

# Package ‘dQTG.seq’

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**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 <soy Zhang@mail.hzau.edu.cn>

**Contact** Yuan-Ming Zhang <soy Zhang@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](https://doi.org/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] (ORCID:  
<<https://orcid.org/0000-0003-2317-2190>>)

**Repository** CRAN

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BSA	<i>BSA data</i>
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### Description

BSA format of F2 dataset.

### Usage

data(BSA)

### Details

Input file for dQTG.seq function.

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Dodata	<i>To perform method</i>
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### 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)
```

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dQTG.seq

*Title The function of dQTG.seq*

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**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)
```

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`Readdata1`*Title readdata function*

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**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)
```

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