Package 'mrMLM.GUI'

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Type Package

Title Multi-Locus Random-SNP-Effect Mixed Linear Model Tools for Genome-Wide Association Study with Graphical User Interface

Version 4.0.2

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Author Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming

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Description Conduct multi-locus genome-wide association study under the framework of multi-locus random-SNP-effect mixed linear model (mrMLM). First, each marker on the genome is scanned. Bonferroni correction is replaced by a less stringent selection criterion for significant test. Then, all the markers that are potentially associated with the trait are included in a multi-locus genetic model, their effects are estimated by empirical Bayes and all the nonzero effects were further identified by likelihood ratio test for true QTL. Wen YJ, Zhang H, Ni YL, Huang B, Zhang J, Feng JY, Wang SB, Dunwell JM, Zhang YM, Wu R (2018) <doi:10.1093/bib/bbw145>.

Depends R (>= 3.5.0),shiny,lars

Imports Rcpp (>= 0.12.14),methods,foreach,ncvreg,coin,shinyjs,data.table,doParallel,sampling,bigmemory,mrMLM,sbl

License GPL (>= 2)

LinkingTo Rcpp,RcppEigen

NeedsCompilation yes

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`mrMLM.GUI-package` *Multi-Locus Random-SNP-Effect Mixed Linear Model Tools for Genome-Wide Association Study with Graphical User Interface*

Description

Description: Conduct multi-locus genome-wide association study under the framework of multi-locus random-SNP-effect mixed linear model (mrMLM). First, each marker on the genome is scanned. Bonferroni correction is replaced by a less stringent selection criterion for significant test. Then, all the markers that are potentially associated with the trait are included in a multi-locus genetic model, their effects are estimated by empirical Bayes and all the nonzero effects were further identified by likelihood ratio test for ture QTL.

Details

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Type:	Package
Version:	4.0.2
Date:	2020-10-8
Depends:	shiny,lars
Imports:	methods,foreach,ncvreg,coin,sampling,data.table,doParallel,shinyjs,bigmemory,mrMLM
License:	GPL version 2 or newer
LazyLoad:	yes

Users can use library(mrMLM.GUI) to start the GUI and use 'mrMLM.GUI()' to restart the programe.

Author(s)

Zhang Ya-Wen, Li Pei, Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

References

1. Zhang YM, Mao Y, Xie C, Smith H, Luo L, Xu S*. Genetics 2005,169:2267-2275. 2. Wang SB, Feng JY, Ren WL, Huang B, Zhou L, Wen YJ, et al. Sci Rep 2016,6:19444. 3. Tamba CL, Ni

YL, Zhang YM*. PLoS Comput Biol 2017,13(1):e1005357. 4. Zhang J, Feng JY, Ni YL, Wen YJ, Niu Y, Tamba CL, et al. Heredity 2018,118(6):517-524. 5. Ren WL, Wen YJ, Dunwell JM, Zhang YM*. Heredity 2018,120(3): 208-218. 6. Wen YJ, Zhang H, Ni YL, Huang B, Zhang J, Feng JY, et al. Brief Bioinform 2018,19(4):700-712. 7. Tamba CL, Zhang YM. bioRxiv,preprint first posted online Jun. 7, 2018, doi:https://doi.org/10.1101/341784. 8. Zhang YW, Tamba CL, Wen YJ, Li P, Ren WL, Ni YL, et al. Genomics, Proteomics & Bioinformatics, Accept.

Examples

```
## Not run:  mrMLM.GUI()
```

`FASTmrEMMA` *To perform GWAS with FASTmrEMMA method*

Description

FAST multi-locus random-SNP-effect EMMA

Usage

```
FASTmrEMMA(gen,phe,outATCG,genRaw,kk,psmatrix,svpal,svmlod,Genformat,Likelihood,CLO)
```

Arguments

`gen`	genotype matrix.
`phe`	phenotype matrix.
`outATCG`	genotype for code 1.
`genRaw`	raw genotype.
`kk`	kinship matrix.
`psmatrix`	population structure matrix.
`svpal`	Critical P-value for selecting variable.
`svmlod`	Critical LOD score for significant QTN.
`Genformat`	Format for genotypic codes.
`Likelihood`	restricted maximum likelihood (REML) and maximum likelihood (ML).
`CLO`	number of CPU.

Author(s)

Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
G1=data(fmegen)
P1=data(mrphe)
G2=data(fmegenraw)
result=FASTmrEMMA(fmegen,mrphe,outATCG=NULL,fmegenraw,kk=NULL,
psmatrix=NULL,0.005,3,1,Likelihood="REML",CLO=1)
```

FASTmrMLM *To perform GWAS with FASTmrMLM method*

Description

FAST multi-locus random-SNP-effect Mixed Linear Model

Usage

```
FASTmrMLM(gen,phe,outATCG,genRaw,kk,psmatrix,svpal,svrad,svmlod,Genformat,CLO)
```

Arguments

gen	genotype matrix.
phe	phenotype matrix.
outATCG	genotype for code 1.
genRaw	raw genotype.
kk	kinship matrix.
psmatrix	population structure matrix.
svpal	Critical P-value for selecting variable.
svrad	Search Radius in search of potentially associated QTN.
svmlod	Critical LOD score for significant QTN.
Genformat	Format for genotypic codes.
CLO	number of CPU.

Author(s)

Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
result=FASTmrMLM(mrgen,mrphe,outATCG=NULL,mrgenraw,kk=NULL,psmatrix=NULL,
0.01,20,3,1,CLO=1)
```

fmegen *Genotype data*

Description

Numeric format of genotype dataset.

Usage

```
data(fmegen)
```

Details

Dataset input of Genotype for FASTmrEMMA function.

Author(s)

Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

fmegenraw *raw genotype data*

Description

Numeric format of raw genotype dataset.

Usage

```
data(fmegenraw)
```

Details

Dataset input of raw genotype for FASTmrEMMA function.

Author(s)

Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

ISIS *To perform GWAS with ISIS EM-BLASSO method*

Description

Iterative Sure Independence Screening EM-Bayesian LASSO

Usage

```
ISIS(gen,phe,outATCG,genRaw,kk,psmatrix,svpal,svmlod,Genformat,CLO)
```

Arguments

gen	genotype matrix.
phe	phenotype matrix.
outATCG	genotype for code 1.
genRaw	raw genotype.
kk	kinship matrix.
psmatrix	population structure matrix.
svpal	Critical P-value for selecting variable.
svmlod	Critical LOD score for significant QTN.
Genformat	Format for genotypic codes.
CLO	number of CPU.

Author(s)

Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
result=ISIS(mrgen,mrphe,outATCG=NULL,mrgenraw,kk=NULL,psmatrix=NULL,
0.01,3,1,CLO=1)
```

mrgen *Genotype data*

Description

Numeric format of genotype dataset.

Usage

```
data(mrgen)
```

Details

Dataset input of Genotype for mrMLM function.

Author(s)

Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

mrgenraw *raw genotype data*

Description

Numeric format of raw genotype dataset.

Usage

```
data(mrgenraw)
```

Details

Dataset input of raw genotype for mrMLM function.

Author(s)

Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

mrMLMFun *To perform GWAS with mrMLM method*

Description

multi-locus random-SNP-effect Mixed Linear Model

Usage

```
mrMLMFun(gen,phe,outATCG,genRaw,kk,psmatrix,svpal,svrad,svmlod,Genformat,CLO)
```

Arguments

gen	genotype matrix.
phe	phenotype matrix.
outATCG	genotype for code 1.
genRaw	raw genotype.
kk	kinship matrix.
psmatrix	population structure matrix.
svpal	Critical P-value for selecting variable
svrad	Search Radius in search of potentially associated QTN.
svmlod	Critical LOD score for significant QTN.
Genformat	Format for genotypic codes.
CLO	number of CPU.

Author(s)

Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
result=mrMLMFun(mrgen,mrphe,outATCG=NULL,mrgenraw,kk=NULL,psmatrix=NULL,
0.01,20,3,1,CLO=1)
```

mrphe *phenotype data*

Description

phenotype dataset.

Usage

```
data(mrphe)
```

Details

Dataset input of phenotype for mrMLM function.

Author(s)

Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

multiplication_speed *Matrix multiplication acceleration algorithm.*

Description

Matrix multiplication acceleration algorithm.

Usage

```
multiplication_speed(A,B)
```

Arguments

A	matrix A.
B	matrix B.

Author(s)

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
## Not run:
A<-matrix(1:10,2,5)
B<-matrix(1:10,5:2)
result<-multiplication_speed(A,B)

## End(Not run)
```

pKWmEB *To perform GWAS with pKWmEB method*

Description

Kruskal-Wallis test with empirical Bayes under polygenic background control

Usage

```
pKWmEB(gen,phe,outATCG,genRaw,kk,psmatrix,svpal,svmlod,Genformat,CLO)
```

Arguments

gen	genotype matrix.
phe	phenotype matrix.
outATCG	genotype for code 1.
genRaw	raw genotype.
kk	kinship matrix.
psmatrix	population structure matrix.
svpal	Critical P-value for selecting variable.
svmlod	Critical LOD score for significant QTN.
Genformat	Format for genotypic codes.
CLO	number of CPU.

Author(s)

Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
result=pKWmEB(mrgen,mrphe,outATCG=NULL,mrgenraw,kk=NULL,psmatrix=NULL,
0.05,3,1,CLO=1)
```

pLARmEB *To perform GWAS with pLARmEB method*

Description

polygene-background-control-based least angle regression plus Empirical Bayes

Usage

```
pLARmEB(gen,phe,outATCG,genRaw,kk,psmatrix,CriLOD,lars1,Genformat,Bootstrap,CLO)
```

Arguments

gen	genotype matrix.
phe	phenotype matrix.
outATCG	genotype for code 1.
genRaw	raw genotype.
kk	kinship matrix.
psmatrix	population structure matrix.
CriLOD	Critical LOD score for significant QTN.
lars1	No. of potentially associated variables selected by LARS.
Genformat	Format for genotypic codes.
Bootstrap	Bootstrap=FALSE indicates the analysis of only real dataset, Bootstrap=TRUE indicates the analysis of both real dataset and four resampling datasets.
CLO	number of CPU.

Author(s)

Zhang Ya-Wen, Li Pei, and Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
result=pLARmEB(mrgen,mrphe,outATCG=NULL,mrgenraw,kk=NULL,psmatrix=NULL,
3,20,1,Bootstrap=FALSE,CLO=1)
```

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