
snsp1m(mk, n1, s0, covp=0.95, fixsens=TRUE, lbmdis=TRUE)
```

Arguments

mk	biomarker values of cases followed by controls.
n1	size of cases.
s0	controlled level of sensitivity or specificity.
covp	norminal level of confidence intervals.
fixsens	fixing sensitivity if True, and specificity otherwise.
lbmdis	larger biomarker value is more associated with cases if True, and controls otherwise.

Value

threshold	estimated threshold, at and beyond which the empirical sensitivity or specificity is the smallest no less than the controlled level s0.
hss	hss[1]: empirical point estimate of specificity at controlled sensitivity, or vice versa; hss[2]: oscillating bias-corrected estimate.
hvar1	estimated variance component from cases if specificity at controlled sensitivity is estimated, or from controls otherwise.
hvar2	estimated variance component from controls if specificity at controlled sensitivity is estimated, or from cases otherwise.
hvar	exact bootstrap variance estimate, =hvar1+hvar2.
btpdf	exact bootstrap probability mass function at (0:n0)/n0 with n0 being the size of controls if sensitivity is controlled, or at (0:n1)/n1 otherwise.
wald_ci	wald_ci[1,]: Wald confidence interval using hss[1]; wald_ci[2,]: Wald confidence interval using hss[2].
pct_ci	percentile confidence interval.
scr_ci	scr_ci[1,]: score confidence interval using hss[1]; scr_ci[2,]: score confidence interval using hss[2].
zq_ci	exact bootstrap version of the BTII in Zhou and Qin (2005, Statistics in Medicine 24, pp 465–477).

Author(s)

Yijian Huang

References

Huang, Y., Parakati, I., Patil, D. H.,and Sanda, M. G. (2023). Interval estimation for operating characteristic of continuous biomarkers with controlled sensitivity or specificity, *Statistica Sinica* 33, 193–214.

Examples

```
## simulate biomarkers of 100 cases and 100 controls
set.seed(1234)
mk <- c(rnorm(100,1,1),rnorm(100,0,1))

## estimate specificity at controlled 0.95 sensitivity
est <- snsp1m(mk, 100, 0.95)
```

`snsp2mp` *Two-biomarker paired comparison in specificity (or sensitivity) at a controlled sensitivity (or specificity) level*

Description

Point estimation and exact bootstrap-based inference

Usage

```
snsp2mp(mk, n1, s0, covp=0.95, fixsens=TRUE, lbmdis=TRUE)
```

Arguments

`mk`	Each of two rows corresponds to a biomarker, cases followed by controls.
`n1`	case size.
`s0`	controlled level of sensitivity or specificity.
`covp`	norminal level of confidence intervals.
`fixsens`	fixing sensitivity if True, and specificity otherwise.
`lbmdis`	larger value of a biomarker is more associated with cases if True, and controls otherwise.

Value

diff	diff[1]: difference of empirical point estimates; hss[2]: difference of oscillating bias-corrected estimates.
btmn	bootstrap mean of the empirical difference.
btva	exact bootstrap variance estimate for diff[1].
btdist	exact bootstrap probability mass function at (-n0:n0)/n0 with n0 being the size of controls if sensitivity is controlled, or at (-n1:n1)/n1 otherwise.
wald_ci	wald_ci[1,]: Wald confidence interval using diff[1]; wald_ci[2,]: Wald confidence interval using diff[2].
pct_ci	percentile confidence interval.
scr_ci	scr_ci[1,]: score confidence interval using diff[1]; scr_ci[2,]: score confidence interval using diff[2].
zq_ci	extension of the BTII in Zhou and Qin (2005, Statistics in Medicine 24, pp 465–477).

Author(s)

Yijian Huang

References

Huang, Y., Parakati, I., Patil, D. H.,and Sanda, M. G. (2023). Interval estimation for operating characteristic of continuous biomarkers with controlled sensitivity or specificity, *Statistica Sinica* 33, 193–214.

Examples

```
## simulate paired biomarkers X and Y, with correlation 0.5, 100 cases and 100 controls
n1 <- 100
n0 <- 100
rho <- 0.5
set.seed(1234)
mkx <- rnorm(n1+n0,0,1)
mky <- rho*mkx + sqrt(1-rho^2)*rnorm(n1+n0,0,1)
mkx <- mkx + c(rep(2,n1),rep(0,n0))
mky <- mky + c(rep(1,n1),rep(0,n0))
mk <- rbind(mkx,mky)

## compare specificity at controlled 0.95 sensitivity
est <- snsp2mp(mk, 100, 0.95)
```

snsp2mup *Two-biomarker unpaired comparison in specificity (or sensitivity) at a controlled sensitivity (or specificity) level*

Description

Point estimation and exact bootstrap-based inference

Usage

```
snsp2mup(mkx, n1x, mky, n1y, s0, covp=0.95, fixsens=TRUE, lbmdisx=TRUE, lbmdisy=TRUE)
```

Arguments

mkx	values of biomarker X, cases followed by controls.
n1x	case size of biomarker X.
mky	values of biomarker Y, cases followed by controls.
n1y	case size of biomarker Y.
s0	controlled level of sensitivity or specificity.
covp	norminal level of confidence intervals.
fixsens	fixing sensitivity if True, and specificity otherwise.
lbmdisx	larger value of biomarker X is more associated with cases if True, and controls otherwise.
lbmdisy	larger value of biomarker Y is more associated with cases if True, and controls otherwise.

Value

diff	diff[1]: difference of empirical point estimates; diff[2]: difference of oscillating bias-corrected estimates.
hvar	exact bootstrap variance estimate for diff[1].
wald_ci	wald_ci[1,]: Wald confidence interval using diff[1]; wald_ci[2,]: Wald confidence interval using diff[2].
pct_ci	percentile confidence interval.
scr_ci	scr_ci[1,]: score confidence interval using diff[1]; scr_ci[2,]: score confidence interval using diff[2].
zq_ci	extension of the BTII in Zhou and Qin (2005, Statistics in Medicine 24, pp 465–477).

Author(s)

Yijian Huang

References

Huang, Y., Parakati, I., Patil, D. H.,and Sanda, M. G. (2023). Interval estimation for operating characteristic of continuous biomarkers with controlled sensitivity or specificity, *Statistica Sinica* 33, 193–214.

Examples

```
set.seed(1234)
## simulate biomarker X with 100 cases and 100 controls
mkx <- c(rnorm(100,2,1),rnorm(100,0,1))
## simulate biomarker Y with 100 cases and 100 controls
mky <- c(rnorm(100,1,1),rnorm(100,0,1))

## compare specificity at controlled 0.95 sensitivity
est <- snsp2mup(mkx, 100, mky, 100, 0.95)
```

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