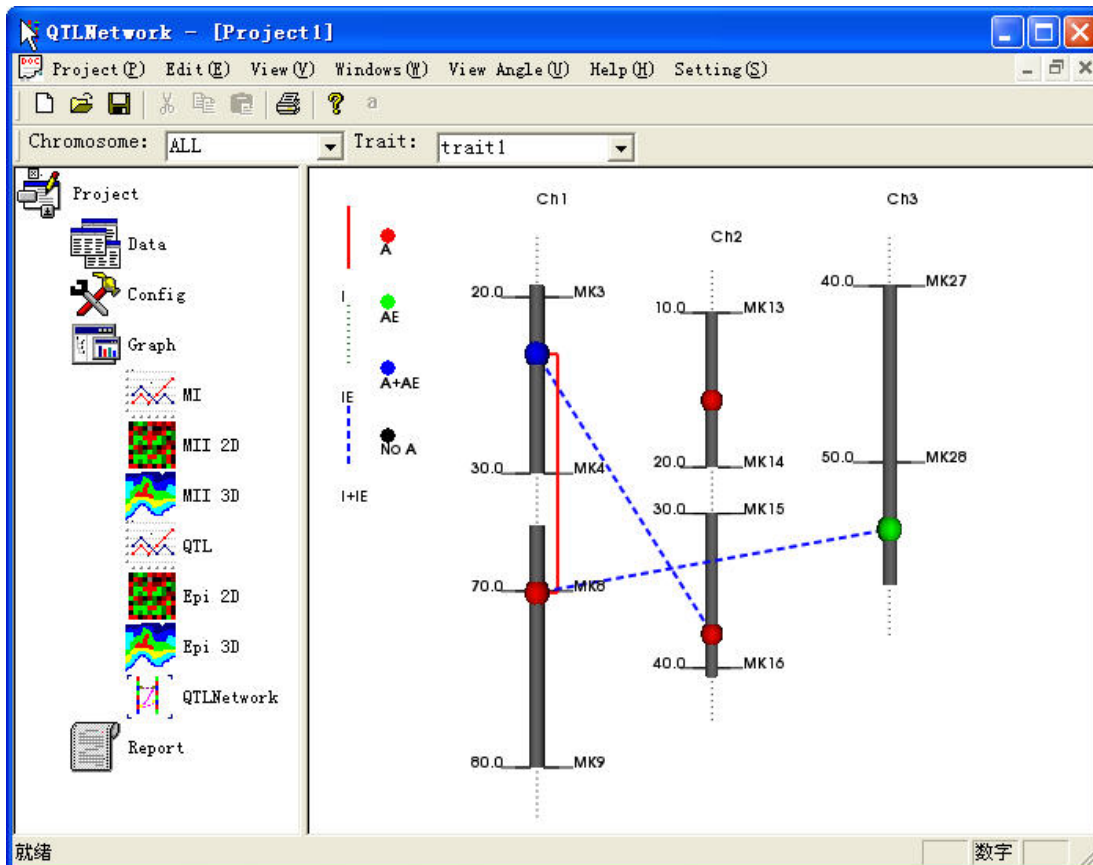


What's new in QTLNetwork-2.2

Software for Mapping QTL with Epistatic and QE Interaction Effects

Zhihong Zhu, Zhixiang Zhu, Xiaoran Tong and Jun Zhu



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Zhejiang University, China

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1. Multiple trait joint analysis for QTL mapping

In this program, multiple traits value within different environment and different replication could be jointly analysed to detect pleiotropic effects. Please find the keyword “_TraitNumber” in the top of the data file, type the number of traits, and then type index of traits which you want to analyse jointly, with connector “+”, the program will search for pleiotropic QTLs in multiple traits. For instance, there are 4 traits in total, the first two are supposed to be analysed jointly, and so do the last two.

```

_Population      DH
_Genotypes       99
_Observations    198
_Environments     yes
_Replications     yes
_TraitNumber     4 1+2 3+4
_TotalMarker     54
_MarkerCode      P1=1    P2=2    F1=3    F1P1=4  F1P2=5

```

2. Triplet interacting QTLs detection by 3 dimension genomic scan

This program is also able to detect possible QTLs involved in triplet interaction. Please find the keyword “_Population” followed with population name. As shown in the following figure, see “T 3D” after population name, where “T” stands for triplet interaction analysis and 3D stands for partial 3D genomic scan, the program would perform triplet QTLs interaction analysis by 3D genomic scan. Also, you can type only the letter “T” to carry out triplet interaction loci detection among individual and epistatic interacting QTLs. Currently, the triplet interaction analysis only works for DH and RIL population.

```

_Population      DH T 3D
_Genotypes       99
_Observations    198
_Environments     yes
_Replications     yes
_TraitNumber     4
_TotalMarker     54
_MarkerCode      P1=1    P2=2    F1=3    F1P1=4  F1P2=5

```

3. Individual genetic effects estimation

As plant and animal breeders also hope to utilize the mapping population to produce new variety or inbred lines, by selecting valuable and beneficial individuals. The program is available to estimate individual genetic effects based on estimation effects of QTLs and QTL by environments interaction effects’ prediction.

Please find the keyword “_Genotypes” with the genotype number following. Typing one decimal fraction less than 1 after the genotype number the program would perform individual genetic effects estimation, and present the result in output file (*.qnk). The scale of the presented results is determined by decimal fraction you typed.

```

_Population      DH
_Genotypes       99 0.1
_Observations    198
_Environments     yes
_Replications     yes
_TraitNumber      4
_TotalMarker      54
_MarkerCode       P1=1    P2=2    F1=3    F1P1=4  F1P2=5

```

The following figure is representation of individual_genotype_value (genetic effects of different genotypes) in *.qnk output files, generated by the input listed above.

```

_general
_for_10%_highest_value
Entry      G      1-15      2-12      3-20      2-12^3-20      2-9^3-7
64         29.2141    10.2334    4.6603    7.7713    2.5815    3.9676
97         26.4951    10.2334    2.7094    8.0333    1.5514    3.9676
48         25.1692    10.2334    4.6603    8.0333    2.6686    -0.4263
42         24.4960    5.1661     4.6603    8.0333    2.6686    3.9676
73         24.1469    5.1661     4.6603    7.7713    2.5815    3.9676
32         21.8212    10.2334    4.6603    7.7713    2.5815    -3.4252
39         21.2788    10.2334    4.6603    7.7713    2.5815    -3.9676
40         21.2788    10.2334    4.6603    7.7713    2.5815    -3.9676
28         18.3514    10.0249    2.7094    8.0333    1.5514    -3.9676

_for_10%_lowest_value
Entry      G      1-15      2-12      3-20      2-12^3-20      2-9^3-7
45        -24.2260    -10.2334    -4.6603    -8.0333    2.6686    -3.9676
65        -24.0511    -10.2334    -4.6603    -7.7713    2.5815    -3.9676
13        -21.0764    -10.2334    2.7094    -8.0333    -1.5514    -3.9676
19        -19.8936    -10.2334    4.6603    -7.7713    -2.5815    -3.9676
6         -19.6571    -10.2334    -4.6603    -7.7713    2.5815    0.4263
74        -19.6571    -10.2334    -4.6603    -7.7713    2.5815    0.4263
93        -18.9838    -5.1661     -4.6603    -7.7713    2.5815    -3.9676
43        -16.7013    -10.2334    4.6603    -8.0333    -2.6686    -0.4263
90        -16.7013    -10.2334    4.6603    -8.0333    -2.6686    -0.4263

```

The program presents sorted individual genetic effects with maximum and minimum estimation, of which scale is determined by the decimal fraction after keyword “_Genotypes”. The estimates are divided into several parts, including general individual genetic effects estimation and individual genetic effects prediction in each specific environment. In each part, the results include individual genetic effects estimation (G) or prediction in each specific environment (G+GE), and genetic effects estimates of individual QTLs and epistatic QTLs where two QTLs are connected with “^”.

For instance, 0.1 is typed after the keyword “_Genotypes”, as a result, 10% largest individual genetic effects and 10% smallest individual genetic effects will be presented in the result file. As shown in the figure above, 9 largest individual genetic effects and 9 smallest individual

genetic effects are listed, and the first part is the general individual genetic effects (G) followed with genetic effects estimates of three individual QTLs (1-15, 2-12, and 3-20) and two epistatic QTLs ($2-12^3-20$ and $2-9^3-7$)

The second part is the individual genetic effects in the first environment (G+GE1) followed with genetic effects estimates of three individual QTLs and two epistatic QTLs in the first environment.

_environment_1						
_for_10%_highest_value						
Entry	G+GE1	1-15	2-12	3-20	$2-12^3-20$	$2-9^3-7$
64	29.2141	10.2334	4.6603	7.7713	2.5815	3.9676
97	26.4951	10.2334	2.7094	8.0333	1.5514	3.9676
48	25.1692	10.2334	4.6603	8.0333	2.6686	-0.4263
42	24.4960	5.1661	4.6603	8.0333	2.6686	3.9676
73	24.1469	5.1661	4.6603	7.7713	2.5815	3.9676
32	21.8212	10.2334	4.6603	7.7713	2.5815	-3.4252
39	21.2788	10.2334	4.6603	7.7713	2.5815	-3.9676
40	21.2788	10.2334	4.6603	7.7713	2.5815	-3.9676
28	18.3514	10.0249	2.7094	8.0333	1.5514	-3.9676
_for_10%_lowest_value						
Entry	G+GE1	1-15	2-12	3-20	$2-12^3-20$	$2-9^3-7$
45	-24.2260	-10.2334	-4.6603	-8.0333	2.6686	-3.9676
65	-24.0511	-10.2334	-4.6603	-7.7713	2.5815	-3.9676
13	-21.0764	-10.2334	2.7094	-8.0333	-1.5514	-3.9676
19	-19.8936	-10.2334	4.6603	-7.7713	-2.5815	-3.9676
6	-19.6571	-10.2334	-4.6603	-7.7713	2.5815	0.4263
74	-19.6571	-10.2334	-4.6603	-7.7713	2.5815	0.4263
93	-18.9838	-5.1661	-4.6603	-7.7713	2.5815	-3.9676
43	-16.7013	-10.2334	4.6603	-8.0333	-2.6686	-0.4263
90	-16.7013	-10.2334	4.6603	-8.0333	-2.6686	-0.4263

The third part is the individual genetic effects in the second environment (G+GE2) followed with genetic effects estimates of three individual QTLs and two epistatic QTLs in the first environment.

_environment_2						
_for_10%_highest_value						
Entry	G+GE2	1-15	2-12	3-20	2-12^3-20	2-9^3-7
64	29.2141	10.2334	4.6603	7.7713	2.5815	3.9676
97	26.4951	10.2334	2.7094	8.0333	1.5514	3.9676
48	25.1692	10.2334	4.6603	8.0333	2.6686	-0.4263
42	24.4960	5.1661	4.6603	8.0333	2.6686	3.9676
73	24.1469	5.1661	4.6603	7.7713	2.5815	3.9676
32	21.8212	10.2334	4.6603	7.7713	2.5815	-3.4252
39	21.2788	10.2334	4.6603	7.7713	2.5815	-3.9676
40	21.2788	10.2334	4.6603	7.7713	2.5815	-3.9676
28	18.3514	10.0249	2.7094	8.0333	1.5514	-3.9676
_for_10%_lowest_value						
Entry	G+GE2	1-15	2-12	3-20	2-12^3-20	2-9^3-7
45	-24.2260	-10.2334	-4.6603	-8.0333	2.6686	-3.9676
65	-24.0511	-10.2334	-4.6603	-7.7713	2.5815	-3.9676
13	-21.0764	-10.2334	2.7094	-8.0333	-1.5514	-3.9676
19	-19.8936	-10.2334	4.6603	-7.7713	-2.5815	-3.9676
6	-19.6571	-10.2334	-4.6603	-7.7713	2.5815	0.4263
74	-19.6571	-10.2334	-4.6603	-7.7713	2.5815	0.4263
93	-18.9838	-5.1661	-4.6603	-7.7713	2.5815	-3.9676
43	-16.7013	-10.2334	4.6603	-8.0333	-2.6686	-0.4263
90	-16.7013	-10.2334	4.6603	-8.0333	-2.6686	-0.4263

4. Replication treatment

This program can consider replication either as simple repetition or as block in experiments, that is providing choices that mapping QTLs based on the mean phenotype value or not. Please find the keyword “_Replications” in the figure below, in the case of replication is employed in the experiment, that is, the keyword is followed with “yes”, an additional ‘B’ or ‘b’ after “yes” would let the program treat replications as block in computation, otherwise, the program would perform QTLs mapping based on averaged phenotype value, which means the replications is treated as repetition of experiments.

```

_Population      DH
_Genotypes       99
_Observations    198
_Environments    yes
_Replications    yes B
_TraitNumber     4
_TotalMarker     54
_MarkerCode      P1=1   P2=2   F1=3   F1P1=4   F1P2=5

```