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A guide to QTL mapping with R/qtl

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List of functions in R/qtl

In this appendix, we list the major functions in R/qtl, organized by topic (rather than alphabetically, as they appear in the help files). Many of the functions listed are not discussed in the book. For those discussed, page numbers (in brackets) indicate the primary reference.

Sample data		
badorder		An intercross with misplaced markers
bristle3		Data on bristle number for Drosophila chromosome 3
bristleX		Data on bristle number for Drosophila X chromosome
fake.4way		Simulated data for a four-way cross
fake.bc		Simulated data for a backcross
fake.f2		Simulated data for an intercross
hyper	[33]	Backcross data on salt-induced hypertension
listeria	[33]	Intercross data on *Listeria monocytogenes* susceptibility
map10	[37]	A 10 cM genetic map modeled after the mouse genome
Input/output		
read.cross	[22]	Read data for a QTL experiment
write.cross	[33]	Write data for a QTL experiment to a file
Simulation		
sim.cross	[36]	Simulate a QTL experiment
sim.map	[37]	Generate a genetic map
Summaries		
qtlversion		Gives the version number of the installed R/qtl package
plot.cross	[35]	Plot various features of a cross object
plot.missing	[36]	Plot a grid of missing genotypes
geno.image		Plot a grid with colored pixels representing different genotypes
plot.pheno	[36]	Histogram or bar plot of a phenotype
plot.info	[70]	Plot the proportion of missing genotype information
summary.cross	[34]	Print a summary of a QTL experiment
summary.map	[38]	Print a summary of a genetic map
nchr, nind, nmar, nphe, totmar [36]		
nmissing	[71]	Number of missing genotypes by marker or individual

ntyped	[72]	Number of genotypes by marker or individual
find.pheno		Find the column number for a particular phenotype
find.marker	[57]	Find the marker closest to a specified position
find.flanking		Find the markers flanking a particular position
find.markerpos	[330]	Find the map positions of a marker
Data manipulation		
clean.cross	[45]	Remove intermediate calculations from a cross
drop.markers	[96]	Remove a set of markers
drop.nullmarkers	[200]	Remove markers without genotype data
fill.geno	[207]	Fill in holes in the genotype data by imputation or the Viterbi algorithm
strip.partials		Replace partially informative genotypes with missing values
markernames	[96]	Pull out the marker names from a cross
pull.map	[54]	Pull out the genetic map from a cross
pull.geno	[55]	Pull out the genotype data as a matrix
pull.pheno	[140]	Pull out a phenotype
replace.map	[65]	Replace the genetic map of a cross
jittermap	[84]	Jitter marker positions slightly so that no two coincide
subset.cross	[100]	Select a subset of chromosomes and/or individuals
c.cross		Combine multiple crosses
switch.order	[62]	Switch the order of markers on a chromosome
movemarker	[57]	Move a marker from one chromosome to another
HMM engine		
argmax.geno		Reconstruct underlying genotypes via the Viterbi algorithm
calc.genoprob	[84]	Calculate conditional genotype probabilities
sim.geno	[94]	Simulate genotypes given observed marker data
Diagnostics		
geno.table	[50]	Create a table of genotypes at each marker
geno.crosstab	[54]	Create a cross-tabulation of genotypes at two markers
checkAlleles	[54]	Identify markers with potentially switched alleles
calc.errorlod	[67]	Calculate genotyping error LOD scores
top.errorlod	[67]	List the genotypes with the highest error LOD values
plot.geno	[67]	Plot the observed genotypes, flagging likely errors
comparecrosses		Compare two cross objects, to see if they are the same
comparegeno	[52]	Calculate the proportion of matching genotypes for each pair of individuals
Genetic mapping		
est.rf	[53]	Estimate pairwise recombination fractions between markers
plot.rf	[55]	Plot recombination fractions
est.map	[64]	Estimate the genetic map
plot.map	[64]	Plot genetic map(s)
ripple	[60]	Assess marker order by permuting adjacent markers
summary.ripple	[61]	Print a summary of the ripple output
compareorder		Compare two orderings of markers on a chromosome
tryallpositions		Test all possible positions for a marker
formLinkageGroups		Partition markers into linkage groups

orderMarkers		Establish marker order, de novo
QTL mapping		
scanone	[84]	Genome scan with a single-QTL model
scantwo	[217]	Two-dimensional genome scan with a two-QTL model
lodint	[120]	Calculate a LOD support interval
bayesint	[120]	Calculate an approximate Bayes credible interval
scanoneboot	[121]	Nonparametric bootstrap to obtain a confidence interval for QTL location
plot.scanone	[79]	Plot output for a one-dimensional genome scan
add.threshold		Add a horizontal line at a LOD threshold to a genome scan plot
plot.scantwo	[217]	Plot output for a two-dimensional genome scan
summary.scanone	[79]	Print a summary of scanone output
summary.scantwo	[220]	Print a summary of scantwo output
max.scanone	[79]	Maximum peak in scanone output
max.scantwo	[238]	Maximum peak in scantwo output
−.scanone	[87]	Subtract LOD scores from multiple scanone results
+.scanone	[195]	Add LOD scores from multiple scanone results
−.scantwo	[87]	Subtract LOD scores from multiple scantwo results
+.scantwo		Add LOD scores from multiple scantwo results
c.scanone	[189]	Combine LOD score columns from multiple scanone results
c.scanoneperm	[223]	Combine multiple batches of permutation replicates from scanone
c.scantwoperm	[223]	Combine multiple batches of permutation replicates from scantwo
cbind.scanoneperm	[189]	Combine LOD score columns from multiple scanone permutation results
effectplot	[125]	Plot phenotype means of genotype groups defined by one or two markers or covariates
effectscan		Plot estimated QTL effects across the whole genome
plot.pxg	[126]	Like effectplot, but as a dot plot of the phenotypes
Multiple QTL models		
makeqtl	[259]	Make a qtl object for use by fitqtl
fitqtl	[260]	Fit a multiple QTL model
summary.fitqtl	[260]	Get a summary of the result of fitqtl
scanqtl	[258]	Perform a multidimensional genome scan
refineqtl	[263]	Refine the QTL locations in a multiple-QTL model
plotLodProfile	[264]	Plot LOD profiles for a multiple-QTL model
addqtl	[267]	Scan for an additional QTL, in a multiple-QTL model
addpair	[269]	Scan for an additional pair of QTL, in a multiple-QTL model
addint	[266]	Add pairwise interactions, one at a time, in a multiple-QTL model
plot.qtl	[260]	Plot the QTL locations on the genetic map
addtoqtl	[272]	Add to a QTL object
dropfromqtl	[274]	Drop a QTL from a QTL object
replaceqtl	[273]	Replace a QTL location in a QTL object with a different position

reorderqtl	[274]	Reorder the QTL in a QTL object
cim	[209]	A (relatively crude) implementation of composite interval mapping
stepwiseqtl	[276]	Stepwise selection for multiple QTL
calc.penalties	[275]	Calculate penalties for use with stepwiseqtl
plotModel	[277]	Plot a graphical representation of a multiple-QTL model