Package 'QTL.gCIMapping'

May 1, 2020

Type Package

Title QTL Genome-Wide Composite Interval Mapping

Version 3.3

Date 2020-4-30

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),MASS,qtl

License GPL (>= 2)

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

LinkingTo Rcpp

NeedsCompilation yes

Repository CRAN

Date/Publication 2020-05-01 07:20:03 UTC

R topics documented:

`DHdata` *DH example data*

Description

GCIM format of DH dataset.

Usage

```
data(DHdata)
```

Details

Input file for WangF function.

Author(s)

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

`Dodata` *Process raw data*

Description

Process raw data for later use

Usage

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

Arguments

`fileFormat`	Dataset format
`Population`	Population type.
`Model`	Random or fixed model.
`readraw`	Raw data.

Author(s)

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

Examples

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

## End(Not run)
```

F2data *F2 example data*

Description

GCIM format of F2 dataset.

Usage

```
data(F2data)
```

Details

Input 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, and 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)
QTL.gCIMapping::markerinsert(mp,geno,map,cl=1,gg1=1,gg2=-1,
gg0=99,flagRIL=1)

## End(Not run)
```

QTL.gCIMapping *QTL Genome-Wide Composite Interval Mapping*

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(file,fileFormat,fileICIMcov,Population,Model,WalkSpeed,
CriLOD,Likelihood,SetSeed,flagrqtl,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).
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.
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:	3.3
Date:	2020-4-30
Depends:	MASS,dplyr,parcor,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, and 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:
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<soyzhang@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<soyzhang@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<soyzhang@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<soyzhang@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<soyzhang@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$pheRaw,Likelihood="REML",SetSeed=11001,
flagrqtl=FALSE,yygg=WEN1re$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