**User Manual for**

QTG-seq\_SmoothLOD

(**version 1.0**)

**MASKED BECAUSE OF DOUBLE BLIND PEER REVIEW**

**Last updated on 14 Oct 2018**

**INTRODUCTION**

**1.1 Why QTG-seq?**

**QTG-seq** is an R package for quickly mapping quantitative trait gene.

QTG-seq v1.0 is able to work on the popular platforms, like Windows, Linux (desktop) and MacOS.

**1.2** **Getting started**

QTG-seq is a package that runs in the R software environment, which can be freely downloaded from https://github.com/caulilin/QTG\_Seq.

**1.2.1 One-Click installation**

Within R environment, the QTG-seq software can be installed directly using the below command:

install.packages(pkgs="QTG-seq")

**1.2.2 Step-by-step installation**

**1.2.2.1 Install the add-on packages**

**Online installation** Within R environment on the internet, the **QTG-seq** package can be installed online, using the below command:

install.packages(pkgs=c("doParallel","dplyr","plyr","rootSolve","data.table","ggplot2"))

**Offline installation** Users should download the below 6 packages from CRAN, github (https://github.com/), or google search:

"doParallel","dplyr","plyr","rootSolve","data.table","ggplot2"

Then, install them offline (under the R environment, select all the 6 packages and install them offline).

**1.2.2.2 Install QTG-seq**

Open R GUI, select "Packages"—"Install package(s) from local files…" and then find the QTG-seq package which you have downloaded on your desktop.

Within R environment, launch the QTG-seq by command:

library(QTG-seq)

**User Manual file U**sers can decompress the QTG-seq package and find the User Manual file (name: **Instruction.pdf**) in the folder of “…/QTG-seq/inst/doc”.

1. **Parameter settings**

|  |  |
| --- | --- |
| **Parameter** | **Meaning** |
| **dir** | Paths of inputting and outputting files in your computer. dir="D:\\Users" |
| **WinSize** | The window size for each SNP in the calculation of smooth LOD, i.e., 25 cM (Magwene et al. 2011). The others recommended trying several window sizes to test if the peaks are over- or under smoothed. |
| **DrawPlot** | DrawPlot=TRUE: one picture output; DrawPlot=FALSE: no picture output |
| **chrom** | chrom="all": To output the results of all the chromosomes; chrom=c(7,8): To output the results of chromosomes 7 and 8 |
| **col** | col=c("blue","red")**:** indicating the blue and red points of smooth LOD scores in adjacent chromosomes |
| **Plotformat** | \*.jpeg, \*.png, \*.tiff and \*.pdf. For example, **Plotformat="jpeg":** the \*.jpeg format of the figure file |
| **Resolution** | Low or High. **Resolution="Low":** the low resolution of the figure file |
| **Results** | Result file: 1) the results of scanning genome with the Chrom, Pos, LOD, Smooth\_LOD and P\_Value columns;  2) significant QTN: having the QTN, Chrom, Pos, LOD, Smooth\_LOD and P\_Value columns |

**Example**

LOD(dir="D:/users",filegen="gen.csv",width=3375000,DrawPlot=TRUE,chrom=c(7,8),col=c("blue","red"),Plotformat1="tiff",Resolution="High")

**Dataset format**

**The format of dataset to be input** The first column, named "**chromosome**", presents chromosome number for each marker. The second column, named "**pos**", stands for positions (bp) of markers on chromosome. The third to sixth column, named "**A in low pool**", "**a in low pool**", "**A in high pool**" and "**a in high pool**", stands for the number of alleles A and a in low pool and those in high pool, respectively.

**Table1. The format of dataset to be input**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chromosome** | **Pos (bp)** | **A in low pool** | **a in low pool** | **A in high pool** | **a in high pool** |
| 1 | 35496 | 202 | 243 | 228 | 232 |
| 1 | 55610 | 36 | 40 | 36 | 50 |
| 1 | 118174 | 125 | 109 | 123 | 122 |
| 1 | 118275 | 171 | 154 | 137 | 162 |
| 1 | 118295 | 186 | 152 | 156 | 161 |
| 1 | 118299 | 192 | 158 | 158 | 160 |

1. **Result**

**The format of dataset to be output** This is the file of final results. The first five columns showed the results of genome scanning, and the last six columns showed the results of the detected QTGs. The chromosome number, position (bp), LOD score, smooth LOD score and P-value for each marker are listed, respectively, in the first five columns. The corresponding information for each identified QTG is listed, respectively, in the last five columns.

**Table 2. The format of dataset to be output**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chrom | Pos | LOD | Smooth\_LOD | P\_Value |  | QTG | Chrom | Pos | LOD | Smooth\_LOD | P\_Value |
| 1 | 35496 | 0.828997 | 0.4425 | 0.153432 |  | 1 | 7 | 135213995 | 5.925758 | 6.213969 | 8.82E-08 |
| 1 | 55610 | 0.542839 | 0.442498 | 0.153433 |  | 2 | 7 | 111501693 | 4.818329 | 3.721323 | 3.48E-05 |
| 1 | 118174 | 0.238635 | 0.442467 | 0.153448 |  |  |  |  |  |  |  |
| 1 | 118275 | 0.647616 | 0.442467 | 0.153448 |  |  |  |  |  |  |  |
| 1 | 118295 | 0.761053 | 0.442467 | 0.153448 |  |  |  |  |  |  |  |
| 1 | 118299 | 0.72107 | 0.442467 | 0.153448 |  |  |  |  |  |  |  |
| 1 | 157091 | 0.38959 | 0.442429 | 0.153466 |  |  |  |  |  |  |  |
| 1 | 157110 | 0.38959 | 0.442429 | 0.153466 |  |  |  |  |  |  |  |
| 1 | 202015 | 0.479482 | 0.442368 | 0.153494 |  |  |  |  |  |  |  |
| 1 | 206547 | 0.219466 | 0.442361 | 0.153497 |  |  |  |  |  |  |  |