

QTL-directed Dependency Graph (QDG) Package in R

Elias Chaibub Neto and Brian S. Yandell

June 27, 2008

This document shows how to generate data, fit a QDG model and plot the inferred graph. We focus on a simple graph, $y_1 \rightarrow y_3$, $y_2 \rightarrow y_3$ and $y_3 \rightarrow y_4$, with QTLs that affect each of the three phenotypes.

```
> library(qdg)
```

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)
```

Use 2 markers per phenotype, samples from the cross.

```
> 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)  
> 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]]  
> 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 into 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 object.

```
> out <- qdgAlgo(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
```

Number of solutions:

```
[1] 1
```

Best solution:

	node1	direction	node2	lod
1	y1	---->	y3	1.6719717
2	y2	---->	y3	0.6870592
3	y3	---->	y4	7.0018203

BIC:

```
lm
2393.154
```

Best solution is solution number:

```
[1] 1
```

Caution:

```
[1] "If one of the solutions is a cyclic graph you should run qdgSEM in order to score the networks using"
```

Plot object.

```
> plot(out)
```

