

SISG Bayes: Exercise 3

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Binomial Data

Introduction

In these notes, in the context of binomial sampling, we look at:

- Specifying a prior distribution
- Prediction.
- Testing.
- Logistic regression.

We analyze allele specific expression (ASE) data, and low birth weight data.

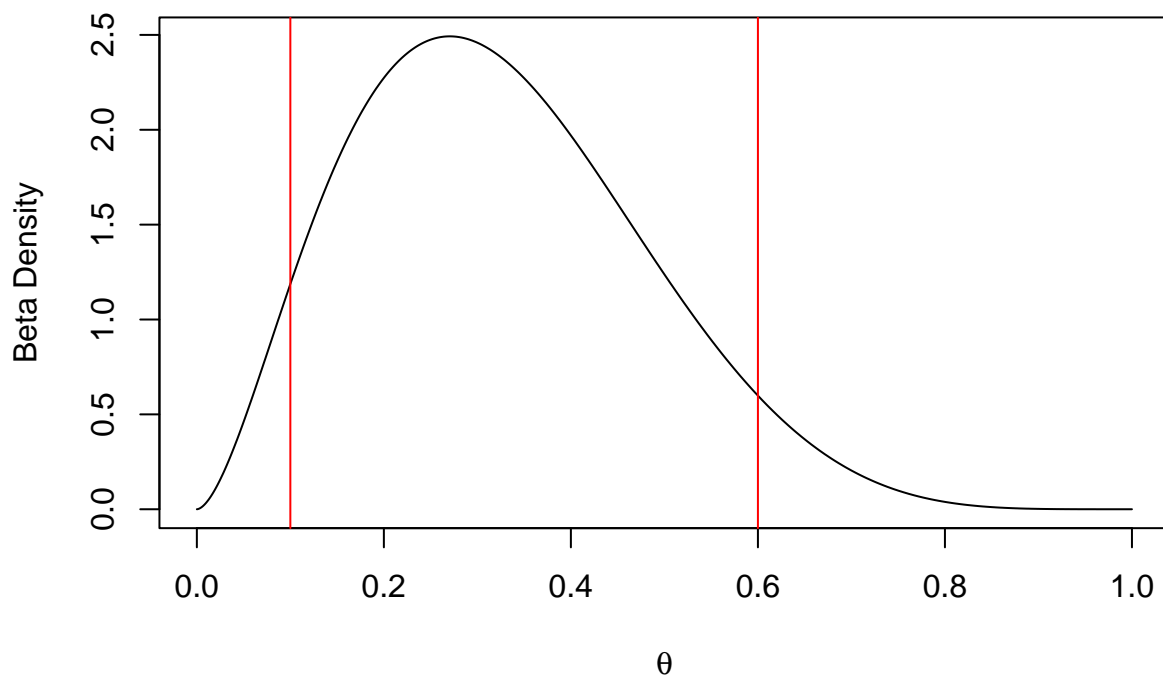
Specifying a prior distribution

The code below finds the beta distribution, i.e. the a and the b, with 5% and 95% points of 0.1 and 0.6.

```
# Function to find a and b
priorch <- function(x,q1,q2,p1,p2){
  (p1-pbeta(q1,x[1],x[2]))^2 + (p2-pbeta(q2,x[1],x[2]))^2 }
p1 <- 0.05
p2 <- 0.95
q1 <- 0.1
q2 <- 0.6
opt <- optim(par=c(1,1),fn=priorch,q1=q1,q2=q2,p1=p1,p2=p2,
  control=list(abstol=1e-8))
cat("a and b are ",opt$par,"\n")
## a and b are 2.730616 5.667462
```

The code below finds the beta distribution, i.e. the a and the b, with 5% and 95% points of 0.1 and 0.6.

```
probvals <- seq(0,1,.001)
plot(probvals,dbeta(probvals,shape1=opt$par[1],shape2=opt$par[2]),
  type="l", xlab=expression(theta),ylab="Beta Density")
abline(v=q1,col="red")
abline(v=q2,col="red")
```



Differences in Binomial Proportions

We consider an example in which we wish to compare allele frequencies between two populations.

Let θ_1 and θ_2 be the allele frequencies in the NE and US population from which the samples were drawn, respectively.

The allele frequencies were 10.69% and 13.21% with sample sizes of 650 and 265, in the NE and US samples, respectively.

We assume independent $\text{Beta}(1,1)$ priors on each of θ_1 and θ_2 .

The y_1 and y_2 data (i.e. the numbers with the allele in the two populations) were reconstructed from figures in the original paper in which only the denominators and the frequencies were given, hence the `floor` function.

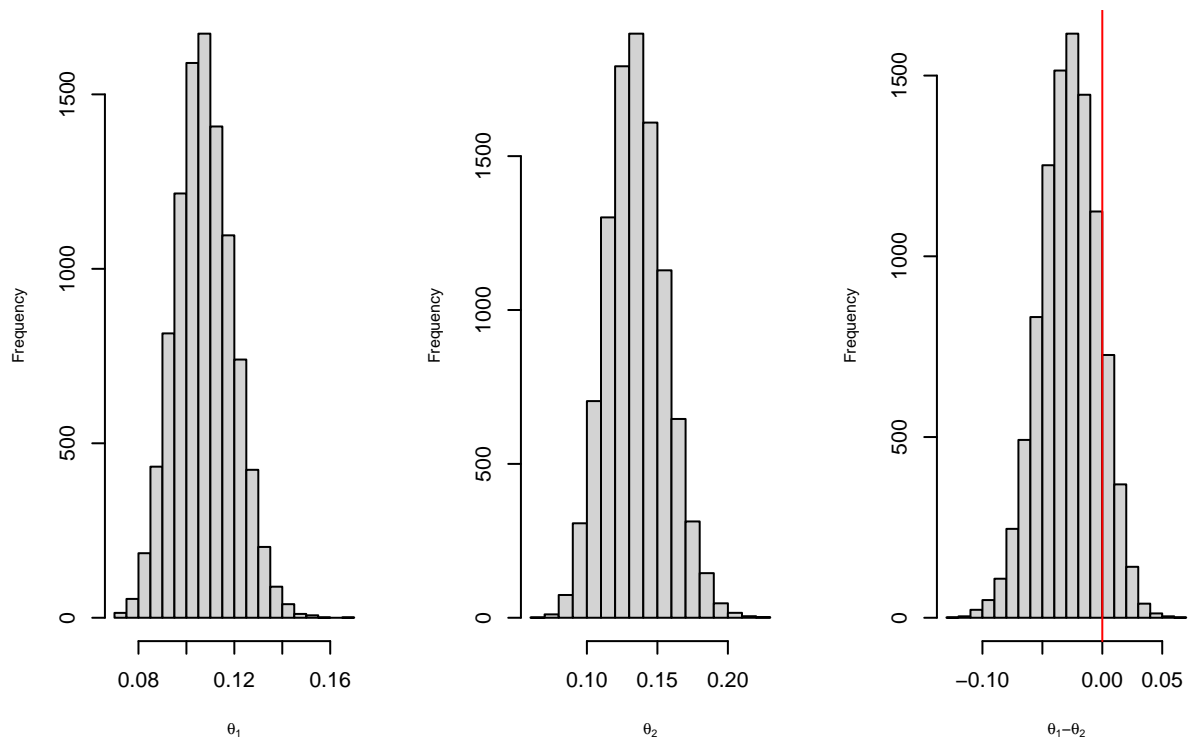
```
N1 <- 650
y1 <- floor(N1*.1069)
N2 <- 265
y2 <- floor(N2*.1321)
nsamp <- 10000
a <- b <- 1
post1 <- rbeta(nsamp,y1+a,N1-y1+b)
post2 <- rbeta(nsamp,y2+a,N2-y2+b)
```

The key step is in constructing a sample estimate of the difference in probabilities $\theta_1 - \theta_2$.

```

par(mfrow=c(1,3))
hist(post1,xlab=expression(theta[1]),main="",cex.lab=0.7)
hist(post2,xlab=expression(theta[2]),main="",cex.lab=0.7)
#
hist(post1-post2,xlab=expression(paste(theta[1],"-",
theta[2])),main="",cex.lab=0.7)
abline(v=0,col="red")
sum(post1-post2>0)/nsamp
## [1] 0.1293

```



ASE Data

Analysis of ASE data

```

download.file("http://faculty.washington.edu/kenrice/sisgbayes/ASEgene.txt",
destfile = "ASEgene.txt")
ASEdat <- read.table("ASEgene.txt",header=TRUE)
head(ASEdat)
##      Y      N
## 1  62  107
## 2  33   59
## 3 658 1550

```

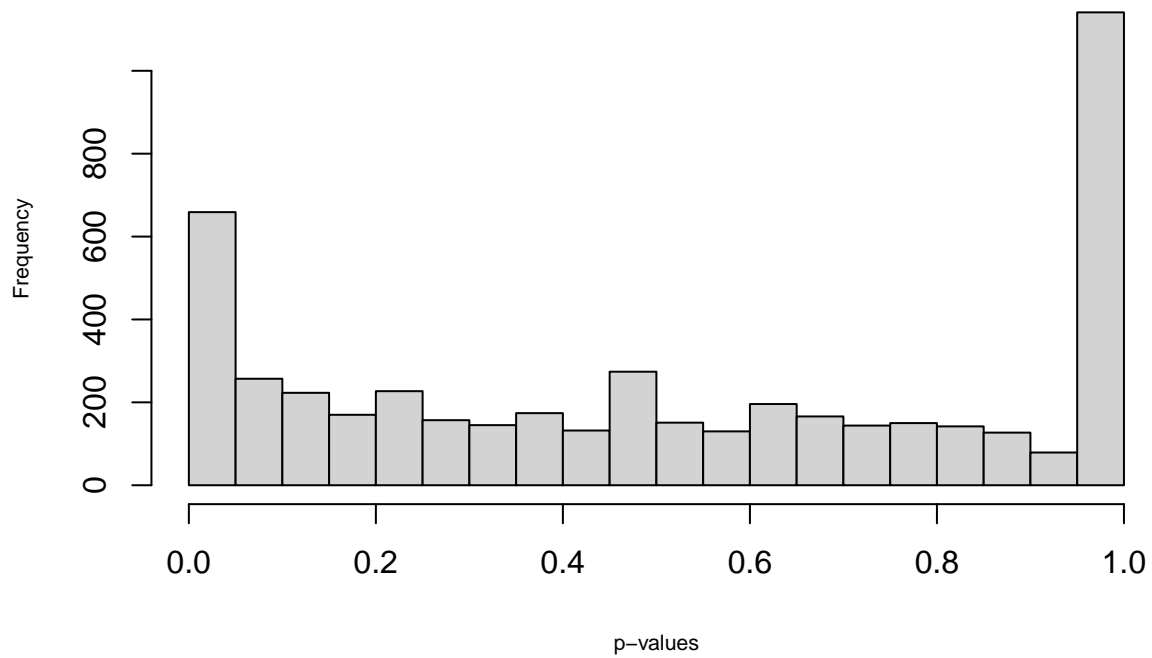
```
## 4 14 61
## 5 57 153
## 6 218 451
dim(ASEdat)
## [1] 4844 2
ngenes <- dim(ASEdat)[1]
pvals <- NULL
for (i in 1:ngenes){
  pvals[i] <- binom.test(ASEdat$Y[i],ASEdat$N[i],
    p=0.5,alternative="two.sided")["p.value"]
}
```

```
# Function to evaluate Bayes factors for a binomial
# likelihood and beta prior, and a point null at p0
BFbinomial <- function(N,y,a,b,p0){
  logPrH0 <- lchoose(N,y) + y*log(p0) + (N-y)*log(1-p0)
  logPrH1 <- lchoose(N,y) + gamma(a+b) - lgamma(a) - lgamma(b) + lgamma(y+a) + lgamma(N-y+b) -lgamma(N)
  logBF <- logPrH0 - logPrH1
  list(logPrH0=logPrH0,logPrH1=logPrH1,logBF=logBF)
}
nsim <- 5000
a <- 1
b <- 1
p0 <- 0.5
```

```
postprob <- logBFR <- rep(0,ngenes)
pcutoff <- 0.05/length(pvals)
for (i in 1:ngenes){
  BFcall <- BFbinomial(ASEdat$N[i],ASEdat$Y[i],a,b,p0)
  logBFR[i] <- -BFcall$logBF
  postprob[i] <- pbeta(0.5,a+ASEdat$Y[i],b+ASEdat$N[i]-ASEdat$Y[i])
}
cat("log BFR > log(150) = ",sum(logBFR>log(150)),"\n")
## log BFR > log(150) = 197
cat("log BFR > log(20) = ",sum(logBFR>log(20)),"\n")
## log BFR > log(20) = 359
cat("p-values > ",pcutoff,sum(pvals<pcutoff),"\n")
## p-values > 1.032205e-05 111
cat("postprobs < 0.01 and > 0.99 ",sum(postprob<0.01),sum(postprob>0.99),"\n")
## postprobs < 0.01 and > 0.99 278 242
```

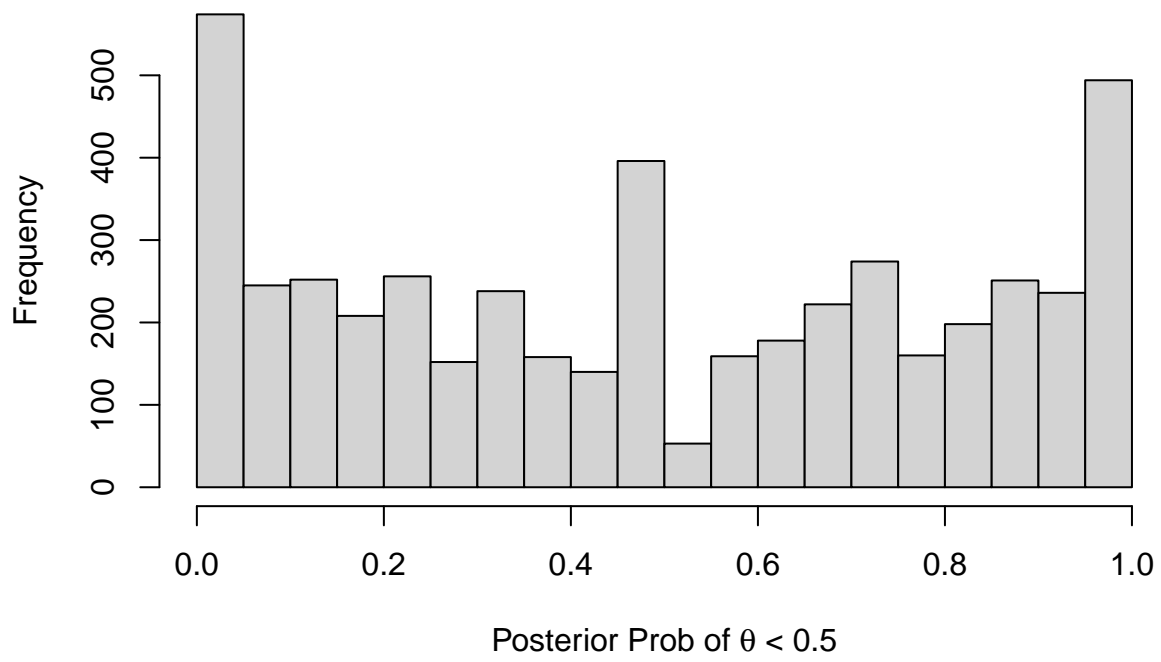
Histogram of p -values for ASE data

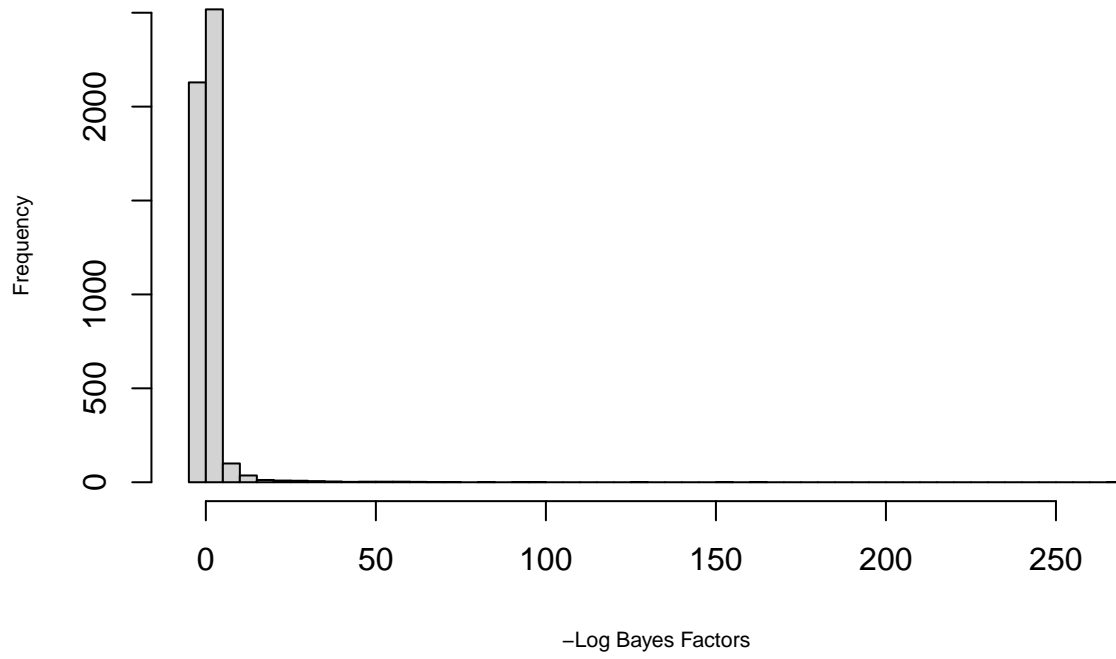
```
hist(pvals,xlab="p-values",main="",nclass=20,cex.lab=0.7,pch=16,cex=0.5)
```

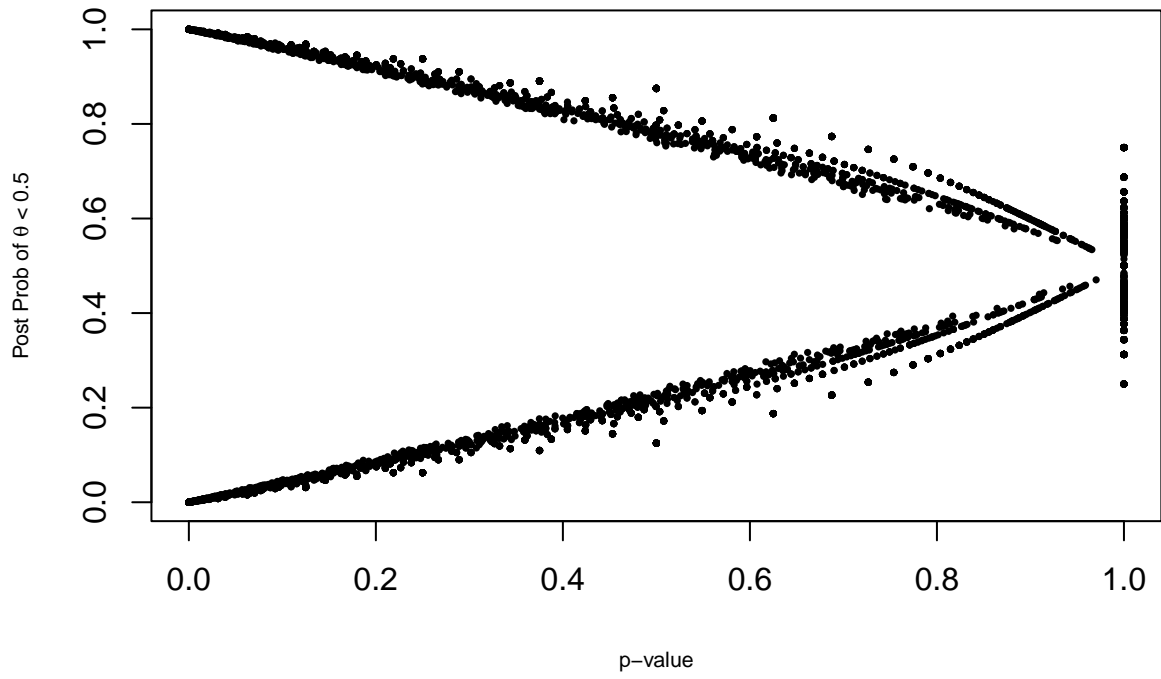


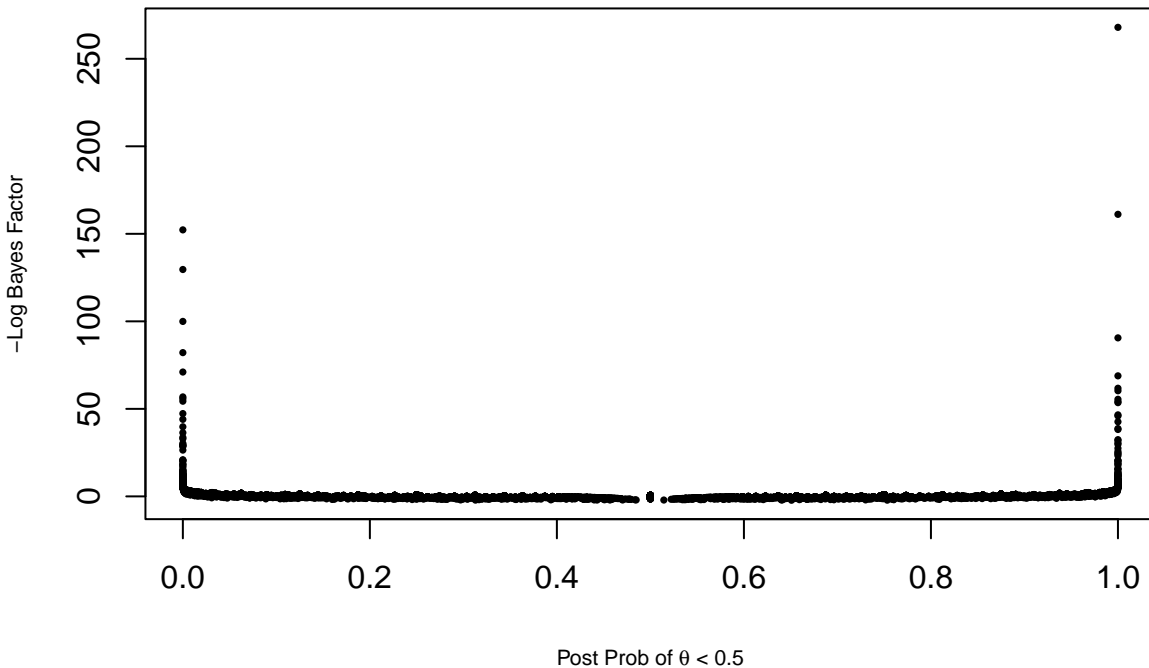
Histogram of posterior probabilities for ASE data

```
hist(postprob,nclass=20,xlab=expression(paste("Posterior Prob of ",theta," < 0.5")),main="",cex.label=0
```









Logistic Regression

LHON example

We consider the LHON example from class

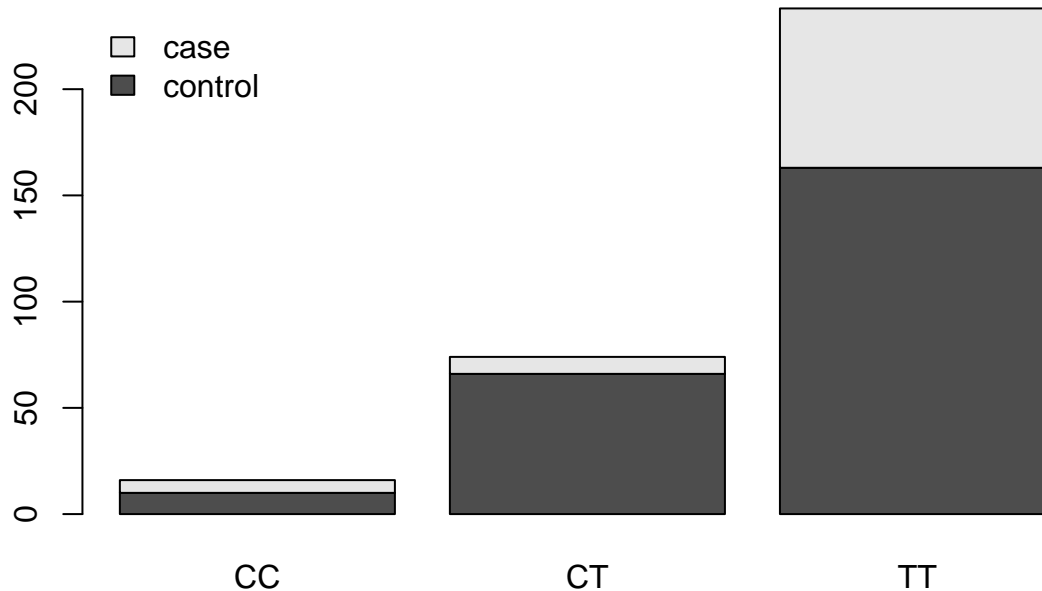
set up data and functions

```
library("ellipse")

lhon <- data.frame( y=c(1,1,1,0,0,0), x=c(0,1,2,0,1,2), n=c(6,8,75,10,66,163) )
dmat <- rbind(lhon$n[4:6], lhon$n[1:3])
names(dmat) <- c("CC", "CT", "TT")

expit <- function(x){exp(x)/(1+exp(x))}
lik <- function(beta){
  probs <- with(lhon, dbinom(y, 1, expit(beta[1] + beta[2]*x)))
  lik <- prod( probs^lhon$n )
}

barplot(dmat, names.arg=c("CC", "CT", "TT"), legend.text=c("case", "control")[2:1],
args.legend=list(x="topleft", bty="n"))
```

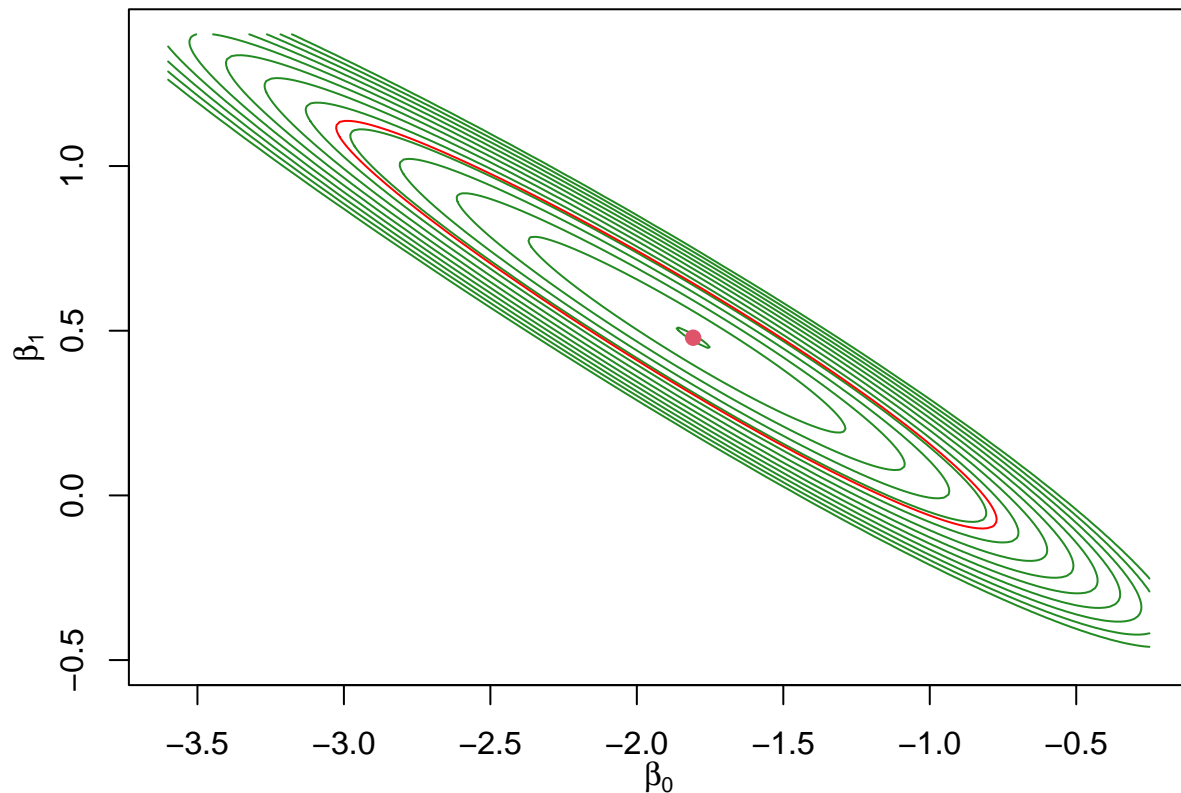


```
knitr::opts_chunk$set(dev = 'pdf')
```

Frequentist logistic regression with glm

```
glm1 <- glm( y~x, family="binomial", weights=n, data=lhon)
round(coef(summary(glm1)), 3)
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.808      0.455  -3.970   0.000
## x              0.479      0.250   1.911   0.056

par(mar=c(3,3,1.5,1.5)+0.2)
b0vals <- seq(-3.6,-0.25,l=201)
b1vals <- seq(-0.5,1.4,l=201)
gg <- expand.grid(b0=b0vals, b1=b1vals)
gg$lik <- apply(gg, 1, lik)
contour(x=b0vals, y=b1vals, z=matrix(gg$lik, 201,201),
        xlab="", ylab="", levels=0.99*lik(coef(glm1))*0.5^(0:12), drawlabels=FALSE, col="forestgreen")
contour(x=b0vals, y=b1vals, z=matrix(gg$lik, 201,201),
        xlab="", ylab="", levels=lik(coef(glm1))/20, drawlabels=FALSE, add=TRUE, col="red")
points(coef(glm1)[1], coef(glm1)[2], pch=19, col=2)
mtext(side=1, expression(beta[0]), line=2)
mtext(side=2, expression(beta[1]), line=2)
```



Logistic regression via rejection sampling (diffuse prior)

```

betahat <- coef(glm( y~x, family="binomial", weights=n, data=lhon))

do.many <- function(bigB){
  #bigB <- 5
  beta.sample <- matrix(NA,bigB,2)
  i <- 1
  while(i<= bigB){
    beta.try <- c(rnorm(1, 0, sqrt(10)), rnorm(1, 0, sqrt(beta1pvar)))
    u <- runif(1)
    if(u < lik(beta.try)/lik(betahat)){
      beta.sample[i,] <- beta.try
      i <- i+1}
  }
  beta.sample
}

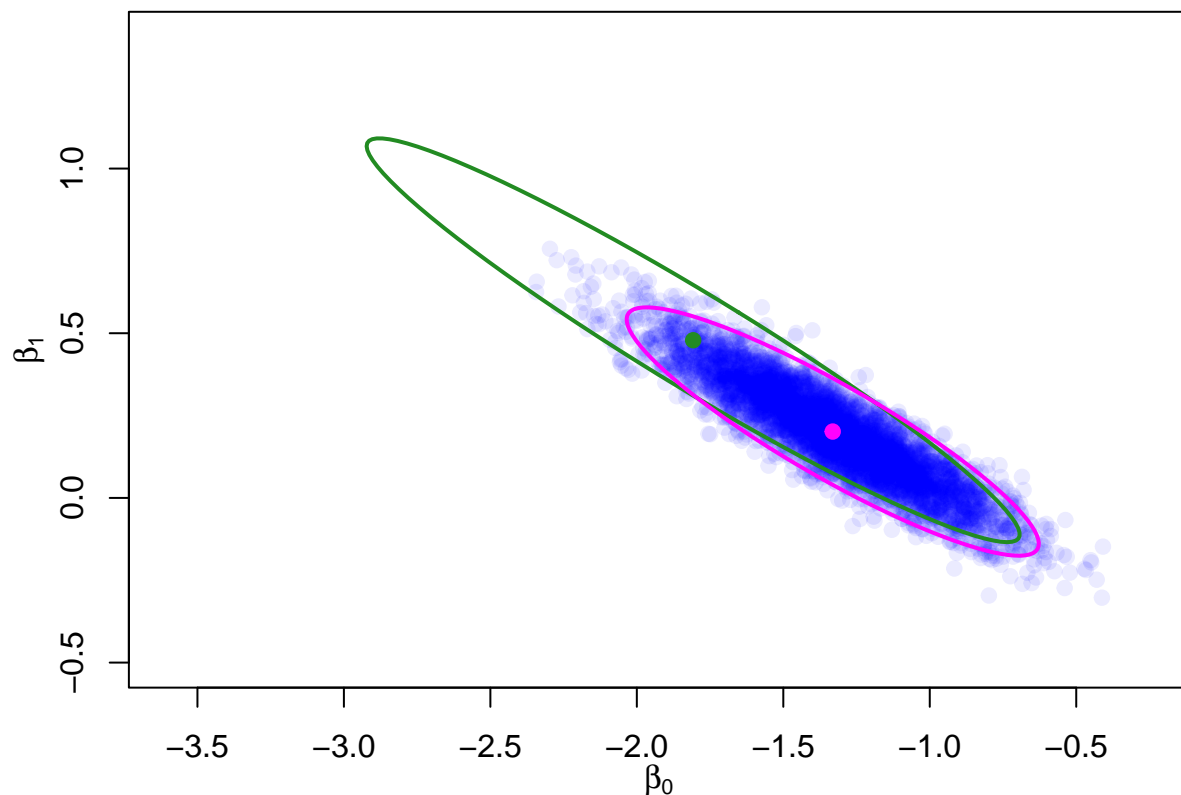
set.seed(4)
#informative prior selection
beta1pvar <- uniroot(function(w){ qnorm(0.975, 0, sqrt(w)) - log(1.5)}, c(0.01, 1))$root
beta.post <- as.data.frame(do.many(5000))
names(beta.post) <- c("beta0","beta1")
cbind( apply(beta.post, 2, mean), apply(beta.post, 2, sd))

```

```
##           [,1]      [,2]
## beta0 -1.331261 0.2874245
## beta1  0.201543 0.1540337
quantile(beta.post[,2], c(0.5, 0.025, 0.975))
##           50%      2.5%      97.5%
##  0.20241657 -0.09472991  0.50796330

par(mar=c(3,3,1.5,1.5)+0.2)
plot(beta1~beta0, data=beta.post, pch=19, col="#0000FF15",
      xlim=c(-3.6,-0.25), ylim=c(-0.5,1.4), xlab="", ylab="")
mtext(side=1, expression(beta[0]), line=2)
mtext(side=2, expression(beta[1]), line=2)

lines(ellipse(vcov(glm1), centre=coef(glm1)), col="forestgreen", lwd=2)
points(x=coef(glm1)[1], y=coef(glm1)[2], pch=19, col="forestgreen")
lines(ellipse(var(beta.post), centre=colMeans(beta.post)), col="magenta", lwd=2)
points(x=mean(beta.post$beta0), y=mean(beta.post$beta1), pch=19, col="magenta")
```

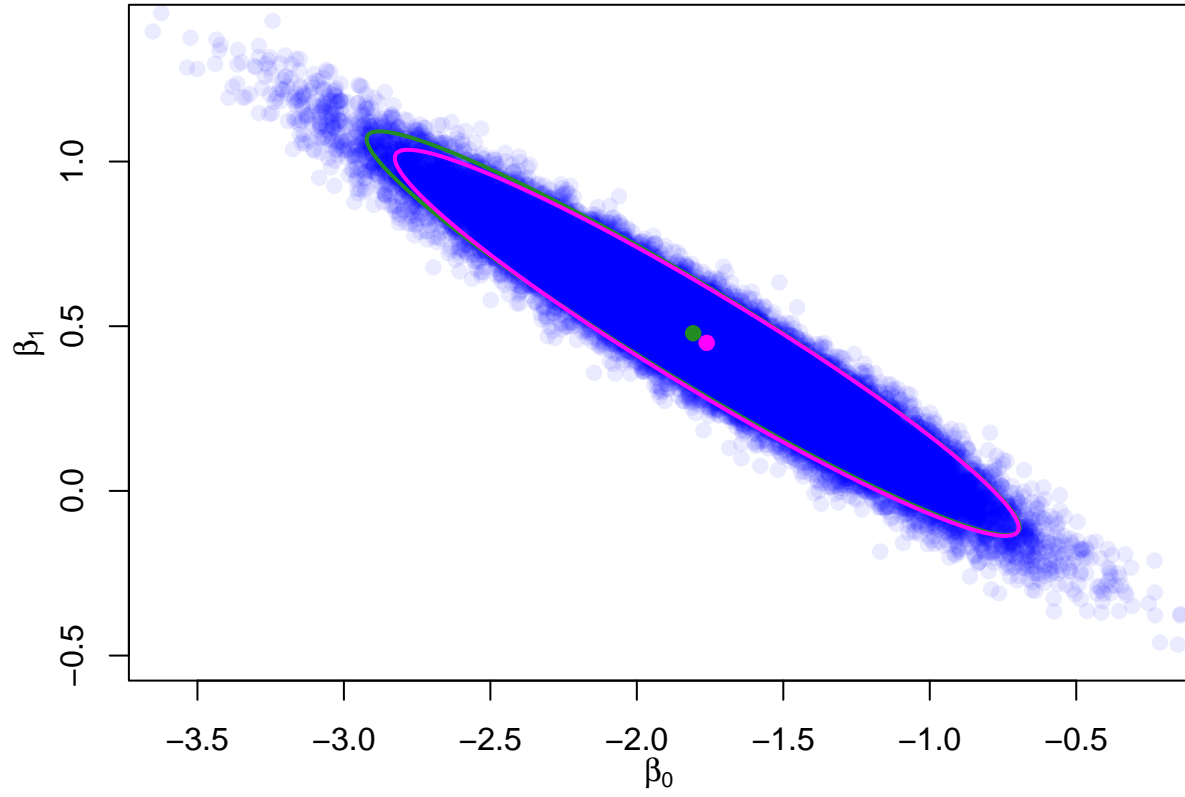


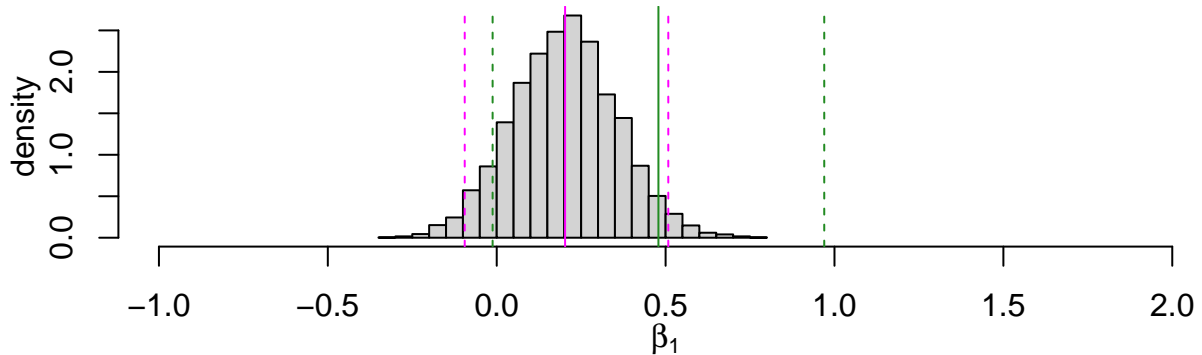
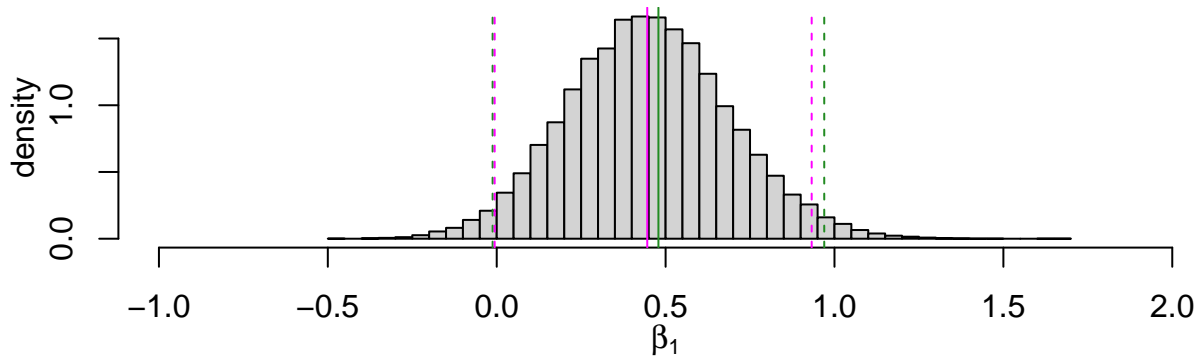
Logistic regression example: comparison of estimates

For the more-diffuse prior:

```
##           [,1]      [,2]
## beta0 -1.7613319 0.4351593
```

```
## beta1  0.4495068 0.2395200
##          50%      2.5%      97.5%
## 0.445647721 -0.006067766 0.932485055
```





```
## null device
##          1
```

We calculate $\Pr(\beta_1 > 0|y)$.

```
round(mean(beta.post[,2]>0),3)
## [1] 0.973
round(mean(beta.post.inf[,2]>0),3)
## [1] 0.905
```

Prediction

Predictions from a Binomial Distribution

We now consider prediction.

Assume $y|\theta \sim \text{binomial}(N, \theta)$ and $\theta \sim \text{beta}(a, b)$.

We suppose we wish to predict the number of successes Z from M trials.

The predictive distribution is

$$\Pr(z|y) = \binom{M}{z} \frac{\Gamma(N+a+b)}{\Gamma(y+a)\Gamma(N-y+b)} \frac{\Gamma(a+y+z)\Gamma(b+N-y+M-z)}{\Gamma(a+b+N+M)}$$

for $z = 0, \dots, M$.

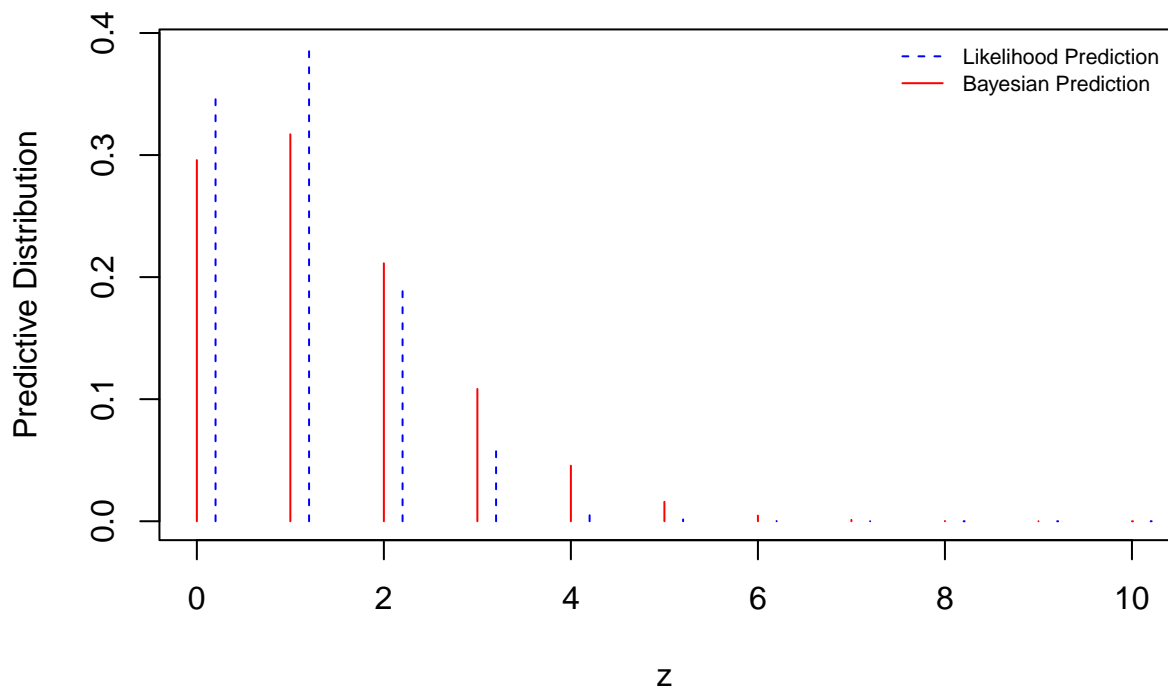
We demonstrate with a uniform prior and observing $y = 2$ successes from $N = 20$ trials, and suppose we wish to predict the number of successes we will see in 10 additional trials.

```
# User written function
binomialpred <- function(a,b,y,N,z,M){
  lchoose(M,z) + lgamma(a+b+N) - lgamma(a+y) - lgamma(b+N-y) +
    lgamma(a+y+z) + lgamma(b+N-y+M-z) - lgamma(a+b+N+M)
}
# Set up the prior and data
a <- b <- 1
y <- 2
N <- 20
M <- 10
```

Along with the Bayesian predictive distribution, we also include a simple approach in which we assume simply take a $\text{binomial}(M, y/N)$ distribution, i.e. assuming the probability is known to be the sample fraction.

```
binpred <- NULL
z <- seq(0,M)
sumcheck <- 0
for (i in 1:(M+1)){
  binpred[i] <- exp(binomialpred(a,b,y,N,z[i],M))
  sumcheck <- sumcheck + binpred[i]
}
likpred <- dbinom(z,M,prob=y/N)
cat("Sum of probs = ",sumcheck,"\n")
## Sum of probs = 1

plot(binpred~z,type="h",col="red",ylim=c(0,max(likpred,binpred)),
     ylab="Predictive Distribution")
points(z+.2,likpred,type="h",col="blue",lty=2)
legend("topright",legend=c("Likelihood Prediction",
                           "Bayesian Prediction"),lty=2:1,col=c("blue","red"),bty="n")
```

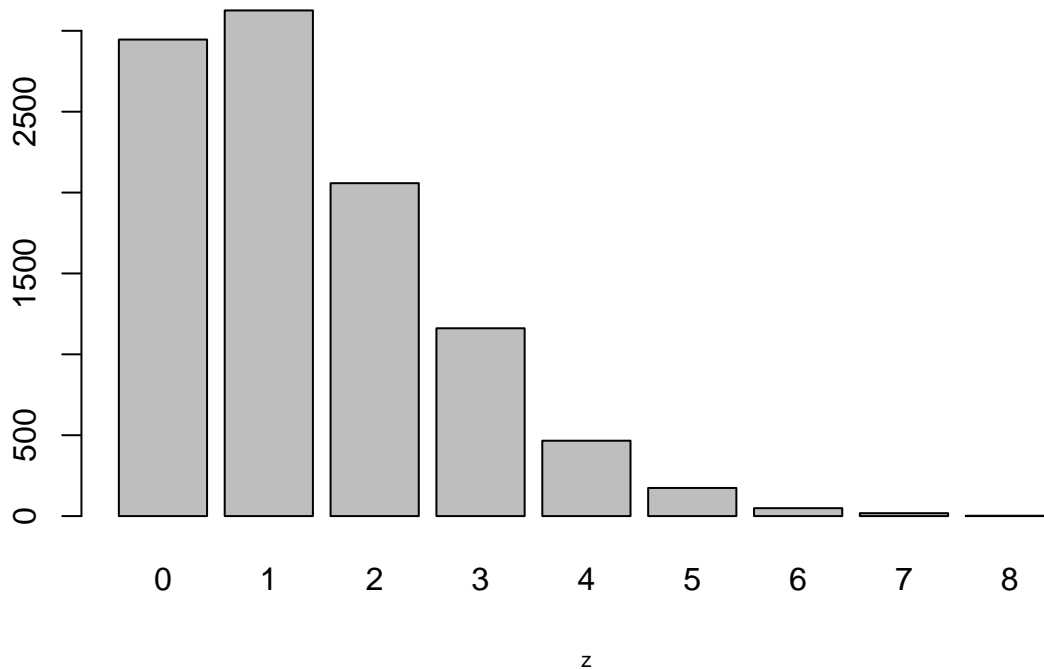


We now simulate directly via:

- Sampling from $\theta^{(s)} \sim p(\theta|y)$, $s = 1, \dots, S$.
- Sampling from $z^{(s)} \sim p(z|\theta)$, $s = 1, \dots, S$.

```
a <- b <- 1; y <- 2; N <- 20; M <- 10
nsim <- 10000
theta <- z <- NULL # This is inefficient but makes method clear
for (s in 1:nsim){
  theta[s] <- rbeta(1,a+y,b+N-y)
  z[s] <- rbinom(1,M,theta[s])
}
```

```
barplot(table(z),xlab="z",cex.lab=0.7)
```



Exercises

- Experiment with the priors $\text{Beta}(a, a)$ for the ASE example. In particular, for $a = 2$:
 - Obtain a histogram of the posterior probabilities $\Pr(\theta < 0.5|y)$, across genes.
 - Plot these posterior probabilities versus the versions under $a = 1$, and comment.
 - How sensitive are the (log) Bayes factors to the prior specification?
 - For how many genes would we reject $H_0 : \theta = 0.5$ if we use a rule of $1/\text{BF} > 150$?
- Redo the logistic regression LHON example, but use the less-diffuse prior on (only) the intercept β_0 , not the log odds ratio β_1 . How do the results compare to using the informative prior on β_1 ?