Package: dQTG.seq (via r-universe)

September 13, 2024

Type Package

Title A BSA Software for Detecting All Types of QTLs in BC, DH, RIL and F2

Version 1.0.2

Maintainer Yuan-Ming Zhang <soyzhang@mail.hzau.edu.cn>

Contact Yuan-Ming Zhang <soyzhang@mail.hzau.edu.cn>

Description The new (dQTG.seq1 and dQTG.seq2) and existing (SmoothLOD, G', deltaSNP and ED) bulked segregant analysis methods are used to identify various types of quantitative trait loci for complex traits via extreme phenotype individuals in bi-parental segregation populations (F2, backcross, doubled haploid and recombinant inbred line). The numbers of marker alleles in extreme low and high pools are used in existing methods to identify trait-related genes, while the numbers of marker alleles and genotypes in extreme low and high pools are used in the new methods to construct a new statistic Gw for identifying trait-related genes. dQTG-seq2 is feasible to identify extremely over-dominant and small-effect genes in F2. Li P, Li G, Zhang YW, Zuo JF, Liu JY, Zhang YM (2022, <doi:10.1016/j.xplc.2022.100319>).

Depends R (>= 3.5.0)

License GPL (>= 2)

Imports BB, data.table, doParallel, openxlsx, qtl, stringr, writexl,vroom, parallel,foreach

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

NeedsCompilation no

Author Pei Li [aut], Yuan-Ming Zhang [aut, cre] (<https://orcid.org/0000-0003-2317-2190>)

Date/Publication 2023-03-22 09:10:06 UTC

Repository https://yuanmingzhang.r-universe.dev

RemoteUrl https://github.com/cran/dQTG.seq

RemoteRef HEAD

RemoteSha 182fe19715e3b04b10d306a3c9f3a722a7d27b02

Contents

`BSA` *BSA data*

Description

BSA format of F2 dataset.

Usage

```
data(BSA)
```

Details

Input file for dQTG.seq function.

`Dodata` *To perform method*

Description

To perform method

Usage

```
Dodata(dir, calculatedata, chr, color1, CLO)
```

Arguments

`dir`	the path of the output
`calculatedata`	the inputdata
`chr`	chromosome
`color1`	the color of the chromosome
`CLO`	the numbers of CPU

Value

list

Examples

```
data(BSA)
dir<- tempdir()
data.calculatedata<-Readdata1(BSA)
Dodata(dir,calculatedata=data.calculatedata,chr="all",color1="blue",CLO=1)
```

---

dQTG.seq *Title The function of dQTG.seq*

Description

Title The function of dQTG.seq

Usage

```
dQTG.seq(dir, filegen, chr, color, CLO)
```

Arguments

dir	the path of the output
filegen	the input data
chr	the chromosome
color	the color
CLO	the numbers of CPU

Value

list

Examples

```
data(BSA)
dQTG.seq(dir=tempdir(),filegen=BSA,chr="all",color="blue",CLO=1)
```

`Readdata1` *Title readdata function*

Description

Title readdata function

Title readdata function

Usage

```
Readdata1(File)
```

```
Readdata1(File)
```

Arguments

`File`	the input file

Value

list

list

Examples

```
data(BSA)
Readdata1(BSA)
data(BSA)
Readdata1(BSA)
```

Index