

Resource Summary Report

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Bionformatics Research Center

RRID:SCR_008540

Type: Tool

Proper Citation

Bionformatics Research Center (RRID:SCR_008540)

Resource Information

URL: <http://statgen.ncsu.edu/qtlcart/>

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Description: QTL Cartographer is a suite of programs to map quantitative traits using a map of molecular markers. The programs are available via an anonymous ftp server. See the README for more information. You will also want a copy of Gnuplot to display plots made by QTL Cartographer. Gnuplot is freely available on the web. Do a search to find the latest version for your operating system. Windows QTL Cartographer Windows QTL Cartographer is a user friendly version of QTL Cartographer. It has a GUI interface and runs under Microsoft Windows. Manual The manual for QTL Cartographer is written in LaTeX2e. An Adobe Portable document format (pdf) version is available with the distribution of the programs. Look in the doc/pdf folder for the manual.pdf file. This file can be printed or viewed using Acrobat Reader, available through the Adobe website. The manual has also been translated into html. It is available through the following link. Please note that the translator is not perfect: The pdf form of the manual is much more accurate. Specifically, latex2html failed to translate figure 2.4 and simply printed 2.3 twice. Man Pages In the UNIX world, it is common to have man pages for programs. We have written such a set of man pages, and these are available with the UNIX distribution. The man pages are also a part of the manual.pdf file. Here is a list of the man pages. 1. Emap 2. Rmap 3. Rqtl 4. Rcross 5. Qstats 6. LRmapqtl 7. SRmapqtl 8. Zmapqtl 9. JZmapqtl 10. Mlmapqtl 11. MultiRegress 12. Prune 13. Preplot 14. Eqtl 15. QTLcart Perl scripts QTL Cartographer comes with some perl scripts to automate repetitive tasks and reformat output files. They are available in the doc/scripts subdirectory of the distribution. Here are the man pages that explain what the scripts can do. 1. Bootstrap.pl is a script for running a bootstrap analysis. 2. CWTupdate.pl is used with Permute.pl for the comparison-wise thresholds. 3. EWThreshold.pl is used with Permute.pl for the experiment-wise thresholds. 4. GetMaxLR.pl is used with Permute.pl for the experiment-wise thresholds. 5. Model8.pl iterates Zmapqtl to find a stable set of cofactors for composite interval mapping. 6. Permute.pl is a script for running a permutation test. 7. Preprawl.pl allows you to reformat and check a Mapmaker data file. 8. SRcompare.pl will compare the set of cofactors in two SRmapqtl output files. 9. SSupdate.pl is used with Bootstrap.pl to update the sum and

sum of squares for the likelihoods and parameter estimates. 10. Vert.pl converts text file line endings between Unix, Macintosh and Windows. 11. Ztrim.pl redisplays Zmapqtl output so that it fits in a terminal window. Data We are now posting published data sets to our web site. A list of links to the ftp subdirectories follows. Each directory contains a set of text files of data. Please read the Readme file in the directory for information on the data. 1. Zeng et al provide data for their paper Genetic architecture of a morphological shape difference between two Drosophila species. If you have any data that you would like to make available via our server, contact Chris Basten. Presentations From time to time, Chris Basten gives presentations on how to use QTL Cartographer. These presentations are created in Microsoft Powerpoint. The source file for the presentation is available with the distribution of the programs. Look in the doc subdirectory. Binary Traits See this for more information on the BTmapqtl module. This is an add-on written in LaurenMcIntyre's lab. BTmapqtl is in the binary directory of the distribution (and is created with a make for the UNIX version).

Abbreviations: BRC

Resource Type: software resource

Resource Name: Bionformatics Research Center

Resource ID: SCR_008540

Alternate IDs: nif-0000-31386

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260725T190649+0000

Ratings and Alerts

No rating or validation information has been found for Bionformatics Research Center.

No alerts have been found for Bionformatics Research Center.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Coelho AVC, et al. (2022) The Brazilian Rare Genomes Project: Validation of Whole Genome Sequencing for Rare Diseases Diagnosis. Frontiers in molecular biosciences, 9, 821582.

- Xie M, et al. (2019) A reference-grade wild soybean genome. *Nature communications*, 10(1), 1216.
- Zhang W, et al. (2019) A cation diffusion facilitator, GmCDF1, negatively regulates salt tolerance in soybean. *PLoS genetics*, 15(1), e1007798.
- Zhang Y, et al. (2018) Genetic dissection and fine mapping of a novel dt gene associated with determinate growth habit in sesame. *BMC genetics*, 19(1), 38.
- Li MW, et al. (2016) QTLs Regulating the Contents of Antioxidants, Phenolics, and Flavonoids in Soybean Seeds Share a Common Genomic Region. *Frontiers in plant science*, 7, 854.
- Kan G, et al. (2016) Identification of novel loci for salt stress at the seed germination stage in soybean. *Breeding science*, 66(4), 530.
- Qi X, et al. (2014) Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. *Nature communications*, 5, 4340.
- Oka A, et al. (2014) Evolutionarily diverged regulation of X-chromosomal genes as a primal event in mouse reproductive isolation. *PLoS genetics*, 10(4), e1004301.
- Kuramata M, et al. (2013) Genetic diversity of arsenic accumulation in rice and QTL analysis of methylated arsenic in rice grains. *Rice (New York, N.Y.)*, 6(1), 3.
- Myřkóv B, et al. (2012) Detection of the quantitative trait loci for α -amylase activity on a high-density genetic map of rye and comparison of their localization to loci controlling preharvest sprouting and earliness. *Molecular breeding : new strategies in plant improvement*, 30(1), 367.
- Pineau C, et al. (2012) Natural variation at the FRD3 MATE transporter locus reveals cross-talk between Fe homeostasis and Zn tolerance in *Arabidopsis thaliana*. *PLoS genetics*, 8(12), e1003120.
- Boggs NA, et al. (2009) Independent S-locus mutations caused self-fertility in *Arabidopsis thaliana*. *PLoS genetics*, 5(3), e1000426.
- Mackay TF, et al. (2009) Q&A: Genetic analysis of quantitative traits. *Journal of biology*, 8(3), 23.