

Package ‘r2redux’

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Title R2 Statistic

Version 1.0.17

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

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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

olkin1_2 function

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

olkin_beta1_2 function

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. $y = x_1 * \beta_1 + x_2 * \beta_2 + e$, 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
var2	Variance of β_2
var1_2	Variance of difference between β_1 and β_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
```

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

Description

This function derives Information matrix for β_1 and β_2 where β_1 and β_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_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

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
```

olkin_beta_ratio *olkin_beta_ratio* function

Description

This function derives variance of β_1^2 / R^2 where β_1 and β_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 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 generate the variance of the proportion, i.e. β_1^2 / R^2 . The outputs are listed as follows.

ratio_var	Variance of ratio
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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
```

r2_beta_var

*r2_beta_var***Description**

This function estimates $\text{var}(\beta_1^2)$ and $\text{var}(\beta_2^2)$, and β_1 and β_2 are regression coefficients from a multiple regression model, i.e. $y = x_1 * \beta_1 + x_2 * \beta_2 + e$, y , x_1 and x_2 are column-standardised (see Olkin and Finn 1995). y is N by 1 matrix having the dependent variable, x_1 is N by 1 matrix having the i th explanatory variable. x_2 is N by 1 matrix having the j th explanatory variable. 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 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 <code>cbind(y,x)</code>
v1	This can be set as $v_1=1$, $v_1=2$, $v_1=3$ or any value between $1 - M$ based on combination
v2	This can be set as $v_2=1$, $v_2=2$, $v_2=3$, or any value between $1 - M$ based on combination
nv	Sample size

Value

This function will estimate the variance of β_1^2 and β_2^2 , and the covariance between β_1^2 and β_2^2 , i.e. the information matrix of squared regression coefficients. β_1 and β_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, x1 and x2 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
```

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

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~x[,1]) and
#R2(y~x[,2]). (here we define R2_1=R2(y~x[,1]) and R2_2=R2(y~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

#output$p$p$nested
#1

#output$p$p$nonnested
#0.5514562

#output$p$p$LRT
#1

#To get the test statistics for the difference between R2(y~x[,1]+x[,2]) and
#R2(y~x[,2]). (here R2_1=R2(y~x[,1]+x[,2]) and R2_2=R2(y~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

#Note: If the directions are not consistent, for instance, if one correlation
#is positive (R_1) and another is negative (R_2), or vice versa, it is crucial
#to approach the interpretation of the comparative test with caution.
#It's important to note that R^2 alone does not provide information about the
#direction or sign of the relationships between predictors and the response variable.

#When faced with multiple predictors common between two models, for example,
#y = any_cov1 + any_cov2 + ... + any_covN + e vs.
#y = PRS + any_cov1 + any_cov2 +...+ any_covN + e

#A more streamlined approach can be adopted by consolidating the various
#predictors into a single predictor (see R code below).

#R
#dat=dat1
#here let's assume, we wanted to test one PRS (dat$V2)
#with 5 covariates (dat$V7 to dat$V11)
#mod1 <- lm(dat$V1~dat$V2 + dat$V7+ dat$V8+ dat$V9+ dat$V10+ dat$V11)
#merged_predictor1 <- mod1$fitted.values
#mod2 <- lm(dat$V1~ dat$V7+ dat$V8+ dat$V9+ dat$V10+ dat$V11)
#merged_predictor2 <- mod2$fitted.values
#dat=data.frame(dat$V1,merged_predictor1,merged_predictor2)

#the comparison can be equivalently expressed as:
#y = merged_predictor1 + e vs.
#y = merged_predictor2 + e

#This comparison can be simply achieved using the r2_diff function, e.g.

#To get the test statistics for the difference between R2(y~x[,1]) and
#R2(y~x[,2]). (here x[,1]= merged_predictor2 (from full model),
#and x[,2]= merged_predictor1 (from reduced model))
#v1=c(1)
#v2=c(2)
#output=r2_diff(dat,v1,v2,nv)
#note that the merged predictor from the full model (v1) should be the first.

#str(output)
#List of 11
#$ rsq1 : num 0.0428
#$ rsq2 : num 0.042
#$ var1 : num 0.0.000158
#$ var2 : num 0.0.000156

```

```

#$ var_diff          : num 2.87e-06
#$ r2_based_p        : num 0.658
#$ r2_based_p_one_tail: num 0.329
#$ mean_diff         : num 0.000751
#$ upper_diff        : num 0.00407
#$ lower_diff        : num -0.00257
#$ p                 :List of 3
#..$ nested         : num 0.386
#..$ nonnested       : num 0.658
#..$ LRT             : num 0.376

#Importantly note that in this case, merged_predictor1 is nested within
#merged_predictor2 (see mod1 vs. mod2 above). Therefore, this is
#nested model comparison. So, output$p$nested (0.386) should be used
#instead of output$p$nonnested (0.658).
#Note that r2_based_p is the same as output$p$nonnested (0.658) here.

##For this scenario, alternatively, the outcome variable (y) can be preadjusted
#with covariate(s), following the procedure in 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_var(dat, v1, nv))

#R
#dat=dat1
#mod <- lm(dat$V1~dat$V7+ dat$V8+ dat$V9+ dat$V10+ dat$V11)
#y_adj=scale(mod$residuals)
#dat=data.frame(y_adj,dat$V2)
#v1=c(1)
#output=r2_var(dat, v1, nv)

#str(output)
#$ var          : num 2e-06
#$ LRT_p        :Class 'logLik' : 0.98 (df=2)
#$ r2_based_p   : num 0.977
#$ rsq          : num 8.21e-07
#$ upper_r2     : num 0.00403
#$ lower_r2     : num -0.000999

#In another scenario where the same covariates, but different
#PRS1 and PRS2 are compared,
#y = PRS1 + any_cov1 + any_cov2 + ... + any_covN + e vs.
#y = PRS2 + any_cov1 + any_cov2 + ... + any_covN + e

#following approach can be employed (see R code below).

#R
#dat=dat1
#here let's assume dat$V2 as PRS1, dat$V3 as PRS2 and dat$V7 to dat$V11 as covariates
#mod1 <- lm(dat$V1~dat$V2 + dat$V7+ dat$V8+ dat$V9+ dat$V10+ dat$V11)
#merged_predictor1 <- mod1$fitted.values
#mod2 <- lm(dat$V1~dat$V3 + dat$V7+ dat$V8+ dat$V9+ dat$V10+ dat$V11)

```

```

#merged_predictor2 <- mod2$fitted.values
#dat=data.frame(dat$V1,merged_predictor2,merged_predictor1)

#the comparison can be equivalently expressed as:
#y = merged_predictor1 + e    vs.
#y = merged_predictor2 + e

#This comparison can be simply achieved using the r2_diff function, e.g.

#To get the test statistics for the difference between R2(y~x[,1]) and
#R2(y~x[,2]). (here x[,1]= merged_predictor2, and x[,2]= merged_predictor1)
#v1=c(1)
#v2=c(2)
#output=r2_diff(dat,v1,v2,nv)

#str(output)
#List of 11
#$ rsq1          : num 0.043
#$ rsq2          : num 0.0428
#$ var1          : num 0.000159
#$ var2          : num 0.000158
#$ var_diff      : num 2.6e-07
#$ r2_based_p    : num 0.657
#$ r2_based_p_one_tail: num 0.328
#$ mean_diff     : num 0.000227
#$ upper_diff    : num 0.00123
#$ lower_diff    : num 0.000773
#$ p             :List of 3
#..$ nested     : num 0.634
#..$ nonnested: num 0.657
#..$ LRT        : num 0.627

#Importantly note that in this case, merged_predictor1 and merged_predictor2
#are not nested to each other (see mod1 vs. mod2 above).
#Therefore, this is nonnested model comparison.
#So, output$p$nonnested (0.657) should be used instead of
#output$p$nested (0.634). Note that r2_based_p is the same
#as output$p$nonnested (0.657) here.

#For the above non-nested scenario, alternatively, the outcome variable (y)
#can be preadjusted with covariate(s), following the procedure in R:
#mod <- lm(y ~ any_cov1 + any_cov2 + ... + any_covN)
#y_adj=scale(mod$residuals)

#R
#dat=dat1
#mod <- lm(dat$V1~dat$V7+ dat$V8+ dat$V9+ dat$V10+ dat$V11)
#y_adj=scale(mod$residuals)
#dat=data.frame(y_adj,dat$V3,dat$V2)

#the comparison can be equivalently expressed as:
#y_adj = PRS1 + e    vs.
#y_adj = PRS2 + e
#then, the comparative significance test can be approximated by using r2_diff function
#To get the test statistics for the difference between R2(y~x[,1]) and
#R2(y~x[,2]). (here x[,1]= PRS1 and x[,2]= PRS2)

```



```

#v1=c(1)
#v2=c(2)
#output=r2_diff(dat,v1,v2,nv)

#str(output)
#List of 11
#$ rsq1          : num 5.16e-05
#$ rsq2          : num 4.63e-05
#$ var1          : num 2.21e-06
#$ var2          : num 2.18e-06
#$ var_diff      : num 1.31e-09
#$ r2_based_p    : num 0.884
#$ r2_based_p_one_tail: num 0.442
#$ mean_diff     : num 5.28e-06
#$ upper_diff    : num 7.63e-05
#$ lower_diff    : num -6.57e-05
#$ p             :List of 3
#..$ nested      : num 0.942
#..$ nonnested   : num 0.884
#..$ LRT         : num 0.942

```

r2_enrich_beta	<i>r2_enrich_beta</i>
----------------	-----------------------

Description

This function estimates $\text{var}(\beta^2/R^2)$, β_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 interger between 1 - M , see Arguments below).

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 $v_1=1$, $v_1=2$, $v_1=3$ or any value between 1 - M based on combination
v2	These can be set as $v_2=1$, $v_2=2$, $v_2=3$, 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 estimate $\text{var}(\beta_1^2/R^2)$, β_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.

beta1_sq	beta1_sq
beta2_sq	beta2_sq
ratio1	beta1_sq/R^2
ratio2	beta2_sq/R^2
ratio_var1	variance of ratio 1
ratio_var2	variance of ratio 2
upper_ratio1	upper limit of 95% CI for ratio 1
lower_ratio1	lower limit of 95% CI for ratio 1
upper_ratio2	upper limit of 95% CI for ratio 2
lower_ratio2	lower limit of 95% CI for ratio 2
enrich_p1	two tailed P-value for beta1_sq/R^2 is significantly different from exp1
enrich_p1_one_tail	one tailed P-value for beta1_sq/R^2 is significantly different from exp1
enrich_p2	P-value for beta2_sq/R^2 is significantly different from (1-exp1)
enrich_p2_one_tail	one tailed P-value for beta2_sq/R^2 is significantly different from (1-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 = 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 (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 expl)
#0.1591692

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

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

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

```

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 cbind(y,x)
v1	This can be set as v1=c(1), v1=c(1,2) or possibly with more values
nv	Sample size

Value

This function will test the null hypothesis for R2. To get the test statistics for R2(y~x[,v1]). The outputs are listed as follows.

rsq	R2
var	Variance of R2
r2_based_p	P-value under the null hypothesis, i.e. R2=0
upper_r2	Upper limit of 95% CI for R2
lower_r2	Lower limit of 95% CI for R2

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

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 $R(y \sim x[,v1])$ 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

#Note: If the directions are not consistent, for instance, if one correlation

```

```
#is positive (R_1) and another is negative (R_2), or vice versa, it is  
#crucial to approach the interpretation of the comparative test with caution.  
#This caution is especially emphasized when applying r_diff()  
#in a nested model comparison involving a joint model
```


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