Package: compareC (via r-universe)

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Type Package

Title Compare Two Correlated C Indices with Right-Censored Survival
Outcome

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Description Proposed by Harrell, the C index or concordance C, is
considered an overall measure of discrimination in survival
analysis between a survival outcome that is possibly right
censored and a predictive-score variable, which can represent a
measured biomarker or a composite-score output from an
algorithm that combines multiple biomarkers. This package aims
to statistically compare two C indices with right-censored
survival outcome, which commonly arise from a paired design and
thus resulting two correlated C indices.

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NeedsCompilation yes

Repository CRAN

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Contents

| compareC | *Testing the difference between two correlated overall* C *indices* |

Description

This is a function used to test if the difference in two correlated overall *C* indices is statistically significant

Usage

```
compareC(timeX, statusX, scoreY, scoreZ)
```

Arguments

timeX	The vector of actual survival time *X*, one survival time for each observation
statusX	The matching vector of event indicator for time *X*, 1 if occured and 0 otherwise
scoreY	The vector of the first measured biomarker or score *Y*, one for each of the same observations
scoreZ	The vector of the second measured biomarker or score *Z*, one for each of the same observations

Value

est.c	The estimated two *C* indices
est.diff_c	The estimated difference of the two *C* indices, i.e.,$C_{XY} - C_{XZ}$
est.vardiff_c	The estimated variance of the difference of two *C* indices
est.varCxy	The estimated variance of the *C* index for *scoreY*
est.varCxz	The estimated variance of the *C* index for *scoreZ*
est.cov	The estimated covariance between the two *C* indices for *scoreY* and that for *scoreZ*
zscore	Z score (test statistic) for hypothesis testing
pval	P value for the comparison of two *C* indices

Note

Under non-random censoring, the returned *p*-value is statistically invalid as the assumption of random censoring is violated.

Author(s)

Le Kang, Weijie Chen

References

Harrell FE, Califf RM, Pryor DB, Lee KL, and Rosati RA. (1982) Evaluating the yield of medical tests. The Journal of the American Medical Association, 247(18), 2543–2546

Pencina MJ and D'Agostino RB. (2004) Overall *C* as a measure of discrimination in survival analysis: model specific population value and confidence interval estimation. Statistics in Medicine, 23(13), 2109–2123

Kang L, Chen W, Petrick NA, and Gallas BD. (2014) Comparing two correlated *C* indices with right-censored survival outcome: a one-shot nonparametric approach. Statistics in Medicine, 34(4), 685–703, doi: 10.1002/sim.6370

See Also

estC,vardiffC

Examples

```
demo(testC)
```

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estC	*Estimation of a single overall* C *index*

Description

This is a function used to estimate a single overall *C* index

Usage

```
estC(timeX, statusX, scoreY)
```

Arguments

timeX	The vector of actual survival time *X*, one survival time for each observation
statusX	The matching vector of event indicator for time *X*, 1 if occured and 0 otherwise
scoreY	The vector of the measured biomarker *Y*, one for each of the same observations, based on which the *C* index is to be estimated

Value

The estimated *C* index

Author(s)

Le Kang, Weijie Chen

References

Harrell FE, Califf RM, Pryor DB, Lee KL, and Rosati RA. (1982) Evaluating the yield of medical tests. The Journal of the American Medical Association, 247(18), 2543–2546

Pencina MJ and D'Agostino RB. (2004) Overall *C* as a measure of discrimination in survival analysis: model specific population value and confidence interval estimation. Statistics in Medicine, 23(13), 2109–2123

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See Also

[vardiffC](),[compareC]()

Examples

```
demo(testC)
```

---

vardiffC	*Variance estimation of the difference between two correlated overall* C *indices*

Description

This is a function used to estimate the variance of the difference between two correlated overall *C* indices

Usage

```
vardiffC(timeX, statusX, scoreY, scoreZ)
```

Arguments

timeX	The vector of actual survival time *X*, one survival time for each observation
statusX	The matching vector of event indicator for time *X*, 1 if occured and 0 otherwise
scoreY	The vector of the first measured biomarker *Y*, one for each of the same observations, based on which the variance of the difference in overall *C* indices is to be estimated
scoreZ	The vector of the second measured biomarker *Z*, one for each of the same observations, based on which the variance of the difference in overall *C* indices is to be estimated

Value

`est.vardiff_c`	The estimated variance of the difference of two *C* indices
`est.varCxy`	The estimated variance of the *C* index for *scoreY*
`est.varCxz`	The estimated variance of the *C* index for *scoreZ*
`est.cov`	The estimated covariance between the two *C* indices for *scoreY* and that for *scoreZ*

Author(s)

Le Kang, Weijie Chen

References

Harrell FE, Califf RM, Pryor DB, Lee KL, and Rosati RA. (1982) Evaluating the yield of medical tests. The Journal of the American Medical Association, 247(18), 2543–2546

Pencina MJ and D'Agostino RB. (2004) Overall *C* as a measure of discrimination in survival analysis: model specific population value and confidence interval estimation. Statistics in Medicine, 23(13), 2109–2123

Kang L, Chen W, Petrick NA, and Gallas BD. (2014) Comparing two correlated *C* indices with right-censored survival outcome: a one-shot nonparametric approach. Statistics in Medicine, 34(4), 685–703, doi: 10.1002/sim.6370

See Also

[estC](#),[compareC](#)

Examples

```
demo(testC)
```

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