Learn QTLNetworkR in 10 minutes

Institute of Bioinformatics of Zhejiang University

What do you expect to learn here?

We will illustrate some essential steps based on the sample files from the home page of QTLNetworkR, providing a quick tutorial of QTLNetworkR. Hopefully, these steps will meet your practice.

GTK+

Make sure the GTK+ is installed on your computer system.

If you do not have the GTK+, please download it here：Windows，MacOS.

R and R packages

R:

Make sure R is installed on your computer system.

If you do not have the GTK+, please download it from the CRAN.

R packages:

Download the following R packages from CRAN and install them in order: RGtk2, cairoDevice, gWidgets and gWidgetsRGtk2

They can also installed directly within R by command:

install.packages(pkgs=c("RGtk2","cairoDevice","gWidgets","gWidgetsRGtk2"))

QTLNetworkR:

Download and install QTLNetworkR from CRAN.

Or you can install QTLNetworkR by command in R:

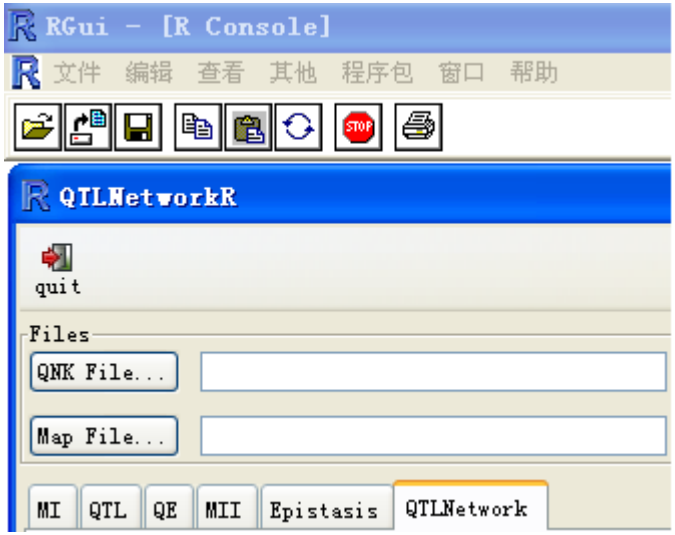
install.packages(pkgs="QTLNetworkR")

Step 1: start QTLNetworkR

Start R by double click 

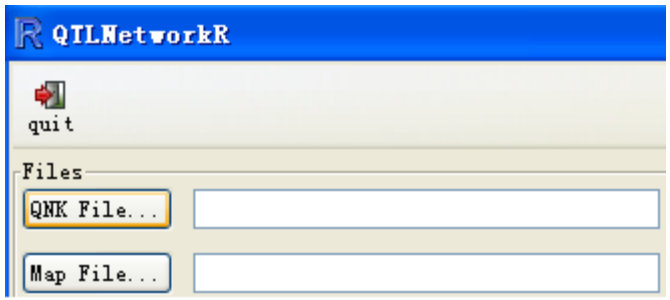
Start QTLNetworkR by command : *Library(QTLNetworkR)*

QTLNetworkR will pop out initially:



Step 2: Load Files

Load QTLNetwork result file and linkage map file by clicking “QNK File…” and “Map File…”:

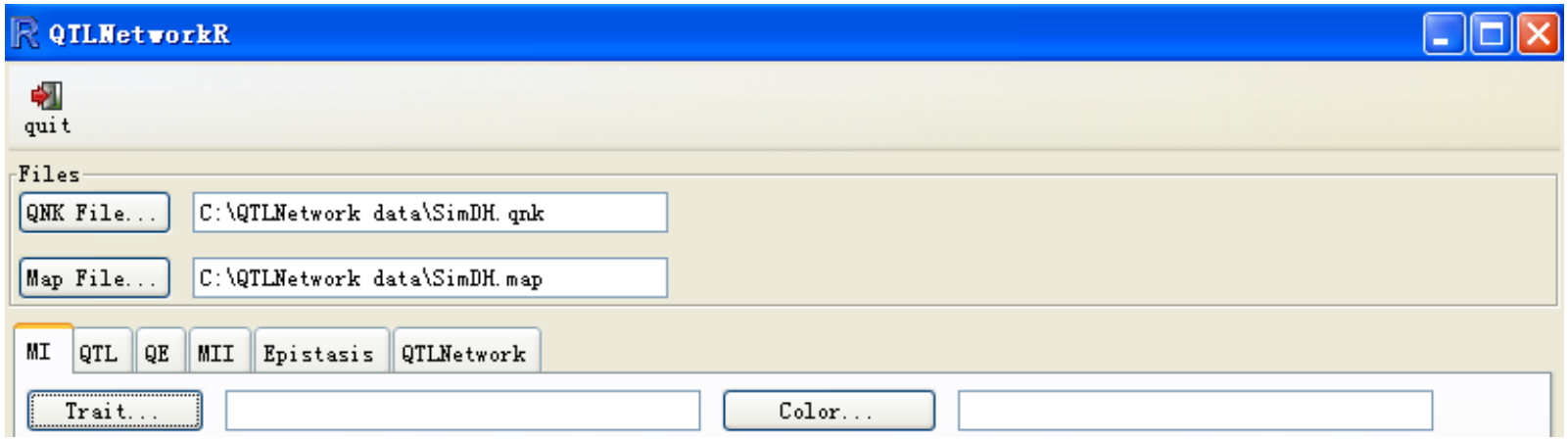


Sample data can be found in the subdirectory ‘./R/library/QTLNetworkR’ with the suffix of “*.map” and “*.qnk”, respectively.

Step3 Go to functions tab, e.g. MI tab

Select traits and colors for marker interval analysis (MI) by clicking

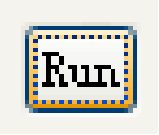
"Trait…" after loading the files:



Step4 Perform the packages

Clicking the “Run” button at the bottom right corner,

the procedure will start to profile.



Congratulations! You’ve completed the steps.