Package 'QTL.gCIMapping'

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Type Package

Title QTL Genome-Wide Composite Interval Mapping

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Description Conduct multiple quantitative trait loci (QTL) and QTL-by-environment interaction (QEI) mapping via ordinary or compressed variance component mixed models with random- or fixed QTL/QEI effects. 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 or on each locus curve are viewed as potential main-effect QTLs and QEIs, all their effects are included in a multi-locus model, their effects are estimated by both least angle regression and empirical Bayes (or adaptive lasso) in back-cross and F2 populations, and true QTLs and QEIs are identified by likelihood ratio test. See Zhou et al. (2022) <doi:10.1093/bib/bbab596> and Wen et al. (2018) <doi:10.1093/bib/bby058>.

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Depends R (>= 3.5.0)

License GPL (>= 2)

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

LinkingTo Rcpp

NeedsCompilation yes

RoxygenNote 7.1.2

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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

Usage

```
Dodata(
  fileFormat = NULL,
  Population = NULL,
  method = NULL,
  Model = NULL,
  readraw = NULL,
  MultiEnv = FALSE
)
```

Arguments

fileFormat	Format of dataset.
Population	Population type.
method	Method "GCIM" or method "GCIM-QEI"
Model	Random or fixed model.
readraw	Raw data.
MultiEnv	Whether to perform multi-environment analysis

Value

a list

Examples

```
data(F2data)
readraw<-Readdata(file=F2data,fileFormat="GCIM",
method="GCIM-QEI",filecov=NULL,
MCIMmap=NULL,MultiEnv=TRUE)
doda<-Dodata(fileFormat="GCIM",Population="F2",
method="GCIM-QEI",Model="Random",
readraw,MultiEnv=TRUE)
```

F2data *F2 example data from 2 environments*

Description

GCIM format of F2 dataset whith GCIM-QEI method.

Usage

```
data(F2data)
```

Details

Input file for ZhouF 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

QTL Genome-Wide Composite Interval Mapping

Usage

```
QTL.gCIMapping(
  file = NULL,
  fileFormat = "GCIM",
  filecov = NULL,
  MCIMmap = NULL,
  Population = NULL,
  method = "GCIM-QEI",
  MultiEnv = FALSE,
  Model = "Random",
  WalkSpeed = 1,
  CriLOD = 3,
  CriDis = 5,
  Likelihood = "REML",
  SetSeed = 11001,
  flagrqtl = FALSE,
  DrawPlot = TRUE,
  PlotFormat = "jpeg",
  Resolution = "Low",
  Trait = NULL,
  dir = NULL,
  CLO = NULL
)
```

Arguments

file	File path and name in your computer.
fileFormat	Format for input file: GCIM, ICIM, Cart, or MCIM.
filecov	Covariate file of QTLIciMapping or QTLNetwork.
MCIMmap	Map file of QTLNetwork.
Population	Population type: F2, BC1, BC2, DH, RIL.
method	Method "GCIM" or method "GCIM-QEI".
MultiEnv	Whether to perform multi-environment analysis.
Model	Random or fixed model.
WalkSpeed	Walk speed for Genome-wide Scanning.
CriLOD	Critical LOD scores for significant QTL.

CriDis	The distance of optimization.
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.
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.
CLO	Number of CPUs.

Examples

```
data(F2data)
QTL.gCIMapping(file=F2data,Population="F2",
MultiEnv=TRUE,Model="Random",CriLOD=3,
Trait=1,dir=tempdir(),CLO=2)
```

Readdata *Read raw data*

Description

Read raw data

Usage

```
Readdata(
  file = NULL,
  fileFormat = NULL,
  method = NULL,
  filecov = NULL,
  MCIMmap = NULL,
  MultiEnv = FALSE
)
```

Arguments

file	Dataset input
fileFormat	Format of dataset.
method	Method "GCIM" or method "GCIM-QEI"
filecov	Covariate file of QTLIciMapping or QTLNetwork.
MCIMmap	Map file of QTLNetwork.
MultiEnv	Whether to perform multi-environment analysis

Value

a list

Examples

```
data(F2data)
Readdata(file=F2data,fileFormat="GCIM",
method="GCIM-QEI",filecov=NULL,
MCIMmap=NULL,MultiEnv=TRUE)
```

WangF *To perform QTL mapping with wang method*

Description

To perform QTL mapping with wang method

Usage

```
WangF(
  pheRaw = NULL,
  genRaw = NULL,
  mapRaw1 = NULL,
  yygg1 = NULL,
  flagRIL = NULL,
  cov_en = NULL,
  Population = NULL,
  WalkSpeed = NULL,
  CriLOD = NULL
)
```

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.
CriLOD	Critical LOD scores for significant QTL.

Value

a list

Examples

```
data(DHdata)
readraw<-Readdata(file=DHdata,fileFormat="GCIM",
method="GCIM",filecov=NULL,MCIMmap=NULL,MultiEnv=FALSE)
DoResult<-Dodata(fileFormat="GCIM",Population="DH",
method="GCIM",Model="Random",readraw,MultiEnv=FALSE)
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)
```

WangS *The second step of wang method*

Description

The second step of wang method

Usage

```
WangS(
  flag = NULL,
  CriLOD = NULL,
  NUM = NULL,
  pheRaw = NULL,
  chrRaw_name = NULL,
  yygg = NULL,
  mx = NULL,
  phe = NULL,
```

```
  chr_name = NULL,
  gen = NULL,
  mapname = NULL,
  CLO = NULL
)
```

Arguments

flag	fix or random model.
CriLOD	Critical LOD scores for significant QTL.
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.

Value

a list

Examples

```
data(DHdata)
readraw<-Readdata(file=DHdata,fileFormat="GCIM",
method="GCIM",filecov=NULL,MCIMmap=NULL,MultiEnv=FALSE)
DoResult<-Dodata(fileFormat="GCIM",Population="DH",
method="GCIM",Model="Random",readraw,MultiEnv=FALSE)
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)
```

WenF *To perform QTL mapping with Wen method*

Description

To perform QTL mapping with Wen method

Usage

```
WenF(
  pheRaw = NULL,
  genRaw = NULL,
  mapRaw1 = NULL,
  yygg1 = NULL,
  cov_en = NULL,
  WalkSpeed = NULL,
  CriLOD = NULL,
  dir = NULL
)
```

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.
CriLOD	Critical LOD scores for significant QTL.
dir	file path in your computer.

Value

a list

Examples

```
data(F2data)
readraw<-Readdata(file=F2data,fileFormat="GCIM",
method="GCIM",filecov=NULL,MCIMmap=NULL,
MultiEnv=FALSE)
DoResult<-Dodata(fileFormat="GCIM",Population="F2",
method="GCIM",Model="Random",readraw,MultiEnv=FALSE)
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())
```

WenS *The second step of Wen method*

Description

The second step of Wen method

Usage

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

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.

Value

a list

Examples

```
data(F2data)
readraw<-Readdata(file=F2data,fileFormat="GCIM",
method="GCIM",filecov=NULL,MCIMmap=NULL,MultiEnv=FALSE)
DoResult<-Dodata(fileFormat="GCIM",Population="F2",
method="GCIM",Model="Random",readraw,MultiEnv=FALSE)
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())
```

ZhouF *To perform QTL mapping with Wen method*

Description

To perform QTL mapping with Wen method

Usage

```
ZhouF(
  pheRaw = NULL,
  genRaw = NULL,
  mapRaw1 = NULL,
  WalkSpeed = NULL,
  CriLOD = NULL,
  dir = NULL
)
```

Arguments

pheRaw	phenotype matrix.
genRaw	genotype matrix.
mapRaw1	linkage map matrix.
WalkSpeed	Walk speed for Genome-wide Scanning.
CriLOD	Critical LOD scores for significant QTL.
dir	file path in your computer.

Value

a list

Examples

```
data(F2data)
readraw<-Readdata(file=F2data,fileFormat="GCIM",
method="GCIM-QEI",filecov=NULL,
MCIMmap=NULL,MultiEnv=TRUE)
DoResult<-Dodata(fileFormat="GCIM",
Population="F2",method="GCIM-QEI",
Model="Random",readraw,MultiEnv=TRUE)
ZhouMatrices<-ZhouF(pheRaw=DoResult$pheRaw,
genRaw=DoResult$genRaw,
mapRaw1=DoResult$mapRaw1,
WalkSpeed=1,CriLOD=3,
dir=tempdir())
```

ZhouMethod *The second step of Zhou method for multiple environments*

Description

The second step of Zhou method for multiple environments

Usage

```
ZhouMethod(
  Model = NULL,
  pheRaw = NULL,
  genRaw = NULL,
  mapRaw = NULL,
  CriLOD = NULL,
  NUM = NULL,
  EnvNum = NULL,
  yygg = NULL,
  genoname = NULL,
  Ax0 = NULL,
  Hx0 = NULL,
  Bx0 = NULL,
  Ax = NULL,
  Hx = NULL,
  Bx = NULL,
  dir = NULL,
  CriDis = NULL,
  CLO = NULL
)
```

Arguments

Model	Random or fixed model.
pheRaw	phenotype matrix.
genRaw	genotype matrix.
mapRaw	linkage map matrix.
CriLOD	Critical LOD scores for significant QTL.
NUM	The serial number of the trait to be analyzed.
EnvNum	The number of environments for each trait is a vector.
yygg	covariate matrix.
genoname	linkage map matrix with pseudo markers inserted.
Ax0	AA genotype matrix.
Hx0	Aa genotype matrix.
Bx0	aa genotype matrix.
Ax	AA genotype matrix with pseudo markers inserted.
Hx	Aa genotype matrix with pseudo markers inserted.
Bx	aa genotype matrix with pseudo markers inserted.
dir	file storage path.
CriDis	The distance of optimization.
CLO	Number of CPUs.

Value

a list

Examples

```
data(F2data)
readraw<-Readdata(file=F2data,fileFormat="GCIM",
method="GCIM-QEI",filecov=NULL,
MCIMmap=NULL,MultiEnv=TRUE)
DoResult<-Dodata(fileFormat="GCIM",
Population="F2",method="GCIM-QEI",
Model="Random",readraw,MultiEnv=TRUE)
ZhouMatrices<-ZhouF(pheRaw=DoResult$pheRaw,
genRaw=DoResult$genRaw,mapRaw1=DoResult$mapRaw1,
WalkSpeed=1,CriLOD=3,dir=tempdir())
OutputZhou<-ZhouMethod(Model="Random",
pheRaw=DoResult$pheRaw,genRaw=DoResult$genRaw,
mapRaw=ZhouMatrices$mapRaw,CriLOD=3,NUM=1,
EnvNum=DoResult$EnvNum,yygg=DoResult$yygg1,
genoname=ZhouMatrices$genoname,
Ax0=ZhouMatrices$Ax0,Hx0=ZhouMatrices$Hx0,
Bx0=ZhouMatrices$Bx0,Ax=ZhouMatrices$Ax,
Hx=ZhouMatrices$Hx,Bx=ZhouMatrices$Bx,
dir=tempdir(),CriDis=5,CLO=2)
```

ZhouMethod_single_env *The second step of Zhou method for single environment*

Description

The second step of Zhou method for single environment

Usage

```
ZhouMethod_single_env(
  Model = NULL,
  pheRaw = NULL,
  genRaw = NULL,
  mapRaw = NULL,
  CriLOD = NULL,
  NUM = NULL,
  yygg = NULL,
  genoname = NULL,
  Ax0 = NULL,
  Hx0 = NULL,
  Bx0 = NULL,
  Ax = NULL,
  Hx = NULL,
```

```
  Bx = NULL,
  dir = NULL,
  CriDis = NULL,
  CLO = NULL
)
```

Arguments

Model	Random or fixed model.
pheRaw	phenotype matrix.
genRaw	genotype matrix.
mapRaw	linkage map matrix.
CriLOD	Critical LOD scores for significant QTL.
NUM	The serial number of the trait to be analyzed.
yygg	covariate matrix.
genoname	linkage map matrix with pseudo markers inserted.
Ax0	AA genotype matrix.
Hx0	Aa genotype matrix.
Bx0	aa genotype matrix.
Ax	AA genotype matrix with pseudo markers inserted.
Hx	Aa genotype matrix with pseudo markers inserted.
Bx	aa genotype matrix with pseudo markers inserted.
dir	file storage path.
CriDis	The distance of optimization.
CLO	Number of CPUs.

Value

a list

Examples

```
data(F2data)
readraw<-Readdata(file=F2data,fileFormat="GCIM",
method="GCIM-QEI",filecov=NULL,
MCIMmap=NULL,MultiEnv=FALSE)
DoResult<-Dodata(fileFormat="GCIM",Population="F2",
method="GCIM-QEI",Model="Random",
readraw,MultiEnv=FALSE)
ZhouMatrices<-ZhouF(pheRaw=DoResult$pheRaw,
genRaw=DoResult$genRaw,mapRaw1=DoResult$mapRaw1,
WalkSpeed=1,CriLOD=3,dir=tempdir())
OutputZhou<-ZhouMethod_single_env(Model="Random",
pheRaw=DoResult$pheRaw,genRaw=DoResult$genRaw,
mapRaw=ZhouMatrices$mapRaw,CriLOD=3,NUM=1,
```

```
yygg=DoResult$yygg1,genoname=ZhouMatrices$genoname,
Ax0=ZhouMatrices$Ax0,Hx0=ZhouMatrices$Hx0,
Bx0=ZhouMatrices$Bx0,Ax=ZhouMatrices$Ax,
Hx=ZhouMatrices$Hx,Bx=ZhouMatrices$Bx,
dir=tempdir(),CriDis=5,CLO=2)
```

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