

Package ‘qtlnet’

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Title Causal Inference of QTL Networks

Description Functions to Simultaneously Infer Causal Graphs and Genetic Architecture.

Includes acyclic and cyclic graphs for data from an experimental cross with a modest number (<10) of phenotypes driven by a few genetic loci (QTL).

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010)

Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes.

Annals of Applied Statistics 4: 320-339.

<doi:10.1214/09-AOAS288>.

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| acyclic | <i>Acyclic graph example</i> |
|---------|------------------------------|

Description

We generate synthetic data (sample size 300) according to a DAG composed by 100 nodes and 107 edges (exactly as in Figure 1). Each phenotype node is affected by three QTLs, and we allow only additive genetic effects. The QTLs for each phenotype are randomly selected among 200 markers, with 10 markers unevenly distributed on each of 20 autosomes. We allowed different phenotypes to potentially share common QTLs. For each phenotype, the regression coefficients with other phenotypes are chosen uniformly between 0.5 and 1; QTL effects are chosen between 0.2 to 0.6; and residual standard deviations are chosen from 0.1 to 0.5. For each realization we apply the QDG algorithm to infer causal directions for the edges of the skeleton obtained by the PC-skeleton algorithm.

Usage

```
data(acyclic)
```

Details

For cyclic graphs, the output of the qdg function computes the log-likelihood up to the normalization constant (un-normalized log-likelihood). We can use the un-normalized log-likelihood to compare cyclic graphs with reversed directions (since they have the same normalization constant). However we cannot compare cyclic and acyclic graphs.

References

Chaibub Neto et al. (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

See Also

[sim.cross](#), [sim.geno](#), [sim.map](#), [skeleton](#), [qdg](#), [graph.qdg](#), [generate.qtl.pheno](#)

Examples

```
## Not run:
## This reproduces Figure 1 exactly.
set.seed(3456789)

tmp <- options(warn=-1)
acyclic.DG <- randomDAG(n = 100, prob = 2 / 99)

options(tmp)

## Simulate cross object using R/qtl routines.
n.ind <- 300
mymap <- sim.map(len=rep(100,20), n.mar=10, eq.spacing=FALSE, include.x=FALSE)
mycross <- sim.cross(map=mymap, n.ind=n.ind, type="f2")
summary(mycross)
mycross <- sim.geno(mycross,n.draws=1)

## Produce 100 QTL at three markers apiece.
acyclic.qtl <- generate.qtl.markers(cross=mycross,n.phe=100)

## Generate data from directed graph.
bp <- runif(100,0.5,1)
stdev <- runif(100,0.1,0.5)
bq <- matrix(0,100,3)
bq[,1] <- runif(100,0.2,0.4)
bq[,2] <- bq[,1]+0.1
bq[,3] <- bq[,2]+0.1
## Generate phenotypes.
acyclic.data <- generate.qtl.pheno("acyclic", cross = mycross,
  bp = bp, bq = bq, stdev = stdev, allqtl = acyclic.qtl$allqtl)

acyclic.qdg <- qdg(cross=acyclic.data,
  phenotype.names=paste("y",1:100,sep=""),
  marker.names=acyclic.qtl$markers,
  QTL=acyclic.qtl$allqtl,
  alpha=0.005,
  n.qdg.random.starts=1,
  skel.method="pcskel")
save(acyclic.DG, acyclic.qtl, acyclic.data, acyclic.qdg,
  file = "acyclic.RData", compress = TRUE)

data(acyclic)

dims <- dim(acyclic.data$pheno)
SuffStat <- list(C = cor(acyclic.data$pheno), n = dims[1])
pc <- skeleton(SuffStat, gaussCItest, p = dims[2], alpha = 0.005)
summary(pc)
```

```
summary(graph.qdg(acyclic.qdg))
gr <- graph.qdg(acyclic.qdg, include.qtl = FALSE)
plot(gr)

## End(Not run)
```

bic.qtlnet
Pre-compute BIC values for qtlnet sampling.

Description

Pre-compute BIC values for qtlnet sampling to speed up MCMC sampling.

Usage

```
bic.qtlnet(cross, pheno.col, threshold, addcov = NULL, intcov = NULL,
  max.parents = 3, parents, verbose = TRUE, ...)
bic.join(cross, pheno.col, ..., max.parents = 3)
data(Pscdbp.bic)
```

Arguments

| | |
|--------------------------|---|
| <code>cross</code> | Object of class <code>cross</code> . See read.cross . |
| <code>pheno.col</code> | Phenotype identifiers from <code>cross</code> object. May be numeric, logical or character. |
| <code>threshold</code> | Scalar or list of thresholds, one per each node. |
| <code>addcov</code> | Additive covariates for each phenotype (NULL if not used). If entered as scalar or vector (same format as <code>pheno.col</code>), then the same <code>addcov</code> is used for all phenotypes. Alternatively, may be a list of additive covariate identifiers. |
| <code>intcov</code> | Interactive covariates, entered in the same manner as <code>addcov</code> . |
| <code>max.parents</code> | Maximum number of parents per node. This reduces the complexity of graphs and shortens run time. Probably best to consider values of 3-5. |
| <code>parents</code> | List containing all possible parents up to <code>max.parents</code> in size. May be a subset |
| <code>verbose</code> | Print iteration and number of models fit. |
| <code>...</code> | Additional arguments passed to internal routines. In the case of <code>bic.join</code> , these are a list of objects produced by <code>bic.qtlnet</code> (see example below). |

Details

The most expensive part of calculations is running [scanone](#) on each phenotype with parent phenotypes as covariates. One strategy is to pre-compute the BIC contributions using a cluster and save them for later use.

We divide the job into three steps: 1) determine parents and divide into reasonable sized groups; 2) compute BIC scores using `scanone` on a grid of computers; 3) compute multiple MCMC runs on a grid of computers. See the example for details.

Value

Matrix with columns:

| | |
|-----------|--|
| code | Binary code as decimal for the parents of a phenotype node, excluding the phenotype. Value is between 0 (no parents) and $2^{(\text{length}(\text{pheno.col}) - 1)}$. |
| pheno.col | Phenotype column in reduced set, in range 1:length(pheno.col). |
| bic | BIC score for phenotype conditional on parents (and covariates). |

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 4: 320-339. <http://dx.doi.org/10.1214/09-AOAS288>

See Also

[mcmc.qtlnet](#), [parents.qtlnet](#)

Examples

```
pheno.col <- 1:13
max.parents <- 12
size.qtlnet(pheno.col, max.parents)

## Not run:
## Compute all phenotype/parent combinations.
## This shows how to break up into many smaller jobs.

#####
## STEP 1: Preparation. Fast. Needed in steps 2 and 3.

pheno.col <- 1:13
max.parents <- 12
threshold <- 3.83

## Load cross object. Here we use internal object.
data(Pscdbp)
## or: load("Pscdbp.RData")
cross <- Pscdbp
## or: cross <- read.cross("Pscdbp.csv", "csv")

## Break up into groups to run on several machines.
## ~53 groups of ~1000, for a total of 53248 scanone runs.
parents <- parents.qtlnet(pheno.col, max.parents)
groups <- group.qtlnet(parents = parents, group.size = 1000)

## Save all relevant objects for later steps.
```

```

save(cross, pheno.col, max.parents, threshold, parents, groups,
     file = "Step1.RData", compress = TRUE)

#####
## STEP 2: Compute BIC scores. Parallelize.

## NB: Configuration of parallelization determined using Step 1 results.
## Load Step 1 computations.
load("Step1.RData")

## Parallelize this:
for(i in seq(nrow(groups)))
{
  ## Pre-compute BIC scores for selected parents.
  bic <- bic.qtlnet(cross, pheno.col, threshold,
                   max.parents = max.parents,
                   parents = parents[seq(groups[i,1], groups[i,2])])

  save(bic, file = paste("bic", i, ".RData", sep = ""), compress = TRUE)
}

#####
## STEP 3: Sample Markov chain (MCMC). Parallelize.

## NB: n.runs sets the number of parallel runs.
n.runs <- 100

## Load Step 1 computations.
load("Step1.RData")

## Read in saved BIC scores and combine into one object.
bic.group <- list()
for(i in seq(nrow(groups)))
{
  load(paste("bic", i, ".RData", sep = ""))
  bic.group[[i]] <- bic
}
saved.scores <- bic.join(cross, pheno.col, bic.group)

## Parallelize this:
for(i in seq(n.runs))
{
  ## Run MCMC with randomized initial network.
  mcmc <- mcmc.qtlnet(cross, pheno.col, threshold = threshold,
                     max.parents = max.parents, saved.scores = saved.scores, init.edges = NULL)

  save(mcmc, file = paste("mcmc", i, ".RData", sep = ""), compress = TRUE)
}

#####
## STEP 4: Combine results for post-processing.

```

```
## NB: n.runs needed from Step 3.
n.runs <- 100

## Combine outputs together.
outs.qtlnet <- list()
for(i in seq(n.runs))
{
  load(paste("mcmc", i, ".RData", sep = ""))
  outs.qtlnet[[i]] <- mcmc
}
out.qtlnet <- c.qtlnet(outs.qtlnet)
summary(out.qtlnet)
print(out.qtlnet)

## End of parallel example.
#####

## End(Not run)

dim(Pscdbp.bic)
```

cyclica

Cyclic graph (a) example

Description

We use a Gibbs sampling scheme to generate a data-set with 200 individuals (according with cyclic graph (a)). Each phenotype is affected by 3 QTLs. We fixed the regression coefficients at 0.5, error variances at 0.025 and the QTL effects at 0.2, 0.3 and 0.4 for the three F2 genotypes. We used a burn-in of 2000 for the Gibbs sampler.

Usage

```
data(cyclica)
```

Details

For cyclic graphs, the output of the qdg function computes the log-likelihood up to the normalization constant (un-normalized log-likelihood). We can use the un-normalized log-likelihood to compare cyclic graphs with reversed directions (they have the same normalization constant). However we cannot compare cyclic and acyclic graphs.

References

Chaibub Neto et al. (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

See Also

[sim.cross](#), [sim.geno](#), [sim.map](#), [skeleton](#), [qdg](#), [graph.qdg](#), [generate.qtl.pheno](#)

Examples

```

## Not run:
bp <- matrix(0, 6, 6)
bp[2,1] <- bp[4,2] <- bp[4,3] <- bp[5,4] <- bp[2,5] <- bp[6,5] <- 0.5
stdev <- rep(0.025, 6)

## Use R/qtl routines to simulate.
set.seed(3456789)
mymap <- sim.map(len = rep(100,20), n.mar = 10, eq.spacing = FALSE,
  include.x = FALSE)
mycross <- sim.cross(map = mymap, n.ind = 200, type = "f2")
mycross <- sim.geno(mycross, n.draws = 1)

cyclica.qtl <- generate.qtl.markers(cross = mycross, n.phe = 6)
mygeno <- pull.geno(mycross)[, unlist(cyclica.qtl$markers)]

cyclica.data <- generate.qtl.pheno("cyclica", cross = mycross, burnin = 2000,
  bq = c(0.2,0.3,0.4), bp = bp, stdev = stdev, geno = mygeno)
save(cyclica.qtl, cyclica.data, file = "cyclica.RData", compress = TRUE)

data(cyclica)
out <- qdg(cross=cyclica.data,
  phenotype.names=paste("y",1:6,sep=""),
  marker.names=cyclica.qtl$markers,
  QTL=cyclica.qtl$allqtl,
  alpha=0.005,
  n.qdg.random.starts=10,
  skel.method="pcskel")

gr <- graph.qdg(out)
gr
plot(gr)

## End(Not run)

```

cyclicb

Cyclic graph (b) example

Description

We use a Gibbs sampling scheme to generate a data-set with 200 individuals (according with cyclic graph (b)). Each phenotype is affected by 3 QTLs. We fixed the regression coefficients at 0.5, error variances at 0.025 and the QTL effects at 0.2, 0.3 and 0.4 for the three F2 genotypes. We used a burn-in of 2000 for the Gibbs sampler.

Usage

```
data(cyclicb)
```


Details

For cyclic graphs, the output of the `qdg` function computes the log-likelihood up to the normalization constant (un-normalized log-likelihood). We can use the un-normalized log-likelihood to compare cyclic graphs with reversed directions (since they have the same normalization constant). However we cannot compare cyclic and acyclic graphs.

References

Chaibub Neto et al. (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

See Also

[sim.cross](#), [sim.geno](#), [sim.map](#), [skeleton](#), [qdg](#), [graph.qdg](#), [generate.qtl.pheno](#)

Examples

```
## Not run:
bp <- matrix(0, 6, 6)
bp[2,1] <- bp[1,5] <- bp[3,1] <- bp[4,2] <- bp[5,4] <- bp[5,6] <- bp[6,3] <- 0.5
stdev <- rep(0.025, 6)

## Use R/qtl routines to simulate.
set.seed(3456789)
mymap <- sim.map(len = rep(100,20), n.mar = 10, eq.spacing = FALSE,
  include.x = FALSE)
mycross <- sim.cross(map = mymap, n.ind = 200, type = "f2")
mycross <- sim.geno(mycross, n.draws = 1)

cyclicb.qtl <- generate.qtl.markers(cross = mycross, n.phe = 6)
mygeno <- pull.geno(mycross)[, unlist(cyclicb.qtl$markers)]

cyclicb.data <- generate.qtl.pheno("cyclicb", cross = mycross, burnin = 2000,
  bq = c(0.2,0.3,0.4), bp = bp, stdev = stdev, geno = mygeno)
save(cyclicb.qtl, cyclicb.data, file = "cyclicb.RData", compress = TRUE)

data(cyclicb)
out <- qdg(cross=cyclicb.data,
  phenotype.names=paste("y",1:6,sep=""),
  marker.names=cyclicb.qtl$markers,
  QTL=cyclicb.qtl$allqtl,
  alpha=0.005,
  n.qdg.random.starts=10,
  skel.method="pcskel")

gr <- graph.qdg(out)
gr
plot(gr)

## End(Not run)
```

cyclicc

*Cyclic graph (c) example***Description**

We use a Gibbs sampling scheme to generate a data-set with 200 individuals (according with cyclic graph (c)). Each phenotype is affected by 3 QTLs. We fixed the regression coefficients at 0.5, (except for $\beta_{5,2}=0.8$) error variances at 0.025 and the QTL effects at 0.2, 0.3 and 0.4 for the three F2 genotypes. We used a burn-in of 2000 for the Gibbs sampler. This example illustrates that even though our method cannot detect reciprocal interactions (e.g. between phenotypes 2 and 5 in cyclic graph (c)), it can still infer the stronger direction, that is, the direction corresponding to the higher regression coefficient. Since $\beta_{5,2}$ is greater than $\beta_{2,5}$, the QDG method should infer the direction from 2 to 5.

Usage

```
data(cyclicc)
```

Details

For cyclic graphs, the output of the qdg function computes the log-likelihood up to the normalization constant (un-normalized log-likelihood). We can use the un-normalized log-likelihood to compare cyclic graphs with reversed directions (since they have the same normalization constant). However we cannot compare cyclic and acyclic graphs.

References

Chaibub Neto et al. (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

See Also

[sim.cross](#), [sim.geno](#), [sim.map](#), [skeleton](#), [qdg](#), [graph.qdg](#), [generate.qtl.pheno](#)

Examples

```
## Not run:
bp <- matrix(0, 6, 6)
bp[2,5] <- 0.5
bp[5,2] <- 0.8
bp[2,1] <- bp[3,2] <- bp[5,4] <- bp[6,5] <- 0.5
stdev <- rep(0.025, 6)

## Use R/qtl routines to simulate map and genotypes.
set.seed(34567899)
mymap <- sim.map(len = rep(100,20), n.mar = 10, eq.spacing = FALSE,
  include.x = FALSE)
mycross <- sim.cross(map = mymap, n.ind = 200, type = "f2")
mycross <- sim.geno(mycross, n.draws = 1)
```

```

## Use R/qdg routines to produce QTL sample and generate phenotypes.
cyclicc.qtl <- generate.qtl.markers(cross = mycross, n.phe = 6)
mygeno <- pull.geno(mycross)[, unlist(cyclicc.qtl$markers)]

cyclicc.data <- generate.qtl.pheno("cyclicc", cross = mycross, burnin = 2000,
  bq = c(0.2,0.3,0.4), bp = bp, stdev = stdev, geno = mygeno)
save(cyclicc.qtl, cyclicc.data, file = "cyclicc.RData", compress = TRUE)

data(cyclicc)
out <- qdg(cross=cyclicc.data,
  phenotype.names=paste("y",1:6,sep=""),
  marker.names=cyclicc.qtl$markers,
  QTL=cyclicc.qtl$allqtl,
  alpha=0.005,
  n.qdg.random.starts=1,
  skel.method="pcskel")

gr <- graph.qdg(out)
plot(gr)

## End(Not run)

```

dist.qtlnet

QTL network diagnostic routines

Description

Various QTLnet diagnostic routines.

Usage

```

dist.qtlnet(qtlnet.object, min.prob = 0.9, method = "manhattan", cex = 5)
edgematch.qtlnet(qtlnet.object, min.prob = 0.9, method = "manhattan", cex = 5)
mds.qtlnet(qtlnet.object, min.prob = 0.9, method = "manhattan", cex = 5)
plotbic.qtlnet(x, ..., smooth = TRUE)

```

Arguments

| | |
|------------------|---|
| qtlnet.object, x | Object of class qtlnet. |
| min.prob | Minimum probability to include edge in network. |
| method | Distance method to be used between columns of connection matrix. Used by dist . (Only used for <code>mds.qtlnet</code> .) |
| cex | Character expansion. (Only used for <code>mds.qtlnet</code> , scaled by range of BIC values.) |
| smooth | Use lowess smoother if TRUE. |
| ... | Additional unused arguments. |

Value

List containing, for each phenotype in the network, a character vector of the QTL names as chr@pos, or pseudomarker name if chr . pos is FALSE.

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 4: 320-339. <http://www.stat.wisc.edu/~yandell/doc/2010/92.AnnApplStat.pdf>

See Also

[mcmc.qtlnet](#)

Examples

```
loci.qtlnet(Pscdbp.qtlnet)
```

```
generate.qtl
```

Generate QTLs and phenotypes from cross object

Description

Generate QTLs and phenotype data for individual examples from cross. These are utility routines to illustrate the examples. They are not meant for users per se.

Usage

```
generate.qtl.markers(cross, n.phe, nqtl = 3)
generate.qtl.pheno(name, cross, bp, bq, stdev, allqtl,
  burnin = 2000, geno)
```

Arguments

| | |
|-------|---|
| cross | object of class cross; see read.cross |
| name | character string for example name |
| bp | vector or matrix of coefficients for dependencies between phenotypes; see cyclic and acyclic examples |
| bq | vector or matrix of coefficients for QTL effects on phenotypes; see cyclic and acyclic examples |
| stdev | vector of standard deviations per phenotype |

| | |
|--------|---|
| allqtl | list of objects of class qtl produced by <code>generate.qtl.sample</code> |
| burnin | number of burnin cycles for MCMC; default is 2000 |
| geno | genotypes at markers, typically extracted with <code>pull.geno</code> |
| n.phe | number of phenotypes |
| nqtl | number of QTL |

See Also

[acyclic](#), [cyclica](#), [cyclicb](#), [cyclicc](#)

Examples

```
## Not run:  
example(acyclic)  
example(cyclica)  
example(cyclicb)  
example(cyclicc)  
  
## End(Not run)
```

| | |
|--------|---------------------------------------|
| glxnet | <i>Generate and graph Glx network</i> |
|--------|---------------------------------------|

Description

This is the Glx network reported in Chaibub Neto et al 2008 and in Ferrara et al 2008. Age was used as an additive covariate and we allowed for sex by genotype interaction. The network differs slightly from the published network due to improved code.

References

Chaibub Neto et al. 2008 Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

Ferrara et al. 2008 Genetic networks of liver metabolism revealed by integration of metabolomic and transcriptomic profiling. *PLoS Genetics* 4: e1000034.

See Also

[qdg](#)

Examples

```

data(glxnet)
glxnet.cross <- calc.genoprob(glxnet.cross)
set.seed(1234)
glxnet.cross <- sim.geno(glxnet.cross)

n.node <- nphe(glxnet.cross) - 2 ## Last two are age and sex.
markers <- glxnet.qtl <- vector("list", n.node)
for(i in 1:n.node) {
  ac <- model.matrix(~ age + sex, glxnet.cross$pheno)[, -1]
  ss <- summary(scanone(glxnet.cross, pheno.col = i,
                      addcovar = ac, intcovar = ac[,2]),
                threshold = 2.999)
  glxnet.qtl[[i]] <- makeqtl(glxnet.cross, chr = ss$chr, pos = ss$pos)
  markers[[i]] <- find.marker(glxnet.cross, chr = ss$chr, pos = ss$pos)
}
names(glxnet.qtl) <- names(markers) <- names(glxnet.cross$pheno)[seq(n.node)]

glxnet.qdg <- qdg(cross=glxnet.cross,
                 phenotype.names = names(glxnet.cross$pheno[, seq(n.node)]),
                 marker.names = markers,
                 QTL = glxnet.qtl,
                 alpha = 0.05,
                 n.qdg.random.starts=10,
                 addcov="age",
                 intcov="sex",
                 skel.method="udgskel",
                 udg.order=6)
glxnet.qdg

## Not run:
gr <- graph.qdg(glxnet.qdg)
plot(gr)

## Or use tkplot().
glxnet.cross <- clean(glxnet.cross)
save(glxnet.cross, glxnet.qdg, glxnet.qtl, file = "glxnet.RData", compress = TRUE)

## End(Not run)

```

 igraph.qtlnet

qtlnet plot using igraph

Description

Plot inferred causal network using igraph package.

Usage

```
igraph.qtlnet(x, edges, loci.list,
             pheno.color = "green", qtl.color = "red", vertex.color,
             include.qtl = TRUE, ...)
## S3 method for class 'qtlnet'
plot(x, ...)
```

Arguments

| | |
|------------------------|---|
| x | Object of class qtlnet. |
| edges | Data frame with first two columns being cause and effect directed phenotype pairs. Typically determined as averaged.net element from call to summary.qtlnet . |
| loci.list | List of character names of loci by phenotype. Typically determined by call to loci.qtlnet . |
| pheno.color, qtl.color | Name of color to use for phenotypes and QTLs, respectively. |
| vertex.color | Vertex colors in order of pheno-pheno edged augmented by loci.list, by default determined by pheno.color and qtl.color. |
| include.qtl | Include QTL in graph if TRUE and loci.list is not NULL. |
| ... | Additional arguments passed to called routines. |

Details

Uses the igraph package to create graph objects. These can be exported to a variety of other modern graphics packages. graph.qtlnet is synonymous with igraph.qtlnet.

Value

Object of class graph created using [graph.data.frame](#).

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. Ann Appl Statist 4: 320-339. <http://www.stat.wisc.edu/~yandell/doc/2010/92.AnnApplStat.pdf>

See Also

[summary.qtlnet](#), [loci.qtlnet](#), [graph.data.frame](#), [tkplot](#)

Examples

```
Pscdbp.graph <- igraph.qtlnet(Pscdbp.qtlnet)
Pscdbp.graph
## Not run:
tkplot(Pscdbp.graph)

## End(Not run)
```

loci.qtlnet

QTL architecture per node as list

Description

Determines QTL that affect each phenotype conditional on the model-averaged network and on covariates.

Usage

```
loci.qtlnet(qtlnet.object, chr.pos = TRUE, merge.qtl = 10, ...)
est.qtlnet(qtlnet.object, ..., verbose = TRUE)
```

Arguments

| | |
|---------------|---|
| qtlnet.object | Object of class qtlnet. |
| chr.pos | Include chromosome and position if TRUE. |
| merge.qtl | Merge QTL within merge.qtl cM of the mean QTL per chromosome across all nodes. No merge if 0 or less. This can reduce the number of QTL nodes to one per chr. |
| ... | Additional unused arguments. |
| verbose | verbose output if TRUE. |

Value

List containing, for each phenotype in the network, a character vector of the QTL names as chr@pos, or pseudomarker name if chr.pos is FALSE.

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 4: 320-339. <http://www.stat.wisc.edu/~yandell/doc/2010/92.AnnApp1Stat.pdf>

See Also[mcmc.qtlnet](#)**Examples**

```
loci.qtlnet(Pscdbp.qtlnet)
```

mcmc.qtlnet

Sample genetic architecture and QTL network

Description

Use MCMC to alternatively sample genetic architecture and QTL network as directed acyclic graphs (DAGs).

Usage

```
mcmc.qtlnet(cross, pheno.col, threshold, addcov = NULL, intcov = NULL,
  nSamples = 1000, thinning = 1, max.parents = 3, M0 = NULL,
  burnin = 0.1, method = "hk", random.seed = NULL, init.edges = 0,
  saved.scores = NULL, rev.method = c("nbhd", "node.edge", "single"),
  verbose = FALSE, ...)
init.qtlnet(pheno.col, max.parents, init.edges)
```

Arguments

| | |
|-------------|--|
| cross | Object of class cross. See read.cross . |
| pheno.col | Phenotype identifiers from cross object. May be numeric, logical or character. |
| threshold | Scalar or list of thresholds, one per each node. |
| addcov | Additive covariates for each phenotype (NULL if not used). If entered as scalar or vector (same format as pheno.col), then the same addcov is used for all phenotypes. Alternatively, may be a list of additive covariate identifiers. |
| intcov | Interactive covariates, entered in the same manner as addcov. |
| nSamples | Number of samples to record. |
| thinning | Thinning rate. Number of MCMC samples is nSamples*thinning. |
| max.parents | Maximum number of parents to a node. This reduces the complexity of graphs and shortens run time. Probably best to consider values of 3-5. |
| M0 | Matrix of 0s and 1s with initial directed graph of row->col if (row,col) entry is 1. Cycles are forbidden (e.g. 1s on diagonal or symmetric 1s across diagonal). Default (if NULL) is sampled by a call to <code>init.qtlnet</code> ; all 0s if <code>init.edges = 0</code> (default). |
| burnin | Proportion of MCMC samples to use as burnin. Default is 0.1 if burnin is TRUE. Must be between 0 and 1. |
| method | Model fitting method for scanone . |

| | |
|--------------|--|
| random.seed | Initialization seed for random number generator. Must be NULL (no reset) or positive numeric. Used in Random . |
| init.edges | Initial number of edges for M_0 , to be sampled using <code>{init.qtlnet}</code> . Chosen uniformly from 0 to the number of possible edges if set to NULL. |
| saved.scores | Updated scores, typically pre-computed by bic.qtlnet . |
| rev.method | Method to use for reversing edges. See details. |
| verbose | Print iteration and number of models fit. |
| ... | Additional arguments. Advanced users may want to supply pre-computed <code>saved.scores</code> to speed up calculations. |

Details

Models are coded compactly as (1)(2|1)(3|1,2,4,5)(4|2)(5|2). Each parenthetical entry is a of form (node|parents); these each require a model fit, for now with [scanone](#).

The [scanone](#) routine is run on multiple phenotypes in the network that could all have the same parents. For instance, for 5 phenotypes, if (1|2,4) is sampled, then do [scanone](#) of this model as well as (3|2,4) and (5|2,4). Setting the hidden parameter `scan.parents` to a value smaller than `length(pheno.col) - 1` (default) disallows multiple trait scanning with more than that number of parents.

The `saved.scores` parameter can greatly reduce MCMC run time, by supplying pre-computed BIC scores. See [bic.qtlnet](#). Another option is to capture `saved.scores` from a previous `mcmc.qtlnet` run with the same phenotypes (and covariates). Caution is advised as only a modest amount of checking can be done.

The `init.qtlnet` routine can be used to randomly find an initial causal network M_0 with up to `init.edges` edges.

MCMC updates include delete, add or reverse edge direction. The early version of this method only considered the edge on its own (`rev.method = "single"`), while the neighborhood method (`rev.method = "nbhd"`) uses the update

Value

List of class `qtlnet`

| | |
|--------------|---|
| post.model | Model code (see details). |
| post.bic | Posterior BIC |
| Mav | Model average of M across MCMC samples. |
| freq.accept | Frequency of acceptance M-H proposals. |
| saved.scores | Saved LOD score for each phenotype and all possible sets of the other phenotypes as parent nodes. |
| all.bic | |
| cross | The cross object with calculated genotype probabilities. |

In addition, a number of attributes are recorded:

| | |
|-------|-------------------------|
| M_0 | Initial network matrix. |
|-------|-------------------------|


```

random.seed = 92387475, verbose = TRUE,
saved.scores = Pscdbp.bic)

## End(Not run)

```

parallel.qtlnet *Code to parallelize use of qtlnet*

Description

This routine calls one of four phases in a parallelized version of qtlnet.

Usage

```
parallel.qtlnet(phase, index = 1, ..., dirpath = ".")
```

Arguments

| | |
|---------|---|
| phase | Phase of parallelization as number 1 through 4. See details. |
| index | Index for phase. Used in phases 2 and 4, and for error codes saved in RESULT.phase.index file. |
| ... | Additional arguments for phases. See details. |
| dirpath | Character string for directory where user can read and write files. When submitting to a cluster, this should remain the default. |

Details

See <http://www.stat.wisc.edu/~yandell/sysgen/qtlnet> for details of implementation in progress. The plan is to run qtlnet via Condor (<https://research.cs.wisc.edu/htcondor/>) to scale up to larger networks, say up to 100 nodes. Most important information is passed in files. Phase 1 imports arguments from the params.txt file, which must have parse-able assignments to the arguments of qtlnet:::qtlnet.phase1. This first phase produces file Phase1.RData, which included objects used by all other phases.

Phase 1 also creates file groups.txt, which for each line has begin and end indices for the parents that would result from a call to [parents.qtlnet](#). Phase 2 should be run the same number of times as the number of lines in file groups.txt. Each run produces a bicN.RData file containing BIC computations. These computations are aggregated in Phase 3 to create Phase3.RData, which contains the saved.scores used for [mcmc.qtlnet](#) runs in Phase 4, which each produce an mcmcN.RData file. The number of runs of Phase 4 is an argument nruns stored in the params.txt file processed in Phase 1. Finally, Phase 5 aggregates the MCMC results from multiple independent runs into one qtlnet object.

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 4: 320-339. <http://www.stat.wisc.edu/~yandell/doc/2010/92.AnnApplStat.pdf>
<http://www.stat.wisc.edu/~yandell/sysgen/qtlnet>

See Also

[mcmc.qtlnet](#), [bic.qtlnet](#)

Examples

```
## Not run:
  parallel.qtlnet("/u/y/a/yandell/public/html/sysgen/qtlnet/condor", 1)

## End(Not run)
```

| | |
|----------------|--|
| parents.qtlnet | <i>Determine and group node-parent combinations.</i> |
|----------------|--|

Description

Routines useful for examining the size of node-parent combinations.

Usage

```
parents.qtlnet(pheno.col, max.parents = 3, codes.only = FALSE)
## S3 method for class 'parents.qtlnet'
summary(object, ...)
size.qtlnet(pheno.col, max.parents = 3)
group.qtlnet(pheno.col, max.parents = 3, n.groups = NULL,
  group.size = 50000, parents = parents.qtlnet(pheno.col, max.parents))
```

Arguments

| | |
|-------------|---|
| pheno.col | Phenotype identifiers from cross object. May be numeric, logical or character. |
| max.parents | Maximum number of parents per node. This reduces the complexity of graphs and shortens run time. Probably best to consider values of 3-5. |
| parents | List containing all possible parents up to max.parents in size. May be a subset |
| codes.only | Return only codes of parents if TRUE. |
| n.groups | Number of groups for parallel computation. Determined from group.size if missing. |
| group.size | Size of groups for parallel computation. See details. |
| object | Object of class parent.qtlnet. |
| ... | Additional arguments ignored. |

Details

The most expensive part of calculations is running `scanone` on each phenotype with parent phenotypes as covariates. One strategy is to pre-compute the BIC contributions using a cluster and save them for later use. The `parents.qtlnet` routine creates a list of all possible parent sets (up to `max.parents` in size). The `size.qtlnet` determines the number of `scanone` calculations possible for a network with nodes `pheno.col` and maximum parent size `max.parents`. The `group.qtlnet` groups the parent sets into roughly equal size groups for parallel computations. See `bic.qtlnet` for further details.

Value

The `size.qtlnet` returns the number of possible `scanone` computations needed for BIC scores.

The `group.qtlnet` produces an index into the parents list created by `parents.qtlnet`. See details.

The `parents.qtlnet` creates a list object with names being the code.

The summary method for such an object is a data frame with `row.names` being the code, a binary code as decimal for the parents of a phenotype node, excluding the phenotype. Value is between 0 (no parents) and $2^{(\text{length}(\text{pheno.col}) - 1)}$. The columns are

| | |
|----------------------|--|
| <code>parents</code> | Comma-separated string of parents to potential child node. |
| <code>n.child</code> | Number of possible child nodes to this parent set. |

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Stat* 4: 320-339. <http://dx.doi.org/10.1214/09-AOAS288>

See Also

`bic.qtlnet`

Examples

```
## Restrict to at most 3 parents per node.
pheno.col <- 1:6
max.parents <- 3
size.qtlnet(pheno.col, max.parents)
parents <- parents.qtlnet(pheno.col, max.parents)
summary(parents)

## Allow an arbitrary number (up to 12) of parents per node.
pheno.col <- 1:13
max.parents <- 12
size.qtlnet(pheno.col, max.parents)
```

```
## Make ~53 groups of ~1000, for a total of 53248 scanone runs.
parents <- parents.qtlnet(pheno.col, max.parents)
n.child <- summary(parents)$n.child
table(n.child)
groups <- group.qtlnet(parents = parents, group.size = 1000)
apply(groups, 1,
      function(group, parents) sapply(parents[seq(group[1], group[2])], length),
      parents)
```

Pscdbp

Cross and qtlnet objects with Ghazalpour et al. (2006) data. Only 13 phenotypes are included.

Description

The R/qtl cross object was created from data at source. The qtlnet object was created using [mcmc.qtlnet](#).

Usage

```
data(Pscdbp)
data(Pscdbp.qtlnet)
```

Source

<https://horvath.genetics.ucla.edu/coexpressionnetwork/>

References

Ghazalpour A, Doss S, Zhang B, Wang S, Plaisier C, Castellanos R, Brozell A, Schadt EE, Drake TA, Lusis AJ, Horvath S (2006) Integrating genetic and network analysis to characterize genes related to mouse weight. PLoS Genetics 2: e130-NA. <http://dx.doi.org/10.1371/journal.pgen.0020130>

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. Ann Appl Statist 4: 320-339. <http://dx.doi.org/10.1214/09-A0AS288>

See Also

[read.cross](#), [mcmc.qtlnet](#)

Examples

```
summary(Pscdbp)
## Not run:
summary(Pscdbp.qtlnet)

## End(Not run)
```

qdg *Produces a directed graph using QDG algorithm*

Description

This function implements the QDG algorithm described in Chaibub Neto et al 2008. It creates and scores QDGs. The computed scores (log-likelihood and BIC) are only valid for acyclic graphs. For cyclic networks qdgSEM should be used to compute the scores.

Usage

```
qdg(cross, phenotype.names, marker.names, QTL, alpha,
    n.qdg.random.starts, addcov = NULL, intcov = NULL,
    skel.method = c("pcskel", "udgskel"), udg.order = 2)
graph.qdg(x, ...)
## S3 method for class 'qdg'
print(x, ...)
## S3 method for class 'qdg'
summary(object, ...)
```

Arguments

| | |
|---------------------|--|
| cross | object of class cross (see read.cross). |
| phenotype.names | character string with names of phenotype nodes corresponding to phenotypes in cross. |
| marker.names | list of character strings, one for each of phenotype.names. Each character string has the marker names for that phenotype. |
| QTL | object of class qt1 (see makeqt1). |
| alpha | significance level threshold for PC or UDG algorithms (for the inference of the graph skeleton. See step 1 of the QDG algorithm). Must be between 0 and 1. |
| n.qdg.random.starts | number of random starts for the QDG algorithm (see step 3 of the QDG algorithm). |
| addcov | names of additive covariates. Must be valid phenotype names in cross. Expanded to include all intcov names. |
| intcov | names of additive covariates. Must be valid phenotype names in cross. |
| skel.method | Either "pcskel" for the PC skeleton algorithm (skeleton) or "udgskel" for the UDG algorithm (approximate.UDG routine defined internal to qdg). |
| udg.order | maximum allowed order of the UDG algorithm. Must be between zero and the number of variables minus 2. |
| x,object | object of class qdg. |
| ... | additional arguments (ignored). |

Details

The log-likelihood and BIC scores are computed based in the factorization of the joint distribution, and hence are only valid for acyclic networks. For cyclic networks these scores are relative to the unnormalized likelihoods. Models include phenotypes and QTLs. The 'udgskel' method for the computation of the skeleton of the causal model should be used for small networks only (the UDG algorithm quickly becomes computationally infeasible as the number of nodes increases).

Value

List object that inherits class "qdg" and "qdg" with components:

| | |
|-----------------|--|
| UDG | Undirected dependency graph from PC skeleton or UDG algorithms. |
| DG | Directed dependency graph before recheck step (output of the step 2 of the QDG algorithm). |
| best.lm | Solution with lowest BIC (best fit to the data). |
| Solutions | Solutions of dependency graph after recheck step (output of steps 3, 4 and 5 of the QDG algorithm.) |
| marker.names | List of character strings, one for each of phenotype.names. Each character string has the marker names for that phenotype. |
| phenotype.names | Character string with names of phenotype nodes corresponding to phenotypes in cross. |

References

Chaibub Neto et al. (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

See Also

[skeleton](#)

Examples

```
## simulate a genetic map (20 autosomes, 10 not equally spaced markers per
## chromosome)
mymap <- sim.map(len=rep(100,20), n.mar=10, eq.spacing=FALSE, include.x=FALSE)

## simulate an F2 cross object with n.ind (number of individuals)
n.ind <- 200
mycross <- sim.cross(map=mymap, n.ind=n.ind, type="f2")

## produce multiple imputations of genotypes using the
## sim.geno function. The makeqtl function requires it,
## even though we are doing only one imputation (since
## we don't have missing data and we are using the
## genotypes in the markers, one imputation is enough)
mycross <- sim.geno(mycross,n.draws=1)
```

```

## sample markers (2 per phenotype)
genotypes <- pull.geno(mycross)
geno.names <- dimnames(genotypes)[[2]]
m1 <- sample(geno.names,2,replace=FALSE)
m2 <- sample(geno.names,2,replace=FALSE)
m3 <- sample(geno.names,2,replace=FALSE)
m4 <- sample(geno.names,2,replace=FALSE)

## get marker genotypes
g11 <- genotypes[,m1[1]]; g12 <- genotypes[,m1[2]]
g21 <- genotypes[,m2[1]]; g22 <- genotypes[,m2[2]]
g31 <- genotypes[,m3[1]]; g32 <- genotypes[,m3[2]]
g41 <- genotypes[,m4[1]]; g42 <- genotypes[,m4[2]]

## generate phenotypes
y1 <- runif(3,0.5,1)[g11] + runif(3,0.5,1)[g12] + rnorm(n.ind)
y2 <- runif(3,0.5,1)[g21] + runif(3,0.5,1)[g22] + rnorm(n.ind)
y3 <- runif(1,0.5,1) * y1 + runif(1,0.5,1) * y2 + runif(3,0.5,1)[g31] +
  runif(3,0.5,1)[g32] + rnorm(n.ind)
y4 <- runif(1,0.5,1) * y3 + runif(3,0.5,1)[g41] + runif(3,0.5,1)[g42] +
  rnorm(n.ind)

## incorporate phenotypes to cross object
mycross$pheno <- data.frame(y1,y2,y3,y4)

## create markers list
markers <- list(m1,m2,m3,m4)
names(markers) <- c("y1","y2","y3","y4")

## create qtl object
allqtls <- list()
m1.pos <- find.markerpos(mycross, m1)
allqtls[[1]] <- makeqtl(mycross, chr = m1.pos[,"chr"], pos = m1.pos[,"pos"])
m2.pos <- find.markerpos(mycross, m2)
allqtls[[2]] <- makeqtl(mycross, chr = m2.pos[,"chr"], pos = m2.pos[,"pos"])
m3.pos <- find.markerpos(mycross, m3)
allqtls[[3]] <- makeqtl(mycross, chr = m3.pos[,"chr"], pos = m3.pos[,"pos"])
m4.pos <- find.markerpos(mycross, m4)
allqtls[[4]] <- makeqtl(mycross, chr = m4.pos[,"chr"], pos = m4.pos[,"pos"])
names(allqtls) <- c("y1","y2","y3","y4")

## infer QDG
out <- qdg(cross=mycross,
  phenotype.names = c("y1","y2","y3","y4"),
  marker.names = markers,
  QTL = allqtls,
  alpha = 0.005,
  n.qdg.random.starts=10,
  skel.method="pcskel")

out
## Not run:
gr <- graph.qdg(out)

```

```

gr
plot(gr)

## End(Not run)

```

| | |
|---------------|---|
| qdg.perm.test | <i>Conduct permutation test for LOD score of edge direction on directed graph</i> |
|---------------|---|

Description

Conduct permutation test for LOD score of edge direction on directed graph.

Usage

```

qdg.perm.test(cross, nperm, node1, node2, common.cov = NULL,
              DG, QTLs, addcov = NULL, intcov = NULL)
## S3 method for class 'qdg.perm.test'
summary(object, ...)
## S3 method for class 'qdg.perm.test'
print(x, ...)

```

Arguments

| | |
|------------|---|
| cross | Object of class cross (see read.cross). |
| nperm | Number of permutations. |
| node1 | Character string with name of a phenotype nodes. |
| node2 | Character string with name of a phenotype nodes. |
| common.cov | Character string with name of common phenotype covariates. |
| DG | Directed graph of class QDG |
| QTLs | List of objects of class qt1. |
| addcov | Names of additive covariates. Must be valid phenotype names in cross. Expanded to include all intcov names. |
| intcov | Names of additive covariates. Must be valid phenotype names in cross. |
| x, object | Object of class qdg.perm.test. |
| ... | Additional arguments ignored. |

Details

qdg.perm.test performs nperm permutation-based test of LOD score for an edge of a directed graph.

Value

List composed by:

| | |
|------------|--|
| pvalue | Permutation p-value. |
| obs.lod | Observed LOD score. |
| PermSample | Permutation LOD scores sample. |
| node1 | Character string with name of a phenotype nodes. |
| node2 | Character string with name of a phenotype nodes. |

References

Chaibub Neto et al. (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.

Examples

```
data(glxnet)
glxnet.cross <- calc.genoprob(glxnet.cross)
set.seed(1234)
glxnet.cross <- sim.geno(glxnet.cross)
## Should really use nperm = 1000 here.
qdg.perm.test(glxnet.cross, nperm = 10, "Glx", "Slc1a2",
  DG = glxnet.qdg$DG, QTls = glxnet.qtl)
```

| | |
|---------|---|
| qdg.sem | <i>Score directed graphs outputed by qdg using structural equation models (SEM)</i> |
|---------|---|

Description

Score directed graphs (cyclic or acyclic) outputed by qdg function using the sem R package.

Usage

```
qdg.sem(qdgObject, cross)
## S3 method for class 'qdg.sem'
print(x, ...)
## S3 method for class 'qdg.sem'
summary(object, ...)
```

Arguments

| | |
|-----------|--|
| qdgObject | list containing the output of <code>qdg</code> . |
| cross | object of class <code>cross</code> (see read.cross). |
| x,object | object of class <code>qdg</code> . |
| ... | extra arguments to <code>print</code> or <code>summary</code> (ignored). |

Details

Fits a SEM to the phenotypes network. QTLs are not included as variables in the model. When additive covariates are used in qdg, qdg.sem fits a SEM model to the residuals of the variables after adjustment of the additive covariates.

Value

List object that inherits class "qdg.sem" and "qdg" composed by:

| | |
|-----------------|--|
| best.SEM | Solution with lowest SEM BIC (best fit to the data). |
| BIC.SEM | Vector with the BIC values of all solutions from qdg. |
| path.coeffs | Path coefficients associated with the best SEM solution. |
| Solutions | Solutions of dependency graph after recheck step (output of steps 3, 4 and 5 of the QDG algorithm.) |
| marker.names | List of character strings, one for each of phenotype.names. Each character string has the marker names for that phenotype. |
| phenotype.names | Character string with names of phenotype nodes corresponding to phenotypes in cross. |
| dropped | Indexes of solutions that were dropped (NULL if none dropped). |

See Also

[qdg sem](#)

Examples

```
## simulate a genetic map (20 autosomes, 10 not equally spaced markers per
## chromosome)
mymap <- sim.map(len=rep(100,20), n.mar=10, eq.spacing=FALSE, include.x=FALSE)

## simulate an F2 cross object with n.ind (number of individuals)
n.ind <- 200
mycross <- sim.cross(map=mymap, n.ind=n.ind, type="f2")

## produce multiple imputations of genotypes using the
## sim.geno function. The makeqtl function requires it,
## even though we are doing only one imputation (since
## we don't have missing data and we are using the
## genotypes in the markers, one imputation is enough)
mycross <- sim.geno(mycross,n.draws=1)

## sample markers (2 per phenotype)
genotypes <- pull.geno(mycross)
geno.names <- dimnames(genotypes)[[2]]
m1 <- sample(geno.names,2,replace=FALSE)
m2 <- sample(geno.names,2,replace=FALSE)
m3 <- sample(geno.names,2,replace=FALSE)
m4 <- sample(geno.names,2,replace=FALSE)
```

```

## get marker genotypes
g11 <- genotypes[,m1[1]]; g12 <- genotypes[,m1[2]]
g21 <- genotypes[,m2[1]]; g22 <- genotypes[,m2[2]]
g31 <- genotypes[,m3[1]]; g32 <- genotypes[,m3[2]]
g41 <- genotypes[,m4[1]]; g42 <- genotypes[,m4[2]]

## generate phenotypes
y1 <- runif(3,0.5,1)[g11] + runif(3,0.5,1)[g12] + rnorm(n.ind)
y2 <- runif(3,0.5,1)[g21] + runif(3,0.5,1)[g22] + rnorm(n.ind)
y3 <- runif(1,0.5,1) * y1 + runif(1,0.5,1) * y2 + runif(3,0.5,1)[g31] +
  runif(3,0.5,1)[g32] + rnorm(n.ind)
y4 <- runif(1,0.5,1) * y3 + runif(3,0.5,1)[g41] + runif(3,0.5,1)[g42] +
  rnorm(n.ind)

## incorporate phenotypes to cross object
mycross$pheno <- data.frame(y1,y2,y3,y4)

## create markers list
markers <- list(m1,m2,m3,m4)
names(markers) <- c("y1","y2","y3","y4")

## create qtl object
allqtls <- list()
m1.pos <- find.markerpos(mycross, m1)
allqtls[[1]] <- makeqtl(mycross, chr = m1.pos[, "chr"], pos = m1.pos[, "pos"])
m2.pos <- find.markerpos(mycross, m2)
allqtls[[2]] <- makeqtl(mycross, chr = m2.pos[, "chr"], pos = m2.pos[, "pos"])
m3.pos <- find.markerpos(mycross, m3)
allqtls[[3]] <- makeqtl(mycross, chr = m3.pos[, "chr"], pos = m3.pos[, "pos"])
m4.pos <- find.markerpos(mycross, m4)
allqtls[[4]] <- makeqtl(mycross, chr = m4.pos[, "chr"], pos = m4.pos[, "pos"])

names(allqtls) <- c("y1","y2","y3","y4")

## infer QDG
out <- qdg(cross=mycross,
  phenotype.names = c("y1","y2","y3","y4"),
  marker.names = markers,
  QTL = allqtls,
  alpha = 0.005,
  n.qdg.random.starts=10,
  skel.method="pcskel")

## Not run:
gr <- graph.qdg(out)
plot(gr)

## Following does not work. Not sure why.
out2 <- qdg.sem(out, cross=mycross)
out2
gr2 <- graph.qdg(out2)
plot(gr2)

```

```
## End(Not run)
```

```
subset.qtlnet      Catenate or subset qtlnet object(s).
```

Description

Multiple qtlnet objects can be catenated together or subsetted by run.

Usage

```
## S3 method for class 'qtlnet'
subset(x, run, ...)
## S3 method for class 'qtlnet'
c(...)
best.qtlnet(x, burnin = attr(x, "burnin"), wh = which.min(meanbic(x, burnin)))
```

Arguments

| | |
|--------|--|
| x | Object of class qtlnet. See mcmc.qtlnet . |
| run | Numeric index to desired run. Must be between 0 and number of runs. |
| burnin | Proportion of MCMC samples to be considered as burnin. Taken from qtlnet object usually. |
| wh | Number identifying which model is best. |
| ... | For c.qtlnet, objects of class qtlnet to be joined. Ignored for subset.qtlnet. |

Details

The catenation is used by [parallel.qtlnet](#) in phase 5 to join together multiple independent MCMC runs. Note that the averaged network and the frequency of acceptance for a derived subset are only based on the saved samples, while the original qtlnet objects used all samples. Thus catenation and subset are not strictly reversible functions.

The `best.qtlnet` routine picks the run with the best (lowest) BIC score on average and returns that run as a qtlnet object. It also produces a trace plot of BIC for all the runs.

Value

Both return an object of class qtlnet.

Author(s)

Brian Yandell

See Also

[mcmc.qtlnet](#)

Examples

```
## Not run:
joined <- c(qtlnet1, qtlnet2)
sub1 <- subset(joined, 1)
best <- best.qtlnet(joined)
## qtlnet1 and sub1 should be nearly identical.

## End(Not run)
```

summary.qtlnet

summary of model average network and posterior table

Description

Print and summary methods for qtlnet objects.

Usage

```
## S3 method for class 'qtlnet'
print(x, cutoff = 0.01, digits = 3, ...)
## S3 method for class 'qtlnet'
summary(object, parent.patterns = FALSE, ...)
## S3 method for class 'summary.qtlnet'
print(x, ...)
check.qtlnet(object, min.prob = 0.9, correct = TRUE, verbose = FALSE, ...)
```

Arguments

| | |
|-----------------|---|
| x, object | Object of class qtlnet. |
| cutoff | Frequency cutoff for model patterns to be displayed. Always shows at least the most common pattern. |
| digits | Number of digits to display for posterior probabilities on directed edges. |
| parent.patterns | Include summary of parent patterns if TRUE. |
| min.prob | Set the minimum posterior probability for inclusion of an edge. |
| correct | Correct min.prob if TRUE. |
| verbose | Print forbidden edges in model-averaged solution if TRUE. |
| ... | Other hidden arguments. These include min.prob, which can also be passed to other igraph.qtlnet and plot.qtlnet routines. |

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 4: 320-339. <http://www.stat.wisc.edu/~yandell/doc/2010/92.AnnApplStat.pdf>

See Also

[mcmc.qtlnet](#)

Examples

```
data(Pscdbp.qtlnet)
print(Pscdbp.qtlnet)
summary(Pscdbp.qtlnet)
```

| | |
|--------------|----------------------------------|
| write.qtlnet | <i>write qtlnet as text file</i> |
|--------------|----------------------------------|

Description

Write resulting graph as text file

Usage

```
write.qtlnet(x, filename, edges, loci.list, include.qtl = TRUE,
            est.list, include.est = TRUE,
            digits = 3, col.names = TRUE, ...)
```

Arguments

| | |
|-------------|---|
| x | Object of class qtlnet. |
| filename | Character string with name of text file (usually ends in .txt). |
| edges | Data frame with first two columns being cause and effect directed phenotype pairs. Typically determined as averaged.net element from call to summary.qtlnet . |
| loci.list | List of character names of loci by phenotype. Typically determined by call to loci.qtlnet . |
| include.qtl | Include QTL in graph if TRUE and loci.list is not NULL. |
| est.list | List of estimates from internal est.qtlnet? |
| include.est | Include estimate if TRUE. |
| digits | Number of significant digits for width. |
| col.names | Character vector of column names. |
| ... | Additional arguments passed to called routines. |

Details

Simple write of causal network, for instance to use with Cytoscape.

Value

Invisibly returns data frame that corresponds to saved file.

Author(s)

Brian S. Yandell and Elias Chaibub Neto

References

Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 4: 320-339. <http://www.stat.wisc.edu/~yandell/doc/2010/92.AnnApplStat.pdf>

See Also

[igraph.qtlnet](#)

Examples

```
## Not run:  
write.qtlnet(Pscdbp.qtlnet, "Pscdbp.txt")  
  
## End(Not run)
```

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