

Package ‘BayesQTLBIC’

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Title Bayesian multi-locus QTL analysis based on the BIC criterion

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Description R package for a non-MCMC approximate multilocus Bayesian model selection approach to the analysis of quantitative trait loci (QTL). The method and models are described in (Ball, R. D. Genetics 159: 1351--1364, 2001; <http://www.genetics.org/cgi/content/abstract/159/3/1351>). Data is assumed to be from a QTL mapping family with DNA markers genotyped along the genome. The QTL mapping problem is represented as a model selection problem, where each model is a linear regression of the trait on a selected set of marker values. The main function `bicreg.qtl()` is based on the S function `bicreg()`--- posterior probabilities for models are approximated from the BIC criterion, calculated for each model in a search of model space using leaps or regsubsets. Additionally, we allow for prior probabilities based on expected numbers of QTL per genome and options to control the size of models considered, and to allow for selectively genotyping from the tails of the phenotypic distribution. Missing values are estimated by multiple imputation, and estimates of marker effects can be obtained conditional on selection or unconditional and free of selection bias. The method relies on 3 approximations: (1.) QTL configuration is represented approximately by configurations with QTL located at marker positions; (2.) Posterior probabilities are given approximately in terms of the BIC criterion; and (3.) The distribution of missing marker values is approximated by multiple imputation, sampling from the distribution of missing values conditional on non-missing values. We have found these are good approximations provided (1.) the marker spacing is

reasonable (less than 30cM); (2.) the sample size is 100 or more for fully genotyped populations; and (3.) around 10 imputations are used and the effect of any given QTL on the trait is not large. Due to limits on the number of markers that can be considered simultaneously the method is generally applied separately to each chromosome or could be iteratively applied to sets of chromosomes using fixed sets of predictors from other chromosomes when analysing a given chromosome.

Depends leaps

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bicreg.models	<i>BIC analysis for a fixed set of models</i>
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Description

bicreg.models evaluates posterior probabilities based on the BIC criterion and prior probabilities for a fixed set of models, typically obtained by sampling from sets of models from separate analyses of individual chromosomes.

Usage

```
bicreg.models(x,y,wt = rep(1, length(y)),which,intercept=TRUE,add.null.model=TRUE,
              n=length(y)/num.imputations,num.imputations=1,delta=1,
              p.sg=1,prior=0.5,eval.markers=TRUE,neval=NULL)
```

Arguments

<code>x</code>	Matrix of independent variables, based on marker genotypes, often from a single chromosome.
<code>y</code>	Vector of values for the dependent variable (trait values).
<code>wt</code>	Vector of weights for regression.
<code>which</code>	Matrix of logical values corresponding to a set of models, the (i,j) element is TRUE if and only if the jth variable is selected in the ith model.
<code>intercept</code>	Add an intercept term.
<code>add.null.model</code>	Add the NULL model.
<code>n</code>	Original sample size, before multiple imputations.
<code>num.imputations</code>	Number of imputations used to construct <code>x</code> , <code>y</code> .
<code>prior</code>	Vector or scalar specifying prior probabilities per marker for a QTL to be in the vicinity of the marker; generally proportional to the distance to flanking markers and total number of QTL expected genome. Defaults to 0.5 which is usually too high.
<code>delta</code>	Adjustment factor for the penalty term in the BIC criterion, default is no adjustment $\delta=1$; (Cf. Broman and Speed 2002); not needed if using subjective prior probabilities and sample size is ample ($p.sg=1$ and $n \geq 100$; Ball 2007).
<code>p.sg</code>	Proportion $p.sg/2$ of each tail is genotyped if selective genotyping is being used; default 1, corresponding to fully genotyped population.
<code>eval.markers</code>	Evaluate model averaged estimates for marker effects (effects of allelic substitution).
<code>neval</code>	Use <code>neval</code> top models on which to evaluate model averaged estimates of marker effects, default NULL, use all models.

Details

Provides posterior probabilities for a fixed set of linear models representing alternative QTL genetic architectures. Provides Bayesian model averaged estimates for effects of QTL or effects of allelic substitution for markers which may be linked to QTL.

Value

`bicreg.models` returns an object of class `bicreg.qtl`.

Author(s)

R.D. Ball, (<rod.ball@scionresearch.com>)

References

Ball, R. D. 2001: Bayesian methods for QTL mapping based on model selection: approximate analysis using the Bayesian Information Criterion. *Genetics* 159: 1351–1364.

See Also

[bicreg.qtl,sample.bicreg.qtl.models](#)

Examples

```
## Not run:
data(ex3n300a.data)
chrom <- rep(1:12,rep(16,12))
marker <- rep(1:16,12)
x <- sapply(ex3n300a.data$Markers,c)
y <- ex3n300a.data$Trait$t1
nchrom <- length(sort(chrom.levels <- unique(chrom)))

quick.demo <- TRUE
if(quick.demo){
  nc <- 2; nsim <- 20;x <- x[,chrom %in% 1:2];
  chrom <- chrom[chrom %in% 1:2]
}else{nc <- 12; nsim <- 200}
chrom.fits <- list()
for(ii in seq(along=chrom.levels[1:nc])){
  cat(paste("*** chromosome",ii,"***","\n"))
  ci <- chrom.levels[ii]
  chrom.sel <- chrom==ci
  chrom.fits[[ii]] <- bicreg.qtl(x[,chrom.sel],y, prior=0.1,nbest=20,nvmax=3)
}
mWhich <- sample.bicreg.qtl.models(chrom.fits,nsim=nsim)
mres <- bicreg.models(x=x,y=y,which=mWhich,prior=0.1)
summary(mres,nbest=38,min.marker.prob=0.05)

## End(Not run)
```

bicreg.qtl

Bayesian QTL analysis using the BIC criterion

Description

Bayesian multi-locus QTL analysis based on Bayesian model selection in linear models using the BIC criterion to calculate approximate posterior probabilities for models.

Usage

```
bicreg.qtl(x, y, wt = rep(1, length(y)), strict = TRUE, OR = 1000,
  maxCol = 31, drop.factor.levels = TRUE, nvmax = 4, nbest = 10,
  intercept = TRUE, do.occam = FALSE, n = length(y)/num.imputations,
  num.imputations = 1, prior = 0.5, delta = 1, p.sg = 1, eval.markers = TRUE,
  neval = NULL, keep.size = 1, method = c("regsubsets", "leaps")[1])
bicreg2(x, y, wt = rep(1, length(y)), strict = FALSE, OR = 1000,
  maxCol = 31, drop.factor.levels = TRUE, nvmax = 4, nbest = 10,
  intercept = TRUE, do.occam = TRUE, n = length(y)/num.imputations,
```

```
num.imputations = 1, prior = 0.5, delta = 1, p.sg = 1, eval.markers = FALSE,
neval = NULL, keep.size = -1, method = c("regsubsets", "leaps")[1])
```

Arguments

x	a matrix of independent variables, based on marker genotypes, often from a single chromosome
y	a vector of values for the dependent variable (trait values)
wt	a vector of weights for regression
strict	logical. FALSE returns all models whose posterior model probability is within a factor of 1/OR of that of the best model. TRUE returns a more parsimonious set of models, where any model with a more likely submodel is eliminated.
OR	a number specifying the maximum ratio for excluding models in Occam's window
maxCol	a number specifying the maximum number of columns in the design matrix (including the intercept) to be kept, i.e. maximum number of markers to include
drop.factor.levels	logical. Indicates whether factor levels can be individually dropped in the step-wise procedure to reduce the number of columns in the design matrix, or if a factor can be dropped only in its entirety.
nvmax	maximum number of variables in a model
nbest	a value specifying the number of models of each size returned to bic.glm by the leaps algorithm.
intercept	add an intercept term
do.occam	do Occam's razor selection
n	original sample size, before multiple imputations
num.imputations	number of imputations used to construct x, y
prior	a vector or scalar specifying prior probabilities per marker for a QTL to be in the vicinity of the marker; generally proportional to the distance to flanking markers and total number of QTL expected genome. Defaults to 0.5 which is usually too high.
delta	adjustment factor for the penalty term in the BIC criterion, default is no adjustment (delta=1); (Cf. Broman and Speed 2002); not needed if using subjective prior probabilities and sample size is ample (p.sg=1 and n >= 100; Ball 2007).
p.sg	proportion genotyped (p.sg/2 per tail), if selective genotyping is being used, default 1, corresponding to fully genotyped population
eval.markers	evaluate model averaged estimates for marker effects (effects of allelic substitution)
neval	use neval top models on which to evaluate model averaged estimates of marker effects, default NULL, use all models
keep.size	keep models up to this size regardless of Occam's razor criterion, e.g. to ensure the intercept only model is available for comparison
method	choice of method, leaps or regsubsets

Details

Provides posterior probabilities for linear models representing alternative QTL genetic architectures, which can be used for Bayesian inference of the number of QTL and probabilities for QTL presence in a region. Provides Bayesian model averaged estimates for effects of QTL or effects of allelic substitution for markers which may be linked to QTL. Posterior probabilities are estimated from the BIC criterion combined with prior information, with adjustments for multiple imputation and selective genotyping. The posterior probability for model M_i is given by:

$$\Pr(M_i) \propto \exp(-\text{BIC}_i/2) \times \pi(M_i)$$

where BIC_i is the value of the BIC criterion and $\pi(M_i)$ is the prior probability for M_i .

Missing marker values can be estimated by multiple imputation, conditional on flanking markers, using `impute.markers`, and the imputed data used as `x.y`.

For selectively genotyped populations (Darvasi and Soller 1992) an adjustment is made to the BIC criterion. Asymptotic convergence is good for fully genotyped families with $n \geq 100$ progeny but requires larger sample sizes for smaller proportions of the tails (p.sg) genotyped.

Value

`bicreg.qtl` returns an object of class `bicreg.qtl`

The function `summary` is used to print a summary of the results.

An object of class `bicreg.qtl` inherits from class `bicreg` and is a list containing at least the following components/attributes:

<code>postprob</code>	the posterior probabilities of the models selected
<code>namesx</code>	the names of the variables
<code>label</code>	labels identifying the models selected
<code>r2</code>	R2 values for the models
<code>bic</code>	values of BIC for the models
<code>size</code>	the number of independent variables in each of the models
<code>which</code>	a logical matrix with one row per model and one column per variable indicating whether that variable is in the model
<code>probne0</code>	the posterior probability that each variable is non-zero (in percent)
<code>n</code>	the sample size before multiple imputation
<code>postprob.size</code>	the marginal posterior probabilities for model sizes
<code>postmean</code>	the posterior mean of each coefficient (from model averaging)
<code>postsd</code>	the posterior standard deviation of each coefficient (from model averaging)
<code>condpostmean</code>	the posterior mean of each coefficient conditional on the variable being included in the model
<code>condpostsd</code>	the posterior standard deviation of each coefficient conditional on the variable being included in the model
<code>ols</code>	matrix with one row per model and one column per variable giving the OLS estimate of each coefficient for each model

se	matrix with one row per model and one column per variable giving the standard error of each coefficient for each model
reduced	a logical indicating whether any variables were dropped before model averaging
dropped	a vector containing the names of those variables dropped before model averaging
call	the matched call that created the bicreg object

and contains the following attributes:

intercept	if an intercept term was added
num.imputations	the number of multiple imputations assumed
p.sg	the proportion genotyped (p.sg/2 per tail)
delta	the value of delta used

Author(s)

R.D. Ball,
 (<rod.ball@scionresearch.com>), based on bicreg from the BMA package by Adrian Raftery,
 Chris Volinski, and Ian Painter.

References

- Ball, R. D. 2001: Bayesian methods for QTL mapping based on model selection: approximate analysis using the Bayesian Information Criterion. *Genetics* 159: 1351–1364.
- Ball, R.D. 2007: Quantifying evidence for candidate gene polymorphisms—Bayesian analysis combining sequence-specific and QTL co-location information. *Genetics* 177: 2399–2416.
- DeSilva, H.N., and Ball, R.D. 2007: Linkage disequilibrium mapping concepts. Chapter 7, pp103–132 In: *Association Mapping in Plants*, N.C. Oraguzie, E.H.A. Rikkerink, S.E. Gardiner, and H.N. DeSilva (Editors), Springer, New York.
- Ball, R.D. 2007: Statistical analysis and experimental design. Chapter 8, pp133–196 In: *Association Mapping in Plants*, N.C. Oraguzie, E.H.A. Rikkerink, S.E. Gardiner, and H.N. DeSilva (Editors), Springer, New York.
- Bogdan, M., Ghosh, J. K., and Doerge, R. W. 2004: Modifying the Schwarz Bayesian information criterion to locate multiple interacting quantitative trait loci. *Genetics* 167: 989–999.
- Broman, K.W. and Speed, T.P. 2002: A model selection approach for the identification of quantitative trait loci in experimental crosses (with discussion). *J Roy Stat Soc B* 64: 641–656, 731–775.
- Darvasi, A. and Soller, M. 1992: Selective genotyping for determination of linkage between a locus and a quantitative trait locus. *Theoretical and Applied Genetics* 85: 353–359.
- Raftery, A. E. 1995: Bayesian model selection in social research (with Discussion). *Sociological Methodology* 1995 (Peter V. Marsden, ed.), pp. 111–196, Cambridge, Mass.: Blackwells.

See Also

[bicreg](#), [summary.bicreg.qtl](#), [DS.gamma](#), [recalc.bicprobs](#) [impute.marker](#)

Examples

```
# simulated backcross progeny
set.seed(1234)
ex1.marker.pos <- seq(5,105,by=10)
chrom <- rep(1:2,rep(length(ex1.marker.pos),2))
ex1.qtldata <- sim.bc.progeny(n=1200,Vp=c(0.1,0.2,0.3,0.15,0.25)/2,
  map.pos=list(chrom=rep(1:2,rep(length(ex1.marker.pos),2)),
    pos=rep(ex1.marker.pos,2)),qtl.pos=list(chrom=rep(1:2,c(3,2)),
      pos=c(40,50,80,30,55)))
ex1n1200c1.bicreg <- bicreg.qtl(x=ex1.qtldata$x[,chrom==1],y=ex1.qtldata$y,OR=1000,
  nbest=10,nvmax=5,prior=0.2,keep.size=1)
# 23 models account for 99% of the probability
cumsum(ex1n1200c1.bicreg$postprob)
# 2 QTL in coupling at 40,50cM can't be resolved
summary(ex1n1200c1.bicreg,nbest=23)
```

DS.gamma

*Darvasi and Soller correction factor gamma***Description**

Calculate Darvasi and Soller correction factor gamma for QTL mapping in selectively genotyped populations

Usage

```
DS.gamma(p)
```

Arguments

p proportion sampled ($p/2$ per sampled tail)

Details

For a given number of individuals genotyped, power of detection of QTL for a continuous trait (assumed normally distributed) is increased if individuals are sampled from the tails of the phenotypic distribution. For small gene effects, if proportion $p/2$ is sampled from each tail of the phenotypic distribution, naive estimates of marker effects are inflated by the factor γ_p (to first order in the size of gene effects) where:

$$\gamma_p = 1 + \Phi^{-1}(1 - p/2) \frac{\phi(\Phi^{-1}(p/2))}{p/2}.$$

Value

the value of γ_p

Author(s)

Rod Ball (<rod.ball@scionresearch.com>)

References

Darvasi, A. and Soller, M. 1992: Selective genotyping for determination of linkage between a locus and a quantitative trait locus. *Theoretical and Applied Genetics* 85: 353–359.

Examples

```
DS.gamma(p = c(0.05,0.1,0.25))
```

ex3n300a.data	<i>Simulated QTL dataset in QTLCartographer format</i>
---------------	--

Description

Simulated data for 300 backcross progeny similar to the example used for testing QTL co-location (Ball (2007)).

Usage

```
ex3n200a.data
```

References

Ball, R. D. 2007: Quantifying evidence for candidate gene polymorphisms—Bayesian analysis combining sequence-specific and QTL co-location information. *Genetics* 177: 2399–2416.

impute.marker	<i>Imputation of missing marker values in QTL progeny</i>
---------------	---

Description

Missing marker values are randomly imputed according to their probability, conditional on non-missing marker values.

Usage

```
impute.marker(m, d, map.function="haldane", marker.values=1:2)
```

```
impute.marker.matrix(m, d, num.imputations = 1, map.function = "haldane",  
marker.values = 1:2)
```

Arguments

<code>m</code>	For <code>impute.marker</code> , a vector of marker haplotype values for a set of linked markers, 1 entry per marker in genome order. For <code>impute.marker.matrix</code> , a matrix with such vectors as rows corresponding to individual genotypes.
<code>d</code>	Inter-marker distances in cM; <code>d[i]</code> is the map distance from marker <code>i</code> to marker <code>i+1</code> (<code>i=1, ..., length(m)-1</code>).
<code>num.imputations</code>	Number of imputations to do.
<code>map.function</code>	Mapping function (Haldane or Kosambi) to use to estimate recombination probabilities.
<code>marker.values</code>	Vector of valid values for markers. Assuming diploid individuals and fully informative markers, the markers inherited from a given parent these would be one of two possible marker values.

Details

For each imputation of each progeny, Missing marker values are randomly generated from their probability distribution, conditional on flanking markers where these exist, as follows. First, marker values not matching an entry of `marker.values` are replaced by missing values. If there are missing values, one is randomly selected and sampled conditionally on any non-missing flanking marker values. The process is repeated (conditional on non-missing values, including originally missing values already sampled) until there are no missing values remaining.

Value

`impute.marker` returns a vector with missing marker values randomly sampled conditional on non-missing values. `impute.marker.matrix` returns a matrix with missing marker values randomly sampled conditional on non-missing values in each row of `m`. If `num.imputations` is an integer greater than 1, `impute.marker.matrix` returns a matrix consisting of the `num.imputations` imputed matrices joined by row.

Author(s)

R.D. Ball <rod.ball@scionresearch.com>

References

Ball, R. D. 2001: Bayesian methods for QTL mapping based on model selection: approximate analysis using the Bayesian Information Criterion. *Genetics* 159: 1351–1364.

See Also

[bicreg.qtl](#)

Examples

```

m <- c(1,1,2,2,1,NA,1,2,NA,1,1,NA)
d <- c(10,11,9,10,21,28,13,6,5,12,7)
impute.marker(m,d,map.function="haldane",marker.values=1:2)

# simulated backcross progeny with ~5% missing marker genotypes
set.seed(1234)
marker.pos <- seq(5,105,by=10)
qtldata200 <- sim.bc.progeny(n=200,Vp=c(0.1,0.2,0.3,0.15,0.25)/2,
  map.pos=list(chrom=rep(1:2,rep(length(marker.pos),2)),
    pos=rep(marker.pos,2)),qtl.pos=list(chrom=rep(1:2,c(3,2)),
    pos=c(40,50,80,30,55)))
x.mv <- qtldata200$x
num.missing <- round(0.05*length(qtldata200$x))
mv.pos <- sample(1:length(c(qtldata200$x)),size=num.missing,replace=FALSE)
x.mv[mv.pos] <- NA
c1.cols <- 1:11
x200c1.imp10 <- impute.marker.matrix(x.mv[,c1.cols],d=diff(marker.pos),
  num.imputations=10)
c2.cols <- 12:22
x200c2.imp10 <- impute.marker.matrix(x.mv[,c2.cols],d=diff(marker.pos),
  num.imputations=10)
x200 <- cbind(x200c1.imp10,x200c2.imp10)

```

map.function.rec	<i>Map functions</i>
------------------	----------------------

Description

Map functions to convert between recombination and physical map distances for the Haldane and Kosambi mapping functions

Usage

```

map.function.rec(d,method="haldane")
map.function.dist(r,method="haldane")

```

Arguments

d	map distance in Morgans
r	recombination distance
method	choice of mapping function

Details

The conversion between physical distance d (Morgans) and recombination probabilities is given by:

$$r = \frac{1}{2}(1 - \exp(-2d))$$

$$d = -\frac{1}{2} \log(1 - 2r)$$

for the Haldane mapping function, and by:

$$r = \frac{1}{2} \frac{1 - \exp(-4d)}{1 + \exp(-4d)}$$

$$d = \frac{1}{4} \log \left(\frac{1 + 2r}{1 - 2r} \right)$$

for the Kosambi mapping function.

Value

the value of r or d

Author(s)

R.D. Ball <rod.ball@scionresearch.com>

References

Liu, B. 1998: Statistical Genomics: Linkage, Mapping and QTL Analysis. Boca Raton, FL: CRC Press LLC.

Examples

```
map.function.rec(d=c(0,0.01,0.1,0.2,1,5),method="haldane")
map.function.rec(d=c(0.01,0.1,0.2,1,5),method="kosambi")
map.function.dist(r=c(0,0.01,0.1,0.2,0.49,0.499,0.5),method="haldane")
map.function.dist(r=c(0,0.01,0.1,0.2,0.49,0.499,0.5),method="kosambi")
```

```
print.summary.bicreg.qtl
```

Print summary of bicreg.qtl objects

Description

print method for summary.bicreg.qtl objects

Usage

```
## S3 method for class 'summary.bicreg.qtl'
print(x,...)
```

Arguments

x object of class 'bicreg.summ'
 ... further arguments to genetic print methods

Author(s)

Rod Ball (<rod.ball@scionresearch.com>)

recalc.bicprobs *Recalculation of posterior probabilities for bicreg.qtl objects*

Description

Posterior probabilities for models, marginal probabilities for model sizes, and marginal probabilities for markers are re-calculated for new values of delta and/or prior probabilities

Usage

```
recalc.bicprobs(obj, old.delta = attr(obj, "delta"), delta = 1, n = obj$n,
  old.prior = attr(obj, "prior"), prior = 0.5, p.sg = 1)
```

Arguments

obj object of class bicreg.qtl
 old.delta value of delta previously used to calculate obj
 delta value of delta for which probabilities are desired
 n sample size used in the BIC calculation (equivalent to sample size before multiple imputations)
 old.prior (scalar) value of prior probability per marker used to calculate obj
 prior (scalar) value of prior probability per marker for which probabilities are desired
 p.sg proportion sampled in tails if selectively genotyping the population

Details

Summary information in obj including BIC values, posterior probabilities for models, marginal probabilities for model size, and marginal probabilities for markers is recalculated with the specified new values of delta and prior

Value

A list with components:

delta	new value of delta used
prior	new value of prior used
bic	new value of bic for each model
,	
postprob	new value of posterior probability for each model
probne0	marginal probabilities for markers to be selected
postprob.size	marginal probabilities for model size

Author(s)

R.D. Ball <rod.ball@scionresearch.com>

See Also

[bicreg.qtl](#), [summary.bicreg.qtl](#)

Examples

```
## Not run: recalc.bicprobs(ex1n1200c1.bicreg,old.prior=0.2,prior=0.1)
```

sample.bicreg.qtl.models

Sampling models for BIC analyses of multiple chromosomes

Description

Models are sampled from each of a set of runs with different sets of independent variables (typically corresponding to multiple chromosomes), according to their posterior probabilities.

Usage

```
sample.bicreg.qtl.models(chrom.fits,nsim,maxtries=10)
```

Arguments

chrom.fits	list of bicreg.qtl objects from separate fits by chromosome or genomic region
nsim	number of models to sample
maxtries	maximum number of retries to get nsim unique models

Details

Each of `nsim` combined models is obtained by randomly sampling one model from each chromosome according to its posterior probability, and combining the `x`-variables from the sampled models.

Value

A list of models represented as a matrix (similar to the which matrix returned by `bicreg.qtl`, whose `(i, j)` element is TRUE if the `i`th sampled model contains the `j`th variable

Author(s)

R.D. Ball, (<rod.ball@scionresearch.com>)

References

Ball, R. D. 2001: Bayesian methods for QTL mapping based on model selection: approximate analysis using the Bayesian Information Criterion. *Genetics* 159: 1351–1364.

See Also

[bicreg.qtl](#), [bicreg.models](#)

Examples

```
## Not run: mWhich200 <- sample.bicreg.qtl.models(chrom.fits,nsim=200)
```

<code>sim.bc.progeny</code>	<i>Simulation of back-cross QTL progeny</i>
-----------------------------	---

Description

Simulate a back-cross QTL progeny with given QTL and markers.

Usage

```
sim.bc.progeny(n, Vp=NULL, map.pos, qtl.pos)
```

Arguments

<code>n</code>	Number of progeny to simulate.
<code>Vp</code>	Vector of variances of QTL effects, as a proportion of total variance. Should sum to less than 1.
<code>map.pos</code>	Vector of map positions for markers, or a list with elements <code>map.pos</code> (vector of map positions for markers) and <code>chrom</code> (vector of corresponding chromosome numbers).
<code>qtl.pos</code>	Vector of map positions for QTL, or a list with elements <code>qtl.pos</code> (vector of QTL positions) and <code>chrom</code> (vector of corresponding chromosome numbers). In case <code>Vp</code> is missing, <code>qtl.pos</code> should also contain elements <code>h2qs</code> (vector of QTL heritabilities) and <code>qtl.effect.signs</code> (vector of effect signs).

Details

Recombinations are simulated randomly along the genome for each progeny, and used to generate marker and QTL genotypes. Random error with variance $1 - \text{sum}(Vp)$ is added to the QTL effects to give simulated trait values y .

Value

sim.bc.progeny returns a list with elements x (matrix of marker values) and y (vector of trait values).

Author(s)

R.D. Ball <rod.ball@scionresearch.com>

Examples

```
set.seed(1234)
ex1.map.pos <- seq(5,105,by=10)
qtldata200 <- sim.bc.progeny(n=200,Vp=c(0.1,0.2,0.3,0.15,0.25)/2,
  map.pos=list(chrom=rep(1:2,rep(length(ex1.map.pos),2)),
  pos=rep(ex1.map.pos,2)),qtl.pos=list(chrom=rep(1:2,c(3,2)),
  pos=c(40,50,80,30,55)))
```

summary.bicreg.qtl *Summary of bicreg.qtl objects*

Description

summary method for bicreg.qtl objects

Usage

```
## S3 method for class 'bicreg.qtl'
summary(object,...)
```

Arguments

object object of class 'bicreg.qtl'
... further arguments to other summary methods

Author(s)

Rod Ball (<rod.ball@scionresearch.com>)

Unique.Rows	<i>Unique rows</i>
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Description

Return indices of unique rows of a matrix

Usage

```
Unique.Rows(x)
```

Arguments

x matrix

Details

The duplicated function is applied to the rows of x

Value

vector of indices of unique rows

Author(s)

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Examples

```
m <- matrix(c(1:3,1:3,2:4,5:7),nc=3,byrow=TRUE)
Unique.Rows(m)
m[Unique.Rows(m),]
```

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