Package 'mrMLM.GUI'

August 25, 2018

Type Package

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

Version 3.2

Date 2018-8-25

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Description Conduct multi-locus genome-wide association study under the framework of 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 model, their effects are estimated by empirical Bayes and true Quantitative Trait Nucleotides (QTN) are identified by likelihood ratio test. 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 shiny,MASS,data.table,doParallel,foreach

Imports methods,openxlsx,stringr,qqman,ggplot2,lars,ncvreg,coin,shinyjs,sampling,bigmemory,mrMLM

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2018-08-25 09:00:02 UTC

R topics documented:

`mrMLM.GUI-package` *Multi-Locus Random-SNP-Effect Mixed Linear Model for Multi-Locus GWAS and Multi-QTL Mapping*

Description

Conduct multi-locus genome-wide association study under the framework of 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 model, their effects are estimated by empirical Bayes and true QTNs are identified by likelihood ratio test.

Details

Package:	mrMLM.GUI
Type:	Package
Version:	3.2
Date:	2018-8-4
Depends:	shiny,MASS,data.table,doParallel,foreach
Imports:	methods,openxlsx,stringr,qqman,ggplot2,lars,ncvreg,coin
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, Ren Wen-Long, Ni Yuan-Li, Zhang Yuan-Ming
Maintainer: Yuan-Ming Zhang<soyzhang@mail.hzau.edu.cn>

References

Methodological implementation of mixed linear models in multi-locus genome-wide association studies. Wen Yang-Jun, Zhang Hanwen, Ni Yuan-Li, Huang Bo, Zhang Jin, Feng Jian-Ying, Wang Shi-Bo, Dunwell Jim M., Zhang Yuan-Ming, Wu Rongling.

Examples

```
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, Ren Wen-Long, Ni Yuan-Li, 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, Ren Wen-Long, Ni Yuan-Li, 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, Ren Wen-Long, Ni Yuan-Li, 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, Ren Wen-Long, Ni Yuan-Li, 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>

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, Ren Wen-Long, Ni Yuan-Li, 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, Ren Wen-Long, Ni Yuan-Li, 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,
3,50,1,Bootstrap=FALSE,CLO=1)
```

Index