

Package ‘mrMLM’

February 9, 2017

Type Package

Title Multi-Locus Random-SNP-Effect Mixed Linear Model for Genome-Wide Association Studies and Linkage Analyses

Version 2.1

Date 2017-02-08

Author Wenlong Ren, Yuanli Ni, Shibo Wang, Yangjun Wen, Bo Huang and Yuanming Zhang

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

Description Conduct multi-locus GWAS and multi-locus QTL mapping under the framework of random-SNP-effect mixed linear model (mrMLM). First, each position (or marker) on the genome is scanned by mrMLM algorithm. Bonferroni correction is replaced by a less stringent selection criterion for significant test. Then, all the markers (or QTL) that are potentially associated with the trait are included in a multi-locus model, their effects are estimated by empirical Bayes and true QTN or QTL are identified by likelihood ratio test.

Depends gWidgets, gWidgetsRGtk2, RGtk2Extras, MASS

Imports RGtk2, methods, openxlsx, stringr, qqman, ggplot2, lars, ncvreg

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2017-02-09 07:02:00

R topics documented:

mrMLM-package 2

Index 3

mrMLM-package

Multi-Locus Random-SNP-Effect Mixed Linear Model for Genome-Wide Association Studies and Linkage Analyses

Description

Conduct multi-locus GWAS and multi-locus QTL mapping under the framework of random-SNP-effect mixed linear model (mrMLM). First, each position (or marker) on the genome is scanned by mrMLM algorithm. Bonferroni correction is replaced by a less stringent selection criterion for significant test. Then, all the markers (or QTL) that are potentially associated with the trait are included in a multi-locus model, their effects are estimated by empirical Bayes and true QTN or QTL are identified by likelihood ratio test.

Details

Package: mrMLM
Type: Package
Version: 2.1
Date: 2017-02-08
Depends: gWidgets,gWidgetsRGtk2,RGtk2Extras,MASS
Imports: RGtk2,methods,openxlsx,stringr,qqman,ggplot2,lars,ncvreg
License: GPL version 2 or newer
LazyLoad: yes

Users can use `library(mrMLM)` to start the GUI and use `'mrMLM()'` to restart the program. Please refer to the documentation section of the project homepage for the usage of FASTmrEMMA.

Author(s)

Ren Wen-Long, Ni Yuan-Li, Wen Yang-Jun, Zhang Jin, Cox Lwaka Tamba, Wang Shi-Bo, Huang Bo, 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

```
library(mrMLM)
```

Index

*Topic **R**

mrMLM-package, [2](#)

*Topic **mrMLM**

mrMLM-package, [2](#)

*Topic **package**

mrMLM-package, [2](#)

*Topic

mrMLM-package, [2](#)

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

mrMLM-package, [2](#)