



Bioinformatics workshop

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Quantitative trait loci mapping using the QTL ICIMapping software



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1- View the .bip file

Header: Lines starting with "*" are remarks and will be ignored in the program
 General Information
 Assuming P1 = P1 x P2, populations available in QTL ICIMapping are:
 1. P1P2P1 = P1 x P1, the first backcrossing where P1 is used as the recurrent parent.
 2. P2P1P1 = P2 x P1, the first backcrossing where P2 is used as the recurrent parent.
 3. P1P1: P1-derived doubled haploids.
 4. M1 or P1B1L: recombination inbred lines through the repeated selfing of P1.
 5. P1B1B1L: recombination inbred lines through the repeated selfing of P1B1P1.
 6. P2P2P1L: recombination inbred lines through the repeated selfing of P2P1P1.
 7. P2: the selfing generation of P1.
 8. P1: the selfing generation of P2.
 9. P1B1P1: the second backcrossing where P1 is used as the recurrent parent.
 10. P2P1P1: the second backcrossing where P2 is used as the recurrent parent.
 11. P1B1B1L: recombination inbred lines through the repeated selfing of P1B1P1.
 12. P2P1P1L: recombination inbred lines through the repeated selfing of P2P1P1.
 13. P1B1P1P2: the selfing generation of P1B1P1.
 14. P2P1P1P2: the selfing generation of P2P1P1.
 15. P1B1P1P2: the selfing generation of P1B1P1P1.
 16. P2P1P1P2: the selfing generation of P2P1P1P1.
 17. P1B1P1P1: P1B1P1-derived doubled haploids.
 18. P2P1P1P1: P2P1P1-derived doubled haploids.
 19. P1B1P1P1P1: P1B1P1P1-derived doubled haploids.
 20. P2P1P1P1P1: P2P1P1P1-derived doubled haploids.
 * Linkage map: 1 for mapping, 2 for simulation.
 4 Mapping Population (see remarks above)
 5 Mapping Function (0 for Kosambi, 1 for Haldane, 3 for Morgan)
 6 Marker Space Type (0 for intervals, 2 for positions)
 7 Marker Space Unit (0 for centimorgan, 2 for Morgan)
 20 Number of Chromosomes (or Linkage Group)
 10 Population size of the mapping population
 0 Number of trials

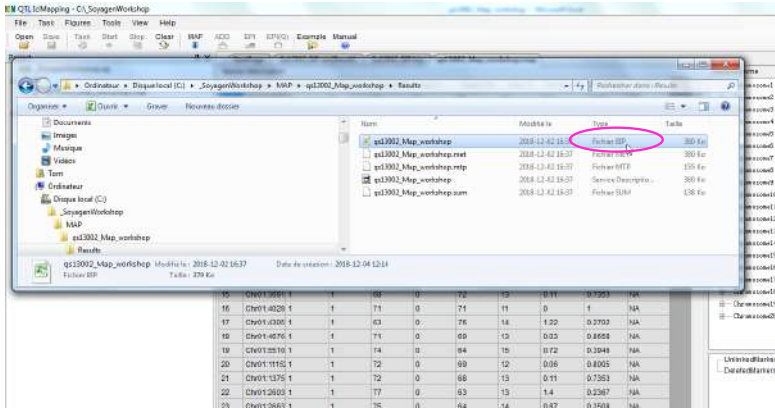
Chromosomes and Linkage	Markers
Chromosome1	60
Chromosome2	60
Chromosome3	64
Chromosome4	64
Chromosome5	70
Chromosome6	51
Chromosome7	64
Chromosome8	68
Chromosome9	68
Chromosome10	71
Chromosome11	71
Chromosome12	20
Chromosome13	37
Chromosome14	40
Chromosome15	42
Chromosome16	34
Chromosome17	47
Chromosome18	43
Chromosome19	32
Chromosome20	25

Linkage map (Marker name followed by position, or the interval length)
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Message
 Welcome to the use of QTL ICIMapping (Version 4.1.0.0)
 C:\Program Files\QTL ICIMapping\qtlmapping.exe read successfully!
 D:\L_QuickTime\QTL ICIMapping\qtlmapping.exe read successfully!

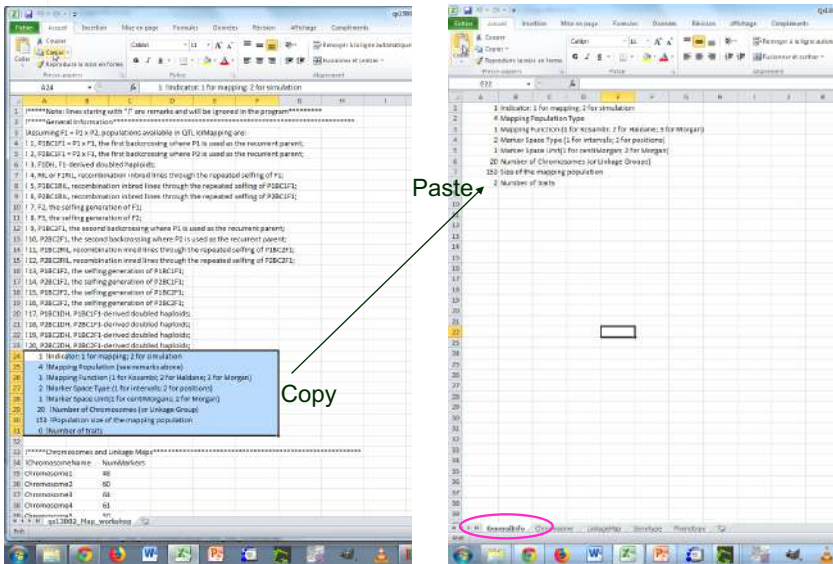
- The .bip file is the input file for the QTL mapping analysis in bi-parental populations
- The .bip file needs to be opened with Excel and reorganized in a new Excel file
- Phenotypes also have to be integrated to this new Excel file

2- Open the .bip file with Microsoft Excel to create a new Excel file



- The .bip file is located in the Results folder
- Open the .bip file with Microsoft Excel

3- Use the .bip file to create a new Excel file



- Produce a new Excel file with the informations from the .bip file
- Copy and paste the datas from the .bip file to separated sheets of the Excel file
- Convert the data to separated columns

Sheet 1: GeneralInfo

3- Use the .bip file to create a new Excel file

- Copy and paste the datas from the .bip file to separated sheets of the Excel file
- Convert the data to separated columns

Sheet 2: Chromosome

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3- Use the .bip file to create a new Excel file

- Copy and paste the datas from the .bip file to separated sheets of the Excel file
- Convert the data to separated columns

Sheet 3: LinkageMap

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3- Use the .bip file to create a new Excel file

- Copy and paste the datas from the .bip file to separated sheets of the Excel file
- Convert the data to separated columns
- Find B and replace by 0
Find A and replace by 2
Find X and replace by -1

Sheet 4: Phenotype

3- Use the .bip file to create a new Excel file

- Place phenotypic data with respect to lines order
- The last step completed the modification of the .bip file, you can now save file as *Microsoft Excel 97-2003 format*

4-Open the .bip file

Open the Excel BIP file created at step 3

5- The BIP directory appears in the menu

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6- Select the parameters for the QTL analysis

❖ Recommended parameters:
Permutation times = 1000
Type 1 Error = 0.05

Missing phenotypic data will not be included in QTL mapping

Mapping parameters: by default

Threshold to declare significant QT

Select mapping method

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7-Start the QTL analysis

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8-View .qic (significant QTLs from additive mapping) results file

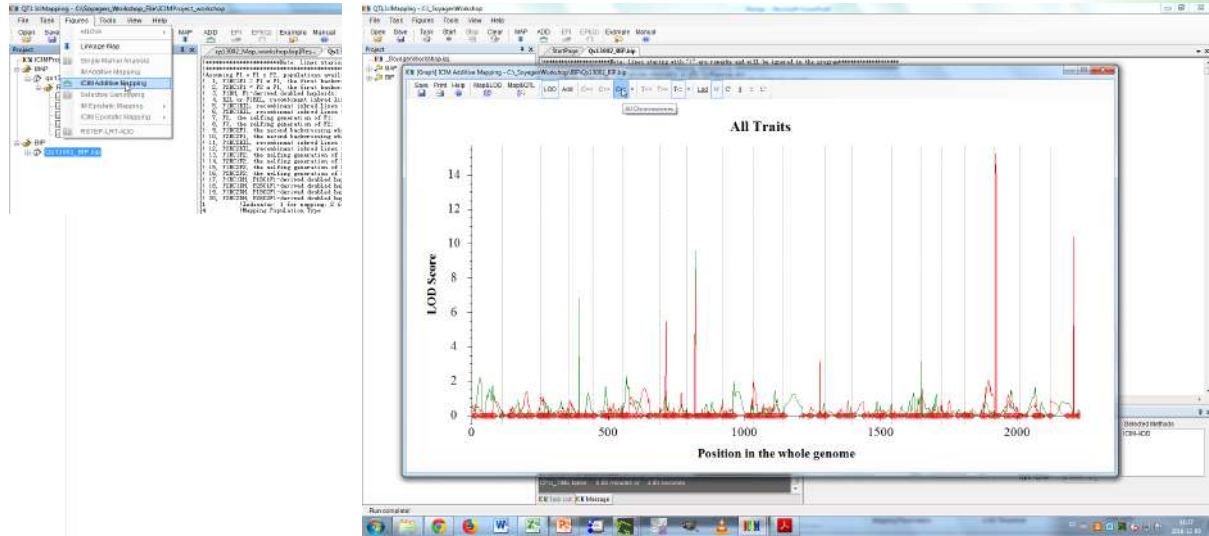
TraitID	TraitName	Chromosome	Position	LeftMarker	RightMarker	LOD	FVE (%)	Add	LeftCI	RightCI
1	FenoleIndex	7	21 0000	Chr07:3432131	Chr07:3655102	5.0254	7.7142	-8.3035	19.5000	22.5000
1	FenoleIndex	8	32 0000	Chr08:3297955	Chr08:3971192	6.2930	12.2151	-11.6690	31.5000	33.5000
1	FenoleIndex	13	65 0000	Chr13:3076306	Chr11:3586555	3.1538	4.5841	-8.8100	62.5000	65.5000
1	FenoleIndex	23	8 0000	Chr23:1748756	Chr18:3461679	15.2254	24.2586	-16.7471	8.5000	8.5000
1	FenoleIndex	27	25 0000	Chr27:4392958	Chr20:4411931	10.2662	15.1131	-13.3689	24.5000	26.5000
2	proteinase	4	58 0000	Chr04:8312906	Chr04:9284101	6.8523	16.1942	0.5102	37.5000	39.5000
2	proteinase	8	32 0000	Chr08:3297955	Chr08:3971192	6.3049	22.6772	-9.6454	31.5000	33.5000
2	proteinase	15	4 0000	Chr15:5529753	Chr15:5776333	3.1487	6.4911	0.3288	2.5000	4.5000

9- View .sta file (basic statistics of phenotypic data and results of analysis of variance)

TraitID	TraitName	SampleSize	Mean	Variance	StdError	Skewness	Kurtosis	Minimum	Maximum	Range	V-test	P-value
1	FenoleIndex	149	63.2303	1106.8204	34.5965	-0.1871	-0.3846	0.7900	151.0000	150.3000	0.8417	0.35218-005
2	proteinase	153	39.7324	1.6685	1.4030	0.3871	-0.3872	38.6900	43.3800	4.6900	0.9843	0.98855-002



10-View QTL map figures

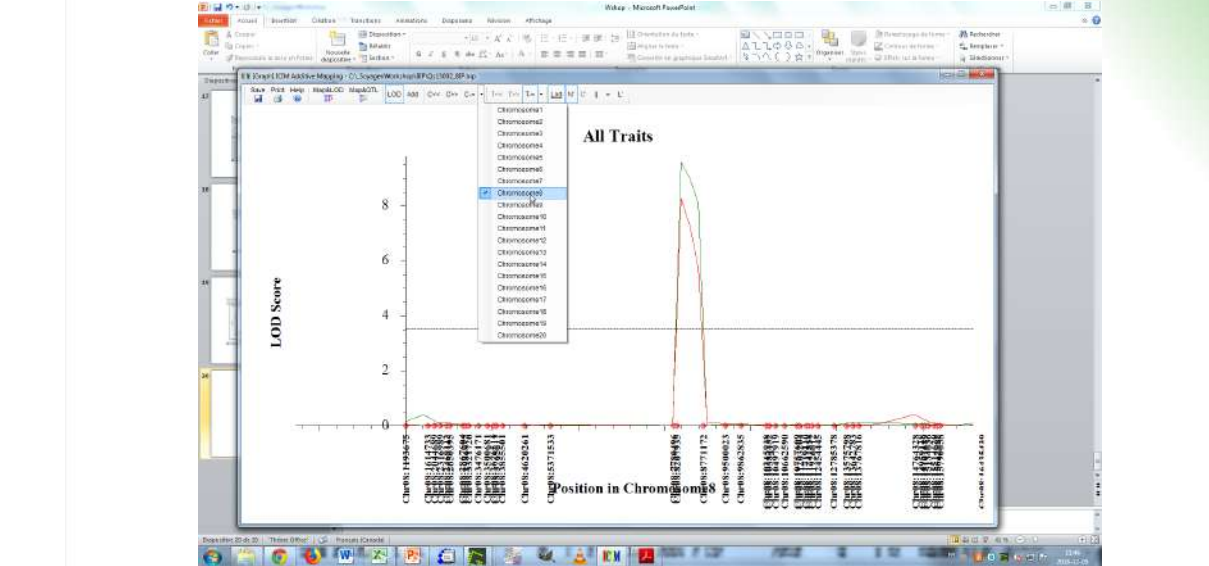


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10-View QTL map figures



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