

# Package ‘r2redux’

August 9, 2023

**Title** R2 Statistic

**Version** 1.0.14

**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.

**License** GPL (>= 3)

**URL** <https://github.com/mommy003/r2redux>

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**NeedsCompilation** no

**Depends** R (>= 2.10)

**LazyData** true

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

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**Repository** CRAN

**Date/Publication** 2023-08-09 08:50:02 UTC

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cc_trf	<i>cc_trf function</i>
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**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
se1	Transformed se on the liability scale
R20	Transformed R2 on the observed scale
se0	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$se1 (transformed se on the liability scale)
#0.008931123

#output$R20 (transformed R2 on the observed scale)
#0.01343616

#output$se0 (transformed se on the observed scale)
#0.000447872
```

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

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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

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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)
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nv	Sample size
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**Value**

This function will be used as source code

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olkin12\_13*olkin12\_13 function*

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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 cbind(y,x1,x2)
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. 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 be used as source code

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olkin1\_2

*olkin1\_2 function*


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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. 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 be used as source code

olkin\_beta1\_2

*olkin\_beta1\_2 function***Description**

This function derives Information matrix for  $\beta_1^2$  and  $\beta_2^2$  where  $\beta_1$  and  $\beta_2$  are regression coefficients from a multiple regression model, i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , 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 $\text{dat}$ is $N$ by 3 matrix having variables in the order of $\text{cbind}(y, x_1, x_2)$
nv	Sample size

**Value**

This function will give information (variance-covariance) matrix of  $\beta_1^2$  and  $\beta_2^2$ . To get information (variance-covariance) matrix of  $\beta_1^2$  and  $\beta_2^2$ . Where  $\beta_1$  and  $\beta_2$  are regression coefficients from a multiple regression model. The outputs are listed as follows.

info	2x2 information (variance-covariance) matrix
var1	Variance of $\beta_1^2$
var2	Variance of $\beta_2^2$
var1_2	Variance of difference between $\beta_1^2$ and $\beta_2^2$

**References**

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

**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

```

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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.  $y = x1 * \beta_1 + x2 * \beta_2 + e$ , 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 Finn, J.D. 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
```

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olkin_beta_ratio	<i>olkin_beta_ratio function</i>
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## Description

This function derives variance of  $\beta_1^2 / R^2$  where  $\beta_1$  and  $\beta_2$  are regression coefficients from a multiple regression model, i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , where  $y$ ,  $x_1$  and  $x_2$  are column-standardised (see Olkin and Finn 1995).

## Usage

```
olkin_beta_ratio(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 $\text{dat}$ is N by 3 matrix having variables in the order of $\text{cbind}(y,x_1,x_2)$
nv	sampel size

**Value**

This function will generate the variance of the proportion, i.e.  $\text{beta1}_2/R^2$ .The outputs are listed as follows.

ratio\_var            Variance of ratio

**References**

Olkin, I. and Finn, J.D. 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=dat2
omat=cor(dat)[1:3,1:3]
#omat
#1.0000000 0.1497007 0.136431
#0.1497007 1.0000000 0.622790
#0.1364310 0.6227900 1.000000

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

#r2redux output

#output$ratio_var (Variance of ratio)
#0.08042288
```

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<i>r2_beta_var</i>	<i>r2_beta_var</i>
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**Description**

This function estimates  $\text{var}(\text{beta1}^2)$  and  $\text{var}(\text{beta2}^2)$ , and beta1 and 2 are regression coefficients from a multiple regression model, i.e.  $y = x1 * \text{beta1} + x2 * \text{beta2} + e$ , y, x1 and x2 are column-standardised (see Olkin and Finn 1995). y is N by 1 matrix having the dependent variable, x1 is N by 1 matrix having the ith explanatory variable. x2 is N by 1 matrix having the jth explanatory variable. v1 and v2 indicates the ith and jth column in the data (v1 or v2 should be a single interger between 1 - M, see Arguments below).

**Usage**

```
r2_beta_var(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=1, v1=2, v1=3 or any value between 1 - M based on combination
v2	This can be set as v2=1, v2=2, v2=3, or any value between 1 - M based on combination
nv	Sample size

**Value**

This function will estimate the variance of  $\beta_1^2$  and  $\beta_2^2$ , and the covariance between  $\beta_1^2$  and  $\beta_2^2$ , i.e. the information matrix of squared regression coefficients.  $\beta_1$  and  $\beta_2$  are regression coefficients from a multiple regression model, i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , where  $y$ ,  $x_1$  and  $x_2$  are column-standardised. The outputs are listed as follows.

beta1_sq	beta1_sq
beta2_sq	beta2_sq
var1	Variance of beta1_sq
var2	Variance of beta2_sq
var1_2	Variance of difference between beta1_sq and beta2_sq
cov	Covariance between beta1_sq and beta2_sq
upper_beta1_sq	upper limit of 95% CI for beta1_sq
lower_beta1_sq	lower limit of 95% CI for beta1_sq
upper_beta2_sq	upper limit of 95% CI for beta2_sq
lower_beta2_sq	lower limit of 95% CI for beta2_sq

**References**

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

**Examples**

```
#To get the 95% CI of beta1_sq and beta2_sq
#beta1 and beta2 are regression coefficients from a multiple regression model,
#i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , where  $y$ ,  $x_1$  and  $x_2$  are column-standardised.

dat=dat2
nv=length(dat$V1)
v1=c(1)
v2=c(2)
output=r2_beta_var(dat,v1,v2,nv)
output
#r2redux output
#output$beta1_sq (beta1_sq)
#0.01118301
```

```

#output$beta2_sq (beta2_sq)
#0.004980285

#output$var1 (variance of beta1_sq)
#7.072931e-05

#output$var2 (variance of beta2_sq)
#3.161929e-05

#output$var1_2 (variance of difference between beta1_sq and beta2_sq)
#0.000162113

#output$cov (covariance between beta1_sq and beta2_sq)
#-2.988221e-05

#output$upper_beta1_sq (upper limit of 95% CI for beta1_sq)
#0.03037793

#output$lower_beta1_sq (lower limit of 95% CI for beta1_sq)
#-0.00123582

#output$upper_beta2_sq (upper limit of 95% CI for beta2_sq)
#0.02490076

#output$lower_beta2_sq (lower limit of 95% CI for beta2_sq)
#-0.005127546

```

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r2\_diff

*r2\_diff function*


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## 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 <code>cbind(y,x)</code>
v1	This can be set as <code>v1=c(1)</code> or <code>v1=c(1,2)</code>
v2	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>
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	two tailed P-value for significant difference between R2_1 and R2_2
r2_based_p_one_tail	one tailed P-value for significant difference
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  $R2(y \sim x[,1])$  and  $R2(y \sim x[,2])$ . (here we define  $R2\_1 = R2(y \sim x[,1])$  and  $R2\_2 = R2(y \sim x[,2])$ )

```
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)
#0.0001436128

#output$var2 (variance of R2_2)
#0.0001451358

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

#output$r2_based_p (two tailed p-value for significant difference)
```

```
#0.5514562

#output$r2_based_p_one_tail(one tailed p-value for significant difference)
#0.2757281

#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  $R^2(y \sim x[,1] + x[,2])$  and
 $R^2(y \sim x[,2])$ . (here  $R2\_1 = R^2(y \sim x[,1] + x[,2])$  and  $R2\_2 = R^2(y \sim x[,1])$ )

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)
#0.0001473686

#output$var2 (variance of R2_2)
#0.0001436128

#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)
#0.4366883

#output$mean_diff (differences between R2_1 and R2_2)
#0.0006042383

#output$upper_diff (upper limit of 95% CI for the difference)
#0.00488788

#output$lower_diff (lower limit of 95% CI for the difference)
#-0.0005576171
```

```

##When faced with multiple predictors, exceeding two in number,
#as seen in the scenario:
#y = PRS vs. y = PRS+any_cov1+any_cov2+...+any_covN
#A more streamlined approach can be adopted by consolidating the various
#predictors (any_cov1, any_cov2, ..., any_covN) into a single predictor,
#following this procedure in R:

#R
#mod <- lm(y ~PRS + any_cov1 + any_cov2 + ... + any_covN)
#merged_predictor <- cbind(any_cov1, any_cov2, ... , any_covN)
#%*% mod$coefficients[3:(2+N)]

#Subsequently, the comparison can be equivalently expressed as:
#y = PRS vs. y = PRS + merged_predictor
#This comparison can be simply achieved using the r2_diff function,
#as exemplified in the second example above.

##In another scenario:
#y = any_cov1 + any_cov2 + ... + any_covN vs.
#y = PRS + any_cov1 + any_cov2 +...+ any_covN

#The same approach applies as
#R
#mod <- lm(y ~PRS + any_cov1 + any_cov2 + ... + any_covN)
#merged_predictor <- cbind(any_cov1, any_cov2, ... , any_covN)
#%*% mod$coefficients[3:(2+N)]

#the comparison can be equivalently expressed as:
#y = merged_predictor vs. y = PRS + merged_predictor

##For this scenario, alternatively, the outcome variable (y) can be preadjusted
#with covariate(s), following the procedure in R:

#R
#mod <- lm(y ~ any_cov1 + any_cov2 + ... + any_covN)
#y_adj=scale(mod$residuals)
#then, the comparative significance test can be approximated by using
#the following model y_adj = PRS

```

---

r2\_enrich\_beta

r2\_enrich\_beta

---

## Description

This function estimates  $\text{var}(\beta_1^2/R^2)$ ,  $\beta_1$  and  $R^2$  are regression coefficient and the coefficient of determination from a multiple regression model, i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , where  $y$ ,  $x_1$  and  $x_2$  are column-standardised (see Olkin and Finn 1995).  $y$  is N by 1 matrix having the

dependent variable, and  $x_1$  is  $N$  by 1 matrix having the  $i$ th explanatory variables.  $x_2$  is  $N$  by 1 matrix having the  $j$ th explanatory variables.  $v_1$  and  $v_2$  indicates the  $i$ th and  $j$ th column in the data ( $v_1$  or  $v_2$  should be a single integer between 1 -  $M$ , see Arguments below).

### Usage

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

### Arguments

<code>dat</code>	$N$ by $(M+1)$ matrix having variables in the order of <code>cbind(y,x)</code>
<code>v1</code>	These can be set as $v_1=1$ , $v_1=2$ , $v_1=3$ or any value between 1 - $M$ based on combination
<code>v2</code>	These can be set as $v_2=1$ , $v_2=2$ , $v_2=3$ , or any value between 1 - $M$ based on combination
<code>nv</code>	Sample size
<code>exp1</code>	The expectation of the ratio (e.g. ratio of # SNPs in genomic partitioning)

### Value

This function will estimate  $\text{var}(\beta_1^2/R^2)$ ,  $\beta_1$  and  $R^2$  are regression coefficient and the coefficient of determination from a multiple regression model, i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , where  $y$ ,  $x_1$  and  $x_2$  are column-standardised. The outputs are listed as follows.

<code>beta1_sq</code>	<code>beta1_sq</code>
<code>beta2_sq</code>	<code>beta2_sq</code>
<code>ratio1</code>	<code>beta1_sq/R^2</code>
<code>ratio2</code>	<code>beta2_sq/R^2</code>
<code>ratio_var1</code>	variance of ratio 1
<code>ratio_var2</code>	variance of ratio 2
<code>upper_ratio1</code>	upper limit of 95% CI for ratio 1
<code>lower_ratio1</code>	lower limit of 95% CI for ratio 1
<code>upper_ratio2</code>	upper limit of 95% CI for ratio 2
<code>lower_ratio2</code>	lower limit of 95% CI for ratio 2
<code>enrich_p1</code>	two tailed P-value for <code>beta1_sq/R^2</code> is significantly different from <code>exp1</code>
<code>enrich_p1_one_tail</code>	one tailed P-value for <code>beta1_sq/R^2</code> is significantly different from <code>exp1</code>
<code>enrich_p2</code>	P-value for <code>beta2_sq/R^2</code> is significantly different from $(1-\text{exp1})$
<code>enrich_p2_one_tail</code>	one tailed P-value for <code>beta2_sq/R^2</code> is significantly different from $(1-\text{exp1})$

### References

Olkin, I. and Finn, J.D. 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, this function estimates
#var (beta1^2/R^2), where
#beta1^2 and R^2 are regression coefficients and the
#coefficient of determination from a multiple regression model,
#i.e.  $y = x_1 * \beta_1 + x_2 * \beta_2 + e$ , where  $y$ ,  $x_1$  and  $x_2$  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 (beta1_sq)
#0.01118301
```

```
#output$beta2_sq (beta2_sq)
#0.004980285
```

```
#output$ratio1 (beta1_sq/R^2)
#0.4392572
```

```
#output$ratio2 (beta2_sq/R^2)
#0.1956205
```

```
#output$ratio_var1 (variance of ratio 1)
#0.08042288
```

```
#output$ratio_var2 (variance of ratio 2)
#0.0431134
```

```
#output$upper_ratio1 (upper limit of 95% CI for ratio 1)
#0.9950922
```

```
#output$lower_ratio1 (lower limit of 95% CI for ratio 1)
#-0.1165778
```

```
#output$upper_ratio2 upper limit of 95% CI for ratio 2)
#0.6025904
```

```
#output$lower_ratio2 (lower limit of 95% CI for ratio 2)
#-0.2113493
```

```
#output$enrich_p1 (two tailed P-value for beta1_sq/R^2 is
#significantly different from exp1)
#0.1591692
```

```
#output$enrich_p1_one_tail (one tailed P-value for beta1_sq/R^2
#is significantly different from exp1)
#0.07958459

#output$enrich_p2 (two tailed P-value for beta2_sq/R2 is
#significantly different from (1-exp1))
#0.000232035

#output$enrich_p2_one_tail (one tailed P-value for beta2_sq/R2
#is significantly different from (1-exp1))
#0.0001160175
```

---

r2_var	<i>r2_var function</i>
--------	------------------------

---

### 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

### 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.

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

**Examples**

```

#To get the test statistics for R2(y~x[,1])
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)
#0.0001436128

#output$r2_based_p (P-value under the null hypothesis, i.e. R2=0)
#1.188162e-10

#output$upper_r2 (upper limit of 95% CI for R2)
#0.06433782

#output$lower_r2 (lower limit of 95% CI for R2)
#0.01764252


#To get the test statistic for R2(y~x[,1]+x[,2]+x[,3])

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

#r2redux output

#output$rsq (R2)
#0.03836254

#output$var (variance of R2)
#0.0001436128

#output$r2_based_p (R2 based P-value)
#1.188162e-10

#output$upper_r2 (upper limit of 95% CI for R2)
#0.06433782

#output$lower_r2 (lower limit of 95% CI for R2)
#0.0176425

```

```

#When comparing two independent sets of PGSS
#Let's assume dat1$V1 and dat2$V2 are independent for this example
#(e.g. male PGS vs. female PGS)

nv=length(dat1$V1)
v1=c(1)
output1=r2_var(dat1,v1,nv)
nv=length(dat2$V1)
v1=c(1)
output2=r2_var(dat2,v1,nv)

#To get the difference between two independent sets of PGSS
r2_diff_independent=abs(output1$rsq-output2$rsq)

#To get the variance of the difference between two independent sets of PGSS
var_r2_diff_independent= output1$var+output2$var
sd_r2_diff_independent=sqrt(var_r2_diff_independent)

#To get p-value (following eq. 15 in the paper)
chi=r2_diff_independent^2/var_r2_diff_independent
p_value=pchisq(chi,1,lower.tail=FALSE)
#to get 95% CI (following eq. 15 in the paper)
uci=r2_diff_independent+1.96*sd_r2_diff_independent
lci=r2_diff_independent-1.96*sd_r2_diff_independent

```

---

*r\_diff**r\_diff function*

---

**Description**

This function estimates  $\text{var}(R(y \sim x[,v1]) - R(y \sim x[,v2]))$  where  $R$  is the correlation between  $y$  and  $x$ ,  $y$  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**

```
r_diff(dat, v1, v2, 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> 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

**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  $R(y \sim x[,v1])$  and  $R(y \sim x[,v2])$ . (here we define  $R\_1 = R(y \sim x[,v1])$  and  $R\_2 = R(y \sim x[,v2])$ ). The outputs are listed as follows.

r1	R_1
r2	R_2
var1	Variance of R_1
var2	variance of R_2
var_diff	Variance of difference between R_1 and R_2
r2_based_p	P-value for significant difference between R_1 and R_2 for two tailed test
r_based_p_one_tail	P-value for significant difference between R_1 and R_2 for one tailed test
mean_diff	Differences between R_1 and R_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 R(y~x[,1]) and
#R(y~x[,2]). (here we define R_1=R(y~x[,1])) and R_2=R(y~x[,2]))

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

#r2redux output

#output$r1 (R_1)
#0.1958636

#output$r2 (R_2)
#0.197006

#output$var1 (variance of R_1)
#0.0009247466

#output$var2 (variance of R_1)
#0.0001451358

#output$var_diff (variance of difference between R_1 and R_2)
#3.65286e-06

#output$r_based_p (two tailed p-value for significant difference between R_1 and R_2)
```

```
#0.5500319

#output$r_based_p_one_tail (one tailed p-value)
#0.2750159

#output$mean_diff
#-0.001142375 (differences between R2_1 and R2_2)

#output$upper_diff (upper limit of 95% CI for the difference)
#0.002603666

#output$lower_diff (lower limit of 95% CI for the difference)
#-0.004888417


#To get the test statistics for the difference between  $R(y \sim x[,1] + [,2])$  and
 $R(y \sim x[,2])$ . (here  $R_1 = R(y \sim x[,1] + x[,2])$  and  $R_2 = R(y \sim x[,1])$ )

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

#output$r1
#0.1974001

#output$r2
#0.197006

#output$var1
#0.0009235848

#output$var2
#0.0009238836

#output$var_diff
#3.837451e-06

#output$r2_based_p
#0.8405593

#output$mean_diff
#0.0003940961

#output$upper_diff
#0.004233621

#output$lower_diff
#-0.003445429
```

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