

Package ‘mrMLM.GUI’

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Type Package

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

Version 3.1

Date 2018-4-25

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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 (2017) <doi:10.1093/bib/bbw145>.

Depends shiny,MASS,data.table,doParallel,foreach

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

License GPL (>= 2)

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mrMLM.GUI-package	<i>Multi-Locus Random-SNP-Effect Mixed Linear Model for Multi-Locus GWAS and Multi-QTL Mapping</i>
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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 QTN are identified by likelihood ratio test.

Details

```

Package:    mrMLM.GUI
Type:      Package
Version:   3.1
Date:      2018-4-25
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 program.

Author(s)

Zhang Ya-Wen, Li Pei, Ren Wen-Long, Ni Yuan-Li, Zhang Yuan-Ming
 Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

References

Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. Wang Shi-Bo,Feng Jian-Ying,Ren Wen-Long,Huang Bo,Zhou Ling,Wen Yang-Jun,Zhang Jin,Jim M. Dunwell,Xu Shizhong*,Zhang Yuan-Ming*

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, Ren Wen-Long, Ni Yuan-Li, Zhang Yuan-Ming
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Examples

```
G1=data(fmegen)
P1=data(mrphe)
G2=data(fmegenraw)
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: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

Examples

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

fmegen	<i>Genotype data</i>
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Description

Numeric format of genotype dataset.

Usage

```
data(fmegen)
```

Details

Dataset input of Genotype for FASTmrEMMA function.

Author(s)

Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

fmegenraw	<i>raw genotype data</i>
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Description

Numeric format of raw genotype dataset.

Usage

```
data(fmegenraw)
```

Details

Dataset input of raw genotype for FASTmrEMMA function.

Author(s)

Maintainer: Yuanming Zhang<soy Zhang@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: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
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: Yuanming Zhang<soy Zhang@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: Yuanming Zhang<soy Zhang@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: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

Examples

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

mrphe	<i>phenotype data</i>
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Description

phenotype dataset.

Usage

data(mrphe)

Details

Dataset input of phenotype for mrMLM function.

Author(s)

Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

pKWmEB	<i>To perform GWAS with pKWmEB method</i>
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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: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
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: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

Examples

```
G1=data(mrgen)
P1=data(mrphe)
G2=data(mrgenraw)
pLARmEB(mrgen, mrphe, outATCG=NULL, mrgenraw, kk=NULL, psmatrix=NULL,
3, 50, 1, Bootstrap=FALSE, CLO=1)
```

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