

# Manual of FsQtlFunMap 1.0

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FsQtlFunMap is a Windows software for functional mapping and can be freely used by anyone who is interested. FsQtlFunMap is used to map quantitative trait loci (QTL) that govern the growth curve of a trait during the development in a full-sib family of diploid species, especially in forest trees. The algorithm is based on interval mapping method, and the growth trajectory is described by Legendre polynomial. The QTL segregation patterns are considered to be sorted into three types, test cross (segregating 1:1),  $F_2$  cross (segregating 1:2:1), and full cross (segregating 1:1:1:1). The model selection criteria of AIC and BIC are applied not only to determine the order of Legendre polynomial, but also to discriminate the QTL segregation pattern. A maximum likelihood approach implemented with EM algorithm provides the estimates of QTL positions and model parameters responsible for growth trajectories. FsQtlFunMap uses the free software, *gnuplot*, to plot likelihood ratio (LR) profiles along the whole genome and the Legendre polynomial curves for each QTL genotype. In practical QTL mapping, the threshold of LR for each QTL model can be obtained through permutations. FsQtlFunMap can be freely downloaded from the webpage: <http://fgbio.njfu.edu.cn/tong/FsQtlFunMap/FsQtlFunMap.htm>.

## 1 Data Format

To use FsQtlFunMap, you must put your data in a text file that contains information about parental linkage phases, map distances between two neighbor markers, and marker genotypes of progeny for each linkage group. The time points and quantitative trait values of progeny are given at the end of the file. The individual marker genotypes for each marker locus and trait values for each trait are given in the same order. For details, please refer to the simulated data file, "Simudata.txt", which can be found in the folder where FsQtlFunMap is installed.

## 2 QTL Mapping

When you have prepared the input data, please open it by clicking the “file” menu and then the option “file open”. The data file will be opened and shown in the main window. Now you can perform QTL mapping by clicking the “Analysis” menu and then the option “QTL Mapping”. A dialog box will pop out to let you choose the order of Legendre polynomial according to the indexes of AIC and BIC. During the procedure of QTL analysis, a series files are generated in the same folder of the data file, which include following types:

- “Trait\*Group\*Order\*Rst.dat”
- “Trait\*Group\*Order\*BcRst.dat”
- “Trait\*Group\*Order\*F2Rst.dat”
- “Trait\*Group\*Order\*FullRst.dat”
- “Trait\*Order\*GenomeLRemfPlot.plt”
- “Trait\*Order\*QTL\*Curv.dat”
- “Trait\*Order\*QTL\*CurvEmfPlot.plt”
- “Trait\*Order\*QtlSummary.sry”

When the computing finishes, the main window will show the summary of QTL mapping, which is saved in the file “Trait\*Order\*QtlSummary.sry”.

## 3 Plots of LOD Profiles and the Curves of QTL Genotypes

After finishing QTL mapping, please click the “Plot” menu and then the option “LOD Profiles”. The system will use *gnuplot* and the file “Trait\*Order\*genomeplot.plt” to plot LOD profiles of the three QTL models for all the linkage groups. The plot is automatically saved in the enhanced metafile format file, “Trait\*Order\*GenomeLRemfPlot.emf”. The system will also use *gnuplot* and the file “Trait\*Order\*QTL\*Curv.dat” to plot curves for each QTL genotype. In the meantime, an eps format of each plot is also generated. Users can modify the files with .plt file name extension to get better plots.

## 4 Parameter Options

When selecting the “Parameter Options” option in the “Analysis” menu, it will pop out a dialog window in which you can set the parameters such as map function, trait number, criterion of QTL model selection, thresholds of LOD, and permutation times. The default thresholds are set based on the permutations for the simulated data.

## 5 Permutations

LR threshold for each QTL model can be obtained through at least 1000 permutations. Because permutations are time needing, you can do permutations on several PCs and pool the results to calculate the thresholds. After you do permutations, the result will be saved in the file, “Trait\*Order\*PermLR.prm”. When you continue to do permutations on the same PC, the results will be appended in the file, “Trait\*Order\*PermLR.prm”. It is worth noting that this file will be deleted if it exists when you select “First Time” on the dialog window of parameter option. If you do permutations for a new trait for the first time, you must select “First Time” on the dialog window of parameter option, and if you continue to do permutations, you must select “Continue” on the dialog window. After the permutation times exceeds 1000, FsQtlFunMap will ask you whether to calculate the thresholds of LR or not.