

# Manual of FsLinkageMap 2.1

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FsLinkageMap is a windows software that can be used to construct genetic linkage maps with molecular markers generated in a full-sib family. It can not only perform linkage analysis but also plot genetic linkage maps. If you are interested, please freely download it from its webpage, <http://fgbio.njfu.edu.cn/tong/FsLinkageMap/FsLinkageMap.htm>.

## 1 Data Format

The data of molecular markers from a full-sib family will be saved in a text file, in which each marker notation with “\*” in advance is put in the first part of a line, the segregation type of the marker in the second part, and the marker genotypes of all individuals in the rest parts. Table 1 shows the notations of possible genotypes for each of seven segregation types (Maliepaard et al, 1997) and Table 2 shows an example of data format used by FsLinkageMap.

Table 1 Notations of Marker Genotypes for Each Segregation Type in a Full-sib Family

Segregation Type	Notations of Marker Genotypes			
abxaa	aa	ab		
aaxab	aa	ab		
abxab	aa	ab	bb	
abxcd	ac	ad	bc	bd
a0xa0	a-	00		
abxa0	a-	ab	b0	
a0xab	a-	ab	b0	



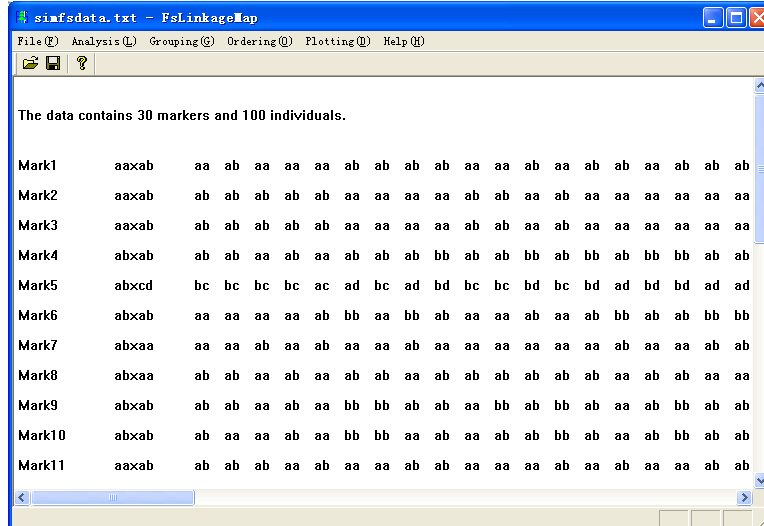


Figure 1: The window of an opened data file

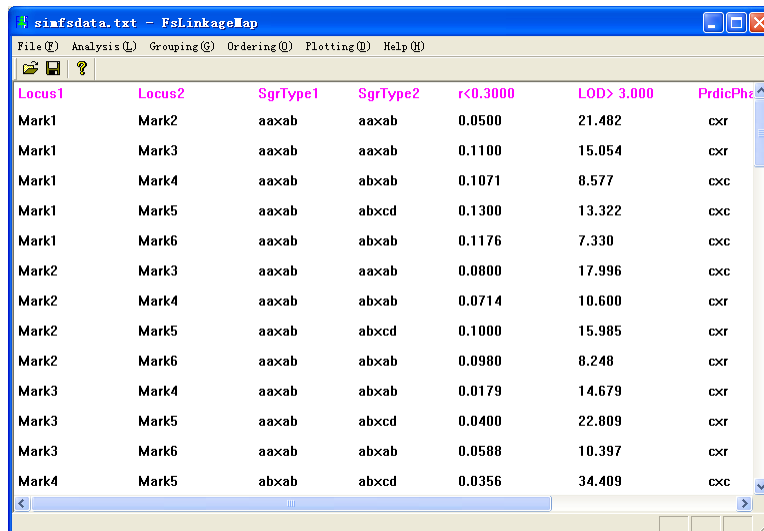


Figure 2: The window of results of two-point linkage analysis

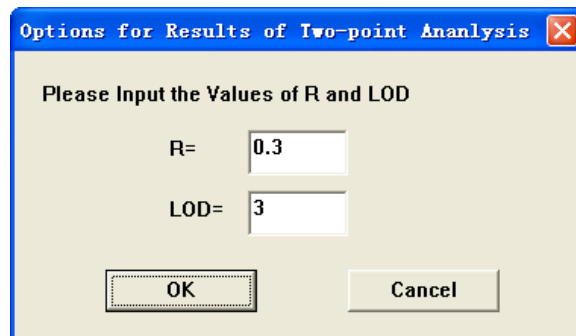


Figure 3: The optional window for results of two-point linkage analysis

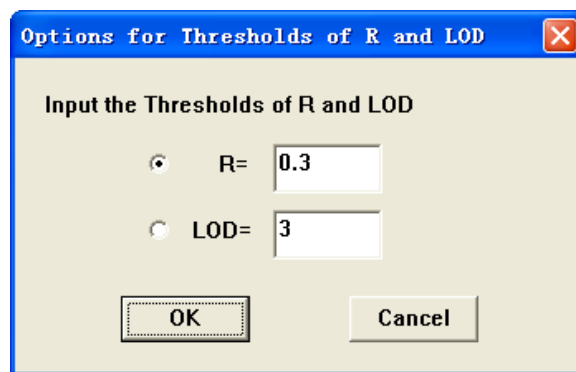


Figure 4: The dialogue window of the thresholds for grouping linkage markers

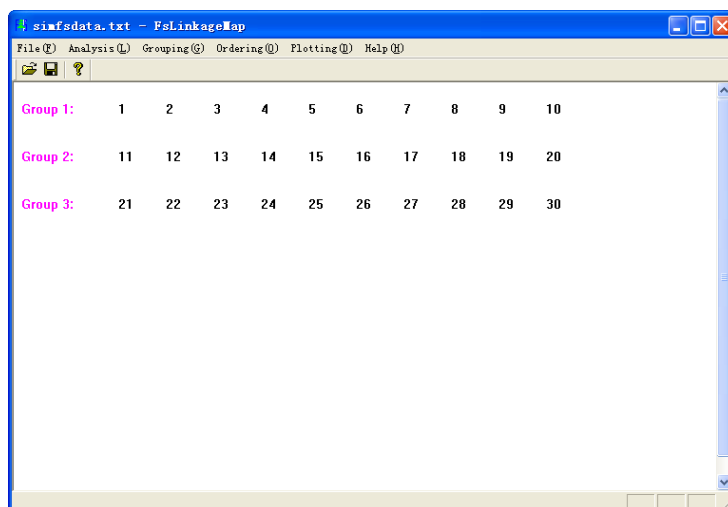


Figure 5: The result of grouping linkage markers

After two-point linkage analysis, you can classify the markers into linkage groups by clicking the option “Linkage Groups” of the menu “Grouping”. You will see the optional dialogue window of the thresholds for grouping linkage markers as fig 4. Filling in proper values of recombination and LOD and pressing the button “OK”, you will see the window of grouping result. You can repeatedly fill in the blanks of the optional dialogue window until you are satisfied in the grouping result.

Finally, you can order the markers of each linkage group. By clicking the option “Calculating” of the menu “Ordering” and waiting for a moment, you can see the ordering result as fig 6 and three files, namely “bestorders.dat”, “maps.dat” and “groupsmknum.dat”, will be generated in the folder where the data file is. The file, “bestorders.dat”, records the result of the optimal orders of linkage groups. And the file, “maps.dat”, records the prediction of multi-linkage phases, the map distances between adjoining two markers and the marker genotypes of progeny for each linkage group according to its optimal orders. The file, “maps.dat”, can be used as the input file of QTL mapping in a full-sib family after properly being modified.

### 3 Drawing Linkage Maps

After ordering the markers of linkage groups, you can draw the linkage map for each linkage group. Clicking the option “Linkage Maps” of the menu “Plotting”, you can see a dialogue window as fig 7. Choosing the map function, filling in the range of linkage groups and pressing the button “OK”, the genetic linkage maps will be shown on the screen as fig 8. The

The screenshot shows a window titled "simfsdata.txt - FsLinkageMap" with a menu bar containing "File (F)", "Analysis (L)", "Grouping (G)", "Ordering (O)", "Plotting (P)", and "Help (H)". Below the menu bar is a toolbar with icons for file operations and help. The main area displays three linkage groups, each with 10 ordered markers:

Ordered Group 1:	1	2	3	4	5	6	7	8	9	10
Ordered Group 2:	11	12	13	14	15	16	17	18	19	20
Ordered Group 3:	21	22	23	24	25	26	27	28	29	30

Figure 6: The result of ordering markers of each linkage group

maps can be saved as a windows metafile (WMF) by clicking the option “Save Maps” of the menu “File”. A WMF file, which quality can not be changed by zooming in or out, can be inserted into a word file.

## 4 Version Update

### 4.1 Version 2.0

FsLinkageMap originally utilizes heuristic search algorithm for ordering the markers of linkage groups. FsLinkageMap2.0 has improved this algorithm by incorporating a local ordering method based on three-point linkage analysis.

In addition, the file, namely “maps.dat”, is generated after the ordering procedure, which can be used as a input file for QTL mapping in a full-sib family.

### 4.2 Version 2.1 (July 31,2014)

Users can modify the three files, “bestorders.dat”, “recombination.dat” and “markerms.dat”, to redraw linkage maps with this new version.

## 5 References

Maliepaard, C., Jansen, J., and Van Ooijen, J. W., 1997 Linkage analysis in a full-sib family of an outbreeding plant species: overview and consequences for applications, *Genetical Research*, 70: 237-250

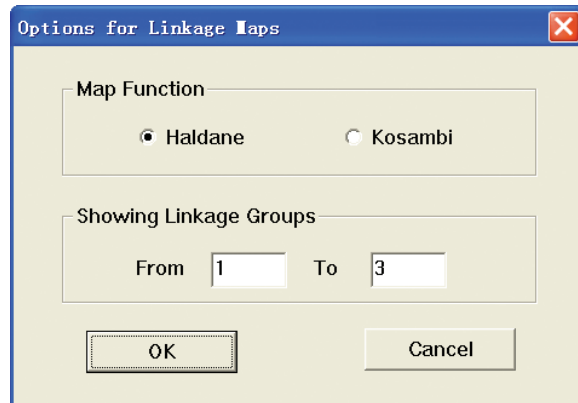


Figure 7: The optional dialogue window of plotting linkage maps

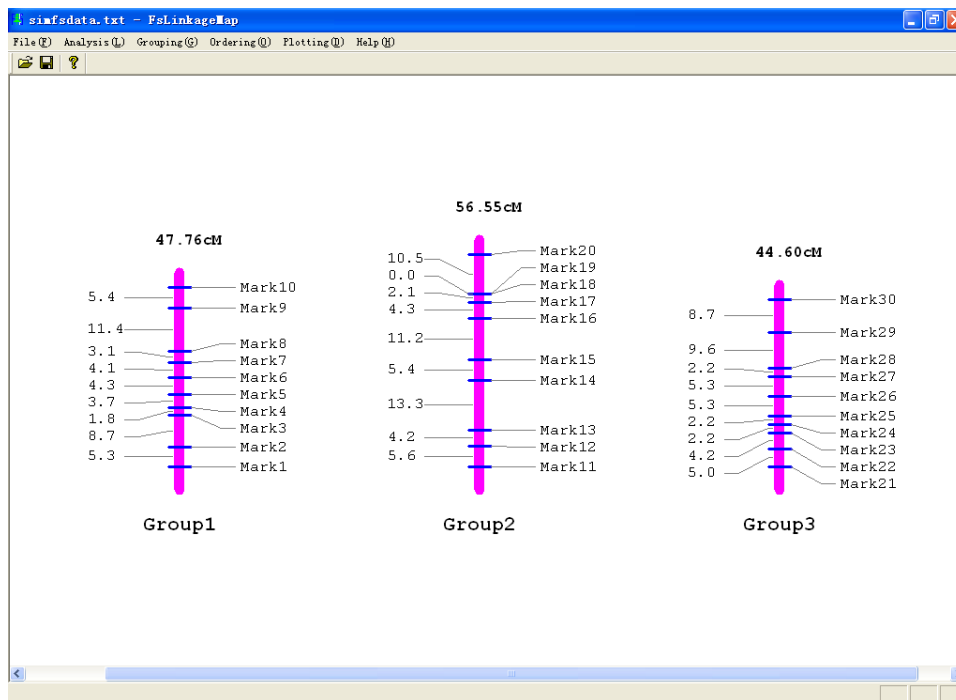


Figure 8: The result of plotting linkage maps