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

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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						

Table 2 Data Format of FsLinkageMap

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2 Data Analysis

After running FsLinkageMap 2.0, please open the data file by clicking the menu "file" and then the option "Open". If the data format is correct, you will successfully open the data file and a window like fig. 1 will be shown on the screen. We provide a simulated data that you can use to construct genetic linkage maps as an example with FsLinkageMap. You can find the simulated data file, "simfsdata.txt", in the folder where FsLinkageMap has been installed.

To perform two-point linkage analysis, please click the menu "analysis" and then the option "Two Point". The result of two-point linkage analysis will be shown as Fig 2, where the first and second columns are notations of two markers, the third and fourth columns are the segregation types of loci 1 and 2 respectively, the fifth and sixth columns are the estimate of recombination and LOD between the two markers, and the seventh column shows the prediction of linkage phase between the two markers. If the prediction of linkage phase between two markers is denoted by "cxr", that means the linkage phase of the first parent in coupling(c) and the second in repulsion(r). Other notations of linkage phases have the similar means. If you choose the option "Options" of menu "Analysis", it will pop out a dialogue window as fig 3. Filling proper values of the recombination and LOD and pressing the button "OK", you will have alternative show for the results of two-point linkage analysis.

In the mean time, four files, namely "recombination.dat", "lod.dat", "phase.dat", and "markernms.dat", are generated in the folder where the data file is. They contain the estimate of recombination, LOD and prediction of linkage phase between any two markers, respectively.

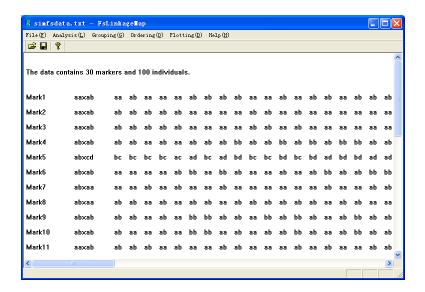


Figure 1: The window of an opened data file

	a.txt - FsLinkag					
	ysis(L) Grouping(G)	Ordering (Q) Plott	ing(D) Help(H)			
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_ocus1	Locus2	SgrType1	SgrType2	r<0.3000	LOD> 3.000	PrdicPha
√lark1	Mark2	aa×ab	aa×ab	0.0500	21.482	c×r
Mark1	Mark3	aa×ab	aa×ab	0.1100	15.054	c×r
Mark1	Mark4	aa×ab	ab×ab	0.1071	8.577	c×c
Mark1	Mark5	aa×ab	ab×cd	0.1300	13.322	c×c
Mark1	Mark6	aa×ab	ab×ab	0.1176	7.330	c×c
Mark2	Mark3	aa×ab	aa×ab	0.0800	17.996	c×c
Mark2	Mark4	aa×ab	ab×ab	0.0714	10.600	c×r
Mark2	Mark5	aa×ab	ab×cd	0.1000	15.985	c×r
Mark2	Mark6	aa×ab	ab×ab	0.0980	8.248	c×r
Mark3	Mark4	aa×ab	ab×ab	0.0179	14.679	c×r
Mark3	Mark5	aa×ab	ab×cd	0.0400	22.809	c×r
Mark3	Mark6	aa×ab	ab×ab	0.0588	10.397	c×r
Mark4	Mark5	ab×ab	ab×cd	0.0356	34.409	cxc
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Figure 2: The window of results of two-point linkage analysis

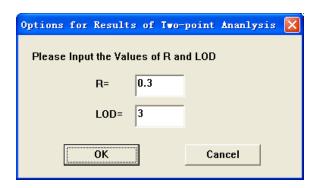


Figure 3: The optional window for results of two-point linkage analysis

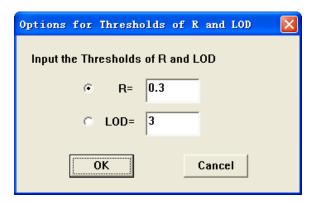


Figure 4: The dialogue window of the thresholds for grouping linkage markers

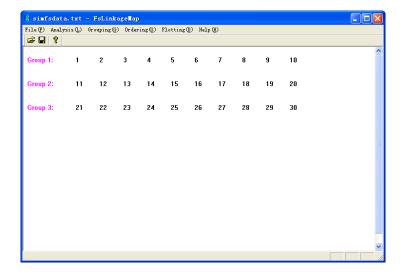


Figure 5: The result of grouping linkage markers

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

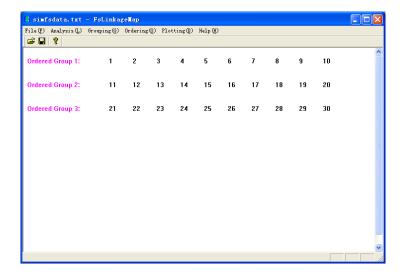


Figure 6: The result of ordering markers of each linkage group

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 "markernms.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

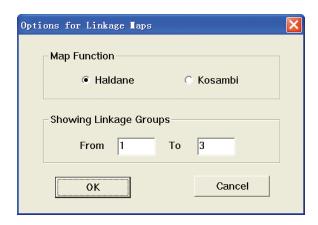


Figure 7: The optional dialogue window of plotting linkage maps

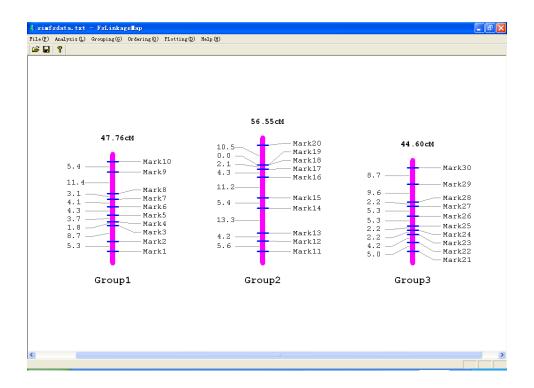


Figure 8: The result of plotting linkage maps