QTL Cartographer

A Reference Manual and Tutorial for QTL Mapping

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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.*

You can usually download a file by using the **get** command with a filename. On Macintoshes, 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

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

```
 -W MacintoshHD:qtlcart:workdir
```

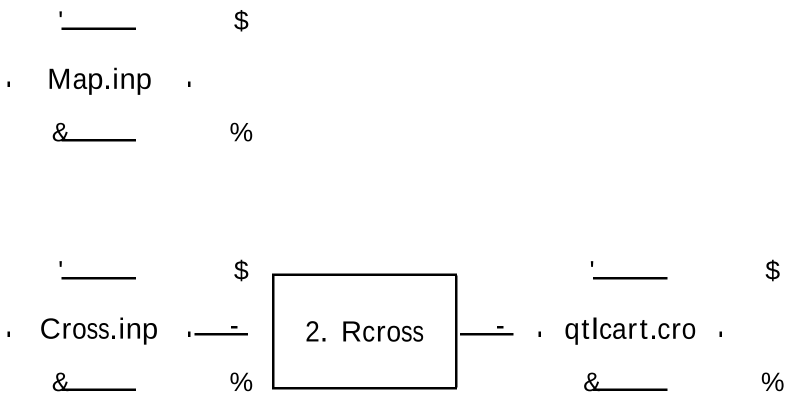
Random Number Seed

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

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.

Program	Extension	Contents	filetype
Rmap	.map	genetic linkage map	Rmap.out
Rqtl	.qtl	QTL model	Rqtl.out
Rcross	.cro	data file (markers, traits)	Rcross.out
Qstats	.qst	Qstats Analysis	Qstats.out

and other files recognized by *QTL Cartographer* are listed in Table 1.6.


Map.inp
Cross.inp
2. Rcross
qtlcart.cro

same concept holds for traits with option 4: Eliminate them in the order of highest to

or a comparison of likelihoods

$$T_2 = \quad 2\sum_{i=1}^{r} n_i(\ln n_i \quad \ln np_i)$$

Both T_1 and T_2 should have a ^{2}

Option	Default	Explanation
-i	qtlcart.cro	Data Input Fin47 cm/F15 tr490 Td[(ot)-3180(qtlcartlrt)-3414

3. Absolute position from left telomere, in Morgans.
4. Likelihood ratio test statistic for

inbreds). For

calculation of r^2

interval is the best position for the QTL.

The information criterion is is a function of the likelihood ratio and the number of

3.6.4 Threshold

If no penalty function is to be used, then it is important to specify the proper threshold for

Option	Default	Explanation

Chapter 5

Tutorial Examples

lpr sends a file to the printer. You can print up to 50 sheets from your account.

alias

1. Start up **Rmap**. Change the working subdirectory, and then the filename stem.

Chapter 6

Input File Formats

Map block

Between the `-start` token and the `-stop`

Command	Followed by	Means
`-filetype`		

```
    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
```

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

Chapter 7

Benchmarks

8.1 QTLCART

NAME

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

SYNOPSIS

QTLcart [**-h**] [**-V**] [**-A**] [**-s** *seed*] [**-W** *workdir*] [**-X**

-e This requires a filename for the log file. It will be appended to if it exists and created if not. The default is *qtlcart.log*.

-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 **QTLCart** is just a wildcard for any of the programs in the suite.

```
0. Continue with these parameters
```

3. **Qstats**, to summarize missing data and calculate some basic statistics on your quan-

8.2 RMAP

NAME

Rmap | Simulate or reformat a map of molecular markers

SYNOPSIS

Rmap

-d You can specify the type of dominance at the trait loci. If we assume inbred parental

-H

OUTPUT

Rcross can produce seven different types of output files. The output formats are specified

7. Prune the data back to one trait. Use the **-t** option with a trait number to select the

EXAMPLES

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

8.7 LRMAPQTL

NAME

LRmapqtl | Single marker QTL analysis.

SYNOPSIS

LRmapqtl [-o[

MODEL

The basic linear model is

PERMUTATION TESTS

```
        echo "Finished"
```

BUGS

It is likely that we will abandon the internal permutation tests in **Zmapqtl**. It is more

-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 *Rqtl.out* and produced by **Rqtl**, **Eqtl** or **MImapqtl**. A new model will be placed in the file specified with the **-O** option. For

NOTES

-S When given an argument, **Preplot**

SEE ALSO

Rao, D. C., B. J. Keats, J. M. Lalouel, N. E. Morton, and S. Lee (1979). A maximum likelihood map of chromosome 1. *A. J. Hum. Genet. 31*, 680{696.

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