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) 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. Wang S-B, Wen Y-J, Ren W-L, Ni Y-L, Zhang J, Feng J-Y, Zhang Y-M (2016) <doi:10.1038/srep29951>.

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Depends MASS,qtl,doParallel,foreach,parallel

License GPL (>= 2)

Imports Rcpp (>= 0.12.17),methods,openxlsx,stringr,data.table,parcor

LinkingTo Rcpp

NeedsCompilation yes

Repository CRAN

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R topics documented:

`f2data` *F2 example data*

Description

GCIM format of F2 dataset.

Usage

```
data(f2data)
```

Details

Dataset input of file for QTL.gCIMapping function.

Author(s)

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`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)

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Examples

```
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)
```

`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,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).

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:	3.1
Date:	2018-10-16
Depends:	MASS,dplyr,parcor,qtl,doParallel
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
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References

Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. Wang Shi-Bo,Wen Yang-Jun,Ren Wen-Long,Ni Yuan-Li,Zhang Jin,Feng Jian-Ying,Zhang Yuan-Ming*

Examples

```
G=data(f2data)
QTL.gCIMapping(file=f2data,fileFormat="GCIM",fileICIMcov=NULL,Population="F2",
Model="Random",WalkSpeed=1,CriLOD=2.5,Likelihood="REML",flagrqtl="FALSE",
DrawPlot="FALSE",PlotFormat="png",Resolution="Low",Trait=1,dir=tempdir())
```

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)

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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)
```

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.

Author(s)

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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>

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,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.
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
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