

Package ‘r2redux’

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Title R2 Statistic

Version 1.0.8

Description R2 statistic for significance test. Variance and covariance of R2 values used to assess the 95% CI and p-value of the R2 difference.

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LazyData true

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R topics documented:

cc_trf	2
dat1	3
dat2	3
olkin12_1	4
olkin12_13	4
olkin12_3	5
olkin12_34	5
olkin1_2	6
olkin_beta1_2	6
olkin_beta_inf	7
r2_diff	8
r2_enrich_beta	11
r2_var	13
Index	15

cc_trf

*cc_trf 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

Value

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

R2l	Transformed R2 on the liability scale
sel	Transformed se on the liability scale
R2O	Transformed R2 on the observed scale
seO	Transformed se on the observed scale

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

#output$R2l (transformed R2 on the liability scale)
#0.2679337

#output$sel (transformed se on the liability scale)
#0.008931123

#output$R2O (transformed R2 on the observed scale)
#0.01343616

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

dat1	<i>Phenotypes and 10 sets of PGSs</i>
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Description

A dataset containing phenotypes and multiple PGSs estimated from 10 sets of SNPs according to GWAS p-value thresholds

Usage

dat1

Format

A data frame with 1000 rows and 11 variables:

- V1** Phenotype, value
- V2** PGS1, for p value threshold ≤ 1
- V3** PGS2, for p value threshold ≤ 0.5
- V4** PGS3, for p value threshold ≤ 0.4
- V5** PGS4, for p value threshold ≤ 0.3
- V6** PGS5, for p value threshold ≤ 0.2
- V7** PGS6, for p value threshold ≤ 0.1
- V8** PGS7, for p value threshold ≤ 0.05
- V9** PGS8, for p value threshold ≤ 0.01
- V10** PGS9, for p value threshold ≤ 0.001
- V11** PGS10, for p value threshold ≤ 0.0001

dat2	<i>Phenotypes and 2 sets of PGSs</i>
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Description

A dataset containing phenotypes and 2 sets of PGSs estimated from 2 sets of SNPs from regulatory and non-regulatory genomic regions

Usage

dat2

Format

A data frame with 1000 rows and 3 variables:

- V1** Phenotype
- V2** PGS1, regulatory region
- V3** PGS2, non-regulatory region

olkin12_1	<i>olkin12_1 function</i>
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Description

olkin12_1 function

Usage

```
olkin12_1(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

Value

This function will be used as source code

olkin12_13	<i>olkin12_13 function</i>
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Description

olkin12_13 function

Usage

```
olkin12_13(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

Value

This function will be used as source code

`olkin12_3`*olkin12_3 function*

Description

olkin12_3 function

Usage

```
olkin12_3(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 <code>cbind(y, x1, x2)</code>
nv	Sample size

Value

This function will be used as source code

`olkin12_34`*olkin12_34 function*

Description

olkin12_34 function

Usage

```
olkin12_34(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 <code>cbind(y, x1, x2)</code>
nv	Sample size

Value

This function will be used as source code

olkin1_2	<i>olkin1_2 function</i>
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Description

olkin1_2 function

Usage

```
olkin1_2(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

Value

This function will be used as source code

olkin_beta1_2	<i>olkin_beta1_2 function</i>
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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, x1 and x2 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, 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

Value

This function will give information (variance-covariance) matrix of β_1^2 and β_2^2 . To get information (variance-covariance) matrix of β_1^2 and β_2^2 . Where β_1 and β_2 are regression coefficients from a multiple regression model. The outputs are listed as follows.

info	2x2 information (variance-covariance) matrix
var1	Variance of β_1^2
var2	Variance of β_2^2
var1_2	Variance of difference between β_1^2 and β_2^2

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 beta1_2 and beta2_2 where
#beta1 and 2 are regression coefficients from a multiple regression model.
dat=dat1
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 beta1^2)
#0.04146276

#output$var2 (variance of beta2^2)
#0.1611112

#output$var1_2 (variance of difference between beta1^2 and beta2^2)
#0.03940878
```

olkin_beta_inf	<i>olkin_beta_inf function</i>
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Description

This function derives Information matrix for beta1 and beta2 where beta1 and 2 are regression coefficients from a multiple regression model, i.e. $y = x1 * beta1 + x2 * beta2 + e$, where y, x1 and x2 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. $omat=cor(dat)$ where dat is N by 3 matrix having variables in the order of cbind(y,x1,x2)
nv	Sample size

Value

This function will generate information (variance-covariance) matrix of beta1 and beta2. The outputs are listed as follows.

info	2x2 information (variance-covariance) matrix
var1	Variance of beta1
var2	Variance of beta2
var1_2	Variance of difference between beta1 and beta2

References

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

Examples

```
#To get information (variance-covariance) matrix of beta1 and beta2 where
#beta1 and 2 are regression coefficients from a multiple regression model.
dat=dat1
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 beta1)
#0.2531406

#output$var2 (variance of beta2)
#0.2530269

#output$var1_2 (variance of difference between beta1 and beta2)
#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 i th 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

Value

This function will estimate significant difference between two PGS (either dependent or independent and joint or single). 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 $R2_2 = R2(y \sim x[,v2])$). The outputs are listed as follows.

rsq1	R2_1
rsq2	R2_2
var1	Variance of R2_1
var2	variance of R2_2
var_diff	Variance of difference between R2_1 and R2_2
r2_based_p	P-value for significant difference between R2_1 and R2_2
mean_diff	Differences between R2_1 and R2_2
upper_diff	Upper limit of 95% CI for the difference
lower_diff	Lower limit of 95% CI for the difference

Examples

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

dat=dat1
nv=length(dat$V1)
v1=c(1)
v2=c(2)
output=r2_diff(dat,v1,v2,nv)
output

#r2redux output

#output$rsq1 (R2_1)
#0.03836254

#output$rsq2 (R2_2)
#0.03881135

#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~x[,v1]+x[,v2]) and
#R2(y~x[,v2]). (here R2_1=R2(y~x[,v1]+x[,v2]) and R2_2=R2(y~x[,v1]))

dat=dat1
nv=length(dat$V1)
v1=c(1,2)
v2=c(1)
output=r2_diff(dat,v1,v2,nv)

#r2redux output

#output$rsq1 (R2_1)
#0.03896678

#output$rsq2 (R2_2)
#0.03836254

#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_beta	r2_enrich_beta
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Description

This function estimates $\text{var}((t1/\text{exp}) - (t2/(1-\text{exp})))$, where $t1 = \text{beta1}^2$ and $t2 = \text{beta2}^2$, and beta1 and beta2 are regression coefficients from a multiple regression model, i.e. $y = x1.\text{beta1} + x2.\text{beta2} + e$, 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, expl)
```

Arguments

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

Value

This function will test the ratio which is significantly different from the expectation. To get the test statistic for the ratio which is significantly different from the expectation. $\text{var}[(t1/\text{exp}) - (t2/(1-\text{exp}))]$, where $t1 = \text{beta1}^2$ and $t2 = \text{beta2}^2$. beta1 and beta2 are regression coefficients from a multiple regression model, i.e. $y = x1.\text{beta1} + x2.\text{beta2} + e$, where y , $x1$ and $x2$ are column-standardised. The outputs are listed as follows.

beta1_sq	$t1$
beta2_sq	$t2$
var1	Variance of $t1$
var2	Variance of $t2$
var1_2	Variance of difference between $t1$ and $t2$
cov	Covariance between $t1$ and $t2$
enrich_p2	P-value for testing the difference between $t1/\text{exp}$ and $t2/(1-\text{exp})$
mean_diff	Difference between $t1/\text{exp}$ and $t2/(1-\text{exp})$
var_diff	Variance of difference, $t1/\text{exp} - t2/(1-\text{exp})$
upper_diff	Upper limit of 95% CI for the mean difference
lower_diff	Lower limit of 95% CI for the mean difference

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/exp) - (t2/(1-exp))], where t1 = beta1^2 and t2 = beta2^2.
#beta1 and beta2 are regression coefficients from a multiple regression model,
#i.e. y = x1.beta1 + x2.beta2 + e, where y, x1 and x2 are column-standardised.

dat=dat2
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$beta1_sq (t1)
#0.01118301

#output$beta2_sq (t2)
#0.004980285

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

#output$var2 (variance of t2)
3.161929e-05

#output$var1_2 (variance of difference between t1 and t2)
#0.000162113

#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

<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> , <code>v1=c(1,2)</code> or possibly with more values
<code>nv</code>	Sample size

Value

This function will test the null hypothesis for R^2 . To get the test statistics for $R^2(y \sim x[,v1])$. The outputs are listed as follows.

<code>rsq</code>	R^2
<code>var</code>	Variance of R^2
<code>r2_based_p</code>	P-value under the null hypothesis, i.e. $R^2=0$
<code>upper_r2</code>	Upper limit of 95% CI for R^2
<code>lower_r2</code>	Lower limit of 95% CI for R^2

Examples

```
#To get the test statistics for R2(y~x[,v1])
dat=dat1
nv=length(dat$V1)
v1=c(1)
output=r2_var(dat,v1,nv)
output

#r2redux output

#output$rsq (R2)
#0.03836254

#output$var (variance of R2)
#0.0001437583

#output$r2_based_p (P-value under the null hypothesis, i.e. R2=0)
#1.213645e-10
```

```
#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 R2 (y~x[,v1]+x[,v2]+x[,v3])

dat=dat1
nv=length(dat$V1)
v1=c(1,2,3)
r2_var(dat,v1,nv)

#r2redux output

#output$rsq (R2)
#0.03917668

#output$var (variance of R2)
#0.0001499374

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

#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, [2](#)
 - r2_diff, [8](#)
 - r2_var, [13](#)
 - *Topic **Transformation**
 - cc_trf, [2](#)
 - *Topic **and**
 - cc_trf, [2](#)
 - *Topic **a**
 - r2_enrich_beta, [11](#)
 - *Topic **beta^2**
 - r2_enrich_beta, [11](#)
 - *Topic **between**
 - cc_trf, [2](#)
 - r2_enrich_beta, [11](#)
 - *Topic **context**
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - *Topic **correlation**
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - *Topic **datasets**
 - dat1, [3](#)
 - dat2, [3](#)
 - *Topic **from**
 - r2_enrich_beta, [11](#)
 - *Topic **information**
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - r2_diff, [8](#)
 - r2_var, [13](#)
 - *Topic **in**
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - *Topic **liability**
 - cc_trf, [2](#)
 - *Topic **matrix**
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - r2_diff, [8](#)
 - r2_var, [13](#)
 - *Topic **multiple**
 - r2_enrich_beta, [11](#)
 - *Topic **observed**
 - cc_trf, [2](#)
 - *Topic **of**
 - cc_trf, [2](#)
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - r2_enrich_beta, [11](#)
 - *Topic **ratio**
 - r2_enrich_beta, [11](#)
 - *Topic **regression**
 - r2_enrich_beta, [11](#)
 - *Topic **scale**
 - cc_trf, [2](#)
 - *Topic **source**
 - olkin12_1, [4](#)
 - olkin12_13, [4](#)
 - olkin12_3, [5](#)
 - olkin12_34, [5](#)
 - olkin1_2, [6](#)
 - *Topic **the**
 - olkin_beta1_2, [6](#)
 - olkin_beta_inf, [7](#)
 - *Topic **variance**
 - r2_diff, [8](#)
 - r2_enrich_beta, [11](#)
 - r2_var, [13](#)
- cc_trf, [2](#)
- dat1, [3](#)
- dat2, [3](#)
- olkin12_1, [4](#)
- olkin12_13, [4](#)
- olkin12_3, [5](#)
- olkin12_34, [5](#)
- olkin1_2, [6](#)
- olkin_beta1_2, [6](#)
- olkin_beta_inf, [7](#)
- r2_diff, [8](#)
- r2_enrich_beta, [11](#)
- r2_var, [13](#)