

# Package ‘jointsum’

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**Title** jointsum

**Version** 0.13

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**Description** Joint analysis using summary statistics.

**Depends** R (>= 3.2.4)

**Imports** MASS

**License** MIT

**Encoding** UTF-8

**LazyData** TRUE

**RoxygenNote** 6.0.1.9000

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JointSum	<i>JointSum</i>
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## Description

Use summary statistics to build a joint linear model for one trait vs. L SNPs or one trait vs. L SNPs + (K-1) traits.

## Usage

```
JointSum(B1, S1, B2=0, S2=0, N, XX=diag(1, nrow=1), YY0, adj_Y=1, lam=0)
```

**Arguments**

B1	a $L \times 1$ matrix containing marginal effects on the trait treated as response.
S1	a $L \times 1$ matrix containing standard errors for B1.
B2	a $L \times (K-1)$ matrix containing marginal effects on the $(K-1)$ traits to adjust for. If $K=1$ , do not specify this.
S2	a $L \times (K-1)$ matrix containing standard errors for B2. If $K=1$ , do not specify this.
N	a $L \times K$ matrix containing sample sizes for each coefficients in B1, B2.
XX	a $L \times L$ estimated covariance matrix for the $L$ SNPs.
YY0	a $K \times K$ estimated correlation matrix for the $K$ traits.
adj_Y	whether traits should be adjusted for. If it is 0, adjust for SNPs only. Otherwise adjust for both SNPs and traits.
lam	a modifying parameter in $[0,1)$ . It is used only if $\text{adj\_Y}=1$ .

**Value**

beta	coefficient estimates (SNPs first).
cov	the covariance matrix for coefficients.
pvalue	p-values for coefficients.
sigma2	estimated mean squared error.

**Author(s)**

Yangqing Deng and Wei Pan.

**References**

Deng, Y., Pan, W. (2017). Conditional analysis of multiple quantitative traits based on marginal GWAS summary statistics. *Genet Epidemiol.* doi: 10.1002/gepi.22046.

**Examples**

```
#2 correlated SNPs, 2 traits
set.seed(13)
x1=rbinom(1000,1,0.3)
x2=c(x1[1:300],rbinom(1000-300,1,0.3))
y2=rnorm(1000)+x1
y1=rnorm(1000)+y2/2

#standardization
x1=x1-mean(x1)
x2=x2-mean(x2)
y1=y1-mean(y1)
y2=y2-mean(y2)

#summary statistics
a=summary(lm(y1~x1-1))$coefficients
b=summary(lm(y1~x2-1))$coefficients
c=summary(lm(y2~x1-1))$coefficients
d=summary(lm(y2~x2-1))$coefficients

B1=as.matrix(c(a[1],b[1]))
```

```

S1=as.matrix(c(a[2],b[2]))
B2=as.matrix(c(c[1],d[1]))
S2=as.matrix(c(c[2],d[2]))
N=matrix(1000,nrow=2,ncol=2)
XX=cov(cbind(x1,x2))
YY0=cor(cbind(y1,y2))

#model Y1 ~ X1 + X2
JointSum(B1,S1,B2,S2,N,XX,YY0,adj_Y=0)
#or
JointSum(B1,S1,N=N[,1],XX=XX,YY0=diag(1),adj_Y=0)

#model Y1 ~ X1 + X2 + Y2
JointSum(B1,S1,B2,S2,N,XX,YY0,adj_Y=1)

#may compare with joint models using individual level data
summary(lm(y1~x1+x2-1))
summary(lm(y1~x1+x2+y2-1))

```

SMI

SMI

## Description

Build a joint linear model for one trait vs.  $q$  SNPs using summary statistics and the MI-type approach.

## Usage

```
SMI(BM, SM, N, Bref, mult=30)
```

## Arguments

BM	a $q \times 1$ matrix containing marginal effects of the $q$ SNPs on the trait.
SM	a $q \times 1$ matrix containing standard errors for BM.
N	a $q \times 1$ matrix containing sample sizes for each coefficient in BM.
Bref	a $nref \times q$ matrix. Reference data with $nref$ subjects and the $q$ SNPs.
mult	the number of imputations for the MI-type approach. When $mult=0$ , do not use the MI-type approach.

## Value

beta	coefficient estimates.
cov	the covariance matrix for coefficients.
chisq	the test statistic for the Wald test (jointly testing the $q$ SNPs).
df	the degree of freedom for the test statistic.
pvalue	the p-value.

## Author(s)

Yangqing Deng and Wei Pan.

**Examples**

```
#2 SNPs, 1 trait
set.seed(190)
x1=rbinom(1000,1,0.3)
x2=c(x1[1:400],rbinom(1000-400,1,0.3))
y1=rnorm(1000)
Bref0=cbind(x1,x2)

#standardization
x1=x1-mean(x1)
x2=x2-mean(x2)
y1=y1-mean(y1)

#summary statistics
a=summary(lm(y1~x1-1))$coefficients
b=summary(lm(y1~x2-1))$coefficients

BM=as.matrix(c(a[1],b[1]))
SM=as.matrix(c(a[2],b[2]))
N=matrix(1000,nrow=2,ncol=1)

#reference data
x1b=rbinom(500,1,0.3)
x2b=c(x1b[1:220],rbinom(500-220,1,0.3))
Bref=cbind(x1b,x2b)

#models using reference data
SMI(BM,SM,N,Bref,mult=1)
SMI(BM,SM,N,Bref,mult=30)

#model using original data
SMI(BM,SM,N,Bref0,mult=1)
```

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