

Manual of FsQtlMap 1.0

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FsQtlMap is a windows software written in VC++6.0 and can be freely used by anyone who is interested. The algorithm is based on interval mapping method and assumes that the segregation pattern in a potential quantitative trait locus (QTL) can be divided into three types, testcross (segregating 1:1), F2 cross (segregating 1:2:1), and full cross (segregating 1:1:1:1) in a full-sib family, which can be generated by hybridizing two outbred parents. FsQtlMap uses Laplace-empirical criterion (LEC) as a model selection criterion to discriminate the QTL segregation ratio. FsQtlMap uses the free software, *gnuplot*, to plot LOD profiles along the linkage groups. In practical QTL mapping, the genome-wide LOD threshold for asserting a peak of the profile to be a QTL can be obtained through permutations for each of the three QTL models. FsQtlMap can be freely downloaded from the webpage: <http://fgbio.njfu.edu.cn/tong/FsQtlMap/FsQtlMap.htm>.

1 Data Format

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

2 QTL Mapping

When you have the formatted 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 do QTL mapping by clicking the "Analysis" menu and then the option "QTL Mapping". During this procedure, a series files are generated in the same folder of the data file, such as "Trait*Group*.data", "Trait*Group*_bc.data", "Trait*Group*_f2.data",

“Trait*Group*_full.data”, “Trait*genomeplot.plt”, “Trait*genomepsplot.plt”, and “Trait*QtlSummary.sry”. When the procedure finishes, the main window will show the summary of QTL mapping which is saved in the file, “Trait*QtlSummary.sry”.

3 LOD Profiles Plot

After having done QTL mapping, please click the “Plot” menu and then the option LOD Profiles. The system will use *gnuplot* and the file “Trait*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*genomeplot.emf”. In the meantime, a ps format of the plot is also generated, which can be transformed into pdf format by Acrobat Distiller.

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, thresholds of LOD and permutation times. The default thresholds are set based on the permutations for the simulated data.

5 Permutations

LOD 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*PermLOD.txt”. When you continue to do permutations on the same PC, the results will be appended in the file, “Trait*PermLOD.txt”. 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, FsQtlMap will ask you whether to calculate the thresholds of LOD or not.