

Package ‘bim’

April 17, 2009

Version 1.01-5

Date 10/9/2006

Author Brian S. Yandell <yandell@stat.wisc.edu>, Hao Wu <hao@jax.org>

Title Bayesian Interval Mapping Diagnostics

Description Functions to sample and interpret Bayesian QTL using MCMC.

Maintainer Brian S. Yandell <yandell@stat.wisc.edu>

Depends stats, qtl

License GPL (>= 2)

URL <http://www.stat.wisc.edu/~yandell/qtl/software/qtlbim>

Repository CRAN

Date/Publication 2006-11-10 10:35:28

R topics documented:

bim.	2
bim.effects	3
bim.fdr	5
bim.model	7
bmapqtl.options	8
Bnapus	9
fisch	11
plot.bim	12
plot.bim.diag	13
plot.bim.loci	14
plot.bim.mcmc	15
plot.bim.model	16
read.bim	17
read.bmapqtl	18
run.bmapqtl	19

subset.bim	21
summary.bim	22
vern	23

Index	25
--------------	-----------

bim. *Bayesian QTL estimation and mapping of loci*

Description

Smooth density, point estimates and HPD regions for QTL loci. Loci are estimated at peaks of density.

Usage

```
bim.qtl(x, cross, nqtl=1, pattern=NULL, exact=FALSE,
        chr, bw=2, levels = seq(.5,.95,by=.05) )
plot.bim.qtl(x, cross, nqtl = 1, pattern = NULL,
             exact = FALSE, chr, bw = 2, qtl,
             level = 0.80, col = "black", add = FALSE, ...)
```

Arguments

x	object of class bim
cross	corresponding object of class cross
nqtl	subset on number of QTL
pattern	subset on chromosome pattern of QTL
exact	subset on exact pattern or number of QTL if true
chr	subset of chromosomes to plot (numerical indices or chromosome names)
bw	bandwidth for loci density
levels	saved levels for HPD region
qtl	QTL estimate information (see value)
level	level for HPD region from <code>seq(.5, .95, by=.05)</code>
col	line color
add	create new plot if FALSE
...	graphical parameters can be given as arguments to plot

Details

Model averaging conditional on at least `nqtl` QTL and at least chromosome `pattern` in model. `bim.qtl` does estimation of density and loci as well as high probability density (HPD) region. `plot.bim.qtl` calls `bim.qtl` and plots the density curve. See [plot.bim.effects](#) for enhanced plots with HPD and effects estimates.

Value

`bim.qtl` returns (and `plot.bim.qtl` silently returns) a list containing:

<code>loci</code>	data frame with <code>chr</code> = chromosome name, <code>x</code> = locus on chromosome, <code>y</code> = height of density
<code>dens</code>	list of density objects by chromosome
<code>hpd</code>	density critical values for high probability density (HPD) region

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/ctl/software/Bmapctl>

See Also

[plot.bim.effects](#)

Examples

```
data( vern )
data( verngeo.bim )

plot.bim.qtl( verngeo.bim, vern, 2 )
```

`bim.effects`

Bayesian QTL map of loci and effects

Description

Histogram of QTL loci plus scatter plots and smooth estimates of QTL effects (additive and dominance-Mather-Jinks model).

Usage

```
plot.bim.effects(x, cross, nctl = 1, pattern = NULL, exact = FALSE,
  chr, bw = 2, ctl, cex, level = .80, project, main, mfc, ... )
bim.effects(x, cross, nctl = 1, pattern = NULL, exact = FALSE, chr,
  bw = 2, ctl)
```

Arguments

<code>x</code>	object of class <code>bim</code>
<code>cross</code>	corresponding object of class <code>cross</code>
<code>nqtl</code>	subset on number of QTL
<code>pattern</code>	subset on chromosome pattern of QTL
<code>exact</code>	subset on exact pattern or number of QTL if true
<code>chr</code>	subset of chromosomes to plot (numerical indices or chromosome names)
<code>bw</code>	bandwidth for loci density
<code>qtl</code>	QTL estimate information (see value)
<code>cex</code>	character expansion for scatter plots
<code>level</code>	level for HPD region from <code>seq(.5, .95, by=.05)</code>
<code>project</code>	project identifier, default is name of <code>x</code> argument
<code>main</code>	title, with default expression <code>(project summaries with m >= nqtl)</code> and substitutions for <code>project</code> and <code>nqtl</code>
<code>mfcoll</code>	parameter to <code>par</code> set to 2 or 3 depending on if dominance is present
<code>...</code>	graphical parameters can be given as arguments to <code>plot</code>

Details

Model averaging conditional on at least `nqtl` and at least chromosome `pattern` QTL in model. `bim.effects` uses `bim.qtl` to estimate the QTL. First row has histogram of loci overlaid with smoothed density estimate (blue line) and HPD regions (red circles along origin). Second row is additive effect; third if present has dominance effect. Smoothing spline fit along scatter plot to estimate mean effects (solid blue line), plus or minus two SDs (dashed blue line; estimated as well by smoothing spline). Simple linear regression used if 50 or fewer samples for a chromosome. Purple triangles indicate marker locations if supplied. Red circles and vertical dashed lines at estimated loci and effects. Vertical black lines delineate chromosomes.

Value

`bim.effects` returns an enhanced version of the `bim.qtl` object, with additional elements

<code>add</code>	additive smoothing spline by chromosome
<code>dom</code>	dominance smoothing spline by chromosome (if present)
<code>est</code>	estimates of QTL
<code>chrom</code>	chromosome name
<code>loci</code>	loci position along chromosome
<code>add</code>	additive effect
<code>add.sd</code>	SD for additive effect
<code>dom</code>	dominance effect (if present)
<code>dom.sd</code>	SD for dominance effect

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[plot.bim](#), [subset.bim](#), [bim.qtl](#)

Examples

```
data( vern )
data( verngeo.bim )

vern.qtl <- bim.effects( verngeo.bim, vern, 2 )
plot.bim.effects( verngeo.bim, vern, 2, qtl = vern.qtl )
```

bim.fdr

Bayesian False Discovery Rate for QTL mapping

Description

Bayesian false discover rate (FDR) applied to QTL mapping. Use `plot.bim.fdr` to determine FDR for HPD level used in `plot.bim.effects`.

Usage

```
bim.fdr(x, cross, nqtl = 1, pattern = NULL, exact = FALSE, chr,
  ..., levels, df=3, qtl)
plot.bim.fdr(x, cross, ..., fdr, critical.value, hpd = NULL )
```

Arguments

<code>x</code>	object of class <code>bim</code>
<code>cross</code>	corresponding object of class <code>cross</code>
<code>nqtl</code>	subset on number of QTL
<code>pattern</code>	subset on chromosome pattern of QTL
<code>exact</code>	subset on exact pattern or number of QTL if true
<code>chr</code>	subset of chromosomes to plot (numerical indices or chromosome names)
<code>levels</code>	probability levels for HPD regions (default every 1 percent)
<code>df</code>	degrees of freedom for smoothing spline estimator of prior on size
<code>qtl</code>	QTL estimate information from <code>bim.qtl</code>
<code>fdr</code>	object returned by call to <code>bim.fdr</code>

critical.value	pFDR guidelines (ignored if hpd provided; default every .05 to .25)
hpd	HPD guidelines
...	graphical parameters can be given as arguments to plot

Details

FDR follows ideas of Storey (<http://www.stat.berkeley.edu/~storey>) adapted to Bayesian setting.

Value

`bim.fdr` returns an enhanced version of the `bim.qtl` object, with additional elements:

levels	HPD levels
size	relative size of HPD region across levels
fdr	false discover rate across levels
hyp	estiamtes for probabilities of hypotheses H0: no QTL at locus, M0: no QTL anywhere, M1: QTL somewhere
prob	cumulative prior probability
spline	spline estimate of cumulative prior probability
hyp	estiamtes for probabilities of hypotheses H0: no QTL at locus, M0: no QTL anywhere, M1: QTL somewhere
fdr	FDR for corresponding HPD levels (chosen by hpd or <code>critical[value settings]</code>)

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[plot.bim.effects](#), [bim.qtl](#)

Examples

```
data( vern )
data( verngeo.bim )

plot.bim.fdr( verngeo.bim, vern, pattern=c(1,1) )
```

bim.model	<i>Bayesian model selection for number and pattern of QTL across genome</i>
-----------	---

Description

Posterior number and pattern of QTL, along with posterior/prior Bayes factor ratios.

Usage

```
bim.model( bim, cross, nqtl = 1, pattern=NULL, exact=FALSE,
           cutoff = 1 )
bim.nqtl( bim )
bim.pattern( bim, cross, nqtl = 1, pattern=NULL, exact=FALSE,
            cutoff = 1 )
```

Arguments

bim	object of class bim
cross	corresponding object of class cross (extracted by bim.cross if not provided)
nqtl	subset on number of QTL
pattern	subset on chromosome pattern of QTL
exact	subset on exact pattern or number of QTL if true
cutoff	percent cutoff for inclusion in model selection

Details

bim.model creates results from both bim.nqtl and bim.pattern.

bim.nqtl estimates posterior frequency of number of QTLs as the margin over all other model parameters. However, note that posterior may be influenced by prior, while Bayes factor is empirically less sensitive for QTL model selection. Bayes factors are ratios of $bf = \text{posterior} / \text{prior}$ ratios.

bim.pattern shows at most 15 model patterns with at least `cutoff %` posterior are returned. Patterns are comma-separated list of chromosomes, with asterisk * for multiple QTL per chromosome. bim is first subsetted using `subset.bim`.

Value

List with items nqtl and pattern, each containing:

posterior	posterior for number of QTL
prior	prior for number of QTL
bf	rank-ordered posterior/prior ratios rescaled so $bf[1] = 1$
bfse	approximate standard error for bf computed using binomial variance

In addition, there is an object param with values for nqtl, pattern, exact and cutoff.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[plot.bim](#), [plot.bim.model](#), [subset.bim](#)

Examples

```
data( verngeo.bim )

bim.model( verngeo.bim )
```

bmapqtl.options *Options Settings for BmapQTL*

Description

This function allows the users to set and examine the options and priors for reversible jump MCMC QTL model search. The options are stored in global hidden variable .bmapqtl.options.

Usage

```
bmapqtl.options(..., reset=FALSE)
```

Arguments

<code>reset</code>	reset options to default settings
<code>...</code>	any options can be defined, using 'name = value'. The available options are listed below.
prior.nqtl	one of "poisson", "geometric" or "uniform" (partial match OK). Default is "geometric".
mean.nqtl	prior for number of QTL (default = 3).
niter	number of iterations (default = 400000).
by	record every <code>by</code> iterations (default = 400).
burnin	proportion of iterations for burnin (default = .05).
preburn	proportion of burnin used for preburn (default = .05).
nqtl	initial number of QTL (default = 0).
init	2-vector with initial mean and variance (see details).
prior.mean	2-vector with prior for mean (see details).
prior.var	2-vector with prior for variance (see details).
prior.add	2-vector with prior for additive effects (see details).
prior.dom	2-vector with prior for dominance effects (see details).
seed	Random number seed. If 0(default), seed will be generated randomly.

Details

Initial mean and variance `init` are used directly if the variance is positive. For values `c(a, -b)` use mean 0 and variance $.5s^2$.

Prior arguments have coded meaning as follows, with a and b non-negative. For the grand mean, `c(a, b)` signifies $\text{Normal}(a, b)$, while `c(a, -b)` stands for $\text{Normal}(\bar{Y}, bS^2)$, with \bar{Y} and S^2 the phenotype mean and variance, respectively. Additive and dominance priors coded as `c(a, b)` have $\text{Normal}(a, b)$; as `c(a, -b)` have $\text{Normal}(0, aS^2)$; as `c(-a, -b)` have $\text{Normal}(0, \beta S^2)$ with $\beta \sim \text{Beta}(2, 10)$ if $a=b=0$ or $\beta \sim \text{Beta}(a, b)$ otherwise. Variance has prior inverse Gamma: $\text{IG}(a, b)$ for `c(a, b)`, or $\text{IG}(a, \text{eqn}\{s^2\})$ for `c(a, -b)`.

Value

A list (in any case) with the previous values of the options changed, or all options when no arguments were given.

Author(s)

Hao Wu, hao@jax.org

See Also

[options](#)

Examples

```
bmapqtl.options()
bmapqtl.options(niter=100000, by=1000)
```

Bnapus

Cross structure for complete Brassica napus data

Description

Contains genotypes and phenotypes for Brassica napus study, including 0- 4- and 8-week vernalization, survival, and 19 chromosomes.

Usage

```
data(Bnapus)
```

Format

See `read.cross` in `library(qtl)` for format.

Details

Traits included are percent winter survival for 1992-3, 1993-4, 1994-5, 1997-8, and 1999-2000 (surv92, surv93, surv94, surv97, surv99, respectively), and days to flowering after no vernalization (flower0), 4 weeks vernalization (flower4) or 8 weeks vernalization (flower8). Percents are of plants alive in the Fall, taken from the middle of rows (totals unavailable). Days to flowering after transplant are averages over four replicates from a RCB design (values by block unavailable). First column has the trait name. The remaining columns identify individual DH line (302-455).

Marker genotype data for Major x Stellar double haploid (DH) population. Double haploids have the same relation of recombination to distance as backcrosses as there is just one meiosis tracked (in F1). However, DH are homozygous at every locus (usually mapped as RI0 lines). Marker genotypes are coded as M = Major, S = Stellar, - = missing. Data columns are

chrom = `B.napus` chromosome (N1, N2, etc.)

order = along chromosome

cM d= istance from proximal end

marker = marker name: E = AFLP; *ec, *tg, *wg = RFLP; *xxx = other markers from Arabidopsis: Lem, eru1, eru2, fad3, isoDia, isoIdh, isoPgi, isoLap, pr2, slg6, Aca1, cor15

Remaining columns are for individual DH lines (identifier 302-455).

Source

Thomas C. Osborn (<mailto:tcosborn@facstaff.wisc.edu>), Department of Agronomy, UW-Madison (<http://agronomy.wisc.edu>).

References

<http://www.stat.wisc.edu/~yandell/qtl/data/osborn/Bnapus>

Ferreira ME, Satagopan J, Yandell BS, Williams PH, Osborn TC (1995) Mapping loci controlling vernalization requirement and flowering time in Brassica napus. Theor Appl Genet 90: 727-732. [original source and analysis]

JM Satagopan, BS Yandell, MA Newton and TC Osborn (1996) Markov chain Monte Carlo approach to detect polygene loci for complex traits. Genetics 144: 805-816. <http://www.genetics.org/cgi/content/abstract/144/2/805> [first MCMC for experimental crosses; analysis of B. napus N2=LG9; see [vern](#) data]

Kole C, Thorman CE, Karlsson BH, Palta JP, Gaffney P, Yandell BS, Osborn TC (2001) Comparative mapping of loci controlling winter survival and related traits in oilseed Brassica rapa and B. napus. Molecular Breeding 1: 329-339. [refined map and reanalysis]

See Also

[read.cross,plot.bim](#)

Examples

```
data(Bnapus)

summary(Bnapus)
plot(Bnapus)
## Not run:
Bnapus.bim = run.bmapqtl(Bnapus, "log10flower8")
## End(Not run)
```

fisch

Eight QTL Stephens and Fisch simulated data

Description

Contains genotypes and phenotypes for data simulated using model in Stephens and Fisch (1998) but with 90 percent heritability.

Usage

```
data(fisch)
data(fisch.bim)
```

Format

fisch is f2 (see [read.cross](#) for format). fisch.bim produced by `link{run.bmapqtl}`.

Author(s)

Brian S. Yandell, <mailto:yandell@stat.wisc.edu>

Source

Patrick J. Gaffney (<mailto:paga@lubrizol.com>), Lubrizol Corp.

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[read.cross](#), [plot.bim](#), [run.bmapqtl](#)

Examples

```
data(fisch)
data(fisch.bim)
```

`plot.bim`*Diagnostics plots for Bayesian interval mapping*

Description

Diagnostic plots highlight putative QTL loci and effects as well as providing graphical model assessment tools.

Usage

```
plot.bim(x, cross, nqtl=1, pattern=NULL, exact=FALSE, chr, ... )
```

Arguments

<code>x</code>	object of class <code>bim</code>
<code>cross</code>	corresponding object of class <code>cross</code>
<code>nqtl</code>	subset on number of QTL
<code>pattern</code>	subset on chromosome pattern of QTL
<code>exact</code>	subset on exact pattern or number of QTL if true
<code>chr</code>	subset of chromosomes to plot (numerical indices or chromosome names)
<code>...</code>	graphical parameters can be given as arguments to <code>plot</code>

Details

Import object `cross` using `read.cross` and simulate Bayesian interval mapping sample object `x` using `run.bmapqtl`, respectively. This routine creates five plots via calls to several other plot routines for `bim` data.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[plot](#), [read.cross](#), [run.bmapqtl](#), [plot.bim.mcmc](#), [plot.bim.loci](#), [plot.bim.model](#), [plot.bim.effects](#), [plot.bim.diag](#)

Examples

```
data( vern )
data( verngeo.bim )

plot.bim( verngeo.bim, vern )
```

plot.bim.diag	<i>Marginal and model-conditional summaries of Bayesian interval mapping diagnostics</i>
---------------	--

Description

A density histogram is drawn for model-averaged summary diagnostics such as LOD, variance, or heritability.

Usage

```
plot.bim.diag(x, nqtl=1, pattern=NULL, exact=FALSE,
             items, mains=items, mfrow, ... )
```

Arguments

x	object of class bim
nqtl	subset on number of QTL
pattern	subset on chromosome pattern of QTL
exact	subset on exact pattern or number of QTL if true
items	diagnostics to be summarized; must be column of data
mains	titles for items
mfrow	plot arrangement parameter for par() (default is rows = number of items by cols = 2)
...	graphical parameters can be given as arguments to plot

Details

Model-averaged density is smooth kernel estimate similar to ordinary histogram. A [boxplot](#) (without outliers) is overlaid for comparison with conditional boxplots. Conditional boxplots by number of QTL may show indication of model bias for small number of QTL. This and [bim.nqtl](#) can help suggest the minimal model. Diagnostic items that make sense to plot are "LOD", "envvar" (environmental variance), "herit" (heritability), "mean" (grand mean), "addvar" (variance of add), "domvar" (variance of add). Marginal and conditional medians are printed.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[plot.bim](#), [density](#), [boxplot](#)

Examples

```
data( verngeo.bim )

plot.bim.diag( verngeo.bim, 2, items = c("LOD","herit") )
```

```
plot.bim.loci
```

Jittered plot of Bayesian QTL loci samples by chromosome

Description

Each point is one locus from the Bayesian QTL estimates, plotted vertically by chromosome, jittered to give a sense of density.

Usage

```
plot.bim.loci(x, cross, nqtl=1, pattern=NULL, exact=FALSE,
  chr, labels=TRUE, amount=.35, cex, ... )
```

Arguments

x	object of class bim
cross	corresponding object of class cross (extracted by bim.cross if not provided)
nqtl	subset on number of QTL
pattern	subset on chromosome pattern of QTL
exact	subset on exact pattern or number of QTL if true
chr	subset of chromosomes to plot (numerical indices or chromosome names)
labels	include marker labels if TRUE
amount	amount of jitter (between 0 and .45)
cex	character expansion (may be invisible if too small—default set by bim.cex)
...	graphical parameters can be given as arguments to plot

Details

Focuses attention on chromosome lengths and concentration of QTL loci estimates. Horizontal blue lines at markers if cross included. Adjust amount and cex to modify look of plot. Most useful when looking at multiple chromosomes.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also[jitter](#), [subset.bim](#)**Examples**

```
data( vern )
data( verngeo.bim )

plot.bim.loci( verngeo.bim, vern, 2 )
```

plot.bim.mcmc *Bayesian MCMC sequence plots for burnin and iterations.*

Description

Plot MCMC burnin and iteration sequences for number of QTL, LOD score, environmental SD, and heritability.

Usage

```
plot.bim.mcmc(x, element = c("burnin", "iter"),
             xlab = c("burnin sequence", "mcmc sequence"),
             items, ylabs = items, types, ... )
```

Arguments

x	object of class bim
element	elements of x to plot
xlab	x-axis labels for elements
items	diagnostic item names to be plotted as time series (default is all names in x\$iter)
ylabs	labels for items
types	line types (default is both for first item—usually number of QTL—and lines for the rest)
...	graphical parameters can be given as arguments to plot

Details

Plots show grey line for saved sequences, usually nearly vertical due to mixing, plus a smoothed curve (blue). Burnin plots should show initial jump in number of QTL during pre-burnin sequence, ideally settling into a well-behaved Markov chain by the end of the burn-in. That is, look for visual evidence of stationarity as flat blue line and even spread of grey. Trend or cyclic pattern indicates Markov chain is not mixing well and needs to be run much longer. No formal assessment is provided.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[run.bmapqtl](#)

Examples

```
data( verngeo.bim )
plot.bim.mcmc( verngeo.bim )
```

plot.bim.model

Graphical model assessment for Bayesian interval mapping

Description

Model-averaged posteriors and posterior/prior ratios for graphical Bayes factor assessment. First row concerns number of QTL, second row evaluates pattern of QTL across chromosomes.

Usage

```
plot.bim.model( x, cross, nqtl = 1, pattern=NULL, exact=FALSE,
  cutoff = 1, assess, ... )
```

Arguments

x	object of class bim or class bim.model
cross	corresponding object of class cross
nqtl	subset on number of QTL
pattern	subset on chromosome pattern of QTL
exact	subset on exact pattern or number of QTL if true
cutoff	percent cutoff for inclusion in model selection
assess	object of class bim.model from bim.model
...	graphical parameters can be given as arguments to plot

Details

`plot.bim.model` uses results (`assess`) of `bim.model` and arranges plots on a single page. If `x` is of class `bim.model`, then `assess` is set to its value and the other arguments are ignored. Left plot is of posterior against model identifier, while right plot assesses Bayes factors. Since Bayes factors are ratios of posterior/prior ratios, a semi-log plot of posterior/prior against model identifier (m = number of QTL or M = model pattern) provides a graphical model assessment tool with a BF threshold yardstick.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/qtl/software/Bmapqtl>

See Also

[bim.model](#)

Examples

```
data( vern )
data( verngeo.bim )

plot.bim.model( verngeo.bim, vern, 2 )
```

read.bim

Read samples from WinQTL output

Description

MCMC samples from WinQTL are organized into an object of class `bim` for diagnostic plots and analysis. This can be used to import MCMC samples from WinQTL or from an optional file saved by `run.bmapqtl`.

Usage

```
read.bim( dir, bimfile, nvalfile = "nval.dat", na.strings="." )
```

Arguments

<code>dir</code>	directory containing files
<code>bimfile</code>	name of MCMC sample file (currently with <code>.z</code> suffix)
<code>nvalfile</code>	parameter file for <code>Bmapqtl</code> program (currently hard-wired)
<code>na.strings</code>	missing value code

Details

Bmapqtl used to operate as a separate external command, but was recently incorporated as a C dynamic library. However, `read.bim` is still useful for output from WinQTL. For information on WinQTL visit <http://statgen.ncsu.edu/qtlcart>.

Value

An object of class 'bim', which is a list with components

<code>bmapqtl</code>	parameter settings for Bmapqtl run
<code>burnin</code>	burnin sequence data frame, containing <code>niter</code> = iteration number, <code>nqtl</code> = number of QTL, <code>LOD</code> = LOD score based on simulated QTL genotypes, <code>mean</code> = grand mean of phenotype, <code>envvar</code> = environmental variance, <code>addvar</code> = additive variance, <code>domvar</code> = dominance variance (if included), and <code>herit</code> = heritability.
<code>iter</code>	MCMC iteration summary data frame, with same elements as <code>burnin</code> .
<code>loci</code>	data frame with MCMC estimates across loci by iteration, containing <code>niter</code> = iteration number, <code>nqtl</code> = number of QTL, <code>chrom</code> = chromosome number, <code>locus</code> = locus position in centi-Morgans, <code>add</code> = additive effect, <code>dom</code> = dominance effect (if included).

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

See Also

[plot.bim](#), [run.bmapqtl](#), [read.bmapqtl](#)

Examples

```
## Not run: verngeo.bim <- read.bim( ".", "verngeo.z" )
```

<code>read.bmapqtl</code>	<i>Read and write options for WinQTL</i>
---------------------------	--

Description

`write.bmapqtl` takes the options and priors in current workspace from `bmapqtl.options` and write it to a (user specified) text file. `read.bmapqtl` opens the file and read the options and priors in.

Usage

```
write.bmapqtl( dir = ".", nvalfile = "nval.dat" )
read.bmapqtl( dir = ".", nvalfile = "nval.dat" )
```

Arguments

dir directory containing files
nvalfile file name for options and priors.

Details

Bmapqtl used to operate as a separate external command using external file `nval.dat`, but was recently incorporated as a C dynamic library. However, `read.bmapqtl` and `write.bmapqtl` are still useful for WinQTL. For information on WinQTL visit <http://statgen.ncsu.edu/qtlcart>.

Value

There is no return value from `write.bmapqtl`.

`read.bmapqtl` returns a list for options and priors. To replace the options and priors in current workspace, use `.bmapqtl.options <- read.bmapqtl()`.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu, Hao Wu, hao@jax.org

See Also

[read.bim](#), [run.bmapqtl](#), [bmapqtl.options](#)

Examples

```
## Not run:  
write.bmapqtl( ".", "nval.dat")  
read.bmapqtl( ".", "nval.dat" )  
## End(Not run)
```

run.bmapqtl

Run Bmapqtl reversible jump MCMC

Description

Run Bmapqtl reversible jump MCMC

Usage

```
run.bmapqtl(cross, pheno=1, chrom=0, result.file="")
```

Arguments

cross	An object of class "cross"
pheno	phenotypic trait number or name
chrom	chromosome number (0 = all). Note that at this stage, it can either be all chromosomes (0) or a single chromosome.
result.file	Result file name. If this is specified, the result will be written to a tab-delimited text file. If it is an empty string (""), result will not be output as a file.

Value

The result is an object of class "bim", which is a list with the following components:

bmapqtl	parameter settings for Bmapqtl run
burnin	burnin sequence data frame, containing <code>niter</code> = iteration number, <code>nqtl</code> = number of QTL, <code>LOD</code> = LOD score based on simulated QTL genotypes, <code>mean</code> = grand mean of phenotype, <code>envvar</code> = environmental variance, <code>addvar</code> = additive variance, <code>domvar</code> = dominance variance (if included), and <code>herit</code> = heritability.
iter	MCMC iteration summary data frame, with same elements as <code>burnin</code> .
loci	data frame with MCMC estimates across loci by iteration, containing <code>niter</code> = iteration number, <code>nqtl</code> = number of QTL, <code>chrom</code> = chromosome number, <code>locus</code> = locus position in centi-Morgans, <code>add</code> = additive effect, <code>dom</code> = dominance effect (if included).

Author(s)

Hao Wu, hao@jax.org

References

<http://www.stat.wisc.edu/~yandell/qtl/data/osborn/Bnapus>

JM Satagopan, BS Yandell, MA Newton and TC Osborn (1996) Markov chain Monte Carlo approach to detect polygene loci for complex traits. *Genetics* 144: 805-816. <http://www.genetics.org/cgi/content/abstract/144/2/805> [first MCMC for experimental crosses; analysis of *B. napus* N2=LG9 (see [vern](#) data)]

JM Satagopan and BS Yandell (1996) Estimating the number of quantitative trait loci via Bayesian model determination. Special Contributed Paper Session on Genetic Analysis of Quantitative Traits and Complex Diseases, Biometrics Section, Joint Statistical Meetings, Chicago, IL. <ftp://ftp.stat.wisc.edu/pub/yandell/revjump.html> [first RJ-MCMC for experimental crosses; analysis of *B. napus* N2=LG9; see [vern](#) data]

Gaffney PJ (2001) An efficient reversible jump Markov chain Monte Carlo approach to detect multiple loci and their effects in inbred crosses. PhD Dissertation, Dept of Statist, UW-Madison. <http://wwwlib.umi.com/dissertations/fullcit/301245>

See Also

[plot.bim](#), [read.bim](#)

Examples

```
data(vern)
## Not run:
bim = run.bmapqtl(vern)
plot(bim)
## End(Not run)
```

subset.bim

Subsetting Bayesian interval mapping data

Description

Subset Bayesian interval mapping iterations on number of QTL and/or chromosome pattern of QTL, using exact match or inclusive subsetting.

Usage

```
## S3 method for class 'bim':
subset(x, cross, nqtl=1, pattern=NULL, exact=FALSE, chr, ... )
```

Arguments

x	object of class bim
cross	corresponding object of class cross
nqtl	subset on number of QTL
pattern	subset on chromosome pattern of QTL
exact	subset on exact pattern or number of QTL if true
chr	subset of chromosomes to plot (numerical indices or chromosome names)
...	additional arguments to subset

Details

Subset to include only iterations with at least `nqtl` number of QTL and at least the `pattern` across chromosomes. `pattern` is a vector of chromosome identities, with repeats for multiple linked QTL on a chromosome. If `exact=FALSE`, then all iterations with at least the given `pattern` and `nqtl` are included. `nqtl` will be reset to `length(pattern)` if it is smaller than this value. Note that `pattern` should be number codes corresponding to those used in the `x` object. At present, chromosome names are not allowed. Further subsets to only include QTL from these iterations that are on chromosomes `chr`.

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/ctl/software/Bmapctl>

See Also

[read.bim](#)

Examples

```
## Not run:  
bim223 <- subset.bim( bim, pattern = c(2,2,3) )  
## End(Not run)
```

summary.bim

Summary of Bayesian interval mapping samples

Description

Quick summary of Bayesian interval mapping samples.

Usage

```
## S3 method for class 'bim':  
summary( object, ... )  
## S3 method for class 'bim.model':  
summary( object, ... )  
## S3 method for class 'bim.ctl':  
summary( object, ... )
```

Arguments

object object of class bim (from [run.bmapctl](#)), bim.model (from [bim.model](#)),
 or bim.ctl (from [bim.ctl](#) or [bim.effects](#))
... additional arguments to [summary](#)

Author(s)

Brian S. Yandell, yandell@stat.wisc.edu

References

<http://www.stat.wisc.edu/~yandell/ctl/software/Bmapctl>

See Also

[run.bmapqtl](#), [bim.model](#), [bim.qtl](#), [bim.effects](#)

Examples

```
data( verngeo.bim )

summary( verngeo.bim )
verngeo.model <- bim.model( verngeo.bim )
summary( verngeo.model )
## estimate QTL density and locate peak(s)
verngeo.qtl <- bim.qtl( verngeo.bim )
## augment bim.qtl with estimates of effects
verngeo.qtl <- bim.effects( verngeo.bim, qtl = verngeo.qtl )
## same idea but with just one call
verngeo.qtl <- bim.effects( verngeo.bim )
```

vern

Eight week vernalization data for Brassica napus

Description

Contains genotypes and phenotypes for 8-week vernalization study used in Satagopan et al. (1996).

Usage

```
data(vern)
data(verngeo.bim)
data(vernpois.bim)
```

Format

See [read.cross](#) for format of `vern`, `verngeo.bim` and `vernpois.bim` created by setting `prior.nqtl` to "geometric" and "poisson", respectively.

Source

Thomas C. Osborn (<mailto:tcosborn@facstaff.wisc.edu>), Department of Agronomy, UW-Madison.

References

<http://www.stat.wisc.edu/~yandell/qtl/data/osborn/Bnapus>

Ferreira ME, Satagopan J, Yandell BS, Williams PH, Osborn TC (1995) Mapping loci controlling vernalization requirement and flowering time in *Brassica napus*. *Theor Appl Genet* 90: 727-732. [original source and analysis]

Kole C, Thorman CE, Karlsson BH, Palta JP, Gaffney P, Yandell BS, Osborn TC (2001) Comparative mapping of loci controlling winter survival and related traits in oilseed Brassica rapa and B. napus. *Molecular Breeding* 1: 329-339. [refined map and reanalysis]

JM Satagopan, BS Yandell, MA Newton and TC Osborn (1996) Markov chain Monte Carlo approach to detect polygene loci for complex traits. *Genetics* 144: 805-816. <http://www.genetics.org/cgi/content/abstract/144/2/805> [first MCMC for experimental crosses; analysis of B. napus N2=LG9; see [vern](#) data]

See Also

[read.cross](#), [plot.bim](#), [run.bmapqtl](#), [bmapqtl.options](#)

Examples

```
data(vern)
data(verngeo.bim)
data(vernpois.bim)
## or use run.bmapqtl to create bim objects:
## Not run:
bmapqtl.options(prior.nqtl="geometric")
verngeo.bim = run.bmapqtl(vern)
bmapqtl.options(prior.nqtl="poisson")
vernpois.bim = run.bmapqtl(vern)
## End(Not run)
```

Index

*Topic **datasets**

Bnapus, 9
fisch, 11
vern, 23

*Topic **file**

read.bim, 17
read.bmapqtl, 18

*Topic **hplot**

bim., 1
bim.effects, 3
bim.fdr, 5
plot.bim, 12

*Topic **models**

bim., 1
bim.effects, 3
bim.fdr, 5
bim.model, 6
plot.bim, 12
plot.bim.diag, 13
plot.bim.loci, 14
plot.bim.mcmc, 15
plot.bim.model, 16
run.bmapqtl, 19

*Topic **utilities**

bmapqtl.options, 8
subset.bim, 21
summary.bim, 22

bim., 1
bim.effects, 3, 22, 23
bim.fdr, 5, 5
bim.model, 6, 16, 17, 22, 23
bim.nqtl, 13
bim.nqtl (*bim.model*), 6
bim.pattern (*bim.model*), 6
bim.qtl, 4–6, 22, 23
bim.qtl (*bim.*), 1
bmapqtl.options, 8, 18, 19, 24
Bnapus, 9
boxplot, 13

density, 13

fisch, 11

jitter, 15

options, 9

plot, 2, 3, 5, 12–16
plot.bim, 4, 7, 10, 11, 12, 13, 18, 21, 24
plot.bim.diag, 12, 13
plot.bim.effects, 2, 6, 12
plot.bim.effects (*bim.effects*), 3
plot.bim.fdr (*bim.fdr*), 5
plot.bim.loci, 12, 14
plot.bim.mcmc, 12, 15
plot.bim.model, 7, 12, 16
plot.bim.qtl (*bim.*), 1

read.bim, 17, 19, 21, 22
read.bmapqtl, 18, 18
read.cross, 10–12, 23, 24
run.bmapqtl, 11, 12, 16, 18, 19, 19, 22–24

subset, 21
subset.bim, 4, 7, 15, 21
summary, 22
summary.bim, 22

vern, 10, 20, 23, 24
verngeo.bim (*vern*), 23
vernpois.bim (*vern*), 23

write.bmapqtl (*read.bmapqtl*), 18