

Package ‘r2redux’

May 25, 2022

Title R2 Statistic

Version 1.0.4

Author Hong Lee, Moksedul Momin

Maintainer Moksedul Momin <cvasu.momin@gmail.com>

Description R2 statistic for significance test.

License GPL (>=3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

NeedsCompilation no

R topics documented:

cc_trf	1
olkin_beta1_2	2
olkin_beta_inf	3
r2_diff	4
r2_enrich	6
r2_enrich_beta	7
r2_var	8

Index	10
--------------	-----------

cc_trf	<i>cc_trf</i> function
--------	------------------------

Description

This function transforms the predictive ability (R2) and its standard error (se) between the observed scale and liability scale

Usage

```
cc_trf(R2, se, K, P)
```

Arguments

R2	R2 or Coefficient of determination on the observed or liability scale
se	Standard error of R2
K	Population prevalence
P	The ratio of cases in the study samples

References

Lee, S. H., Goddard, M. E., Wray, N. R., and Visscher, P. M. A better coefficient of determination for genetic profile analysis. *Genetic epidemiology*,(2012). 36(3): p. 214-224.

Examples

```
To get the transformed R2
output=cc_trf(0.06, 0.002, 0.05, 0.05)

output$R2l (transformed R2 to the liability scale)
0.2679337

output$se1 (transformed se to the liability scale)
0.008931123

output$R2O (transformed R2 to the observed scale)
0.01343616

output$seO (transformed se to the observed scale)
0.000447872
```

olkin_beta1_2	<i>olkin_beta1_2 function</i>
---------------	-------------------------------

Description

This function derives Information matrix for β_1^2 and β_2^2 where β_1 and β_2 are regression coefficients from a multiple regression model, i.e. $y = x_1 \cdot \beta_1 + x_2 \cdot \beta_2 + e$, where y , x_1 and x_2 are column-standardised, (i.e. in the context of correlation coefficients, see Olkin and Finn 1995).

Usage

```
olkin_beta1_2(omat, nv)
```

Arguments

omat	3 by 3 matrix having the correlation coefficients between y , x_1 and x_2 , i.e. $\text{omat} = \text{cor}(\text{dat})$ where dat is N by 3 matrix having variables in the order of $\text{cbind}(y, x_1, x_2)$
nv	sample size

References

Olkin, I. and J.D. Finn, Correlations redux. Psychological Bulletin, 1995. 118(1): p. 155. Momin, M.M., Lee, S. Wray, N. and S. Lee, S.H. The variance and covariance of the coefficients of determination for genetic profile analysis (will be subbitted soon)

Examples

To get information (variance-covariance) matrix of β_1^2 and β_2^2 where β_1 and 2 are regression coefficients from a multiple regression model.

```
dat=read.table("test_ukbb_thresholds_scaled") (see example files)
omat=cor(dat)[1:3,1:3]
omat
1.0000000 0.1958636 0.1970060
0.1958636 1.0000000 0.9981003
0.1970060 0.9981003 1.0000000

nv=length(dat$V1)
output=olkin_beta1_2(omat,nv)
output

output$info (2x2 information (variance-covariance) matrix)
0.04146276 0.08158261
0.08158261 0.16111124

output$var1 (variance of  $\beta_1^2$ )
0.04146276

output$var2 (variance of  $\beta_2^2$ )
0.1611112

output$var1_2 (variance of difference between  $\beta_1^2$  and  $\beta_2^2$ )
0.03940878
```

olkin_beta_inf	<i>olkin_beta_inf</i> function
----------------	--------------------------------

Description

This function derives Information matrix for β_1 and β_2 where β_1 and 2 are regression coefficients from a multiple regression model, i.e. $y = x_1 \cdot \beta_1 + x_2 \cdot \beta_2 + e$, where y , x_1 and x_2 are column-standardised (see Olkin and Finn 1995).

Usage

```
olkin_beta_inf(omat, nv)
```

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

References

Olkin, I. and J.D. Finn, Correlations redux. Psychological Bulletin, 1995. 118(1): p. 155.

Examples

To get information (variance-covariance) matrix of β_1^2 and β_2^2 where β_1 and 2 are regression coefficients from a multiple regression model.

```
dat=read.table("test_ukbb_thresholds_scaled") (see example files)
omat=cor(dat)[1:3,1:3]
omat
1.0000000 0.1958636 0.1970060
0.1958636 1.0000000 0.9981003
0.1970060 0.9981003 1.0000000

nv=length(dat$V1)
output=olkin_beta_inf(omat,nv)
output

output$info (2x2 information (variance-covariance) matrix)
0.2531406 -0.2526212
-0.2526212 0.2530269

output$var1 (variance of  $\beta_1^2$ )
0.2531406

output$var2 (variance of  $\beta_2^2$ )
0.2530269

output$var1_2 (variance of difference between  $\beta_1^2$  and  $\beta_2^2$ )
1.01141
```

r2_diff

r2_diff function

Description

This function estimates $\text{var}(R^2(y \sim x[,v1]) - R^2(y \sim x[,v2]))$ where R^2 is the R squared value 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 ith column in the x matrix (v1 or v2 can be multiple values between 1 - M, see Arguments below)

Usage

```
r2_diff(dat, v1, v2, nv)
```

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) or v1=c(1,2)
v2	This can be set as v2=c(2), v2=c(3), v2=c(1,3) or v2=c(3,4)
nv	sample size

Examples

To get the test statistics for the difference between $R2(y \sim x[,v1])$ and $R2(y \sim x[,v2])$. (here we define $R2_1 = R2(y \sim x[,v1])$ and $R2_2 = R2(y \sim x[,v2])$)

```
dat=read.table("test_ukbb_thresholds_scaled") (see example files)
nv=length(dat$V1)
v1=c(1)
v2=c(2)
output=r2_diff(dat,v1,v2,nv)
output

r2redux output

output$var1 (variance of R2_1)
0.0001437583

output$var2 (variance of R2_2)
0.0001452828

output$var_diff (variance of difference between R2_1 and R2_2)
5.678517e-07

output$r2_based_p (p-value for significant difference between R2_1 and R2_2)
0.5514562

output$mean_diff (differences between R2_1 and R2_2)
-0.0004488044

output$upper_diff (upper limit of 95% CI for the difference)
0.001028172

output$lower_diff (lower limit of 95% CI for the difference)
-0.001925781
```

To get the test statistics for the difference between $R2(y \sim x[,v1] + x[,v2])$ and $R2(y \sim x[,v2])$. (here $R2_1 = R2(y \sim x[,v1] + x[,v2])$ and $R2_2 = R2(y \sim x[,v1])$)

```
dat=read.table("test_ukbb_thresholds_scaled") (see example files)
nv=length(dat$V1)
v1=c(1,2)
v2=c(1)
output=r2_diff(dat,v1,v2,nv)
output

r2redux output
```

```

output$var1 (variance of R2_1)
0.0001475195

output$var2 (variance of R2_2)
0.0001437583

output$var_diff (variance of difference between R2_1 and R2_2)
2.321425e-06

output$r2_based_p (p-value for significant difference between R2_1 and R2_2)
0.4369177

output$mean_diff (differences between R2_1 and R2_2)
0.0006042383

output$upper_diff (upper limit of 95% CI for the difference)
0.004887989

output$lower_diff (lower limit of 95% CI for the difference)
-0.0005574975

```

r2_enrich

r2_enrich

Description

This function estimates $\text{var}(t1/(t1+t2))$ where $t1 = R2(y \sim x[,v1] + x[,v2]) - R2(y \sim x[,v1])$ and $t2 = R2(y \sim x[,v1] + x[,v2]) - R2(y \sim x[,v2])$ where $R2$ is the R squared value 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 $v2$ should be a single interger between $1 - M$, see Arguments below)

Usage

```
r2_enrich(dat, v1, v2, nv, expl)
```

Arguments

dat	N by $(M+1)$ matrix having variables in the order of <code>cbind(y,x)</code>
nv	sample size
expl	The expectation of the ratio (e.g. # SNPs for the genomic region of interest / total # SNPs in genomic partitioning)
v1/v2	These can be set as $v1=1$ and $v2=2$, $v1=2$ and $v2=1$, $v1=3$ and $v2=2$, or any combination as long as the value is between $1 - M$

r2_enrich_beta	r2_enrich_beta
----------------	----------------

Description

This function estimates $\text{var}(t1/(t1+t2))$ where $t1 = \text{beta1}^2$ and $t2 = \text{beta2}^2$, and beta1 and beta2 are regression coefficients from a multiple regression model, i.e. $y = x1\beta_1 + x2\beta_2 + e$, where y , $x1$ and $x2$ are column-standardised (see Olkin and Finn 1995). y is N by 1 matrix having the dependent variable, and $x1$ is N by 1 matrix having the i th explanatory variables. $x2$ is N by 1 matrix having the j th explanatory variables. $v1$ and $v2$ indicates the i th and j th column in the data ($v1$ or $v2$ should be a single interger between $1 - M$, see Arguments below). Note that $r2_enrich$ (above) and $r2_enrich_beta$ is equivalent (identical p-value derived).

Usage

```
r2_enrich_beta(dat, v1, v2, nv, exp1)
```

Arguments

dat	N by $(M+1)$ matrix having variables in the order of <code>cbind(y,x)</code>
nv	sample size
exp1	The expectation of the ratio (e.g. ratio of # SNPs in genomic partitioning)
v1/v2	These can be set as $v1=1$ and $v2=2$, $v1=2$ and $v2=1$, $v1=3$ and $v2=2$, or any combination as long as the value is between $1 - M$

References

Olkin, I. and J.D. Finn, Correlations redux. Psychological Bulletin, 1995. 118(1): p. 155.

Examples

```
To get the test statistic for the ratio which is significantly
different from the expectation.
var(t1/(t1+t2)), where t1 = beta1^2 and t2 = beta2^2.
beta1 and beta2 are regression coefficients from a multiple regression model,
i.e.  $y = x1\beta_1 + x2\beta_2 + e$ , where  $y$ ,  $x1$  and  $x2$  are column-standardised
```

```
dat=read.table("test_ukbb_enrichment_choles") (see example file)
nv=length(dat$V1)
v1=c(1)
v2=c(2)
expected_ratio=0.04
output=r2_enrich_beta(dat,v1,v2,nv,expected_ratio)
output
```

```
r2redux output
```

```
output$var1 (variance of t1)
7.072931e-05
```

```
output$var2 (variance of t2)
```

```

3.161929e-05

output$var1_2 (difference between t1 and t2)
0.000162113

output$beta1_sq (t1)
0.01118301

output$beta2_sq (t2)
0.004980285

output$cov (covariance between t1 and t2)
-2.988221e-05

output$enrich_p2 (p-value for testing the difference between t1/exp and t2/(1-exp))
0.1997805

output$mean_diff (difference between t1/exp and t2/(1-exp))
0.2743874

output$var_diff (variance of difference, t1/exp - t2/(1-exp))
0.04579649

output$upper_diff (upper limit of 95% CI for the mean difference)
0.6938296

output$lower_diff (lower limit of 95% CI for the mean difference)
-0.1450549

```

r2_var

r2_var function

Description

This function estimates $\text{var}(R^2(y \sim x[,v1]))$ where R^2 is the R squared value of the model, where R^2 is the R squared value 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 i th column in the x matrix ($v1$ can be multiple values between $1 - M$, see Arguments below)

Usage

```
r2_var(dat, v1, nv)
```

Arguments

dat	N by $(M+1)$ matrix having variables in the order of <code>cbind(y,x)</code>
v1	This can be set as <code>v1=c(1)</code> , <code>v1=c(1,2)</code> or possibly with more values
nv	sample size

Examples

To get the test statistics for $R^2(y \sim x[,v1])$

```
dat=read.table("test_ukbb_thresholds_scaled") (see example file)
nv=length(dat$V1)
v1=c(1)
output=r2_var(dat,v1,nv)
```

r2redux output

```
output$var (variance of R2)
0.0001437583
```

```
output$r2_based_p (P-value under the null hypothesis, i.e.  $R^2=0$ )
1.213645e-10
```

```
output$mean_r2 (R2)
0.03836254
```

```
output$upper_r2 (upper limit of 95% CI for R2)
0.06435214
```

```
output$lower_r2 (lower limit of 95% CI for R2)
0.01763347
```

To get the test statistic for $R^2(y \sim x[,v1]+x[,v2]+x[,v3])$

```
dat=read.table("test_ukbb_thresholds_scaled") (see example file)
nv=length(dat$V1)
v1=c(1,2,3)
outout=r2_var(dat,v1,nv)
output
```

r2redux output

```
output$var (variance of R2)
0.0001499374
```

```
output$r2_based_p (R2 based P-value)
7.461267e-11
```

```
output$mean_r2 (R2)
0.03917668
```

```
output$upper_r2 (upper limit of 95% CI for R2)
0.06538839
```

```
output$lower_r2 (lower limit of 95% CI for R2)
0.01821657
```

Index

- *Topic **R2**
 - cc_trf, 1
 - r2_diff, 4
 - r2_enrich, 6
 - r2_var, 8
- *Topic **Transformation**
 - cc_trf, 1
- *Topic **and**
 - cc_trf, 1
- *Topic **a**
 - r2_enrich_beta, 7
- *Topic **beta²**
 - r2_enrich_beta, 7
- *Topic **between**
 - cc_trf, 1
 - r2_enrich, 6
 - r2_enrich_beta, 7
- *Topic **context**
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
- *Topic **correlation**
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
- *Topic **from**
 - r2_enrich_beta, 7
- *Topic **information**
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
 - r2_diff, 4
 - r2_var, 8
- *Topic **in**
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
- *Topic **liability**
 - cc_trf, 1
- *Topic **matrix**
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
 - r2_diff, 4
 - r2_var, 8
- *Topic **multiple**
 - r2_enrich_beta, 7
- *Topic **observed**
 - cc_trf, 1
- *Topic **of**
 - cc_trf, 1
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
 - r2_enrich, 6
 - r2_enrich_beta, 7
- *Topic **ratio**
 - r2_enrich, 6
 - r2_enrich_beta, 7
- *Topic **regression**
 - r2_enrich_beta, 7
- *Topic **scale**
 - cc_trf, 1
- *Topic **the**
 - olkin_beta1_2, 2
 - olkin_beta_inf, 3
- *Topic **variance**
 - r2_diff, 4
 - r2_enrich, 6
 - r2_enrich_beta, 7
 - r2_var, 8
- cc_trf, 1
- olkin_beta1_2, 2
- olkin_beta_inf, 3
- r2_diff, 4
- r2_enrich, 6
- r2_enrich_beta, 7
- r2_var, 8