

Package ‘gskat’

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Type Package

Title GEE_KM

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Description Family based association test via GEE Kernel Machine score test

License GPL (>= 2)

LazyData yes

LazyLoad yes

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gskat-package

Family based association test via kernel machine regression score test

Description

R package for GEE_SKAT.

Details

Package: gskat
Type: Package
Version: 1.0
Date: 2012-12-30
License: GPL-2
LazyLoad: yes

Author(s)

XUEFENG WANG Maintainer: Xuefeng Wang <pwxfor@gmail.com>

gdata*Sample Data*

Description

Sample data

Usage

data(gdata)

Format

The format is:

gskat_score	<i>Perform GEE_SKAT Score Test</i>
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Description

This function performs family based marker set based association (score test) based on the GEE_SKAT.

Usage

```
gskat_score(pedDat, F1=FALSE)
```

Arguments

pedDat	Input Family Data: A list including four data matrix: ID, y, X, Z. ID: Pedigree ID matrix, having four columns are the Family ID (FID), Individual ID (IID), Paternal ID (FAT), Maternal ID (MAT), respectively. y: binary phenotype coded as 0, 1 X: covariate matrix, including the intercept column Z: SNP genotypes coded 0/1/2 (minor allele count).
F1	If TRUE, use identity working corr. matrix

Value

pval	Returns p-value
ifault	fault indicator from the davies method: 0: no error, 1: requested accuracy could not be obtained, 2: round-off error possibly significant, 3: invalid parameters, 4: unable to locate integration parameters

Author(s)

Xuefeng Wang

Examples

```
gskat_score(gdata)
```

gskat_score_pert	<i>Perform GEE_SKAT Score Test (perturbation)</i>
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Description

This function performs family based marker set based association (score test) based on the GEE_SKAT.

Usage

```
gskat_score_pert(pedDat, F1=FALSE, pw="Rade", np=10000)
```

Arguments

pedDat	Input Family Data: A list including four data matrix: ID, y, X, Z. ID: Pedigree ID matrix. The four columns are the Family ID (FID), Individual ID (IID), Paternal ID (FAT), Maternal ID (MAT), respectively. y: binary phenotype coded as 0, 1 X: covaraite matrix, including the intercept column Z: SNP genotypes coded 0/1/2 (minor allele count).
F1	If TRUE, use identity working corr. matrix
pw	Perturbation method. "Rade":Rademacher; "Norm": Normal distribution
np	number of perturbed samples. default=10000

Value

pval	Returns p-value
Ts	Score statistic
mu_Ts	Theoretical mean of Ts
var_Ts	Theoretical variance of Ts
PM	Empirical mean of Ts based on the perturbation
PV	Empirical variance of Ts based on the perturbation

Author(s)

Xuefeng Wang

Examples

```
gskat_score_pert(gdata)
```

gskat_seq

Perform GEE_KM Score Test with sequencing data

Description

This function performs family based marker set based association (score test) based on the GEE_KM.

Usage

```
gskat_seq(y, XC, Z, ID, impute.method="fixed", SNP.weights=NULL,
w_a=1, w_b=25, resampling=TRUE, pw="Rade", Uc=TRUE, sW=FALSE, np=10000)
```

Arguments

y	binary phenotype coded as 0, 1
XC	covaraite matrix, including the intercept column
Z	SNP genotypes coded 0/1/2 (minor allele count)
ID	ID: Pedigree ID matrix, having four columns are the Family ID (FID), Individual ID (IID), Paternal ID (FAT), Maternal ID (MAT), respectively.
impute.method	default is fixed method i.e. fill with means
SNP.weights	If NULL, the default beta (1,25) desensity will be used, or a custimoized weight vector may be used
w_a	The first parameter of the beta density in the weight function
w_b	The second parameter of the beta density in the weight function
resampling	If TRUE, resampling will be applied
pw	r.v. used in the perturbation, "Norm"=Normal , "Rade"=Rademacher
Uc	Score centered or not
sW	standardize weights
np	No. of perturbed samples

Value

p1	Returns asymptotic p-value
p2	Returns resampling p-value

Author(s)

Xuefeng Wang

Examples

```
# gskat_score(gdata)$p2
```

gskat_seq_cont	<i>Perform GEE_KM Score Test with sequencing data for continuous traits</i>
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Description

This function performs family based marker set based association (score test) based on the GEE_KM.

Usage

```
gskat_seq_cont(y, XC, Z, ID, impute.method="fixed", SNP.weights=NULL,
w_a=1, w_b=25, resampling=TRUE, pw="Rade", Uc=TRUE, sW=FALSE, np=10000)
```

Arguments

y	binary phenotype coded as 0, 1
XC	covariate matrix, including the intercept column
Z	SNP genotypes coded 0/1/2 (minor allele count)
ID	ID: Pedigree ID matrix, having four columns are the Family ID (FID), Individual ID (IID), Paternal ID (FAT), Maternal ID (MAT), respectively.
impute.method	default is fixed method i.e. fill with means
SNP.weights	If NULL, the default beta (1,25) desensity will be used, or a custimoized weight vector may be used
w_a	The first parameter of the beta density in the weight function
w_b	The second parameter of the beta density in the weight function
resampling	If TRUE, resampling will be applied
pw	r.v. used in the perturbation, "Norm"=Normal , "Rade"=Rademacher
Uc	Score centered or not
sW	standardize weights or not
np	No. of perturbed samples

Value

p1	Returns asymptotic p-value
p2	Returns resampling p-value

Author(s)

Xuefeng Wang

Examples

```
# gskat_seq_cont(y, XC=X, Z, ID)
```

score.RFAM_IC_burden *Burden test based on GEE_SKAT*

Description

This function performs burden test based on the GEE_SKAT.

Usage

```
score.RFAM_IC_burden(y, XC, Z, FID)
```

Arguments

y	binary phenotype coded as 0, 1
XC	covaraite matrix, WITHOUT the intercept column.
Z	SNP genotypes coded 0/1/2 (minor allele count).
FID	Family ID

Value

Returns p-value

Author(s)

Xuefeng Wang

See Also

geeglm_wrap; gee_wrap

Examples

```
Z1=genoC(gdata$Z)
score.RFAM_IC_burden(y=gdata$y, XC=gdata$X[, -1], Z=Z1, FID=gdata$ID[, 1])
```

score_FSKAT_IC_pertu *GEE_SKAT for rare variants*

Description

This function performs GEE_SKAT score test based on the davies and perturbation method

Usage

```
score_FSKAT_IC_pertu(y, XC, Z, ID, w_a=1, w_b=5, pw="Rade", Uc=FALSE, sW=TRUE, np=10000)
```

Arguments

y	binary phenotype coded as 0, 1
XC	covaraite matrix, WITHOUT the intercept column.
Z	SNP genotypes coded 0/1/2 (minor allele count).
ID	Pedigree ID matrix. The four columns are the Family ID (FID), Individual ID (IID), Paternal ID (FAT), Maternal ID (MAT), respectively.
w_a	The first parameter of the beta density in the weight function
w_b	The second parameter of the beta density in the weight function
pw	perturbatio method: "Rade"=Rademacher; "Norm"=Normal
Uc	Score centered or not
sW	standardize weights or not
np	No. of perturbed samples

Value

pval_davies	Returns p-value from davies method
ifault	fault indicator from the davies method: 0: no error, 1: requested accuracy could not be obtained, 2: round-off error possibly significant, 3: invalid parameters, 4: unable to locate integration parameters
PM	Empirical mean of Ts based on perturbation
mu_Ts	Theoretical mean of Ts
PV	Empirical variance of Ts based on perturbation
var_Ts	Theoretical variance of Ts
pval_pert	Returns p-value from perturbation method

Author(s)

Xuefeng Wang

See Also

score.RFAM_IC_burden

Examples

```
score_FSKAT_IC_pertu(y=gdata$y, XC=gdata$X[, -1], Z=gdata$Z, ID=gdata$ID)
```


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