

# Package ‘QTL.gCIMapping’

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**Type** Package

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

**Version** 3.3.1

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

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

## Description

Conduct multiple quantitative trait loci (QTL) mapping under the framework of random-QTL-effect linear mixed model. First, each position on the genome is detected in order to obtain 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 population or by adaptive lasso in F2 population, and true QTL are identified by likelihood ratio test. See Wen et al. (2018) <doi:10.1093/bib/bby058>.

**Encoding** UTF-8

**Depends** R (>= 3.5.0), MASS, qtl

**License** GPL (>= 2)

**Imports** Rcpp (>= 0.12.17), methods, openxlsx, stringr, data.table, glmnet, doParallel, foreach

**LinkingTo** Rcpp

**NeedsCompilation** yes

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DHdata	<i>DH example data</i>
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### Description

GCIM format of DH dataset.

### Usage

`data(DHdata)`

### Details

Input file for WangF function.

### Author(s)

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

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Dodata	<i>Process raw data</i>
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### Description

Process raw data for later use

### Usage

`Dodata(fileFormat,Population,Model,readraw)`

### Arguments

<code>fileFormat</code>	Dataset format
<code>Population</code>	Population type.
<code>Model</code>	Random or fixed model.
<code>readraw</code>	Raw data.

**Author(s)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**Examples**

```
## Not run:  
data(DHdata)  
readraw<-Readdata(file=DHdata,fileFormat="GCIM",fileICIMcov=NULL)  
doda<-Doddata(fileFormat="GCIM",Population="DH",Model="Random",readraw)  
  
## End(Not run)
```

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F2data

*F2 example data*

---

**Description**

GCIM format of F2 dataset.

**Usage**

```
data(F2data)
```

**Details**

Input file for WenF function.

**Author(s)**

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

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markerinsert

*To insert marker in genotype.*

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

**Examples**

```
## Not run:
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,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,3,3,3,3,3,3,3,
1,1,1,2,2,2,3,3,3,3,3,3,1,2,3,4,5,6,7,8,9,10,11,12),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,c1=1,gg1=1,gg2=-1,
gg0=99,flagRIL=1)

## End(Not run)
```

---

QTL.gCIMapping

*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,SetSeed,flagqtl,DrawPlot,PlotFormat,Resolution,Trait,dir)
```

**Arguments**

file	File path and name in your computer, i.e., "D:/Users/GCIM_Format_DH.csv".
fileFormat	Format for input file (GCIM, ICIM, Cart).
fileICIMcov	File path and name in your computer, i.e., "D:/Users/ICIM_Cov.csv".
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 REML (restricted maximum likelihood ) and ML(maximum likelihood).
SetSeed	In which the cross validation experiment is needed. Generally speaking, the random seed in the cross-validation experiment was set as 11001. If some known genes are not identified by the seed, users may try to use some new random seeds. At this case, one better result may be obtained.
flagrqt1	This parameter is only for F2 population, flagrqt1="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 flagrqt1="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,i.e.,PlotFormat="tiff".
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,i.e., "D:/Users".

**Details**

Package: QTL.gCIMapping  
 Type: Package  
 Version: 3.3.1  
 Date: 2020-10-8  
 Depends: MASS, qtl  
 Imports: methods, openxlsx, stringr, Rcpp  
 License: GPL version 2 or newer  
 LazyLoad: yes

**Note**

The User Manual file (name: Instruction.pdf) in the folder of ".../QTL.gCIMapping/inst/doc".

**Author(s)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
 Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**References**

1. 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.
2. Wen Yang-Jun, Zhang Ya-Wen, Zhang Jin, Feng Jian-Ying, Jim M. Dunwell, Zhang Yuan-Ming\*. An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2. *Briefings in Bioinformatics* 2019, 20(5): 1913-1924.
3. Zhang Ya-Wen, Wen Yang-Jun, Jim M. Dunwell, Zhang Yuan-Ming\*. QTL.gCIMapping.GUI v2.0: An R software for detecting small-effect and linked QTLs for quantitative traits in bi-parental segregation populations. *Computational and Structural Biotechnology Journal* 2020, 18: 59-65.
4. Wen Yang-Jun, Zhang Ya-Wen, Zhang Jin, Feng Jian-Ying, Zhang Yuan-Ming\*. The improved FASTmrEMMA and GCIM algorithms for genome-wide association and linkage studies in large mapping populations. *The Crop Journal* 2020, 8(5): 723-732.

**Examples**

```
## Not run:
data(F2data)
QTL.gCIMapping(file=F2data,Population="F2",WalkSpeed=1,CriLOD=2.5,
Trait=1,dir=tempdir())

## End(Not run)
```

---

 Readdata

*Read raw data*


---

**Description**

Read raw data which have not been transformed

**Usage**

```
Readdata(file,fileFormat,fileICIMcov)
```

**Arguments**

file	Dataset input
fileFormat	Format of dataset .
fileICIMcov	Format of covariate file of QTLiCIMapping.

**Author(s)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**Examples**

```
## Not run:  
data(F2data)  
Readdata(file=F2data,fileFormat="GCIM",fileICIMcov=NULL)  
  
## End(Not run)
```

---

WangF

*To perform QTL mapping with wang method*

---

**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)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**Examples**

```
## Not run:
data(DHdata)
readraw<-Readdata(file=DHdata,fileFormat="GCIM",fileICIMcov=NULL)
###
DoResult<-Dodata(fileFormat="GCIM",Population="DH",Model="Random",readraw)
###
ws<-WangF(pheRaw=DoResult$pheRaw,genRaw=DoResult$genRaw,
mapRaw1=DoResult$mapRaw1,yygg1=DoResult$yygg1,
flagRIL=DoResult$flagRIL,cov_en=DoResult$cov_en,
Population="DH",WalkSpeed=1,CriLOD=2.5)

## End(Not run)
```

---

WangS

---

*The second step of wang method*


---

**Description**

Genome-wide Composite Interval Mapping

**Usage**

```
WangS(flag,CriLOD,NUM,pheRaw,chrRaw_name,yygg,mx,phe,chr_name,gen,
mapname,CLO)
```

**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.
CLO	Number of CPUs.

**Author(s)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>



**Examples**

```

## Not run:
data(DHdata)
###
readraw<-Readdata(file=DHdata,fileFormat="GCIM",fileICIMcov=NULL)
###
DoResult<-Dodata(fileFormat="GCIM",Population="DH",Model="Random",readraw)
###
W1re<-WangF(pheRaw=DoResult$pheRaw,genRaw=DoResult$genRaw,
mapRaw1=DoResult$mapRaw1,yygg1=DoResult$yygg1,
flagRIL=DoResult$flagRIL,cov_en=DoResult$cov_en,
Population="DH",WalkSpeed=1,CriLOD=2.5)
###
ws<-WangS(flag=DoResult$flag,CriLOD=2.5,NUM=1,pheRaw=DoResult$pheRaw,
chrRaw_name=W1re$chrRaw_name,yygg=W1re$yygg,mx=W1re$mx,phe=W1re$phe,
chr_name=W1re$chr_name,gen=W1re$gen,mapname=W1re$mapname,CLO=1)

## End(Not run)

```

---

WenF

---

*To perform QTL mapping with Wen method*


---

**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)**

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

## Examples

```
## Not run:
data(F2data)
###
readraw<-Readdata(file=F2data,fileFormat="GCIM",fileICIMcov=NULL)
###
DoResult<-Dodata(fileFormat="GCIM",Population="F2",Model="Random",readraw)
###
wf<-WenF(pheRaw=DoResult$pheRaw,genRaw=DoResult$genRaw,
mapRaw1=DoResult$mapRaw1,yygg1=DoResult$yygg1,
cov_en=DoResult$cov_en,WalkSpeed=1,CriLOD=2.5,
dir=tempdir())

## End(Not run)
```

---

WenS

*The second step of Wen method*

---

## 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,SetSeed,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.
SetSeed	random seed set in which,the cross validation is needed.
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)

Zhang Ya-Wen, Wen Yang-Jun, Wang Shi-Bo, and Zhang Yuan-Ming  
 Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

### Examples

```
## Not run:
data(F2data)
###
readraw<-Readdata(file=F2data,fileFormat="GCIM",fileICIMcov=NULL)
###
DoResult<-Dodata(fileFormat="GCIM",Population="F2",Model="Random",readraw)
###
WEN1re<-WenF(pheRaw=DoResult$pheRaw,genRaw=DoResult$genRaw,
mapRaw1=DoResult$mapRaw1,yygg1=DoResult$yygg1,
cov_en=DoResult$cov_en,WalkSpeed=1,CriLOD=2.5,
dir=tempdir())
###
ws<-WenS(flag=DoResult$flag,CriLOD=2.5,NUM=1,
pheRaw=DoResult$pheRaw,Likelihood="REML",SetSeed=11001,
flagrqt1=FALSE,yygg=WEN1re$yygg,mx=WEN1re$mx,
phe=WEN1re$phe,chr_name=WEN1re$chr_name,
v.map=WEN1re$v.map,gen.raw=WEN1re$gen.raw,
a.gen.orig=WEN1re$a.gen.orig,
d.gen.orig=WEN1re$d.gen.orig,n=WEN1re$n,
names.insert2=WEN1re$names.insert2,
X.ad.tran.data=WEN1re$X.ad.tran.data,
X.ad.t4=WEN1re$X.ad.t4,dir=tempdir())

## End(Not run)
```

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