QTL Cartographer
QTL Cartographer

A Reference Manual and Tutorial for QTL Mapping

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Contents

List of Figures 8
List of Tables 9

1 Introduction 10
  1.1 General Overview ........................................... 10
  1.1.1 Definition of the Problem ................................. 10
  1.1.2 Experimental Design ...................................... 11
  1.1.3 Genetic Linkage Maps .................................... 13
  1.2 Programming Philosophy ..................................... 13
  1.3 Copyright Information and Acknowledgments .................. 13
    1.3.1 QTL Cartographer Copyright Information ................. 13
    1.3.2 Citing QTL Cartographer ................................ 14
    1.3.3 Gnuplot Copyright Information ............................ 14
    1.3.4 LINPACK Copyright Information ........................... 15
    1.3.5 Numerical Recipes in C Information ...................... 15
  1.4 How to Get and Install QTL Cartographer ..................... 16
    1.4.1 MS-Windows ............................................. 17
    1.4.2 UNIX .................................................. 17
    1.4.3 Macintosh .............................................. 18
  1.5 Getting Help .................................................. 18
    1.5.1 Mailing List ............................................ 19
    1.5.2 Bug Reports ............................................ 19
    1.5.3 Contacts ............................................... 20
  1.6 General Usage of the Programs ................................ 20
    1.6.1 Options for all programs ................................ 21
    1.6.2 Filenaming Conventions .................................. 25

2 Simulating/Reformatting Data 28
  2.1 Rmap ....................................................... 29
    2.1.1 Simulating a Map ....................................... 30
    2.1.2 Using MAPMAKER/EXP files ............................... 31
    2.1.3 QTL Cartographer user input format ...................... 31
CONTENTS

2.1.4 Command Line Options ........................................... 31
2.2 Rqtl ................................................................. 33
2.3 Rcross ............................................................... 35
  2.3.1 Simulating Data .................................................. 35
  2.3.2 Translating Data ............................................... 37
  2.3.3 Output ........................................................... 37
2.4 Prune ................................................................. 41
  2.4.1 Pruning Datasets Interactively ................................. 42
  2.4.2 Recreating Datasets ........................................... 43
3 Analysis ............................................................... 47
  3.1 Qstats ............................................................... 47
    3.1.1 Command Line Options ...................................... 50
    3.1.2 Segregation .................................................. 50
  3.2 LRmapqtl ........................................................... 51
    3.2.1 Simple Linear Regression .................................. 51
    3.2.2 Output ....................................................... 52
    3.2.3 Permutation Tests .......................................... 53
  3.3 SRmapqtl ........................................................... 53
    3.3.1 Output ....................................................... 54
  3.4 Zmapqtl ............................................................. 55
    3.4.1 Computational Methodology .................................. 55
    3.4.2 Models ....................................................... 56
    3.4.3 Zmapqtl Options ............................................ 57
    3.4.4 Output ....................................................... 60
  3.5 JZmapqtl ............................................................ 63
    3.5.1 JZmapqtl Options ............................................ 63
    3.5.2 Output ....................................................... 63
    3.5.3 Usage Hints ................................................ 64
  3.6 MImapqtl ............................................................ 65
    3.6.1 MImapqtl Options ............................................ 66
    3.6.2 QTL Search .................................................. 71
    3.6.3 Epistatic Interactions ..................................... 71
    3.6.4 Threshold ................................................... 72
4 Visualization of Results ............................................. 73
  4.1 Eqtl ................................................................. 73
    4.1.1 Options ....................................................... 75
  4.2 Preplot ............................................................... 76
    4.2.1 Printing Results ............................................ 77
  4.3 GNUPLOT .............................................................. 78
    4.3.1 Basic GNUPLOT ................................................ 78
## Tutorial Examples

5.1 General tactics and notes ........................................ 79
5.2 Basic Macintosh ............................................. 80
5.3 Basic Windows ................................................ 80
5.3.1 Navigating disks ........................................ 80
5.4 Basic Unix .................................................... 81
5.4.1 Help! ....................................................... 81
5.4.2 Basic filesystem commands ............................... 81
5.4.3 Curious? .................................................. 82
5.4.4 Other commands ........................................ 82
5.5 Simulating and Analyzing data .............................. 83
5.6 Analyzing simulated data .................................. 84
5.7 Analyzing real data ......................................... 84
5.8 Analyzing a MAPMAKER data set ....................... 85
5.8.1 Using MAPMAKER/EXP ................................. 85
5.8.2 Using the MAPMAKER files ....................... 86

## Input File Formats

6.1 Genetic Linkage Maps ...................................... 88
6.1.1 MAPMAKER output files ............................... 88
6.1.2 Rmap input files ..................................... 88
6.1.3 Rmap output files ................................... 93
6.2 QTL information ............................................ 94
6.2.1 Rqtl input files ...................................... 94
6.2.2 Rqtl output files .................................... 98
6.3 Data files .................................................... 99
6.3.1 MAPMAKER raw files ................................. 99
6.3.2 Rcross input files .................................. 99

## Benchmarks

7. UNIX Man Pages ............................................... 107
8.1 QTLCART .................................................. 108
8.2 RMAP ....................................................... 113
8.3 RQTL ....................................................... 117
8.4 RCROSS .................................................... 120
8.5 PRUNE ...................................................... 124
8.6 QSTATS .................................................... 127
8.7 LRMAPQTL .................................................. 129
8.8 SRMAPQTL .................................................. 131
8.9 ZMAPQTL .................................................... 133
8.10 JZMAPQTL .................................................. 139
8.11 MIMAPQTL .................................................. 143
8.12 PREPLOT .................................................. 150
List of Figures

1.1 Basic Cross ................................................................. 11
2.1 Reformatting Data ...................................................... 29
2.2 Simulating Data ......................................................... 29
3.1 Analysis Schematic ..................................................... 48
4.1 Visualization Schematic ............................................... 74
6.1 Input format for a map.inp file ...................................... 89
6.2 Example of a Model input file ....................................... 95
6.3 Example of a cross.inp file .......................................... 100
## List of Tables

1.1 Summary of Experimental Design Codes .................................. 12  
1.2 Subroutines from *Numerical Recipes in C* ............................ 15  
1.3 Contact for Help .......................................................... 21  
1.4 Command Line Options for all programs ................................. 22  
1.5 Standard Filename Extensions and File types for Output Files ...... 26  
1.6 Miscellaneous Files and File types .................................... 26  
2.1 Command Line Options for Rmap ........................................ 32  
2.2 Command Line Options for Rmap ........................................ 33  
2.3 Command Line Options for Rqtl ......................................... 34  
2.4 Command Line Options for Rcross ..................................... 35  
2.5 Command Line Options for Prune ...................................... 41  
3.1 Command Line Options for Qstats ....................................... 50  
3.2 Command Line Options for LRmapqtl .................................. 52  
3.3 Command Line Options for SRmapqtl .................................. 53  
3.4 Command Line Options for Zmapqtl ................................... 58  
3.5 Examples of Interim Files for Model 6 ................................ 59  
3.6 Command Line Options for JZmapqtl .................................. 64  
3.7 Coded variables ............................................................ 66  
3.8 Command Line Options for MImapqtl .................................. 67  
4.1 Command Line Options for Eqtl ........................................ 75  
4.2 Command Line Options for Preplot .................................... 77  
4.3 Filename extensions for Preplot output ................................. 77  
7.1 Timings for Interval Mapping ............................................ 105  
7.2 Timings for Composite Interval Mapping ............................... 106  
7.3 Timings for Multiple Interval Mapping ................................. 106
Chapter 1

Introduction

1.1 General Overview

QTL Cartographer is a suite of programs for mapping quantitative trait loci (QTLs) onto a genetic linkage map. The general experimental paradigm begins with a pair of inbred parental lines that differ in the trait of interest and in the set of marker genotypes. The programs use linear regression, interval mapping (Lander and Botstein 1989) or composite interval mapping (Zeng 1993; Zeng 1994) methods to dissect the underlying genetics of the quantitative traits. Mapping is done onto a set of linked genetic markers with known recombination frequencies. Genetic linkage maps and data files can be imported from MAPMAKER (Lander et al. 1987). The mapping program uses a dynamic algorithm that allows a host of statistical models to be fitted and compared, including various gene actions (additive and dominance), QTL-environment interactions, and close linkage.

This package consists of several programs written in C to perform various tasks, including simulating, reformatting or analyzing data and visualizing the results of the analyses. Presently, the mapping programs can handle data from backcrosses, intercrosses and recombinant inbreds, as well as a few other experimental designs (see Table 1.1).

All input and output files are plain text and can be viewed or imported into many text editors and graphics packages on various computing platforms. The programs were originally written for the UNIX operating system and have since been ported to the Macintosh and Microsoft Windows operating systems. Present development is on a Macintosh using Metroworks Codewarrior. Both Macintosh and Windows binaries are created using Metroworks. The UNIX distribution is of the source code. This project is ongoing and suggestions are welcome for further improvements and enhancements. The source code and compiled binaries are freely available and may be obtained by anyone over the internet.

1.1.1 Definition of the Problem

Often traits in plants and animals are influenced by many genes rather than a single locus (Falconer and MacKay 1996, for an excellent general review). These traits are termed quantitative traits and the loci that control these traits quantitative trait loci, abbreviated henceforth as QTLs. An important goal in genetics and breeding is to identify and
characterize QTLs, especially those that contribute to variation in quantitative traits both within and between populations or species. The recent advances in molecular biology have allowed the construction of genetic linkage maps based on molecular markers. Such genetic linkage maps can span the genome at regular intervals. The experimenter can then look for correlations between these mapped markers and the trait of interest in controlled breeding experiments to gain insight into the regions of the genome that control the trait.

1.1.2 Experimental Design

The paradigm for the programs in the *QTL Cartographer* package is that of highly inbred lines with very little genetic variation within lines but variation between lines. We shall refer to these inbred lines as parental lines and denote them by the symbols $P_1$ and $P_2$. As a general rule, the $P_1$ lines will correspond to the “high” lines with respect to the trait of interest, that is they will have mean values larger than the $P_2$ or “low” lines. These parental lines can be crossed to produce $F_1$ lines which are heterozygous for both markers and QTLs. One can then cross the $F_1$ populations with either parental line to produce backcrosses. The symbols $B_1$ and $B_2$ will refer to backcrosses involving the $P_1$ and $P_2$ lines, respectively. Alternatively, the $F_1$ lines can be intercrossed to produce $F_2$ lines.

In each of these cases, the resultant lines will have variation in both the trait of interest and the underlying quantitative trait loci and marker genotypes. These crosses are illustrated in Figure 1.1. We can then look for correlations between the trait in question and marker genes that have been mapped previously.

![Figure 1.1: Basic Cross](image-url)

```plaintext
QTL Cartographer
```
We have also included options for more complex experimental designs, including recombinant inbred lines, general \(F_t\) lines produced by selfing or random crossing of \(F_{t-1}\) lines, etc. The programs in the \textit{QTL Cartographer} system will need to know the type of experimental design used to create the data. This design is encoded by a string of characters. If the letter \(i\) stands for some integer, then the possible crosses will be \(B_i\), \(SF_i\), \(RF_i\), \(RI_i\), \(T(XX)SF_i\) and \(T(XX)RF_i\). The \(B\) stands for a backcross and the integer attached to it will indicate the parental line to which the \(F_1\) line was crossed to (either 1 or 2). If there was repeated backcrossing to one of the parental lines, this can be indicated by attaching two integers to the \(B\): \(B_{ij}\) indicates that there were \(j\) generations of backcrossing to parental line \(i\). \(B_{11}\) is equivalent to \(B_1\). \(SF_i\) stands for selfed intercross lines and the integer indicates the generation (\(i = 2, 3, \ldots\)). \(RF_i\) stands for randomly mated intercross lines. \(RI\) means recombinant inbred lines, and the integer can take on one of three values: 0, 1, and 2. A 1 indicates \(RI\) lines derived by selfing, a 2 by sib mating and a 0 means doubled haploid lines.

<table>
<thead>
<tr>
<th>Design</th>
<th>Code</th>
<th>Example</th>
</tr>
</thead>
<tbody>
<tr>
<td>Backcross to (P_i)</td>
<td>(B_i)</td>
<td>B1</td>
</tr>
<tr>
<td>Backcross (j) times to (P_i)</td>
<td>(B_{ij})</td>
<td>B13</td>
</tr>
<tr>
<td>Selfed generation (i) intercross</td>
<td>(SF_i)</td>
<td>SF3</td>
</tr>
<tr>
<td>Randomly mated generation (i) intercross</td>
<td>(RF_i)</td>
<td>RF2</td>
</tr>
<tr>
<td>Doubled Haploid</td>
<td>(RI_0)</td>
<td>RI0</td>
</tr>
<tr>
<td>Recombinant Inbred via selfing</td>
<td>(RI_1)</td>
<td>RI1</td>
</tr>
<tr>
<td>Recombinant Inbred via sib mating</td>
<td>(RI_2)</td>
<td>RI2</td>
</tr>
<tr>
<td>Testcross of (SF_i) to (P_j)</td>
<td>(T(B_j)SF_i)</td>
<td>T(B1)SF3</td>
</tr>
<tr>
<td>Testcross of (SF_i) for (j) generations</td>
<td>(T(SF_{i+j})SF_i)</td>
<td>T(SF4)SF3</td>
</tr>
<tr>
<td>Testcross of (RF_i) to (P_j)</td>
<td>(T(B_j)RF_i)</td>
<td>T(B1)RF3</td>
</tr>
<tr>
<td>Design III</td>
<td>(T(D3)SF_i)</td>
<td>T(D3)SF5</td>
</tr>
</tbody>
</table>

Table 1.1: Summary of Experimental Design Codes

The \(T\) indicates that the data are the result of a test cross. For a test cross, genotyping is done on an intercross (\(SF_i\) or \(RF_i\)) and phenotyping on a cross derived from that intercross. The first part of the string, \(T(XX)\) indicates that phenotyping is done on the \(XX\) population and the second part (\(SF_i\) or \(RF_i\)) indicates the genotyped population. \(XX\) can be a \(B_1\), \(B_2\), \(SF_i\) or \(D_3\) for \(SF_i\) lines or \(B_1\) or \(B_2\) for \(RF_i\) lines. \(D_3\) stands for Design III experiments (Cockerham and Zeng 1996).

All of the above experimental designs can be simulated, and all but the Design III experiments can be analyzed. Table 1.1 lists all the experimental designs and their \textit{QTL Cartographer} codes. The experimental designs of Table 1.1 can be specified in Rcross for simulations or in certain data input files (see Section 6.3.2).
1.1.3 Genetic Linkage Maps

A known genetic linkage map will be required for the analysis. A good genetic linkage map will comprise a set of Mendelian marker loci that are evenly spaced and span the genome. Average intermarker distances of 5 to 10 centimorgans would be optimal. We have provided ways to simulate linkage maps as well as to convert linkage map information into a format suitable for QTL Cartographer. Presently the user has two options for genetic linkage map input. The first is a format designed for the QTL Cartographer system that allows for free annotation of the data file. An example is given in (6.1.2). A second option allows the user to import the results of a MAPMAKER session. This is covered in more detail in (2.1) and (5.8.1).

1.2 Programming Philosophy

These programs were originally developed on a UNIX workstation. Consequently, the programming philosophy is heavily influenced by the UNIX operating system. All the programs have command line options which mimic those of regular UNIX commands. We have added interactive menus so as to make the programs more user friendly on Macintoshes and PCs running Microsoft Windows™.

There are a number of different programs in the package rather than one program that does everything. In this way, each program does a small job, and the user can combine the programs as a group to do a complete analysis. The user can examine the input and output files for each step and have a better idea of what the programs are doing. All input and output files are plain ASCII text. They can be transferred to any platform and viewed or edited there.

We have also been influenced by the Free Software Foundation in that we charge no fee for this program package. We have attempted to integrate these programs with other free software (most notably GNUPLOT and MAPMAKER).

1.3 Copyright Information and Acknowledgments

1.3.1 QTL Cartographer Copyright Information

Copyright (C) 1994-2001 C. J. Basten, B. S. Weir and Z.-B. Zeng
Permission to use, copy, and distribute this software and its documentation for any purpose with or without fee is hereby granted, provided that the above copyright notice appear in all copies and that both that copyright notice and this permission notice appear in supporting documentation.

Permission to modify the software is granted, but not the right to distribute the modified code. Modifications are to be distributed as patches to released version.

This software is provided “as is” without express or implied warranty.
1.3.2 Citing QTL Cartographer

In publications, you should cite our original short announcement (Basten, Weir, and Zeng 1994) and this manual.


1.3.3 Gnuplot Copyright Information

We suggest that you download and make use of the fine plotting package GNUPLTO (Williams and Kelley 1993), which we use as the graphics engine to display the results of analyses. GNUPLTO is freely available for UNIX, Macintosh and MS-Windows machines. It is quite easy to use, produces nice results and all the input files are plain text. We reprint the copyright information for GNUPLTO verbatim:

GNUPLTO copyright information:

Copyright (C) 1986 - 1993 Thomas Williams, Colin Kelley

Permission to use, copy, and distribute this software and its documentation for any purpose with or without fee is hereby granted, provided that the above copyright notice appear in all copies and that both that copyright notice and this permission notice appear in supporting documentation.

Permission to modify the software is granted, but not the right to distribute the modified code. Modifications are to be distributed as patches to released version.

This software is provided "as is" without express or implied warranty.

AUTHORS

Original Software:
  Thomas Williams, Colin Kelley.

Gnuplot 2.0 additions:
  Russell Lang, Dave Kotz, John Campbell.

Gnuplot 3.0 additions:
CHAPTER 1. INTRODUCTION

Gershon Elber and many others.

For more information on GNUPLLOT, see the documentation that comes with the program.

1.3.4 LINPACK Copyright Information

We have translated some of the FORTRAN procedures of LINPACK (Dongarra et al. 1979) into C. We have used all of the basic linear algebra subroutines (BLAS) as well as subroutines to do the QR factorization of the matrix $X$ of the linear system

$$\vec{y} = X \cdot \vec{b}$$

These include the subroutines SQRST, STRSL, SPODI, SQRSL and SQRDC. Not all of the optimizations have been translated. These subroutines are used quite extensively in the analysis modules. The original FORTRAN subroutines are Copyright (C) 1979 by the Society for Industrial and Applied Mathematics.

1.3.5 Numerical Recipes in C Information

We have made extensive use of the ideas from *Numerical Recipes in C* (Press, Flannery, Teukolsky, and Vetterling 1988). The source file “Utilities.c” contains subroutines for allocating memory that are derived from the functions for creating arbitrary offset vectors and matrices in Appendix D. We have also used modified versions of the subroutines listed in Table 1.2. The original subroutines are Copyright (C) 1987, 1988 Numerical Recipes Software.

<table>
<thead>
<tr>
<th>subroutine</th>
<th>section</th>
</tr>
</thead>
<tbody>
<tr>
<td>indexx()</td>
<td>8.3</td>
</tr>
<tr>
<td>moment()</td>
<td>13.1</td>
</tr>
<tr>
<td>sort()</td>
<td>8.2</td>
</tr>
<tr>
<td>gammeln()</td>
<td>6.1</td>
</tr>
<tr>
<td>gammmp()</td>
<td>6.2</td>
</tr>
<tr>
<td>gasdev()</td>
<td>7.2</td>
</tr>
<tr>
<td>gcf()</td>
<td>6.2</td>
</tr>
<tr>
<td>gser()</td>
<td>6.2</td>
</tr>
<tr>
<td>poidev()</td>
<td>7.3</td>
</tr>
<tr>
<td>betai()</td>
<td>6.3</td>
</tr>
<tr>
<td>beta()</td>
<td>6.1</td>
</tr>
<tr>
<td>betacf()</td>
<td>6.3</td>
</tr>
</tbody>
</table>

Table 1.2: Subroutines from *Numerical Recipes in C*
1.4 How to Get and Install QTL Cartographer

Point your web browser to “http://statgen.ncsu.edu/statgen” and follow the link to software, and from there to QTL Cartographer. You can then follow the link to the ftp site and shift-click on the files you want to download.

QTL Cartographer is also downloadable via anonymous ftp at statgen.ncsu.edu. Use “ftp” as your username and your email address as the password. Here is an example.

username: ftp
password: basten@statgen.ncsu.edu

Next, change directory into the distribution subdirectory, /pub/qtlcart, and view what is available. For example,

ftp> cd /pub/qtlcart
ftp> ls
ChangeLog
QTLCartMac.sea.hqx
QTLCartWin.zip
QTLCart.tar.Z
README
gnuplot.exe
gnuplot.sit.hqx
gnuplot.tar.Z
1.10b/
1.12f/
1.13g/
1.14d/
swang/

Download the appropriate version. Presently, the following versions are available.

- QTLCartWin.zip is for Microsoft Windows. These are 32 bit applications. You will need an unzip utility to unpack this file. There should be an unzip utility in the Windows system folder.

- QTLCartMac.sea.hqx is for Macintoshes

- QTLCart.tar.Z is for UNIX

- gnuplot files are the distributions of GNUPLOT for various platforms

- The 1.10b, 1.12f, 1.13g and 1.14d are directories containing older versions of QTL Cartographer

- The swang directory contains Shengchu Wang’s Windows front-end for QTL Cartographer
CHAPTER 1. INTRODUCTION

You can usually download a file by using the get command with a filename. On Macintosches, using the server mode may require you to use the put command, as you are putting the files onto your local machine rather than getting them from the remote server. It is best to do the transfer in an empty subdirectory so that you don’t inadvertently delete some important files. You will also want to download the README file if you don’t already have a copy of it. The README file in the /pub/qtlcart subdirectory will often be more recent than the one in the archive.

The manual.pdf file is an Adobe Portable Document File of the manual and the UNIX manpages. It is contained within the distribution for each platform in a subdirectory doc/pdf (or the folder pdf inside the folder doc. You can view or print these files with Adobe Acrobat Reader, which is freely available from Adobe (http://www.adobe.com).

The following sections indicate how to install the programs onto various computing platforms.

1.4.1 MS-Windows

Download the file QTLCartWin.zip in binary format to your computer’s hard drive. Move the program to a directory where you want QTL Cartographer to reside. Use the program unzip utility to unpack the MS-Windows distribution (this can be done with a double-click).

The programs will be unpacked in the directory you choose. You will want to do this in a directory created for QTL Cartographer, so let’s assume that it is c:\qtlcart.

You may also want to download GNUPLOT for MS-Windows. In binary format, get the self-extracting archive gnuplot.exe. Put it in a subdirectory (say C:\gnuplot) and while in that subdirectory, run gnuplot from the DOS command line.

The programs can be run by double clicking their icons in the Windows Explorer application. An alternate method is to open a Command Window and type in the program names.

You can view the output files in any text editor, although you should be aware that some editors in MS-Windows cannot load large files.

1.4.2 UNIX

Download the file QTLCart.tar.Z in binary form from statgen.ncsu.edu. It is in the same directory that README file came from. On your local machine, create a subdirectory for the distribution, then move the file QTLCart.tar.Z to it. Uncompress and untar the file as follows:

```
% uncompress QTLCart.tar.Z
% tar xf QTLCart.tar
```

Follow these steps to compile and install QTL Cartographer:

1. Move into the src directory and edit the file LocalD.h. It is annotated and you can follow the directions in the file if compilation doesn’t work the first time.
2. You will also need to edit the Makefile and choose a compiler. The default is gcc, which is the compiler used on our Sun workstations running Solaris. If you don’t have gcc, you might try cc. Finally, you will want to set the install directory. By default it is BINDIR = /usr/local/bin, but you can change it to whatever you wish. Note that to install the programs in the install subdirectory, you will need write permissions for that subdirectory.

3. Change into the root directory of the distribution and make the programs:

   \% make install

4. The binaries will be in the BINDIR subdirectory. Make sure that this subdirectory is in your path variable, and then rehash.

Presently, we use gcc version 2.95.2 on our Sun Workstations under Solaris 2.7. If you have troubles compiling, you may need to update your operating system or compiler.

1.4.3 Macintosh

You will need a Macintosh with a power pc chip. Download the file QTLCartMac.sea.hqx. Use StuffitExpander or BinHex4 to unbinhex the self-extracting archive. Double click the QTLCart.sea file to unpack the binaries and supplemental files. Some programs such as Netscape or Fetch will unbinhex the files for you, although they may require a helper application.

Once the file QTLCart.sea.hqx has been unpacked, you will have a folder called bin with the programs in it. You can simply double click on any of them to start them up. You will first be presented with a console window. All you need to do is click on OK to get to the interactive menu for setting options. Note that when you double click on a QTL Cartographer program, you will get a command line interface window: You can simply click “OK” here to get the menu. You can also enter command line options in that box if you like.

1.5 Getting Help

All three distributions come with a doc subdirectory. This subdirectory contains a README.doc file in plain text format explaining what is in the five subdirectories of this subdirectory.

html This contains the manual pages in hypertext markup language. You can view these files in any web browser. They are also the files available online at http://statgen.ncsu.edu/qtlcart/cartographer.html

ppt Contains a PowerPoint slide presentation that Chris Basten gives to introduce QTL Cartographer. You will need Microsoft Powerpoint to view it.

pdf Contains the QTL Cartographer manual in Adobe portable document format. You will need Adobe’s Acrobat reader to view and print this file. Acrobat Reader is free and can be obtained from http://www.adobe.com.
txt Contains files in plain text. It includes some sample input files, announcements and a list of program changes.

scripts Contains a number of c shell and perl scripts to automate repetitive tasks such as bootstrapping and permutation tests. These scripts are mainly for UNIX platforms.

You can also get up to date documentation via the World Wide Web by pointing your web browser to http://statgen.ncsu.edu/statgen and following the link to Software and from there to QTL Cartographer.

1.5.1 Mailing List

The address for the mailing list server is MajorDomo@statgen.ncsu.edu. Please join the mailing list for QTL Cartographer. It will be a forum for problems you may have in using the programs, and we will post announcements of updates and bug fixes. To subscribe, send the following two line message to the server:

subscribe qtlcart
end

The second line in the message stops MajorDomo from interpreting your .sig. Note that the subject line of your mail message will be ignored. If the subscription was successful, you will receive a confirmation note saying as much. You may also put an email address after the “subscribe qtlcart” (on the same line) to subscribe that address:

subscribe qtlcart basten@statgen.ncsu.edu
end

A message like the above with “unsubscribe” rather than “subscribe” would unsubscribe the address. The command “help” would cause the server to return a list of commands that can be sent to the MajorDomo server. Remember that all commands should be directed to MajorDomo@statgen.ncsu.edu, while messages for people on the list go to qtlcart@statgen.ncsu.edu.

1.5.2 Bug Reports

Send any bug reports to qtlcart-bug@statgen.ncsu.edu. There is certain information that will greatly aid in diagnosing the problem. The QTL Cartographer distribution should come with a file called problems.txt with the following questions in it:

1. Computing platform

(a) What machine are you using? Is it a
i. UNIX based workstation?
ii. PC running Windows?
iii. PowerPC based Macintosh?

(b) What operating system is it running?
(c) What is the version of the Operating system?
(d) How much memory and free hard disk space do you have?

2. Programs

(a) Which program is giving you trouble, and what parameter values were used?
(b) Are the input files simulated or real?
(c) Would it be possible to send me the input files, the log file and the resource file (qtlcart.rc)?
(d) When the program crashed, did it give any diagnostics?
(e) When did you download the programs?
(f) What is the version number? (This is valid for programs downloaded after 1 January 1996, and supersedes the previous question.)

When reporting a problem, try to include the answers to all of the questions above. Some of them may not be relevant for you particular case and can be ignored. Email is generally the best way to report problems as the messages stay on a queue until they are dealt with.

One of the most difficult steps in using the QTL Cartographer system is to reformat datasets. Question 2(c) above asks whether you would be willing to send us your data in order to diagnose a problem. We would like to emphasize that if you send us your data files, they will be kept in the strictest confidence. Data files sent to us are stored on a machine which cannot be accessed by the network. We will also delete your data files upon your request.

1.5.3 Contacts

For any other problems with QTL Cartographer, contact Christopher J. Basten via any of the methods listed in Table 1.3. In general, email is the best method for indicating a problem. Chris may not always get back to you right away, but will try to.

1.6 General Usage of the Programs

The programs in the QTL Cartographer suite all have the same look and feel and are heavily influenced by UNIX programs. They can be used as command line programs, or in an interactive mode where a menu of options is presented. Some command line options that are common to all the programs are discussed in 1.6.1. The new user should become familiar with these options. In addition to the command line interface, all the programs have an interactive menu for setting options. The user need only start up any program in
the suite and a list of options will appear. Selecting the number of an option will allow the user to change the value of the option. When all options are set to the user’s satisfaction, choosing a zero ‘0’ will cause the program to run. Choosing the penultimate numbered option will allow you to exit the program without changing any files. The last option saves any parameters you have set before exiting.

### 1.6.1 Options for all programs

Table 1.4 shows the command line parameters that are valid for all the programs in *QTL Cartographer*.

**Working directory**

A working subdirectory (folder) to hold all input and output files is a convenient way to organize your work. We suggest using a different subdirectory (folder) for each data set. In the UNIX world, you can simply change into such a subdirectory and run the programs. In the Macintosh and MS-Windows environs, you need to run the programs from where they reside and specify where the working directory is. Use the `-W` command line option to specify a working directory, or set it in the interactive menu. Be sure to follow the conventions of the particular operating system that you are working on. For UNIX, you might specify it as

```bash
-W /home/myaccount/qtlcart/workdir
```

While for MS-Windows it might look like

```cmd
-W C:\qtlcart\workdir
```

And on a Macintosh, assuming that your Hard drive is called “MacintoshHD”,

---

**Table 1.3: Contact for Help**

<table>
<thead>
<tr>
<th>Name</th>
<th>Dr. Christopher J. Basten</th>
</tr>
</thead>
<tbody>
<tr>
<td>Email</td>
<td><a href="mailto:basten@statgen.ncsu.edu">basten@statgen.ncsu.edu</a></td>
</tr>
<tr>
<td>Phone</td>
<td>(919)515-1934</td>
</tr>
<tr>
<td>Fax</td>
<td>(919)515-7315</td>
</tr>
<tr>
<td>Address</td>
<td>Bioinformatics Research Center</td>
</tr>
<tr>
<td></td>
<td>1523 Partners II Building</td>
</tr>
<tr>
<td></td>
<td>North Carolina State University</td>
</tr>
<tr>
<td></td>
<td>Raleigh, NC 27695-7566 USA</td>
</tr>
<tr>
<td>Courier</td>
<td>840 Main Campus Drive</td>
</tr>
<tr>
<td></td>
<td>Raleigh NC 27606</td>
</tr>
<tr>
<td>MajorDomo</td>
<td><a href="mailto:MajorDomo@statgen.ncsu.edu">MajorDomo@statgen.ncsu.edu</a></td>
</tr>
<tr>
<td>Bug Report</td>
<td><a href="mailto:qtlcart-bug@statgen.ncsu.edu">qtlcart-bug@statgen.ncsu.edu</a></td>
</tr>
</tbody>
</table>
The programs will automatically add a file separator to the end of the path if you don’t put it in. Thus

-\W MacintoshHD:qtlcart:workdir:

is equivalent to the first incarnation of the Macintosh work directory. The Macintosh file separator “:\” is equivalent to the DOS “\” and the UNIX “/”.

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-e</td>
<td>qtlcart.log</td>
<td>Error and Log File</td>
</tr>
<tr>
<td>-s</td>
<td>795793333</td>
<td>Random Number Seed</td>
</tr>
<tr>
<td>-h</td>
<td>(off)</td>
<td>Show help and exit</td>
</tr>
<tr>
<td>-R</td>
<td>qtlcart.rc</td>
<td>Resource File</td>
</tr>
<tr>
<td>-W</td>
<td>(none)</td>
<td>Working Directory</td>
</tr>
<tr>
<td>-A</td>
<td>(off)</td>
<td>Automatic mode</td>
</tr>
<tr>
<td>-X</td>
<td>qtlcart</td>
<td>Filename Stem</td>
</tr>
<tr>
<td>-V</td>
<td>(on)</td>
<td>Verbosity</td>
</tr>
</tbody>
</table>

Table 1.4: Command Line Options for all programs

You may also use relative pathnames for the working subdirectory. In the UNIX and Windows environments, a single period (.) means from here and a pair of periods (..) indicates one higher directory level. Thus,

-\W ..\workdir

would indicate go up one level from the binary subdirectory, where you will find a workdir subdirectory. In UNIX it might look like

-\W ../workdir

For the Macintosh you use extra colons: If the binaries are in the bin.ppc folder inside the qtlcart folder, then

-\W ::workdir:

would indicate that there is a folder called workdir in the qtlcart, whereas

-\W :workdir:

would indicate that the workdir folder is inside the bin.ppc folder.

Listing options

Using the -h option will print out a list of all command line options and their values. The program will then exit without doing anything. I find this most useful when I just want a reminder of what the programs expect. This may not seem as useful now that there is an interactive menu to set options, but if you only want to use the programs in batch mode, it is a quick way to see what the values of all parameters are.
CHAPTER 1. INTRODUCTION

Random Number Seed

Many of the simulation programs make use of a pseudo-random number generator that requires a seed. If none is provided, the number of seconds since some date in the past is used. The \(-s\) option allows you to specify a seed for the random number generator. You can use this to repeat simulations to see if the same answers are obtained. If you don’t use this option, the random number seed is set to the number of seconds since some arbitrary past date (for example, 1 January 1970 for Sun Workstations). The random number seed is printed to the output files of the programs on the first line. This means that if you don’t specify a random number seed, each file should have a unique identifier associated with it. This identifier will also be written to the log file.

If you run a shell script loop on a really fast machine, each turn of the loop may take less than one second. This can be important if you are using the default random number seed, in that separate invocations of the program in a loop might get the same random number seed. For example, consider the pseudo code to produce 1,000 simulated data sets:

\[
i = 1 \\
while (i < 1000) \{
    Rcross -A -V -o qtlcart.cro.$i \\
    i = i + 1
\}
\]

It is possible that each loop in the above code could take a fraction a second, and groups of output files would then be identical. You would want to put a \texttt{sleep} command in the loop to avoid this problem.

Verbosity

For debugging purposes and simply to inform the user about what is happening, many diagnostic messages will be printed out as the programs run. The user can turn these diagnostic messages off. When the messages are displayed, we refer to this as the verbosity mode. The verbosity mode can be turned off by using the the \(-V\) option. This means that the time and summary of options will not be printed on the standard output at runtime. This is a useful flag for batch files. Most of the messages printed to the screen are also printed to the log file.

Automatic Mode

By default, when the user starts up a program, an interactive menu for setting program options is displayed. The opposite of this is the Automatic mode. The \(-A\) flag turns off the interactive setting of program options. This is another flag useful for batch programming. The automatic mode should only be used by those familiar with the \textit{QTL Cartographer} programs.
CHAPTER 1. INTRODUCTION

Resource File

A resource file is an ASCII text file that keeps track of the parameters that the user specifies in using the programs. The same file is read and updated by all the programs in the suite. You can specify a resource file using the -R option. It is `qtlcart.rc` by default and should be in the directory that you are currently working in (for UNIX machines) or where the binaries are (for PCs and Macintoshes). If you change any options (either via the command line or the menus), they will be saved to the file specified. If you decide to use a file other than `qtlcart.rc` as the resource file, you will need to specify it for each program you run.

Initially, the user may want to create a resource file with three lines in it. The two lines will specify the working subdirectory and a “stem” for filenames. Here is an example of a resource file for the Macintosh version of the programs:

```
-workdir ::test: # (The working directory)
-stem corn # (Stem for filenames)
```

The working directory must be specified according to the rules of the operating system. This was explained in using the -W option in previous section. In the above example, a relative pathname was used. The programs will assume that there is a directory (folder) called `test` in the directory (folder) one level up from the directory (folder) that the applications reside in. The analogous lines for the MS-Windows version would look like:

```
-workdir ..\test\ # (The working directory)
-stem corn # (Stem for filenames)
```

The working directory must exist before you run QTL Cartographer.

Filename stem

The filename stem is an important concept in the usage of QTL Cartographer. Beginning with version 1.12, the QTL Cartographer programs utilize the filename stem “qtlcart”. All files are then named using this stem and filename extensions relevant to the filetype. In the resource file example above, the “-stem” entry specifies “corn” as a stem for filenames. This means that when new files are created, they will have the stem “corn” followed by a logical extension. An example would be `corn.map` for a genetic linkage map. With some practice, you will be able to know the contents of a file by its extension. You can set the filename stem on the command line with the -X option.

Log File

It’s often useful to keep a log of the work done using the programs. The -e option can be used to specify the log or error file. Each time a program in the QTL Cartographer system runs, a summary of all the parameters and options is written to the log file. The file also keeps track of when the program was run and may contain other diagnostic information. The log file is appended to with each run rather than overwritten.
CHAPTER 1. INTRODUCTION

Remember that the log file is appended to during each invocation of any of the programs. This is something to keep in mind if you do a bootstrap in a batch file. After a thousand replications, the log file will tend to grow large. The batch file examples included with the QTL Cartographer system (see 2.4.2) take this into account by saving a copy of the log file before running the bootstrap, and deleting the large (and unnecessary) log file at the end.

Interactive Mode

The default behavior for the QTL Cartographer programs is to present the user with a menu of numbered options. This menu is in a loop, so the user can pick options and change them, one at a time. When satisfied that the proper options have been set, selecting “0” will tell the program to continue. There will always be an option to quit without doing anything. This will be the last numbered option.

When “0” is chosen, the programs will present a summary of the options and continue. At termination, the options will be written to the resource file so that the options and parameter values are remembered.

There are a few options that can only be set or changed in this interactive menu. One of these is the aforementioned filename stem which will be explained in greater detail in the next section.

A feature that is not apparent from the interactive menu is that of rewriting the resource file without doing any calculations. There is a quit command, which is the penultimate numbered command. If you choose the quit command, you will exit without rewriting the resource file. It is possible to change parameters in the menu and save them without running the program: Simply select the last value. The program will overwrite the resource file and exit without doing anything else. This is a feature for all the programs of the suite.

1.6.2 Filenaming Conventions

The QTL Cartographer system reads and creates many files and each has a default name. For example, the default output file for Rmap is qtlcart.map. We find it convenient to specify a filename stem and allow for the filename extension to indicate which program created it, and what it contains. Suppose we were working on a corn data set. We might use “corn” as the filename stem. Then Rmap would write its output to corn.map and its error messages to corn.log. Rqtl would write its output to corn.qtl, etc. Table 1.5 summarizes the standard file name extensions in the QTL Cartographer system. Beginning with version 1.12, the default behavior of QTL Cartographer is to use a filename stem: If none is given, then “qtlcart” will be the stem. Unless specifically written in the qtlcart.rc file, the old default names of Rmap.out, Rqtl.out, etc., will no longer be used. These old default names will be used as filetype identifiers. In the output files, there will be a token “-filetype” followed by a token from the fourth column of Tables 1.5-1.6. Note that Zmapqtl creates some interim files, and that Preplot will create many other files in addition to the GNUPLOT control file: See Section 4.2 for details. The “-filetype” specifier will greatly aid programs such as Rmap and Rcross in translating files. As QTL Cartographer
develops, this feature will be used more extensively. Once the stem is set in the menu, it will be remembered as long as a resource file is present.

<table>
<thead>
<tr>
<th>Program</th>
<th>Extension</th>
<th>Contents</th>
<th>-filetype</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rmap</td>
<td>.map</td>
<td>genetic linkage map</td>
<td>Rmap.out</td>
</tr>
<tr>
<td>Rqtl</td>
<td>.qtl</td>
<td>QTL model</td>
<td>Rqtl.out</td>
</tr>
<tr>
<td>Rcross</td>
<td>.cro</td>
<td>data file (markers, traits)</td>
<td>Rcross.out</td>
</tr>
<tr>
<td>Qstats</td>
<td>.qst</td>
<td>Qstats Analysis</td>
<td>Qstats.out</td>
</tr>
<tr>
<td>LRmapqtl</td>
<td>.lr</td>
<td>Single Marker Analysis</td>
<td>LRmapqtl.out</td>
</tr>
<tr>
<td>SRmapqtl</td>
<td>.sr</td>
<td>Stepwise Regression Analysis</td>
<td>SRmapqtl.out</td>
</tr>
<tr>
<td>Zmapqtl</td>
<td>.z</td>
<td>IM-CIM Results</td>
<td>Zmapqtl.out</td>
</tr>
<tr>
<td>JZmapqtl</td>
<td>.z#</td>
<td>Multitrait Results</td>
<td>JZmapqtl.out</td>
</tr>
<tr>
<td>Prune</td>
<td>.mpb</td>
<td>Pruned genetic linkage map</td>
<td>Rmap.out</td>
</tr>
<tr>
<td>Prune</td>
<td>.crb</td>
<td>Pruned data file</td>
<td>Rcross.out</td>
</tr>
<tr>
<td>Preplot</td>
<td>.plt</td>
<td>Gnuplot Control file</td>
<td>Preplot.plt</td>
</tr>
<tr>
<td>Eqtl</td>
<td>.eqt</td>
<td>Summary of Zmapqtl Results</td>
<td>Eqtl.out</td>
</tr>
<tr>
<td>MImapqtl</td>
<td>.mim</td>
<td>MImapqtl results</td>
<td></td>
</tr>
</tbody>
</table>

Table 1.5: Standard Filename Extensions and File types for Output Files

In addition to the files specified in the table, we assume that files with extensions “maps” and “raw” are MAPMAKER genetic linkage map and raw data files, respectively. These

<table>
<thead>
<tr>
<th>Program</th>
<th>Example</th>
<th>Contents</th>
<th>-filetype</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rmap</td>
<td>qtlcartm.inp</td>
<td>genetic linkage map</td>
<td>map.inp</td>
</tr>
<tr>
<td>Rmap</td>
<td>qtlcart.maps</td>
<td>MAPMAKER/EXP output</td>
<td>mapmaker.maps</td>
</tr>
<tr>
<td>Rqtl</td>
<td>qtlcartq.inp</td>
<td>genetic model file</td>
<td>qtls.inp</td>
</tr>
<tr>
<td>Rcross</td>
<td>qtlcartc.inp</td>
<td>data file (markers, traits)</td>
<td>cross.inp</td>
</tr>
<tr>
<td>Rcross</td>
<td>qtlcart.raw</td>
<td>MAPMAKER/EXP input</td>
<td>mapmaker.raw</td>
</tr>
<tr>
<td>Zmapqtl</td>
<td>qtlcart.z3c</td>
<td>Perm. test interim file</td>
<td>ZipermC.out</td>
</tr>
<tr>
<td>Zmapqtl</td>
<td>qtlcart.z3e</td>
<td>Perm. test interim file</td>
<td>ZipermE.out</td>
</tr>
<tr>
<td>Zmapqtl</td>
<td>qtlcart.z3a</td>
<td>Bootstrap interim file</td>
<td>Ziboot.out</td>
</tr>
<tr>
<td>Eqtl</td>
<td>qtlcart.z3b</td>
<td>Bootstrap summary file</td>
<td>Ziboots.out</td>
</tr>
<tr>
<td>Zmapqtl</td>
<td>qtlcart.z3i</td>
<td>Jackknife interim file</td>
<td>Zijack.out</td>
</tr>
<tr>
<td>MImapqtl</td>
<td>qtlcart.res</td>
<td>Residuals dataset file</td>
<td>Rcross.out</td>
</tr>
<tr>
<td>MImapqtl</td>
<td>qtlcart.mqt</td>
<td>Model output file</td>
<td>Rqtl.out</td>
</tr>
<tr>
<td>Eqtl</td>
<td>qtlcart.z3j</td>
<td>Jackknife summary file</td>
<td>Zijacks.out</td>
</tr>
</tbody>
</table>

Table 1.6: Miscellaneous Files and File types
and other files recognized by *QTL Cartographer* are listed in Table 1.6.
Chapter 2

Simulating/Reformatting Data

The first phase in using QTL Cartographer is to create some data. You have two options for this: You can either simulate a data set or collect one yourself. The end result will be to have two files. One will contain the information on a genetic linkage map (marker order, chromosome assignment and recombination fractions) and the other a data set from a cross, which contains the markers, trait values and other explanatory variables. QTL Cartographer cannot create a genetic linkage map from a data set: You will have to use another program such as MAPMAKER/EXP for that task.

Figures 2.1–2.2 present a schematic of the data simulation/reformatting process. There are four main programs involved in this phase: Rmap, Rqtl, Rcross and Prune. Rmap is a program designed to create random genetic linkage maps, or reformat linkage maps that were prepared by MAPMAKER/EXP. Rqtl is a program that creates a genetic model for simulation. One can specify the positions, effects and the number of loci for each trait, or have the program do it randomly. Finally, Rcross uses the genetic linkage map and the model to create a random data set, by simulating a cross. Rcross can also reformat MAPMAKER/QTL raw data files or specially formatted data files. The fourth member of this group is Prune. With Prune, the user can eliminate individuals, markers or traits from the data set. In addition, Prune allows one to bootstrap or permute the data, as well as to simulate missing markers.

Regardless of whether the data are simulated or real, the important output files from this step are the genetic linkage map and the data set. We will refer to these files as qtlcart.map and qtlcart.cro, although you can name them anything you like. In fact, we generally decide on a filename stem and use filename extensions to indicate what is in the various files. If we were working on a corn data set, we might have files corn.map and corn.cro for the genetic linkage map and marker/trait data set, respectively. The naming scheme would be consistent throughout the analysis.

One note on the behavior of Rmap, Rqtl and Rcross. If you choose to translate a data file, then the parameters for simulations are unnecessary and they disappear from the interactive menu. If you specify no input file for any of these programs (by entering a period “.” all by itself for the input filename), then the simulation parameters will reappear for the user to change.
2.1 Rmap

Originally, the program Rmap was designed to simulate a genetic linkage map. The “R” in Rmap was meant to convey the meaning of “Random Map”. Since then we have included the ability to translate genetic linkage map information from various formats into that required by the QTL Cartographer system. Thus, the “R” can now mean reformat or random.

If you have no data, you can simulate a genetic linkage map. Rmap allows the user to specify the number of chromosomes, markers per chromosome and average intermarker distance for the simulation. You can also specify standard deviations for the latter two quantities. This would yield a simulated map that better approximates one that you might actually produce in the lab. Finally, you can also specify whether you want some genetic
material outside the most telomeric markers on the chromosomes.

Rmap can also read in files in three formats. The first format is the same as its output format. We will refer to this as “Rmap.out” filetype format. This feature is provided so that you can create as set of output files that GNUPLOT can read and display a graphic representation of your markers.

The second format is that which is produced by MAPMAKER (Lander et al. 1987; Lincoln et al. 1992): We will refer to it as a “mapmaker.maps” filetype format. Rmap will read in the MAPMAKER output and reformat into the “Rmap.out” format. The third format is defined in Section 6.1.2 and in the file map.inp included with the distribution of the programs. Remember: Rmap will overwrite output files. If you specify an output file that already exists, Rmap will destroy it when creating a new file. For this reason, we recommend that all work is done in a working subdirectory on copies of the original input files.

2.1.1 Simulating a Map

As an exercise in learning to use the programs, you can simulate a genetic linkage map. The main parameters that you will need to specify are the haploid number of chromosomes, average number of markers per chromosome, and average intermarker distance between consecutive markers. You can also simulate linkage maps in which the telomeres don’t have marker information.

To see how Rmap simulates a genetic linkage map, denote the number of chromosomes by \( c \), the average number of markers per chromosome by \( m \) and the average intermarker distance by \( d \) in centimorgans. Furthermore, the average amount of “tail” DNA (DNA outside the most telomeric markers) will be specified by \( t \), again in centimorgans. The standard deviations of \( m \) and \( d \) will by \( \sigma_m \) and \( \sigma_d \), respectively. All of these variables can be specified by command line options, the resource file or by the interactive menu. The standard deviation of \( t \) will be \( \sigma_t = (\frac{t}{d})\sigma_d \). For each chromosome, Rmap decides how many markers are on that chromosome by picking a random number from a normal distribution with mean \( m \) and standard deviation \( \sigma_m \). Once this is done, the amount of DNA between consecutive markers is simulated as a normal random variable with mean \( d \) and standard deviation \( \sigma_d \). Finally, the amount of telomeric or tail DNA is simulated as a normal random variable with mean \( t \) and standard deviation \( \sigma_t \). Setting a standard deviation equal to zero means that the quantity in question is not a random variable, but set equal to its mean value.

The parameters \( c, m, d, t, \sigma_m \) and \( \sigma_d \) can be set using the command line options of Table 2.1 or in the interactive menu. Note that if an input file is specified, all these parameters are ignored and Rmap attempts to translate the input file.

An alternate method of simulating the genetic linkage map can be invoked by changing the simulation mode parameter from 0 to 1 using the -M command line option. In this version, the length of the chromosomes will be normally distributed with mean \( d \) and standard deviation \( \sigma_d \). The number of markers on a chromosome will still be normally distributed with mean \( m \) and standard deviation \( \sigma_m \), but will be placed on the chromosome following a uniform distribution. You should set the values of \( d \) and \( \sigma_d \) to appropriate
levels, as they are for chromosome length rather than intermarker distance in this mode. For example, if you want roughly the same results from this mode as that in the original, then set \( d = 16 \times 10 = 160 \) in this mode.

2.1.2 Using MAPMAKER/EXP files

*QTL Cartographer* has the added capability of reading map files generated by MAPMAKER/EXP (Lander et al. 1987; Lincoln et al. 1992). Genetic marker order and chromosome assignment may be accomplished using MAPMAKER/EXP. Once map order is established, chromosomes may be saved to external files using the following MAPMAKER/EXP commands (in MAPMAKER/EXP):

```plaintext
make chromosome c1
seq M1 M2 M5 M4 M3
attach c1
framework c1
```

A chromosome c1 is defined, and the marker order (for example: M1, M2, M5, M4, M3) assigned. The “attach” and “framework” commands tell MAPMAKER/EXP to save this marker order on chromosome c1. See Section 5.8.1 for a more detailed example of using MAPMAKER/EXP to create the genetic linkage map.

After all chromosomes are defined and marker order assigned, exit MAPMAKER/EXP. You will find files in your directory with the extensions, “*.data”, “*.maps”, “*.traits”, “*.xmaps”. The “*.raw” file contains the original genotype and phenotype information. The “*.maps” file contains the saved marker order per assigned chromosome, as well as the estimated recombination fractions between each marker in the established order. On MS-DOS machines, the extension may be “*.map” rather than “*.maps”. It would be a good idea to rename this file with a “*.mps” ending, so as not to confuse QTL Cartographer with its own genetic linkage map file.

The map order, chromosome, and recombination fraction estimate information may be used in *QTL Cartographer* by specifying “*.maps” as the input file for Rmap. The “*.raw” file is the input for the Rcross utility.

2.1.3 QTL Cartographer user input format

The third format is one defined for the *QTL Cartographer* system. It is similar to the MAPMAKER output format, but has commands embedded in the file to allow the program to read in the data more easily. There is an example and further explanation of this format in Section 6.1.2. It can be annotated quite freely; the example file map.inp is self documenting.

2.1.4 Command Line Options

Table 2.1 summarizes the command line options for Rmap. Most of these were explained in 2.1.1. The default options in Table 2.1 would produce a genetic linkage map on four
chromosomes with 16 markers each. The markers would be equally spaced at 10 centimorgan intervals and would span the genome.

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td></td>
<td>Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.map</td>
<td>Output File</td>
</tr>
<tr>
<td>-f</td>
<td>1</td>
<td>Map Function</td>
</tr>
<tr>
<td>-p</td>
<td>0.0</td>
<td>Map function parameter</td>
</tr>
<tr>
<td>-g</td>
<td>1</td>
<td>Output Flag</td>
</tr>
<tr>
<td>-c</td>
<td>4</td>
<td>Chromosomes</td>
</tr>
<tr>
<td>-m</td>
<td>16</td>
<td>Markers per Chromosome</td>
</tr>
<tr>
<td>-vm</td>
<td>0.0</td>
<td>Standard deviation of Markers per Chromosome</td>
</tr>
<tr>
<td>-d</td>
<td>10.0</td>
<td>Intermarker Distance (cM)</td>
</tr>
<tr>
<td>-vd</td>
<td>0.0</td>
<td>Standard deviation of Intermarker Distance</td>
</tr>
<tr>
<td>-t</td>
<td>0.0</td>
<td>Tails (Flanking DNA, in cM)</td>
</tr>
<tr>
<td>-M</td>
<td>0</td>
<td>Simulation Mode (0,1)</td>
</tr>
</tbody>
</table>

Table 2.1: Command Line Options for Rmap

Map Function

A map function is a mathematical relationship between recombination probabilities and map distances measured in centimorgans or Morgans. QTL Cartographer presently allows for eight map functions specified by an integer. The numbers 1, 2 or 3 correspond to the Haldane, Kosambi and Morgan (formerly Fixed) mapping functions, respectively. The default is the Haldane mapping function. If \( r \) corresponds to the recombination frequency between a pair of markers and \( d_M \) is the distance between them in Morgans, then the Haldane mapping function is defined by

\[
d_M = -\frac{1}{2} \ln(1 - 2r) \tag{2.1}
\]

\[
r = \frac{1}{2} \left[ 1 - \exp(-2d_M) \right] \tag{2.2}
\]

The Kosambi function is

\[
r = \frac{1 - \exp(-4d_M)}{2[1 + \exp(-4d_M)]} \tag{2.3}
\]

\[
d_M = \frac{1}{4} \ln \left[ \frac{1 + 2r}{1 - 2r} \right] \tag{2.4}
\]

and the Morgan function assumes \( d_M = r \), which is complete interference. All eight mapping functions are discussed at length in Ben Liu’s book (Liu 1998). We direct the reader there for the details. Table 2.2 lists the mapping functions and their integer codes for QTL Cartographer. Some of these map functions require an extra parameter. This parameter can be set in the Rmap menu. See Section 10.3.1 of Liu (1998) for the details.
### Table 2.2: Command Line Options for Rmap

<table>
<thead>
<tr>
<th>Code</th>
<th>Reference</th>
<th>Note</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Haldane (1919)</td>
<td>default</td>
</tr>
<tr>
<td>2</td>
<td>Kosambi (1944)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Morgan (1994)</td>
<td>“Fixed”</td>
</tr>
<tr>
<td>4</td>
<td>Carter and Falconer (1951)</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Rao et al. (1979)</td>
<td>$0 \leq p \leq 1$</td>
</tr>
<tr>
<td>6</td>
<td>Sturt (1976)</td>
<td>$L$</td>
</tr>
<tr>
<td>7</td>
<td>Felsenstein (1979)</td>
<td>$-\infty &lt; K &lt; \infty$, $K \neq 2$</td>
</tr>
<tr>
<td>8</td>
<td>Karlin (1984)</td>
<td>binomial, $N &gt; 0$</td>
</tr>
</tbody>
</table>

#### Output Flags

The output flag takes on values of 1, 2 or 3. A 1 indicates that Rmap should output a file in the “Rmap.out” format. A 2 indicates that a set of files that can be plotted in GNUPLOT should be created while a 3 indicates that both should be done. The option to display the map in GNUPLOT allows a general overview of the spacing of markers. If you choose to create the GNUPLOT files, then Rmap will write one file per chromosome summarizing the linkage information. Each file will have two columns: The first indicating the position of the marker from the telomere and the second for the chromosome number. The file for chromosome 1 will be Chrom.1, and other files are named accordingly. Finally, a control file, Chrom.plt, will have the plotting commands understood by GNUPLOT. This file should be loaded by GNUPLOT to view the linkage map. Marker names are not written on the map.

#### Input Files

Again, note that if an input file is specified, all options from “Chromosomes” down in Table 2.1 will be ignored and Rmap will attempt to translate the input file. Remember that Rmap overwrites any files with the same name as its output file, so avoid giving your input and output files the same name.

### 2.2 Rqtl

Given a genetic linkage map, Rqtl can place a random set of quantitative trait loci on the map. The program simulates the positions and effects (additive, dominance and epistatic) of the QTL. It can also reformat a given set of QTLs defined in an input file of filetype “qtls.inp” that is explained in Section 6.2.1. The given set of QTLs might be made up by the user, or a set of estimates from a previous analysis of a data set. Table 2.3 presents the command line options for Rqtl. The default values from the table tell Rqtl to simulate nine QTLs for one trait.
For simulations, the user can specify the average number of QTLs per trait, the number of traits, and parameters for dominance and additive effects. Epistatic effects are simulated with the same parameters used for the dominance effects. We use the convention that \( Q_1 \) alleles are from \( P_1 \) lines and \( Q_2 \) from \( P_2 \) lines.

Dominance can take on the values 1, 2, 3 or 4. 1 means no dominance, while 2 means \( Q_1 \) is dominant and 3 means \( Q_2 \) is dominant. A value of 4 means that dominance for each QTL will be random in magnitude and sign. The degree of dominance will be a Beta random variable \( d \) with shape parameters \( \beta_1, \beta_2 \). The density function for \( d \) is

\[
f(d) = \begin{cases} \frac{d^{\beta_1-1}(1-d)^{\beta_2-1}}{B(\beta_1,\beta_2)} & \beta_1, \beta_2 > 0; -1 \leq d \leq 1 \\ 0 & \text{otherwise} \end{cases}
\]

where

\[
B(\beta_1,\beta_2) = \frac{\Gamma(\beta_1)\Gamma(\beta_2)}{\Gamma(\beta_1 + \beta_2)} \tag{2.6}
\]

and \( \Gamma(x) \) is the gamma function

\[
\Gamma(x) = \int_0^\infty y^{x-1}e^{-y}dy
\]

Epistatic effects are generated from the same distribution as the dominance effects. For a \( k \) QTL model, there are \( 2^k(k-1) \) potential dominance effects. For each unordered pair of loci, there are Additive by Additive, Additive by Dominance, Dominance by Additive and Dominance by Dominance terms, and thus \( 4k(k-1)/2 \) possible epistatic interactions. Only a proportion of these will be nonzero, with that proportion specified by the -E option. The proportion should be in the range \([0.0, 1.0]\).

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>(None)</td>
<td>Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.qtl</td>
<td>Output File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-t</td>
<td>1</td>
<td>Number of Traits</td>
</tr>
<tr>
<td>-q</td>
<td>9</td>
<td>Number of QTL per Trait</td>
</tr>
<tr>
<td>-b</td>
<td>2.0</td>
<td>Additive effect parameter beta</td>
</tr>
<tr>
<td>-1</td>
<td>2.0</td>
<td>Dominance effect parameter ( \beta_1 )</td>
</tr>
<tr>
<td>-2</td>
<td>2.0</td>
<td>Dominance effect parameter ( \beta_2 )</td>
</tr>
<tr>
<td>-d</td>
<td>1</td>
<td>Dominance</td>
</tr>
<tr>
<td>-E</td>
<td>0.0</td>
<td>Proportion of Epistatic Effects</td>
</tr>
</tbody>
</table>

Table 2.3: Command Line Options for Rqtl

The additive effects of the QTLs are independent, identically distributed random variables sampled from the gamma distribution (Zeng 1992, page 993, equation 12) and reprinted here:

\[
f(a) = \frac{\beta^a a^{\beta-1}e^{-a\beta}}{\Gamma(\beta)}, \quad 0 < a < \infty, \quad 0 < \beta < \infty \tag{2.7}
\]
CHAPTER 2. SIMULATING/REFORMATTING DATA

The shape parameter $\beta$ allows a wide variety of different genetic models to be generated. The additive effect of substituting an $Q_1$ allele for an $Q_2$ allele is $a$. When multiple traits are simulated, the number of QTLs per trait is simulated as a random variable with mean specified by the $-q$ option.

If an input file is specified, then it is translated into a format readable by Rcross and the options in Table 2.3 from “Number of Traits” and below are ignored. The input file format “qtls.inp” is defined in Section 6.2.1. This input file format will allow a wide variety of genetic models to be simulated.

2.3 Rcross

Rcross uses the information generated by Rmap and Rqtl and randomly simulates a data set. Alternatively, it can also reformat MAPMAKER raw data files and “ cross.inp” filetype formatted files. Table 2.4 presents the options for Rcross. The default values would create a simulated sample of 200 individuals backcrossed to $P_1$ with a heritability of 0.5 for the quantitative trait.

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>(None)</td>
<td>Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.cro</td>
<td>Output File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-q</td>
<td>qtlcart.qtl</td>
<td>QTL Data File</td>
</tr>
<tr>
<td>-n</td>
<td>200</td>
<td>Sample Size</td>
</tr>
<tr>
<td>-c</td>
<td>1</td>
<td>Type of Cross</td>
</tr>
<tr>
<td>-H</td>
<td>0.5</td>
<td>Heritability</td>
</tr>
<tr>
<td>-I</td>
<td>0</td>
<td>Interactive flag</td>
</tr>
<tr>
<td>-g</td>
<td>0</td>
<td>Output format</td>
</tr>
<tr>
<td>-E</td>
<td>-1.000000</td>
<td>Environmental Variance (used if $&gt; 0$)</td>
</tr>
</tbody>
</table>

Table 2.4: Command Line Options for Rcross

2.3.1 Simulating Data

Rcross will simulate a dataset using the genetic linkage map prepared by Rmap and the genetic model prepared by Rqtl. The user can specify the sample size, type of cross and heritability or environmental variance. An interactive mode allows the user to generate arbitrary crosses. Rcross can automatically generate backcrosses, intercrosses or any of the other experimental designs defined in Section 1.1.2. Below we describe how each individual is created. The process is repeated as many times as are necessary to get the sample size specified.
CHAPTER 2. SIMULATING/REFORMATTING DATA

QTL Cartographer

Generation of Individuals

For generating backcrosses or intercross samples, the parental lines are known. Individuals in the \( F_1 \) are all heterozygous, and all pairs of loci are in coupling. Samples derived from \( F_2 \) and later crosses need to take into account the different possible parents. This section explains how individuals are simulated in a general way.

We assume that there is one or two parental samples that will be used to create the next generation. Refer to these as lines 1 and 2. We assume monoecious, diploid individuals. To generate a new individual, one parent is selected from line 1 and one from line 2. If line 1 and line 2 are the same sample (for example, crossing two \( F_2 \) lines to form an \( F_3 \)) then selfing is a possibility. Once the parents have been selected, gametes are produced, one from each parent.

The first step in producing gametes is to simulate recombination. We assume that the number of crossovers on each chromosome is distributed as a Poisson random variable with mean equal to the length of the chromosome in Morgans. A separate random integer is generated for each chromosome subject to the Poisson, and this indicates the number of crossovers on that chromosome. These crossovers are placed on the chromosome subject to a uniform distribution.

Once the crossovers are in place, gametes are generated. Starting with the first chromosome, one of the two homologs is chosen at random. This chromosome is followed until a crossover is encountered, at which point the other homolog is used. At the end of the first chromosome, a homolog from the second chromosome is chosen at random and the process continues. At the end, a gamete is created which contains the markers and QTLs. The gametes from each parent are then combined to form a new individual. Genetic values are calculated from the genotypes of the new individual using Cockerham’s general genetic model for the partitioning of genetic variance (Cockerham 1954). Phenotypic values can then be generated based on the genetic variance and the heritability.

Phenotypic Values

Phenotypic values are calculated from the genotypic values for each individual for each trait. Each individual’s phenotypic value is calculated from its genotypic value with an environmental effect determined by the heritability \( h^2 \). The individual’s genotypic value is based on the alleles it inherited at the quantitative trait loci. To calculate genetic values, we use Cockerham’s general genetic model (Cockerham 1954).

\[
G_i = \sum_{r=1}^{m} a_r x_{ir} + \sum_{r=1}^{m} d_r z_{ir} + \sum_{r \neq s} b_{rs}^{AA} x_{ir} x_{is} + \sum_{r \neq s} b_{rs}^{AD} x_{ir} z_{is} \\
+ \sum_{r \neq s} b_{rs}^{DA} z_{ir} x_{is} + \sum_{r \neq s} b_{rs}^{DD} z_{ir} z_{is} \quad (2.8)
\]

The parameters \( a_r, d_r \) are the additive and dominance effects of QTL \( r \). The \( b \)’s are epistatic interactions. The superscripts on the \( b \)’s are for the type of interaction: We distinguish between additive by additive (AA), additive by dominance (AD), dominance
CHAPTER 2. SIMULATING/REFORMATTING DATA

QTL Cartographer

by additive (DA) and dominance by dominance (DD) interactions. The $x$ and $z$ are coded variables denoting the genotype of the QTL. The $x_{ir}$ take on values (1, 0, −1) for QTL genotypes (QQ, Qq, qq), while the $z_{ir}$ are 1/2 for heterozygotes and −1/2 for homozygotes.

This results in a vector of genotypic values, one entry per individual in the simulated data set. The genetic variance is the sample variance of this vector of genotypic values. Call it $\sigma_g^2$. The environmental variance, $\sigma_e^2$ is defined by

$$\sigma_e^2 = \sigma_g^2 \left( \frac{1}{h^2} - 1 \right)$$

(2.9)

where $h^2$ is the heritability of the trait. The extra environmental effect is taken from a normal distribution with mean 0 and variance $\sigma_e^2$. If the environmental variance is specified, the heritability is ignored and the environmental variance is used directly. For each individual in the data set, a random variable with mean zero and variance $\sigma_e^2$ is generated and added to the genotypic value. This is the phenotypic value of that individual, and is printed in the output file.

2.3.2 Translating Data

Similar to Rmap and Rqtl, Rcross can translate files in a pair of special formats. The first format is the input format for MAPMAKER/QTL. These would be the MAPMAKER/QTL “*.raw” files. Simply invoke Rcross and specify that the input file is one of these files. The parameters that are for simulations are then ignored. REMEMBER: The first two words of a MAPMAKER/QTL raw file should be “data type”. Older versions of Rcross cannot process comments at the beginning of a raw file. In fact, it depends on those first two words to recognize the file as a MAPMAKER/QTL raw file. Beginning with version 1.12, comments will be allowed in the beginning of a “mapmaker.raw” file if you include the “-filetype mapmaker.raw” indicator within the first 100 lines of your file. It is usually best to put this on the first line. Rcross will recognize the command and translate the file appropriately. You might want to get into the habit of putting the “-filetype” token (with an appropriate identifier) in your input files, as it will become more important in future releases of QTL Cartographer. There are two other things to keep in mind when using MAPMAKER/QTL files. The first is that marker and trait names are truncated to eight characters in the output: Versions of QTL Cartographer prior to 1.12 will be tripped up by this. Secondly, MAPMAKER/EXP has been known to translate underscores “_” as minus signs “−” in its output, so you might want to avoid them.

The other format is one designed for the QTL Cartographer system. It is defined in the file cross.inp included with the distribution and outlined in Section 6.3.2. Finally, Rcross can read files in it’s own output format (filetype “Rcross.out”) for translation to “mapmaker.raw” or “cross.inp” filetype formats.

2.3.3 Output

The flag -g can be used to indicate the output format of Rcross. In contrast to the input formats, there are five options for output. Rcross will write output in a format suitable
for MAPMAKER if the -g option is used with the integer 2, while a cross.inp formatted file will be written with the value 1. Using a value of 3 produces a file suitable for input into Splus or R, while a 4 generates a SAS program file. The integers 5 and 6 tell Rcross to produce files suitable for import into PLABQTL (Utz and Melchinger 1996): Use 5 if you want the matrix format and 6 for the vector format.

The default is what we term the qtlcart.cro format, and is indicated by using zero with the -g option. Here is an example of the output of Rcross.

```
# 1472574604    filetype Rcross.out
#
# QTL Cartographer V. 1.12c, March, 1997
#
-n 300 is the sample size
-p 63 is one more than the number of markers
-cross B1 is the type of cross
-traits 1 is the number of traits
-Names of the traits...
   1 Trait.1
-otraits 0 is the number of other traits
#
-s
   1 1
   1 1 1 1 1 1 2 2 2 2 2 1 1 1 1 1
   2 2 2 2 2 2 1 1 1 1 1 1 1 1 1 1
   2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1
   1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
    7.035406650635
   2 1
   1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
   1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1
   3.555115422473
   3 1
   2 1 1 1 1 2 2 2 2 2 2 1 2 2 2 2
   1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
   2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1
   2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1
    4.165996548162
.
.
.
-e
```

The section prior to the ‘-s’ token is self-explanatory. The area between the ‘-s’ and
the ‘-e’ is the data. It starts with an identification number (1, 2, 3, etc), and is followed by a “1”. At the moment this number “1” is ignored. With the convention that $A_1$ alleles originated from the $P_1$ line and $A_2$ from the $P_2$, marker genotypes will be encoded with the following integer values:

- 2 for $A_1A_1$
- 1 for $A_1A_2$
- 0 for $A_2A_2$
- 12 for $A_1-$, that is individuals with at least one dominant $A_1$ allele
- 10 for $A_2-$, that is individuals with at least one dominant $A_2$ allele
- -1 for unknown genotypes. Rcross read something but could not translate it.
- -2 is also for unknown genotypes. In this case, no data had been read in.

The trait values follow the marker genotypes, and finally the “other” (categorical or qualitative) traits follow at the end. The sequence repeats for all individuals. Note that there is a permissible range for trait values. By default, all trait values must be real numbers with absolute value less than one million ($10^6$). Any trait value that is less than negative one million is treated as a missing phenotype by the programs.

Other Traits

Other traits can be thought of as qualitative or categorical traits. Examples include sex, brood, plot, etc. In some cases these factors will have been “regressed out”, that is a regression of the quantitative trait of interest on the categorical trait will have been performed and the residuals used as the phenotypes in the analysis. Presently, they can be input via a file of filetype “cross.inp” but not automatically analyzed. One includes these other traits in the regression model by prepending a plus sign (+) to the other trait name. For example,

```
+Names of the other traits...
  1 +Sex
  2 -Line
```

would incorporate a Sex effect in the regression model, while ignoring the Line effect.

Interface with R and Splus

If -g is used with the integer 3, then Rcross will create a file with all the trait, marker and categorical data that is suitable for loading into Splus or R. In addition, it will create data frames for the different types of data and set up a set of commands to do one-factor ANOVA of each trait on each marker, and each trait on each categorical trait. From there, the user can do higher level ANOVA analyses in R or Splus. In the output you will see data frames with names Markers$markernname, Traits$traitname, and Ottraits$otraitname,
where *markername* is the name of a specific marker, *traitname* is the name of a specific trait and *otraitname* is the name of a specific categorical trait. If markers have no names, then the data for marker Y on chromosome X will be in *Markers$XmY*. A similar convention holds for traits and categorical traits: the trait numbered Z will go into *Traits$Z* and categorical trait W will go into *OTraits$W*. The output file will have filetype *RSplus.inp*.

Once the *RSplus.inp* file has been created, it can be imported into *Splus* or *R* with the *source* command. Here is an example of using *R* in a UNIX environment using the *mletest.cro* file has been converted with *Rcross* and the `-g 3` option:

```r
prompt % Rcross -X mletest -i mletest.cro -o mletest.r -g 3 -A -V
prompt % R

R : Copyright 2000, The R Development Core Team
Version 1.0.0 Patched (April 4, 2000)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type "?license" or "?licence" for distribution details.

R is a collaborative project with many contributors.
Type "?contributors" for a list.

Type "demo()" for some demos, "help()" for on-line help, or "help.start()" for a HTML browser interface to help.
Type "q()" to quit R.

> source("mletest.r")

.....lots of output that looks like....

Response: Traits$Trait.1

<table>
<thead>
<tr>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.34</td>
<td>0.34</td>
<td>0.0978</td>
<td>0.7547</td>
</tr>
<tr>
<td>298</td>
<td>1038.21</td>
<td>3.48</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

> q()
prompt %

The ANOVA of the trait on marker 16 from chromosome 4 has a p-value of 0.7547, indicating little evidence of linkage with a QTL.

Since the output is going into *R*, you need to take care in naming your markers, traits and categorical traits. Special characters like underscores and dollar signs mean something to *R* and should be avoided.
CHAPTER 2. SIMULATING/REFORMATTING DATA

Interface with SAS

Similar to the R/Splus output option, you may use -g 4 to get a conversion of your data to SAS format. The file will contain all the data and a set of PROC ANOVA statements for each trait on each marker and categorical trait. Note that there is a RUN statement at the very end of the output file, so that if you load it into SAS, then all the ANOVA’s will be done automatically. You will need to take care with marker, trait and categorical trait names. See the SAS documentation for limitations.

2.4 Prune

Prune takes a genetic linkage map and a data set as input. The user can either eliminate some of the data (markers or traits), bootstrap, permute or simulate missing data. Table 2.5 summarizes the command line options for Prune.

Originally, Prune was strictly a command line program. In adding the interactive menu it became necessary to add a second level of interaction. When Prune is invoked in the interactive mode, the user will see a menu in which all the parameters of Table 2.5 can be set. The user will then proceed to another interactive menu in which data manipulation can be performed. The second menu will list actions that can be taken. The user selects an action and provides the proper values at which time the action is taken. This second menu is in a loop. The user can continue to take actions until the option to quit is chosen. At the end, the data set is printed out. A few actions can be done automatically. They are bootstrapping, permuting and simulating missing data. These are provided so that Prune can be run in a batch file for permutation tests or bootstrap experiments.

The output files of Prune may include a genetic linkage map and a data file. If markers had been eliminated, then the linkage map is regenerated to take this into account. The new output files will have the extensions .mpb and .crb, and filename stems specified by the -o option.

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-o</td>
<td>qtlcart</td>
<td>Output Filename Stem</td>
</tr>
<tr>
<td>-e</td>
<td>qtlcart.log</td>
<td>Error File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Data File</td>
</tr>
<tr>
<td>-s</td>
<td>860436420</td>
<td>Random Number Seed</td>
</tr>
<tr>
<td>-I</td>
<td>1</td>
<td>Interactive mode (0,1)⇒(no,yes)</td>
</tr>
<tr>
<td>-b</td>
<td>0</td>
<td>B (1), P (2), M (3) or D (4)</td>
</tr>
<tr>
<td>-M</td>
<td>0.100000</td>
<td>Percent missing data to simulate</td>
</tr>
</tbody>
</table>

Table 2.5: Command Line Options for Prune
2.4.1 Pruning Datasets Interactively

The pruning of datasets occurs in an interactive menu. After setting parameters in the first menu, continue on to the second interactive menu where actions can be taken. The second interactive menu looks like this:

You can loop through items 1-6, but 7-11 terminate.

<table>
<thead>
<tr>
<th>No.</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Eliminate A- marker systems (P1 dominant)</td>
</tr>
<tr>
<td>2.</td>
<td>Eliminate a- marker systems (P2 dominant)</td>
</tr>
<tr>
<td>3.</td>
<td>Eliminate marker m on chromosome c</td>
</tr>
<tr>
<td>4.</td>
<td>Eliminate trait t</td>
</tr>
<tr>
<td>5.</td>
<td>Eliminate individuals with missing phenotypes for trait t</td>
</tr>
<tr>
<td>6.</td>
<td>Eliminate individuals with more than m% missing markers</td>
</tr>
<tr>
<td>7.</td>
<td>Bootstrap the data</td>
</tr>
<tr>
<td>8.</td>
<td>Permute the traits in the data</td>
</tr>
<tr>
<td>9.</td>
<td>Simulate m% missing markers</td>
</tr>
<tr>
<td>10.</td>
<td>Simulate m% dominant markers</td>
</tr>
<tr>
<td>11.</td>
<td>Simulate m% selective genotyping</td>
</tr>
<tr>
<td>12.</td>
<td>Write modified dataset and exit</td>
</tr>
<tr>
<td>13.</td>
<td>Exit without writing anything</td>
</tr>
</tbody>
</table>

Pick a number to do an action...

Dominant Markers

There are actions to eliminate dominant markers from the data set. These options were included at a time when Zmapqtl and LRmapqtl couldn’t analyze dominant markers. With the addition of subroutines to analyze dominant markers, the need for these options has lessened. Selecting option 1 or 2 in the second interactive menu eliminates one dominant markers or one type or the other.

Eliminating markers and traits

Option 3 of the interactive menu has an action to eliminate a specific marker. You should be aware that the order of elimination is important. If all the markers to be eliminated are on separate chromosomes, the order is unimportant. If two markers from the same chromosome are to be eliminated, higher numbered marker should be eliminated first. The same concept holds for traits with option 4: Eliminate them in the order of highest to lowest. You will need to know the marker number and chromosome number rather than the marker name to use this option.
Culling sparse data

Some markers or traits may have been typed for a small proportion of individuals in the dataset. Such markers or traits can be eliminated from the dataset. Option 5 will allow you to specify a trait number, and then eliminate individuals with missing data for that trait. Choosing option 6 will require a tolerance level for the percentage of missing marker data. The \(-M\) option specifies this number, which must be in the range \((0.0, 100.0)\). If option 6 is selected, Prune will eliminate individuals with this percentage of missing marker data.

Resampling data

Options 7, 8 and 9 allow the user to bootstrap, permute or simulate missing data for the dataset. If a bootstrap is chosen, then a new dataset of the same size will be resampled (with replacement) from the original data. A permutation simply permutes the trait values. The simulation of missing data requires a percentage level to simulate: That percentage of markers will then be set to unknown. These options are examined in more detail in Section 2.4.2.

Selecting 7, 8 or 9 will do the requested action, write the output and exit. The other options require you to specify when to write and exit. You also have the option of exiting without writing anything.

2.4.2 Recreating Datasets

Command Line Actions

When you use the \(-b\) option with an integer value from one to six, Prune will take one action, print out a new dataset and exit. There are six possible actions, and some require that you use the \(-M\) option with a percentage as well. The six possible actions are listed below: use the number preceding the action with the \(-b\) option to do that action.

1. Bootstrap the data. This option samples individuals with replacement to produce a new data set of the same size as the original.

2. Permute the data. This option will randomly shuffle the traits against the genotypic arrays. If there are multiple traits, then there is a shuffling for each trait. If you want to keep trait arrays together, see item six below.

3. Simulate missing markers. This option requires you to specify a percent \((0 - 100\%)\) of missing marker information. Prune will then randomly reset that percentage of marker data to unknown.

4. Simulate dominant markers. Again, you need to specify the percentage of dominant marker systems. A random set of markers are chosen and converted to dominant markers. The direction is random \((50/50 each way)\) for each marker chosen.

5. Simulate selective genotyping. The \(-M\) option specifies what proportion of individuals that are typed. Do this with single trait data sets. The individuals are ordered
according to their trait values, and one-half the specified proportion in the tails are retained in the output. The individuals in the middle of the distribution are deleted from the data set.

6. Permute the data. This is the same as option 2 above except that with multi-trait data sets, there is a shuffling of the trait arrays against the genotype arrays. If you think the traits are correlated, you can use this to maintain that correlation. A value of 12 is the same as this option.

Bootstrapping

The -b option with a value of 1 tells Prune to create a single bootstrapped data set. This option should be used alone. It will sample the data set with replacement, creating a new data set of the same sample size and writing it to the file qtlcart.crb. Of course, you can change the output file name by changing the output filename stem with the -o option. Using Prune, one can perform a bootstrap experiment on the data set. This is much easier to do on a UNIX workstation than a Macintosh or MS-Windows machine because it can be automated in a batch file.

Suppose qtlcart is the filename stem, and use m as the integer code for the model, h for the hypothesis test, and r for the number of repetitions, then this snippet of pseudo-code will do a bootstrap analysis

\[
\text{Zmapqtl -A -V -X qtlcart -M } m \\
\text{SSupdate -I } h < \text{qtlcart.z} > \text{qtlcart.z.boot} \\
\text{move qtlcart.z qtlcart.z.save} \\
\text{i } = 1 \\
\text{while (i } < r \text{)} \{} \\
\text{Prune -A -V -i qtlcart.cro -b 1} \\
\text{Zmapqtl -A -V -M } m \text{-i qtlcart.crb} \\
\text{SSupdate -I } h \text{-f qtlcart.z.boot } < \text{qtlcart.z} > \text{qtlcart.z.new} \\
\text{move qtlcart.z.new qtlcart.z.boot} \\
\text{delete qtlcart.z} \\
\text{i } = i + 1 \\
\text{\}} \\
\text{SSupdate -I } h \text{-c -f qtlcart.z.boot } > \text{qtlcart.z.booted} \\
\text{move qtlcart.z.save qtlcart.z}
\]

Except for the while loop line, the symbols <,>,>> above are for input and output redirection. SSUpdate is a Perl script available with the distribution of the programs (look in doc for a scripts subdirectory). Note that the work is done in the while loop. For each repetition, a bootstrapped data set is created with Prune. This data will be placed in the file ending with .crb. Zmapqtl then analyzes this bootstrapped data. The script SSUpdate reads the results of the Zmapqtl run and updates a file with the sum and sum of squares of the test statistic and estimates of effects. Also, SSUpdate is run to initialize the boot file, so you will need to run Zmapqtl on the original data before doing the bootstrap. When this is finished, the script runs SSUpdate with the -c option to get the mean and variance of the likelihood ratio, additive effect and dominance effect at each
test site. There is a \texttt{c} shell script called \texttt{Bootstrap} in the \texttt{scripts} subdirectory of the distribution that implements the above idea.

\textbf{Permutation Tests}

\texttt{Zmapqtl} can perform permutation tests using interval mapping, but if you want to do a proper permutation test using composite interval mapping and reselecting your background markers during each permutation, you will need to do it in a batch file similar to the one for bootstrapping. \texttt{Prune} can create a single permuted dataset by using the \texttt{-b} option with a value of 2 or 6. If you use 2, then each trait is permuted against the genotypes. Alternatively, using a 6 means that the traits as a block are permuted against the genotypes to retain any correlation the traits may have.

Suppose \texttt{qtlcart} is the filename stem, and use \texttt{m} as the integer code for the model, \texttt{c} for the \texttt{Zmapqtl} output file column to test, and \texttt{r} for the number of repetitions, then this snippet of psuedo-code will do a permutation test

\begin{verbatim}
Zmapqtl -A -V -X qtlcart -M m
GetMaxLR -i < qtlcart.z > qtlcart.z.ewt
CWTupdate -C c < qtlcart.z > qtlcart.z.cwt
move qtlcart.z qtlcart.z.save
i = 1
while (i < r) {
    Prune -A -V -i qtlcart.cro -b 2
    Zmapqtl -A -V -M m -i qtlcart.crb
    GetMaxLR -i -C c < qtlcart.z >> qtlcart.z.ewt
    CWTupdate -f qtlcart.z.cwt -C c < qtlcart.z >> qtlcart.z.new
    move qtlcart.z.new qtlcart.z.cwt
    delete qtlcart.z
    i = i + 1
}
EWThreshold < qtlcart.z.ewt
move qtlcart.z.save qtlcart.z
\end{verbatim}

The \texttt{Perl} scripts \texttt{GetMaxLR}, \texttt{EWThreshold} and \texttt{CWTupdate} are in the \texttt{doc/scripts} subdirectory. A \texttt{c} shell example script, \texttt{Permute}, also resides there.

You could also have \texttt{SRmapqtl} redo the stepwise regression in the above script so that the background markers in composite interval mapping reflect the permuted data set rather than the original. There is a small quirk in this type of simulation if you are using \texttt{SRmapqtl} with stepwise forward-backward regression and \texttt{Zmapqtl} with model 6. Sometimes a permuted data set will result in no markers being sufficiently correlated with the trait of interest to be added in the forward phase of the stepwise regression. Thus, \texttt{Zmapqtl} will think there are no markers to be used as covariates, and default to interval mapping. Thus, you may not get the exact number of permutations specified to the above script.
Simulating Missing Data

You can also use Prune to simulate missing data. You set the amount of missing marker data you would like to simulate with the \texttt{-M} option. This will be a percent, and should be specified before you invoke the bootstrap option, which actually does the simulation. Use a value of 3 to tell Prune to randomly set some of the markers to missing. Over the entire data set, approximately the percentage of markers that had been set with the \texttt{-M} option will be set to -10. The results will be in a file with the filename extension “.crb”. Similar to simulating missing data, some of the markers can be made dominant by using a value of 4 with the bootstrap option. The percentage of markers transformed is set with the \texttt{-M}. The direction of dominance is random: Half of those changed will convert the \texttt{P}$_1$ allele to dominant, while the other half will convert the \texttt{P}$_2$ allele.

If you use a value of 5 with \texttt{-b} and specify a percentage for \texttt{-M}, then you can investigate how selective genotyping compares to having typed all the individuals. As an example, suppose you have a data set typed for 500 individuals and use \texttt{-M} 20 and \texttt{-b} 5. The individuals are ordered with respect to the trait of interest and those whose trait values are in the lowest 10\% are retained along with those in the highest 10\%. Those in the 10 to 90 percent range are deleted. A new data set with the “.crb” filename extension will contain the results.
Chapter 3

Analysis

A recent review (Doerge, Zeng, and Weir 1997) summarizes the statistical issues for mapping QTLs. It is the best place to start for a general overview of the analytical methods used in QTL Cartographer.

Figure 3.1 shows a schematic of the analysis procedure. There are five programs in this step. Qstats does some basic quantitative genetic statistics and summarizes missing data. It is a useful program to run at the beginning of your analysis. LRmapqtl does single maker analysis using linear regression. It also runs very fast and will give some idea of where QTLs are. SRmapqtl does stepwise regression, either forward, backward or forward with backward elimination. The program Zmapqtl implements interval mapping (Lander and Botstein 1989) and composite interval mapping (Zeng 1993; Zeng 1994) for a single trait at a time. JZmapqtl is an extension to multitrait mapping (Jiang and Zeng 1995). Multiple interval mapping (Kao and Zeng 1997; Kao, Zeng, and Teasdale 1999; Zeng, Kao, and Basten 1999) is available in MImapqtl.

The basic requirements for using these three programs is a genetic linkage map and a data file. The linkage map should be of filetype format “Rmap.out” and the data file of “Rcross.out”. Whether the files are simulated, real or bootstrapped data is irrelevant: The analysis is the same regardless of the origin of the data.

3.1 Qstats

Qstats is a good place to start in analyzing your data. It computes some basic statistics on the quantitative traits and summarizes missing data. Let \( \{y_1, y_2, \ldots, y_n\} \) be a vector of quantitative trait values. For each trait in turn, it calculates the sample size \( n \), mean \( \bar{y} = \frac{1}{n} \sum_{i=1}^{n} y_i \), variance \( s^2 = \frac{1}{n-1} \sum_{i=1}^{n} (y_i - \bar{y})^2 \), standard deviation \( s = \sqrt{s^2} \), skewness, kurtosis and average deviation, \( \frac{1}{n} \sum_{i=1}^{n} |y_i - \bar{y}| \). The coefficient of variation is the sample standard deviation divided by the sample mean.

Lynch and Walsh (1998) provide a lucid explanation of some of the statistics calculated by Qstats. Let the kth sample moment be \( M(k) = \frac{1}{n} \sum_{i=1}^{n} y_i^k \). Clearly, \( M(1) = \bar{y} \). Using
the notation $\bar{y}^k = M(k)$, we can estimate the sample variance with

$$s^2 = \frac{n}{n-1} (\bar{y}^2 - \bar{y}^2)$$  \hspace{1cm} (3.1)

An estimate of the skewness is

$$Skw(y) = \frac{n^2}{(n-1)(n-2)} (\bar{y}^3 - 3\bar{y}\bar{y}^2 + 2\bar{y}^3)$$

The standard error of skewness depends on the underlying distribution but can be approximated by $\sqrt{6/n}$. The coefficient of skewness, $k_3$ is

$$k_3 = \frac{Skw(y)}{s^3}$$

where the sample standard deviation, $s = \sqrt{s^2}$, is estimated from (3.1). Kurtosis is estimated by

$$Kur(y) = \frac{n^2(n+1)}{(n-1)(n-2)(n-3)} (\bar{y}^4 - 4\bar{y}^3\bar{y} + 6\bar{y}^2\bar{y}^2 - 3\bar{y}^4)$$

and the coefficient of kurtosis is

$$k_4 = \frac{Kur(y) - 3s^4}{s^4}$$
Like skew, the standard error of kurtosis is dependent upon the population distribution. We give the estimate $\sqrt{\frac{24}{n}}$. A test of normality for the vector $y$ then involves the test statistic

$$S = \frac{nk_3^2}{6} + \frac{nk_4^2}{24}$$

which is distributed as a $\chi^2$ with two degrees of freedom. The critical values for the rejection of normality are 5.99 and 9.21 for tests at the 5% and 9% levels, respectively.

An example of the output follows:

<table>
<thead>
<tr>
<th>Sample Size..............</th>
<th>119</th>
</tr>
</thead>
<tbody>
<tr>
<td>M(1)..........................</td>
<td>0.4349</td>
</tr>
<tr>
<td>M(2)..........................</td>
<td>0.2184</td>
</tr>
<tr>
<td>M(3)..........................</td>
<td>0.1195</td>
</tr>
<tr>
<td>M(4)..........................</td>
<td>0.0694</td>
</tr>
<tr>
<td>Mean Trait Value...........</td>
<td>0.4349</td>
</tr>
<tr>
<td>Variance...................</td>
<td>0.0295</td>
</tr>
<tr>
<td>Standard Deviation.......</td>
<td>0.1718</td>
</tr>
<tr>
<td>Coefficient of Variation..</td>
<td>0.3951</td>
</tr>
<tr>
<td>Average Deviation.........</td>
<td>0.1398</td>
</tr>
<tr>
<td>Skw..LW(24)..................</td>
<td>-0.0010</td>
</tr>
<tr>
<td>....Sqrt(6/n)...............</td>
<td>0.2245</td>
</tr>
<tr>
<td>Kur..LW(29)..................</td>
<td>0.0022</td>
</tr>
<tr>
<td>....Sqrt(24/n).............</td>
<td>0.4491</td>
</tr>
<tr>
<td>k3...LW(24)..................</td>
<td>-0.1922</td>
</tr>
<tr>
<td>k4...LW(28)..................</td>
<td>-0.5250</td>
</tr>
<tr>
<td>S (5%: 5.99, 1%: 9.21)....</td>
<td>2.0992</td>
</tr>
</tbody>
</table>

In the above example, LW(i) refers to a page number in Lynch and Walsh (1998) where one can find an explanation of the quantity. The value of the test statistic $S$ is 2.0992, thus one would fail to reject the hypothesis that this trait is normally distributed.

After the basic statistics, Qstats draws a histogram of the quantitative trait. It is a simple histogram in that the range of the data are divided into 50 equally sized bins, and the number of data points falling into each bin are counted and plotted. A small table following the histogram gives the sample size, minimum, first quartile, median, second quartile and maximum.
3.1.1 Command Line Options

Table 3.1 summarizes the command line options for Qstats. There are very few of them. You can specify the data set, genetic linkage map file and output file. In addition, all the global options of Table 1.4 are valid.

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Data Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.qst</td>
<td>Output File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
</tbody>
</table>

Table 3.1: Command Line Options for Qstats

Another function of Qstats is to summarize the missing data for markers, traits and individuals. Following the histogram, there will be a table. For each trait, it will present a summary of missing data for each marker in turn. The table will consist of seven columns. The first three columns indicate the chromosome, marker number and name of the marker (if there is a marker name). The fourth column specifies what type of marker Qstats thinks it is. There are three types that are recognized. The first is codominant and is indicated by a “co” token. The other two are dominant markers and Qstats distinguishes between marker systems in which $A_1$ is dominant to $A_2$ (indicated by the token “A-”) and those in which $A_2$ is dominant to $A_1$ (“a-”). Column 5 has the counts of individuals with data for the marker, while column 6 has the counts of individuals with both marker and trait data. Column seven is just the ratio of columns 5 and 6.

At the end of the Qstats output file, there will be a summary of missing data for each individual in the data set. Qstats will indicate the number of marker systems, quantitative traits and categorical traits. It will then have a table with seven columns. Column 1 is for the individual. Column 2 indicates the number of markers for which the individual is typed, and Column 3 indicates a percent. Columns 4 and 5 do the same for traits while columns 6 and 7 summarize the data for categorical traits.

Something to keep in mind is that some of the analyses require large sample sizes. For example, if the sample sizes are too small, the ECM algorithm may fail in Zmapqtl. When difficulties in analysis are encountered, check the missing data summaries in the Qstats output: Such problems often correspond to areas with a lot of missing data.

3.1.2 Segregation

Qstats also tests for adherence to Mendelian segregation at all marker loci. For a given locus, suppose there are $r$ genotypic classes. Let $p_i$ be the expected frequency, and $n_i$ the observed count for the $i$th class. For a sample of size $n$, the expected counts will be $np_i$ and the observed frequencies will be $n_i/n$. We can construct a test statistics based on a contingency table

$$T_1 = \sum_{i=1}^{r} \frac{(n_i - np_i)^2}{np_i} = n \sum_{i=1}^{r} \frac{(n_i/n - p_i)^2}{p_i}$$
or a comparison of likelihoods

\[ T_2 = -2 \sum_{i=1}^{r} n_i (\ln n_i - \ln np_i) \]

Both \( T_1 \) and \( T_2 \) should have a \( \chi^2 \) distribution with one degree of freedom for backcrosses and recombinant inbred lines and two degrees of freedom for intercrosses. Both statistics are calculated and presented in a table in the \texttt{Qstats} output.

### 3.2 LRmapqtl

\texttt{LRmapqtl} fits the data to a simple linear regression model. For each marker in turn, it fits a simple linear model to the trait data. It is a quick way to get an idea of where the QTLs may reside.

#### 3.2.1 Simple Linear Regression

For each marker in turn, \texttt{LRmapqtl} fits the phenotypic data to the linear model

\[ y_i = b_0 + b_1 x_i + e \]  

(3.2)

where \( y_i \) is the phenotype of the \( i \)th individual and \( x_i \) is an indicator variable for the marker genotype. Generally,

\[
  x_i = \begin{cases} 
    2 & \text{if } A_1A_1 \\
    1 & \text{if } A_1A_2 \\
    0 & \text{if } A_2A_2 
  \end{cases}
\]

but for \( B_1 \) crosses

\[
  x_i = \begin{cases} 
    1 & \text{if } A_1A_1 \\
    0 & \text{if } A_1A_2 
  \end{cases}
\]

If the marker is missing or dominant, then an expected value for the marker is calculated from the flanking markers (Fisch, Ragot, and Gay 1996; Jiang and Zeng 1997). The regression parameters \( b_0 \) and \( b_1 \) can be estimated, and \( e \) is assumed to have a normal distribution.

\texttt{LRmapqtl} can also take into account categorical traits, that is other variables such as sex or brood, in its analysis. If your data set contains such information, then there should be a list of the names of these other variables near the beginning of the “Rcross.out” formatted file. These names might look as follows:

- Names of the other traits...
  1. Sex
  2. Line

If you would like to include “Sex” and “Sex by Marker interaction” terms in your analysis, then you need to indicate as much to \texttt{LRmapqtl}. If you prefix the name of one of these variables with a plus sign (+), then it will be incorporated into the linear model.
CHAPTER 3. ANALYSIS

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Data Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.lr</td>
<td>Output File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-r</td>
<td>0</td>
<td>Number of permutations</td>
</tr>
<tr>
<td>-t</td>
<td>1</td>
<td>Trait to analyze</td>
</tr>
</tbody>
</table>

Table 3.2: Command Line Options for LRmapqtl

- Names of the other traits...
  1 +Sex
  2 Line

In LRmapqtl, this would consider both Sex and Sex by Marker interaction terms. In Zmapqtl and SRmapqtl, the Sex by Marker term wouldn’t be incorporated, but the Sex factor would. All other variables that have no + sign at the beginning of their names will be ignored in the analysis. For the above example, a pair of models will be considered:

\[
y_i = b_0 + b_1x_i + b_2Sex + b_3Sex \times x_i + e \quad (3.3)
\]
\[
y_i = b_0 + b_2Sex + e \quad (3.4)
\]

The output will give probabilities that the marker is significant.

Table 3.2 shows the command line options specific to LRmapqtl. As with Qstats, there are few parameters to change. The -t option allows you to specify a trait to analyze. It is trait 1 by default. If you only have one trait, you can ignore this option. If your data set has more than one trait, you can analyze a specific trait by using -t with an integer from 1 to the number of traits. If you want LRmapqtl to analyze all traits, use a value greater than the number of traits.

3.2.2 Output

LRmapqtl prints out a histogram of the trait (identical to the one from Qstats), and the results of simple linear regression. The results are displayed in a table with seven columns. The first column indicates the chromosome, while the second gives the number of the marker on the chromosome. The name of the marker can be found in the genetic linkage map file. The next two columns correspond to the parameters in the linear model (Equation 3.2). Column three is the intercept and column four the slope of the least squares regression line fit to the data. Column five is a likelihood ratio test statistic for the model, and column six is the \(F\) statistic. Column seven is the tail probability of the \(F\) statistic assuming one and \(n-1\) degrees of freedom in the numerator and denominator, respectively. Asterisks attached to these probabilities indicate significance of the \(F\) statistics: Significance at the 5%, 1%, 0.1% and 0.01% levels are indicated by one, two, three and four asterisks, respectively.

The results of running LRmapqtl are used in Zmapqtl for analysis models four and five (see Section 3.4.2).
3.2.3 Permutation Tests

The \(-r\) option tells \texttt{LRmapqtl} to perform a permutation test (Churchill and Doerge 1994). The argument to \(-r\) indicates how many permutations should be performed. In each permutation, the phenotypes are shuffled relative to the genotypes over individuals and the analysis is redone. The results are summarized at the end of the \texttt{LRmapqtl} output file.

3.3 SRmapqtl

\texttt{SRmapqtl} uses the technique of stepwise regression to search for QTLs. For forward and backward regression, it simply ranks the markers for their effect on the quantitative trait. In forward stepwise regression (FS), each marker in turn is tested for its effect on the quantitative trait using linear regression. That marker with the largest partial F-statistic is assigned rank 1 and included in all subsequent analyses. Step two tests all the remaining markers, and assigns rank 2 to the marker with the largest partial F-statistic. This is repeated until all the markers have been ranked.

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.sr</td>
<td>Output File</td>
</tr>
<tr>
<td>-e</td>
<td>qtlcart.log</td>
<td>Error File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-s</td>
<td>860437285</td>
<td>Random Number Seed</td>
</tr>
<tr>
<td>-M</td>
<td>0</td>
<td>FS, BE or FB (0,1,2)?</td>
</tr>
<tr>
<td>-t</td>
<td>1</td>
<td>Trait to analyze</td>
</tr>
<tr>
<td>-F</td>
<td>0.1</td>
<td>Size: (p(F_{in}) =)</td>
</tr>
<tr>
<td>-B</td>
<td>0.1</td>
<td>Size: (p(F_{out}) =)</td>
</tr>
<tr>
<td>-u</td>
<td>100</td>
<td>Maximum number of steps</td>
</tr>
</tbody>
</table>

Table 3.3: Command Line Options for \texttt{SRmapqtl}

Backward elimination regression (BE) starts with all markers in the model. In the first step, each marker in turn is removed and a partial F-statistic is calculated. That marker with the smallest partial F statistic is given the lowest rank and removed from subsequent analyses. This is repeated until all the markers have been ranked.

The above methods seek only to rank the markers: They make no effort to determine whether adding or deleting a marker makes a significant difference for the fit of the model to the data. A third method (FB) is to start with forward stepwise regression, but only keep adding markers while the p-value of the partial F statistic of the marker to be added is below a defined threshold, \(p(F_{in})\). When a step is reached in which no more markers can be added, all of the markers are retested to see if they are still significant. Each marker in turn is deleted from the model, a p-value is calculated for the partial F-statistic, and if the p-value is greater than a specified level \(p(F_{out})\), it is deleted.
You can put a hard limit on the number of steps in the regression analysis with the -u option. The program has internal limits based on the sample size (it won’t allow more parameters than sample points), but you can lower this further. It defaults to 100, which is generally more markers than you will need to rank. If SRmapqtl seems to run forever, you might run it with this parameter set to a reasonable number, say 20.

As with LRmapqtl, any traits that begin with a plus sign are also used in the regression model. Unlike LRmapqtl, no interaction terms are used. The command line parameters for SRmapqtl are listed in Table 3.3. One added feature is that if you use the -t option with an integer value one greater than the number of traits, then all traits will be analyzed in turn.

3.3.1 Output

For the specified trait, SRmapqtl will output a small table:

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Marker</th>
<th>Rank</th>
<th>F-Stat</th>
<th>DOF</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>2</td>
<td>13.38778</td>
<td>114</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>4</td>
<td>10.12742</td>
<td>110</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>5</td>
<td>3.55528</td>
<td>108</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>3</td>
<td>11.15490</td>
<td>112</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>1</td>
<td>28.85236</td>
<td>116</td>
</tr>
</tbody>
</table>

The first two columns indicate the chromosome and marker. The third column gives the rank of that marker as determined by the stepwise regression mode of choice. Then there will be an F-statistic indicating the difference between having that variable in the model or not. Finally, the DOF (degrees of freedom) for the numerator of that F statistic is given. For forward stepwise or backward elimination, SRmapqtl will try to rank all of the markers no matter how small the F statistic is. For the forward regression with backward elimination, the program proceeds to add variables until the F statistic p-value is less than that specified by the -F option (0.1 by default). Then SRmapqtl rechecks all the variables added and will eliminate any with an F statistic p-value less than the value given with the -B option.

In general, the FB method is probably the best method for picking background markers to be used with model 6 in Zmapqtl and JZmapqtl. To this end, SRmapqtl should be run prior to using either module. Zmapqtl and JZmapqtl will read the results of SRmapqtl and use the markers that are ranked. You can specify an upper bound to the number of background parameters to be used in Zmapqtl. JZmapqtl will use all the markers that are listed for all traits in its analysis: The FB method thus selects only a subset of significant markers.

Be aware that SRmapqtl tries to determine how many markers can be analyzed at once. The number of parameters has to be smaller than the sample size. If you try to use
backward regression, and there are more markers than individuals, then SRmapqtl will
default to forward stepwise regression and rank as many markers as possible. You should
be aware that when dominance can be estimated, each marker will count two towards the
total number of parameters and you will need a sample size of at least twice the number of
markers to do backward elimination.

3.4 Zmapqtl

Zmapqtl implements interval and composite interval mapping. There are also options to
perform a permutation test (Churchill and Doerge 1994; Doerge and Churchill 1996).

3.4.1 Computational Methodology

Composite interval mapping (Zeng 1993; Zeng 1994) combines interval mapping with mul-
tiple regression. The statistical model is defined as

\[ Y = x^*b^* + z^*d^* + XB + E \]  

(3.5)

where

- \( Y \) is a vector of trait values
- \( b^* \) and \( d^* \) are the additive and dominance effects of the putative QTL being tested
- \( x^* \) and \( z^* \) are indicator variable vectors specifying the probabilities of an individual
  being in different genotypes for the putative QTL constructed by flanking makers
- \( B \) is the vector of effects of other selected markers fitted in the model
- \( X \) is the marker information matrix for those selected markers
- \( E \) is the error vector.

Estimates of the parameters are obtained by maximum likelihood through an ECM
(for Expectation/Conditional Maximization) algorithm (Meng and Rubin 1993). In each
E-step, the probability of an individual being in different genotypes of the putative QTL is
updated. In the CM-step, the estimation of parameters \( b^* \) and \( d^* \) is separated from that of
\( B \), and each group is estimated conditional on the others. This procedure is implemented
for numerical consideration. As \( x^* \) and \( z^* \) are separated from \( X \), \( X \) is unchanged in each
iteration, and its costly recalculation is avoided.

For an \( F_2 \) population, the hypotheses for testing are \( H_0 : b^* = 0 \) and \( d^* = 0 \) and
\( H_3 : b^* \neq 0 \) or \( d^* \neq 0 \). This is performed through a likelihood ratio test procedure. In
addition, it is possible to test hypotheses on \( b^* \) and \( d^* \) individually. For a backcross data
set, dominance cannot be estimated and \( d^* \) is dropped from Equation 3.5.

The trait will have a variance \( s^2 \). Under the null hypothesis

\[ H_0 : Y = XB + E \]
CHAPTER 3. ANALYSIS

the sample variance of the residuals will be $s^2_0$. For a given alternative model, say

$$H_1 : Y = x^* b^* + z^* d^* + X B + E$$

the variance of the residuals would be $s^2_1$. With this in mind we can calculate the proportion of variance explained by a QTL at the test site. The quantity is usually called $r^2$ and estimated by

$$r^2 = \frac{s^2_0 - s^2_1}{s^2}$$

An alternative estimate would use the total variance. Denote it by

$$r^2_t = \frac{s^2 - s^2_1}{s^2}$$

$r^2$ is the proportion of the variance explained by the QTL conditioned on the background markers and any explanatory variables. $r^2_t$ is the proportion of the total variance explained by the QTL and the the background markers and any explanatory variables. Generally, $r^2_t \geq r^2$

3.4.2 Models

When we speak of models for analysis, we mean to specify the markers used as cofactors in composite interval mapping. There are presently six models for analysis.

1. Use all the markers to control for the genetic background. This is model 1 from Zeng (1994).

2. Use all unlinked markers to control for the genetic background. This is model 2 from Zeng (1994).

3. Don’t use any markers to control for the genetic background. This is also known as interval mapping and is the same as Lander and Botstein’s method (Lander and Botstein 1989).

4. This is an ad-hoc model. One marker from each chromosome (except for the chromosome on which we are testing) is used to control for the genetic background. The results of LRmapqtl are scanned, and the marker that showed the highest test statistic from each chromosome is used.

5. This is another ad-hoc model. Two markers from each chromosome are used to control for the genetic background. They are the top two markers as determined by LRmapqtl. In addition, all the other markers on the chromosome of the test position that are more than 10 cM away from the flanking markers are also thrown in. It may be ad-hoc, but tends to work best at this time. The value of 10 centimorgans can be changed with the -w option.

6. Model six will be explained in the next subsection.
7. Model seven requires the results of a prior run of \texttt{Zmapqtl} and \texttt{Eqtl}. Initially, the user may want to run \texttt{Zmapqtl} with interval mapping, summarize the positions and effects of that analysis using \texttt{Eqtl}, and then use those estimates as the covariates in the regression model. Virtual markers are created at the best estimates for the positions of the QTLs.

8. Model eight is similar to model seven except that instead of using virtual markers, the nearest flanking markers to the putative QTL are used as cofactors. As in model seven, \texttt{Eqtl} is run after \texttt{Zmapqtl}, and a table of markers with arbitrary ranks are written to the \texttt{SRmapqtl.out} file. You should set the number of background parameters to more than the number of QTL identified by \texttt{Eqtl}.

\textbf{Zmapqtl Model Six}

Model 6 requires two additional parameters. One is the number of markers to control for the genetic background ($n_p$), and the other is a window size ($w_s$). When invoked, the program will read in the results of a prior run of \texttt{SRmapqtl} to pick the most important markers to control for the genetic background. Then, when testing at any point on the genome, it will use up to $n_p$ of these markers. If \texttt{SRmapqtl} didn’t rank as many markers as specified with $n_p$, then $n_p$ is reset to the number of markers ranked. The window size will block out a region of the genome on either side of the markers flanking the test site. Since these flanking regions are tightly linked to the testing site, if we were to use them as background markers we would then be eliminating the signal from the test site itself.

Note that if $w_s = 0.0$ and $n_p$ equals the total number of markers, then Model 6 reduces to Model 1. If $w_s$ is large (say the size of the largest chromosome) and $n_p$ equals the number of markers, then Model 2 is the result. If $n_p$ is zero, then Model 3 is the result. In the future, we will recommend that people use model 3 or model 6 for analysis. The default values of 5 for $n_p$ and 10 for $w_s$ should be good starting points for Model 6. Increasing $n_p$ will allow better resolution for mapping linked QTLs.

\textbf{3.4.3 Zmapqtl Options}

Table 3.4 shows the command line options specific to \texttt{Zmapqtl}. One can select a trait to analyze, a model for analysis and a walking speed along the genome (that is, the interval between successive analysis points). The user can analyze just one chromosome or the entire genome. Finally, permutation tests or bootstraps can be performed by setting the number of permutations or bootstraps to a number greater than 0. Explanatory variables such as Sex or Line are automatically included in the analysis if their names are preceded by a plus sign in the data file. This is similar to \texttt{LRmapqtl}, except that interaction terms are not yet used.

\textbf{Traits and Chromosomes}

The \texttt{-t} option allows the user to specify which trait in a data set with multiple traits is to be analyzed. For multiple trait analysis, use \texttt{JZmapqtl}. If you set the trait number to one
CHAPTER 3. ANALYSIS

QTL Cartographer

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.z</td>
<td>Output File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-l</td>
<td>qtlcart.lr</td>
<td>LRmapqtl Results file</td>
</tr>
<tr>
<td>-S</td>
<td>qtlcart.sr</td>
<td>SRmapqtl Results file (Model 6)</td>
</tr>
<tr>
<td>-M</td>
<td>3</td>
<td>Model</td>
</tr>
<tr>
<td>-t</td>
<td>1</td>
<td>Trait to analyze</td>
</tr>
<tr>
<td>-c</td>
<td>0</td>
<td>Chromosome to analyze</td>
</tr>
<tr>
<td>-d</td>
<td>2.0</td>
<td>Walking speed in cM</td>
</tr>
<tr>
<td>-n</td>
<td>5</td>
<td>Number of Background Parameters (Model 6)</td>
</tr>
<tr>
<td>-w</td>
<td>10.0</td>
<td>Window Size in cM</td>
</tr>
<tr>
<td>-r</td>
<td>0</td>
<td>Number of Permutations</td>
</tr>
<tr>
<td>-b</td>
<td>0</td>
<td>Number of Bootstraps</td>
</tr>
</tbody>
</table>

Table 3.4: Command Line Options for Zmapqtl

more than the total number of traits, then all traits (except for those whose names begin with a minus sign) will be analyzed in succession: This only works with models 1, 2, 3 and 6.

One can also limit the analysis to a single chromosome with the -c option.

Background Parameters and Window Sizes

For models 5 and 6, one can specify the size of the window ($w_s$) on either side of the test interval that is blocked from having markers in the background. This option is ignored for all models except 5 and 6. The number of background parameters ($n_p$) is only used with model 6 and is explained above.

Permutations, Bootstraps and Jackknives

Zmapqtl allows for permutation tests and bootstrap or jackknife resamplings. The former is a way to determine experimentwise significance levels and comparisonwise probabilities (Churchill and Doerge 1994; Doerge and Churchill 1996). Phenotypes are shuffled against genotypes and the analyses are redone. For each test position, the comparisonwise probability or $P$ value is the proportion of permuted datasets that have test statistics less than the observed data set test statistic. It should correspond to the probability of the observed test statistic assuming a $\chi^2$ distribution with one degree of freedom. For the experimentwise significance level, the highest test statistic in each permutation is recorded, and these are ordered at the end of the permutations. The 90, 95, 97.5 and 99th percentile values are then the experimentwise significance levels at $\alpha = 0.1$, 0.05, 0.025 and 0.01, respectively. Permutation tests are done for interval mapping within Zmapqtl, and interim results are stored in the files qtlcart.z3c and qtlcart.z3e. There are two distinct ways to perform the
permutation test in \textit{QTL Cartographer}. The first is simply to have \texttt{Zmapqtl} do the permuting and analysis: You would then use `-r` with the number of permutations to perform. If you choose to do the permutation test entirely within \texttt{Zmapqtl}, you must set the number permutations to a value larger than number of permutations already completed. In this way, if you started a permutation test and your machine crashed before the test was complete, you can restart \texttt{Zmapqtl} and finish it from where it left off.

An alternative way to do the permutation test is in a batch file. For composite interval mapping, one might want to reselect the background markers with \texttt{SRmapqtl} in each permutation. To this end, one would need to permute the traits, reselect the background markers and then run the composite interval mapping. The pseudo code example in Section 2.4.2 shows how to do this without the \texttt{SRmapqtl} step.

In the bootstrap, new datasets are created from the original by sampling with replacement. New datasets are the same size as the original. The statistics are redone and printed out. See the section \texttt{Prune} as to how to do bootstrapping.

<table>
<thead>
<tr>
<th>Interim file</th>
<th>Created during</th>
<th>Contains</th>
</tr>
</thead>
<tbody>
<tr>
<td>qtlcart.z6e</td>
<td>permutation test</td>
<td>Experimentwise state</td>
</tr>
<tr>
<td>qtlcart.z6c</td>
<td>permutation test</td>
<td>Comparisonwise state</td>
</tr>
<tr>
<td>qtlcart.z6a</td>
<td>bootstrap resampling</td>
<td>Iteration (i) bootstrap</td>
</tr>
<tr>
<td>qtlcart.z6b</td>
<td>bootstrap resampling</td>
<td>Iteration (i + 1) bootstrap</td>
</tr>
<tr>
<td>qtlcart.z6i</td>
<td>jackknife resampling</td>
<td>Iteration (i) jackknife</td>
</tr>
<tr>
<td>qtlcart.z6j</td>
<td>jackknife resampling</td>
<td>Iteration (i + 1) jackknife</td>
</tr>
</tbody>
</table>

Table 3.5: Examples of Interim Files for Model 6

Jackknife resampling is performed by calculating \(n\) (the sample size) new estimates of the parameters: The \(i\)th estimate is calculated by deleting individual \(i\) from the dataset. The standard deviation over these \(n\) new estimates provides an estimate of the standard deviation for the test statistic and additive and dominance effects. You invoke the Jackknife by setting the number of bootstraps to 2. \texttt{Zmapqtl} uses two interim files to perform the jackknife. If you are using Model 6 in \texttt{Zmapqtl} and your filename stem is qtlcart, then these files will be called qtlcart.z6i and qtlcart.z6j. These files contain the sum and sum of squares up to the previous and current iteration, as \texttt{Zmapqtl} runs. Initially, the qtlcart.z6i file contains columns of zeros: This is the sum before any iterations are performed. Subsequently, qtlcart.z6j will contain the interim state after each odd-numbered iteration, while qtlcart.z6i will contain the state after each even-numbered iteration. If individual \(i\) has no trait data, then the \(i\)th iteration will be skipped. For this reason, one cannot be sure that the file ending in “\(j\)” is the last iteration for odd sample sizes. It is best to look at both files at the conclusion of a jackknife experiment, and rename the interim file with the greater number of iterations to qtlcart.z6i. It this is done, then \texttt{Eqtl} will recognize it and calculate the means and sample standard deviations of the test statistic and effects.

To clarify the interim file names, we consider an example using Model 6 in \texttt{Zmapqtl} and the default filename stem “qtlcart”. Table 3.5 lists the interim file names. \texttt{Eqtl} auto-
matically looks for files named “qtlcart.z6e”, “qtlcart.z6a” and “qtlcart.z6i”. These files will be processed and the appropriate calculations done. Eqtl will overwrite the “qtlcart.z6b” and “qtlcart.z6j” files after completing its calculations, so if you want to save them, do so before running Eqtl. If you chose to use another model (say model 3), then the “6” in the filenames of Table 3.5 would be a “3”.

3.4.4 Output

Here is a truncated example of the output of Zmapqtl for a backcross.

```plaintext
# 890840384  -filetype Zmapqtl.out
# QTL Cartographer V. 1.13b, March 1998
# This output file (qtlcart.z) was created by Zmapqtl...
# It is 10:39:44 on Wednesday, 25 March 1998
#
#
#The position is from the left telomere on the chromosome
-window 10.00 Window size for models 5 and 6
-background 5 Background parameters in model 6
-Model 6 Model number
-trait 1 Analyzed trait [Trait_1]
cross B2 Cross
# Test Site  * Like. Ratio Test Statistics  *  Additive
   c  m position H0:H1 R2(0:1) TR2(0:1) H1:a S1
-3
1  1  0.0001  0.411  0.002  0.473  0.027  1.531
1  2  0.0133  0.016  0.000  0.472  0.005  1.542
1  2  0.0333  0.023  0.000  0.472  0.006  1.547
1  2  0.0533  0.031  0.000  0.472  0.008  1.554
1  2  0.0733  0.041  0.000  0.472  0.009  1.563
1  2  0.0933  0.052  0.000  0.472  0.010  1.572
1  2  0.1133  0.063  0.000  0.472  0.011  1.582
1  2  0.1333  0.073  0.000  0.472  0.012  1.593
...
```

For a backcross, let $a$ be the additive effect. We have two hypotheses:

- $H_0$: no QTL effect at the test position, i.e. $a = 0$
- $H_1$: There is a QTL effect at the test position, i.e. $a \neq 0$

The first eight columns correspond to

1. Chromosome of test position
2. Left flanking marker of test position
3. Absolute position from left telomere, in Morgans.

4. Likelihood ratio test statistic for $H_1 / H_0$. It is a $\chi^2$ random variable with one degree of freedom for any position, meaning that a value of 3.84 or higher is evidence for a QTL. The significance level over more positions will be higher due to multiple testing.

5. $r^2$

6. $r^2_t$

7. Estimate of $a$ (the additive effect) under $H_1$

8. Test statistic $S$ for the normality of the residuals under $H_1$

The last 13 columns are not shown because they are only valid for $F_2$ design experiments. They would all be zeros if shown.

The output for an $F_2$ design (or any design in which dominance effects can be estimated) is similar, but has more information. For an $F_2$, you can estimate additive ($a$) and dominance ($d$) parameters at each position. Thus, there are four hypotheses.

- $H_0$: $a = 0$, $d = 0$
- $H_1$: $a \neq 0$, $d = 0$
- $H_2$: $a = 0$, $d \neq 0$
- $H_3$: $a \neq 0$, $d \neq 0$

and twelve full columns of output, corresponding to all possible hypothesis tests and parameter estimates. The 21 columns correspond to

1. Chromosome of test position.
2. Left flanking marker of test position.
3. Absolute position from left telomere, in Morgans.
4. Likelihood ratio test statistic for $H_2 / H_0$.
5. Likelihood ratio test statistic for $H_1 / H_0$.
6. Likelihood ratio test statistic for $H_3 / H_0$.
7. Estimate of $a$ (the additive effect) under $H_1$.
8. Estimate of $a$ (the additive effect) under $H_3$.
9. Estimate of $d$ (the dominance effect) under $H_2$.
10. Estimate of $d$ (the dominance effect) under $H_3$.
11. Likelihood ratio test statistic for $H_2 / H_0$.
12. Likelihood ratio test statistic for $H_1 / H_0$.
13. $r^2$ for $H_2 / H_0$.
14. $r^2$ for $H_1 / H_0$. 
15. $r^2$ for $\frac{H_3}{H_0}$.
16. $r^2$ for $\frac{H_1}{H_0}$.
17. $r^2$ for $\frac{H_2}{H_0}$.
18. $r^2$ for $\frac{H_3}{H_0}$.
20. $S$ for $H_2$.

**Permutation Test output**

If you chose to do a permutation test (Churchill and Doerge 1994) for the purpose of estimating experiment specific threshold values, `Zmapqtl` will create two auxiliary files to store interim comparisonwise and experimentwise test statistics. If the filename stem is “qtlcart” and the model for analysis is “6”, then these files will be “qtlcart.z6c” and “qtlcart.z6e”. The former file should look something like this:

```
#Row Chrom Mark Position Original P-Val Count -perm 899
-start
 1 1 1 0.00010 0.00000 0.982202 883
 2 1 1 0.02010 0.00000 0.976641 878
```

whose columns are

1. Integer indicating the row.
2. Chromosome of test position.
3. Left flanking marker of test position.
4. Absolute position of test from left telomere, in Morgans.
5. Likelihood ratio test statistic of actual data. For backcrosses, this is $\frac{H_1}{H_0}$, while for $F_2$’s, it is $\frac{H_3}{H_0}$.
6. Proportion of permuted data sets with an LR greater than or equal to the observed LR.
7. Actual count of the number of permuted data sets with an LR greater than or equal to the observed LR.

In each step of the permutation test, this file is rewritten and the number following the “-perm” token incremented. This way, if the computer crashes during a run, `Zmapqtl` can be restarted from where it left off. If you were running `Zmapqtl` with 1,000 permutations, and the process stopped at 899 as above, then restarting `Zmapqtl` with 1,000 permutations will begin with permutation 900 and continue to 1,000.
The second file, “qtlcart.z6e”, will contain two columns of numbers: the permutation and the maximal likelihood ratio over the genome in that permutation. Each permutation will add a line to the output. When enough permutations have been done, Eqtl can be run to summarize the experimentwise levels. A small table will be written to the log file that looks like:

```
-start
   Performed 899 permutations of the phenotypes and genotypes
Here are the Experimentwise significance levels for different alpha
Permutation significance level for alpha = 0.1 : 11.6858
Permutation significance level for alpha = 0.05 : 13.3108
Permutation significance level for alpha = 0.025 : 14.6669
Permutation significance level for alpha = 0.01 : 16.8008
-end of shuffling results
```

For each shuffle, the largest likelihood ratio test statistic over all test positions is saved in the file. At the end of the shuffling, these maximum values are sorted, and the \((1 - \alpha) \times 899\) th largest is the experimentwise significance level for a test of size \(\alpha\). The number of permutations can be changed from 899 to any integer from 0 to 10,000. This upper bound could be made higher by changing the appropriate definition in the Main.h source file and recompiling. In general, we find that 1000 permutations is a sufficient number. In a test, values of 1000 and 17,000 were used with little difference in the ultimate comparisonwise and experimentwise values.

### 3.5 JZmapqtl

**JZmapqtl** implements interval and composite interval mapping for multiple traits (Jiang and Zeng 1995). It is very similar to **Zmapqtl** except that it can jointly analyze more than one trait. It is best used after **Zmapqtl** when one suspects that two traits are correlated.

#### 3.5.1 JZmapqtl Options

Table 3.6 shows the command line options specific to **JZmapqtl**. Most are the same as those for **Zmapqtl**. One thing to note is that there is no facility for permutation tests or bootstraps at this time.

#### 3.5.2 Output

**JZmapqtl** will create a number of different output files depending on the number of traits in the joint analysis. There will be one file per trait that has estimates for the parameters for that trait. These files will end in `.z#`, where `#` is a number indicating the trait. There will be one other file, ending in `.z0` that contains the results of the joint likelihood ratio.

The joint results file ending in `.z0` will have four columns corresponding to the chromosome, marker, markername and test position. Then there will be column giving the joint likelihoods for the test position for all possible hypothesis tests (see next section).
CHAPTER 3. ANALYSIS

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Input File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.z</td>
<td>Output File</td>
</tr>
<tr>
<td>-e</td>
<td>qtlcart.log</td>
<td>Error File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-S</td>
<td>qtlcart.sr</td>
<td>SRmapqtl results (Model 6)</td>
</tr>
<tr>
<td>-E</td>
<td>qtlcart.eqt</td>
<td>Eqtl results (Model 7)</td>
</tr>
<tr>
<td>-s</td>
<td>893339277</td>
<td>Random Number Seed</td>
</tr>
<tr>
<td>-M</td>
<td>3</td>
<td>Model [3,6,7], 3=&gt;1M</td>
</tr>
<tr>
<td>-t</td>
<td>1</td>
<td>Trait to analyze</td>
</tr>
<tr>
<td>-c</td>
<td>0</td>
<td>Chromosome to analyze (0=all)</td>
</tr>
<tr>
<td>-d</td>
<td>2.000000</td>
<td>Walking speed in cM</td>
</tr>
<tr>
<td>-n</td>
<td>5</td>
<td>Number of Background Parameters (Model 6)</td>
</tr>
<tr>
<td>-w</td>
<td>10.000000</td>
<td>Window Size in cM (Model 6)</td>
</tr>
<tr>
<td>-I</td>
<td>1</td>
<td>Hypothesis test</td>
</tr>
</tbody>
</table>

Table 3.6: Command Line Options for JZmapqtl

The single trait files, ending in .z#, will have the results for the numbered trait. In addition to the chromosome, marker, markername and test position, the likelihood ratio and parameter estimates will be given. All columns are labelled, and the parameters are the same as explained in the Zmapqtl section.

3.5.3 Usage Hints

Trait Selection

You can select traits to include in the analysis in three ways. Suppose that you have \( t \) traits in your data file.

1. Set the trait to analyze at 0, so that no traits except those beginning with a + (plus sign) are analyzed. You would need to edit the .cro file first to prepend a + to all traits you want in the analysis.

2. Set the trait to a value in the range 1 – \( t \), inclusive. You will then get single trait results for the selected trait.

3. Set the trait to a value greater than \( t \). All traits will be put in the analysis, unless they begin with a – (minus sign).

Hypothesis tests

You need to set the hypothesis test for \( SF_x \) and \( RF_x \) crosses. The default of 1 is fine for crosses in which there are only two marker genotypic classes (backcrosses and recombinant
inbreds). For \( SF_x \) and \( RF_x \), values of 30, 31 or 32 are valid. Recall that we have the following hypotheses:

1. \( H_0 : a = d = 0 \)
2. \( H_1 : a \neq 0, d = 0 \)
3. \( H_2 : a = 0, d \neq 0 \)
4. \( H_3 : a \neq 0, d \neq 0 \)

For 30, we test \( H_3 : H_0 \). For 31, we test \( H_3 : H_0, H_3 : H_1 \) and \( H_1 : H_0 \). For 32, we test \( H_3 : H_0, H_3 : H_2 \) and \( H_2 : H_0 \). 30 is probably fine for initial scans.

Also, if you do only have two genotypic classes, then 10 is the same as 1 for the hypothesis test.

Model 6

For Model 6, be sure to run \texttt{SRmapqtl} first. Once done, \texttt{JZmapqtl} will use all markers that are significant for any of the traits in the analysis. We need to work out a better way to select the cofactors. Now it uses any markers that are significant for any trait. Also, be sure to use FB regression, or else you will end up using all markers as cofactors.

It is a good idea to edit the \texttt{SRmapqtl.out} file prior to running \texttt{JZmapqtl} with model 6. It might be best to pick out the top two or three ranked markers for each trait so as not to use too many cofactors.

G x E Analysis

One special case of G x E analysis has been incorporated into \texttt{JZmapqtl}, namely the situation where a set of genotypes is raised in more than one environment. The value of the trait in each environment is treated as a separate trait for the common genotype. For this type of data, use hypothesis 14 or 34 to invoke the G x E analysis. Hypothesis 14 is for data with two marker genotypes, while 34 is for three marker genotypes. There will be an extra column in the output that give a likelihood ratio for a G x E effect versus no effect. When running Eqtl subsequent to doing a G x E analysis, be sure to specify the same hypothesis test.

3.6 MImapqtl

MImapqtl implements QTL mapping analysis for multiple QTL in multiple intervals for a single trait in a single environment. It can begin analysis from an initial model specifying the positions of QTL, or \textit{de novo}, that is with no initial model. If given an initial model, the program will estimate the parameters, refine the estimates of QTL positions within intervals, test the significance of all parameters, search for more QTL, search for epistatic interactions and finally calculate the \( r^2 \) and breeding values for the model. If analysis is initiated \textit{de novo}, then there will be a search for QTL, a search for interactions and
calculation of $r^2$ and breeding values. **MImapqtl** can also do a single pass search for a new QTL and create a likelihood ratio profile for a new putative QTL given any initial model.

For $m$ putative QTL, the model is

$$y_i = \mu + \sum_{r=1}^{m} \alpha_r x_{ir}^* + \sum_{r=1}^{m} \delta_r z_{ir}^* + \sum_{r \neq s} \beta_{rs}^{AA} x_{ir}^* x_{is}^* + \sum_{r \neq s} \beta_{rs}^{AD} x_{ir}^* z_{is}^*$$

$$+ \sum_{r \neq s} \beta_{rs}^{DA} z_{ir}^* x_{is}^* + \sum_{r \neq s} \beta_{rs}^{DD} z_{ir}^* z_{is}^* + e_i$$

(3.6)

where $y_i$ is the trait and $e_i$ the residual for individual $i$. The parameters $\alpha_r$, $\delta_r$ are the additive and dominance effects of QTL $r$. The $\beta$’s are epistatic interactions. The superscripts on the $\beta$’s are for the type of interaction: We distinguish between additive by additive (AA), additive by dominance (AD), dominance by additive (DA) and dominance by dominance (DD) interactions. There is also a mean denoted by $\mu$ and a variance for the residuals ($\sigma^2$) which are assumed to have a normal distribution and mean zero. The $x^*$ and $z^*$ are coded variables denoting the genotype of the putative QTL. If there are only two marker genotypic classes, the $z^*$’s are all set to zero. Otherwise, $z_{ir}^* = 0.5$ for a heterozygote and $-0.5$ for a homozygote. The $x_{ir}^*$ are defined differently for different crosses and are shown in Table 3.7.

The sum over $r \neq s$ means over all unordered QTL pairs and we use the convention $r > s$.

<table>
<thead>
<tr>
<th>z*</th>
<th>x*</th>
</tr>
</thead>
<tbody>
<tr>
<td>QQ</td>
<td>B1</td>
</tr>
<tr>
<td>-1/2</td>
<td>1/2</td>
</tr>
<tr>
<td>Qq</td>
<td>1/2</td>
</tr>
<tr>
<td>qQ</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 3.7: Coded variables

The likelihood function of the data given the model is a mixture of normal distributions

$$L(E, \mu, \sigma^2 | Y, X) = \prod_{i=1}^{n} \left[ \sum_{j=1}^{g^m} p_{ij} \phi(y_i | \mu + D_j E, \sigma^2) \right]$$

(3.7)

In (3.7), the $p_{ij}$ are the probabilities of the multilocus genotypes conditioned on marker data. The variable $g$ is the number of genotypic classes for the experimental design: For backcrosses and recombinant inbred lines, $g = 2$, while for intercrosses it is $g = 3$. In practice, it is often infeasable to do the sum over all $g^m$ multilocus genotypes: We use a subset of the most frequent genotypes. The parameters are in $E$ while the coded indicator variables are in $D$. $\phi(y_i | \mu, \sigma^2)$ is the normal density function with mean $\mu$ and variance $\sigma^2$. We use an EM (expectation maximization) algorithm to obtain maximum likelihood parameter estimates (Kao and Zeng 1997; Zeng, Kao, and Basten 1999).

3.6.1 **MImapqtl Options**

Table 3.8 shows the command line options specific to **MImapqtl**.
CHAPTER 3. ANALYSIS

Table 3.8: Command Line Options for MImapqtl

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-i</td>
<td>qtlcart.cro</td>
<td>Data File</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.mim</td>
<td>Output File</td>
</tr>
<tr>
<td>-e</td>
<td>qtlcart.log</td>
<td>Error File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-E</td>
<td>qtlcart.eqt</td>
<td>Initial model file</td>
</tr>
<tr>
<td>-O</td>
<td>qtlcart.mqt</td>
<td>Output model file</td>
</tr>
<tr>
<td>-s</td>
<td>1590337669</td>
<td>Random Number Seed</td>
</tr>
<tr>
<td>-t</td>
<td>1</td>
<td>Trait to analyze</td>
</tr>
<tr>
<td>-q</td>
<td>19</td>
<td>Maximum number of QTL to fit</td>
</tr>
<tr>
<td>-k</td>
<td>19</td>
<td>Maximum number of epistatic interactions</td>
</tr>
<tr>
<td>-d</td>
<td>2.000000</td>
<td>Walking speed in cM</td>
</tr>
<tr>
<td>-S</td>
<td>1</td>
<td>Information criterion [1-6]</td>
</tr>
<tr>
<td>-L</td>
<td>0.000000</td>
<td>Threshold for adding/dropping parameters</td>
</tr>
<tr>
<td>-I</td>
<td>smprtSeC</td>
<td>Work code</td>
</tr>
<tr>
<td>-p</td>
<td>0</td>
<td>Phase of analysis</td>
</tr>
</tbody>
</table>

If you choose to begin analysis from some initial model, it should be formatted as an Rqtl output file and specified with the -E option. For data sets with multiple traits, you can specify the trait to analyze with the t option. If the specified trait is 0, then all traits whose names begin with a plus sign (+) will be analyzed (one at a time). If the specified trait is larger than the number of traits, then all traits will be analyzed one at a time, unless their names begin with a minus sign (−).

You may specify a maximal number of QTL and epistatic interactions to fit in the model. The limitations of C on a 32 bit computer mean that you can only fit up to 19 QTL in a cross with three marker genotypes (SFx and RFx lines). Thus, 19 will be a hard limit on the number of loci at this time. In practice, it is not wise to try to fit more than $2\sqrt{n}$ parameters, where $n$ is the sample size. Thus, MImapqtl will automatically adjust this number so that it is no greater than $2\sqrt{n}$ for backcrosses and recombinant inbred lines, $\sqrt{n}$ for lines with three marker genotypes (since each QTL has an additive and a dominance effect). Once main effects are fitted for the QTL, MImapqtl searches for epistatic effects. Again, it will only try to fit up to $2\sqrt{n}$ parameters so only $2\sqrt{n}$ minus the number of main effects will be fitted. For example, if you have a sample size of 400, then $2\sqrt{400} = 40$. For an SF2 line, if you find 10 QTL, then 20 parameters have been fitted (10 additive and 10 dominance effects). Thus, there will be up to $40 - 20 = 20$ possible epistatic effects that can be fitted.

The walking speed is identical to that in Zmapqtl and JZmapqtl and is used during the refinement of QTL positions and the search for new QTL. For the refinement of QTL position, for each QTL, the position is moved within the QTL interval from one end to the other and an information criterion is calculated for each position. The minium over the
interval is the best position for the QTL.

The information criterion is a function of the likelihood ratio and the number of parameters that gives an indication of how good the model fits the data. This is a function in form

$$I(L_k, k, n) = -2(\log(L_k) - kc(n)/2)$$

where $L_k$ is the likelihood for a $k$ parameter model and $c(n)$ is a penalty function and $\log$ is the natural log function. The penalty function $c(n)$ takes one of six forms:

1. $c(n) = \log(n)$ (Schwarz 1978)
2. $c(n) = 2$ (Akaike 1969)
3. $c(n) = 2\log(\log(n))$ (Hannan and Quinn 1979)
4. $c(n) = 2\log(n)$ (Broman 1997)
5. $c(n) = 3\log(n)$ (Broman 1997)
6. $c(n) = 0$

Use the numbers above with the `-S` option to indicate which information criterion you want to use. When comparing a model with $k$ parameters to one with $k - 1$ parameters, if $I(L_{k-1}, k - 1, n) - I(L_k, k, n)$ is greater than the threshold value specified with the `-L` option, then the parameter is considered significant. During a scan over the entire genome, if the maximum of $I(L_{k-1}, k - 1, n) - I(L_k, k, n)$ is greater than the threshold, then that position parameter is retained. A non-zero penalty function supersedes the requirement of a true threshold. Therefore, if using one of the first five penalty functions, you can use a threshold of 0.0. For function six (that is, no penalty), it is best to do a permutation test to determine the initial threshold.

In general, it is probably best to start with information criterion 1 with a threshold of 0.0. We have done some initial simulations to support the utility of this approach. If no QTL are identified using information criterion 1, then one could use no penalty function and do a permutation test for the threshold.

Phase of Analysis

It is often a good idea to rerun an analysis for various reasons. Think of each run as a “phase” or step. For example, the first phase might be to identify QTL main effects. The second phase would then test the significance of each QTL just identified. The third phase might be to refine the positions of the remaining QTL and the fourth phase to estimate interactions. It is convenient to use the phase variable for this type of analysis. The phase variable, if set to an integer value greater than zero, will modify the names of the output file and the model input and output files. For a filename stem `qtlcart` and phase $N$, the output file will be `qtlcartPhaseN.mim`. The output model will be placed in `qtlcartPhaseN.mqt`, and the input model will be assumed to be `qtlcartPhaseN-1.mqt`. The phase variable is set with
the -p option, and if greater than zero, will be incremented at the end of each successful run of MImapqtl.

Here is a sequence using the example dataset mletest.cro along with its map file mletest.map, both of which come with the programs. Assume that these two files have been placed in an empty subdirectory which is now the current working directory.

\[
\%
MImapqtl -A -V -I smprtSeC -L 0.0 -S 1 -p 1 -X mletest &
\]

\[
\%
MImapqtl -A -V -I sMPrTseC &
\]

\[
\%
MImapqtl -A -V -I sMPRtseC &
\]

\[
\%
MImapqtl -A -V -I sMPrtsBC &
\]

The first invocation sets the filename stem, the information criterion and threshold for adding parameters and indicates that it is phase 1. The -I option tells MImapqtl to search for additive QTL. The second invocation tests each QTL found in the first phase. The third step refines the positions of all remaining QTL. The fourth step searches for more QTL (and probably won’t find any). The fifth step searches for interactions between the identified putative QTL. The phase variable is updated after each step, so MImapqtl knows where to find the results from the previous step. The work code specified by the -I option is explained in the next section.

**Work Code**

The Work Code must be specified with an eight (8) letter string. Each letter in the string is a flag to tell the program whether to do a certain step. Some of the flags have options to modify the behavior of that step. The eight letter string starts from position 0 and continues on to position 7. In general, a lower case letter indicates that the function should be skipped, while an upper case letter tells MImapqtl to do the step. The labels on the items below indicate the positions.

0. Scan flag

This can take on values S or s. If S, then MImapqtl will go into scan mode, that is it will scan the genome for a new QTL beginning with any model. At the end of this scan, it will print out a likelihood profile for the existence of a new QTL. The user can then plot the values and decide where to place a new QTL.

1. Model flag

This flag tells MImapqtl whether to use the initial model specified with the -E option. If M, then MImapqtl will begin its analysis with the initial model. If m, then it will start the analysis from a state with no QTL. If you use m, then you should also specifyprt in positions 2, 3 and 4. For example, smprtSEC would make sense: It would search for QTL de novo.

2. Parameter flag
Use a \textbf{P} here if you want \texttt{MImapqtl} to re-estimate the parameters in the initial model. Use a \texttt{p} if you want to skip this step. The case of this position should almost always match that of position 1: It makes little sense to estimate parameters in a model without any parameters.

3. Refine position flag

Use an \textbf{R} here if you want \texttt{MImapqtl} to refine the position estimates in the initial model. Use an \texttt{r} if you want to skip this step. If you don’t have an initial model, then this should be \texttt{r}. This is most useful if your initial model was generated from a run of \texttt{Zmapqtl} or \texttt{JZmapqtl}. The \textbf{R} value causes the position to be optimized within the current interval. If you want to extend the refinement to adjacent intervals, use \textbf{A}.

4. Test flag

For initial models, you may want to test the significance of all parameters before searching for new QTL. Use a \textbf{T} here if you want \texttt{MImapqtl} to test the significance of the parameters in the initial model. Use a \texttt{t} if you want to skip this step. If you don’t have an initial model, then this should be \texttt{t}. This position also allows you to test the dominance effects alone: You can use \texttt{D} in place of \texttt{T}. Finally, you can test the current set of epistatic interactions by using a \textbf{E} in this position.

5. Search flag

Use an \textbf{S} here if you want \texttt{MImapqtl} to search for more QTL. Use an \texttt{s} if you want to skip this step. You can also specify an \textbf{A} if you only want to search for the additive effects of putative QTL (that is, don’t search for dominance effects in crosses with three marker genotypes). Finally, if you use a \texttt{D} here, \texttt{MImapqtl} will only search for dominance effects at putative QTL locations that don’t already have them.

6. Epistasis flag

Use an \textbf{E} here if you want \texttt{MImapqtl} to search for epistatic effects. Use an \texttt{e} if you want to skip this step. If you want to use a backward elimination approach, then use a \textbf{B} in this position. The backward elimination approach will only be used if the number of possible interactions plus the number of main effects is less than \(2\sqrt{n}\). If you want to relax this restriction, then use a \textbf{U} in place of the \textbf{B}.

7. Covariance flag

Use a \textbf{C} here if you want \texttt{MImapqtl} to calculate the variance-covariance matrix, \(r^2\) values and breeding values for the final model. Use a \texttt{c} if you want to skip this step. You may also use an \textbf{R} in this position. In that case, \texttt{MImapqtl} will calculate the residuals for the final model, replace the trait values with the residuals and print out a new data set with the same markers to a file (\texttt{stem.res} by default, where \texttt{stem} is the filename stem). If the phase variable is set to a number \(N\) greater than zero, then the residual data set will be written to \texttt{stemPhaseN.res}. The \textbf{C} and \textbf{R} options are mutually exclusive.
CHAPTER 3. ANALYSIS

The default work code is \texttt{smprtSeC}, which searches for QTL starting with an initial model containing no QTL. If you want to do an analysis within an initial model, then \texttt{sMPrtSeC} would be appropriate. For a scan to find a new QTL, you might use \texttt{SPrtSec} recursively, adding a QTL in each step.

If you have a model and simply want to create a new data set with the residuals replacing the traits, then use \texttt{sMPrtseR} as the work code.

3.6.2 QTL Search

For a model with \( k \) QTL and information criterion \( I(L_k, k, n) \), we search for \( k + 1 \)st QTL over all intervals that do not presently have a QTL in them. For each of these intervals, we walk along the interval and calculate the information criterion \( I(L_{k+1}, k + 1, n) \) for the presence of a QTL. We keep track of the minimum information criterion (equivalent to the maximum likelihood) within each interval. When all intervals have been tested, the minimum over intervals is determined and compared to the information criterion of the \( k \) QTL model. If \( I(L_k, k, n) - I(L_{k+1}, k + 1, n) \) is greater than the threshold, the QTL at that site is retained in the model. The process repeats until no new QTL are retained.

If \texttt{MImapqtl} is run in scan mode (\texttt{S} in position 0 of the work code), then the quantity \( I(L_k, k, n) - I(L_{k+1}, k + 1, n) \) is written to the output file for each tested position. This yields a likelihood ratio profile giving the strength of evidence for a new QTL at the tested sites.

For crosses with three marker genotypic classes, both an additive and a dominant effect are added when testing for a new QTL. One can scan for additive effects only with the \texttt{A} option used in position five of the work code. If a \texttt{D} is used in this position, the search for dominance effects is restricted to previously identified QTL.

3.6.3 Epistatic Interactions

Once QTL have been identified, the program can search for interactions. For each pair of QTL, the information criterion is calculated with an interaction effect. The minimum over all pairs is compared to the information criterion of a model without the epistatic effect. If the difference is greater than the threshold, the effect is retained and the process is repeated. In each step, the new effect is tested within the backgound of all the QTL main effects as well as previously identified interactions.

For crosses with two marker genotypic classes, only additive by additive effects are tested. For those with three classes, additive by dominance, dominance by additive and dominance by dominance effects are also tested.

By default, \texttt{MImapqtl} does a forward stepwise search for epistatic terms. If you want to try a backward elimination approach, use a \texttt{B} instead of an \texttt{E} in the appropriate position. Also, be aware that if there are too many epistatic terms, the request for a backward elimination approach will be ignored in favor of a forward search. \texttt{MImapqtl} only allows for \( 2\sqrt{n} \) parameters. If you want to relax this constraint, then use a \texttt{U} instead of the \texttt{B}. \texttt{MImapqtl} will then allow for up to \( n - 1 \) parameters.
3.6.4 Threshold

If no penalty function is to be used, then it is important to specify the proper threshold for adding and dropping parameters. If the threshold is too low, then no QTL will be found. If too high, then $\text{MImapqtl}$ will continue to find QTL until it reaches its upper limit. One can specify a low threshold and limit the number of QTL to find. Alternatively, one can perform a permutation test to get an initial threshold. We do this using a shell script to cycle through the $\text{Prune}$ and $\text{MImapqtl}$ commands for a predetermined number of repetitions.

Suppose $\text{qtlcart}$ is the filename stem, and use $m$ as the work code, $s$ for the type I error rate, $c$ for the output column to process, and $r$ for the number of repetitions, then this snippet of pseudo-code will do a permutation analysis for $\text{MImapqtl}$.

```bash
echo "\n-start" > qtlcart.mim.ewt
i = 1
while (i < r) {
    Prune -A -V -i qtlcart.cro -b 2
    MImapqtl -A -V -I -m -S ic -i qtlcart.crb
    GetMaxLR -r i -C c < qtlcart.mim >> qtlcart.mim.ewt
    delete qtlcart.mim
    i = i + 1
}
echo "\n-end" >> qtlcart.mim.ewt
EWThreshold < qtlcart.mim.ewt
```

The programs $\text{GetMaxLR}$ and $\text{EWThreshold}$ are $\text{Perl}$ scripts that come with the UNIX distribution of the programs. There is also a c shell script called $\text{PermuteMI}$ that can be modified for your particular data set. Use the script on the original data to obtain an initial threshold. This threshold can be used with $\text{MImapqtl}$ and the $\text{SmprtSeR}$ work code to find a QTL and compute residuals. From there, a new permutation test can be run to get a new threshold to search for more QTL.
Chapter 4

Visualization of Results

The final step in analyzing your data will be to summarize your results, either graphically or as a compact set of estimates for QTL positions and effects. We have provided some utilities that read the output of the analysis programs and reformat it for use in graphics packages. The freeware program GNUPLOT is recommended as a graphics engine, but the results could be plotted in any plotting package on any machine. All of the results from the analysis programs are simple text files, and all the reformatted files are also simple text.

Figure 4.1 is a schematic of the programs and files that are involved in this step. Eqtl is a utility that quickly picks out the possible QTLs from the results of Zmapqtl. Preplot can read the output of Rqtl, LRmapqtl, Zmapqtl, M1mapqtl and Eqtl and produce simple files containing two columns of text corresponding to the values for the abscissa and ordinate of a plot. These files in turn can be plotted by GNUPLOT, or imported into various plotting packages on various platforms.

4.1 Eqtl

Zmapqtl outputs a great deal of information: Often the experimenter will want a quick summary of the positions and effects of the QTLs. The program Eqtl scans the output of Zmapqtl and reformats it. Part of the output of Eqtl is identical to the output format of Rqtl. This is convenient if the experimenter would like to do simulation studies with a set of estimated QTLs. The output of Eqtl can be used as the input to Rcross (with the appropriate genetic linkage map), and new data sets can be simulated to examine the power of the different methods to detect the QTLs. Finally, the output of Eqtl can be read by Zmapqtl and used to create virtual markers to be used as covariates in composite interval mapping (see model seven of Section 3.4.2).

The remaining output is more readable and is appropriate if the experimenter is not interested in doing further simulations. The positions of the QTL are given in Morgans from the telomere rather than recombination frequencies from the flanking markers.

Eqtl also appends some output to the SRmapqtl.out file. Once putative QTL are identified, Eqtl determines which markers are closest to these QTL and writes them to the SRmapqtl.out file. These markers will be in a table similar to the output of SRmapqtl.
itself. They can be read by Zmapqtl when running model 8.

In addition to reformatting the output of Zmapqtl, Eqtl will automatically detect whether a permutation test, jackknife or bootstrap experiment had been done. If such results exist, Eqtl will open and summarize them. For example, if you do a permutation test with Zmapqtl using interval mapping, an interim file qtlcart.z3e is created and appended to for each permutation. Eqtl will read this file and calculate experimentwise threshold values from it. Standard significance thresholds will be written to the log file. The user can specify a type I error rate (size) and Eqtl will calculate a threshold value relevant to it. Once done, the threshold value will be remembered and used by subsequent runs of Eqtl or Preplot.

For bootstrap results from Zmapqtl using interval mapping, Eqtl looks for a file qtlcart.z3a. If found, Eqtl will read in the sums and sums of squares of the likelihood ratio, additive effect and dominance effect at each position and print the mean and sample standard deviations into a summary file (qtlcart.z3d). Eqtl does similar calculations for the jackknife results that would be in qtlcart.z3i.

Table 4.1 shows the command line options specific to Eqtl.
CHAPTER 4. VISUALIZATION OF RESULTS

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-z</td>
<td>qtlcart.z</td>
<td>(Composite) Interval Mapping Results</td>
</tr>
<tr>
<td>-o</td>
<td>qtlcart.eqt</td>
<td>Output File</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-M</td>
<td>3</td>
<td>Model from Zmapqtl</td>
</tr>
<tr>
<td>-H</td>
<td>1</td>
<td>Hypothesis Test (30,31,32) for F2</td>
</tr>
<tr>
<td>-S</td>
<td>10.0</td>
<td>Significance threshold</td>
</tr>
<tr>
<td>-a</td>
<td>0.05</td>
<td>Size ($\alpha$)</td>
</tr>
<tr>
<td>-L</td>
<td>0</td>
<td>Output LOD scores? (0=no,1=yes)</td>
</tr>
</tbody>
</table>

Table 4.1: Command Line Options for Eqtl

4.1.1 Options

Files

Similar to other programs in the QTL Cartographer system, the input and output files can be specified. A genetic linkage map and a file containing the results of Zmapqtl must exist and be properly specified to Eqtl.

Which Results?

The output file from Zmapqtl may contain the results of analyzing different traits using different models. Furthermore, in $F_2$ and other populations in which dominance can be estimated, it is possible to test different sets of hypotheses. The user can specify which results from the Zmapqtl output file to process. The -M option tells Eqtl to examine the results from using the specified analysis model. An integer value should be given after the -M option. By default, Eqtl looks for the results from Model 3, or interval mapping. If you have done composite interval mapping, with say model 6, then you should specify -M 6 on the command line (or in the interactive menu). If model 6 was the last model run in Zmapqtl, then Eqtl should already be aware of that fact.

The output file may also contain results from different traits. The default trait is 1, but can be changed with the -t option. Of course, some users may choose to have a different output file for each trait in turn, and then the -z and -t options should be used together. Remember that at the beginning of each set of results in the Zmapqtl output file, the trait is specified. Eqtl looks to match this.

For $F_2$ design experiments, various hypothesis tests can be performed. These are explained in the previous chapter. Using -H with an integer allows you to specify which hypothesis test results to use. Presently, the choices are 1, 2 and 3 for the $H_3 : H_0$, $H_3 : H_1$ and $H_3 : H_2$ comparisons, respectively.

Other Options

Eqtl essentially finds the peaks in the likelihood ratio graph of the results from Zmapqtl.
CHAPTER 4. VISUALIZATION OF RESULTS

QTL Cartographer

It goes along the chromosome, and determines whether the likelihood ratio test statistic is increasing or decreasing. Upon a change, it picks out the position and estimates of other parameters. The user can specify that the peaks of interest need be higher than some “Significance threshold” to be considered QTLs. The default is 3.84, that is, any peak that is less than 3.84 is ignored. This can be changed with the -S option. If you have run Zmapqtl and done a permutation test, Eqtl automatically reads the output and sets the significance threshold subject to the value of the size, set with the -a option. For a size of $\alpha$, the the 100(1 − $\alpha$)-percentile is calculated from the experimentwise test values.

The final option is a flag to output LOD scores rather than likelihood ratios. The default behavior of the QTL Cartographer system is to use a likelihood ratio test statistic (LR) rather than a LOD score. For a hypotheses $H_i$, let $L_i$ be the likelihood of the data given the hypothesis. For a pair of hypotheses $H_0$ and $H_1$, this would yield $L_0$ and $L_1$. The LOD score is defined as

$$LOD = -\log \frac{L_0}{L_1}$$

The likelihood ratio test statistic (LR) is

$$LR = -2 \ln \frac{L_0}{L_1} = -2 \ln 10^{-LOD} = 2(\ln 10)LOD = 4.605LOD$$

and thus

$$LOD = -\log \exp\left(-\frac{LR}{2}\right) = \frac{1}{2}(\log e)LR = 0.217LR$$

4.2 Preplot

Preplot re_formats the output of the analysis programs so that they may be plotted by GNUPLOT. The output files could be imported into any programs. The default behavior of Preplot is what we term the “automagic” mode. Preplot reads the Zmapqtl output file, determines what analyses have been done, and then reformats all of these analyses in a logical way. There will be a separate graph for each trait and each chromosome. Preplot will attempt to put the results from different models in Zmapqtl and from LRmapqtl on the graphs, along with any information from the Rqtl, Eqtl and MImapqtl output file (if they exist), and a significance threshold (which can be set in the interactive menu or on the command line).

Table 4.2 shows the command line options specific to Preplot. In general, it will not be necessary to change any options to Preplot. Most of the proper values should have been set by other programs in the QTL Cartographer suite. You might want to use the -L command to tell Preplot to convert LR values into LOD scores. In any case, the output of Preplot is ready for import into GNUPLOT. There will be a number of output files. One is a plot control file, that has commands that GNUPLOT understands. The other files simply contain two columns of numbers for the $x$ and $y$ coordinates to plot. The names of the files indicate what the numbers are for. They all start with a lower case $c$, which indicates chromosome. Following the $c$ is an integer indicating which chromosome, then there is a $t$ followed by an integer indicating the trait. Then there is a period and a
CHAPTER 4. VISUALIZATION OF RESULTS

QTL Cartographer

<table>
<thead>
<tr>
<th>Option</th>
<th>Default</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>-o</td>
<td>qtlcart</td>
<td>Gnuplot Control File Name</td>
</tr>
<tr>
<td>-m</td>
<td>qtlcart.map</td>
<td>Genetic Linkage Map File</td>
</tr>
<tr>
<td>-q</td>
<td>qtlcart.qtl</td>
<td>QTL or Estimated QTL file</td>
</tr>
<tr>
<td>-l</td>
<td>qtlcart.lr</td>
<td>LRmapqtl Output File</td>
</tr>
<tr>
<td>-z</td>
<td>qtlcart.z</td>
<td>Zmapqtl Output File</td>
</tr>
<tr>
<td>-S</td>
<td>10.0</td>
<td>Significance Threshold</td>
</tr>
<tr>
<td>-T</td>
<td>x11</td>
<td>Terminal</td>
</tr>
<tr>
<td>-L</td>
<td>0</td>
<td>Output LOD scores? (0=no,1=yes)</td>
</tr>
<tr>
<td>-i</td>
<td>1</td>
<td>Hypothesis (for F2 design)</td>
</tr>
</tbody>
</table>

Table 4.2: Command Line Options for Preplot

file extension that indicates the results contained in the file. For the results of composite interval mapping, the “.z” filename extension will be followed by an integer from 1 to 7 indicating the model used for the analysis. For example, the file c2t3.z6 would have the results of composite interval mapping for trait 3 on chromosome 2 in it.

4.2.1 Printing Results

One option that is useful to change is the “Terminal” setting. This will be set correctly if all you want to do is view the graphs on your screen with GNUPLOT. If you want to get a hardcopy printout, you have two alternate choices for the “Terminal” option. If you have a postscript printer, then use “postscript” as the terminal. Run Preplot, and then run GNUPLOT as explained in Section 4.3. You will not see any output, but a file qtlcart.ps will be created (or stem.ps, where “stem” is your filename stem). This file can be sent to any postscript printer. The other alternative is “hpljii”, which does something similar for HP-LaserJet II’s (the output file will be stem.hp). You could use the “hpljii” option for “Terminal”, and then edit the stem.plt file to change the type of printer to anything that GNUPLOT supports: See the GNUPLOT manual (Williams and Kelley 1993) for more details.

<table>
<thead>
<tr>
<th>Extension</th>
<th>Meaning</th>
</tr>
</thead>
<tbody>
<tr>
<td>s</td>
<td>Significance Threshold</td>
</tr>
<tr>
<td>lr</td>
<td>Linear Regression results</td>
</tr>
<tr>
<td>z#</td>
<td>Composite interval mapping results</td>
</tr>
<tr>
<td>q</td>
<td>Quantitative trait locus data (from Rqtl)</td>
</tr>
</tbody>
</table>

Table 4.3: Filename extensions for Preplot output
CHAPTER 4. VISUALIZATION OF RESULTS

4.3 GNUPLOT

GNUPLOT is free plotting software available for UNIX, Macintosh and Windows machines. It is an interactive package. The basic idea behind the program is to read in simple files of numbers and plot them. The files of numbers contain two columns, one for the abscissa and one for the ordinate. Preplot takes care of reformatting the output of the analysis so that GNUPLOT can read the results and plot them. We have placed copies of GNUPLOT for the three platforms on our ftp server.

4.3.1 Basic GNUPLOT

In many ways, GNUPLOT is similar to MAPMAKER in that it is an interactive, command driven program. Once GNUPLOT has been started, the user can type “help” to get information on how to use the program. There are commands to change the terminal type, load files and specify the output device. Thus, one can view or print the images created by GNUPLOT.

If you have run GNUPLOT, you should have a plot control file with a “.plt” extension. Suppose that this file was stem.plt. You can start up GNUPLOT and issue the command

```
gnuplot> load "stem.plt"
```

to see the plot specified by stem.plt.

See the GNUPLOT manual for more information on this program (Williams and Kelley 1993). Of special interest may be the different types of printers supported by GNUPLOT. If you choose “postscript” as your terminal type in Preplot, then you will find a pair of lines on the stem.plt file that look like this:

```
set term postscript
set output "stem.ps"
```

You can change the token “postscript” token in that file to any printer that GNUPLOT supports and sent the stem.ps file to that printer.

78
Chapter 5

Tutorial Examples

5.1 General tactics and notes

Below, we outline some general exercises using QTL Cartographer. These exercises were used at North Carolina State University in a class (Statistics 591o), in the Summer Institute in Statistical Genetics. We have also done presented these labs in South Africa and New Zealand. At NCSU, we have used the Statistics Instructional Computing Laboratory (SICL), which is equipped with Sun workstations running Solaris, but the exercises can be done on any platform that QTL Cartographer runs on. We have also done these exercises in labs with Windows NT workstations.

As a general rule, we suggest creating a separate subdirectory (folder) for each data set. Copy the original input files into that subdirectory. This will help to organize your work. In addition, since you will be working with copies, your original files will be safe.

Beginning with the first program you run, a resource file called qtlcart.rc is created and updated for each subsequent program. This file keeps track of all the parameters and file names that you use. In addition, a log file will record which specific parameters were used with which specific programs, and when the programs were run. Thus, the qtlcart.rc file keeps track of the current settings, and the qtlcart.log file records the history of parameter settings. You can look at any of these files or any other files that QTL Cartographer creates by opening them in any text editor.

Macintoshes and PCs work a little differently than the examples below. They maintain one copy of the qtlcart.rc file in the subdirectory (folder) where the applications are located. You can specify a working subdirectory (folder) in any of the QTL Cartographer programs, and this will be recorded in the qtlcart.rc file. The Introduction has more extensive instructions on how to do this. If you are on a Macintosh or a PC, create a subdirectory (folder) called “qwork” in the subdirectory (folder) where the binaries are. If you are on a UNIX machine, create the “qwork” subdirectory in your root directory.

There is a web page for QTL Cartographer

http://statgen.ncsu.edu/qtlcart/cartographer.html

which is the good place to keep abreast of new information. The “readme” file from the ftp server is linked to the web page. The programs are also linked to the web page, so you
can download them using some web browsers. The entire manual as well as the man pages have been translated into html.

5.2 Basic Macintosh

The MacOS is so easy to use that little instruction is necessary. I would recommend getting a copy of BBEdit Lite for viewing and editing text files. It is freeware and can open large files as long as you have the memory. BBEdit Lite can also view and convert text files with DOS, UNIX or Macintosh line endings. Other free programs such as Fetch to download files, NiftyTelnet to access UNIX servers and Acrobat Reader to view and print documents are also useful.

5.3 Basic Windows

This is a quick summary of some basic commands and techniques for working in the Windows NT environment: Other versions of Windows from 95 up should be similar.

Logging in  Using “control+alt+delete” will bring up the login screen. Click in the login box and type your login name. Press tab to get to the password box and type your password and a return. If you then see a timer (which looks like a little clock), you’ll know you have succeeded: Just wait while the windowing system starts up.

Logging out  You may want to empty the trash before you log out. Right-click on the recycle bin and select “empty” to do so. When you want to log out, simply click the left mouse button on the Start icon and select shutdown. This will bring up a menu. Select the “Close all programs and logon as a different user” option and then click “OK”.

5.3.1 Navigating disks

I generally use Windows Explorer to navigate the disks. You can click on files, copy them and paste them in different directories to make copies of files. If you are not familiar with Windows Explorer, take a few minutes to play with it. You can double click on the “My Computer” icon and icons therein to explore your hard drive.

Viewing files

There are a lot of options for viewing files. Generally I recommend using Notepad. It is a simple text editor with a fixed width font. You can find it under “Start → Programs→ Accessories → Notepad”. When you try to open a file, be sure to tell Notepad to look for files of type “All Files”. If you don’t, then Notepad will only show files with a “.txt” extension.

Windows NT does not like files to be accessed by two programs at once. Be sure to clear out Notepad by creating a new file before running any programs that might read or write to a file that you are viewing.
CHAPTER 5. TUTORIAL EXAMPLES

Command Prompt
Clicking on “Start → Programs → Command Prompt” brings up a command line window for DOS commands. You can ftp or telnet from this window if you wish to transfer files or logon to an account elsewhere. There is a text editor that can be started with the command edit that will allow you to view files. Again, take care not to open files that are being accessed by other programs.

Transferring Files
You can start a Command Prompt and from there ftp files to your home account. You will need the IP number or hostname and domain name to do this. Simply start up the Command Prompt, type in the drive from which you want to transfer files, and cd to the directory where the files are. Then, ftp to your home machine and put the files there. Use “quit” to kill ftp and “exit” to get back to Windows. Here is an example.

c:\> k:
k:\> cd module5
k:\module5> ftp mymachine.somedomain.net
ftp> prompt
ftp> mput *
ftp> quit
k:\module5> exit

In the above example, the k: drive is the users home directory at North Carolina State University. If you are not at NCSU, then you may or may not have the k: drive.

5.4 Basic Unix
This is meant to be a quick summary of some basic Unix commands. One thing to keep in mind is that Unix is case sensitive. Feel free to practice any of the following commands (but be careful with rm and mv).

5.4.1 Help!
The man command is one of the most important for the novice and experienced user. If you would like to know what it does, type man man at the prompt in a command window. You can use it to get information on most of the commands below.

5.4.2 Basic filesystem commands
Here is a list of basic commands for seeing, copying and moving the files in your directory, creating new subdirectories and navigating. Go ahead and experiment with these commands.
• **ls** is a command to list the files in the present working directory. You can give it options, for example **ls -l** will give listings with more information about the files than **ls**.

• **pwd** tells you where you are. This can be useful if you have created many subdirectories.

• **cd** allows you to change the current working directory. You can give it an absolute or a relative argument. **cd ..** would move you to the next highest subdirectory. **cd /ncsu/pams046/bin** would move you to the /ncsu/pams046/bin subdirectory, etc.

• **mkdir** allows you to create a subdirectory. **mkdir test** would create the subdirectory **test**. **rmdir** would remove it. You can only remove empty subdirectories.

• **rm** allows you to remove a file. It is aliased as **rm -i**, which means that it will ask if you really want to remove the file. **rm filename** would remove the file **filename**.

• **mv** moves a file. **mv file.orig file.new** would move the file **file.orig** to **file.new**. You can think of it as renaming.

• **cp** copies one or more files. **cp file1 file2** copies the file **file1** to the file **file2**. **cp file1 file2 direct** would copy the files **file1 file2** to the directory **direct**.

• **chmod** is a rather complex command to change the permissions on files. You can write batch files, and use **chmod** to allow execution of them.

• **more** will display the contents of a file. Use it as **more filename**. While in **more**, typing a **q** will get you out.

5.4.3 Curious?

There are a couple of commands to find out who is on your machine and what they are doing. **w**, **who** and **finger** tell you who is logged on to your machine and what they are doing. You can also use **finger** to get info on a user on another machine. Try **finger basten@statgen.ncsu.edu**.

5.4.4 Other commands

• **rlogin**, **telnet** and **ftp** allow you to initiate sessions on other machines. You need to supply the IP address or nickname of the machine with these commands.

• **exit** closes a terminal window and **clear** clears it.

• **history** shows the last 40 commands issued. They will be numbered, and you can rerun them with an exclamation point and the number of the command, *e.g.*, **!23** would run the command numbered 23 in the **history** list.
5. Simulating and Analyzing data

Assuming that you have a “qwork” subdirectory (folder), create a new subdirectory (folder) within it. You can call it anything you like, but for the purposes of illustration it will be referred to as “example1”. Thus, your working directory for this example will be “qwork:example1” if on a Macintosh or “qwork\example1” if on a PC. If you are on a UNIX machine, cd into the “qwork/example1” subdirectory and don’t worry about setting a working subdirectory. Also note that if you are using a PC, the program names will all have an “.exe” ending.

In this exercise, you will simulate a genetic linkage map, then a model and finally a data set. This data will then be analyzed.

1. Start up Rmap. Select the option to change the filename stem. Change the filename stem to “sim”. You can change any parameters that you like. We suggest changing the variances of markers per chromosome and intermarker distance to values other than 0.0. In each case, a value of 2 or 3 would work well for the purposes of this exercise. Don’t change the output format. If you are on a Macintosh or MS-Windows machine, be sure to set the proper working subdirectory (folder). When satisfied with the parameter values, select “0” to run the program. Look at the output (sim.map).

2. Start up Rqtl. You probably don’t need to change any parameters. You can run this program with the “0” option. Look at the output (sim.qtl).

3. Start up Rcross. Again, you do not need to change any parameters, but you could try a different experimental design. Select the number associated with the experimental design. Change its value from “B1” to “SF3” (or whatever you like from Table 1.1). Run this program with the “0” option. Look at the output (sim.cro). From this point on, the analyses will utilize this file and the “sim.map” file.

4. Start up Qstats and run it without changing any parameters. Look at the output (sim.qst).

5. Start up LRmapqtl and run it without changing any parameters. Look at the output (sim.lr).

6. Start up SRmapqtl. You might want to change the analysis model from its default value of “0” (forward stepwise regression) to “2” (forward regression with backward elimination). Run it and look at the output (sim.sr).

7. Start up Zmapqtl. You won’t need to change any parameters. Tell it to go ahead with the analysis and look at the output (sim.z).
CHAPTER 5. TUTORIAL EXAMPLES

QTL Cartographer

8. Start up Zmapqtl again. This time, choose “Model for Analysis” and change it to “6”. Tell it to go ahead with the analysis, and look at the output (which will be appended to what you did in the first run).

9. Start up Preplot. Don’t change any parameters: Go ahead with the program.

10. If you are on a Macintosh, move the GNUPLOT binary into the working subdirectory and double click it. If on PC or UNIX machine, start up GNUPLOT. From the GNUPLOT command line, type in

   load “sim.plt”

   (If you are on a PC, you may need to go through the file menu and search for the “sim.plt” file.) This should display graphical results. Press returns when requested.

11. Start up Eqtl. Go ahead with the analysis. Look at the output (sim.eqt).

5.6 Analyzing simulated data

Create a working subdirectory (call it “mletest”) and copy the simulated data sets into it. The simulated datasets called “mletest.map” and “mletest.cro” come from Zeng (1994). They are in the “doc” folder for the Macintosh versions, in the same place as the binaries on PCs and in the “example” subdirectory in the UNIX version. These are properly formatted, and can be analyzed with Qstats, LRmapqtl, etc. Do the following:

1. Proceed with the analysis programs as in the previous example. Be sure to set the proper filename stem (mletest) and working subdirectory. Run Qstats, LRmapqtl, SRmapqtl and Zmapqtl. Look at the output after each run.

2. Start up Preplot. Don’t change any parameters: Go ahead with the program.

3. Start up GNUPLOT. From the GNUPLOT command line, type in

   load “mletest.plt”

   This should display graphical results. See the first example for the specifics of PCs and Macintoshes.

4. Start up Eqtl. Go ahead with the analysis. Look at the output (mletest.eqt).

5.7 Analyzing real data

Create a new working subdirectory called “realdat” in you “qwork” subdirectory. Copy the realdat*.inp files into it. There should be two files: “realdatm.inp” and “realdatc.inp”. The former is a genetic linkage map in the standard input format (map.inp). The latter is a file with marker and trait data in the standard input format (cross.inp). This is a real data set kindly provided by Juan Medrano (Horvat and Medrano 1995). It has also been used as an example in a review on the statistical issues in QTL mapping (Doerge, Zeng, and Weir 1997). You will now translate the data files into the QTL Cartographer format, and then analyze the data.

84
1. Start up **Rmap**. Change the working subdirectory, and then the filename stem. You can use “realdat” for the stem. Now, select item 1 from the menu and enter “realdatm.inp”. Now run the program. **Rmap** should read in the prepared genetic linkage map file and reformat it properly.

2. Start up **Rcross**. Select item 1 from the menu and enter “realdatc.inp”. Now run the program. **Rcross** should read in the prepared data file, match marker names from this data file to those in the map file, and reformat the data properly. Look at the output.

3. Proceed with the analysis programs as in the previous examples. Run **Qstats**, **LRmapqtl**, **SRmapqtl** and **Zmapqtl**. Look at the output after each run.

4. Start up **Preplot**. Don’t change any parameters: Go ahead with the program.

5. Start up **GNUPLOT**. From the **GNUPLOT** command line, type in
   
   ```load "realdat.plt"
   ```
   This should display graphical results.

6. Start up **Eqtl**. Go ahead with the analysis. Look at the output (realdat.eqt).

### 5.8 Analyzing a MAPMAKER data set

#### 5.8.1 Using MAPMAKER/EXP

You will need **MAPMAKER/EXP** for this part. If you don’t want to use **MAPMAKER/EXP**, then you can use the already prepared files that come with the distribution. Otherwise, ftp to genome.wi.mit.edu and cd to `/distribution/mapmaker` to get the programs. A file `sample.raw` comes with **MAPMAKER/EXP**.

Each number is a command in a sequence to be done in **MAPMAKER/EXP**. Anything inside of square braces are comments and should not be typed into **MAPMAKER/EXP**. Start up **MAPMAKER/EXP** in an appropriate subdirectory and proceed with these commands:

1. prepare data sample.raw
   
   [Input the data from the raw file.]

2. photo sample.tutorial
   
   [Save what you do in a log file.]

3. sequence 1 2 3 4 5 6 7 8 9 10 11 12
   
   [Start with all markers.]

4. group
   
   [Group them into linkage groups]

5. sequence { 1 2 3 5 7 }
   
   [Use randomly ordered group 1 makers.]

6. compare
   
   [Compare all orders. For each in turn, calculate the Likelihood.]

7. sequence 1 3 2 5 7
   
   [Decide that this is the best order and specify it.]
8. map [Print the map to the screen. This attaches distances as well.]
9. sequence 4 6 8 9 10 11 12 [Now use the rest of the markers.]
10. list loci [Summarize the number of informative progeny.]
11. lod table [Show pairwise distances and linkage LOD scores.]
12. sequence {8 9 10 11 12} [Use a randomly ordered subset of markers from group 2.]
13. compare [Compare all orders. For each in turn, calculate the Likelihood.]
14. sequence order1 [Use the best order from the compare command.]
15. try 4 6 [Try all possible positions of markers 4 and 6. Also, try unlinked idea.]
16. sequence 4 11 8 12 9 6 10 [This is the best sequence.]
17. make chromosome c1 [Create chromosome 1.]
18. sequence 1 3 2 5 7 [Specify the sequence of markers on chromosome 1.]
19. attach c1 [Attach the sequence to chromosome 1.]
20. framework c1 [Create the framework (puts in distances) for chromosome 2.]
21. make chromosome c2 [Create chromosome 2.]
22. sequence 4 11 8 12 9 6 10 [Specify the sequence of markers on chromosome 2.]
23. attach c2 [Attach the sequence to chromosome 2.]
24. framework c2 [Create the framework (puts in distances) for chromosome 2.]
25. quit [Exit the program. The map will be in sample.maps.]

On a UNIX machine, you will now have a file called sample.maps. On a PC, it will be called sample.map. It will be one of these two on a Macintosh. Rename this output file to sample.mps, and use it along with the sample.raw file for the next part.

5.8.2 Using the MAPMAKER files

Create a new working subdirectory called mm in you qwork subdirectory. Copy the sample.* files into it. There should be two files: sample.mps and sample.raw. The former is a genetic linkage map created by MAPMAKER/EXP. The latter is MAPMAKER/QTL raw file. You will now translate the data files into the QTL Cartographer format, and then analyze the data.

1. Start up Rmap. Select the option to change the filename stem. Change the filename stem to “sample” and set the proper working subdirectory. Then select the input file option and change it to “sample.mps”. Then go ahead with the analysis. Look at the output (sample.map).
2. Start up **Rcross**. Select the input file option and change it to “sample.raw”. Then go ahead with the analysis. Look at the output (sample.cro).

3. Proceed with the analysis programs as in the previous examples. Run **Qstats**, **LRmapqtl**, **SRmapqtl** and **Zmapqtl**. Look at the output after each run.

4. Start up **Preplot**. Don’t change any parameters: Go ahead with the program.

5. Start up **GNUPLOT**. From the **GNUPLOT** command line, type in

```
load "sample.plt"
```

This should display graphical results.

6. Start up **Eqtl**. Go ahead with the analysis. Look at the output (sample.eqt).
Chapter 6

Input File Formats

All of the input and output files in the QTL Cartographer system are plain text, and can thus be viewed by virtually any text editor or word processor on any platform. The input files for many of the programs will have embedded commands that start with a minus sign (-). Care should be taken not to have stray tokens such as ‘-Chromosome’ in input files. Also, the case of commands is generally very important: When in doubt use the exact case that is specified here.

6.1 Genetic Linkage Maps

6.1.1 MAPMAKER output files

Rmap can translate the output of MAPMAKER into the format required by the QTL Cartographer system. Use the .maps file that is the output of MAPMAKER as the input to Rmap and it will be translated automatically. An alternate format has been designed for those who don’t have the MAPMAKER files.

6.1.2 Rmap input files

The general method of inputting data for this format is by tokens. Tokens are just collections of characters surrounded by whitespace (spaces, carriage returns, tabs, line feeds). The maximum length of any token must be less than 64 (and this may be increased in the future). An example of this format is given in Figure 6.1.

First line

It is critical that the first line start with a pound symbol, a space, a number, the word bychromosome, a -filetype token, and the map.inp token as shown below:

# 123456789 bychromosome -filetype map.inp

space space space space
# 123456789  bychromosome  -filetype map.inp
# Look for documentation at the end
-type positions
-function 1
-Units cM
-chromosomes 2
-maximum 5
-named yes
-start
-Chromosome 1
  Marker1_1  0.0
  Marker1_2  10.2
  Marker1_3  34.1
  Marker1_4  43.3
  Marker1_5  52.1
-Chromosome 2
  Marker2_1  0.0
  Marker2_2  13.7
  Marker2_3  19.1
  Marker2_4  24.8
-stop
-end

Figure 6.1: Input format for a map.inp file
The spaces are necessary, because the input is token based. The program will read the second token in the file as a long integer and use it as an identifier for the file. Thus, each file should have a unique identifier following the pound symbol.

The `-filetype map.inp` tells the QTL Cartographer programs that this is a `map.inp` formatted file. The `bychromosome` word is a vestige of an idea that simply needs to hang around.

**Tokens**

A token is any string of non-whitespace surrounded by whitespace. Each time a token begins with a minus sign (-), it is read to determine what follows it. The next token is then read and processed. The program will ignore any token that it doesn’t recognize. The tokens that are recognized as commands in a `map.inp` file are `-type`, `-function`, `-param`, `-Units`, `-chromosomes`, `-maximum`, `-end`, `-named`, `-start`, `-stop`, `-skip`, `-unskip`, and `-Chromosome`.

Note that only the first letter of these tokens is actually necessary (except for `-start`, `-stop` and `-skip`, which require more letters to distinguish between them).

Case is important. `-Units` is different from `-units`.

**Meanings of commands**

The file in Figure 6.1 also has commands embedded into it. `Rmap` recognizes any token that begins with a minus sign (-) as an embedded command. Some commands require that the following token be a number or piece of information. The following table gives a list of tokens that the program recognizes, their purpose and what the next token should be.

<table>
<thead>
<tr>
<th>Commands</th>
<th>Followed by</th>
<th>Means</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>-type</code></td>
<td>positions</td>
<td>Marker positions are given</td>
</tr>
<tr>
<td><code>-type</code></td>
<td>intervals</td>
<td>Marker intervals are given</td>
</tr>
<tr>
<td><code>-function</code></td>
<td>integer 1-8</td>
<td>Code for the map function: Details in manual</td>
</tr>
<tr>
<td><code>-param</code></td>
<td>real number</td>
<td>Extra parameter needed for some map functions</td>
</tr>
<tr>
<td><code>-Units</code></td>
<td>cM, M or r</td>
<td>Units are in centiMorgans (cM), Morgans (M) or recombination frequencies (r)</td>
</tr>
<tr>
<td><code>-chromosomes</code></td>
<td>integer &gt; 0</td>
<td>Haploid number of chromosomes</td>
</tr>
<tr>
<td><code>-maximum</code></td>
<td>integer &gt; 0</td>
<td>Maximum number of markers on any chromosome. Needed for array allocation.</td>
</tr>
<tr>
<td><code>-named</code></td>
<td>yes or no</td>
<td>Says whether markers will have names.</td>
</tr>
<tr>
<td><code>-skip</code></td>
<td></td>
<td>Tells <code>Rmap</code> to skip everything until an <code>end</code> of the <code>-skip</code>. These cannot be within a <code>-start</code> to <code>-stop</code> block</td>
</tr>
<tr>
<td><code>-unskip</code></td>
<td></td>
<td>Start of a map block</td>
</tr>
<tr>
<td><code>-start</code></td>
<td></td>
<td>End of a map block</td>
</tr>
<tr>
<td><code>-stop</code></td>
<td></td>
<td>End of the file</td>
</tr>
<tr>
<td><code>-Chromosome</code></td>
<td>integer, string</td>
<td>Gives the number of the chromosome (if integer) or the name (if a string)</td>
</tr>
</tbody>
</table>
Map block

Between the -start token and the -stop token, you should have a repeating sequence of a -Chromosome token followed by an integer or sting, then markers ordered, with their names followed by the appropriate distances. You should be consistent with the tokens following the -Chromosome token: Either have them all be unique chromosome names or unique integers from 1 to the number of chromosomes indicted with the -chromosomes token.

This example has the markers followed by their positions in centiMorgans. Please give all markers unique names.

```
-named yes
-start
-Chromosome 1
  Marker1_1 0.0
  Marker1_2 10.2
  Marker1_3 34.1
  Marker1_4 43.3
  Marker1_5 52.1
-Chromosome 2
  Marker2_1 0.0
  Marker2_2 13.7
  Marker2_3 19.1
  Marker2_4 24.8
-stop
```

In the above, the line Marker1_2 10.2 means that Marker1_2 is on chromosome 1 at position 10.2 cM from the left telomere. If you want to give the chromosomes names, then the above could have been

```
-named yes
-start
-Chromosome X
  Marker1_1 0.0
  Marker1_2 10.2
  Marker1_3 34.1
  Marker1_4 43.3
  Marker1_5 52.1
-Chromosome First
  Marker2_1 0.0
  Marker2_2 13.7
  Marker2_3 19.1
  Marker2_4 24.8
-stop
```

If -named had a value of no in the preamble, then the format of the distances would be:
QTL Cartographer

CHAPTER 6. INPUT FILE FORMATS

- named
- start
- Chromosome 1  0.0  10.2  34.1  43.3  52.1
- Chromosome 2  0.0  13.7  19.1  24.8
- stop

That is, the names would be skipped.

You can also create a map where the markers are not on the telomeres. If you are inputting the map based on positions, then

- start
- Chromosome 1
  Marker1_1  5.0
  Marker1_2  10.2
  Marker1_3  34.1
  Marker1_4  43.3
  Marker1_5  52.1
  Telomere   55.3
- Chromosome 2
  Marker2_1  4.0
  Marker2_2  13.7
  Marker2_3  19.1
  Marker2_4  24.8
  Telomere   27.4
- stop

would mean that there is DNA outside of the first and last markers on a Chromosome. The keyword ‘Telomere’ is recognized by Rmap as a telomere and not as a marker.

If you are inputting intervals, then the same map would look like

- start
- Chromosome 1
  Telomere   5.0
  Marker1_1  5.2
  Marker1_2  23.9
  Marker1_3  9.2
  Marker1_4  8.8
  Marker1_5  3.2
- Chromosome 2
  Telomere   4.0
  Marker2_1  9.7
  Marker2_2  5.4
  Marker2_3  4.7
  Marker2_4  2.6
- stop

92
That is, you need to indicate that the telomeric DNA comes first. These two maps should give
the same result when run through \texttt{Rmap}.

\textbf{WARNING:} do not use 'Telomere' as a marker name. This keyword is case sensitive, so 'telomere' is not the same as 'Telomere'.

\textbf{Termination}

The \texttt{-end} token will tell \texttt{Rmap} to stop reading the file and to the translation. The token \texttt{-quit} will do the same thing.

\textbf{Annotation}

You can annotate this file as much as you want. Just don’t put in any extra stuff in the
\texttt{-start} to \texttt{-stop} block. Everything after the \texttt{-end} token is ignored. Before the \texttt{-start} token, only the \texttt{-type, -function, -param, -units, -chromosomes} and \texttt{-maximum} tokens are processed. The token following each of these is read and the information used in the program.

The format of the information in \texttt{-start} to \texttt{-stop} block is unimportant. You just need whitespaces around each piece of information. All the marker names and their distances could be on one line.

\textbf{Usage}

If this file were called \texttt{map.inp}, then
\begin{verbatim}
% Rmap -A -V -i map.inp
\end{verbatim}
would convert this file to the format required for the other programs in the \textit{QTL Cartographer} system.

\subsection*{6.1.3 Rmap output files}

\texttt{Rmap} overwrites any file that has the same name as specified as the output file. Be careful not to destroy any important files. The output file will contain the values of the parameters used, the names of chromosomes and markers (if a translation was made) and the linkage map.
6.2 QTL information

You can specify a genetic model and use it for simulation by translating it with Rqtl. This would be useful if you want to do some “what-if” experiments.

6.2.1 Rqtl input files

The input format is similar to that for Rmap. Figure 6.2 is an example of an input file for a QTL model.

First line

It is critical that the first line start with a pound symbol, a space, a number, a -filetype token and the qtls.inp filetype:

```
# 12345789 -filetype qtls.inp
```

The spaces are necessary, because the input is token based. The program will read the second token in the file as a long integer and use it as an identifier for the file. Thus, each file should have a unique identifier following the pound symbol.

The -filetype qtls.inp tells the QTL Cartographer programs that this is a qtls.inp formatted file.

Tokens

A token is any string of non-whitespace surrounded by whitespace. Each time a token begins with a -, it is read to determine what follows it. The next token is then read and processed. The program will ignore any token that it doesn’t recognize. The tokens that are recognized in a qtls.inp file are -Units, -end, -named, -start, -stop, -skip, -unskip, -interactions and -filetype.

Usually, only the first letter of these tokens is actually necessary (except for -start, -stop and -skip, which require more letters to distinguish between them).

Case is important. -Units is correct and is different from -units, which will be ignored.

Meanings of commands

The file in Figure 6.2 also has commands embedded into it. Rqtl recognizes any token that begins with a minus sign (-) as an embedded command. Some commands require that the following token be a number or piece of information. The following table gives a list of tokens that the program recognizes, their purpose and what the next token should be.
# 12345789 -filetype qtls.inp # Documentation at end

-Units cM
-named yes

-start qtls 3
Trait_1 4
   1  9.1  0.75  0.0
   1  89.1  0.5  0.0
   3  68.4  0.22  0.0
   4  43.2  0.95  0.0
Trait_2 2
   2  93.4  0.42  0.0
   4  33.2  0.90  0.0
Trait_3 1
   1  33.4  0.84  0.2
-stop qtls

-interactions
-trait Trait_1
   1  2  AA  0.01
   1  2  AD  0.02
   1  2  DA  0.031
   1  2  DD  0.04
   1  3  AA  0.01
   1  3  AD  0.02
   1  3  DA  0.032
   1  3  DD  0.05
   2  3  AA  0.01
   2  3  AD  0.02
   2  3  DA  0.03
   2  3  DD  0.0
-trait Trait_2
   1  2  AA  0.01
   1  2  AD  0.02
   1  2  DA  0.03
   1  2  DD  0.04
-trait Trait_3
-stop interactions
-end

Figure 6.2: Example of a Model input file
CHAPTER 6. INPUT FILE FORMATS

<table>
<thead>
<tr>
<th>Command</th>
<th>Followed by</th>
<th>Means</th>
</tr>
</thead>
<tbody>
<tr>
<td>-filetype</td>
<td>qtls.inp</td>
<td>Tells \texttt{Rqtl} what to expect in the format.</td>
</tr>
<tr>
<td>-Units</td>
<td>cM or M</td>
<td>cM for centiMorgans and M for Morgans.</td>
</tr>
<tr>
<td>-named</td>
<td>yes or no</td>
<td>Answers whether the traits will have names.</td>
</tr>
<tr>
<td>-start</td>
<td>qtls</td>
<td>Begin data defining QTLs</td>
</tr>
<tr>
<td>-interactions</td>
<td></td>
<td>Begin data on defining interactions</td>
</tr>
<tr>
<td>-skip</td>
<td></td>
<td>Tells \texttt{Rqtl} to skip everything until an -unskip</td>
</tr>
<tr>
<td>-unskip</td>
<td></td>
<td>which is the end of the -skip. These cannot be within a -start to -stop block or a -interactions to -stop block</td>
</tr>
<tr>
<td>-stop</td>
<td></td>
<td>End of a qtls or interactions block</td>
</tr>
<tr>
<td>-end</td>
<td></td>
<td>End of the file</td>
</tr>
</tbody>
</table>

\textbf{QTLs block}

After the -\texttt{start} token, there should be the token \texttt{qtls} and a number to indicate the number of traits to be modelled. For example, -\texttt{start qtls 3} means that there will be QTLs for 3 traits. After this there should be a repeating sequence of a trait name, number of loci for that trait, then the chromosome, position, additive and dominance effects for each locus. This example has the loci followed by their positions in centiMorgans (from the telomere). Please give all traits unique names.

Here is an example of the repeating sequence:

\begin{verbatim}
Trait_Name  #loci
chrom pos a d
chrom pos a d
. . . .
. . . .
. . . .
chrom pos a d

Trait_Name  #loci
chrom pos a d
chrom pos a d
. . . .
. . . .
. . . .
chrom pos a d
\end{verbatim}

Our specific example was

\begin{verbatim}
-start qtls 3
Trait_1 4
1  9.1  0.75 0.0
1  89.1  0.5 0.0
3  68.4  0.22 0.0
\end{verbatim}
4  43.2  0.95  0.0
Trait_2  2
   2  93.4  0.42  0.0
   4  33.2  0.90  0.0
Trait_3  1
   1  33.4  0.84  0.2
-stop qtls

Now, consider the block

Trait_1  4
   1  9.1  0.75  0.0
   1  89.1  0.5  0.0
   3  68.4  0.22  0.0
   4  43.2  0.95  0.0

and think of them as being numbered consecutively:

Trait_1  4
1.  1  9.1  0.75  0.0
2.  1  89.1  0.5  0.0
3.  3  68.4  0.22  0.0
4.  4  43.2  0.95  0.0

and for the second trait, the numbering starts from 1 again:

Trait_2  2
1.  2  93.4  0.42  0.0
2.  4  33.2  0.90  0.0

These numberings will be used to define the interactions.

Interactions

For a QTL with k loci, there are \( \frac{k(k-1)}{2} \) unordered pairs of loci. We can define epistatic interactions for each of these pairs. Epistatic interactions come in four types, thus there are \( 2^k \) possible interactions. The abbreviations for the types are:

<table>
<thead>
<tr>
<th>Interaction</th>
<th>Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Additive by additive</td>
<td>AA</td>
</tr>
<tr>
<td>2. Additive by dominance</td>
<td>AD</td>
</tr>
<tr>
<td>3. Dominance by additive</td>
<td>DA</td>
</tr>
<tr>
<td>4. Dominance by dominance</td>
<td>DD</td>
</tr>
</tbody>
</table>

If an interaction is not defined in the `-interactions` block, then it will be set to zero. To define the interactions, we have a block that looks similar to that defining QTL main effects. The token `-interactions` is followed by the `-trait` token with a traitname and
then a repeating sequence of QTL1 QTL2 Type Value tokens. Thus, the line
1 2 AA 0.01
means that QTL 1 (chromosome 1 position 9.1) and QTL 2 (chromosome 1 position 89.1)
have an additive by additive effect of 0.01. Note that the QTL with a smaller number
ALWAYS comes before that with the larger number. Note that in the example file, there
were no interactions between QTL 4 and any of the other QTL for the first trait. If an
interaction term is missing, its value is zero.

Termination
The -end token will tell Rqtl to stop reading the file and to the translation. The token
-quits will do the same thing.

Annotation
You can annotate the input file as much as you want. Be careful to not put annotation in
the -start to -stop or -interactions to -stop blocks. Also, don’t use words that begin
with a minus sign, or put such words in a -skip to -unskip block. Finally, anything after
an -end or -quit token will be ignored.

Usage
If this file were called qtls.inp, then
% Rqtl -A -V -i qtls.inp
would convert this file to the format required for the other programs in the QTLcartographer
system. The above assumes that an appropriate map file exists.

6.2.2 Rqtl output files
Rqtl overwrites any file that has the same name as specified as the output file. Be careful
not to destroy any important files. The output file will contain the genetic model in a
format suitable for input into Rcross.
6.3 Data files

These are files that contain marker and trait data. The output format of Rcross is rather difficult for the user to read and create manually. We have therefore provided ways to translate other formats.

6.3.1 MAPMAKER raw files

Rcross will convert MAPMAKER raw files for use in the QTL Cartographer system. You will first need to use MAPMAKER to create a genetic linkage map. Then convert the map into the “Rmap.out” format for use with Rcross. Then, use Rcross to convert the MAPMAKER raw data file into the “Rcross.out” format.

6.3.2 Rcross input files

We have also defined a format for your data. It is similar to the input formats for Rmap and Rqtl. Input is token based, and the data file has embedded commands to indicate to Rcross what it is reading. An example of such a file is given in Figure 6.3.

First line

It is critical that the first line start with a pound symbol, a space, a number, a -filetype token, and the cross.inp filetype:

```
# 123456789 -filetype cross.inp
```

The spaces are necessary, because the input is token based. The program will read the second token in the file as a long integer and use it as an identifier for the file. Thus, each file should have a unique identifier following the pound symbol.

The -filetype cross.inp tells the QTL Cartographer programs that this is a cross.inp formatted file.

Tokens

A token is any string of non-whitespace surrounded by whitespace. Each time a token begins with a minus sign (-), it is assumed to be a command and the token following it is processed. The program will ignore any token that it doesn’t recognize. The tokens that are recognized as commands in a cross.inp file are -traits, -SampleSize, -TranslationTable, -end, -Cross, -case, -skip, -unskip, -quit and -start.

Note that only the first letter of these tokens is actually necessary (except for -start, -stop and -skip, which require more letters to distinguish between them). Case is important. -Units is different from -units.

Extra whitespace is ignored, so you can put in spaces, tabs, carriage returns, etc, to format your data in an understandable fashion.
# 123456787 -filetype cross.inp

# Documentation at the end
-Cross B1
-traits 2
-otraits 2
-SampleSize 10
-case no
-TranslationTable
  AA  2  2
  Aa  1  1
  aa  0  0
  A-  12 12
  a-  10 10
  -- -1 -1

-start markers
Marker1_1 2 2 2 2 2 1 1 1 1 1
Marker1_2 2 2 2 1 1 1 1 1 1 1
Marker1_3 1 2 2 2 1 1 1 1 1 1
Marker1_4 1 1 2 2 1 1 1 1 1 1
Marker1_5 2 2 2 2 2 1 1 1 1 1
Marker2_1 2 1 1 2 2 1 1 1 1 1
Marker2_2 2 2 2 1 1 1 1 1 1 1
Marker2_3 2 2 1 1 1 1 2 2 2 2
Marker2_4 2 1 1 1 1 1 1 1 1 1

-stop markers

-missingtrait .

-start traits
Trait_1 5.0 5.3 6.2 4.1 5.5 5.8 6.7 6.1 . 6.4
Trait_2 15.0 15.3 16.2 24.1 25.5 25.8 16.7 26.1 33.2 16.4

-stop traits

-start otroits
Sex M F M M M F F M F F
Brood 1 1 1 1 2 2 2 2

-stop otroits

-quit

Figure 6.3: Example of a cross.inp file
Meanings of commands

<table>
<thead>
<tr>
<th>Token</th>
<th>Followed by</th>
<th>Means</th>
</tr>
</thead>
<tbody>
<tr>
<td>-Cross</td>
<td>string</td>
<td>type of cross See (1.1.2)</td>
</tr>
<tr>
<td>-traits</td>
<td>integer</td>
<td>number of traits</td>
</tr>
<tr>
<td>-otraits</td>
<td>integer</td>
<td>number of categorical variables</td>
</tr>
<tr>
<td>-SampleSize</td>
<td>integer</td>
<td>sample size</td>
</tr>
<tr>
<td>-case</td>
<td>yes or no</td>
<td>whether comparisons are case sensitive</td>
</tr>
<tr>
<td>-TranslationTable</td>
<td>table</td>
<td>table for marker translation</td>
</tr>
<tr>
<td>-skip</td>
<td></td>
<td>Tells Rcross to skip everything until an</td>
</tr>
<tr>
<td>-unskip</td>
<td></td>
<td>which is the end of the -skip. These</td>
</tr>
<tr>
<td></td>
<td></td>
<td>cannot be within a -start to -stop block</td>
</tr>
<tr>
<td>-start</td>
<td>string</td>
<td>Start of a block of markers, traits or otraits</td>
</tr>
<tr>
<td>-stop</td>
<td></td>
<td>End of a block</td>
</tr>
<tr>
<td>-end</td>
<td></td>
<td>End of the file</td>
</tr>
</tbody>
</table>

The -case token changes how strings are matched. Put a yes here if comparisons are case dependant. With no, all names of individuals, markers and traits are converted to lower case to make comparisons.

Marker Translation

You can define how markers are translated. Here is the default translation table

-TranslationTable

\[
\begin{array}{ccc}
AA & 2 & 2 \\
Aa & 1 & 1 \\
aa & 0 & 0 \\
A- & 12 & 12 \\
a- & 10 & 10 \\
-- & -1 & -1 \\
\end{array}
\]

Note a few things in the above translation table. There are six rows and three columns. There must be a token in all 18 positions of the table. The first column is the genotype. The program assumes that the A allele is diagnostic for the High (parental 1) line and the a allele is diagnostic for the Low (parental 2) line. A minus sign (-) means the allele is unknown. Dominant as well as codominant markers can be encoded. The middle column is how the output of these genotypes will be encoded while the right (3rd) column is how you will code the input of this file. The above TranslationTable maps 2 to 2, 1 to 1, 0 to 0, etc. Just about any set of tokens can be used for the third column, but DO NOT change the first two columns. If you encoded your \( P_1 \) homozygotes as \( BB \), heterozygotes as \( Bb \), etc, your translation table might appear as

-TranslationTable

\[
\begin{array}{ccc}
AA & 2 & BB \\
\end{array}
\]
CHAPTER 6. INPUT FILE FORMATS

QTL Cartographer

Aa  1  Bb
aa  0  bb
A-  12  B-
a-  10  b-
--  -1  --

Anything in the following data file that is not recognized (doesn’t match something in column 3) will become unknown (-1) in the output.

REMEMBER: You need all 18 tokens following the ~TranslationTable command and the first two columns can’t be altered. You can only alter the last column.

Crosses

You need to define the type of cross. See (1.1.2) for more on the different crosses and the symbols used by the QTL Cartographer system.

Data Input by Markers and Trait

One way to organize the data is by markers. For each marker, you give the genotypes of the individuals. The order of the individuals has to be the same for each marker. Below is an example. After the ~start markers, the program expects a repeating sequence of marker name, then n marker genotypes where n is the sample size. The marker names should match those in the Map file.

~start markers
Marker1_1 2 2 2 2 1 1 1 1 1 1 1 1 1 1 1
Marker1_2 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1
Marker1_3 1 2 2 2 2 1 1 1 1 1 1
Marker1_4 1 1 2 2 2 1 1 1 1 1 1
Marker1_5 2 2 2 2 2 1 1 1 1 1 1
Marker2_1 2 1 1 2 2 1 1 1 1 1 1
Marker2_2 2 2 1 1 1 1 1 1 1 1 1
Marker2_3 2 2 1 1 1 2 2 2 2 2 2
Marker2_4 2 1 1 1 1 1 1 1 2 2 2
~stop markers

The traits are encoded in the same fashion. After the ~start traits tokens, the program expects a repeating sequence of trait name and then n values for the sample. The order of the individuals has to be the same as in the markers. Also, you can specify the token for a missing trait with ~missingtrait.

If you want a lone period to indicate a missing datum.

~start traits
Trait_1  5.0  5.3  6.2  4.1  5.5  5.8  6.7  6.1  .  6.4

102
CHAPTER 6. INPUT FILE FORMATS

Trait_2 15.0 15.3 16.2 24.1 25.5 25.8 16.7 26.1 33.2 16.4
-stop traits ... indicates the end of the trait data.

Categorical (otraits) are other traits that will be stored as character strings. These will be things such as sex, brood, eye color, etc. Each token should be less than 64 characters in length. The -missingtrait token can be reused with a different token if desired.

-start otraits
Sex M F M M F F M F F
Brood 1 1 1 1 2 2 2 2
-stop otraits

Data Input by individuals

If the -start and -stop tokens are followed by the work 'individuals', then data will be read in by individuals.

Another way to organize the data is by individuals. The program expects that the markers are ordered from marker 1 on chromosome 1, marker 2 on chromosome 1, ..., to the last marker on the last chromosome. Since the individuals are named, they can be in any order.

-start individuals markers
Ind_1 2 2 1 1 2 2 2 2
Ind_2 2 2 2 1 2 1 2 1
Ind_3 2 2 2 2 2 1 2 1
Ind_4 2 1 2 2 2 1 1 1
Ind_5 2 1 2 2 2 1 1 1
Ind_6 1 1 1 1 1 1 1 1
Ind_7 1 1 1 1 1 1 2 1
Ind_8 1 1 1 1 1 1 2 1
Ind_9 1 1 1 1 1 1 2 2
Ind_10 1 1 1 1 1 1 2 2
-stop individuals markers

The traits are done similarly. All the traits have to be in this block. Each column is for a different trait. After the -start token, put individuals followed by traits, then the number of traits (2), then the names of the traits, then indicate whether the individuals are named. Here they are, but if they weren’t, put an notnamed token where the 'named' token presently is. otraits below are done in the same fashion.

-start individuals traits 2 Trait_1 Trait_2 named
Ind_1 5.0 15.0
Ind_2 5.3 15.3
Ind_3 6.2 16.2
Ind_4 4.1 24.1
CHAPTER 6. INPUT FILE FORMATS

Ind_5 5.5 25.5
Ind_6 5.8 25.8
Ind_7 6.7 16.7
Ind_8 6.1 26.1
Ind_9 . 33.2
Ind_10 6.4 16.4
~stop individuals traits

~start individuals otraits 2 sex brood named
Ind_1 M 1
Ind_2 F 1
Ind_3 M 1
Ind_4 M 1
Ind_5 M 1
Ind_6 F 2
Ind_7 F 2
Ind_8 M 2
Ind_9 F 2
Ind_10 F 2
~stop individuals otraits

Termination

The ~end token will tell Rcross to stop reading the file and to the translation. The token ~quit will do the same thing.

Annotation

You can annotate the input file as much as you want. Be careful to not put annotation in the ~start to ~stop blocks. Also, don’t use words that begin with a minus sign, or put such words in a ~skip to ~unskip block. Finally, anything after an ~end or ~quit token will be ignored.

Usage

If this file were called cross.inp, then
% Rcross -i cross.inp

would convert this file to the format required for the other programs in the QTL Cartographer system. The above assumes that an appropriate map file exists.
Chapter 7

Benchmarks

Tables 7.1-7.2 summarize the timings for Zmapqtl to do interval mapping (Lander and Botstein 1989) and composite interval mapping (Zeng 1993; Zeng 1994) on various computing platforms under different operating systems. All timings were done in the winter of 1999. The simulated data set has been used previously (Zeng 1994) and consists of a genetic linkage map that has four chromosomes with 16 markers on each chromosome. The markers are evenly spaced at 10 cM and the simulated data has one trait. The entire genome was scanned at a walking speed of 2 cM. The programs were run in automatic mode, with no recourse to the interactive menus. They indicate the amount of time to read in the data, perform the analysis and write the output.

Table 7.1 summarizes the timings for interval mapping.

<table>
<thead>
<tr>
<th>Machine</th>
<th>Speed (Mhz)</th>
<th>Time (seconds)</th>
<th>Ratio to UltraSparc 60</th>
</tr>
</thead>
<tbody>
<tr>
<td>PowerMac G3</td>
<td>266</td>
<td>7</td>
<td>1.7</td>
</tr>
<tr>
<td>PowerMac G3</td>
<td>400</td>
<td>5</td>
<td>1.3</td>
</tr>
<tr>
<td>Sparc 10</td>
<td>36</td>
<td>34</td>
<td>8.5</td>
</tr>
<tr>
<td>UltraSparc 2170</td>
<td>167</td>
<td>8</td>
<td>2.0</td>
</tr>
<tr>
<td>UltraSparc 60</td>
<td>300</td>
<td>4</td>
<td>1.0</td>
</tr>
<tr>
<td>Pentium, NT 4.0</td>
<td>260</td>
<td>8</td>
<td>2.0</td>
</tr>
<tr>
<td>Pentium, NT 4.0</td>
<td>450</td>
<td>4</td>
<td>1.0</td>
</tr>
</tbody>
</table>

Table 7.1: Timings for Interval Mapping

Table 7.2 summarizes timings for composite interval mapping. The model for analysis was Model 6 with a window size set to 10.0 cM and using up to 5 markers to control for the genetic background. Some of the ratios for the same machine change from interval mapping to composite interval mapping. Model 6 uses quite a lot more double precision arithmetic, and this may account for the differences.

For $N$ replications of a permutation test or bootstrap, the computing time should be less than $N$ times the values in Tables 7.1-7.2. The jackknife analysis should be around $n$ times these values (where $n$ is the sample size).
CHAPTER 7. BENCHMARKS

<table>
<thead>
<tr>
<th>Machine</th>
<th>Speed (Mhz)</th>
<th>Time (seconds)</th>
<th>Ratio to UltraSparc 60</th>
</tr>
</thead>
<tbody>
<tr>
<td>PowerMac G3</td>
<td>266</td>
<td>7</td>
<td>1.2</td>
</tr>
<tr>
<td>Sparc 10</td>
<td>36</td>
<td>45</td>
<td>7.5</td>
</tr>
<tr>
<td>UltraSparc 2170</td>
<td>167</td>
<td>10</td>
<td>1.7</td>
</tr>
<tr>
<td>UltraSparc 60</td>
<td>300</td>
<td>6</td>
<td>1.0</td>
</tr>
<tr>
<td>Pentium, NT 4.0</td>
<td>260</td>
<td>10</td>
<td>1.7</td>
</tr>
</tbody>
</table>

Table 7.2: Timings for Composite Interval Mapping

<table>
<thead>
<tr>
<th>System</th>
<th>Speed (Mhz)</th>
<th>Time (seconds)</th>
<th>Ratio to best</th>
</tr>
</thead>
<tbody>
<tr>
<td>Macintosh G3</td>
<td>400</td>
<td>1569</td>
<td>1.18</td>
</tr>
<tr>
<td>UltraSparc 10</td>
<td>440</td>
<td>1699</td>
<td>1.27</td>
</tr>
<tr>
<td>Pentium III</td>
<td>866</td>
<td>1333</td>
<td>1.0</td>
</tr>
</tbody>
</table>

Table 7.3: Timings for Multiple Interval Mapping

The MImapqtl module was run on three systems for the mletest data set with information criterion 1 and a threshold of 0.0. Timings are presented in Table 7.3. The systems ran MacOS 8.6, Solaris 8 and Windows 2000, respectively for the Macintosh, UltraSparc and Pentium III machines. The analytic results were the same on all platforms. MImapqtl is sensitive to the number of parameters in the model it is analyzing. In this example, 10 QTL were identified. the first stages of QTL identification proceed quickly, but the program slows down significantly as more parameters are used. This is something to keep in mind if you decide to search for epistatic terms. If there are a lot of main effects, then a backward elimination method for finding epistatic interactions may take a prohibitavely long time.
Chapter 8

UNIX Man Pages

In the UNIX world, a standard way of providing online documentation of programs is to write man pages. These are ASCII text files with embedded troff commands. UNIX versions of QTL Cartographer have man pages for all the programs in the suite. On a UNIX system, if the man pages are in the correct subdirectory (in essence, if the subdirectory that contains the man pages is defined in the environmental variable MANPATH), then you can get the online help with a command such as

% man Rmap

We provide html versions of the man pages on the web server for Macintosh and Windows users. If you have World Wide Web access, first point your browser to our home page:

http://statgen.ncsu.edu/

Then, click on Statistical Genetics, and then on the Software link. You will then be able to click on the QTL Cartographer link. Follow it to the online man pages. You can also access the rest of the QTL Cartographer manual. The manual is written in \LaTeX\ and has been translated into HTML by the program html2latex.

The complete set of man pages are reprinted here for your benefit. Here follow the \LaTeX\ formatted versions of the man pages.

Since the documentation will change regularly, it is a good idea to check the Web site for the current online manual. The Web pages will always be updated with the manual updates.
8.1 QTLCART

NAME

QTLcart — A rudimentary front end for the QTL Cartographer system.

SYNOPSIS


DESCRIPTION

QTLcart does not actually exist. It is intended to be the front end to a set of programs collectively known as QTL Cartographer. This man page explains the options that are valid in all the programs of the QTL Cartographer suite. It also outlines how to get started using the programs.

OPTIONS

The following options can be used with any of the programs in the QTL Cartographer suite. The current programs are Rmap, Rqtl, Rcross, Qstats, LRmapqtl, SRmapqtl, JZmapqtl, Eqtl, Prune, and Preplot.

- h Prints out the current values of all program options, and information on what the program does. It then exits.

- V Turns the verbosity mode off. The programs in the suite print out messages while running. This option turns off those messages. This is useful for batch files.

- A Skips the interactive screen for setting options. All programs start up with a menu that allows setting of options. This turns the menu off. It is also very useful for batch files.

- R The programs will read the default parameters from a file specified with this option. If a file called qtlcart.rc is in the current working directory, it will be opened by default and all parameter values read. If no such file exists, then default parameter values will be assumed, and the file will be created.

- W This option allows one to set the work directory. This directory must exist. All the input files must be in this directory and the output files will be placed there.

- s This requires a long integer to act as the random number seed. By default, it is the value returned by the ANSI C function time(), which is usually the number of seconds since some arbitrary past date (often 1 January 1970). This number will also be used as a unique identifier on the first line of the output file.

This can be a useful option. It is recorded in the log file when any program is run. It is possible to recreate exactly what was done using the log file.
\textbf{\texttt{-e}} This requires a filename for the log file. It will be appended to if it exists and created if not. The default is \texttt{qtlcart.log}.

\textbf{\texttt{-X}} Give a filename stem. All output will start with this stem and have extensions indicating what is in them.

**EXAMPLES**

For all the following examples, assume that \texttt{QTLCart} is just a wildcard for any of the programs in the suite.

\begin{verbatim}
% QTLcart -R resource.file
\end{verbatim}

\texttt{QTLcart} will read option values from the file \texttt{resource.file}. The other programs do this, and except for \texttt{Preplot}, will regenerate the file upon exit.

\begin{verbatim}
% QTLcart -X corn
\end{verbatim}

Will set the filename stem to \texttt{corn}. The output files will then have names beginning with \texttt{corn} and logical extensions. For example, the map file will be placed in \texttt{corn.map} and the file containing the data from a cross will be in \texttt{corn.cro}. Filenaming conventions follow the old DOS 8+3 due to historical reasons.

**GLOBAL COMMAND LINE OPTIONS**

All the parameters for \texttt{QTLcart} are also parameters for the other programs in the QTL Cartographer system.

**GLOBAL BEHAVIOR**

All the programs in the QTL Cartographer suite behave in the same general way. They were originally UNIX programs and can be run as such (using command line options). More recently, we have added an interactive menu that allows the user to set parameters. Once inside any of the programs, all the parameters of the program are displayed with their current values. The user chooses whichever parameter he or she wishes to change by selecting a number. The menu is in a loop. Choosing 0 will end the loop and proceed with the current parameter values.

The menu is also where one can get online help. Online help will be a numbered option in the list of parameters. Choose it and specify the location of the help file if the program couldn’t find it.

When the programs begin to run, they will print out their parameter values to a log file (\texttt{qtlcart.log} by default).

Here is an example of the \texttt{Qstats} menu:

\begin{verbatim}
No. | Options | Values:
--- | --- | ---
\end{verbatim}
0. Continue with these parameters
1. Data Input File qtlcart.cro
2. Output File qtlcart.qst
3. Error File qtlcart.log
4. Genetic Linkage Map File qtlcart.map
5. Random Number Seed 961681144

---------------------------------------------
6. Specify Resource File qtlcart.rc
7. Change Filename stem qtlcart
8. Change Working Directory:
9. Quit
10. Quit, but update the Resource File

Please enter a number...

This menu is in a loop. To change a parameter, select its number and press return. You will be prompted for a new value or filename. You can clear out a filename or working directory by inputting a single period (.). When satisfied that the parameters are set correctly, you can select 0 to run the program. If you want to quit, simply select 10. Selecting 11 will update the resource file with any parameter changes you have made.

RESOURCE FILE

The resource file keeps track of the most current parameter values used in the programs. Each time the user runs a program, the program accepts new values for parameters and writes them to the resource file. This is unlike the log file which keeps track of the parameters used at the time of running each program. The resource file that is generated by the programs in the suite is self-documenting. Look in the qtlcart.rc file.

WORKING DIRECTORY

You can specify a working directory (or folder) with the -W option. This directory (folder) must exist prior to running any of the programs. The directory can be relative or complete, and should have the standard directory delimiter appended to it. For example

-W /home/user/qtlcart/work/

would use /home/user/qtlcart/work as the working directory. All input and output files would have to be in this directory. For a Windows system, the line might be

-W c:\qtlcart\work\n
whereas a Macintosh would require

-W HardDrive:qtlcart:work:
The equivalent line in the resource file would have `-workdir` instead of just `-W`.

In UNIX, you can set a path variable pointing to the programs and simply set your current working directory to the working directory. For Mac, you double click the icons and should use a working directory variable. Relative paths are also possible. For example, if the programs reside in a `bin` folder in the `qtlcart` folder on a Macintosh, then you can have a `data` folder in the `qtlcart` folder and use

```
-W ::data:
```

as the working directory. The two colons mean go up one level and then go into the `data` folder.

**FILENAME STEM**

The filename stem is an important concept in the usage of this package. Beginning with version 1.12, the programs utilize the filename stem `qtlcart`. All files are then named using this stem and filename extensions relevant to the filetype. For example, if the `-X` option is followed by `corn`, then when new files are created, they will have the stem `corn` followed by a logical extension. An example would be `corn.map` for a genetic linkage map. With some practice, you will be able to know the contents of a file by its extension.

**USING THE INDIVIDUAL PROGRAMS**

For now it is best to use the individual programs rather than the front end. If you have no data, then you would use the programs in the following order:

1. `Rmap`, to create a random map of markers.
2. `Rqtl`, to generate a random genetic model for the map.
3. `Rcross`, to create a random cross.
4. `LRmapqtl`, to do a simple linear regression of the data on the markers.
5. `SRmapqtl`, to do a stepwise linear regression of the data on the markers to rank the markers.
6. `Zmapqtl`, to do interval or composite interval mapping.
7. `Preplot`, to reformat the output of the analysis for `GNUPlot`.
8. `GNUPlot`, to see the results graphically.

If you have data, then you might use the programs in the following order:

1. `Rmap`, to reformat the output of MAPMAKER or a standard input file.
2. `Rcross`, to reformat your data.
3. **Qstats**, to summarize missing data and calculate some basic statistics on your quantitative traits.

4. **LRmapqtl**, to do a simple linear regression of the data on the markers.

5. **SRmapqtl**, to do a stepwise linear regression of the data on the markers to rank the markers. This should be run with model 2.

6. **Zmapqtl**, to do interval or composite interval mapping. This should be run twice, once with model 3 and a second time with model 6.

7. **Preplot**, to reformat the output of the analysis for Gnuplot.

8. **GNUPLOT**, to see the results graphically.

We recommend that the new user tries a simulation to gain an understanding of the programs.

**REFERENCES**


**BUGS**

Many UNIX systems have been known to get upset when trying to run the QTL Cartographer programs from out of the front end. It has something to do with the memory management. Try running the individual programs one by one. A good test is to simply run each program without changing any parameters.

**SEE ALSO**

Rmap(1), Rqtl(1), Rcross(1), Qstats(1), LRmapqtl(1), SRmapqtl(1), JZmapqtl(1), Eqtl(1), Prune(1), Preplot(1), MImapqtl(1)

**AUTHORS**

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8.2 RMAP

NAME

Rmap — Simulate or reformat a map of molecular markers

SYNOPSIS


DESCRIPTION

Rmap creates a random map of molecular markers. The user specifies the number of chromosomes, the number of markers per chromosome and the average intermarker distance. If one specifies standard deviations for the number of markers and the average intermarker distances, they will vary subject to the normal distribution. The output gives a table of markers by chromosomes, with the distances between consecutive markers (in centiMorgans) in the table.

If you specify an input file, Rmap will open it, determine if it is in the same format as Rmap outputs, and process it based in the value given to -g. If the input file is the output of MAPMAKER, then the map will be reformatted from MAPMAKER into the Rmap output format.

Finally, there is a standard input format that Rmap can translate, and is defined in the file map.inp that comes with the distribution of the programs. Note that if the user specifies an input file, no simulations will be done and the latter half of the command line options are ignored.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This should be used with a filename indicating where the output will be written. Rmap will overwrite the file if it exists, and create a new file if it does not. If not used, then Rmap will use qtlcart.map.

-i You can use this option to specify an input filename. This file must exist and have one of three formats: Rmap.out, map.inp or mapmaker.mps. Rmap will attempt to identify the format of the file and translate it to another format. If you specify an input file, then the simulation parameters will be ignored.

113
-g Requires an integer to indicate the output format. You can use a 1 for the default output format, a 2 for GNUPlot output or a 3 for both. If you use a 2 or a 3, then you can use GNUPlot to see a primitive looking linkage map.

-f Requires an integer option to specify the mapping function. Rmap can use the Haldane, Kosambi, fixed or a number of other functions. The default is to use the Haldane function, which is specified with a 1. Using a 2 invokes the Kosambi mapping function. A 3 means that a fixed function is used and thus the distance in Morgans is the recombination fraction. The type of mapping function used would then be recorded in the output and all following analyses will use this function. One must edit the map file to change this if not using Rmap.

-p Requires a real number. Some map functions need an extra parameter, and this allows the user to specify it. See the manual for details.

-c This allows you to specify the number of chromosomes if you are simulating a genetic linkage map. It is 4 by default. If you are translating a file, then this will be ignored as will the remaining options.

-m This allows you to specify the average number of markers per chromosome in a simulation. The default is 16.

-vm This allows you to specify the standard deviation in the number of markers per chromosome. The number of markers per chromosome will have a normal distribution with mean given in the previous option, and the standard deviation specified here. If zero, then each chromosome will have the same number of markers.

-d Rmap uses the value given after this option as the average intermarker distance (in centiMorgans) for a simulation. It is 10 centiMorgans by default.

-vd The intermarker distance will have a normal distribution with mean set by the previous option and standard deviation specified with this option. It is 0.0 by default, which means that the intermarker distances between consecutive markers will all be the same. Set it to a positive value to have intermarker distances vary at random.

-t You can simulate maps where there are no markers on the telomeres with this option. Give this option a value of tails and Rmap puts an average of tails Morgans of genetic material on the ends of the chromosomes. By default, it is 0.0. If the standard deviation for intermarker distance is greater than 0.0, then then the amount of flanking DNA will have a normal distribution with mean given here and standard deviation proportional to that of the standard deviation of intermarker distances.

-M Allows you to specify an alternate simulation mode. If the -M option is used with a value of 1, then the intermarker distance will be used as the chromosome length (so you should make it longer), and the markers are placed on the chromosomes following the uniform distribution.
INPUT FORMAT

**Rmap** recognizes three types of files. The first is the *Rmap.out* format that *Rmap* itself creates. The second is a special format defined in the example file *map.inp* included in the distribution. The third format is the output of **MAPMAKER**. If the input file is a **MAPMAKER** output file, *Rmap* translates this file into its own format. If the input file is already in the correct format, *Rmap* will output it dependant upon the flag given to the `-g` option. The units of intermarker distances will be in centiMorgans in the output.

EXAMPLES

```
% Rmap -o Map.out -c 23 -vm 3 -vd 1 -t 5
```

Simulates a random map where the number of markers on each of 23 chromosomes has a normal distribution with mean 16 and standard deviation 3. The intermarker distance is normally distributed with mean 10 cM and standard deviation 1. There will be some genetic material outside the flanking markers on each chromosome, with a mean length of 5 cM and standard deviation 0.5.

```
% Rmap -o Map.out -i map.mps
```

Opens the file *map.mps*, tries to determine its format, and translates it if possible. The output will be written to the file *Map.out*. The extension *.mps* should be used with **MAPMAKER** output files and the string `-filetype mapmaker.mps` should be put somewhere in the first twenty lines of the file.

REFERENCES


BUGS

Note that if **MAPMAKER** outputs an intermarker distance of 0.00 cM, then *Rmap* will translate it to 0.0001 cM. In fact, all intermarker distances of 0.0 will be reset to 0.0001 cM.

SEE ALSO

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8.3 RQTL

NAME

Rqtl — Place a set of estimated or randomly generated QTLs on a molecular map.

SYNOPSIS

Rqtl [ -o output ] [ -i input ] [ -m mapfile ] [ -b beta ] [ -t Traits ] [ -q QTLperTrait ] [ -d dominance ] [ -1 beta1 ] [ -2 beta2 ] [ -E prop ]

DESCRIPTION

Rqtl will translate a genetic model or simulate a random model for use by Rcross to simulate a data set. It places a specified number of QTLs (Quantitative Trait Loci) on the molecular map created or translated by Rmap. For simulations, they are placed randomly on the map, and the additive, dominance and epistatic effects are also determined. The molecular map could be a random one produced by Rmap, or a real one in the same format as the output of Rmap.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. Rqtl will overwrite the file if it exists, and create a new file if it does not. If not used, then Rqtl will use qtlcart.qtl.

-i This requires an input filename. This file must exist. Rqtl will attempt to identify the format of the file and translate it to another format. This file should contain a genetic model defining a set of QTL and including their positions and effects. See the file qtls.inp for the format.

-m This requires a filename that must exist. Rqtl will read the genetic linkage map from this file.

-t This allows the user to specify the number of traits to simulate. It is 1 by default.

-q This requires an integer argument. It allows the user to specify the number of QTL that affect the trait. If one trait is simulated, then exactly this number of QTL will be created. If more than one trait are simulated, then the number of QTL per trait will vary but have mean value specified here. The default is 9.
-d You can specify the type of dominance at the trait loci. If we assume inbred parental lines with line one marker trait alleles all Q and line two trait alleles all q, then use a 1 for no dominance, a 2 for complete dominance of Q over q, a 3 for complete dominance of q over Q, and a 4 for dominance that is random in direction and magnitude for each locus. It is 1 by default, that is no dominance.

-b Specifies the parameter needed to determine the additive effect of a QTL. It is 0.5 by default. See Zeng (1992) equation (12) and accompanying text for a discussion of this parameter. It is not the allelic effect of a QTL allele, rather it is the shape parameter in the beta distribution.

-1, -2 Allows you to specify the two parameters used to determine the dominance effect of a QTL. The effect is simulated from a beta distribution. See the manual for more details.

-E For a k QTL model, there will be 2k(k+1) potential epistatic terms. This option sets the proportion of epistatic interactions that will be non-zero in a simulated model. The effects are generated with the same beta function used for the dominance effects.

INPUT FORMAT

The input format of the molecular map should be the same as that of the output format from the program Rmap.

If a file is specified with the -i option, then that file will be read for the positions and effects of the QTLs. The format of this file should be identical to that of the output of Rqtl, or of a special format defined in the file qtls.inp included with the distribution.

EXAMPLES

% Rqtl -d 2

Places 9 QTLs on the map in Rmap.out. There is complete dominance of A over a.

% Rqtl -i qtls.inp -o test.qtl

Reads the file qtls.inp and translates it into the output format of Rqtl. The output is written to the file test.qtl, which is overwritten if it exists.

REFERENCES

BUGS
The \texttt{-t} option for the number of traits is rather primitive at this time. The number of QTLs and their effects are randomly determined, with means given in the other options.

SEE ALSO
\texttt{Rmap(1)}, \texttt{Rcross(1)}, \texttt{Qstats(1)}, \texttt{LRmapqtl(1)}, \texttt{SRmapqtl(1)}, \texttt{Zmapqtl(1)}, \texttt{JZmapqtl(1)}, \texttt{Eqtl(1)}, \texttt{Prune(1)}, \texttt{Preplot(1)}, \texttt{QTLcart(1)}

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8.4 Rcross

NAME

Rcross — Simulate or reformat a data set.

SYNOPSIS


DESCRIPTION

Rcross performs a random cross or reformats a data set. Cross types include F1 backcrosses to the P1 or P2, F2 crosses produced by selfing or random mating, recombinant inbred lines as well as a few others. It simulates marker and trait data. The markers simulated come from a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The QTL model could be a random set produced by Rqtl or an estimated set in the same format as the output of Rqtl.

Rcross can also translate files from three different formats. If the user chooses to translate a file, then the simulation options are ignored.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. Rcross will overwrite the file if it exists, and create a new file if it does not. If not used, then Rcross will use qtlcart.cro. This output is in a format suitable for any of the mapping programs.

-i This requires an input filename. This file must exist. Rcross will attempt to identify the format of the file and translate it to another format. Specifying a file with this option turns off the simulation parameters below.

-m Rcross requires a genetic linkage map. This option require the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-q Rcross needs a genetic model to simulate a data set. It will read from the file specified by this option. The file specified should contain a genetic model in the same format as the output of Rqtl. The default file is qtlcart.qtl.
-H Allows the user to specify the heritability for the trait. If used, it requires a value in
the range 0.0 to 1.0. It is 0.5 by default.

-E Allows the user to specify an environmental variance for the trait. If used, it requires a
positive value and will disable the heritability. This is ignored by default.

-I is the flag to turn on interactive crosses. By default, it has a value of 0. To do interactive
crosses, use this option with the value 1.

-c Allows the user to specify the type of cross. It requires a string such as B1, SF2 or RI1.
See below for more on the values of the cross.

-g This option requires an integer from 0 to 6 to indicate the output format. The default
is 0. See below for the seven different output options.

-n This is the sample size of the offspring. It is 200 by default and requires some integer
value greater than 0 if used.

INPUT FORMAT
The input format of the molecular map should be the same as that of the output format from
the program Rmap. The input form of the QTL data should be that of the output format
from Rqtl. If an input file for the data is used, then it can have one of two formats. The first
is identical to the raw files required by MAPMAKER. You must first use MAPMAKER
to create a genetic map, then run the map through Rmap to reformat it, then use the map
and the original raw file to reformat the data for subsequent use.
An alternative format is defined in a file cross.inp that is included with the distribution.
The file can be annotated freely. Look at the cross.inp file and use it as a template for your
data.

OUTPUT OPTIONS
Rcross can produce five different types of output files. You can use the -g command line
option with any integer from 0 to 6 or use these numbers in the text menu to change the
output format. The numbers correspond to these types of output files.

0. qtlcart.cro
This is the default and standard format for the analysis programs in the QTL Car-
tograher package.

1. cross.inp
This is a standard input format designed for Rcross.

2. mapmaker.raw
This is the MAPMAKER raw format.
3. qtlcart.r
   This format is suitable for import into the programs R or Splus. All the data will be written into the file and embedded in commands that allow R/Splus to read it. In addition, Rcross writes a set of commands to do ANOVA analyses of each trait on each marker and categorical trait.

4. qtlcart.sas
   This format is a SAS program that has all the data and a set of PROC ANOVA commands to do the same ANOVA analyses as with the R/Splus option above.

5. plabqtl0.qdt
   This will produce a file suitable for input into PLABQTL. The data will be in the matrix format. See the PLABQTL manual for more details.

5. plabqtl1.qdt
   This will produce a file suitable for input into PLABQTL. The data will be in the vector format. See the PLABQTL manual for more details.

CROSSES
   A pair of inbred parental lines (P1 and P2) that differ in the trait of interest and marker genotypes are crossed to produce an F1 generation. All crosses are then derived from these lines. Backcrossing to P1 is encoded by B1, and to P2 by B2. Selfed intercrosses of generation i are encoded by SFi. Randomly mated intercrosses of generation i are encoded by RFi. Recombinant inbreds created by selfing have the code RI1, while those by sib-mating are RI2. Doubled haploids have the code RI0. A test cross of an SFi line to a Pj line is encoded by T(Bj)SFi. The QTL Cartographer manual explains some other crosses that are possible. Note that the UNIX shell may interpret ( and ) so they should either be quoted, or the cross entered into the interactive menu.
   Rcross uses the general genetic model developed by Cockerham (1954).

EXAMPLES
   % Rcross -A -V -c SF2 -n 1000
   Does a selfed F2 cross with 1000 offspring using the linkage map in qtlcart.map and the model in qtlcart.qtl. The command line options -A and -V turn off the interactive menu and the verbosity mode, respectively.
   % Rcross -i cross.raw
   Reads from the file cross.raw, tries to determine its format, and translates it if possible. The file cross.raw could be a MAPMAKER/QTL formatted file, a cross.inp formatted file or one that is already in the Rcross.out format.
REFERENCES


BUGS

If you use the interactive mode, you can print out the results of crosses. The analysis of these arbitrary crosses has not been fully integrated into the other programs.

SEE ALSO


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8.5 PRUNE

NAME
Prune — Prune or resample the data set.

SYNOPSIS

DESCRIPTION
Prune allows one to eliminate markers or traits. It removes the data from the file containing
the cross and reconstructs the molecular map. It requires a molecular map that could be a
random one produced by Rmap, or a real one in the same format as the output of Rmap.
The sample could be a randomly generated one from Rcross or a real one in the same
format as the output of Rcross.
Prune also does bootstraps, permutations and simulations of missing or dominant mark-
ers.

OPTIONS
See QTLcart(1) for more information on the global options -h for help, -A for automatic,
-V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e
to specify the log file, -s to specify a seed for the random number generator and -X stem
to specify a filename stem. The options below are specific to this program.
If you use this program without specifying any options, then you will get into a menu
that allows you to set them interactively.

-o This requires a filename stem for output. Prune will overwrite the file ending in .crb
if it exists, and create a new file if it does not. If not used, then Prune will use
qtlcart.crb. If the map is recreated, then a new map file will be written to qtlcart.mp
by default or a file ending in mpb with the specified stem.

-i This requires an input filename. This file must exist. It should be in the same format as
the output of Rcross. The default file is qtlcart.cro.

-m Prune requires a genetic linkage map. This option requires the name of a file containing
the map. It should be in the same format that Rmap outputs. The default file is
qtlcart.map.

-I Sets the interactive level. A zero means that Prune will do what it needs to without
asking (the default for bootstraps, permutations or missing data simulations). A one
means that the user will be put into a repeating loop to manipulate the data set. It
has a value 1 by default, but using the -b option disables it.
This sets a level for the elimination of individuals with this much missing marker data, or for the simulation of missing or dominant markers when used with the -b option.

-b Prune will read in the map and data file and do one of AUTOMATIC ACTIONS described in the section of the same name below. A value of zero means that this option is ignored.

INPUT FORMAT

The input format of the molecular map should be the same as that of the output format from the program Rmap. The input format of the individual data should be the same as the output format of the program Rcross.

AUTOMATIC ACTIONS

There are a number of automatic actions that can be performed using the -b option. You will use one of the numbers below with the option to tell Prune to do that action. A new dataset is then printed to a file stem.crb, where stem is the filename stem. Note that if you give a nonzero value to this option, the interactive flag is turned off.

1. Perform a bootstrap resampling of the data. Sampling of individuals is done with replacement to create a sample of the same size as the original.

2. Permute the traits against genotype arrays. If there are multiple traits in the data set, then each trait will be shuffled against the genotype arrays.

3. Simulate missing markers. The percent of missing marker data should be specified with the -M option, and it should be an number in the range of 0 to 100 percent.

4. Simulate dominant markers. The percent of dominant marker data should be specified with the -M option, and it should be an number in the range of 0 to 100 percent. The direction of dominance is random.

5. Simulate selective genotyping. The percent of typed individuals should be specified with the -M option, and it should be an number in the range of 0 to 100 percent. This will print out individuals with trait values in the tails of the overall distribution. The value specified will be the sum of these tails: Each tail will have half of the total. This will apply to whichever trait was last analyzed, or trait 1 if all the traits had been analyzed. It is probably best to do this with single trait data sets.

6. Permute the traits against genotype arrays. If there are multiple traits in the data set, then entire trait arrays will be shuffled against the genotype arrays. This contrasts with option 2 above which permutes the traits independently. If you think the traits are correlated and you want to maintain that correlation, use this option. Otherwise, use option 2.
EXAMPLES

% Prune -m example.map -i example.cross -o exout

Puts the user into an interactive menu for eliminating traits, markers, etc.

% Prune -m example.map -i example.cross -o exout -b 1

The -b option creates a new sample from the old. The new sample is created by resampling the original sample with replacement. Phenotypes and genotypes are kept together. The new sample will have the same sample size as the old one. It will be written to exout.crb. No new map will be written.

% Prune -m example.map -i example.cross -o exout -b 5 -M 20.0

Here, the -b option tells Prune to selectively genotype. We specify 20.0 percent with the -M option meaning that those individuals with trait values falling in the lower and upper 10 percent tails are retained, and the middle 80 percent are removed.

BUGS

You can eliminate multiple markers in the interactive loop. You should be aware that the order marker elimination is important. If all the markers to be eliminated are on separate chromosomes, the order is unimportant. If two markers from the same chromosome are to be eliminated, order should be to eliminate the highest numbered marker. The same concept holds for traits: eliminate them in the order of highest to lowest.

Do not try to eliminate any markers or traits AND do a bootstrap, permutation or simulation of missing markers in the same run.

SEE ALSO

Rmap(1), Rqtl(1), Rcross(1), Qstats(1), LRmapqtl(1), SRmapqtl(1), JZmapqtl(1), Eqtl(1), Preplot(1), QTLcart(1)

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CHAPTER 8. UNIX MAN PAGES

8.6 QSTATS

NAME

Qstats — Calculate basic statistics for a QTL dataset.

SYNOPSIS

Qstats [-o output] [-i input] [-m mapfile]

DESCRIPTION

Qstats does some basic statistics on a dataset of quantitative traits. It plots a histogram and calculates the sample size, mean, variance standard deviation, skewness, kurtosis, and average deviation for a quantitative trait. The program also summarizes missing marker and trait data, as well as determining the marker types (dominant or codominant). Finally, Qstats will test whether markers are segregating at random. It requires a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The sample could be a randomly generated one from Rcross or a real one in the same format as the output of Rcross.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. Qstats will append the file if it exists, and create a new file if it does not. If not used, then Qstats will use qtlcart.qst.

-i This requires an input filename. This file must exist. It should be in the same format as the output of Rcross. The default file is qtlcart.cro.

-m Qstats requires a genetic linkage map. This option require the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

INPUT FORMAT

The input format of the molecular map should be the same as that of the output format from the program Rmap. The input format of the individual data should be the same as the output format of the program Rcross.
EXAMPLES

% Qstats -i corn.cro -m corn.map

Calculates basic statistics on the dataset in corn.cro using the genetic linkage map in corn.map. The program will display an interactive menu for setting options and print out messages to the screen while running. These can be turned off with -A and -V, respectively. If the dataset in corn.cro has more than one trait, then all traits will be analyzed.

REFERENCES


BUGS

Are there any other statistics that we can do? Your suggestions are welcome.

SEE ALSO

Rmap(1), Rqtl(1), Rcross(1), LRmapqtl(1), SRmapqtl(1), Zmapqtl(1), JZmapqtl(1), Eqtl(1), Prune(1), Preplot(1), QTLCart(1)

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8.7 LRMAPQTL

NAME
LRmapqtl — Single marker QTL analysis.

SYNOPSIS
LRmapqtl [-o output] [-i input] [-m mapfile] [-r reps] [-t trait]

DESCRIPTION
LRmapqtl uses simple linear regression to map quantitative trait loci to a map of molecular markers. It requires a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The sample could be a randomly generated one from Rcros or a real one in the same format as the output of Rcros.

OPTIONS
See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

-0 This requires a filename for output. LRmapqtl will append the file if it exists, and create a new file if it does not. If not used, then LRmapqtl will use qtlcart.lr.

-i This requires an input filename. This file must exist. It should be in the same format as the output of Rcros. The default file is qtlcart.cro.

-m LRmapqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-r LRmapqtl will do a permutation test a la Churchill and Doerge (1994). This option specifies the number of permutations to do. It is zero by default, which means no permutation test is done. If used, you must specify a positive integer. Usually, 1,000 is sufficient.

-t Use this to specify which trait LRmapqtl will analyze. If this number is greater than the number of traits, then all traits will be analyzed. The default is to analyze trait 1 only.
MODEL
The basic linear model is

\[
\text{Trait} = \text{Mean} + \text{Slope} \times \text{Marker} + \text{Error}
\]

The marker value will be in the range [-1, 1] inclusive. Two hypotheses are compared. The null hypothesis is that the Slope is zero. The alternate is that the Slope is non-zero. A p-value for the likelihood ratio of these two hypotheses is calculated for each marker-trait combination. LRmapqtl outputs a table with parameter estimates, F statistics, Likelihood ratios and p-values.

INPUT FORMAT
The input format of the molecular map should be the same as that of the output format from the program Rmap. The input format of the individual data should be the same as the output format of the program Rcross.

EXAMPLES
\[
\% \text{LRmapqtl -i corn.cro -m corn.map}
\]
Calculates the regression coefficients for each marker on the dataset in corn.cro using the genetic linkage map in corn.map.

REFERENCES

BUGS
SEE ALSO
Rmap(1), Rqtl(1), Rcross(1), Qstats(1), SRmapqtl(1), Zmapqtl(1), JZmapqtl(1), Eqtl(1), Prune(1), Preplot(1), QTLcart(1)

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8.8 SRMAPQTL

NAME
SRmapqtl — Map quantitative traits on a molecular map.

SYNOPSIS
SRmapqtl [ -o output ] [ -i input ] [ -m mapfile ] [ -t trait ] [ -M Model ] [ -F pFin ] [ -B pFout ] [ -u MaxSteps ]

DESCRIPTION
SRmapqtl uses stepwise regression to map quantitative trait loci to a map of molecular markers. It requires a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The sample could be a randomly generated one from Rcross or a real one in the same format as the output of Rcross.

This program should be run before Zmapqtl if you want to use composite interval mapping. The results will be used to pick markers background control in composite interval mapping. The main result from using this program is to rank the markers in terms of their influence on the trait of interest.

OPTIONS
See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. SRmapqtl will append the file if it exists, and create a new file if it does not. If not used, then SRmapqtl will use qtlcart.sr.

-i This requires an input filename. This file must exist. It should be in the same format as the output of Rcross. The default file is qtlcart.cro.

-m SRmapqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-t Use this to specify which trait SRmapqtl will analyze. If this number is greater than the number of traits, then all traits will be analyzed. The default is to analyze trait 1 only.

-M This tells SRmapqtl what type of analysis to perform. Use a 0 for forward stepwise (FS) regression, a 1 for backward elimination (BE) and a 2 for forward regression with a backward elimination step at the end (FB). It is probably best to use Model 2 here.
-F Requires a real number in the range 0.0 to 1.0. This is a threshold p value for adding markers in model 2 during the forward stepwise regression step. The default is 0.05.

-B Requires a real number in the range 0.0 to 1.0. This is a threshold p value for deleting markers in model 2 during the backward elimination step. It should probably be the same as the previous option. The default is 0.05.

-u Requires an integer valued argument. This allows you to specify a hard limit to the number of steps in a forward regression analysis. It is valid for models 0 and 2. By default, it is 100.

INPUT FORMAT
The input format of the molecular map should be the same as that of the output format from the program Rmap. The input format of the individual data should be the same as the output format of the program Rcross.

EXAMPLES

% SRmapqtl -i corn.cro -m corn.map -M 2

Does a forward stepwise regression with a backward elimination step for the dataset in corn.cro using the genetic linkage map in corn.map.

REFERENCES

BUGS
Forward and backward regression should probably use the thresholds for adding and deleting markers from the model. When that feature is added, the -F and -B options will have more use.

SEE ALSO

Rmap(1), Rqtl(1), Rcross(1), Qstats(1), LRmapqtl(1), Zmapqtl(1), JZmapqtl(1), Eqtl(1), Prune(1), Preplot(1), QTLcart(1)

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CHAPTER 8. UNIX MAN PAGES

QTL Cartographer

8.9 ZMAPQTL

NAME

Zmapqtl — Composite interval mapping module

SYNOPSIS


DESCRIPTION

Zmapqtl uses composite interval mapping to map quantitative trait loci to a map of molecular markers. It requires a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The sample could be a randomly generated one from Rcross or a real one in the same format as the output of Rcross. In addition, the program requires the results of the stepwise linear regression analysis of SRmapqtl for composite interval mapping.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. Zmapqtl will append the file if it exists, and create a new file if it does not. If not used, then Zmapqtl will use qtlcart.z.

-i This requires an input filename. This file must exist. It should be in the same format as the output of Rcross. The default file is qtlcart.cro.

-m Zmapqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-t Use this to specify which trait Zmapqtl will analyze. If this number is greater than the number of traits, then all traits will be analyzed. The default is to analyze trait 1 only.

-l Allows the user to specify the name of the file containing results from LRmapqtl. Zmapqtl reads those results and uses the information to choose cofactors for some of the analysis methods.
-S Allows the user to specify the name of the file containing results from SRmapqtl. Zmapqtl reads the results and uses the information to choose cofactors for composite interval mapping model 6.

-M Zmapqtl assumes the specified model (see below) in the analysis. Model 3 is default.

-c The user can specify a specific chromosome for Zmapqtl to analyze. If zero, then all will be analyzed.

-d Zmapqtl walks along the chromosome at a rate that can be specified with this option. The default is to do an analysis every 2 centiMorgans along the chromosome.

-n Use this to indicate how many background parameters Zmapqtl uses in composite interval mapping. This is used only with model 6, and gives an upper bound. If fewer than this number of markers are ranked in the SRmapqtl.out file, then less than the specified number of markers will be used.

-w Zmapqtl blocks out a region of this many centiMorgans on either side of the markers flanking the test position when picking background markers. It is 10 by default and is only used in models 5 and 6. We refer to it as the window size.

-r Zmapqtl can do a permutation test to determine the threshold for rejecting the null hypothesis of no QTL at a site. By default, this option sets the number of permutations equal to 0, which means no permutation test is run. You can set it to a number $\geq 10000$ to do the test. See Churchill and Doerge (1994) for more details. The results are in an interim file. Use Eqtl to summarize them when enough repetitions have been done. You need to run Zmapqtl without permutations or bootstraps at least once before you can do the permutation tests. This option only allows for interval mapping (Model 3) or composite interval mapping (Model 6).

-b When used with argument 1, Zmapqtl will do a single bootstrap. You need to run Prune to actually create the bootstrapped data set: This option merely analyzes it and stores summary statistics in an interim file qtlcart.s3b by default, for model 3. You should also run Zmapqtl without bootstraps or permutation tests before doing a bootstrap analysis.

When used with an argument 2, Zmapqtl will do a jackknife analysis. Again, Zmapqtl should be run without this argument prior to doing a jackknife.

INPUT FORMAT

The input format of the molecular map should be the same as that of the output format from the program Rmap. The input format of the individual data should be the same as the output format of the program Rcros.
EXAMPLES

```
% Zmapqtl
```

Calculates the likelihood ratio test statistics of the dataset in `qtlcart.cro` using the map in `qtlcart.map`.

```
% nice Zmapqtl -A -V -i corn.cro -m corn.map -M 6 -r 500 &
```

Calculates the likelihood ratio test statistics of the dataset in `corn.cro` using the map in `corn.map`. Model 6 is used for analysis and a permutation test with 500 replications is performed. The program is nice’d as a courtesy to other users, and run in the background so that the user can logout and relax.

MODELS

Different parameters for the `-M` option allow for the analysis of the data assuming different models. Models 1–3 were described in Zeng (1993, 1994).

1. Fit all the background markers

2. Fit all unlinked background markers

3. Fit only the mean (Lander and Botstein (1989) method)

4. Fit a subset of the other markers, namely those unlinked markers with the highest correlation with the trait on each chromosome.

5. This model uses a pair of markers from each other chromosome and all linked markers that fall outside a window around the flanking markers. This window extends to 10 cM beyond the markers immediately flanking the test position. The window size can be changed with the `-w` option.

6. This model uses a specified number of markers that fall outside a window around the flanking markers. This window extends to 10 cM beyond the markers immediately flanking the test position. The number of markers are set by the `-n` option. You need to run `SRmapqtl` to rank the markers before using model 6.

7. This model requires that you have already run `Zmapqtl` and `Eqtl`. It reads in the estimated QTL from the `Eqtl.out` file and uses them as virtual markers to control for the genetic background. All identified markers are used that do not fall within the window.

8. Like model 7, this requires a prior run of `Zmapqtl` and `Eqtl`. Instead of using virtual markers, `Zmapqtl` uses the closest flanking markers to identified QTL. Again, all of these markers outside the window are used.

The default is to fit only the mean, that is to use interval mapping.
PERMUTATION TESTS

Churchill and Doerge (1994) describe a method to calculate the threshold values for quantitative trait mapping that we have implemented in this program. Basically, it does a permutation of the trait values and the genotypes and redoes the analysis. Over the number of replicates, two types of thresholds are defined: "experimentwise" and "comparisonwise". We calculate the experimentwise thresholds, but only give p values for the comparisonwise values to save on storage space. The p values give the proportion of permuted replicates that have loglikelihood ratios larger than the observed ratios.

If you choose to do permutation tests, you need to run \texttt{Zmapqtl} with the model of choice prior to doing the permutation test. Also, if the program terminates prematurely, you can restart it from where it left off to complete the permutation test.

REFERENCES


CAVEATS

Model 7 has not been extensively tested. Remember that you will need to run \texttt{Zmapqtl} with some other model (say 3 or 6) and then run \texttt{Eqtl} prior to using model 7.

Model 8 requires a prior run of \texttt{Zmapqtl} and \texttt{Eqtl} as well. There is a shell script called \texttt{Model8.csh} in the \texttt{scripts} subdirectory that allows you to easily iterate using model 8. Try using it to see whether your set of cofactors (or estimated QTL) becomes stable after a few iterations. A low threshold may lead to adding and dropping putative QTL over consecutive analyses using Model 8. Here is the shell script:

```csh
#!/usr/bin/csh
#
# Run Model 8 iteration
# Copyright 2001 Christopher J. Basten
# Usage:
# Model8 bindir stem siglevel iterations max_nbp
# bindir is the binary subdirectory
# stem is the filename stem
# siglevel is the significance level to declare a QTL
```
# iterations is the number of iterations
# max_nbp is the maximal number of background parameters.
#
if ( $1 == '-h' ) then
    echo " Usage: Model8.csh bindir stem siglevel iterations max_nbp"
    echo "Where"
    echo " bindir = QTL Cart. binary directory"
    echo " stem = filename stem"
    echo " siglevel = Significance level to declare a QTL"
    echo " iterations = number of iterations"
    echo " max_nbp = maximal number of background parameters"
    echo ""
    echo "Now exiting"
    exit
endif
set bindir=$1
set stem=$2
set siglevel=$3
set iterations=$4
set maxnbp=$5
$bindir/Qstats -X $stem -A -V
$bindir/Zmapqtl -A -V -M 3
$bindir/Eqtl -A -V -S $siglevel
#
# Save the original files
#
/usr/bin/mv $stem.eqt $stem.eqt.0
/usr/bin/mv $stem.z $stem.z.0
/usr/bin/cp $stem.sr $stem.sr.0
#
# Use model 8 iteratively with cofactors from previous run.
#
set i=1
while ( $i < $iterations )
    echo "Doing iteration $i"
    $bindir/Zmapqtl -A -V -M 8 -n $maxnbp
    /usr/bin/rm $stem.sr
    $bindir/Eqtl -A -V -S $siglevel
    /usr/bin/cp $stem.sr $stem.sr.$i
    /usr/bin/mv $stem.eqt $stem.eqt.$i
    /usr/bin/mv $stem.z $stem.z.$i
@ i++
end
/usr/bin/rm $stem.sr
echo "Finished"

BUGS
It is likely that we will abandon the internal permutation tests in Zmapqtl. It is more efficient to use Prune and a batch file to do the same job. This paradigm will allow users to do permutation tests with any of the programs.

SEE ALSO
Rmap(1), Rqtl(1), Rcros(1), Qstats(1), LRmapqtl(1), SRmapqtl(1), JZmapqtl(1), Eqtl(1), Prune(1), Preplot(1), QTLcart(1)

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CHAPTER 8. UNIX MAN PAGES

8.10 JZMAPQTL

NAME

JZmapqtl — Multitrait mapping module

SYNOPSIS


DESCRIPTION

JZmapqtl uses (composite) interval mapping to map quantitative trait loci to a map of molecular markers and can analyze multiple traits simultaneously. It requires a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The sample could be a randomly generated one from Rcross or a real one in the same format as the output of Rcross. In addition, the program requires the results of the stepwise linear regression analysis of SRmapqtl for composite interval mapping.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. JZmapqtl will append the file if it exists, and create a new file if it does not. If not used, then JZmapqtl will use qtlcart.zj, where the j indicates the trait analyzed and the zero'th file contains joint mapping.

-i This requires an input filename. This file must exist. It should be in the same format as the output of Rcross. The default file is qtlcart.cro.

-m JZmapqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-t Use this to specify which trait JZmapqtl will analyze. If this number is greater than the number of traits, then all traits will be analyzed unless the trait name begins with a minus sign. If a negative number is given, then only traits beginning with a plus sign will be analyzed. The default is to analyze trait 1 only.
-E Allows the user to specify the name of the file containing results from \texttt{Eqtl}. \texttt{JZmapqtl} reads those results and uses the information to choose cofactors for some of the analysis methods.

-S Allows the user to specify the name of the file containing results from \texttt{SRmapqtl}. \texttt{JZmapqtl} reads the results and uses the information to choose cofactors for composite interval mapping model 6.

-M \texttt{JZmapqtl} assumes the specified model (see below) in the analysis. Model 3 is default.

-c The user can specify a specific chromosome for \texttt{Zmapqtl} to analyze. If zero, then all will be analyzed.

-d \texttt{Zmapqtl} walks along the chromosome at this rate. The default is to do an analysis every 2 centiMorgans along the chromosome.

-n Use this to indicate how many background parameters \texttt{JZmapqtl} uses in composite interval mapping. This is used only with model 6, and gives an upper bound. If fewer than this number of markers are ranked in the \texttt{SRmapqtl.out} file, then less than the specified number of markers will be used.

-w \texttt{JZmapqtl} blocks out a region of this many centiMorgans on either side of the markers flanking the test position when picking background markers. It is 10 by default and is only used in models 5 and 6. We refer to it as the \textit{window size}.

-I \texttt{JZmapqtl} requires the user to specify which hypotheses to test. For backcrosses, there are two hypotheses numbered 1 and 0. Use 10 for backcrosses or a 14 to do GxE tests as well. For crosses in which there are three genotypic classes, there are hypotheses 0, 1, 2, and 3. Use 30, 31, 32 in that case or 34 to do GxE. These are explained in greater detail in the manual.

**INPUT FORMAT**

The input format of the molecular map should be the same as that of the output format from the program \texttt{Rmap}. The input format of the individual data should be the same as the output format of the program \texttt{Rcross}.

**EXAMPLES**

```bash
% JZmapqtl
```

Calculates the likelihood ratio test statistics of the dataset in \texttt{qtlcart.cro} using the map in \texttt{qtlcart.map}.

```bash
% nice JZmapqtl -A -V -i corn.cro -m corn.map -M 6 -t 3 -I 34 &
```
Calculates the likelihood ratio test statistics of the dataset in *corn.cro* using the map in *corn.map*. Model 6 is used for analysis. This file has two traits, so specifying trait 3 means that both traits are analyzed. Hypothesis 34 means that GxE interactions are also analyzed. The program is nice’d as a courtesy to other users, and run in the background so that the user can logout and relax.

**MODELS**

Different parameters for the `-M` option allow for the analysis of the data assuming different models. See the *Zmapqtl* man page for explanations of models 3 and 6. These are the only models available in *JZmapqtl*.

**REFERENCES**


**BUGS**

*Preplot* ignores the output at present. So far, the program only does joint mapping and one form of GxE. Tests for close linkage, pleiotropic effects and other environmental effects will be added in the future.

**HINTS**

You can select traits to include in the analysis in three ways:

- **a.** Set the trait to analyze at 0, so that no traits except those beginning with a `+` (plus sign) are analyzed. You would need to edit the `.cro` file first to prepend a `+` to all traits you wanted in the analysis.
- **b.** Set the trait to a value in the range `[1-t]` inclusive, where `t` is the number of traits in the `.cro` file. You will then get single trait results.
- **c.** Set the trait to a value greater than `t`. Then all traits will be put in the analysis, unless they begin with a minus sign `[-]`. As in a. above, you would need to edit the `.cro` file to minus out some traits.
You need to set the hypothesis test for SFx and RFx crosses. The default of 10 is ok for crosses in which there are only two marker genotypic classes (BCx, RIx). To test GxE, use 14. For SFx and RFx, values of 30, 31 or 32 are valid, and a 34 invokes the GxE test. Recall that we have the following hypotheses:

1. H0: $a = d = 0$
2. H1: $a \neq 0$, $d = 0$
3. H2: $a = 0$, $d \neq 0$
4. H3: $a \neq 0$, $d \neq 0$

For 30, we test H3:H0. For 31, we test H3:H0, H3:H1 and H1:H0. For 32, we test H3:H0, H3:H2 and H2:H0. 30 is probably fine for initial scans. Hypothesis 34 does a test for H3:H0 as well as the GxE.

For Model 6, be sure to run SRmapqtl first. Once done, JZmapqtl will use all markers that are significant for any of the traits in the analysis. We need to work out a better way to select the cofactors. Presently we use any markers that are significant for any trait. Also, be sure to use FB regression (Model 2 in SRmapqtl), or else you will end up using all markers as cofactors.

SEE ALSO

Rmap(1), Rqtl(1), Rcross(1), Qstats(1), LRmapqtl(1), SRmapqtl(1), Zmapqtl(1), Eqtl(1), Prune(1), Preplot(1), QTLcart(1)

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8.11 MIMAPQTL

NAME

MImapqtl — Multiple Interval mapping module

SYNOPSIS


DESCRIPTION

MImapqtl uses multiple interval mapping to map quantitative trait loci to a map of molecular markers. It requires a molecular map that could be a random one produced by Rmap, or a real one in the same format as the output of Rmap. The sample could be a randomly generated one from Rcross or a real one in the same format as the output of Rcross. In addition, the program can use an initial genetic model. This model will most likely be produced by running Eqt1 on the results of a Zmapqtl run, but could be the results of a prior run of MImapqtl.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. MImapqtl will append the file if it exists, and create a new file if it does not. If not used, then MImapqtl will use qtlcart.mim.

-i This requires an input filename. This file must exist. It should be in the same format as the output of Rcross. The default file is qtlcart.cro.

-m MImapqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-t Use this to specify which trait MImapqtl will analyze. If this number is greater than the number of traits, then all traits will be analyzed unless the trait name begins with a minus sign. If a negative number is given, then only traits beginning with a plus sign will be analyzed. The default is to analyze trait 1 only.
-E Allows the user to specify the name of the file containing the genetic model for input. This file should be in the format of \texttt{Rqtl.out} and produced by \texttt{Rqtl}, \texttt{Eqtl} or \texttt{MImapqtl}. A new model will be placed in the file specified with the \texttt{-O} option. For an initial analysis (phase 0), this will default to \texttt{qtlcart.eqt}.

-\texttt{O} Allows the user to specify the name of the file containing the genetic model for output. For an initial analysis (phase 0), this will default to \texttt{qtlcart.mqt}.

-\texttt{q MImapqtl} has a limit to the number of QTL it can analyze. For 32 bit machines, this is 19 QTL. For 64 bit machines, this can be 31. If you set this to a number higher than that allowed, it will be reset to the maximum allowed for the machine type.

-\texttt{k} The user can specify the maximum number of epistatic terms allowed in the model.

-\texttt{d MImapqtl} walks along an interval at this rate during the refinement of QTL positions and the search for more QTL.

-\texttt{S} Requires an integer value to indicate the information criterion for declaring the presence or absence of a parameter. Information criteria are explained below.

-\texttt{L} Requires a real value to indicate the threshold for adding or deleting parameters to a model. Comparisons are made based on the information criterion function specified with the \texttt{-S} option above. The default is 3.84. If this is set too low, the program will continue to find QTL until it hits the upper limit. If set too high, it will not find any QTL.

-\texttt{I} Requires an eight character string that codes for what the program should do. See below for more explanation.

-\texttt{p} is used with an integer to specify the phase of the analysis. See below for more explanation.

FILES

You will need a map of molecular markers, \texttt{qtlcart.map} and a data set, \texttt{qtlcart.cro}. You can also specify an initial genetic model, \texttt{qtlcart.qtl}.

The input format of the molecular map should be the same as that of the output format from the program \texttt{Rmap}. The input format of the individual data should be the same as the output format of the program \texttt{Rcross}. If you use an initial genetic model, it should be of the same format as an \texttt{Rqtl} output file. The output of \texttt{Eqtl} will also have such a model, as will the output of \texttt{MImapqtl} itself.

\texttt{MImapqtl} can produce three types of output files. Most results will be put in the \texttt{qtlcart.mim} file, while the \texttt{Rqtl} formatted output file will be \texttt{qtlcart.mqt}. If you choose to calculate residuals, they will be placed in \texttt{qtlcart.res}, which will have the same format as an \texttt{Rcross} output file.
NOTES

ANALYSIS

If MImapqtl is invoked and an initial model is provided, it will do the following seven steps:

1. **Initial Model**
   Read in the initial model and convert it to a usable format. The model is read from the file specified by the -E option and must exist.

2. **Parameter Estimation**
   Estimate all parameters in the initial model. If used, then the initial model simply specifies the positions of the QTL.

3. **Refine Positions**
   Refine the estimates of the positions of all QTL in the initial model. This refinement occurs in the interval where the QTL resides. This is not an option to search other intervals for QTL.

4. **Test parameters**
   Test each parameter in the initial model for significance. This follows a backward elimination procedure, and those parameters that do not lead to a significant improvement in fit are dropped. The threshold for dropping parameters is specified by the -L option. The information criterion is calculated for the model with and without the tested parameter, and the difference must be greater than the threshold for the effect to be retained.

5. **Search for QTL**
   Search for more QTL. This follows a forward stepwise procedure, whereby the genome is scanned, the most likely place for a new QTL is determined, and if it results in a significant improvement, is retained.

6. **Epistasis search**
   Search for epistatic interactions between the QTL in the model. This will do all pairwise combinations of the QTL that survive steps 4 and 5.

7. **Calculate predictions**
   Calculate breeding values, the Variance-Covariance matrix and R2 values for the parameters.

If the user specifies that no initial model is to be used, then the analysis starts with step 5 above.

WORK CODE

The **Work Code** must be specified with an 8 letter string. Each letter in the string is a flag to tell the program whether to do a certain step. Some of the flags have options to
modify the behavior of that step. The 8 letter string starts from position 0. The remaining positions (1–7) correspond to the steps given in the previous section.

1. **Scan flag**
   This can take on values S or s. If S, then **MImapqtl** will go into scan mode. It will do one pass in the search for QTL phase, and print out positions and a likelihood profile to the output file. The user can then plot the values and decide where to place a new QTL.

2. **Model flag**
   Tells **MImapqtl** whether to use the initial model specified with the -E option. If M, then use the model, and if m, don’t use it. If you use m, then you should also specify **prt** in positions 2, 3 and 4. For example, **smprtSEC** would make sense: It would search for QTL de novo.

3. **Parameter flag**
   Use a P here if you want **MImapqtl** to re-estimate the parameters in the initial model. Use a p if you want to skip this step. The case of this position should almost always match that of position 1.

4. **Refine position flag**
   Use an R here if you want **MImapqtl** to refine the position estimates in the initial model. Use an r if you want to skip this step. If you don’t have an initial model, then this should be r. You can also extend the refinement of position to the immediate adjacent intervals by using A in this position.

5. **Test flag**
   Use a T here if you want **MImapqtl** to test the significance of the parameters in the initial model. Use a t if you want to skip this step. If you don’t have an initial model, then this should be t. You can use D in place of T in order to test dominance effects only, but this is only relevant with three marker classes. Finally, if you want to test any existing epistatic interactions, then use E.

6. **Search flag**
   Use an S here if you want **MImapqtl** to search for more QTL. Use an s if you want to skip this step. You can also specify a A if you only want to search for the additive effects of putative QTL (that is, don’t search for dominance effects in Fx lines). Finally, if you use a D here, **MImapqtl** will only search for dominance effects at QTL locations that don’t already have them.

7. **Epistasis flag**
   Use an E here if you want **MImapqtl** to search for epistatic effects. Use an e if you want to skip this step. By default, the **MImapqtl** does a forward stepwise search for epistatic terms. If you want to try a backward elimination approach, use a B in this position, but be aware that if there are too many epistatic terms, the request will be ignored in favor of a forward search. Finally, a U in this position will do a backward
elimination approach but the limit to the number of parameters will be the sample size minus one.

8. Covariance flag
   Use a C here if you want MImapqtl to calculate the variance-covariance matrix, R2 values and breeding values for the final model. Use a c if you want to skip this step. If you specify an R in this spot, then for the current model, the residuals for the trait being analyzed are calculated and used as the new trait values. These residuals are written to a file stem.res where stem is the filename stem.

The default string is smprtSeC, which tells MImapqtl to scan for QTL without an initial model, where the the additive and dominance effects are treated as a unit.

INFORMATION CRITERIA

See Kao, Zeng and Basten (1999) for more detailed information on the information criteria. We use

\[ IC(k) = -2(\log(L) - k \ c(n) / 2) \]

where L is the likelihood for a k-parameter model and \( \log \) is the natural log function. The penalty function \( c(n) \) takes one of six forms:

1. \( c(n) = \log(n) \)
2. \( c(n) = 2 \)
3. \( c(n) = 2 \log(\log(n)) \)
4. \( c(n) = 2 \log(n) \)
5. \( c(n) = 3 \log(n) \)
6. \( c(n) = 0 \)

Use the numbers above with the -S option to indicate which information criterion you want to use. If you use penalty functions 1 through 5 above, then you should also specify a threshold of 0.0 with the -L function. Penalty function 6 is equivalent to no penalty function and requires an experimentwise threshold value that might be obtained via a permutation test.

ANALYSIS PHASE

MImapqtl can read a genetic model and proceed with various tasks as explained above. This leads to the idea of repeating the analysis with the results of a previous run of the program. One can think of doing the analysis in steps or phases. The default is to set the phase to zero. If the phase is set to zero, then the default input file for a genetic model is
qtlcart.eqt, the output is qtlcart.mqt and the general output file is qtlcart.mim. At the end of the analysis, the phase remains 0.

If one sets the phase to a positive integer (generally starting with 1), then the default input is to assume that input and output files follow a rule. Assume the filename stem is qtlcart and the phase is $i$. The input genetic model will be set to qtlcartPhase$-i$.mqt, the output genetic model will be written to qtlcartPhase$-i$.mqt, and the general output file will be qtlcartPhase$-i$.mim. At the end of the analysis, the phase variable $i$ will be incremented by one and recorded in the qtlcart.rc file. This makes it easier for the program (and the user) to keep track of previous and current results. Also note that if you used an R in position 7 of the workcode, then the output file containing a new dataset with the residuals replacing the trait values will be put in qtlcartPhase$-i$.res.

EXAMPLES

% MImapqtl -I smprtSeC

Calculates the best model for the dataset in qtlcart.cro using the map in qtlcart.map and the model in qtlcart.eqt, but only searches for main effects (additive and dominance).

Here is a sequence using the example dataset mletest.cro along with its map file mletest.map, both of which come with the programs. Assume that these two files have been placed in an empty subdirectory which is now the current working directory.

% MImapqtl -A -V -I smprtSeC -L 0.0 -S 1 -p 1 -X mletest &
% MImapqtl -A -V -I smprtSeC &
% MImapqtl -A -V -I sMPrtSeC &
% MImapqtl -A -V -I sMPrtSeC &
% MImapqtl -A -V -I sMPrtsBC &

The first invocation sets the filename stem, the information criterion and threshold for adding parameters and indicates that it is phase 1. The -I option tells MImapqtl to search for additive QTL. The second invocation tests each QTL found in the first phase. The third step refines the positions of all remaining QTL. The fourth step searches for more QTL (and probably won’t find any). The fifth step searches for interactions between the identified putative QTL. The phase variable is updated after each step, so MImapqtl knows where to find the results from the previous step.

REFERENCES


**CAVEATS**

We are still doing some simulations to determine the best information criterion to use. At present, the default of 1 with a threshold of 0.0 seems to work well for a variety of data sets. If the default detects no QTL, then you might try information criteria 2, 3 or 6.

**BUGS**

Still under development: We hope to add the joint analysis of multiple traits in multiple environments. We are also working on the output formats.

The A option for refining positions in the work code does not yet behave correctly. It tends to place all putative QTL at the left flanking marker of an interval. If you use this option, then re-run `MImapqtl` with an R in position four to better refine the position estimate of the QTL.

**SEE ALSO**

`Rmap(1), Rqtl(1), Rcross(1), Qstats(1), LRmapqtl(1), SRmapqtl(1), Zmapqtl(1), JZmapqtl(1), Eqtl(1), Prune(1), Preplot(1), QTLcart(1)`

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8.12 PREPLOT

NAME

Preplot — Process results of LRmapqtl and Zmapqtl for input to gnuplot

SYNOPSIS


DESCRIPTION

Preplot reformats the output of LRmapqtl and Zmapqtl so that it can be plotted by GNUPLOT. It requires a molecular map that was used in the analysis of the data with LRmapqtl and Zmapqtl.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename stem for output. Preplot will overwrite the file if it exists, and create a new file if it does not. If not used, then Preplot will use qtlcart. The GNUPLOT file will be qtlcart.plt in that case.

-m Zmapqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-l This requires an input filename. This file must exist. It should be in the same format as the output of LRmapqtl. The default file is qtlcart.lr.

-q This requires an input filename. This file may or may not exist. It should be in the same format as the output of Rqtl. The default file is qtlcart.qtl.

-z This requires an input filename. This file must exist. It should be in the same format as the output of Zmapqtl. The default file is qtlcart.z.

-T Allows the user to set the output terminal. Valid options can be found in the GNUPLOT manual. The default is x11 on UNIX, mac for Macintosh and windows for MS-Windows.
-S When given an argument, **Preplot** will use this significance threshold. It is 3.84 by default.

-H **Preplot** will get results for this hypothesis test from the **Zmapqtl** output file. Test 1 is the default, which is the only value for a backcross.

-L If given an argument of 1, **Preplot** will output LOD scores instead of the LR test statistics.

**EXAMPLES**

```
% Preplot -L 1
```

**Preplot** will automagically reformat your results to be plotted by **GNUPLOT**, converting the likelihood ratio test statistics into LOD scores along the way.

**REFERENCES**


**CAVEATS**

**Preplot** will search for the output files from **Rqtl**, **Eqtl** and **M1mapqtl** and try to process them. If you don’t want them processed, rename or move the files. Note that **Preplot** only searches for files with names `stem.eqt`, `stem.qtl` and `stem.mqt`, where `stem` is the filename stem.

**BUGS**

**Preplot** ignores **JZmapqtl** output.

**SEE ALSO**

**Rmap(1)**, **Rqtl(1)**, **Rcross(1)**, **Qstats(1)**, **LRmapqtl(1)**, **SRmapqtl(1)**, **JZmapqtl(1)**, **Eqtl(1)**, **Prune(1)**, **Zmapqtl(1)**, **QTLcart(1)**

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151
CHAPTER 8. UNIX MAN PAGES

8.13 EQTL

NAME

Eqtl — Summarize the output of Zmapqtl

SYNOPSIS

Eqtl [ -o output ] [ -z zmapfile ] [ -m mapfile ] [ -t trait ] [ -M Model ] [ -a size ] [ -S threshold ] [ -L lod ]

DESCRIPTION

Eqtl reformats the prodigious output of Zmapqtl. The output file has a section that is suitable for input to Rcross. There are other sections to the output that are more readable. Eqtl can also detect whether a bootstrap, permutation or jackknife analysis was performed and process the interim files produced by those analyses.

OPTIONS

See QTLcart(1) for more information on the global options -h for help, -A for automatic, -V for non-Verbose -W path for a working directory, -R file to specify a resource file, -e to specify the log file, -s to specify a seed for the random number generator and -X stem to specify a filename stem. The options below are specific to this program.

If you use this program without specifying any options, then you will get into a menu that allows you to set them interactively.

-o This requires a filename for output. Eqtl will overwrite the file if it exists, and create a new file if it does not. If not used, then Eqtl will use qtlcart.eqt.

-z This requires an input filename. This file must exist. It should be in the same format as the output of Zmapqtl. The default file is qtlcart.z.

-m Eqtl requires a genetic linkage map. This option requires the name of a file containing the map. It should be in the same format that Rmap outputs. The default file is qtlcart.map.

-H Allows the user to specify which hypothesis test results to process. Use values 10 or 14 for data with two marker classes, and 30, 31, 32, 34 for those with three marker classes.

-S Tells Eqtl the significance threshold. It assumes that the test statistic is significant if greater than this value. It is 3.84 by default.

-a Eqtl uses the specified size (alpha) to determine the significance threshold from the experiment-wise permutation results. If used, the -S option is ignored, and the significance threshold is set and saved from the experiment-wise permutation test results. The size is 0.05 by default.
-L If used with argument 1, it causes LOD scores to be output rather than the LR statistics. It is 0 by default.

INPUT FORMAT
The input format of the molecular map should be the same as that of the output format from the program Rmap. The input format of the individual data should be the same as the output format of the program Rcross. The other files should have been created by Zmapqtl. Take care that Zmapqtl completed its analysis: An incomplete qtlcart.z file can cause Eqtl to crash.

EXAMPLES

% Eqtl -m example.map -z example.z -S 13.2

reprocesses the results of example.z based on the map in example.map using a significance threshold of 13.2.

BOOTSTRAPS, JACKKNIVES AND PERMUTATIONS
If Zmapqtl was used to do a bootstrap experiment or a permutation test, then there will be interim results files. With the default filename stem and model 3, there will be files qtlcart.z3c and qtlcart.z3e if a permutation test was done, and qtlcart.z3a if a bootstrap was done. Eqtl automatically detects these files and processes their results. It will open a qtlcart.z3e file and determine an experimentwise threshold based on the size specified with the -a option.

If the qtlcart.z3a file exists, then Eqtl opens it and computes the means and standard deviations, at each test site, of the likelihood ratio test statistic, additive effect and dominance effect. The results are printed to qtlcart.z3b.

The jackknife procedure produces a qtlcart.z3i that Eqtl opens computes the means and standard deviations, at each test site of the likelihood ratio test statistic, additive effect and dominance effect. The results are printed to qtlcart.z3j.

REFERENCES

BUGS
If the resource file indicates that there are more than one trait, then Eqtl will try to estimate positions and additive effects for all the traits. This will even if no analysis was done on the extra traits. The output file will then have some null estimates.

When doing a jackknife with Zmapqtl, the user should check that the file ending in the letter i is truly the last version of the interim jackknife file. Zmapqtl switches between a file ending in i and another ending in j, so check both and move the j file onto the i file if required.

If you set the significance threshold too high, then Eqtl may find no QTL in the qtlcart.z output. If this is the case, then Eqtl will crash.
SEE ALSO
Rmap(1), Rqtl(1), Rcross(1), Qstats(1), LRmapqtl(1), SRmapqtl(1), JZmapqtl(1), Zmapqtl(1), Prune(1), Preplot(1), QTLcart(1)

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Bibliography


Index

-A, 108
-B, 132
-E, 118, 121, 140, 144
-F, 132
-H, 121, 151, 152
-I, 121, 124, 140, 144
-L, 144, 151, 153
-M, 114, 125, 131, 134, 140
-O, 144
-R, 108
-S, 134, 140, 144, 151, 152
-T, 150
-V, 108
-W, 108
-X, 109
-a, 152
-b, 118, 125, 134
-c, 114, 121, 134, 140
-d, 114, 118, 134, 140, 144
-e, 109
-f, 114
-g, 114, 121
-h, 108
-i, 113, 117, 120, 124, 127, 129, 131, 133, 139, 143
-k, 144
-l, 133, 150
-m, 114, 117, 120, 124, 127, 129, 131, 133, 139, 143, 150, 152
-n, 121, 134, 140
-o, 113, 117, 120, 124, 127, 129, 131, 133, 139, 143, 150, 152
-p, 114, 144
-q, 117, 120, 144, 150
-r, 129, 134
-s, 108
-t, 114, 117, 129, 131, 133, 139, 143
-u, 132
-vd, 114
-vm, 114
-w, 134, 140
-z, 150, 152
0. qtlcart.cro, 121
1. Scan flag, 146
1. c(n) = log(n), 147
1. Initial Model, 145
1. cross.inp, 121
1. Model flag, 146
2. c(n) = 2, 147
2. Parameter Estimation, 145
2. mapmaker.raw, 121
2. Parameter flag, 146
3. c(n) = 2 log(log(n)), 147
3. Refine Positions, 145
3. qtlcart.r, 122
3. Refine postion flag, 146
4. c(n) = 2 log(n), 147
4. Test parameters, 145
4. qtlcart.sas, 122
4. Test flag, 146
5. c(n) = 3 log(n), 147
5. Search for QTL, 145
5. plabqtl0.qdt, 122
5. Search flag, 146
6. c(n) = 0, 147
6. Epistasis search, 145
6. Epistasis flag, 146
7. Calculate predictions, 145

INDEX

Covariance flag, 147
a., 141
additive effect, 34
ANALYSIS, 145
ANALYSIS PHASE, 147
AUTOMATIC ACTIONS, 125
b., 141
background parameter, 57
beta distribution, 34
bootstrap, 25, 44, 58, 74
BOOTSTRAPS, JACKKNIVES AND PER-
MUTATIONS, 153
bug, 19
c., 141
categorical trait, 39, 51
CAVEATS, 136, 149, 151
command line, 20
composite interval mapping, 45, 55, 63,
105
covariate, 45, 73
cross
advanced intercross, 12
backcross, 11, 60
Design III, 12
doubled haploid, 12
intercross, 11, 61
recombinant inbred line, 12
repeated backcross, 12
test cross, 12
CROSSES, 122
dominance, 34, 42
ECM algorithm, 55
EQTL, 152
Eqtl, 63, 73
options, 75
output, 73
experimentwise significance level, 63
FILENAME STEM, 111
filename stem, 28
ftp server, 16, 79, 85
gamma distribution, 34
gamma function, 34
genetic linkage map, 11, 13, 30, 35
GLOBAL BEHAVIOR, 109
GLOBAL COMMAND LINE OPTIONS,
109
GNUPLLOT, 14, 30, 33, 77, 78
heritability, 35–37
HINTS, 141
inbred line, 11
INFORMATION CRITERIA, 147
INPUT FORMAT, 115, 118, 121, 125, 127,
130, 132, 134, 140, 153
install
Macintosh, 18
MS-Windows, 17
UNIX, 17
interactive menu, 23, 25, 41
interval mapping, 45, 55, 63, 105
jackknife, 58, 74
JZMAPQTL, 139
JZmapqtl, 63
option, 63
least squares, 52
linear regression, 51
LINPACK, 15
LOD, 76
log file, 24
LR, 76
LRMAPQTL, 129
LRmapqtl, 51
options, 52
output, 52
Macintosh, 13, 16, 21, 44
binhex, 18
install, 18
StuffitExpander, 18
mailing list, 19
INDEX

<table>
<thead>
<tr>
<th>MAPMAKER</th>
<th>13, 26, 31, 37, 88, 99</th>
</tr>
</thead>
<tbody>
<tr>
<td>mapping function</td>
<td>32</td>
</tr>
<tr>
<td>Fixed</td>
<td>32</td>
</tr>
<tr>
<td>Haldane</td>
<td>32</td>
</tr>
<tr>
<td>Kosambi</td>
<td>32</td>
</tr>
<tr>
<td>maximum likelihood</td>
<td>55</td>
</tr>
<tr>
<td>MIMAPQTL</td>
<td>143</td>
</tr>
<tr>
<td>Mmapqtl</td>
<td>65</td>
</tr>
<tr>
<td>option</td>
<td>66</td>
</tr>
<tr>
<td>missing data</td>
<td>50</td>
</tr>
<tr>
<td>MODEL</td>
<td>130</td>
</tr>
<tr>
<td>MODELS</td>
<td>135, 141</td>
</tr>
<tr>
<td>MS-Windows</td>
<td>13, 21, 44</td>
</tr>
<tr>
<td>GNUPLOT</td>
<td>17</td>
</tr>
<tr>
<td>Windows Explorer</td>
<td>17</td>
</tr>
<tr>
<td>multiple interval mapping</td>
<td>65</td>
</tr>
<tr>
<td>Note</td>
<td>22–24, 28, 30, 31, 33, 37, 54</td>
</tr>
<tr>
<td>OPTIONS</td>
<td>108, 113, 117, 120, 124, 127, 129, 131, 133, 139, 143, 150, 152</td>
</tr>
<tr>
<td>OUTPUT OPTIONS</td>
<td>121</td>
</tr>
<tr>
<td>permutation test</td>
<td>45, 53, 55, 58, 62, 74, 76</td>
</tr>
<tr>
<td>PERMUTATION TESTS</td>
<td>136</td>
</tr>
<tr>
<td>phenotype</td>
<td>36</td>
</tr>
<tr>
<td>PREPLOT</td>
<td>150</td>
</tr>
<tr>
<td>Preplot</td>
<td></td>
</tr>
<tr>
<td>automagic</td>
<td>76</td>
</tr>
<tr>
<td>options</td>
<td>76</td>
</tr>
<tr>
<td>printing</td>
<td>77, 78</td>
</tr>
<tr>
<td>PRUNE</td>
<td>124</td>
</tr>
<tr>
<td>Prune</td>
<td>41, 59</td>
</tr>
<tr>
<td>interactive menu</td>
<td>42</td>
</tr>
<tr>
<td>QSTATS</td>
<td>127</td>
</tr>
<tr>
<td>Qstats</td>
<td>47</td>
</tr>
<tr>
<td>options</td>
<td>50</td>
</tr>
<tr>
<td>QTL</td>
<td>10, 33</td>
</tr>
<tr>
<td>QTL CART</td>
<td>108</td>
</tr>
<tr>
<td>RCROSS</td>
<td>120</td>
</tr>
<tr>
<td>Recross</td>
<td>35</td>
</tr>
<tr>
<td>input</td>
<td>37, 99</td>
</tr>
<tr>
<td>output</td>
<td>37</td>
</tr>
<tr>
<td>REFERENCES</td>
<td>112, 115, 118, 123, 128, 130, 132, 136, 141, 148, 151, 153</td>
</tr>
<tr>
<td>RESOURCE FILE</td>
<td>110</td>
</tr>
<tr>
<td>resource file</td>
<td>24, 79</td>
</tr>
<tr>
<td>RMAP</td>
<td>113</td>
</tr>
<tr>
<td>Rmap</td>
<td>29</td>
</tr>
<tr>
<td>input</td>
<td>88</td>
</tr>
<tr>
<td>input format</td>
<td>30, 31</td>
</tr>
<tr>
<td>options</td>
<td>30, 31</td>
</tr>
<tr>
<td>output</td>
<td>33, 93</td>
</tr>
<tr>
<td>RQTL</td>
<td>117</td>
</tr>
<tr>
<td>Rqtl</td>
<td>33</td>
</tr>
<tr>
<td>input</td>
<td>33, 35, 94</td>
</tr>
<tr>
<td>output</td>
<td>73, 98</td>
</tr>
<tr>
<td>sample</td>
<td></td>
</tr>
<tr>
<td>average deviation</td>
<td>47</td>
</tr>
<tr>
<td>kurtosis</td>
<td>47</td>
</tr>
<tr>
<td>mean</td>
<td>47</td>
</tr>
<tr>
<td>skewness</td>
<td>47</td>
</tr>
<tr>
<td>standard deviation</td>
<td>47</td>
</tr>
<tr>
<td>variance</td>
<td>47</td>
</tr>
<tr>
<td>simulation</td>
<td></td>
</tr>
<tr>
<td>cross</td>
<td>35</td>
</tr>
<tr>
<td>gametes</td>
<td>36</td>
</tr>
<tr>
<td>genetic linkage map</td>
<td>30</td>
</tr>
<tr>
<td>genetic model</td>
<td>34</td>
</tr>
<tr>
<td>missing data</td>
<td>43, 46</td>
</tr>
<tr>
<td>QTL</td>
<td>34</td>
</tr>
<tr>
<td>random number seed</td>
<td>23</td>
</tr>
<tr>
<td>recombination</td>
<td>36</td>
</tr>
<tr>
<td>trait</td>
<td>37</td>
</tr>
<tr>
<td>SRMAPQTL</td>
<td>131</td>
</tr>
<tr>
<td>SRmapqtl</td>
<td>45, 57</td>
</tr>
<tr>
<td>output</td>
<td>54</td>
</tr>
<tr>
<td>standard deviation</td>
<td>59</td>
</tr>
<tr>
<td>stepwise regression</td>
<td>45, 53</td>
</tr>
<tr>
<td>backward</td>
<td>53</td>
</tr>
<tr>
<td>forward</td>
<td>53</td>
</tr>
<tr>
<td>forward-backward</td>
<td>53</td>
</tr>
<tr>
<td>token</td>
<td>88</td>
</tr>
<tr>
<td>UNIX</td>
<td>13, 16, 20</td>
</tr>
<tr>
<td>install</td>
<td>17</td>
</tr>
</tbody>
</table>

160
USING THE INDIVIDUAL PROGRAMS, 111

variance
   environmental, 35, 37
   genetic, 37
verbosity, 23
virtual marker, 73

web site, 19, 79
window size, 57
WORK CODE, 145
WORKING DIRECTORY, 110
working directory, 21, 24, 79

ZMAPQTL, 133
Zmapqtl, 45, 55
   model, 56
   option, 57
   output, 60
   virtual marker, 57