

MapChart: Software for the Graphical Presentation of Linkage Maps and QTLs

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Over the last 15 years a wealth of linkage maps and quantitative trait loci (QTL) mapping results have become available. The pace of generating this genetic information is accelerating owing to advances in molecular marker technology and the development of software for linkage analysis and QTL mapping.

A graphical presentation of this information is often needed, both for publication purposes and for easy and intuitive interpretation. However, the development of tools for the graphical presentation of linkage maps and QTLs has lagged behind.

DrawMap (Van Ooijen 1994) was an early program capable of drawing genetic linkage maps. However, the output of this program was not very well suited for use in modern word processors and presentation software. Authors in this field have therefore, of necessity, resorted to the use of general graphics software to compose charts of their linkage and QTL maps. This is always a laborious process, with sometimes disappointing results. Also, each time a map is recalculated when new data become available, this process has to be repeated. For this reason I developed MapChart, a software package that takes as input the linkage and QTL data and generates charts of linkage maps and QTLs. These charts can easily be exported to word processing or presentation software. The charts are exported as vector graphics

(Windows enhanced metafiles) rather than bitmaps, which makes them easy to rescale and to edit further if desired.

User Interface

MapChart has a standard Windows interface, with a main menu, toolbar, and pop-up menus. The manual is available from the Help menu in the form of an HTML file with index and links.

Several maps can be opened simultaneously, each in their own subwindow. A map window consists of two tab sheets. One sheet shows a text editor with the map data, the other shows the chart pages. The chart pages can be shown at several magnifications, from a full-page view to a view at printer resolution. Both the charts and the map data can be printed, saved to files, or copied to the Windows clipboard.

Charts

MapChart displays charts of a series of linkage groups. A linkage group chart consists of a vertical bar on which the map positions and names of loci are indicated. Next to the bar, QTL intervals and QTL graphs can be shown, and sections of the bar can be highlighted. Linkage group charts can also be split into segments, which can be useful if they are too large to fit on the page. All the elements of the charts can be formatted with their own color, fill style, text font, etc. An example of a linkage group chart with some of these elements is shown in Figure 1.

By default the linkage groups are shown side by side on one or more pages, but they can also be shifted up or down to align homologous parts. Further, extra horizontal spacing or page breaks can be inserted between linkage groups to emphasize grouping (e.g., corresponding male and female linkage groups), and linkage group charts can be aligned vertically

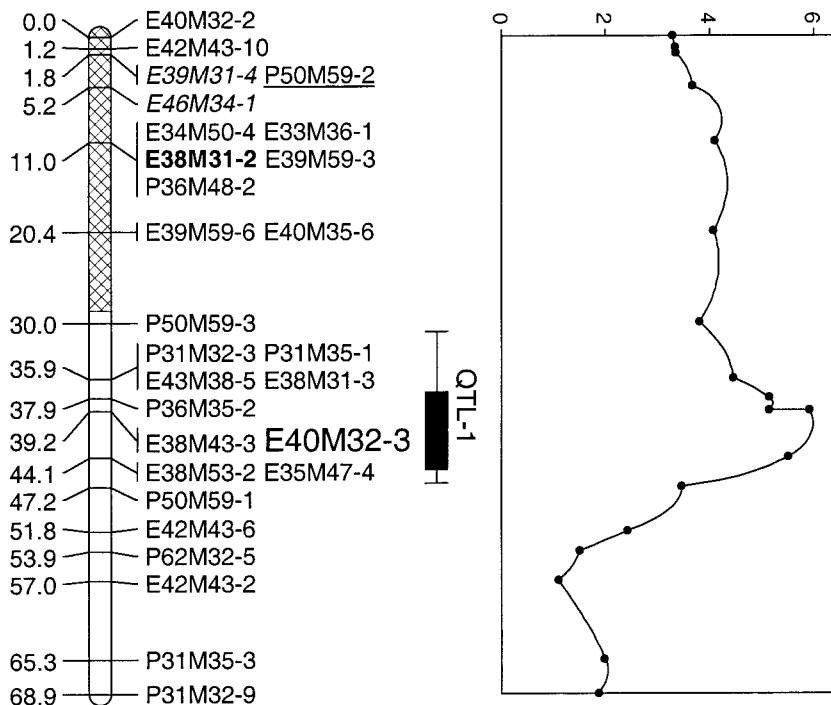


Figure 1. Chart of one linkage group, showing the bar, loci in various font styles and font sizes, positions (as absolute map positions), a cross-hatched bar segment, a 1 and 2 LOD QTL interval, and a QTL LOD graph.

(e.g., if they represent parts of the same chromosome).

Data and Formatting

Linkage Data

MapChart imports linkage data from map files, produced by software for linkage analysis. Map files are composed of a sequence of linkage groups, each with a header line specifying the linkage group title, followed by a sequence of lines with locus names and map positions. MapChart will draw basic charts from these data without further editing. Such map files are exported by JoinMap 3.0 (Van Ooijen and Voorrips 2001) or are easily assembled from the output of JoinMap 2.0 (Stam 1993; Stam and Van Ooijen 1995). Some mapping software, for example, MapMaker (Lander et al. 1987; Lincoln et al. 1990), presents linkage maps in terms of distances between loci; in this case conversion to map positions is necessary.

QTLs, Graphs, and Bar Segments

To each linkage group a QTLs section, a graphs section, and/or a bar segments section can be added. QTL intervals and bar segments are specified by their start and endpoints; for QTLs an inner and an outer interval (e.g., a 1 LOD and 2 LOD interval) can be specified. Graphs are specified by a reference to a text file containing the map positions and function values (e.g., LOD values) of graph points. Such graph files can be derived from the output of QTL mapping software such as MapMaker/QTL (Lincoln and Lander 1990) or QTL Cartographer (Basten et al. 1999) by extracting the relevant data columns. The output of MapQTL (Van Ooijen 2000; Van Ooijen and Maliepaard 1996) can be read without further editing.

Chart Options

Many chart options are available to adjust the general appearance of the charts.

These include the fonts, scaling, and sizing of different elements, a choice of which elements appear on the right and left side of the bar, the page setup, etc. Also, several options for displaying the map positions of loci are available: as absolute map positions, as intervals between loci, as ticks at fixed intervals, or no position indication at all.

Formatting Individual Elements

The appearance of individual chart elements can be adjusted by adding formatting information. Depending on the chart element, this formatting may include font size and style (bold, italics, underlined), color, fill style, line style, and symbol style. For loci, additional text (e.g., an indication of the linkage phase, skewness of segregation, etc.) can be specified; this text is shown in a separate column next to the locus name.

Tools

The creation of a chart with all the elements and formatting described above may require the specification of many parameters. MapChart supplies several tools to help with this task. First, if charts are too large to fit on the page, the AutoFit utility can be used to find a suitable combination of chart options. Second, users can save their own preferred default chart options, which will be used for all new charts. Finally, when a new version of a map has been calculated (e.g., with additional loci), all the formatting of chart elements from the previous version of the map can be automatically transferred to the new map. This makes it easy to generate presentable charts each time a map changes.

Availability

MapChart is available for Microsoft Windows 95 and Windows NT 3.5 or higher

operating systems. It has been developed over a period of 2 years, and the current version (2.0, February 2001) incorporates many suggestions from early users. MapChart can be downloaded and a free license ordered from the website at <http://www.joinmap.nl>. The installation package includes example files illustrating the various features of MapChart.

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References

- Basten CJ, Weir BS, and Zeng Z-B, 1999. QTL Cartographer version 1.13. Raleigh, NC: Department of Statistics, North Carolina State University.
- Lander ES, Green P, Abrahamson J, Barlow A, Daly MJ, Lincoln SE, and Newberg L, 1987. MAPMAKER: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations. *Genomics* 1:174-181.
- Lincoln SE, Daly MJ, and Lander ES, 1990. Constructing genetic linkage maps with MAPMAKER: a tutorial and reference manual. Technical Report. Cambridge, MA: Whitehead Institute for Biomedical Research.
- Lincoln SE and Lander ES, 1990. Mapping genes controlling quantitative traits using MAPMAKER/QTL. Technical Report. Cambridge, MA: Whitehead Institute for Biomedical Research.
- Stam P, 1993. Construction of integrated genetic maps by means of a new computer package: JoinMap. *Plant J* 3:739-744.
- Stam P and Van Ooijen JW, 1995. JoinMap[™] version 2.0: software for the calculation of genetic linkage maps. Wageningen: CPRO-DLO.
- Van Ooijen JW, 1994. DrawMap: a computer program for drawing genetic linkage maps. *J Hered* 85:66.
- Van Ooijen JW, 2000. MapQTL[™] version 4.0: user friendly power in QTL mapping. Addendum to the manual of version 3.0. Wageningen: Plant Research International.
- Van Ooijen JW and Maliepaard C, 1996. MapQTL[™] version 3.0: software for the calculation of QTL positions on genetic maps. *Plant Genome IV Conference*, San Diego, CA, 1996. Available at (<http://www.intl-pag.org/pag/4/abstracts/p316.html>).
- Van Ooijen JW and Voorrips RE, 2001. JoinMap[®] version 3.0: software for the calculation of genetic linkage maps. Wageningen: Plant Research International.
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