

# Simulating molecular regulatory networks using *qpgraph*

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## 1 Introduction

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The theoretical substrate used by *qpgraph* to estimate network models of molecular regulatory interactions is that of graphical Markov models (GMMs). A useful way to understand the underpinnings of these models is to simulate them and simulate data from them. More importantly, these simulated data may serve the purpose of verifying properties of GMM estimation procedures, such as correctness or asymptotic behavior. Here we illustrate the functionalities of *qpgraph* to perform these simulations. The interface provided by *qpgraph* tries to comply with the available functions in the base R *stats* package for simulating data from probability distributions and the names of functions described below for the purpose of simulating graphs, models and data follow the convention:

`r<objectclass>(n, ...)`

where *<objectclass>* refers to the class of object (in a broad sense, not just a formal S3 or S4 class) being simulated and *n* is the number of observations to simulate. Except for the case of data, since the simulated observations are other than R atomic types of objects, when  $n > 1$ , these functions return simulated observations in the form of a list with *n* elements.

## 2 Simulation of graphs

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An undirected graph  $G$  is a mathematical object defined by a pair of sets  $G = (V, E)$  where  $V = \{1, \dots, p\}$  is the vertex set and  $E \subseteq (V \times V)$  is the edge set. In the context of GMMs *labeled* undirected graphs are employed to represent conditional (in)dependencies among random variables (r.v.'s)  $X = \{X_1, \dots, X_p\}$  indexed by the vertices in  $V$  whose values occur on equal footing. Stepwise data generating processes can be represented by directed graphs. In the context of GMMs one may also consider so-called *marked* graphs, which are graphs with *marked* vertices grouped into two subsets, one associated to discrete variables and another to continuous ones. A graph with a single type of vertices, i.e., that is not marked, it is also called *pure*. Different types of graphs determine different GMM classes. For a comprehensive description of different GMM classes and more elaborate descriptions of the terminology and notation used in this vignette the reader may consult the book of Lauritzen (1996).

The first step to simulate a GMM consists of simulating its associated graph. While there are many R packages that provide procedures to simulate graphs, *qpgraph* provides its own minimal functionality for this purpose tailored to ease the downstream simulation of GMMs. This functionality allows the user to simulate undirected graphs according to two main criteria, the type of graph (pure or marked) and the type of model to simulate the random graph.

The simplest type of model to simulate random undirected graphs is the so-called Erdős-Rényi which is generated by either including an edge between every pair of vertices with a pre-specified probability or drawing a graph uniformly at random among those with a pre-specified number of edges. In the context of exploring the performance of GMM structure estimation procedures under different degrees of sparseness of the underlying graph, it is handy to work with the so-called

$d$ -regular graphs (Harary, 1969). These are graphs with a constant degree vertex  $d$  which, in one hand, make the graph density a linear function of  $d$  and, on the other hand, bound the smallest minimal separator between any two vertices (Castelo and Roverato, 2006, see pg. 2646).

To specify the parameters that define one specific type of graph we want to simulate *qpgraph* provides the following functions that build parameter objects which can be used afterwards to simulate graphs through a single call to the function `rgraphBAM()`:

```
> library(qpgraph)
> args(erGraphParam)

function (p = 4L, m = 4L, prob = NA_real_, labels = as.character(1:p))
NULL

> args(erMarkedGraphParam)

function (pI = 1L, pY = 3L, m = 4L, prob = NA_real_, Ilabels = paste0("I",
  1:pI), Ylabels = paste0("Y", 1:pY))
NULL

> args(dRegularGraphParam)

function (p = 4L, d = 2L, exclude = as.integer(NULL), labels = as.character(1:p))
NULL

> args(dRegularMarkedGraphParam)

function (pI = 1L, pY = 3L, d = 2L, exclude = as.integer(NULL),
  Ilabels = paste0("I", 1:pI), Ylabels = paste0("Y", 1:pY))
NULL
```

As we can see from their default values, a single call without arguments already define some small graphs on 5 vertices:

```
> erGraphParam()

Erdos-Renyi pure graph parameter object
No. of pure vertices: 4
No. of edges: 4
Vertex labels: 1, 2, 3, 4

> erMarkedGraphParam()

Erdos-Renyi marked graph parameter object
No. of marked vertices: 4
No. of dot (I) vertices: 1
No. of circle (Y) vertices: 3
No. of edges: 4
Dot (I) vertex labels: I1
Circle (Y) vertex labels: Y1, Y2, Y3

> dRegularGraphParam()

d-regular pure graph parameter object
No. of pure vertices: 4
Constant degree: 2
Vertex labels: 1, 2, 3, 4

> dRegularMarkedGraphParam()

d-regular marked graph parameter object
No. of marked vertices: 4
No. of dot (I) vertices: 1
No. of circle (Y) vertices: 3
```

```

Constant degree: 2
Dot (I) vertex labels: I1
Circle (Y) vertex labels: Y1, Y2, Y3

```

The objects returned by these functions belong to different S4 classes derived from the following two main ones, *graphParam* and *markedGraphParam*:

```

> showClass("graphParam")

Class "graphParam" [package "qpgraph"]

Slots:

Name:      p      labels
Class:     integer character

Known Subclasses: "erGraphParam", "dRegularGraphParam"

```

```

> showClass("markedGraphParam")

Class "markedGraphParam" [package "qpgraph"]

Slots:

Name:      pI      pY      Ilabels      Ylabels
Class:     integer integer character character

Known Subclasses: "erMarkedGraphParam", "dRegularMarkedGraphParam"

```

While this level of detail is not crucial for the end-user, knowing the distinction between these two main types of graph parameter objects, *graphParam* and *markedGraphParam*, may help to get more quickly acquainted with the type of arguments we need in calls described below to simulate GMMs.

Finally, the function *rgraphBAM()* simulates one or more random graphs as objects of the class *graphBAM* defined in the *graph* package. Its arguments are:

```

> args(rgraphBAM)

function (n, param, ...)
NULL

```

where *n* is the number of graphs to simulate (default *n*=1) and *param* is an object generated by one of the previous parameter functions. A couple of minimal examples are:

```

> rgraphBAM(erGraphParam())

A graphBAM graph with undirected edges
Number of Nodes = 4
Number of Edges = 4

> rgraphBAM(n=2, dRegularGraphParam())

[[1]]
A graphBAM graph with undirected edges
Number of Nodes = 4
Number of Edges = 4

[[2]]
A graphBAM graph with undirected edges
Number of Nodes = 4
Number of Edges = 4

```

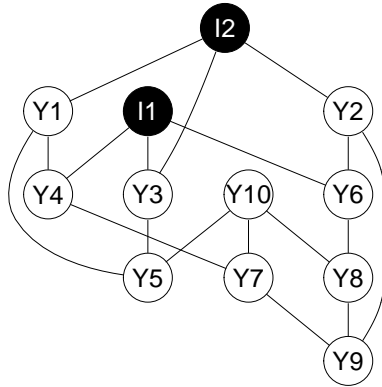


Figure 1: A random 3-regular marked undirected graph.

In a slightly more elaborate example, if we would like to simulate a  $d$ -regular graph on 2 discrete vertices and 5 continuous ones with a constant degree  $d = 3$ , we would make the following call to `rgraphBAM()`, which we previously seed to enable the reader reproducing the same graph shown here:

```
> set.seed(1234)
> g <- rgraphBAM(dRegularMarkedGraphParam(pI=2, pY=10, d=3))
> plot(g)
```

where the last `plot` function call is defined (overloaded) in the *qpggraph* package to ease plotting the graph which is displayed in Figure 1. This function uses the plotting capabilities from the *Rgraphviz* package and further arguments, such as `layoutType`, can be passed downstream to the *Rgraphviz* plotting function to fine tune the display of the graph.

### 3 Simulation of undirected Gaussian GMMs

Undirected Gaussian GMMs are multivariate normal models on continuous r.v.'s  $X_V = \{X_1, \dots, X_p\}$  determined by an undirected graph  $G = (V, E)$  with  $V = \{1, \dots, p\}$  and  $E \subseteq (V \times V)$ . In particular, the zero-pattern of the inverse covariance matrix corresponds to the missing edges in  $G$  (Lauritzen, 1996). Therefore, simulating this type of GMM amounts to simulate a covariance matrix whose inverse matches the missing edges of a given, or simulated, undirected graph in its zero pattern and whose scaled covariance matches a given marginal correlation on the cells corresponding to present edges. This can be easily accomplished with *qpggraph* using the function `rUGgmm`:

```
> args(rUGgmm)

function (n, g, ...)
NULL
```

where `n` corresponds to the number of undirected Gaussian GMMs we want to simulate (default `n=1` and `g` corresponds to either a *graphParam* object, a *graphBAM* object or a matrix. This depends on whether we want to simulate both the graph and the covariance matrix underlying the GMM, by providing a *graphParam* object, or we just want to simulate the covariance matrix given a graph specified as either a *graphBAM* object, an squared and symmetric adjacency matrix or a two-column matrix describing an edge set. Examples of these are the following:

```
> rUGgmm(dRegularGraphParam(p=4, d=2))

Undirected Gaussian graphical Markov model
with 4 r.v. and 4 edges.

> rUGgmm(matrix(c(0, 1, 0, 1,
+               1, 0, 1, 0,
```

```
+           0, 1, 0, 1,
+           1, 0, 1, 0), nrow=4, byrow=TRUE))
```

```
Undirected Gaussian graphical Markov model
with 4 r.v. and 4 edges.
```

```
> rUGgmm(matrix(c(1, 2,
+                 2, 3,
+                 3, 4,
+                 4, 1), ncol=2, byrow=TRUE))
```

```
Undirected Gaussian graphical Markov model
with 4 r.v. and 4 edges.
```

These three calls to `rUGgmm()` return objects of class *UGgmm* containing undirected Gaussian GMMs with an underlying graph structure formed by a single undirected cycle on four vertices. The elements of an *UGgmm* object can be quickly explored with the `summary()` function call:

```
> set.seed(12345)
> gmm <- rUGgmm(dRegularGraphParam(p=4, d=2))
> summary(gmm)
```

```
Undirected Gaussian graphical Markov model
with 4 r.v. and 4 edges.
```

```
Graph density: 67%
```

```
Degree distribution of the undirected graph:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2	2	2	2	2	2

```
Distribution of marginal correlations for present edges:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.3352	0.5963	0.7587	0.6958	0.8582	0.9305

```
Distribution of partial correlations for present edges:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.8236	-0.6656	-0.5352	-0.4232	-0.2928	0.2014

and the individual elements that are available to the user can be accessed as if it were a *list* object:

```
> class(gmm)
[1] "UGgmm"
attr(,"package")
[1] "qpgraph"
> names(gmm)
[1] "X"      "p"      "g"      "mean"   "sigma"
> gmm$X
[1] "1" "2" "3" "4"
> gmm$p
[1] 4
> gmm$g
```

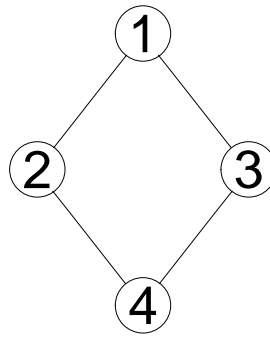


Figure 2: A 4-cycle undirected graph.

A graphBAM graph with undirected edges

Number of Nodes = 4

Number of Edges = 4

```
> gmm$mean
```

```
[1] 0 0 0 0
```

```
> gmm$sigma
```

4 x 4 Matrix of class "dspMatrix"

	1	2	3	4
1	1.1854830	0.8687971	1.0001179	0.4717917
2	0.8687971	0.9152916	0.7026960	0.6299566
3	1.0001179	0.7026960	0.9745280	0.3188662
4	0.4717917	0.6299566	0.3188662	0.9285910

We can also directly plot the *UGgmm* object to see the underlying undirected graph and, in this particular example, note how the zeroes of the inverse covariance match the missing edges shown in Figure 2.

```
> plot(gmm)
```

```
> round(solve(gmm$sigma), digits=1)
```

	1	2	3	4
1	9.5	-3.4	-7.2	0.0
2	-3.4	5.9	0.0	-2.3
3	-7.2	0.0	8.2	0.9
4	0.0	-2.3	0.9	2.3

Further arguments to *rUGgmm()* can be the desired mean marginal correlation derived from the cells of the covariance matrix that match the present edges in the underlying graph (*rho*=0.5), the minimum tolerance at which the iterative matrix completion algorithm that builds the covariance matrix stops (*tol*=0.001) and whether the function should report progress on the calculations (*verbose*=FALSE). It is important to set the latter argument *verbose*=TRUE when we want to simulate an undirected Gaussian GMM with more than, let's say, 200 vertices, since around that number of vertices and beyond the simulation of the covariance matrix becomes computationally demanding, specially when the underlying graph is not very sparse. Further technical information on the algorithms employed to simulate the covariance matrix can be found in the help pages of the *qpgraph* functions *qpG2Sigma()*, *qpRndWishart()*, *qpIPF()* and *qpHTF()* which are called by the procedures described here.

Finally, to simulate multivariate normal observations from the undirected Gaussian GMM we just need to use the *rmvnorm()* function from the *mvtnorm* package which is overloaded in the *qpgraph* package to take directly an *UGgmm* object, as follows:

```
> rmvnorm(10, gmm)

      1      2      3      4
[1,]  1.8203501  0.93389886  1.432134453 -0.1917191
[2,]  0.3276189 -0.04621885  0.004281742  0.8140006
[3,]  1.2455715  0.92583029  1.462412069 -0.1502647
[4,] -1.0649416 -1.43363508  0.025905355 -1.0810069
[5,]  0.8215409  0.92693851  0.457389128  1.0147731
[6,]  3.6015946  2.99690308  3.073395574  1.4028879
[7,] -0.3178426  0.04528419 -0.970752819  1.4148364
[8,] -0.9758867 -0.22685242 -1.549907669 -0.7448294
[9,]  1.6800263  0.99249248  1.773751270 -0.6969221
[10,] -0.0824054  0.09107758 -0.560575698 -0.2894250
```

Note that with sufficient data we can directly recover the zero-pattern of the inverse covariance matrix:

```
> set.seed(123)
> X <- rmvnorm(10000, gmm)
> round(solve(cov(X)), digits=1)

      1      2      3      4
1  9.6 -3.4 -7.3  0.0
2 -3.4  5.9  0.0 -2.2
3 -7.3  0.0  8.1  0.9
4  0.0 -2.2  0.9  2.3

> round(solve(gmm$sigma), digits=1)

      1      2      3      4
1  9.5 -3.4 -7.2  0.0
2 -3.4  5.9  0.0 -2.3
3 -7.2  0.0  8.2  0.9
4  0.0 -2.3  0.9  2.3
```

However, such a sample size would be exceptional and for more limited sample size but still with  $p < n$  the user may use the *qpgraph* function `qpPAC()` which performs zero-partial correlation tests and when  $p \gg n$ , then the user may estimate non-rejection rates [Castelo and Roverato \(2006\)](#) with the `qpNrr()` function and simplify the saturated model such that it may become possible to apply `qpPAC()`.

Obviously, gene expression data, either from microarrays or log-transformed count data, are far from being multivariate normal. However, many available methods for estimating molecular regulatory networks from expression data, such as *qpgraph*, make such an assumption and simulating data from undirected Gaussian GMMs can help us to test these methods under a controlled experiment, learning their basic properties and obvious pitfalls with such a clean data.

## 4 Simulation of homogeneous mixed GMMs

Mixed GMMs are GMMs for multivariate data defined by mixed discrete and continuous r.v.'s,  $X = \{I, Y\}$  where  $I = \{I_1, \dots, I_{p_I}\}$  denote discrete r.v.'s and  $Y = \{Y_1, \dots, Y_{p_Y}\}$  denote continuous ones. This class of GMMs are determined by marked graphs  $G = (V, E)$  with  $p$  marked vertices  $V = \Delta \cup \Gamma$  where  $\Delta = \{1, \dots, p_I\}$  are plotted with dots and index the discrete r.v.'s in  $I$  and  $\Gamma = \{1, \dots, p_Y\}$  are denoted by circles and index the continuous r.v.'s in  $Y$ .

In the context of molecular regulatory networks and, particularly, of genetical genomics data where we associate discrete r.v.'s to genotypes and continuous ones to expression profiles, we make the assumption that discrete genotypes affect gene expression and not the other way around. Under this assumption, we will consider the underlying graph  $G$  not only with mixed vertices but also with mixed edges, where some are directed and represented by arrows and some are undirected. More concretely  $G$  will be a partially-directed graph with arrows pointing from discrete vertices to continuous ones and undirected edges between continuous vertices. From this restricted definition of a partially-directed graph it

follows immediately that there are no semi-directed (direction preserving) cycles and allows one to interpret these GMMs also as *chain graphs*, which are graphs formed by undirected subgraphs connected by directed edges (Lauritzen, 1996). Currently, the *graph* and *Rgraphviz* packages, in which *qpgraph* relies to handle and plot graph objects, do not directly allow one to define and work with partially-directed graphs. However, in the functionality described below *qpgraph* tries to hide to the user complications derived from this fact.

A second important assumption *qpgraph* makes is that the joint distribution of the r.v.'s in  $X$  is a conditional Gaussian distribution (also known as CG-distribution) by which continuous r.v.'s follow a multivariate normal distribution  $\mathcal{N}_{\Gamma}(\mu(i), \Sigma(i))$  conditioned on the joint levels  $i \in \mathcal{I}$  from the discrete variables in  $I$ .

A third and final assumption is that the conditional covariance matrix is constant across  $i \in \mathcal{I}$ , the joint levels of  $I$ , i.e.,  $\Sigma(i) \equiv \Sigma$ . This implies that we are actually simulating the so-called *homogeneous* mixed GMMs. In the context of genetical genomics data, this assumption implies that genotype alleles affect only the mean expression level of genes and not the correlations between them.

Two restrictions currently constrain further the type of mixed GMMs we can simulate with *qpgraph*. The first one is that discrete variables are simulated under marginal independence between them and the second one is that every continuous variable cannot be associated to more than one discrete variable. As we shall see below, the first restriction does not apply when simulating expression quantitative trait loci data in experimental crosses, as genotype marker data is simulated by another package, the *qtl* package (Broman et al., 2003). We are working to remove the second restriction in the near future and enable multiple discrete variables having linear additive effects and interaction effects, on a common continuous variable.

Similarly to how we did it with undirected Gaussian GMMs, simulating mixed GMMs is done with a call to the function `rHMgmm()`:

```
> args(rHMgmm)

function (n, g, ...)
NULL
```

where `n` corresponds to the number of mixed GMMs we want to simulate (default `n=1` and `g` corresponds to either a *markedGraphParam* object, a *graphBAM* object or a matrix. Note that the first assumption made before enables specifying the underlying partially-directed graph just as we did for an undirected one, since directed edges are completely determined by the vertex type at their endpoints (discrete to continuous). Examples of these are the following:

```
> rHMgmm(dRegularMarkedGraphParam(pI=1, pY=3, d=2))

Homogeneous mixed graphical Markov model
with 1 discrete and 3 continuous r.v., and 4 edges.

> rHMgmm(matrix(c(0, 1, 0, 1,
+                1, 0, 1, 0,
+                0, 1, 0, 1,
+                1, 0, 1, 0), nrow=4, byrow=TRUE), I=1)

Homogeneous mixed graphical Markov model
with 1 discrete and 3 continuous r.v., and 4 edges.

> rHMgmm(matrix(c(1, 2,
+                2, 3,
+                3, 4,
+                4, 1), ncol=2, byrow=TRUE), I=1)

Homogeneous mixed graphical Markov model
with 1 discrete and 3 continuous r.v., and 4 edges.
```

These three calls to `rHMgmm()` return objects of class *HMgmm* containing homogenous mixed GMMs with an underlying graph structured formed by one discrete vertex pointing to two continuous ones which are themselves forming an undirected connected component with a fourth vertex, all together forming an undirected cycle on four vertices. Just as with *UGgmm* objects, the elements of an *HMgmm* object can be quickly explored with the `summary()` function call:



```
> set.seed(12345)
> gmm <- rHMgmm(dRegularMarkedGraphParam(pI=1, pY=3, d=2))
> summary(gmm)
```

Homogeneous mixed graphical Markov model  
with 1 discrete and 3 continuous r.v., and 2 edges.

Graph density: 33% (all edges) 33% (mixed edges) 67% (continuous edges)

Degree distribution of the vertices in the graph:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2	2	2	2	2	2

Distribution of marginal correlations for present continuous edges:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.7822	0.8063	0.8304	0.8304	0.8545	0.8786

Distribution of partial correlations for present continuous edges:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.7536	-0.6937	-0.6339	-0.6339	-0.5740	-0.5142

Distribution of additive linear effects for present mixed edges:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1	1	1	1	1	1

and again the individual elements that are available to the user can be accessed as if it were a *list* object:

```
> class(gmm)
[1] "HMgmm"
attr(,"package")
[1] "qpgraph"
> names(gmm)
[1] "X"      "I"      "Y"      "p"      "pI"     "pY"     "g"      "mean"   "sigma"
[10] "a"      "eta2"
> gmm$X
[1] "I1" "Y1" "Y2" "Y3"
> gmm$I
[1] "I1"
> gmm$Y
[1] "Y1" "Y2" "Y3"
> gmm$p
[1] 4
> gmm$pI
[1] 1
> gmm$pY
[1] 3
> gmm$g
```

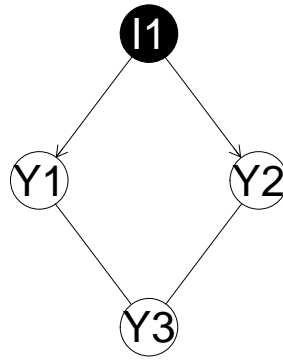


Figure 3: Homogeneous mixed graphical (chain) model with one discrete variable and three continuous ones forming an undirected cycle on four vertices.

A graphBAM graph with undirected edges

Number of Nodes = 4

Number of Edges = 4

```
> gmm$mean()
```

	Y1	Y2	Y3
1	0.4720734	0.9669291	0.7242007
2	1.4720734	1.9669291	1.7934027

```
> gmm$sigma
```

3 x 3 Matrix of class "dspMatrix"

	Y1	Y2	Y3
Y1	0.3986118	0.6302970	0.4720734
Y2	0.6302970	2.1100639	0.9669291
Y3	0.4720734	0.9669291	0.7242007

```
> gmm$a
```

Y1	Y2	Y3
1	1	NA

```
> gmm$eta2
```

	Y1	Y2	Y3
0.35494969	0.09638361	NA	

We can also directly plot the *HMgmm* object and *qpgraph* will use the necessary instructions from the *graph* and *Rgraphviz* libraries to display a partially-directed graph as the one shown in Figure 3.

```
> plot(gmm)
```

Further arguments to *rHMgmm()* are all we described previously for the *rUGgmm()* function plus the desired additive linear effect (*a*=1) of the discrete levels (alleles in the genetics context) on the continuous variables (genes in the genetics context). To simulate conditional multivariate normal observations from the homogeneous mixed GMM we use the *rcmvnorm()* function, which uses its pure continuous counterpart *rmvnorm()* from the *mvtnorm* package, but which is defined in the *qpgraph* package as it needs to calculate the corresponding conditional mean vectors  $\mu(i)$ :

```
> rcmvnorm(10, gmm)
```

	I1	Y1	Y2	Y3
1	1	0.69288009	0.78201846	0.84474686

```

2  1 -0.07511924 -2.25118979 -0.07484308
3  1  0.30898513  2.16129006  0.45379595
4  1  0.44373890  1.73438953  0.69000584
5  1  0.03144977  1.35426519  0.95480862
6  1 -0.34614962  0.13665093 -0.45059696
7  2  1.45888312  1.52702362  1.81217248
8  1  0.17087970  0.19890662  0.67766218
9  1  0.32224897  0.05164234  1.09247428
10 2  1.39579255  0.68223679  1.48814816

```

Note that with sufficient data we can directly recover the zero-pattern of the inverse *conditional* covariance matrix:

```

> set.seed(123)
> X <- rcmvnorm(10000, gmm)
> csigma <- (1/10000)*sum(X[, gmm$I] == 1)*cov(X[X[, gmm$I]==1, gmm$Y]) +
+          (1/10000)*sum(X[, gmm$I] == 2)*cov(X[X[, gmm$I]==2, gmm$Y])
> round(solve(csigma), digits=1)

      Y1  Y2  Y3
Y1 11.1  0.0 -7.2
Y2  0.0  1.2 -1.6
Y3 -7.2 -1.6  8.3

> round(solve(gmm$sigma), digits=1)

      Y1  Y2  Y3
Y1 11.0  0.0 -7.2
Y2  0.0  1.2 -1.6
Y3 -7.2 -1.6  8.2

```

and that the sample sample mean vectors and additive effects approach the ones specified in the model according to the mixed associations between the discrete and continuous variables:

```

> smean <- apply(X[, gmm$Y], 2, function(x, i) tapply(x, i, mean), X[, gmm$I])
> smean

      Y1      Y2      Y3
1 0.4637072 0.942311 0.7123249
2 1.4657407 1.985921 1.7951299

> gmm$mean()

      Y1      Y2      Y3
1 0.4720734 0.9669291 0.7242007
2 1.4720734 1.9669291 1.7934027

> abs(smean[1, ] - smean[2, ])

      Y1      Y2      Y3
1.002033 1.043610 1.082805

> gmm$a

Y1 Y2 Y3
1  1 NA

```

## 5 Simulation of eQTL models of experimental crosses

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We illustrate in this section how we can use *qpgraph* in conjunction with the *qtl* package (Broman et al., 2003) to simulate expression quantitative trait loci (eQTL) models of experimental crosses and data from them. This functionality employs the previously described procedures to simulate an homogeneous mixed GMM that represents the underlying model of regulatory *cis*-eQTL, *trans*-eQTL and gene-gene associations, although this fact appears hidden to the user.

More concretely, the *qpgraph* package defines an object class called *eQTLcross* which basically holds a genetic map of the genotype markers (as defined by the *map* class in the *qtl* package from Broman et al., 2003) and an homogeneous mixed GMM defining the underlying molecular regulatory network that connects genotypes with genes and genes themselves, where we use the term *gene* to refer to a gene expression profile.

In a similar vein to the way we simulated before graphs and GMMs, we need to create a parameter object that defines the main features of the eQTL model we want to simulate. This is done through the function *eQTLcrossParam()* which by default defines some minimal eQTL model:

```
> eQTLcrossParam()
```

```
eQTL backcross parameter object defining 20 markers,
20 genes, 20 cis-eQTL and 0 trans-eQTL.
```

```
cis-eQTL associations occur within 1.0 cM of a gene
and all eQTL are located at 0.0 cM from a marker.
```

```
Gene network parameters are defined by a
```

```
d-regular pure graph parameter object
No. of pure vertices: 20
Constant degree: 2
Vertex labels: g1, g2, g3, g4, g5, g6 ...
```

```
> args(eQTLcrossParam())
```

```
function (map = do.call("class<-", list(list(`1` = do.call("class<-",
  list(do.call("names<-", list(seq(0, 100, length.out = 20),
    paste0("m", 1:20))), "A"))), "map")), type = "bc", genes = 20,
  cis = 1, trans = as.integer(NULL), cisr = 1, d2m = 0, networkParam = dRegularGraphParam())
NULL
```

To simulate an *eQTLcross* object *qpgraph* provides the function *reQTLcross()* giving as first argument the number of *eQTLcross* objects we want to simulate and a *eQTLcrossParam* object:

```
> reQTLcross(n=2, eQTLcrossParam())
```

```
[[1]]
```

```
eQTL backcross model with 20 markers, 20 genes,
20 eQTL and 20 gene-gene expression associations.
```

```
[[2]]
```

```
eQTL backcross model with 20 markers, 20 genes,
20 eQTL and 20 gene-gene expression associations.
```

When the first argument *n* is omitted, then *n*=1 is assumed by default. Other arguments to *reQTLcross()* are the mean marginal correlation between genes (*rho*=0.5), the magnitude of the linear additive effect of the simulated eQTL

associations ( $a=1$ ), the minimum tolerance of the matrix completion algorithm that is involved in the construction of the conditional covariance matrix ( $\text{tol}=0.001$ ) and whether progress on the calculations should be shown `verbose=FALSE`.

To simulate a larger *eQTLcross* object we load an example genetic map object called `map10` from the *qtl* package (Broman et al., 2003):

```
> data(map10, package="qtl")
> class(map10)

[1] "map"

> head(lapply(map10, head))

$`1`
      D1M1      D1M2      D1M3      D1M4      D1M5      D1M6
0.000000  9.769231 19.538462 29.307692 39.076923 48.846154

$`2`
      D2M1      D2M2      D2M3      D2M4      D2M5      D2M6
0.000000 10.36364 20.72727 31.09091 41.45455 51.81818

$`3`
      D3M1      D3M2      D3M3      D3M4      D3M5      D3M6
0.000000  9.933333 19.866667 29.800000 39.733333 49.666667

$`4`
D4M1 D4M2 D4M3 D4M4 D4M5 D4M6
0.0 10.5 21.0 31.5 42.0 52.5

$`5`
      D5M1      D5M2      D5M3      D5M4      D5M5      D5M6
0.000000 10.22222 20.44444 30.66667 40.88889 51.11111

$`6`
      D6M1      D6M2      D6M3      D6M4      D6M5      D6M6
0.000  9.375 18.750 28.125 37.500 46.875
```

and using it in combination with a larger number of genes (100) we can easily simulate this larger *eQTLcross* object:

```
> eqtl <- reQTLcross(eQTLcrossParam(map=map10, genes=100))
> class(eqtl)

[1] "eQTLcross"
attr(,"package")
[1] "qpgraph"

> eqtl

eQTL backcross model with 187 markers, 100 genes,
100 eQTL and 100 gene-gene expression associations.
```

which, as we can see, it corresponds a backcross model with 100 genes each of them associated to a *cis*-eQTL, and with a certain underlying gene network embedded into an homogeneous mixed GMM that forms part of this object and which can be accessed as follows:

```
> eqtl$model

Homogeneous mixed graphical Markov model
with 100 discrete and 100 continuous r.v., and 200 edges.
```

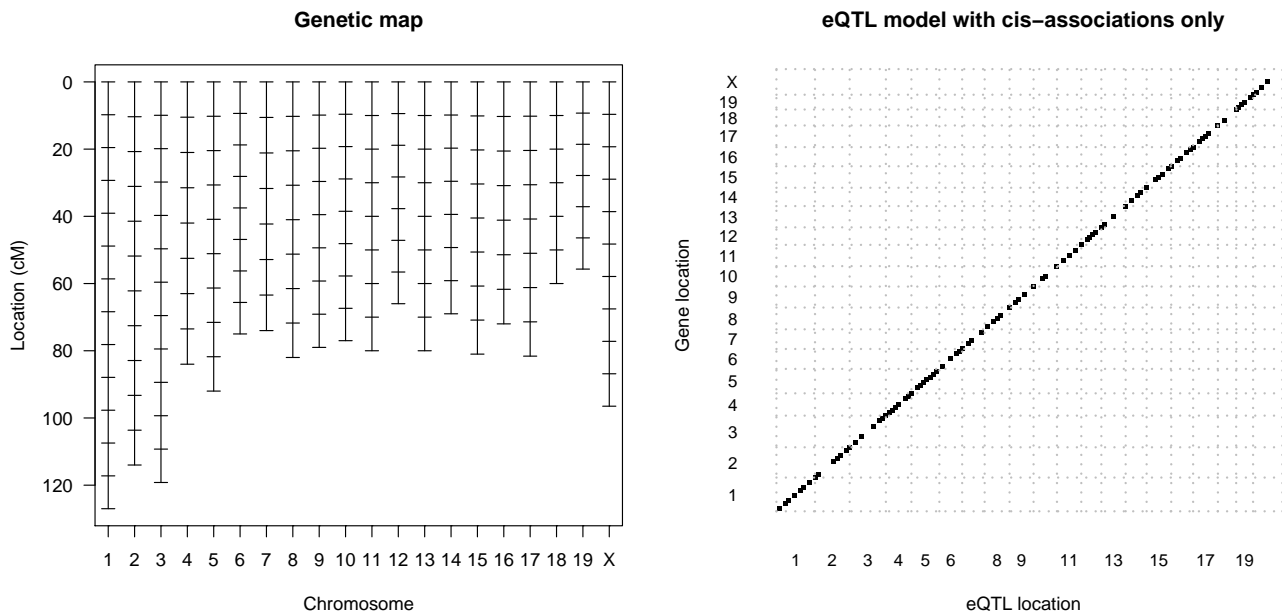


Figure 4: A genetic map simulated with the *qtl* package (Broman et al., 2003) on the left, and on the right, an eQTL model simulated using the genetic map with the *qpgraph* package.

A dot plot describing the eQTL associations along the given genetic map can be obtained by calling the `plot` function with the *eQTLcross* object as argument. In Figure 4 we see on the right panel such a plot, and on the left panel the genetic map plotted by the `plot` function defined in the *qtl* package (Broman et al., 2003) to plot genetic maps.

```
> par(mfrow=c(1,2))
> plot(map10)
> plot(eqt1, main="eQTL model with cis-associations only")
```

A somewhat more complex eQTL model with *trans* associations can be simulated by using the `trans` argument as follows:

```
> set.seed(123)
> eqt1 <- reQTLcross(eQTLcrossParam(map=map10, genes=100,
+                                cis=0.5, trans=c(5, 5)), a=5)
```

In this call, `cis=0.5` indicates that 50% of the genes should have *cis*-eQTL associations and among the remaining ones, 10 will be associated to two *trans*-eQTL affecting 5 genes each of the two. We have also increased the default additive linear effect from the default value `a=1` to `a=5` which corresponds to a very strong linear additive effect from genotype markers on gene expression. We can examine the *cis* and *trans* associations of the *eQTLcross* object with the `ciseQTL()` and `transeQTL()` functions:

```
> head(ciseQTL(eqt1))

  chrom location  QTL gene a
1     1  29.30769 QTL1  g2  5
2     1  68.38462 QTL2  g3  5
3     1  78.15385 QTL3  g5  5
4     2  31.09091 QTL4  g7  5
5     2  51.81818 QTL5  g9  5
6     2  62.18182 QTL6 g10  5

> transeQTL(eqt1)
```

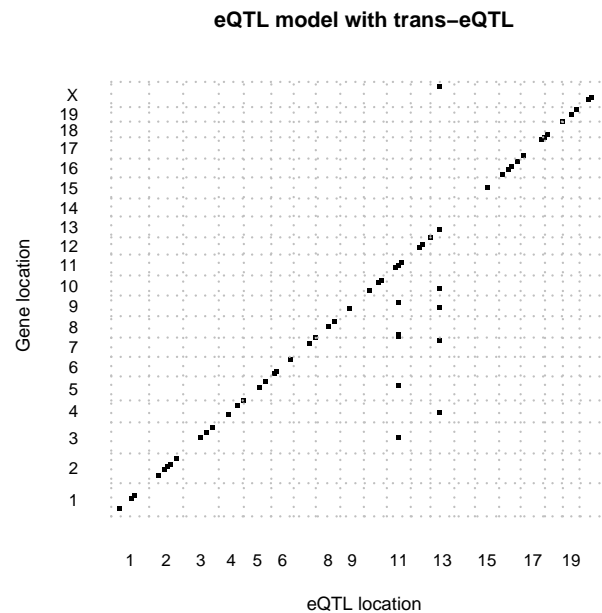


Figure 5: An eQTL model including trans-acting associations simulated using the genetic map from Fig. 4.

	chrom	location	QTL	gene	a
1	11	40	QTL29	g15	5
2	11	40	QTL29	g27	5
3	11	40	QTL29	g39	5
4	11	40	QTL29	g41	5
5	11	40	QTL29	g49	5
6	13	30	QTL34	g23	5
7	13	30	QTL34	g37	5
8	13	30	QTL34	g48	5
9	13	30	QTL34	g52	5
10	13	30	QTL34	g99	5

and examine where the eQTL associations occur and what genes map to *trans*-eQTL, as shown in Figure 5.

```
> plot(eqt1, main="eQTL model with trans-eQTL")
```

Using this *eQTLcross* object we can simulate data from the corresponding experimental cross with the function `sim.cross()` from the *qtl* package (Broman et al., 2003) but which is overloaded in *qpgraph* to plug the eQTL associations into the corresponding genetic loci:

```
> set.seed(123)
> cross <- sim.cross(map10, eqt1)
> cross
```

This is an object of class "cross".

It is too complex to print, so we provide just this summary.

Backcross

No. individuals: 100

No. phenotypes: 100

Percent phenotyped: 100

```

No. chromosomes:      20
Autosomes:           1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19
X chr:               X

Total markers:        187
No. markers:          14 12 13 9 10 9 8 9 9 9 9 8 9 8 9 8 9 7 7 11
Percent genotyped:    100
Genotypes (%):
  Autosomes:          AA:49.3  AB:50.7
  X chromosome:       AA:54.1  AB:45.9

```

Note that here, the genotype data is simulated by the procedures implemented in the *qtl* package (Broman et al., 2003) and *qpgraph* adds to that simulation the eQTL and gene network associations. Thus, while the `rHMgmm()` function described in the previous section, does not simulate correlated discrete variables, here the genotypes will be correlated according to the input arguments of the `sim.cross()` function in *qtl* (mainly, the `map.function` argument that converts genetic distances into recombination fractions) and which can be passed through the previous call to `sim.cross()`.

Let's focus on a specific simulated eQTL, concretely on the second one of the following list:

```

> allcis <- ciseQTL(eqt1)
> allcis[allcis$chrom==1, ]

  chrom location  QTL gene a
1     1 29.30769 QTL1  g2 5
2     1 68.38462 QTL2  g3 5
3     1 78.15385 QTL3  g5 5

> gene <- allcis[2, "gene"]
> chrom <- allcis[2, "chrom"]
> location <- allcis[2, "location"]

```

Find out the genes connected to gene g3 in the underlying regulatory network:

```

> connectedGenes <- graph::inEdges(gene, eqt1$model$g)[[1]]
> connectedGenes <- connectedGenes[connectedGenes %in% eqt1$model$Y]
> connectedGenes

[1] "g36" "g46"

```

Now, using the *qtl* package (Broman et al., 2003) and its `scanone()` function, we perform a simple QTL analysis by marker regression using the expression profiles from genes g3, g36, g46 as phenotypes<sup>1</sup>:

```

> library(qtl)
> out.mr <- scanone(cross, method="mr", pheno.col=c(gene, connectedGenes))

```

By using the plotting functionalities of the *qtl* package (Broman et al., 2003) we can examine the LOD score profile of these three genes on chromosome 1 where the eQTL of gene g3 is located:

```

> plot(out.mr, chr=chrom, ylab="LOD score", lodcolumn=1:3, col=c("black", "blue", "red"), lwd=2)
> abline(v=allcis[allcis$gene == gene, "location"])
> legend("topright", names(out.mr)[3:5], col=c("black", "blue", "red"), lwd=2, inset=0.05)

```

We can observe in Figure 6 that not only the directly associated gene g3 seems to have an eQTL at position 68.4 cM, but also the genes g36, g46 connected to g3 in the underlying gene network. Using a permutation procedure implemented in *qtl*, we calculate LOD score thresholds that yield genome-wide statistical significant eQTL associations:

<sup>1</sup>Note that when we load below the *qtl* package (Broman et al., 2003), the definition of `sim.cross()` in *qpgraph* gets masked by the original definition of this function in *qtl*. This means we would need, from that point on, to use the notation `qpgraph::sim.cross()` to call the *qpgraph* definition of this function unless we detach *qtl* from the search path



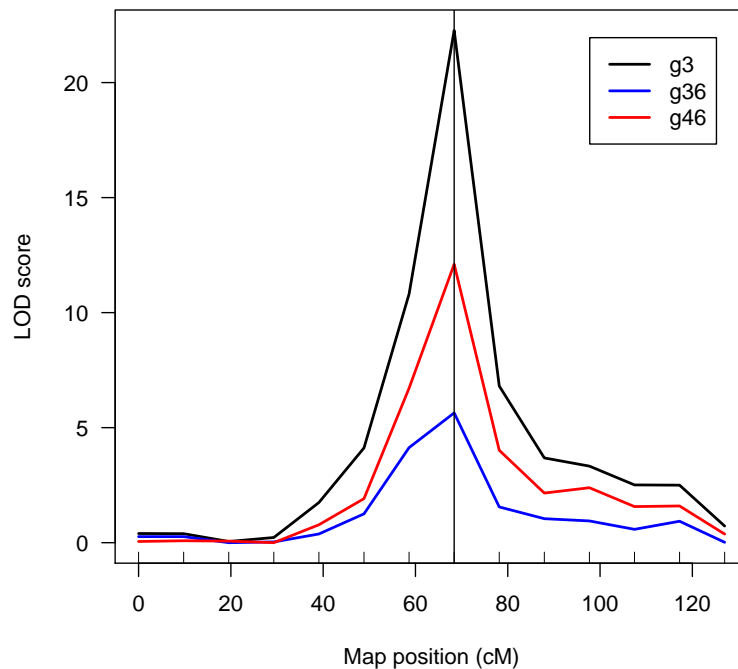


Figure 6: Profile of LOD scores for three genes with direct and indirect eQTL.

```
> out.perm <- scanone(cross, method="mr", pheno.col=c(gene, connectedGenes),
+                     n.perm=100, verbose=FALSE)
> summary(out.perm, alpha=c(0.05, 0.10))
```

LOD thresholds (100 permutations)

	g3	g36	g46
5%	2.44	2.57	2.92
10%	2.29	2.39	2.49

and examine which genotype markers yield such significant associations to these the expression profiles of these genes:

```
> summary(out.mr, perms=out.perm, alpha=0.05)
```

	chr	pos	g3	g36	g46
D1M8	1	68.4	22.26	5.64	12.10
D7M6	7	52.9	5.22	17.16	2.75
D13M4	13	30.0	4.37	5.22	9.89
DXM3	X	19.3	3.74	3.28	3.80

Notice that the directly associated gene g3 as well as the indirectly associated ones g36, g46 have genome-wide significant LOD scores on the same eQTL located at 68.4 cM in chromosome 1.

## 6 Session information

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```
> toLatex(sessionInfo())
```

- R version 3.1.1 (2014-07-10), x86\_64-apple-darwin10.8.0

- Locale: en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: qpgraph 1.20.2, qtl 1.32-10
- Loaded via a namespace (and not attached): annotate 1.42.1, AnnotationDbi 1.26.0, Biobase 2.24.0, BiocGenerics 0.10.0, BiocStyle 1.2.0, DBI 0.2-7, digest 0.6.4, genefilter 1.46.1, GenomeInfoDb 1.0.2, GGBase 3.26.0, graph 1.42.0, grid 3.1.1, IRanges 1.22.10, lattice 0.20-29, Matrix 1.1-4, mvtnorm 1.0-0, parallel 3.1.1, Rgraphviz 2.8.1, RSQLite 0.11.4, snpStats 1.14.0, splines 3.1.1, stats4 3.1.1, survival 2.37-7, tools 3.1.1, XML 3.98-1.1, xtable 1.7-3

## References

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- Broman, K. W., Wu, H., Sen, S., and Churchill, G. A. (2003). R/qtl: Qtl mapping in experimental crosses. *Bioinformatics*, 19(7):889–90.
- Castelo, R. and Roverato, A. (2006). A robust procedure for gaussian graphical model search from microarray data with  $p$  larger than  $n$ . *J Mach Learn Res*, 7:2621–2650.
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