

# Package ‘R2ROC’

November 24, 2023

**Title** AUC Statistics

**Version** 1.0.1

**Description** Area under the receiver operating characteristic curves (AUC) statistic for significance test. Variance and covariance of AUC values used to assess the 95% Confidence interval (CI) and p-value of the AUC difference for both nested and non-nested model.

**License** GPL (>=3)

**URL** <https://github.com/mommy003/R2ROC>

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

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**Depends** R (>= 2.10)

**LazyData** true

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auc\_diff

*auc\_diff function***Description**

This function estimates  $\text{var}(\text{AUC}(y \sim x[,v1]) - \text{AUC}(y \sim x[,v2]))$  where AUC is the Area Under ROC curve of the model,  $y$  is  $N$  by  $1$  matrix having the dependent variable, and  $x$  is  $N$  by  $M$  matrix having  $M$  explanatory variables.  $v1$  or  $v2$  indicates the  $i$ th column in the  $x$  matrix ( $v1$  or  $v2$  can be multiple values between  $1 - M$ , see Arguments below)

**Usage**

```
auc_diff(dat, v1, v2, nv, kv)
```

**Arguments**

<code>dat</code>	$N$ by $(M+1)$ matrix having variables in the order of <code>cbind(y,x)</code>
<code>v1</code>	This can be set as <code>v1=c(1)</code> or <code>v1=c(1,2)</code>
<code>v2</code>	This can be set as <code>v2=c(2)</code> , <code>v2=c(3)</code> , <code>v2=c(1,3)</code> or <code>v2=c(3,4)</code>
<code>nv</code>	Sample size
<code>kv</code>	Population prevalence

**Value**

This function will estimate significant difference between two PRS (either dependent or independent and joint or single). To get the test statistics for the difference between  $\text{AUC}(y \sim x[,v1])$  and  $\text{AUC}(y \sim x[,v2])$  (here we define  $\text{AUC1} = \text{AUC}(y \sim x[,v1])$  and  $\text{AUC2} = \text{AUC}(y \sim x[,v2])$ ). The outputs are listed as follows.

<code>mean_diff</code>	AUC differences between AUC1 and AUC2
<code>var</code>	Variances of AUC differences
<code>upper_diff</code>	Upper value of the differences
<code>lower_diff</code>	Lower value of the differences
<code>p</code>	Two tailed P-value for significant difference between AUC1 and AUC2
<code>p_one_tail</code>	One tailed P-value for significant difference
<code>heller_p</code>	P-value based on Heller's test for significant difference
<code>heller_upper_diff</code>	Upper limit of 95% CI for the difference based on Heller's test
<code>heller_lower_diff</code>	Lower limit of 95% CI for the difference based on Heller's test

**Examples**

```
#To get the test statistics for the difference between AUC(y=x[,1])
#and AUC(y=x[,2])
dat=dat1 #(this example embedded within the package)
nv=length(dat$V1)
kv=sum(dat$V1)/length(dat$V1)# pop. prevalence estimated from data
#R2ROC also allows users to estimate AUC using pre-adjusted phenotype
```

```

#In that case, users need to specify kv
#eg. kv=0.10 for dat2 (dat2 embedded within the package)
v1=c(1)
v2=c(2)
output=auc_diff(dat,v1,v2,nv,kv)

#R2ROC output
#output$mean_diff (mean difference of AUC1 and AUC2)
#0.1756046

#output$var (variance of AUC difference)
#9.274356e-05

#output$upper_diff (upper limit of 95% CI for difference)
#0.1944801

#output$lower_diff (lower limit of 95% CI for difference)
#0.1567292

#output$p (two-tailed P-value for the differences is
#significantly different from zero)
#2.747031e-74

#output$p_one_tail (one-tailed P-value for the differences
#is significantly different from zero)
#1.373515e-74

#To get the test statistics for the difference between
#AUC(y=x[,1]+x[,2]) and AUC(y=x[,2])
dat=dat1 #(this example embedded within the package)
nv=length(dat$V1)
kv=sum(dat$V1)/length(dat$V1)# pop. prevalence estimated from data
#R2ROC also allows users to estimate AUC using pre-adjusted phenotype
#In that case, users need to specify kv
#eg. kv=0.10 for dat2 (dat2 embedded within the package)
v1=c(1,2)
v2=c(2)
output=auc_diff(dat,v1,v2,nv,kv)

#R2ROC output
#output$mean_diff (mean difference of AUC1 and AUC2)
#0.1793682

#output$var (variance of AUC difference)
#0.0001190366

#output$upper_diff (upper limit of 95% CI for difference)
#0.2007526

#output$lower_diff (lower limit of 95% CI for difference)
#0.1579839

#output$p (two-tailed P-value for the differences is
#significantly different from zero)
#9.87014e-61

```

```
#output$p_one_tail (one-tailed P-value for the differences
#is significantly different from zero)
#4.93507e-61

#output$heller_p (two-tailed P-value based on Hellers test
#for the differences is significantly different from zero)
#4.2085e-237

#output$heller_upper_diff (upper limit of 95% CI for
#difference based on Hellers test)
#0.2013899

#output$heller_lower_diff (lower limit of 95% CI for
#difference based on Hellers test)
#0.1586212
```

---

auc\_trf

*auc\_trf* function

---

## Description

This function transforms the observed scale predictive ability (R2) and its standard error (SE) to AUC with its SE

## Usage

```
auc_trf(R2, se, kv)
```

## Arguments

R2	R2 or coefficient of determination on the observed scale
se	Standard error of R2
kv	Population prevalence

## Value

This function will transform the observed R2 and its s.e between to AUC. Output from the command is the lists of outcomes.

auc	Transformed AUC
se	SE of transformed AUC

## References

Wray, Naomi R., et al. "The genetic interpretation of area under the ROC curve in genomic profiling." *PLoS genetics* 6.2 (2010): e1000864.

Lee, Sang Hong, et al. "A better coefficient of determination for genetic profile analysis." *Genetic epidemiology* 36.3 (2012): 214-224.

## Examples

```
#To get the transformed AUC

output=auc_trf(0.04, 0.002, 0.05)
output

#output$auc (transformed AUC)
#0.7522887

#output$se (se of transformed AUC)
#0.005948364
```

---

auc\_var

*auc\_var function*

---

## Description

This function estimates  $\text{var}(\text{AUC}(y \sim x[,v1]))$  where AUC is the Area Under ROC curve of the model, y is N by 1 matrix having the dependent variable, and x is N by M matrix having M explanatory variables. v1 indicates the ith column in the x matrix (v1 can be multiple values between 1 - M, see Arguments below)

## Usage

```
auc_var(dat, v1, nv, kv)
```

## Arguments

dat	N by (M+1) matrix having variables in the order of cbind(y,x)
v1	This can be set as v1=c(1), v1=c(1,2) or possibly with more values
nv	Sample size
kv	Population prevalence

## Value

This function will test the null hypothesis for AUC. To get the test statistics for  $\text{AUC}(y \sim x[,v1])$ . The outputs are listed as follows.

auc	AUC
var	Variance of AUC
upper_auc	Upper limit of 95% CI for AUC
lower_auc	Lower limit of 95% CI for AUC

## Examples

```
#To get the AUC for AUC(y=x[,1])

dat=dat1 #(this example embedded within the package)
nv=length(dat$V1)
kv=sum(dat$V1)/length(dat$V1)# pop. prevalence estimated from data
#R2ROC also allows users to estimate AUC using pre-adjusted phenotype
#In that case, users need to specify kv
#eg. kv=0.10 for dat2 (dat2 embedded within the package)
v1=c(1)
output=auc_var(dat,v1,nv,kv)

#R2ROC output
#output$auc (AUC)
#0.7390354

#output$var (variance of AUC)
#7.193337e-05

#output$upper_auc (upper limit of 95% CI for AUC)
#0.7556589

#output$lower_auc (lower limit of 95% CI for AUC)
#0.7224119

#output$p
9.28062e-175 (two-tailed P-value for the AUC is significantly different from 0.5)

#output$p_one_tail (one-tailed P-value for the AUC is significantly different from 0.5)
4.64031e-175
```

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dat1

*Raw phenotypes and 2 sets of discovery PGSs*


---

## Description

A dataset containing raw phenotypes and multiple PGSs estimated two independent discovery population

## Usage

```
dat1
```

## Format

A data frame with 10000 rows and 3 variables:

**V1** Phenotype, raw case-control data

**V2** PGS1, for discovery population 1

**V3** PGS2, for discovery population 2

dat2

*Pre-adjusted phenotypes and 2 sets of discovery PGSs***Description**

A dataset containing preadjusted phenotypes and multiple PGSs estimated two independent discovery population

**Usage**

dat2

**Format**

A data frame with 10000 rows and 3 variables:

**V1** Phenotype, preadjusted case-control data

**V2** PGS1, for discovery population 1

**V3** PGS2, for discovery population 2

olkin\_auc1

*olkin\_auc1 function***Description**

olkin\_auc1 function

**Usage**

```
olkin_auc1(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. $\text{omat} = \text{cor}(\text{dat})$ where dat is N by 3 matrix having variables in the order of cbind(y, x1, x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code

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olkin_auc12	<i>olkin_auc12 function</i>
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**Description**

olkin\_auc12 function

**Usage**

```
olkin_auc12(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. $\text{omat} = \text{cor}(\text{dat})$ where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code

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olkin_auc12_1	<i>olkin_auc12_1 function</i>
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**Description**

olkin\_auc12\_1 function

**Usage**

```
olkin_auc12_1(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. $\text{omat} = \text{cor}(\text{dat})$ where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code



---

olkin\_auc12\_13      *olkin\_auc12\_13 function*


---

**Description**

olkin\_auc12\_13 function

**Usage**

```
olkin_auc12_13(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. $\text{omat} = \text{cor}(\text{dat})$ where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code

---

olkin\_auc12\_3      *olkin\_auc12\_3 function*


---

**Description**

olkin\_auc12\_3 function

**Usage**

```
olkin_auc12_3(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. $\text{omat} = \text{cor}(\text{dat})$ where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code

---

olkin\_auc12\_34      *olkin\_auc12\_34 function*


---

**Description**

olkin\_auc12\_34 function

**Usage**

```
olkin_auc12_34(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. omat=cor(dat) where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code

---

olkin\_auc1\_2      *olkin\_auc1\_2 function*


---

**Description**

olkin\_auc1\_2 function

**Usage**

```
olkin_auc1_2(omat, nv, kv)
```

**Arguments**

omat	3 by 3 matrix having the correlation coefficients between y, x1 and x2, i.e. omat=cor(dat) where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size
kv	Population prevalence

**Value**

This function will be used as source code

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