Package ‘correctedAUC’

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Type Package

Title Correcting AUC for Measurement Error

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Depends R (>= 3.1.0), stats

Imports ICC, mnormt

Description Correcting area under ROC (AUC) for measurement error based on probit-shift model.

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Contents

`AUCest.Reiser` *Calculate AUC corrected for measurement error based on Reiser's (2000) method*

Description

Calculate AUC corrected for measurement error based on Reiser's (2000) method.

Usage

```
AUCest.Reiser(
  datFrame,
  sidVar = "subjID",
  obsVar = "y",
  grpVar = "grp",
  repVar = "myrep",
  alpha = 0.05)
```

Arguments

`datFrame`	a data frame with at least the following columns: `y`: numerical vector of observations; `subjID`: vector of subject ids; `grp`: group indicator: 1 means case; and 0 means conrol; `myrep`: integer vector indicating replication. should be consecutive positive integer starting from 1.
`sidVar`	character. variable name for subject id in the data frame `datFrame`.
`obsVar`	character. variable name for observations in the data frame `datFrame`.
`grpVar`	character. variable name for group indictor in the data frame `datFrame`.
`repVar`	character. variable name for replication indictor in the data frame `datFrame`.
`alpha`	confidence interval level $100(1-\alpha\%$

Value

A list of 4 elements

`AUC.c`	AUC corrected for measurement error based on Reiser's (2000) method.
`sd.AUC.c`	standard error of the estimated AUC corrected for measurement error based on Reiser's (2000) method.
`AUC.c.low`	lower bound of the `AUC.c`.
`AUC.c.upp`	upper bound of the `AUC.c`.

Author(s)

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References

Rosner B, Tworoger S, Qiu W (2015) Correcting AUC for Measurement Error. J Biom Biostat 6:270. doi:10.4172/2155-6180.1000270

Examples

```
set.seed(1234567)
tt=genSimDataReiser(
     nX = 100,
     nY = 100,
     sigma.X2 = 1,
     mu.X = 0.25,
     sigma.Y2 = 1,
     mu.Y = 0,
     sigma.epsilon2 = 0.5,
     sigma.eta2 = 0.5)

print(dim(tt$datFrame))
print(tt$datFrame[1:2,1:3])
print(tt$theta2)
print(tt$mu.true)
print(tt$AUC.true)

res = AUCest.Reiser(
  datFrame = tt$datFrame,
  sidVar = "subjID",
  obsVar = "y",
  grpVar = "grp",
  repVar = "myrep",
  alpha = 0.05)
print(res)
```

`AUCest.Rosner` *Calculate AUC.c for measurement error based on probit-shift model*

Description

Calculate AUC.c for measurement error based on probit-shift model.

Usage

```
AUCest.Rosner(
  datFrame,
  sidVar = "subjID",
  obsVar = "y",
  grpVar = "grp",
  repVar = "myrep",
  alpha = 0.05)
```

Arguments

`datFrame`	a data frame with at least the following columns: `y`: numerical vector of observations; `subjID`: vector of subject ids; `grp`: group indicator: 1 means case; and 0 means conrol; `myrep`: integer vector indicating replication. should be consecutive positive integer starting from 1.
`sidVar`	character. variable name for subject id in the data frame `datFrame`.
`obsVar`	character. variable name for observations in the data frame `datFrame`.
`grpVar`	character. variable name for group indictor in the data frame `datFrame`.
`repVar`	character. variable name for replication indictor in the data frame `datFrame`.
`alpha`	confidence interval level $100(1-\alpha\%$

Value

A list of 9 elements:

`AUC.obs`	AUC estimated based on the Mann-Whitney statistic.
`AUC.c`	AUC corrected for measurement error based on the probit-shift model.
`ICC.x`	intra-class correlation for cases.
`ICC.y`	intra-class correlation for controls
`mu.mle`	maximum likelihood estimate of μ (i.e., the shift between the case distribution and the control distribution after probit transformation)
`AUC.obs.low`	lower bound of the `AUC.obs`.
`AUC.obs.upp`	upper bound of the `AUC.obs`.
`AUC.c.low`	lower bound of the `AUC.c`.
`AUC.c.upp`	upper bound of the `AUC.c`.

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References

Rosner B, Tworoger S, Qiu W (2015) Correcting AUC for Measurement Error. J Biom Biostat 6:270. doi:10.4172/2155-6180.1000270

Examples

```
set.seed(1234567)
tt=genSimDataModelIII(
  nX = 100,
  nY = 100,
  mu = 0.25,
  lambda = 0,
  sigma.X2 = 1,
  sigma.Y2 = 1,
```

```
    sigma.e.X = 1,
    sigma.e.Y = 1)

  print(dim(tt$datFrame))
  print(tt$datFrame[1:2,1:3])
  print(tt$AUC.true)

  res = AUCest.Rosner(
    datFrame = tt$datFrame,
    sidVar = "subjID",
    obsVar = "y",
    grpVar = "grp",
    repVar = "myrep",
    alpha = 0.05)
  print(res)
```

`genSimDataModelII` *Generate one simulated data set based on Model II in Rosner et al's (2015) manuscript*

Description

Generate one simulated data set based on Model II in Rosner et al's (2015) manuscript.

Usage

```
genSimDataModelII(
  nX,
  nY,
  mu,
  lambda,
  sigma.X2,
  sigma.Y2,
  sigma.e.X,
  sigma.e.Y)
```

Arguments

`nX`	integer. number of cases.
`nY`	integer. number of controls.
`mu`	difference of means between the case distribution and control distribution.
`lambda`	mean for controls.
`sigma.X2`	variance of the true value for cases.
`sigma.Y2`	variance of the true value for controls.
`sigma.e.X`	variance of the random error term for cases.
`sigma.e.Y`	variance of the random error term for controls.

Details

The Model II in Rosner et al.'s (2005) manuscript:

$$X_{ik,obs} = X_{i,true} + \epsilon_{ik},\ \log\left(X_{i,true}\right) \sim N\left(\lambda + \mu, \sigma_X^2\right), \epsilon_{ik} \sim N\left(0, \sigma_\epsilon^2\right), i = 1, \ldots, n_X, k = 1, 2$$

$$Y_{jl,obs} = Y_{j,true} + \xi_{jl},\ \log\left(Y_{j,true}\right) \sim N\left(\lambda, \sigma_Y^2\right), \xi_{jl} \sim N(0, \sigma_\eta^2), j = 1, \ldots, n_Y, l = 1, 2$$

Value

A list of 2 elements:

`datFrame`	A data frame with 4 elements: `y`: observations; `subjID`: subject ID; `grp`: group indicator; `myrep`: replication indicator.
`AUC.true`	true AUC value

Author(s)

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References

Rosner B, Tworoger S, Qiu W (2015) Correcting AUC for Measurement Error. J Biom Biostat 6:270. doi:10.4172/2155-6180.1000270

Examples

```
set.seed(1234567)
tt=genSimDataModelII(
  nX = 100,
  nY = 100,
  mu = 0.25,
  lambda = 0,
  sigma.X2 = 1,
  sigma.Y2 = 1,
  sigma.e.X = 1,
  sigma.e.Y = 1)

print(dim(tt$datFrame))
print(tt$datFrame[1:2,1:3])
print(tt$AUC.true)
```

`genSimDataModelIII` *Generate one simulated data set based on Model III in Rosner et al's (2015) manuscript*

Description

Generate one simulated data set based on Model III in Rosner et al's (2015) manuscript.

Usage

```
genSimDataModelIII(
  nX,
  nY,
  mu,
  lambda,
  sigma.X2,
  sigma.Y2,
  sigma.e.X,
  sigma.e.Y)
```

Arguments

`nX`	integer. number of cases.
`nY`	integer. number of controls.
`mu`	difference of means between the case distribution and control distribution.
`lambda`	mean for controls.
`sigma.X2`	variance of the true value for cases.
`sigma.Y2`	variance of the true value for controls.
`sigma.e.X`	variance of the random error term for cases.
`sigma.e.Y`	variance of the random error term for controls.

Details

The Model III in Rosner et al.'s (2005) manuscript:

$$X_{ik,obs} = X_{i,true} + \epsilon_{ik},\ \log\left(X_{i,true}\right) \sim N\left(\lambda + \mu, \sigma_X^2\right),\ \log\left(\epsilon_{ik}\right) \sim N\left(0, \sigma_\epsilon^2\right), i = 1, \ldots, n_X, k = 1, 2$$

$$Y_{jl,obs} = Y_{j,true} + \xi_{jl},\ \log\left(Y_{j,true}\right) \sim N\left(\lambda, \sigma_Y^2\right),\ \log\left(\xi_{jl}\right) \sim N(0, \sigma_\eta^2), j = 1, \ldots, n_Y, l = 1, 2$$

Value

A list of 2 elements:

`datFrame`	A data frame with 4 elements: `y`: observations; `subjID`: subject ID; `grp`: group indicator; `myrep`: replication indicator.
`AUC.true`	true AUC value

Author(s)

Bernard Rosner <stbar@channing.harvard.edu>, Shelley Tworoger <nhsst@channing.harvard.edu>, Weiliang Qiu <stwxq@channing.harvard.edu>

References

Rosner B, Tworoger S, Qiu W (2015) Correcting AUC for Measurement Error. J Biom Biostat 6:270. doi:10.4172/2155-6180.1000270

Examples

```
set.seed(1234567)
tt=genSimDataModelIII(
  nX = 100,
  nY = 100,
  mu = 0.25,
  lambda = 0,
  sigma.X2 = 1,
  sigma.Y2 = 1,
  sigma.e.X = 1,
  sigma.e.Y = 1)

print(dim(tt$datFrame))
print(tt$datFrame[1:2,1:3])
print(tt$AUC.true)
```

`genSimDataReiser` *Generate one simulated data set based on Reiser's (2000) model*

Description

Generate one simulated data set based on Reiser's (2000) model. The true AUC will also be calculated.

Usage

```
genSimDataReiser(
  nX = 100,
  nY = 100,
  sigma.X2 = 1,
  mu.X = 0.25,
  sigma.Y2 = 1,
  mu.Y = 0,
  sigma.epsilon2 = 0.5,
  sigma.eta2 = 0.5)
```

Arguments

`nX`	integer. number of cases.
`nY`	integer. number of controls.
`sigma.X2`	variance of the true value for cases.
`mu.X`	mean of the true value for cases.
`sigma.Y2`	variance of the true value for controls.
`mu.Y`	mean of the true value for controls.
`sigma.epsilon2`	variance of the random error term for cases.
`sigma.eta2`	variance of the random error term for controls.

Details

Reiser's (2000) measurement error model is:

$$X_{ik,obs} = X_{i,true} + \epsilon_{ik}, X_{i,true} \sim N\left(\mu_X, \sigma_X^2\right), \epsilon_{ik} \sim N\left(0, \sigma_\epsilon^2\right), i = 1, \ldots, n_X, k = 1, 2$$

$$Y_{jl,obs} = Y_{j,true} + \xi_{jl}, Y_{j,true} \sim N\left(\mu_Y, \sigma_Y^2\right), \xi_{jl} \sim N(0, \sigma_\eta^2), j = 1, \ldots, n_Y, l = 1, 2$$

Value

A list of 4 elements:

`datFrame`	A data frame with 4 elements: `y`: observations; `subjID`: subject ID; `grp`: group indicator; `myrep`: replication indicator.
`theta2`	$(sigma.epsilon2 + sigma.eta2)/(sigma.X2 + sigma.Y2)$
`mu.true`	$mu.X - mu.Y$
`AUC.true`	true AUC value

Author(s)

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References

Rosner B, Tworoger S, Qiu W (2015) Correcting AUC for Measurement Error. J Biom Biostat 6:270. doi:10.4172/2155-6180.1000270

Examples

```
set.seed(1234567)
tt=genSimDataReiser(
     nX = 100,
     nY = 100,
     sigma.X2 = 1,
     mu.X = 0.25,
     sigma.Y2 = 1,
```

```
     mu.Y = 0,
     sigma.epsilon2 = 0.5,
     sigma.eta2 = 0.5)

print(dim(tt$datFrame))
print(tt$datFrame[1:2,1:3])
print(tt$theta2)
print(tt$mu.true)
print(tt$AUC.true)
```

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