Package ‘aSPU’

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Title Adaptive Sum of Powered Score Test

Description R codes for the (adaptive) Sum of Powered Score (‘SPU’ and ‘aSPU’) tests, inverse variance weighted Sum of Powered score (‘SPUw’ and ‘aSPUw’) tests and gene-based and some pathway based association tests (Pathway based Sum of Powered Score tests (‘SPUpath’), adaptive ‘SPUpath’ (‘aSPUpath’) test, ‘GEEaSPU’ test for multiple traits - single ‘SNP’ (single-nucleotide-polymorphism) association in generalized estimation equations, ‘MTaSPUs’ test for multiple traits - single ‘SNP’ association with Genome Wide Association Studies (‘GWAS’) summary statistics, Gene-based Association Test that uses an extended Simes procedure (‘GATES’), Hybrid Set-based Test (‘HYST’) and extended version of ‘GATES’ test for pathway-based association testing (‘GATES-Simes’). 

The tests can be used with genetic and other data sets with covariates. The response variable is binary or quantitative. Summary; (1) Single trait-‘SNP’ set association with individual-level data (‘aSPU’, ‘aSPUw’, ‘aSPUr’), (2) Single trait-‘SNP’ set association with summary statistics (‘aSPUs’), (3) Single trait-pathway association with individual-level data (‘aSPUpath’), (4) Single trait-pathway association with summary statistics (‘aSPUsPath’), (5) Multiple traits-single ‘SNP’ association with individual-level data (‘GEEaSPU’), (6) Multiple traits-single SNP association with summary statistics (‘MTaSPUs’), (7) Multiple traits-‘SNP’ set association with summary statistics(‘MTaSPUsSet’), (8) Multiple traits-pathway association with summary statistics(‘MTaSPUsSetPath’).

Author Il-Youp Kwak and others (See Author(s) in each function manual)

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Suggests knitr

VignetteBuilder knitr

Imports Rcpp (>= 0.12.1)

Depends R(>= 3.1.0), gee, MASS, mvtnorm, fields, matrixStats

License GPL-3

LinkingTo Rcpp, RcppArmadillo

URL https://github.com/ikwak2/aSPU
aspu

Sum of Powered Score (SPU) tests and adaptive SPU (aSPU) test for single trait - SNP set association.

Description

It gives p-values of the SPU tests and aSPU test.
**Usage**

```r
aSPU(Y, X, cov = NULL, resample = c("perm", "sim", "boot"),
    model = c("gaussian", "binomial"), pow = c(1:8, Inf), n.perm = 1000)
```

**Arguments**

- **Y**: Response or phenotype data. It can be a disease indicator; =0 for controls, =1 for cases. Or it can be a quantitative trait. A vector with length n (number of observations).
- **X**: Genotype or other data; each row for a subject, and each column for an SNP (or a predictor). The value of each SNP is the # of the copies for an allele. A matrix with dimension n by k (n : number of observation, k : number of SNPs (or predictors)).
- **cov**: Covariates. A matrix with dimension n by p (n : number of observation, p : number of covariates).
- **resample**: Use "perm" for residual permutations, "sim" for simulations from the null distribution, and "boot" for parametric bootstrap.
- **model**: Use "gaussian" for a quantitative trait, and use "binomial" for a binary trait.
- **pow**: power used in SPU test. A vector of the powers.
- **n.perm**: number of permutations or bootstraps.

**Value**

A list object, Ts : test statistics for the SPU tests (in the order of the specified pow) and finally for the aSPU test. pvs : p-values for the SPU and aSPU tests.

**Author(s)**

Il-Youp Kwak, Junghi Kim, Yiwei Zhang and Wei Pan

**References**

- Wei Pan, Junghi Kim, Yiwei Zhang, Xiaotong Shen and Peng Wei (2014) A powerful and adaptive association test for rare variants, Genetics, 197(4), 1081-95
- Junghi Kim, Jeffrey R Wozniak, Bryon A Mueller, Xiaotong Shen and Wei Pan (2014) Comparison of statistical tests for group differences in brain functional networks, NeuroImage, 1;101:681-694

**See Also**

- `aSPUw`

**Examples**

```r
data(exdat)
```

```r
## example analysis using aSPU test on exdat data.
```
Adaptive Sum of powered score (SPU) tests (SPU and aSPU) (distribution based).

Description

It gives the p-values of the SPU(1), SPU(2) and minP tests and aSPU test based on the distribution.

Usage

```r
aSPUd(Y, X, cov = NULL, model = c("gaussian", "binomial"))
```

Arguments

- **Y**: Response or phenotype data. It can be a disease indicator; =0 for controls, =1 for cases. Or it can be a quantitative trait. A vector with length n (number of observations).
- **X**: Genotype or other data; each row for a subject, and each column for an SNP (or a predictor). The value of each SNP is the # of the copies for an allele. A matrix with dimension n by k (n: number of observation, k: number of SNPs (or predictors)).
- **cov**: Covariates. A matrix with dimension n by p (n: number of observation, p: number of covariates).
- **model**: Use "gaussian" for a quantitative trait, and use "binomial" for a binary trait.

Value

p-values for SPU(1), SPU(2), minP tests and aSPU test.

Author(s)

Il-Youp Kwak and Wei Pan
References

Wei Pan, Junghi Kim, Yiwei Zhang, Xiaotong Shen and Peng Wei (2014) A powerful and adaptive association test for rare variants, Genetics, 197(4), 1081-95

Junghi Kim, Jeffrey R Wozniak, Bryon A Mueller, Xiaotong Shen and Wei Pan (2014) Comparison of statistical tests for group differences in brain functional networks, NeuroImage, 1;101:681-694

See Also

aSPU

Examples

data(exdat)

## example analysis using aSPU test on exdat data.
out <- aSPUd(exdat$Y, exdat$X, cov = NULL, model = "binomial")

out

aSPUpath Pathway based Sum of Powered Score tests (SPUpath) and adaptive SPUpath (aSPUpath) test for single trait - pathway association.

Description

It gives p-values of the SPUpath tests and aSPUpath test.

Usage

aSPUpath(Y, X, cov = NULL, model = c("binomial", "gaussian"), snp.info,
gene.info, pow = c(1:8, Inf), pow2 = c(1, 2, 4, 8), n.perm = 200,
usePCs = F, varprop = 0.95)

Arguments

Y Response or phenotype data. It can be a disease indicator; =0 for controls, =1 for cases. Or it can be a quantitative trait. A vector with length n (number of observations).

X Genotype or other data; each row for a subject, and each column for an SNP (or a predictor). The value of each SNP is the # of the copies for an allele. A matrix with dimension n by k (n : number of observation, k : number of SNPs (or predictors)).

cov Covariates. A matrix with dimension n by p (n :number of observation, p : number of covariates).

model Use "gaussian" for a quantitative trait, and use "binomial" for a binary trait.
snp.info  SNP information matrix, the 1st column is SNP id, 2nd column is chromosome #, 3rd column indicates SNP location.
gene.info  GENE information matrix, The 1st column is GENE id, 2nd column is chromosome #, 3rd and 4th column indicate start and end positions of the gene.
pow    SNP specific power(gamma values) used in SPUpath test.
pow2    GENE specific power(gamma values) used in SPUpath test.
n.perm  number of permutations.
usePCs  indicating whether to extract PCs and then use PCs of X.
varprop the proportion of the variations explained (cutoff) that determines how many top PCs to use.

Value

P-values for SPUpath tests and aSPUpath test.

Author(s)

Il-Youp Kwak and Wei Pan

References


See Also

simPathAR1Snp

Examples

```r
## Not run: dat1<-simPathAR1Snp(nGenes=20, nGenes1=5, nSNPlim=c(1, 20), nSNP0=1, LOR=.2, n=100, MAFlim=c(0.05, 0.4), p0=0.05 )
## End(Not run)

# p-values of SPUpath and aSPUpath tests.
## Not run: p.pathaspu<- aSPUpath(dat1$Y, dat1$X, snp.info = dat1$snp.info, gene.info = dat1$gene.info, model = "binomial", pow=1:8, pow2=c(1, 2, 4, 8), n.perm=1000)
## End(Not run)

p.pathaspu
## pow = 1:8 and pow2 = 1,2,4,8
## So, there are 8*4 = 32 SPUpath p-values.
## SPUpath.i,j corresponds pow = i , pow2 = j
## The last element, aSPUpath gives aSPUpath p-value.
```
aSPUr

Robust Sum of powered score (SPU) tests and aSPU test for a quantitative trait

Description

The test is based on the Huber loss function and using the parametric bootstrap for inference (i.e. bootstrapping residuals).

Usage

aSPUr(Y, X, cov = NULL, pow = c(1:8, Inf), B = 1000, C = 1.345)

Arguments

Y
a vector of quantitative traits (QTs).

X
Genotype or other data; each row for a subject, and each column for an SNP (or a predictor). The value of each SNP is the # of the copies for an allele. A matrix with dimension n by k (n : number of observation, k : number of SNPs (or predictors) ).

cov
Covariates. A matrix with dimension n by k2 (n : number of observation, k2 : number of covariates).

pow
power used in SPUr test. A vector of the powers.

B
number of bootstraps.

C
Constant in huber loss function. C = 1.345 is chosen to maintain a high efficiency for a Normal error.

Value

p-values of the SPUr tests in the order of supplied pow values; finally, the p-value of the aSPUr test (that combines the SPUs tests with pow by taking their min P-value and adjust for multiple testing).

Author(s)

Yiwei Zhang and Wei Pan

References

Peng Wei, Ying Cao, Yiwei Zhang, Zhiyuan Xu, Il-Youp Kwak, Eric Boerwinkle, Wei Pan (in press) On Robust Association Testing for Quantitative Traits and Rare Variants, G3.

See Also

aSPU
Examples

```r
data(exdat)

## example analysis using aSPU test on exdat data.

QT <- jitter(exdat$Y)

out <- aSPU(Y = QT, X = exdat$X, cov = NULL, B = 100)

out

## This is a vector of p-values for SPUr and aSPUr tests.
## SPU1 to SPUInf corresponds with the option pow=c(1:8, Inf)
## They are p-values for corresponding SPUr tests.
## The last element is p-value of aSPUr test.
```

---

**aSPUs**

*Sum of Powered Score (SPUs) tests and adaptive SPU (aSPUs) test for single trait - SNP set association with GWAS summary statistics.*

---

### Description

It gives p-values of the SPUs tests and aSPUs test with GWAS summary statistics.

### Usage

```r
aSPUs(Zs, corSNP, pow = c(1:8, Inf), n.perm = 1000, Ps = FALSE, prune = TRUE)
```

### Arguments

- **Zs**: Z-scores for each SNPs. It could be P-values if the Ps option is TRUE.
- **corSNP**: Correlation matrix of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).
- **pow**: power used in SPU test. A vector of the powers.
- **n.perm**: number of permutations or bootstraps.
- **Ps**: TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.
- **prune**: if it is TRUE, do pruning before the test using pruneSNP function.

### Value

A list object, **Ts**: test statistics for the SPU tests (in the order of the specified pow) and finally for the aSPU test. **pvs**: p-values for the SPUs and aSPUs tests.
**aSPUsD**

*Author(s)*

Il-Youp Kwak and Wei Pan

*References*


*See Also*

aSPUw aSPU aSPUsPath

*Examples*

```r
data(kegg9)
## example analysis using aSPUM test.
g <- kegg9$gene.info[1,1]  # SOAT1
## Take snps mapped on gene "SOAT1" from the information of gene.info and snp.info.
snps <- which(( kegg9$snp.info[,2] == kegg9$gene.info[kegg9$gene.info[,1] == g, 2] ) &
              (kegg9$snp.info[,3] > kegg9$gene.info[kegg9$gene.info[,1] == g, 3] ) &
## Take subsets
newP <- kegg9$np[snps];
ldsub <- kegg9$ldmatrix[snps, snps];

## Get p-value for gene SOAT1. Read vignette for details.
out <- aSPUs(newP, corSNP=ldsub , pow=c(1:8, Inf), n.perm=100, Ps=TRUE)

out$Ts
# This is a vector of Test Statistics for SPUM and aSPUM tests.
# SPUs1 to SPUsInf corresponds with the option pow=c(1:8, Inf)
# They are SPUs test statistics.
# The last element aSPUs is minimum of them, aSPUs statistic.

out$pvs
# This is a vector of p-values for SPUs and aSPUs tests.
# SPUs1 to SPUsInf corresponds with the option pow=c(1:8, Inf)
# They are p-values for corresponding SPUs tests.
# The last element is p-value of aSPUs test.
```

**Description**

*aSPUsD* *Sum of Powered Score (SPUs) tests and adaptive SPU (aSPUs) test for single trait - SNP set association with GWAS summary statistics (distribution based).*

It gives p-values of the SPUs tests and aSPUs test with GWAS summary statistics.
Usage

aSPUsD(Zs, corrSNP, Ps = FALSE)

Arguments

Zs  
Z-scores for each SNPs. It could be P-values if the Ps option is TRUE.

corrSNP  
Correlation matrix of the SNPs to be tested; estimated from a reference panel
(based on the same set of the reference alleles as used in calculating Z-scores).

Ps  
TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.

Value

pvs : p-values for the SPUsD and aSPUsD tests.

Author(s)

Il-Youp Kwak and Wei Pan

References


See Also

aSPUs aSPU

Examples

data(kegg9)
## example analysis using aSPUM test.
g <- kegg9$gene.info[1,1]  # SOAT1
## Take snps mapped on gene "SOAT1" from the information of gene.info and snp.info.
snps <- which( (kegg9$snp.info[,2] == kegg9$gene.info[kegg9$gene.info[,1] == g, 2] ) &
              (kegg9$snp.info[,3] > kegg9$gene.info[kegg9$gene.info[,1] == g, 3] ) &
## Take subsets
newP <- kegg9$np[snps] ;
ldsub <- kegg9$ldmatrix[snps, snps];
## Get p-value for gene SOAT1. Read vignette for details.
out <- aSPUsD(newP, corrSNP=ldsub, Ps=TRUE)

out
**Description**

It gives p-values of the SPUsPath tests and aSPUsPath test with GWAS summary statistics.

**Usage**

```r
aSPUsPath(Zs, corSNP, pow = c(1, 2, 4, 8, Inf), pow2 = c(1, 2, 4, 8),
            snp.info, gene.info, n.perm = 1000, Ps = FALSE, prune = TRUE)
```

**Arguments**

- **Zs**: Z-scores for each SNPs. It could be P-values if the Ps option is TRUE.
- **corSNP**: Correlation matrix of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).
- **pow**: SNP specific power(gamma values) used in SPUsPath test.
- **pow2**: GENE specific power(gamma values) used in SPUsPath test.
- **snp.info**: SNP information matrix, the 1st column is SNP id, 2nd column is chromosome #, 3rd column indicates SNP location.
- **gene.info**: GENE information matrix, The 1st column is GENE id, 2nd column is chromosome #, 3rd and 4th column indicate start and end positions of the gene.
- **n.perm**: number of permutations.
- **Ps**: TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.
- **prune**: if it is TRUE, do pruning before the test using pruneSNP function.

**Value**

P-values for SPUsPath tests and aSPUsPath test.

**Author(s)**

Il-Youp Kwak and Wei Pan

**References**


**See Also**

aSPUs
**Examples**

```r
data(kegg9)

# p-values of SPUw and aSPUw tests.
out.a <- aSPUwPath(kegg9$snp, corSNP = kegg9$ldmatrix, pow=c(1:8, Inf),
                   pow2 = c(1,2,4,8),
                   snp.info=kegg9$snp.info, gene.info = kegg9$gene.info,
                   n.perm=10, Ps = TRUE)

out.a
```

**aSPUw**

*Inverse variance weighted Sum of Powered Score tests (SPUw) and adaptive SPUw (aSPUw) test for single trait - SNP set association.*

**Description**

It gives the p-values of the SPUw tests and aSPUw test based on the permutations of the residuals or simulations from the null distribution.

**Usage**

```r
aSPUw(y, x, cov = NULL, resample = c("perm", "sim", "boot"),
      model = c("gaussian", "binomial"), pow = c(1:8, Inf), n.perm = 1000)
```

**Arguments**

- **y**  
  Response or phenotype data. It can be a disease indicator; =0 for controls, =1 for cases. Or it can be a quantitative trait. A vector with length n (number of observations).

- **x**  
  Genotype or other data; each row for a subject, and each column for an SNP (or a predictor). The value of each SNP is the # of the copies for an allele. A matrix with dimension n by k (n : number of observation, k : number of SNPs (or predictors)).

- **cov**  
  Covariates. A matrix with dimension n by p (n :number of observation, p : number of covariates).

- **resample**  
  Use "perm" for residual permutations, "sim" for simulations from the null distribution, and "boot" for parametric bootstrap.

- **model**  
  Use "gaussian" for a quantitative trait, and use "binomial" for a binary trait.

- **pow**  
  power used in SPU test. A vector of the powers.

- **n.perm**  
  number of permutations or bootstraps.

**Value**

A list object, Ts : Test Statistics for the SPUw and aSPUw test. pvs : p-values for the SPUw and aSPUw test.
estcov

Author(s)
Il-Youp Kwak, Junghi Kim and Wei Pan

References
Junghi Kim, Jeffrey R Wozniak, Bryon A Mueller, Xiaotong Shen and Wei Pan (2014) Comparison of statistical tests for group differences in brain functional networks, Neuroimage, 1;101:681-694

See Also
aSPU

Examples

```r
data(exdat)
out <- aSPUw(exdat$Y, exdat$X, pow = c(1:8, Inf), n.perm = 1000)

out$Ts
# This is a vector of Test Statistics for SPU and aSPU tests.
# SPU1 to SPUInf corresponds with the option pow=c(1:8, Inf)
# They are SPU test statistics.
# The last element aSPU is minimum of them, aSPU statistic.

out$pvs
# This is a vector of p-values for SPU and aSPU tests.
# SPU1 to SPUInf corresponds with the option pow=c(1:8, Inf)
# They are p-values for corresponding SPU tests.
# The last element is p-value of aSPU test.
```

Description
Estimate the covariance matrix of multiple traits based on their (null) summary Z-scores.

Usage

```r
estcov(allZ)
```

Arguments

- `allZ` matrix of summary Z-scores for all SNP, each row for SNP; each column for single trait.

Value
estimated correlation matrix.
Author(s)

Junghi Kim, Yun Bai and Wei Pan

References

Junghi Kim, Yun Bai and Wei Pan (2015) An Adaptive Association Test for Multiple Phenotypes with GWAS Summary Statistics, Genetic Epidemiology, 8:651-663

See Also

MTaSPUs minP

Examples

# -- n.snp: number of SNPs
# -- n.trait: number of traits
# -- n.subject: number of subjects

n.snp <- 100
n.trait <- 10
n.subject <- 1000
traits <- matrix(rnorm(n.subjects*n.trait), n.subjects, n.trait)
v <- cov(traits)
allZ <- rmvnorm(n.snp, sigma=v)
colnames(allZ) <- paste("trait", 1:n.trait, sep="")
rownames(allZ) <- paste("snp", 1:n.snp, sep="")

r <- estcov(allZ)
MTaSPUs(Z = allZ, v = r, B = 100, pow = c(1:4, Inf), transform = FALSE)
MTaSPUs(Z = allZ[,1], v = r, B = 100, pow = c(1:4, Inf), transform = FALSE)
minP(Zi= allZ[1,], r = r)

An example data set

Data

The exdat data set is list of three objects. exdat$Y is a vector of length 1000, 500 0s and 500 1s. exdat$X is a matrix of 1000 by 10. This simulated X matrix is assumed to be rare variants. All elements are 0, 1 or 2. exdat$SNP0indx is a vector of length 10. The values are 1 or 0, 0 indicate corresponding column of X matrix have no association with Y vector.

Usage

data(exdat)
Examples

```r
data(exdat)
exdat$x[c(1:10, 501:510), ]
exdat$y[c(1:10, 501:510)]

# 3rd and 10th column of X have no association with Y
exdat$snp0indx
```

---

**GATES2**

**Gene-based Association Test that uses an extended Simes procedure (GATES) for single trait - SNP set association**

---

**Description**

Get the p-value of GATES. Usually it is used to get genomewise p-values. This function is taken from postgwas package. There is a little modification of the code GATES in postgwas package. 1) The approximated matrix may have negative eigen value, we modified it not to have negative values; 2) we added one more return (the key gene location) for Hyst method.

**Usage**

```r
GATES2(ldmatrix, p)
```

**Arguments**

- `ldmatrix` numeric. A correlation matrix of SNPs, dimensions matching the p and snps arguments.
- `p` p-value for each SNPs.

**Value**

A p-value of GATES and the key gene location (to be used by Hyst).

**Author(s)**

Milan Hiersche(taken from pastgwas package), Il-Youp Kwak(modified a little)

**References**


**See Also**

`Hyst`, `GatesSimes`
Examples

```r
simula <- simPathAR1Snps(nGenes=20, nGenes1=1, nSNPlim=c(1, 20), nSNP0=1:3,
LOR=.2, rholim=c(0,0),
n=100, MAFlim=c(0.05, 0.4), p0=0.05)
Ps <- getlogitp(simula$Y, simula$X)

## get correlation of SNPs using controls
ldmat <- cor(simula$X[ simula$Y == 0, ])

o.pvec = order(Ps)
ldmat <- ldmat[o.pvec, o.pvec]
(gatesp <- GATES2(ldmat, sort(Ps))[1])
```

---

**GatesSimes**

*GATES-Simes test for single trait - pathway association.*

**Description**

Get the p-value of GATES-Simes. It uses an extended Simes procedure to combine GATES p-values across multiple genes in a pathway.

**Usage**

`GatesSimes(pvec, ldmatrix, snp.info, gene.info)`

**Arguments**

- `pvec`  
  p-values for each SNP.

- `ldmatrix`  
  numeric. A correlation matrix of SNPs with dimensions matching the length of `pvec` (the number of SNPs).

- `snp.info`  
  SNP information matrix, the 1st column is SNP id, 2nd column is chromosome #, 3rd column indicates SNP location.

- `gene.info`  
  GENE information matrix, The 1st column is GENE id, 2nd column is chromosome #, 3rd and 4th column indicate start and end positions of the gene.

**Value**

A p-value.

**Author(s)**

Il-Youp Kwak and Wei Pan
References
Hongsheng Gui, Miaoxin Li, Pak C Sham and Stacey S Cherny (2011) Comparisons of seven algorithms for pathway analysis using the WTCCC Crohn’s Disease BMC Research Notes, 4:386

See Also
Hyst GATES2

Examples

```r
simula <- simPathAR1Snp(nGenes=20, nGenes1=1, nSNP1im=c(1, 20), nSNP0=1:3, LOR=.2, rho1im=c(0,0), n=100, MAFlim=c(0.05, 0.4), p0=0.05)
logitp <- getlogitp(simula$Y, simula$X)

## get correlation of SNPs using controls
ldmat <- cor(simula$X[ simula$Y == 0 , ])
out <- GatesSimes(pvec = logitp, ldmatrix = ldmatrix, snp.info = simula$snp.info, gene.info = simula$gene.info)
out
d
```

**GEEaSPU**

The SPU and aSPU tests for multiple traits - single SNP association in generalized estimating equations.

Description
It gives p-values of the GEESPU tests and GEEaSPU test.

Usage

```r
GEEaSPU(traits, geno, Z = NULL, model = c("binomial", "gaussian"),
        gamma = c(1:8, Inf), n.sim = 1000, corstr = "independence")
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>traits</td>
<td>trait matrix. The row for individuals and the column for traits.</td>
</tr>
<tr>
<td>geno</td>
<td>A matrix of genetic information.</td>
</tr>
<tr>
<td>Z</td>
<td>covariates.</td>
</tr>
<tr>
<td>model</td>
<td>Use &quot;gaussian&quot; for a quantitative trait, and use &quot;binomial&quot; for a binary trait.</td>
</tr>
<tr>
<td>gamma</td>
<td>power used in GEEaSPU test. A vector of the powers.</td>
</tr>
<tr>
<td>n.sim</td>
<td>number of simulations.</td>
</tr>
<tr>
<td>corstr</td>
<td>a character string specifying the correlation structure. The following are permitted: &quot;independence&quot;, &quot;fixed&quot;, &quot;stat_M_dep&quot;, &quot;non_stat_M_dep&quot;, &quot;exchangeable&quot;, &quot;AR-M&quot; and &quot;unstructured&quot;</td>
</tr>
</tbody>
</table>
getlogitp

Value
p-values for the GEE-SPU and GEE-aSPU test.

Author(s)
Junghi Kim, Wei Pan and Il-Youp Kwak

References

Examples

traits <- matrix(rnorm(100*5, 0,1), ncol=5)
Z <- rnorm(100, 2, 0.5)
geno <- rbinom(100, 2, 0.5)
out <- GEEaSPU(traits, geno, Z = NULL, model = "gaussian",
gamma = c(1:8,Inf), n.sim = 100)

getlogitp

Get the p-values of the multiple SNPs based on the Wald test in a logistic regression model.

Description
Get p-value using logistic regression for each of the multiple SNPs

Usage
getlogitp(Y, X)

Arguments
Y Response or phenotype data. It can be a disease indicator; =0 for controls, =1 for cases.
X Genotype or other data; each row for a subject, and each column for an SNP (or a predictor). The value of each SNP is the # of the copies for an allele. A matrix with dimension n by p (n: number of observation, p: number of SNPs (or predictors)).

Value
p-values for each SNPs.
See Also

GATES2 GatesSimes Hyst

Examples

```r
simula <- simPathAR1Snp(nGenes=20, nGenes1=1, nSNPlim=c(1, 20), nSNP0=1:3,
LOR=.2, rhoLim=c(0,0),
n=100, MAFlim=c(0.05, 0.4), p0=0.05)
logitp <- getlogitp(simula$Y, simula$X)
```

Hyst

HYST (Hybrid Set-based Test) for single trait - pathway association

Description

Get a p-value using HYST.

Usage

```r
Hyst(pvec, ldmatrix, snp.info, gene.info)
```

Arguments

- `pvec`: p-values for each SNP.
- `ldmatrix`: numeric. A correlation matrix of SNPs with dimensions matching the length of pvec (the number of SNPs).
- `snp.info`: SNP information matrix, the 1st column is SNP id, 2nd column is chromosome #. 3rd column indicates SNP location.
- `gene.info`: GENE information matrix. The 1st column is GENE id, 2nd column is chromosome #. 3rd and 4th column indicate start and end positions of the gene.

Value

A p-value.

Author(s)

Il-Youp Kwak and Wei Pan

References

See Also

GatesSimes GATES2

Examples

```r
simula <- simPathAR1Snp(nGenes=20, nGenes1=1, nSNPlim=c(1, 20), nSNP0=1:3,
LOR=.2, rholim=c(0,0),
n=100, MAFlim=c(0.05, 0.4), p0=0.05)
logitp <- getlogitp(simula$Y, simula$X)

## get correlation of SNPs using controls
ldmat <- cor(simula$X[ simula$Y == 0, ])
out <- Hyst(pvec = logitp, ldmatrix = ldmat, snp.info = simula$snp.info,
            gene.info = simula$gene.info)
```

kegg9

A subset of coronary artery disease (CAD) data

Description

Data on coronary artery disease, myocardial infarction have been contributed by CARDIoGRAM-plusC4D investigators and have been downloaded from www.CARDIOGRAMPLUSC4D.ORG

The data set contains P value data for coronary artery disease (CAD). We mapped these SNPs to the 9th KEGG pathway.

gene.info is a contains 16 gene information of 9th Kegg pathway. The 1st column is the name of the gene, 2nd column is the chromosome number, 3rd column is where the gene starts and 4th column is where the gene ends.

snp.info contains 330 snp informations mapped on this Kegg pathway. The 1st column is the rsID of the SNP, 2nd column is the chromosome number and the 3rd column is the location of the SNP.

Ps is a vector containing p-value information for mapped SNPs.

The ‘PPs’ is a list object contains the SNP information for each genes. For example, PPs$CEL contains snp.info matrix mapped on gene ‘CEL’. The 1st column is the rsID of the SNP, 2nd column is the chromosome number, the 3rd column is the location of the SNP and the 4th column is p-value of the SNP.

nP is a subvector of Ps. These are SNPs on reference population(Hapmap CEU phase 2 data, downloadable from plink, SNPs with MAF less than 5 percent omitted)

ldmatrix is a correaltion matrix of SNPs from the reference population.

Usage

```r
data(kegg9)
```
References


Examples

data(kegg9)

## gene informations
kegg9$gene.info

## SNPs mapped on 3rd and 4th gene in 9th Kegg pathway
kegg9$PPs[3:4]

## snp information
kegg9$snp.info

## The 1st 10 P-values of SNPs mapped on 9th Kegg pathway.
kegg9$snP[1:10]

## correlation matrix among those SNPs
kegg9$ldmatrix[1:10,1:10]

---

**minP**

*minP test.*

Description

Return exact minP test p-value for multiple traits - single SNP association.

Usage

`minP(Zi, r)`

Arguments

- **Zi** a vector of summary Z-scores for single SNP
- **r** estimated correlation matrix based on the summary Z-scores (output of estcov)

Value

return exact minP test

Author(s)

Jungho Kim, Yun Bai and Wei Pan
References

Junghi Kim, Yun Bai and Wei Pan (2015) An Adaptive Association Test for Multiple Phenotypes with GWAS Summary Statistics, Genetic Epidemiology, 8:651-663

See Also

estcov, MTaSPUs

Examples

```r
# -- n.snp: number of SNPs
# -- n.trait: number of traits
# -- n.subject: number of subjects

n.snp <- 100
n.trait <- 10
n.subject <- 1000
traits <- matrix(rnorm(n.subject*n.trait), n.subject, n.trait)
v <- cov(trait)
alZ <- rmvnorm(n.snp, sigma=v)
colnames(alZ) <- paste("trait", 1:n.trait, sep="")
rownames(alZ) <- paste("snp", 1:n.snp, sep="")

r <- estcov(alZ)
MTaSPUs(Z = alZ, v = r, B = 100, pow = c(1,4, Inf), transform = FALSE)
MTaSPUs(Z = alZ[,1], v = r, B = 100, pow = c(1,4, Inf), transform = FALSE)
minP(Zi = alZ[,1], r = r)
```

---

**MTaSPUs**

*The SPU and aSPU tests for multiple traits - single SNP association with GWAS summary statistics.*

**Description**

SNP based adaptive association test for multiple phenotypes with GWAS summary statistics.

**Usage**

`MTaSPUs(Z, v, B, pow, transform = FALSE)`

**Arguments**

- `Z` matrix of summary Z-scores, SNPs in rows and traits in columns. Or a vector of summary Z-scores for a single snp
- `v` estimated correlation matrix based on the summary Z-scores (output of estcov)
MTaSPUs

B  number of Monte Carlo samples simulated to compute p-values, the maximum number of MC simulations is 1e8
pow  power used in SPU test. A vector of the powers.
transform  if TRUE, the inference is made on transformed Z

Value
compute p-values for SPU(gamma) i.e. pow=1:8, and infinity aSPU, based on the minimum p-values over SPU(power) each row for single SNP

Author(s)
Junghi Kim, Yun Bai and Wei Pan

References
Junghi Kim, Yun Bai and Wei Pan (2015) An Adaptive Association Test for Multiple Phenotypes with GWAS Summary Statistics, Genetic Epidemiology, 8:651-663

See Also
minP estcov

Examples

# -- n.snp: number of SNPs
# -- n.trait: number of traits
# -- n.subject: number of subjects
n.snp <- 100
n.trait <- 10
n.subjects <- 1000
traits <- matrix(rnorm(n.subjects*n.trait), n.subjects, n.trait)
v <- cov(traits)
allZ <- rmvnorm(n.snp, sigma=v)
rownames(allZ) <- paste("snp", 1:n.snp, sep="")
colnames(allZ) <- paste("trait", 1:n.trait, sep="")

r <- estcov(allZ)
MTaSPUs(Z = allZ, v = r, B = 100, pow = c(1:4, Inf), transform = FALSE)
MTaSPUs(Z = allZ[1,], v = r, B = 100, pow = c(1:4, Inf), transform = FALSE)
minP(Zi= allZ[1,], r = r)
MTaSPUsSet

*gene-Multitrait Sum of Powered Score (MTSPUsSet) tests and adaptive MTSPUsSet (MTaSPUsSet) test for multi trait - SNP set association with GWAS summary statistics.*

Description

It gives p-values of the MTSPUsSet tests and MTaSPUsSet test with GWAS summary statistics.

Usage

```r
MTaSPUsSet(Zs, corSNP, corPhe, pow = c(1, 2, 4, 8), pow2 = c(1, 2, 4, 8), 
n.perm = 5000, Ps = FALSE, prune = TRUE)
```

Arguments

- **Zs**: Z-score matrix. row represent SNPs and column represent traits. It could be P-values if the Ps option is TRUE.
- **corSNP**: Correlation matrix of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).
- **corPhe**: Correlation matrix of phenotypes to be tested; Estimated from Z-scores.
- **pow**: SNP specific power(gamma values) used in MTSPUsSet test.
- **pow2**: GENE specific power(gamma values) used in MTSPUsSet test.
- **n.perm**: number of permutations or bootstraps.
- **Ps**: TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.
- **prune**: if it is TRUE, do pruing before the test using pruneSNP function.

Value

A vector object, MTSPUsSet test P values and MTaSPUsSet P value.

Author(s)

Il-Youp Kwak and Wei Pan

References


See Also

MTaSPUsSetC
**Examples**

```r
data(SAMD11)
attach(SAMD11)
## example analysis using MTaSPUsSet test.
(outFZ <- MTaSPUsSet(ZsF, corSNP=corSNPF, corPhe = corPheF,
pow=c(1,2,4,8), pow2 = c(1,2,4,8), n.perm=10, Ps=FALSE))
```

| MTaSPUsSetC | gene-Multitrait Sum of Powered Score (MTSPUsSet) tests and adaptive MTSPUsSet (MTaSPUsSet) test for multi trait - SNP set association with GWAS summary statistics. (C coded version) |

**Description**

It gives p-values of the MTSPUsSet tests and MTaSPUsSet test with GWAS summary statistics.

**Usage**

```r
MTaSPUsSetC(Zs, corSNP, corPhe, pow = c(1, 2, 4, 8), pow2 = c(1, 2, 4, 8),
n.perm = 5000, Ps = FALSE)
```

**Arguments**

- **Zs**
  - Z-scores for each SNPs. It could be P-values if the Ps option is TRUE.
- **corSNP**
  - Correlation matirx of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).
- **corPhe**
  - Correlation matirx of phenotypes to be tested; Estimated from Z-scores.
- **pow**
  - SNP specific power(gamma values) used in MTSPUsSet test.
- **pow2**
  - GENE specific power(gamma values) used in MTSPUsSet test.
- **n.perm**
  - number of permutations or bootstraps.
- **Ps**
  - TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.

**Value**

A vector object, MTSPUsSet test P values and MTaSPUsSet P value.

**Author(s)**

Il-Youp Kwak and Wei Pan

**References**

Il-Youp Kwak, Wei Pan (2016) Gene- and pathway-based association tests for multiple traits with GWAS summary statistics
MTaSPUsSetPath

See Also

MTaSPUsSet

Examples

data(SAMD11)
attach(SAMD11)
## example analysis using aSPUM test.
(outFZC <- MTaSPUsSetC(ZsF, corSNP=corSNPF, corPhe = corPheF,
pow=c(1,2,4,8), pow2 = c(1,2,4,8), n.perm=10, Ps=FALSE))

MTaSPUsSetPath  Multitraits - Pathway based Sum of Powered Score tests (MTSPUsSetPath) and adaptive MTSPUsSetPath (MTaSPUsSetPath) test for multi trait - pathway association with GWAS summary statistics.

Description

It gives p-values of the MTSPUsSetPath tests and MTaSPUsSetPath test with GWAS summary statistics.

Usage

MTaSPUsSetPath(Zs, corPhe, corSNP, pow1 = c(1, 2, 4, 8), pow2 = c(1, 2, 4, 8), pow3 = c(1, 2, 4, 8), snp.info, gene.info, n.perm = 1000,
Ps = FALSE, prune = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zs</td>
<td>Z-score matrix. row represent SNPs and column represent traits. It could be P-values if the Ps option is TRUE.</td>
</tr>
<tr>
<td>corPhe</td>
<td>Correlation matrix of phenotypes to be tested; Estimated from Z-scores.</td>
</tr>
<tr>
<td>corSNP</td>
<td>Correlation matrix of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).</td>
</tr>
<tr>
<td>pow1</td>
<td>SNP specific power(gamma values) used in MTSPUsSetPath test.</td>
</tr>
<tr>
<td>pow2</td>
<td>GENE specific power(gamma values) used in MTSPUsSetPath test.</td>
</tr>
<tr>
<td>pow3</td>
<td>Trait specific power(gamma values) used in MTSPUsSetPath test.</td>
</tr>
<tr>
<td>snp.info</td>
<td>SNP information matrix, the 1st column is SNP id, 2nd column is chromosome #, 3rd column indicates SNP location.</td>
</tr>
<tr>
<td>gene.info</td>
<td>GENE information matrix, The 1st column is GENE id, 2nd column is chromosome #, 3rd and 4th column indicate start and end positions of the gene.</td>
</tr>
<tr>
<td>n.perm</td>
<td>number of permutations.</td>
</tr>
<tr>
<td>Ps</td>
<td>TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.</td>
</tr>
<tr>
<td>prune</td>
<td>if it is TRUE, do pruning before the test using pruneSNP function.</td>
</tr>
</tbody>
</table>
**Value**

P-values for MTSPUsSetpath tests and MTaSPUsSetpPath test.

**Author(s)**

Il-Youp Kwak and Wei Pan

**References**


**See Also**

MTaSPUsSetC, MTaSPUsSet

**Examples**

```r
Zs <- cbind( c( 0.3, 0.2, 0.1, 0.5, 1.2),
             c(-1, -3,-1, 1, 1.2) )
varSNP = cbind( c( 1, 1, 0, 0, 0),
                c(0,0,0,0,0),
                c(0,0,0,1,0),
                c(.11,.0,0,1) )
varPhe = cbind( c( 1, -1),
               c(-1,1) )
gene.info = data.frame( Gnm = c( "G1", "G2"),
                        chr = c(1,3),
                        loc1 = c(0,0), loc2 = c(10,10) )
snp.info = data.frame( rsid = c("rs1", "rs2", "rs3", "rs4", "rs5"),
                     chr = c(1,1,3,3,3), loc = c(1,2,1,2,3) )
out <- MTaSPUsSetPath(Zs, corPhe = varPhe, corSNP = varSNP,
                      n.perm = 100, snp.info = snp.info, gene.info = gene.info)
out
```

**Description**

It gives p-values of the MTSPUsSet tests MTScore and MTaSPUsSet_Score test with GWAS summary statistics.
Usage

\[ \text{MTaSPUsSetScore}(Zs, \text{corSNP}, \text{corPhe}, \text{pow} = c(1, 2, 4, 8), \text{pow2} = c(1, 2, 4, 8), n\text{.perm} = 5000, \text{Ps} = \text{FALSE}) \]

Arguments

- **Zs**: Z-score matrix. Row represent SNPs and column represent traits. It could be P-values if the Ps option is TRUE.
- **corSNP**: Correlation matrix of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).
- **corPhe**: Correlation matrix of phenotypes to be tested; Estimated from Z-scores.
- **pow**: SNP specific power (gamma values) used in MTaSPUsSetScore test.
- **pow2**: GENE specific power (gamma values) used in MTaSPUsSetScore test.
- **n.perm**: number of permutations or bootstraps.
- **Ps**: TRUE if input is p-value, FALSE if input is Z-scores. The default is FALSE.

Value

A vector object, MTaSPUsSet test, MTScore test P values and MTaSPUsSet_Score P value.

Author(s)

Il-Youp Kwak and Wei Pan

References

Il-Youp Kwak, Wei Pan (2016) Gene- and pathway-based association tests for multiple traits with GWAS summary statistics

See Also

- **MTaSPUsSetC**

Examples

data(SAMD11)
attach(SAMD11)
### example analysis using aSPUM test.
(outFZ <- MTaSPUsSetScore(ZsF, corSNP=corSNPF, corPhe = corPheF, 
                          pow=c(1,2,4,8), pow2 = c(1,2,4,8), n_perm=10, Ps=FALSE))
plotPmat

Image plot of P-value matrix.

Description

It gives a P-value image for a given P-value matrix.

Usage

plotPmat(Ps, zlim = NULL, main = NULL, yl = NULL, xlab = "SNPs", thresh = -log(5e-08, 10), trait.names = NULL)

Arguments

- **Ps**: P-value matrix. Row represent traits, column represent SNPs
- **zlim**: -log 10 transformed p value range.
- **main**: main title.
- **yl**: it controls the location of trait names.
- **xlab**: label for x axis. Default is "SNPs".
- **thresh**: Default is set to widely used genome wise threshold -log(5e-8,10).
- **trait.names**: A vector of trait names.

Value

Image of P-values matrix.

Author(s)

Il-Youp Kwak and Wei Pan

References


See Also

aSPUs
Examples

```r
## Say we have 3 traits and their p-values at 5 SNPs.
Ps <- rbind( c(0.001, 0.4, 0.5, 0.0000001, .1),
              c(0.03, 0.3, 0.3, 0.00001, .2),
              c(0.01, 0.2, 0.4, 0.001, .0001) )

## We can visualize it using plotPmat function.
plotPmat(Ps)
```

---

```r
pruneSNP

Prune SNPs (related to aSPUs, aSPUsPath, MTaSPUsSet)
```

**Description**

When correlation matrix have highly correlated SNPs, the performance of aSPUs, aSPUsPath and MTaSPUsSet are not very good. Do pruning using this function.

**Usage**

```
pruneSNP(corSNP, rup = 0.95, rdown = -0.95)
```

**Arguments**

- `corSNP`: Correlation matrix of the SNPs to be tested; estimated from a reference panel (based on the same set of the reference alleles as used in calculating Z-scores).
- `rup`: pruning criteria, erase one SNP when correlation between two SNPs are larger than this value.
- `rdown`: pruning criteria, erase one SNP when correlation between two SNPs are smaller than this value.

**Value**

A list object `pruned.corSNP` and `to.erase`. `pruned.corSNP` is pruned correlation matrix. `to.erase` is SNP index to erase to get purged object. (i.e. `corSNP[-to.erase, -to.erase] = pruned.corSNP`)

**Author(s)**

Il Youp Kwak

**See Also**

`aSPUs` `aSPUsPath` `MTaSPUsSet`
Examples

data(kegg9)
## example analysis using aSPUM test.
g <- kegg9$gene.info[1,1]  # SOAT1
## Take snps mapped on gene "SOAT1" from the information of gene.info and snp.info.
snps <- which( (kegg9$snp.info[,2] == kegg9$gene.info[kegg9$gene.info[,1] == g, 2] ) &
               (kegg9$snp.info[,3] > kegg9$gene.info[kegg9$gene.info[,1] == g, 3] ) &
## Take subsets
newP <- kegg9$sNP[snps];
ldsub <- kegg9$ldmatrix[snps, snps];

prSNP <- pruneSNP(ldsub)
newP <- newP[-prSNP$to.erase]
ldsub <- ldsub[-prSNP$to.erase, -prSNP$to.erase ]

## Get p-value for gene SOAT1. Read vignette for details.
out <- aSPUs(newP, corSNP=ldsub , pow=c(1:8, Inf), n.perm=100, Ps=TRUE)

out$Ts
# This is a vector of Test Statistics for SPUM and aSPUM tests.
# SPUs1 to SPUsInf corresponds with the option pow=c(1:8, Inf)
# They are SPUs test statistics.
# The last element aSPUs is minimum of them, aSPUs statistic.

out$pvs
# This is a vector of p-values for SPUs and aSPUs tests.
# SPUs1 to SPUsInf corresponds with the option pow=c(1:8, Inf)
# They are p-values for corresponding SPUs tests.
# The last element is p-value of aSPUs test.

---

SAMD11

An example data for MTaSPUsSet test

Description

Genetic Investigation of ANthropometric Traits (GIANT) consortium data contain P-values of 2.7 million SNPs with six anthropometric traits that are well established to represent body size and shape: height, weight, BMI, waist circumference (WC), hip circumference (HIP). The data is downloadable from https://www.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_files
We mapped SNPs on gene SAMD11. This subdata contains P values, Z scores of SNPs mapped on gene SAMD11. It also contains correlation among SNPs and correlation among phenotypes for demonstrated example of MTaSPUsSet test.

Usage

data(SAMD11)
References

Examples
data(SAMD11)

## Z-scores for man
SAMD11$Zsm

## P-values for man
SAMD11$Psm

## correlation among SNPs for man
SAMD11$corSNPM

## correlation among phenotypes for man
SAMD11$corPheM

---

**simPathAR1Snp**  
*Simulating a pathway with multiple SNPs.*

Description
It gives a simulated SNPs consisting of multiple genes in a pathway. Each SNPs from a latent multivariate Gaussian variable with an AR1 correlation structure.

Usage
```r
simPathAR1Snp(nGenes = 10, nGenes1 = 5, nSNPs = NULL, ncSNPs = NULL,  
    nSNPlim = c(1, 20), nSNP0 = 1:3, LOR = 0.3, n = 100,  
    MAFlim = c(0.05, 0.4), rholim = c(0, 0), p0 = 0.05, noncausal = FALSE)
```

Arguments
- **nGenes**: The number of total genes.
- **nGenes1**: The number of causal genes.
- **nSNPs**: A vector, length matched with total number of genes. Each elements of vector indicate the number of SNPs in the gene. Default is nSNPs = NULL, in this case the number of nSNPs randomly selected from nSNPlow to nSNPup.
- **ncSNPs**: A vector, length matched with total number of genes. Each elements of vector indicate the number of causal SNPs in the gene. Default is ncSNPs = NULL, in this case the number of ncSNPs are randomly selected from nSNP0.
If `nSNPs = NULL`, the number of SNPs in Gene randomly selected from Unif(`nSNPlim[1]`,

If `ncSNPs = NULL`, the number of causal SNPs in Gene randomly selected from
`nSNP0`. Default is 1:3.

Association in log OR between a causal SNP and outcome.

# of cases (= # of controls).


the SNPs in each gene are from a latent Normal variable with a AR(rho) corr
structure, rho’s are drawn from Unif(`rholim[1]`, `rholim[2]`); the SNPs in diff
genes are independant.

background disease prevalence; i.e. intercept=log(p0/(1-p0)).

exclude causal SNPs if TRUE, it is the simulation set up d in the paper(Pan et al
2015).

a list of the binary outcome Y (=0 or 1) and SNPs (=0, 1 or 2); Y is a vector of length 2n; X is a
matrix of 2n by nSNP.

See Also

aSPUpath

Examples

```r
# Simulation set up A a) in the paper (Pan et al 2015)
## Not run: simul <- simPathAR1Snp(nGenes=20, nGenes1=1, nSNPlim=c(1, 20), nSNP0=1:3,
##                  LOR=2, rholim=c(0,0),
##                  n=100, MAFlim=c(0.05, 0.4), p0=0.05)
## End(Not run)

# Simulation set up A b) in the paper
# simulb <- simPathAR1Snp(nGenes=20, nGenes1=1, nSNPlim=c(1, 100), nSNP0=1:3,
#                  LOR=2, rholim=c(0,0),
#                  n=100, MAFlim=c(0.05, 0.4), p0=0.05)
```
Description

Genetic Investigation of ANthropometric Traits (GIANT) consortium data contain P-values of 2.7 million SNPs with six anthropometric traits that are well established to represent body size and shape: height, weight, BMI, waist circumference (WC), hip circumference (HIP). The data is downloadable from https://www.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_files

We mapped SNPs on gene LCORL, RASA2, STK33 and RPGRIP1L. This subdata contains P values, correlation matrices for demonstrated example of MTaSPUsSet test.

Usage

data(someGs)

References


Examples

data(someGs)

```r
## P-values for LCORL
someGs$LCORL[[1]]
```

```r
## correlation matrix for LCORL
someGs$LCORL[[2]]
```

```r
## P-values for RASA2
someGs$RASA2[[1]]
```

```r
## correlation matrix for LCORL
someGs$RASA2[[2]]
```

# See vignettes for more details.
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