

# Package ‘QTL.gCIMapping.GUI’

May 1, 2020

**Type** Package

**Title** QTL Genome-Wide Composite Interval Mapping with Graphical User Interface

**Version** 2.1

**Date** 2020-4-30

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## 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),shiny,MASS,qt1

**License** GPL (>= 2)

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

**LinkingTo** Rcpp

**NeedsCompilation** yes

**Repository** CRAN

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QTL.gCIMapping.GUI-package

*QTL Genome-Wide Composite Interval Mapping with Graphical User Interface*

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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.GUI()

## Details

Package:	QTL.gCIMapping.GUI
Type:	Package
Version:	2.1
Date:	2020-4-30
Depends:	shiny,MASS,dplyr,parcor,qt1
Imports:	methods,openxlsx,stringr,Rcpp
License:	GPL version 2 or newer
LazyLoad:	yes

## Author(s)

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

**References**

An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2. Wen Yang-Jun, Zhang Ya-Wen, Zhang Jin, Feng Jian-Ying, Jim M. Dunwell, Zhang Yuan-Ming\*

**Examples**

```
## Not run: QTL.gCIMapping.GUI()
```

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gen	<i>genotype example data</i>
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**Description**

GCIM format of DH genotype dataset.

**Usage**

```
data(gen)
```

**Details**

Dataset input of file for WangF function.

**Author(s)**

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

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genf2	<i>genotype example data</i>
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**Description**

GCIM format of F2 genotype dataset.

**Usage**

```
data(genf2)
```

**Details**

Dataset input of file for WenF function.

**Author(s)**

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

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map

*map example data*

---

**Description**

GCIM format of DH map dataset.

**Usage**

data(map)

**Details**

Dataset input of file for WangF function.

**Author(s)**

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

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mapf2

*map example data*

---

**Description**

GCIM format of F2 map dataset.

**Usage**

data(mapf2)

**Details**

Dataset input of file for WenF function.

**Author(s)**

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



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phe *phenotype example data*

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**Description**

GCIM format of DH phenotype dataset.

**Usage**

data(phe)

**Details**

Dataset input of file for WangF function.

**Author(s)**

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

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phef2 *phenotype example data*

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**Description**

GCIM format of F2 phenotype dataset.

**Usage**

data(phef2)

**Details**

Dataset input of file for WenF function.

**Author(s)**

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

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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)

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

## Examples

```
## Not run:  
data(gen)  
data(phe)  
data(map)  
wf<-WangF(pheRaw=phe, genRaw=gen, mapRaw1=map, yygg1=NULL,  
flagRIL=0, cov_en=NULL, 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, Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**Examples**

```
## Not run:
data(gen)
data(phe)
data(map)
W1re<-WangF(pheRaw=phe, genRaw=gen, mapRaw1=map, yygg1=NULL,
flagRIL=0, cov_en=NULL, Population="DH", WalkSpeed=1, CriLOD=2.5)
###
ws<-WangS(flag=1, CriLOD=2.5, NUM=1, pheRaw=phe,
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)
```



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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)

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

## Examples

```
## Not run:  
data(genf2)  
data(phef2)  
data(mapf2)  
wf<-WenF(pheRaw=phef2,genRaw=genf2,mapRaw1=mapf2,  
yygg1=NULL,cov_en=NULL,WalkSpeed=1,CriLOD=2.5,dir=tempdir())  
  
## End(Not run)
```

---

WenS

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*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,setseed,flagrqt1,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.
flagrqt1	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, Zhang Yuan-Ming  
Maintainer: Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**Examples**

```
## Not run:
data(genf2)
data(phef2)
data(mapf2)
WEN1re<-WenF(pheRaw=phef2,genRaw=genf2,mapRaw1=mapf2,
yygg1=NULL,cov_en=NULL,WalkSpeed=1,CriLOD=2.5,dir=tempdir())
###
ws<-WenS(flag=1,CriLOD=2.5,NUM=1,pheRaw=phef2,
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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