

Welcome to QTLNetworkR Project

1. Introduction

QTLNetworkR, a R package, aims to provide a user-friendly and platform-independent tool to visualize QTL mapping results generated by QTLNetwork. It works both on the Windows, Linux/FreeBSD and MacOS platforms. The GUI is based on available add-on package RGtk2, via the aid of another package gWidgetsRGtk2. Functions for visualizing are developed by package lattice and grid that are distributed with R by default.

2. Installation

2.1 install GTK+

Because RGtk2 depends on GTK+, you may need to install GTK+ before install RGtk2. For windows user, you can do this:

download GTK+ [here](#)

Run the resulting file. This is an automated installer which will help you complete the installation of Gtk2 libraries.

For Mac OS users, you can do this:

Download GTK+ [here](#).

Run the resulting file.

In Linux, you may or may not upgrade the GTK libraries depending on your distribution.

There are more details on RGtk2 at [RGtk2's home page](#).

2.2 install R

Download R from [CRAN](#) and install it.

2.3 install the R packages

The following R packages are needed: RGtk2, cairoDevice, gWidgets and gWidgetsRGtk2.

Install them in order, as some depend on others. All can be downloaded from [CRAN](http://CRAN.R-project.org).

2.4 Install QTLNetworkR

The QTLNetworkR package is freely available [here](#), you can download and install. You can also install it directly within R by command:

```
install.packages("QTLNetworkR",repos="http://R-Forge.R-project.org")
```

3. Running

The procedure is described below. First you can launch QTLNetworkR by command `library(QTLNetworkR)` within R, after that you will see the QTLNetworkR GUI like the following dialog.

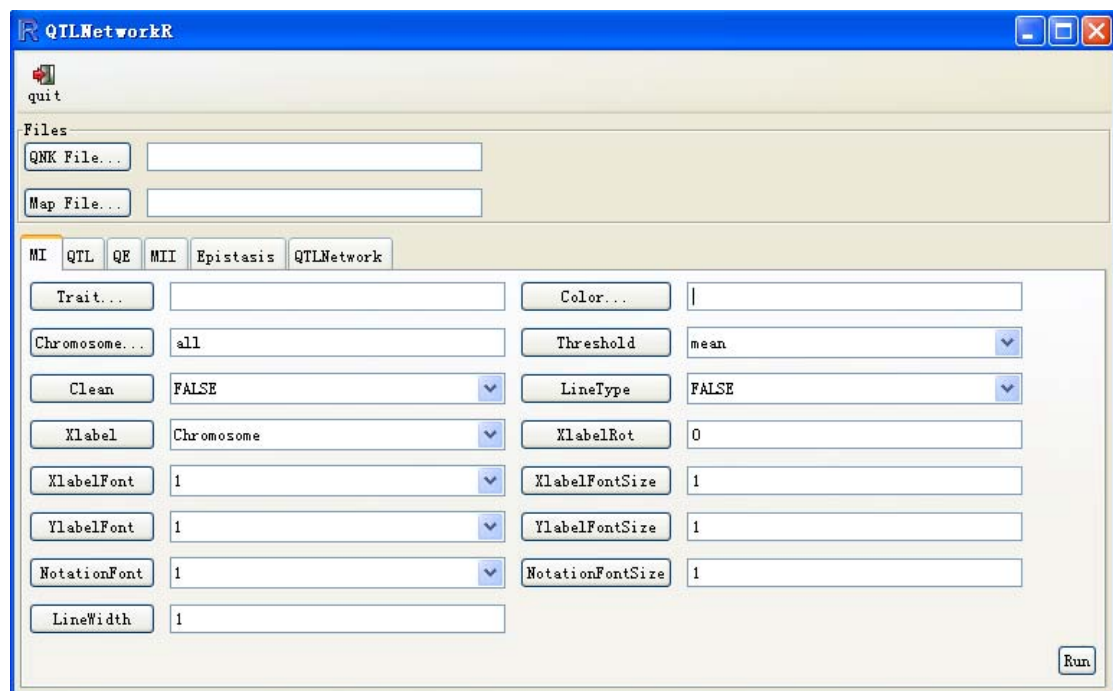


Figure 1. A snapshot of the GUI of QTLNetworkR with tabbed page of MI.

To restart the GUI, the command `QTLNetworkR()` can be issued.

User can use the Browse... button to load QTL mapping results file and linkage file, and the

blank will show the path and filename after the files are chosen. All these files should be located correctly. Six functions are devised presented by a notebook with six tabbed pages, From left to right are “MI”, “QTL”, “QE”, “MII”, “Epistasis” and “QTLNetwork” respectively. The detailed information of this notebook can be found in Chapter 4. After that, Users can set parameters for visualization. At last, click the button of “Run” to start the program.

Warning: Do not edit the map file (*.map) and the result file (*.qnk) from QTLNetwork, otherwise QTLNetworkR may crashed with some unpredictable error.

4. Graphic Configuration

Six tabbed pages named “MI”, “QTL”, “QE”, “MII”, “Epistasis” and “QTLNetwork” are for F -statistic profiles of marker interval analysis, one-dimensional genome scan for putative QTL, QTL-by-environment interaction, marker interval interaction analysis, two dimensional genome scan for epistasis and in summary, the predicted genetic architecture, respectively. After loading linkage map file and QTL mapping result files generated by QTLNetwork, users can click one of them to set graphic configuration to perform the program. Let’s start it one by one.

MI&QTL:

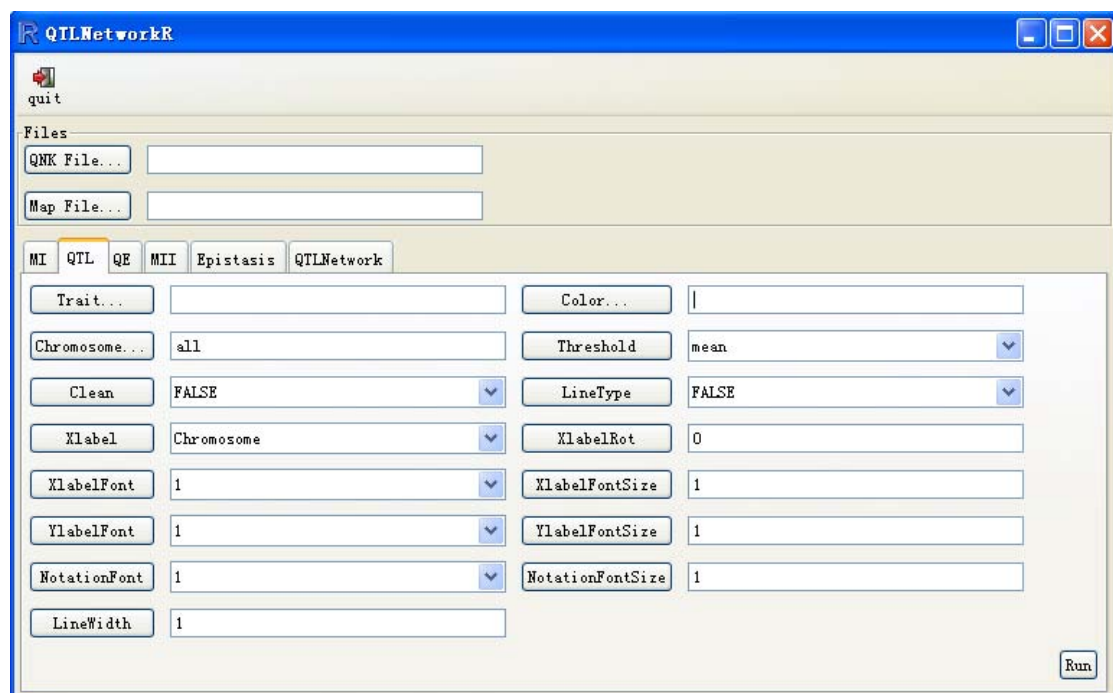


Figure 2. A snapshot of the GUI of QTLNetworkR with tabbed page of QTL.

Trait... - Click this option to select traits.

Color... -Click this option to select colors. (Warning: make sure the number of colors same with traits, otherwise, the program will be stopped)

Chromosome...: Click this option to select chromosomes, if the selected ones including “all”, others will be ignored. The default value is ”all”

Threshold: “each” means show threshold with each trait respectively, but “mean” will only show threshold by mean., click the drop-down menu change threshold value

Clean: If “yes”, the field below threshold will turn out blank.

LineType: If “yes”, the line of each traits will turn out different, solid, dashed and so on. But R only provides 8 types of line.

Xlabel: The types of x-axis label, “chromosome” to show chr add chromosome number without space between them or “Length” to show each length of chromosomes, respectively.

XlabelRot: Angle of rotation for x-axis label.

XlabelFont: Font of x-axis label.

Table 1. Font families and font face in R

1	Roman or upright face
2	Bold face
3	Slanted or italic face
4	Bold and slanted face

XlabelFontSize: Font size of x-axis label.

YlabelFont: Font of y-axis label.

YlabelFontSize: Font size of y-axis label.

NotationFont: Font of notation on the top.

NotationFontSize: Font size of notation on the top.

LineWidth: Width of Line.

QE

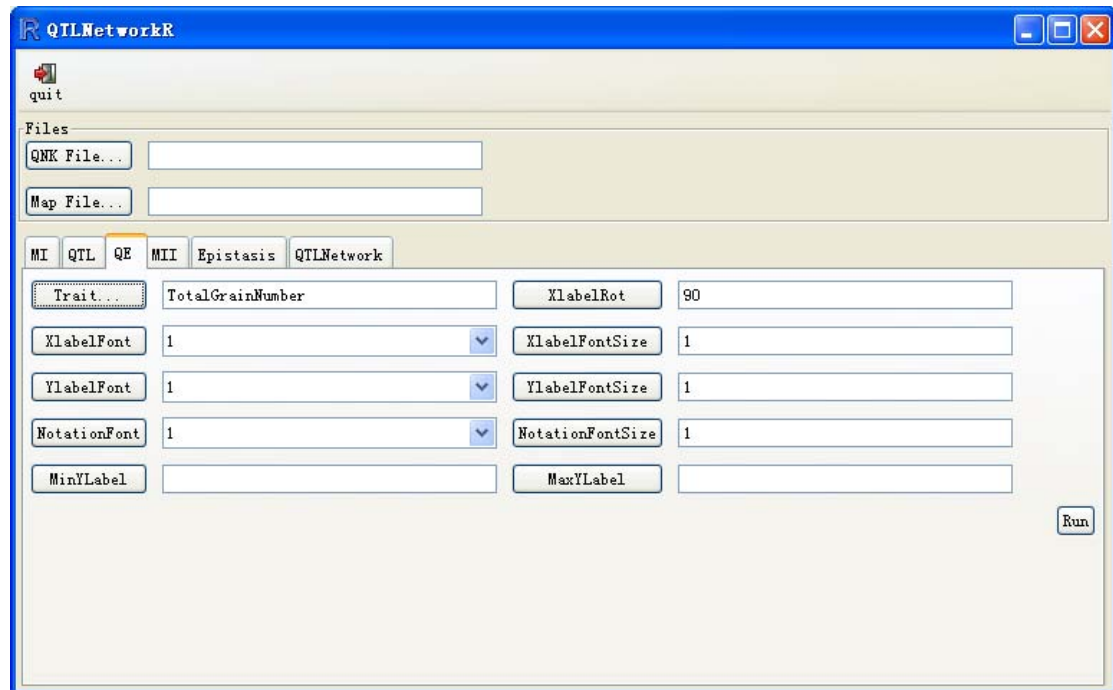


Figure 3. A snapshot of the GUI of QTLNetworkR with tabbed page of QE.

Trait... - Click this option to select trait.

XlabelRot: Angle of rotation for x-axis label.

XlabelFont: Font of x-axis label.

XlabelFontSize: Font size of x-axis label.

YlabelFont: Font of y-axis label.

YlabelFontSize: Font size of y-axis label.

NotationFont: Font of notation on the top.

NotationFontSize: Font size of notation on the top.

MinYLabel(MaxYlabel): Minimum (Maximum) of y-axis label, if blank, the scale will be calculated by the program itself.

MII

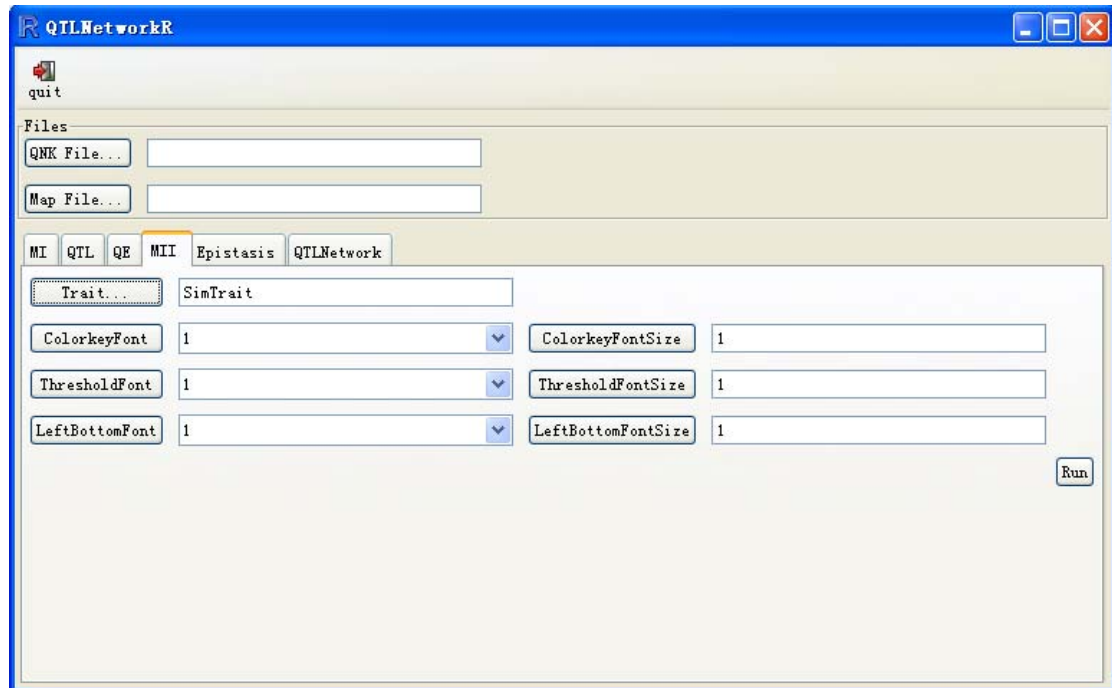


Figure 4. A snapshot of the GUI of QTLNetworkR with tabbed page of MII.

Trait... - Click this option to select trait.

ColorkeyFont: Font of color key scale.

ColorkeyFontSize: Font size of color key scale.

ThresholdFont: Font of threshold legend on color key.

ThresholdFontSize: Font size of threshold legend on color key.

LeftBottomFont: Font of left and bottom (or x and y-axis) labels which show the position on its chromosomes.

LeftBottomFontSize: Font size of left and bottom (or x and y-axis) label.

Epistasis

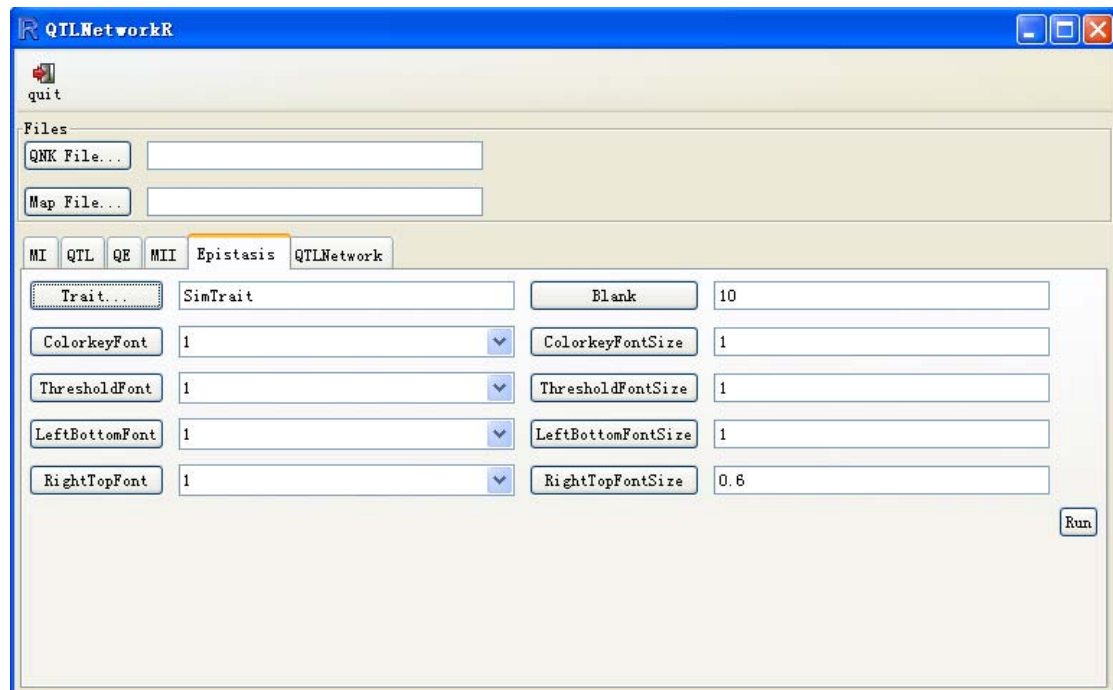


Figure 5. A snapshot of the GUI of QTLNetworkR with tabbed page of Epistasis.

Trait... - Click this option to select trait.

Blank: The distance between two epistasis regions.

ColorkeyFont: Font of color key scale.

ColorkeyFontSize: Font size of color key scale.

ThresholdFont: Font of threshold label on color key.

ThresholdFontSize: Font size of threshold label on color key.

LeftBottomFont: Font of left and bottom (or x and y-axis) label.

LeftBottomFontSize: Font size of left and bottom (or x and y-axis) label.

RightTopFont: Font of right and top labels which show which chromosome it belongs to.

RightTopFontSize: Font size of right and top label.

QTLNetwork:

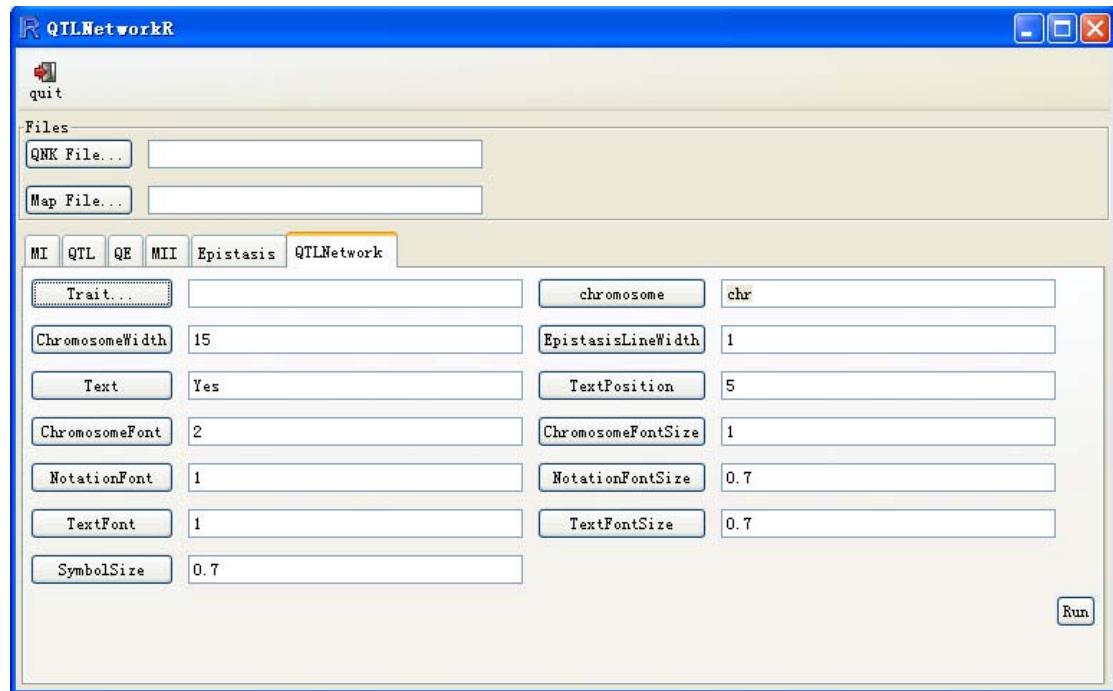


Figure 2. A snapshot of the GUI of QTLNetworkR with tabbed page of QTLNetwork..

Trait... - Click this option to select trait.

Chromosome: Mark appears at the left side of the chromosomes, and it will turn out "chr" by default.

ChromosomeWidth: The chromosome height.

EpistasisLineWidth: Width of epistasis line.

ChromosomeFont: Font of chromosome at the left.

ChromosomeFontSize: Font size of chromosome at the left.

NotationFont: Font of notation at the top.

NotationFontSize: Font size of notation at the top.

TextFont: Font of the text for indicating QTLs in the plot.

TextFontSize: Font size of the text for indicating QTLs in the plot.

SymbolSize: Size of the symbols representing QTLs.