

# Package ‘QTL.gCIMapping’

June 16, 2018

**Type** Package

**Title** QTL Genome-Wide Composite Interval Mapping

**Version** 3.0

**Date** 2018-6-13

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**Description** Conduct multiple quantitative trait loci (QTL) mapping under the framework of random-QTL-effect mixed linear model. First, each position on the genome is detected in order to construct a negative logarithm P-value curve against genome position. Then, all the peaks on each effect (additive or dominant) curve are viewed as potential QTL, all the effects of the potential QTL are included in a multi-QTL model, their effects are estimated by empirical Bayes in doubled haploid or by adaptive lasso in F2, and true QTL are identified by likelihood ratio test. Wang S-B, Wen Y-J, Ren W-L, Ni Y-L, Zhang J, Feng J-Y, Zhang Y-M (2016) <doi:10.1038/srep29951>.

**Encoding** UTF-8

**Depends** MASS, qtl, doParallel, foreach, parallel

**License** GPL (>= 2)

**Imports** Rcpp (>= 0.12.17), methods, openxlsx, stringr, data.table, parcor

**LinkingTo** Rcpp

**NeedsCompilation** yes

**Repository** CRAN

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f2data	<i>F2 example data</i>
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**Description**

GCIM format of F2 dataset.

**Usage**

```
data(f2data)
```

**Details**

Dataset input of file for QTL.gCIMapping function.

**Author(s)**

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

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markerinsert	<i>To insert marker in genotype.</i>
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**Description**

a method that can insert marker in genotype.

**Usage**

```
markerinsert(mp,geno,map,c1,gg1,gg2,gg0,flagRIL)
```

**Arguments**

mp	linkage map matrix after insert.
geno	genotype matrix.
map	linkage map matrix.
c1	walk speed.
gg1	raw covariate matrix.
gg2	code for type 1.
gg0	code for missing.
flagRIL	RIL population or not.

**Author(s)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
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**Examples**

```
mp=matrix(c(197.9196,198.7536,199.5876,200.4216,201.2453,
202.0691,202.8928,203.7521,204.6113,205.4706,206.3298,207.1891,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,3,3,3,3,3,3,
1,1,1,2,2,2,3,3,3,3,3,1,2,3,4,5,6,7,8,9,10,11,12),12,5)
map=matrix(c(1,1,1,1,197.9196,200.4216,202.8928,207.1891),4,2)
geno=matrix(c(1,99,99,99),1,4)
QTL.gCIMapping::markerinsert(mp,geno,map,cl=1,gg1=1,gg2=-1,gg0=99,flagRIL=1)
```

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 QTL.gCIMapping

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*QTL Genome-Wide Composite Interval Mapping*


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**Description**

Conduct multiple quantitative trait loci (QTL) mapping under the framework of random-QTL-effect mixed linear model. First, each position on the genome is detected in order to construct a negative logarithm P-value curve against genome position. Then, all the peaks on each effect (additive or dominant) curve are viewed as potential QTL, all the effects of the potential QTL are included in a multi-QTL model, their effects are estimated by empirical Bayes in doubled haploid or by adaptive lasso in F2, and true QTL are identified by likelihood ratio test.

**Usage**

```
QTL.gCIMapping(file,fileFormat,fileICIMcov,Population,Model,WalkSpeed,CriLOD,
Likelihood,flagqrtl,DrawPlot,PlotFormat,Resolution,Trait,dir)
```

**Arguments**

file	File path and name in your computer.
fileFormat	Format for input file (GCIM, ICIM, Cart).
fileICIMcov	File path and name in your computer.
Population	BC1, BC2, DH, RIL, F2.
Model	Random (random model) or Fixed (fixed model) for QTL effects.
WalkSpeed	Walk speed for Genome-wide Scanning.(WalkSpeed=1)
CriLOD	Critical LOD scores for significant QTL (CriLOD=2.5).
Likelihood	This parameter is only for F2 population, including restricted maximum likelihood (REML) and maximum likelihood (ML).

flagrqtl	This parameter is only for F2 population, flagrqtl="FALSE" in the first running. If the other software detects only one QTL in a neighborhood but this software finds two linked QTLs (one with additive effect and another with dominant effect) in the region, let flagrqtl="TRUE"
DrawPlot	This parameter is for all the populations, including FALSE and TRUE, DrawPlot=FALSE indicates no figure output, DrawPlot=TRUE indicates the output of the figure against genome position.
PlotFormat	This parameter is for all the figure files, including *.jpeg, *.png, *.tiff and *.pdf.
Resolution	This parameter is for all the figure files, including Low and High.
Trait	Trait=1:3 indicates the analysis from the first trait to the third trait.
dir	This parameter is for the save path.

### Details

Package: QTL.gCIMapping  
 Type: Package  
 Version: 3.0  
 Date: 2018-6-13  
 Depends: MASS,dplyr,parcor,qt1,doParallel  
 Imports: methods,openxlsx,stringr,Repp  
 License: GPL version 2 or newer  
 LazyLoad: yes

### Author(s)

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

### References

Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. Wang Shi-Bo, Wen Yang-Jun, Ren Wen-Long, Ni Yuan-Li, Zhang Jin, Feng Jian-Ying, Zhang Yuan-Ming\*

### Examples

```

G=data(f2data)
QTL.gCIMapping(file=f2data,fileFormat="GCIM",fileICIMcov=NULL,Population="F2",
Model="Random",WalkSpeed=1,CriLOD=2.5,Likelihood="REML",flagrqtl="FALSE",
DrawPlot="FALSE",PlotFormat="png",Resolution="Low",Trait=1:1,dir=tempdir())
  
```

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WangF *To perform QTL mapping with wang method*

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**Description**

Genome-wide Composite Interval Mapping

**Usage**

WangF(pheRaw, genRaw, mapRaw1, yygg1, flagRIL, cov\_en, Population, WalkSpeed, CriLOD)

**Arguments**

pheRaw	phenotype matrix.
genRaw	genotype matrix.
mapRaw1	linkage map matrix.
yygg1	the transformed covariate matrix .
flagRIL	if RIL or not.
cov_en	raw covariate matrix.
Population	population flag.
WalkSpeed	Walk speed for Genome-wide Scanning.(WalkSpeed=1).
CriLOD	Critical LOD scores for significant QTL (CriLOD=2.5).

**Author(s)**

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WangS *The second step of wang method*

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**Description**

Genome-wide Composite Interval Mapping

**Usage**

WangS(flag, CriLOD, NUM, pheRaw, chrRaw\_name, yygg, mx, phe, chr\_name, gen, mapname)

**Arguments**

flag	fix or random model.
CriLOD	LOD score.
NUM	The number of trait.
pheRaw	Raw phenotype matrix.
chrRaw_name	raw chromosome name.
yygg	covariate matrix.
mx	raw genotype matrix.
phe	phenotype matrix.
chr_name	chromosome name.
gen	genotype matrix.
mapname	linkage map matrix.

**Author(s)**

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 WenF

*To perform QTL mapping with Wen method*

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**Description**

An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2

**Usage**

WenF(pheRaw, genRaw, mapRaw1, yygg1, cov\_en, WalkSpeed, CriLOD, dir)

**Arguments**

pheRaw	phenotype matrix.
genRaw	genotype matrix.
mapRaw1	linkage map matrix.
yygg1	the transformed covariate matrix .
cov_en	raw covariate matrix.
WalkSpeed	Walk speed for Genome-wide Scanning.(WalkSpeed=1).
CriLOD	Critical LOD scores for significant QTL (CriLOD=2.5).
dir	file path in your computer.

**Author(s)**

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

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WenS

*The second step of Wen method*

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### **Description**

An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2

### **Usage**

```
WenS(flag,CriLOD,NUM,pheRaw,Likelihood,flagrqtl,yygg,mx,phe,chr_name,v.map,  
gen.raw,a.gen.orig,d.gen.orig,n,names.insert2,X.ad.tran.data,X.ad.t4,dir)
```

### **Arguments**

flag	random or fix model.
CriLOD	LOD score.
NUM	the number of trait.
pheRaw	raw phenotype matrix .
Likelihood	likelihood function.
flagrqtl	do CIM or not.
yygg	covariate matrix.
mx	raw genotype matrix.
phe	phenotype matrix.
chr_name	chromosome name.
v.map	linkage map matrix.
gen.raw	raw genotype matrix.
a.gen.orig	additive genotype matrix.
d.gen.orig	dominant genotype matrix.
n	number of individual.
names.insert2	linkage map after insert.
X.ad.tran.data	genotype matrix after insert.
X.ad.t4	genotype matrix.
dir	file storage path.

### **Author(s)**

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