Package 'betafam'

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Title Detecting rare variants for quantitative traits using nuclear families

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Description To detecting rare variants for quantitative traits using nuclear families, the linear combination methods are proposed using the estimated regression coefficients from the multiple regression and regularized regression as the weights.

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R topics documented:

`betafam` *Detecting rare variants for quantitative traits uing nuclear families*

Description

To detecting rare variants for quantitative traits using nuclear families, the linear combination methods are proposed using the estimated regression coefficients from the multiple regression and regularized regression as the weights.

Usage

```
betafam(ped,group.threshold=-1,fix.group.index=NULL, fix.weight=NULL,mute.SMM=TRUE,trait=c("binary"
```

Arguments

ped	input data, has same format with PLINK but having column names. The PED file is a white-space (space or tab) delimited file: the first six columns are mandatory: FID: Family ID; IID: Individual ID; FA: Paternal ID; MO: Maternal ID; SEX: Sex (1=male; 2=female; other=unknown); PHENO: Phenotype; Genotypes (column 7 onwards) should also be white-space delimited; they are coded as 0, 1 and 2, indicating the number of coding allele, and NA is for missing genotype.
group.threshold	optional, indicates the minor allele frequency threshold that alleles will be grouped marker in the pre-group step before the linear combination test; default is -1, which means all markers are not grouped.
fix.group.index	optional, indicates the fixed grouping index for each marker regardless of the group.threshold value. The length of this vector equals the number of markers. For example, if fix.group.index=c(1,1,2,2,2), the first two markers will be grouped and the last three will grouped together marker in the pre-group step. Default is NULL, which means no pre-group is to be done.
fix.weight	optional, indicates the fixed weight for each marker in the pre-group step. The length of this vector equals the number of markers. Default is NULL, which means the weight on each marker is automatically specified by 1/sqrt(q(1-q)), where q is the minor allele frequency.
mute.SMM	indicates whether or not the multi-marker test, same as FBAT -m test, should be calculated; default is TRUE.
trait	taking values as c("binary","qtl"),indicates the trait type, either binary ("binary") or quantitative ("qtl").
LC.test	taking values as c("LC.true","LC","sig.LC","LC.mreg","LC.lasso","LC.elasticnet"), indicates which test should be included in the linear combination methods. See details in the reference paper.
sig.LC.cutoff	indicates the pvalue threshold for grouping the markers with pvalue< sig.LC.cutoff in the sig.LC test; default is 0.
true.beta	indicates the true beta values used as the weights in the linear combination methods for simulation use only. Alternatively, this could be used as fixed weights given by the user.
ped2multifam	indicates whether or not a pedigree could be separated into multiple nuclear families. Default is FALSE.
useParInRegression	indicates whether or not parents will be used in the linear regression for estimating the weights. Default is FALSE.
trace	indicates whether or not the intermediate outcomes should be printed; default is FALSE.

Value

single.P	pvalues for the sigle marker tests.
minP	minimum pvalue for the sigle marker tests.
Z	test statistic Z=S-E(S).
Z.stat	Z statistics for each marker or group.
Zk.var	variance calculating by parental genotypes.
allele.weight	frequency-determined weights.
group.index	group index used in the pre-group step.
Ngroup	number of groups in the pre-group step.
sigma	empirical variance matrix.
inv.sigma	inverse sigma.
SMM.stat	multiple marker test statistic
SMM.pvalue	pvalue on the multiple marker test.
why.SMM.na	reason that the SMM test does not exist.
LC.beta	estimated betas in the LC test based on the single marker regression.
LC.stat	LC test statistic
LC.pvalue	pvalue on the LC test
sig.LC.beta	estimated betas in the sig.LC test.
sig.LC.stat	sig.LC test statistic
sig.LC.pvalue	pvalue on the sig.LC test
true.LC.beta	estimated betas in the true.LC test.
true.LC.stat	true.LC test statistic
true.LC.pvalue	pvalue on the true.LC test
mreg.LC.beta	estimated betas in the mreg.LC test.
mreg.LC.stat	mreg.LC test statistic
mreg.LC.pvalue	pvalue on the mreg.LC test
lasso.LC.beta	estimated betas in the lasso.LC test.
lasso.LC.stat	lasso.LC test statistic
lasso.LC.pvalue	pvalue on the lasso.LC test
elasticnet.LC.beta	estimated betas in the elasticnet.LC test.
elasticnet.LC.stat	elasticnet.LC test statistic
elasticnet.LC.pvalue	pvalue on the elasticnet.LC test
runtime	runtime of this program.
fam.info	nuclear families in the ped data.

References

Guo W , Shugart YY, Detecting Rare Variants for Quantitative Traits Using Nuclear Families (manuscript).

Examples

```
#example.ped<-read.table("example.ped",head=1,stringsAsFactors=F)
#library(glmnet)
#test<-betafam(ped=example.ped,trace=TRUE)
#test$elasticnet.LC.pvalue
```

`call.moment` *Calculating the expectation and variance of the offspring's genotype conditional on parental genotypes.*

Description

The expectation and variance are calculated with respect to parental genotypes at a single marker under the null distribution of parental random transmission using Mendel's laws.

Usage

```
call.moment(father,mother)
```

Arguments

`father`	indicates the father's genotype, coded as 0, 1 and 2.
`mother`	indicates the mother's genotype, coded as 0, 1 and 2.

Value

`mean`	expecation of the offspring's genotype.
`var`	variance of the offspring's genotype.

References

Guo W , Shugart YY, Detecting Rare Variants for Quantitative Traits Using Nuclear Families (manuscript).

Examples

```
call.moment(1,1)
```

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