

# Package ‘gskat’

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**Type** Package

**Title** GEE\_KM

**Version** 1.0

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**Description** Family based association test via GEE Kernel Machine score test

**License** GPL (>= 2)

**LazyData** yes

**LazyLoad** yes

**Depends** R (>= 2.10), CompQuadForm, e1071, gee, geepack, Matrix

**NeedsCompilation** no

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## R topics documented:

gskat-package . . . . .	2
gdata . . . . .	2
gskat_score . . . . .	3
gskat_score_pert . . . . .	3
gskat_seq . . . . .	4
gskat_seq_cont . . . . .	5
score.RFAM_IC_burden . . . . .	6
score_FSKAT_IC_pertu . . . . .	7

<b>Index</b>	<b>9</b>
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gskat-package

*Family based association test via kernel machine regression score test*

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**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>

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gdata*Sample Data*

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**Description**

Sample data

**Usage**

data(gdata)

**Format**

The format is:

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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)
```

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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)
```

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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
```

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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) density will be used, or a customized 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)
```

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score.RFAM\_IC\_burden *Burden test based on GEE\_SKAT*

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**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)
```



# Index

\*Topic **datasets**

gdata, [2](#)

\*Topic **package**

gskat-package, [2](#)

gdata, [2](#)

gskat (gskat-package), [2](#)

gskat-package, [2](#)

gskat\_score, [3](#)

gskat\_score\_pert, [3](#)

gskat\_seq, [4](#)

gskat\_seq\_cont, [5](#)

score.RFAM\_IC\_burden, [6](#)

score\_FSKAT\_IC\_pertu, [7](#)