

```

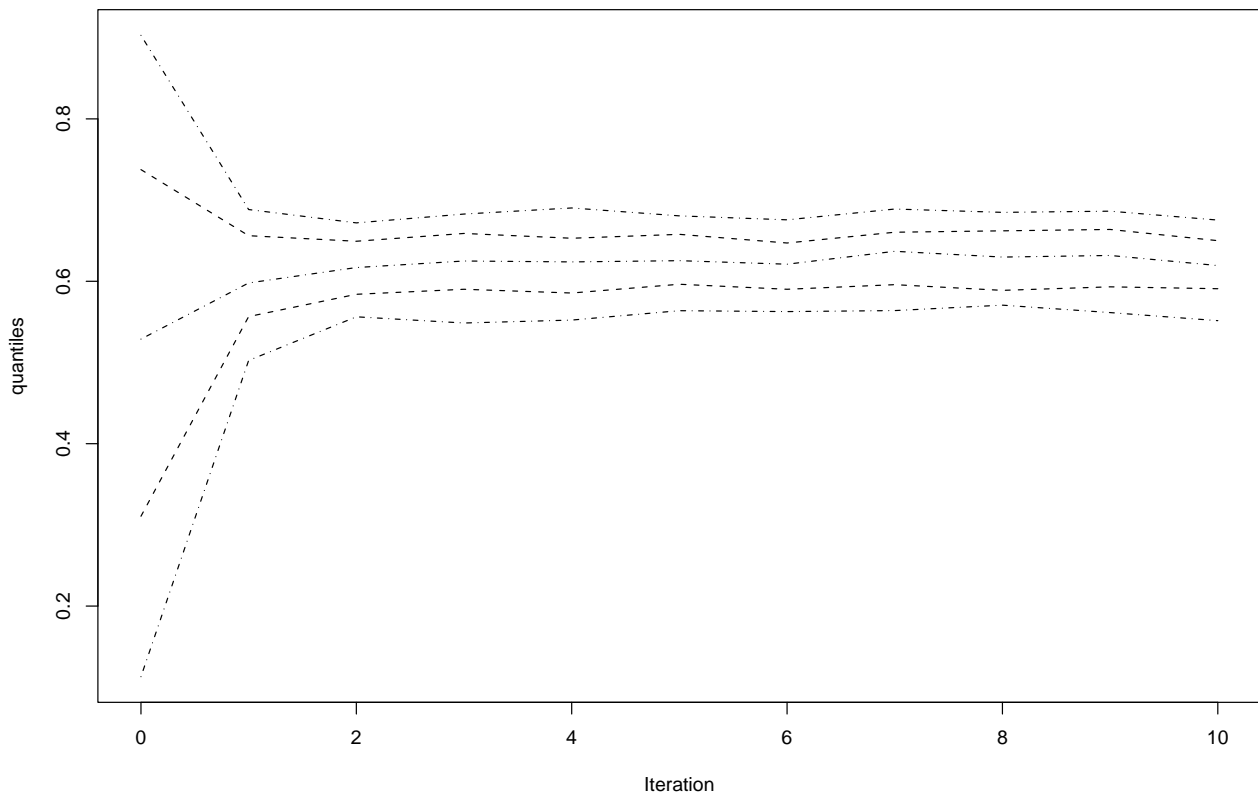
# The Data Augmentation algorithm for the genetic linkage example
#

geneticda <- function(y, N, R,
                     alpha=c(0.1,0.25,0.5,0.75,0.9))
{
# y is the data set
# N is the number of theta samples
# R is the number of iterations
# alpha is

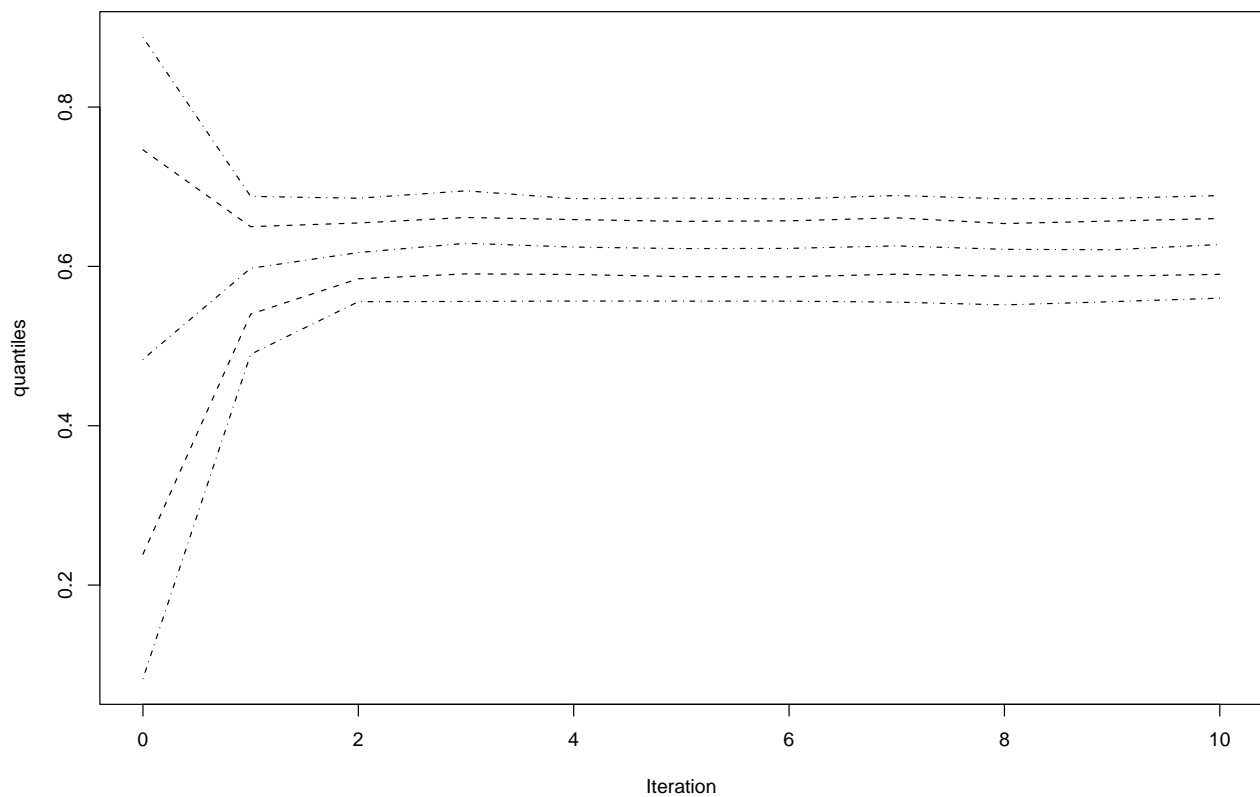
qq <- matrix(NA, R+1, length(alpha))
theta <- runif(N)
qq[1,] <- quantile(theta, alpha)
for (i in 2:(R+1)) {
  X2 <- rbinom(N, y[1], theta/(2+theta))
  II <- sample(N,N,replace=T)
  theta <- rbeta(N, y[4]+X2[II]+1, y[2]+y[3]+1)
  qq[i,] <- quantile(theta, alpha)
}
list(theta=theta, Z=X2, quantiles=qq)
}

```

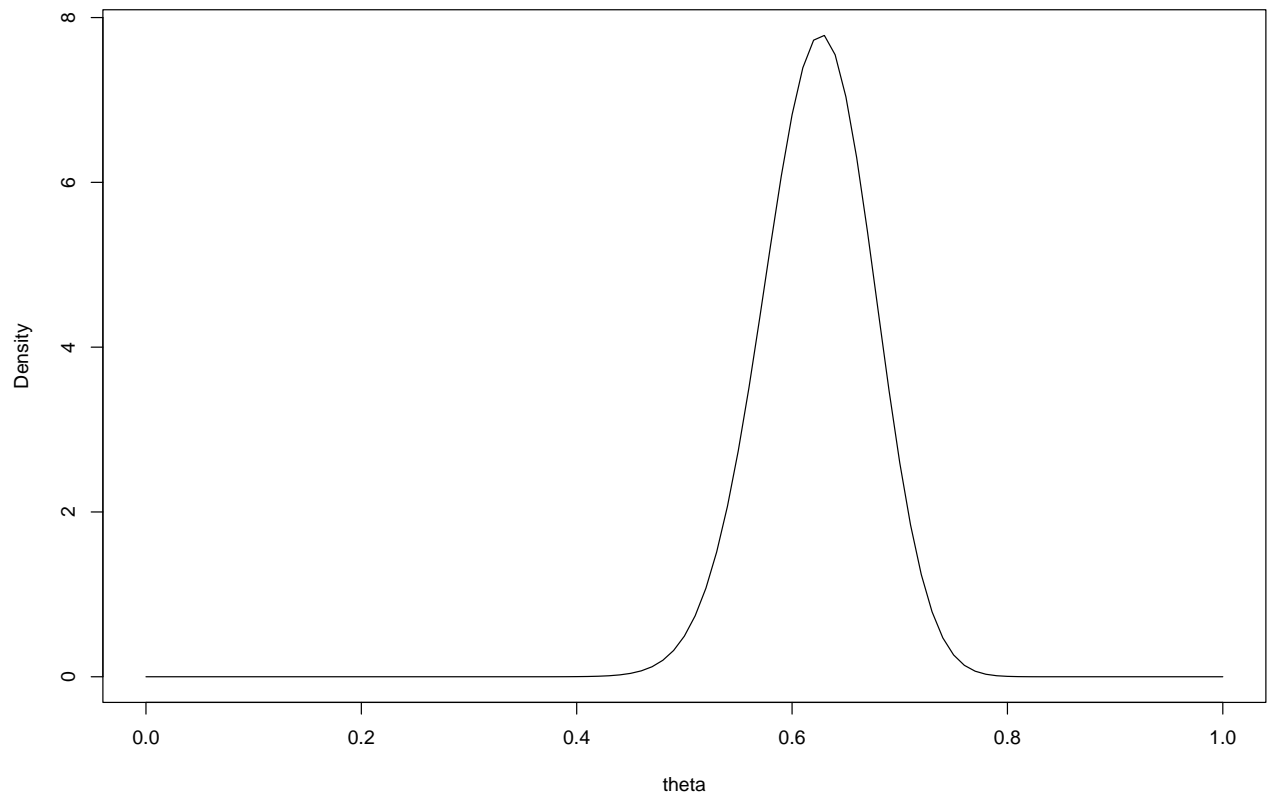
```
gda1 <- geneticda(c(125,18,20,34), 100, 10)
plot(rep(0:10,5), gda1$q, type="n", xlab="Iteration",
     ylab="quantiles")
for (i in 1:5) lines(0:10,gda1$q[,i], lty=2*(1+i%%2))
```



```
gda2 <- geneticda(c(125,18,20,34), 1000, 10)
plot(rep(0:10,5), gda1$q, type="n", xlab="Iteration",
     ylab="quantiles")
for (i in 1:5) lines(0:10,gda2$q[,i], lty=2*(1+i%%2))
```



Approximation to posterior with Mixture of Betas



```
mean(gda2$theta)
[1] 0.6243596
mean(gda2$theta^2)
[1] 0.3922873
hist(gda2$theta,prob=T,xlab='theta')
```

