Package 'QTL.gCIMapping.GUI'

October 12, 2022

Type Package

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

Version 2.1.1

Date 2020-10-8

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

Maintainer Yuanming Zhang<soyzhang@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 radio test. See Wen et al. (2018) <doi:10.1093/bib/bby058>.

Encoding UTF-8

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

License GPL (>= 2)

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

LinkingTo Rcpp

NeedsCompilation yes

Repository CRAN

Date/Publication 2020-10-12 04:40:12 UTC

R topics documented:

`QTL.gCIMapping.GUI-package`

QTL Genome-Wide Composite Interval Mapping with Graphical User Interface

---

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 radio test.

Usage

```
QTL.gCIMapping.GUI()
```

Details

Package:	QTL.gCIMapping.GUI
Type:	Package
Version:	2.1.1
Date:	2020-10-8
Depends:	shiny,MASS,qtl
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<soyzhang@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()
```

---

gen *genotype example data*

Description

GCIM format of DH genotype dataset.

Usage

```
data(gen)
```

Details

Dataset input of file for WangF function.

Author(s)

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

---

genf2 *genotype example data*

Description

GCIM format of F2 genotype dataset.

Usage

```
data(genf2)
```

Details

Dataset input of file for WenF function.

Author(s)

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

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<soyzhang@mail.hzau.edu.cn>

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<soyzhang@mail.hzau.edu.cn>

markerinsert *To insert marker in genotype.*

Description

a method that can insert marker in genotype.

Usage

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

Arguments

mp	linkage map matrix after insert.
geno	genotype matrix.
map	linkage map matrix.
cl	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, Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@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,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,2,2,2,3,3,3,3,3,3,
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)
mark_insert<-QTL.gCIMapping::markerinsert(mp,geno,map,cl=1,gg1=1,gg2=-1,
gg0=99,flagRIL=1)

## End(Not run)
```

phe *phenotype example data*

Description

GCIM format of DH phenotype dataset.

Usage

```
data(phe)
```

Details

Dataset input of file for WangF function.

Author(s)

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

phef2 *phenotype example data*

Description

GCIM format of F2 phenotype dataset.

Usage

```
data(phef2)
```

Details

Dataset input of file for WenF function.

Author(s)

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

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, Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@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<soyzhang@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)
```

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, Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@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 *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, Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@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,flagrqtl=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)
```

Index