

Program input/output and comments from the Mapmaker analysis of data file araba.raw.

Mapmaker Screen Command and Output	Comments
<pre>***** * Output from: Wed Mar 4 14:13:03 1998 * * * * MAPMAKER/EXP * * (version 3.0b) * * * *****</pre>	
<pre>1> photo araba 'photo' is on: file is 'araba.out'</pre>	<p>photo is the command to have the program keep an exact record of all of the commands you issue and the program output. The syntax is photo <filename>. For example, photo araba will create a file called araba.out. The file will be in the same directory as your data file.</p>
<pre>2> prepare data araba.raw preparing data from file 'araba.raw'... ok RI (selfing) data (101 individuals, 8 loci)... ok unable to run file 'araba.prep'... skipping initialization saving genotype data in file 'araba.data'... ok saving map data in file 'araba.maps'... ok</pre>	<p>prepare data command instructs the program prepare the data in file araba.raw for analysis.</p>
<pre>3> sequence all sequence #1= all</pre>	<p>sequence all command tells the program which to analyze all loci. all is the variable. See other forms of the sequence command below.</p>
<pre>4> group 3 30 Linkage Groups at min LOD 3.00, max Distance 30.0 group1= 1 2 3 4 5 6 7 8</pre>	<p>group command instructs the program to create linkage groups based on the criteria lod>3.0 and distance<30 cM. These can be varied.</p>
<pre>5> lod Bottom number is LOD score, top number is centimorgan distance: 1 2 3 4 5 6 7 2 4.2 17.18 3 8.1 4.4 12.19 16.38 4 18.1 24.0 31.4 5.84 3.92 2.57 5 6.3 11.0 16.3 15.3 14.43 9.68 6.75 7.12 6 28.2 40.1 53.1 10.7 31.0 3.27 1.64 0.86 10.12 2.85 7 9.5 5.7 2.3 35.5 17.4 62.6 11.32 14.87 20.79 2.15 6.62 0.57 8 10.8 17.1 21.0 7.2 6.3 17.6 22.1 9.90 6.18 4.86 13.28 14.43 6.43 4.80</pre>	<p>lod command asks for a table of cM distances (top) and the associated lod value of that distance. Here is where some of the art of using Mapmaker comes in. You want to select loci that are not too close, but not too far apart. The loci that are selected are 1,3,4,5 and 8. Look at the table to see the distances. This step takes practice.</p>

<pre>6> sequence {1 3 4 5 8} sequence #2= {1 3 4 5 8}</pre>	<p>sequence {1 3 4 5 8} in brackets means to work with these loci, but not in any particular order.</p>
<pre>7> compare Best 20 orders: 1: 3 1 5 8 4 Like: 0.00 2: 3 1 5 4 8 Like: -6.67 3: 1 3 5 8 4 Like: -7.32 4: 5 1 3 8 4 Like: -8.50 5: 5 8 4 1 3 Like: -8.73 6: 3 5 1 8 4 Like: -9.08 7: 1 5 8 4 3 Like: -9.74 8: 4 5 8 1 3 Like: -9.88 9: 4 3 1 5 8 Like: -10.49 10: 5 4 8 1 3 Like: -11.07 11: 5 3 1 8 4 Like: -11.12 12: 5 1 3 4 8 Like: -11.25 13: 5 8 4 3 1 Like: -11.46 14: 5 1 8 4 3 Like: -13.33 15: 3 5 8 4 1 Like: -13.93 16: 5 8 1 3 4 Like: -14.08 17: 1 5 4 8 3 Like: -14.09 18: 3 5 1 4 8 Like: -14.13 19: 1 5 3 8 4 Like: -14.14 20: 1 3 5 4 8 Like: -14.18 order1 is set</pre>	<p>compare command instructs the program to look at all possible orders and return the order and the associated LOD value. The sequences are given in the best possible order. Because the LOD value is a logarithmic value, the 3 1 4 5 8 order is $10^{6.67}$ more likely than the next order. This can also be read that odds that the second order is correct is 1 in $10^{6.67}$. Clearly the first order is best.</p> <p>This is a critical step in mapping. When you select this order, you are selecting your framework with which the remainder of you map will be built. Because this is a critical step, researchers often require that the framework order have a LOD value greater than 3.0 the second possible order.</p>
<pre>8> sequence 3 1 5 8 4 sequence #3= 3 1 5 8 4</pre>	<p>sequence 3 1 5 8 4 command tells the program to set this exact order</p>
<pre>9> try 2 6 7 2 6 7 ----- 3 -4.81 -9.54 0.00 0.00 -18.94 -1.58 1 -8.82 -18.98 -18.25 -18.79 -15.08 -24.35 5 -24.30 -7.41 -27.78 -17.58 0.00 -19.46 8 -21.86 -10.47 -21.93 ----- 4 -94.98 -107.57 -96.42 ----- INF BEST</pre>	<p>The try command places loci into all possible intervals of the map and returns the LOD value associated with each interval. The best fit is into the interval where the LOD value is 0.00. But it is not that simple. To build a robust map, the locus should not be placed into an interval if the LOD value associated with another interval is less than LOD=2.0. Some researchers use a cut off of LOD=3.0, especially for dominant acting markers such as RAPDs.</p> <p>try 2 6 7 is the command to test how well loci 2, 6 and 7 fit into all of the intervals defined by the sequence fixed in the previous command. Only loci 2 and 6 can be placed because the LOD values associated with the next best intervals are all greater than 2.0. Loci 7 can not be placed at this time.</p>
<pre>10> sequence 3 2 1 5 8 4 6 sequence #4= 3 2 1 5 8 4 6</pre>	<p>sequence 3 2 1 5 8 4 fixes our new sequence based on the try command.</p>

11> **try 7**

```

      7
-----
3 | 0.00 |
  | -2.04 |
2 |      |
  | -12.13 |
1 |      |
  | -18.32 |
5 |      |
  | -24.31 |
8 |      |
  | -28.21 |
4 |      |
  | -29.39 |
6 |      |
  | -21.35 |
-----
INF | -21.99 |
-----
BEST -121.22

```

try 7 attempts to place locus 7 at an appropriate interval. The results show that the locus 7 should be placed at the end next to locus 4.

12> **sequence 7 3 2 1 5 8 4 6**
sequence #5= 7 3 2 1 5 8 4 6

sequence 7 3 2 1 5 8 4 is fixed.

13> **map**

```

=====
Map:
Markers      Distance
7 m246       2.2 cM
3 g4553      4.0 cM
2 g4532      4.0 cM
1 g4133      6.4 cM
5 m216       6.8 cM
8 m251       7.1 cM
4 g6842     10.5 cM
6 m220
-----
41.1 cM    8 markers    log-likelihood= -121.22
=====

```

map outputs the linkage map defined by the sequence from the previous command. The way to read the map is that the distance between locus m246 and g4553 is 2.2 cM. etc. The total map distance is 41.1 cM.

14> **ripple**

```

=====
Map To Test:
Markers      Distance
7 m246       2.2 cM
3 g4553      4.0 cM
2 g4532      4.0 cM
1 g4133      6.4 cM
5 m216       6.8 cM
8 m251       7.1 cM
4 g6842     10.5 cM
6 m220
-----
41.1 cM    8 markers    log-likelihood= -121.22
=====
Window-size: 5 Log-likelihood Threshold: 2.00
Comparing maps with ALL flanking markers...

compare {7 3 2 1 5}... ok
compare ...{3 2 1 5 8}... ok
compare ...{2 1 5 8 4}... ok
compare ...{1 5 8 4 6}    ok

```

ripple command tests your map against a specific LOD criteria. The criteria (default if not parameters are given) are seen in the following statement:

Window-size: 5 Log-likelihood
Threshold: 2.00

The command looks at five loci at a time, first 7 3 2 1 8, next 3 2 1 5 8 and so on. It checks to ensure that the loci are placed in proper order passed on a criteria of LOD>2.0. **This is another test for the robustness of your map. Our map passes this test.**

If you are building a LOD 3.0 map, your parameters should be 5 3.0 and the command is **ripple 5 3.0**.

15> **quit**

```

save data before quitting? [yes] y
saving map data in file 'araba.maps'... ok
saving two-point data in file 'araba.2pt'... ok

...goodbye...

```

quit exits you from the program. You are prompted to save your data. This is a good idea.