

# Package ‘mrMLM’

December 20, 2016

**Type** Package

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

**Version** 2.0

**Date** 2016-12-19

**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, ggplot2, qqman

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2016-12-20 10:19:38

## R topics documented:

mrMLM-package . . . . . 2

**Index** . . . . . 4

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: 2.0  
 Date: 2016-12-19  
 Depends: gWidgets,gWidgetsRGtk2,RGtk2Extras,MASS  
 Imports: RGtk2,methods,openxlsx,stringr,ggplot2,qqman  
 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 mrMLM.

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

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

**References**

1. 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\*. Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. *Scientific Reports* 2016, 6: 19444.
2. Wang Shi-Bo, Wen Yang-Jun, Ren Wen-Long, Ni Yuan-Li, Zhang Jin, Feng Jian-Ying, Zhang Yuan-Ming\*. Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. *Scientific Reports* 2016, 6: 29951.
3. Wen Yang-Jun, Zhang Hanwen, Ni Yuan-Li, Huang Bo, Zhang Jin, Feng Jian-Ying, Wang Shi-Bo, Jim M. Dunwell, Zhang Yuan-Ming\*, Wu Rongling\*. Methodological implementation of mixed linear models in multi-locus genome-wide association studies. *Briefings in Bioinformatics* 2016, DOI: 10.1093/bib/bbw145
4. Zhang Yuan-Ming et al. Mapping quantitative trait loci using naturally occurring genetic variance among commercial inbred line of maize (*Zea mays* L.). *Genetics* 2005, 169:2267-2275.

**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](#)