AdvStDaAn, Worksheet, Week 10

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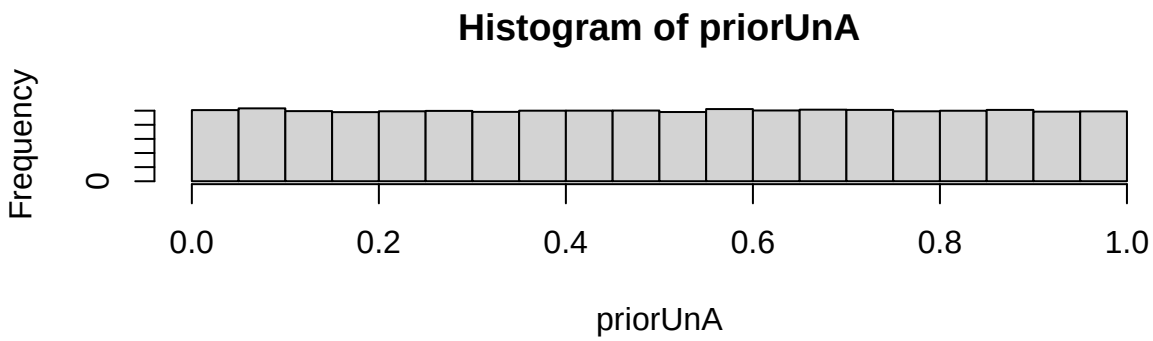
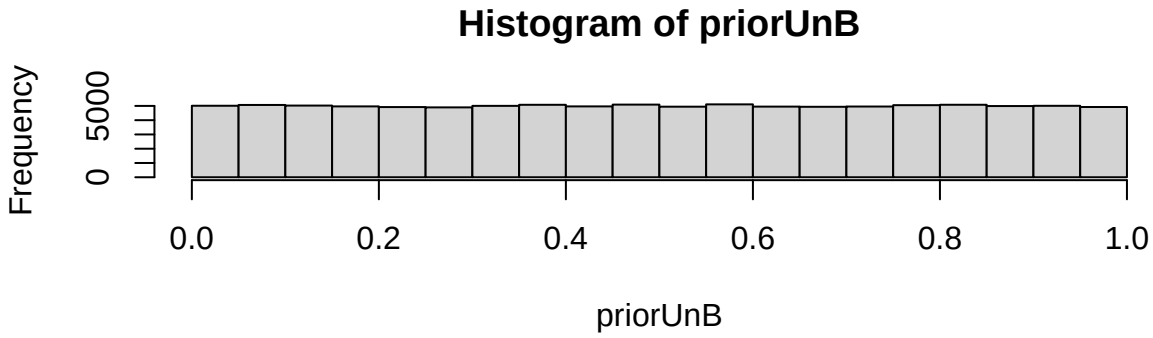
Contents

Task 1

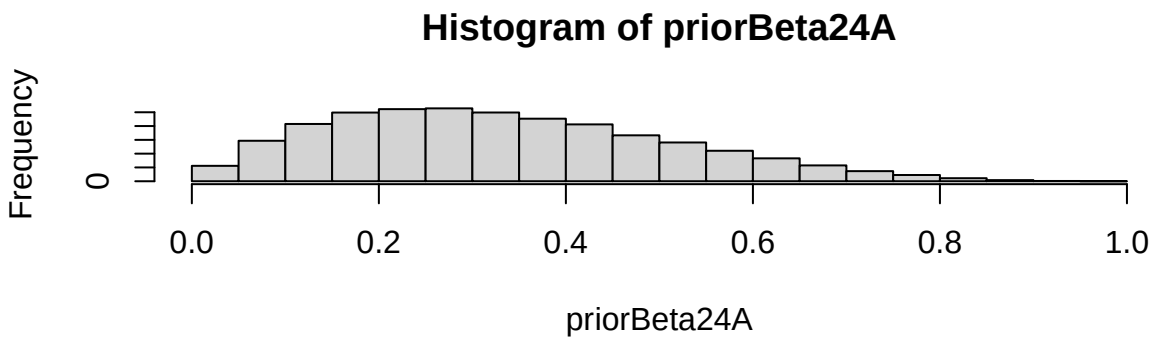
Study the influence of prior assumptions on the results of a Bayesian analysis. Remember Swedish Fish Inc.'s two advertising alternatives: - method A: 6 out of 16 signed up and - method B: 10 out of 16 signed up. Use an uninformative prior, a Beta(2, 4) prior and the more informative Beta(3, 25) prior for the signup rates θ_A and θ_B and compare the resulting marginal posterior distributions.

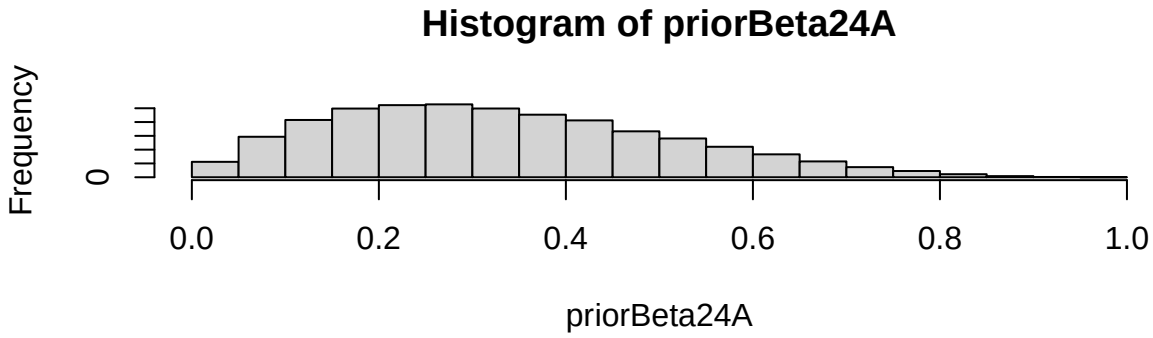
```
# Simulate n random draws from the different priors
n = 100000

par(mfrow=c(2,1))
# uninformative prior:
priorUnA <- runif(n)
hist(priorUnA) # Eyball the prior
priorUnB <- runif(n)
hist(priorUnB) # Eyball the prior
```



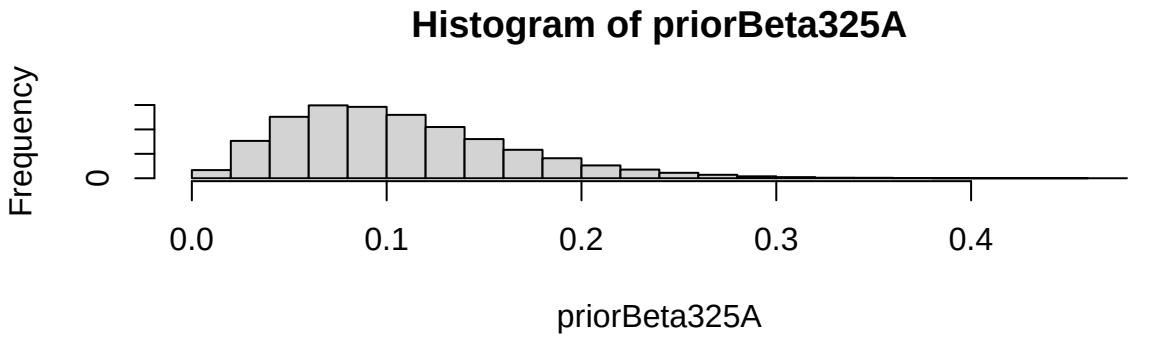


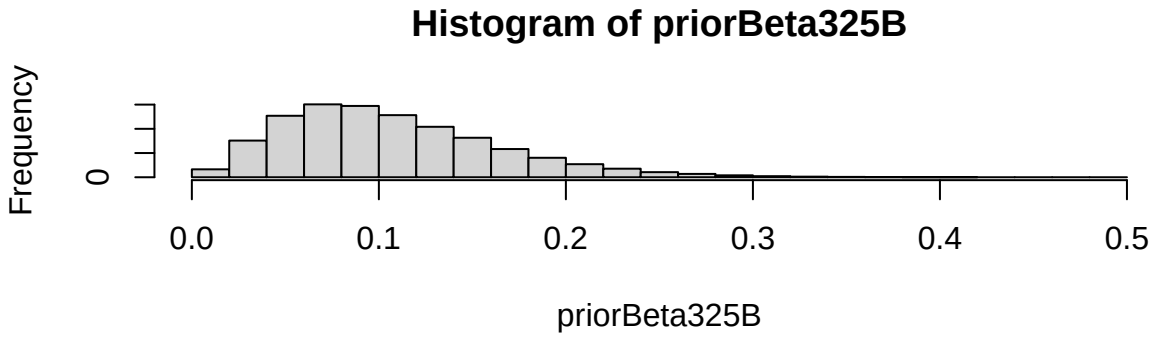

```
# beta(2, 4) prior
priorBeta24A <- rbeta(n, 2, 4)
hist(priorBeta24A)
priorBeta24B <- rbeta(n, 2, 4)
hist(priorBeta24A)
```






```
# beta(3, 25) prior
priorBeta325A <- rbeta(n, 3, 25)
hist(priorBeta325A)
priorBeta325B <- rbeta(n, 3, 25)
hist(priorBeta325B)
```

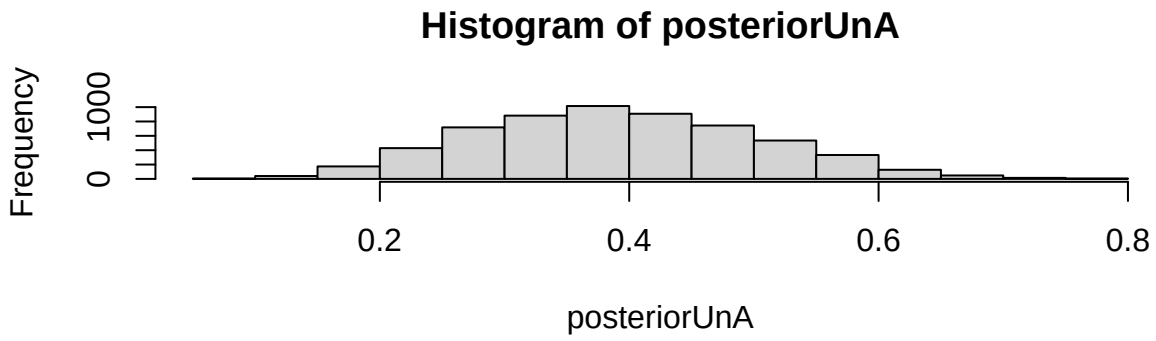


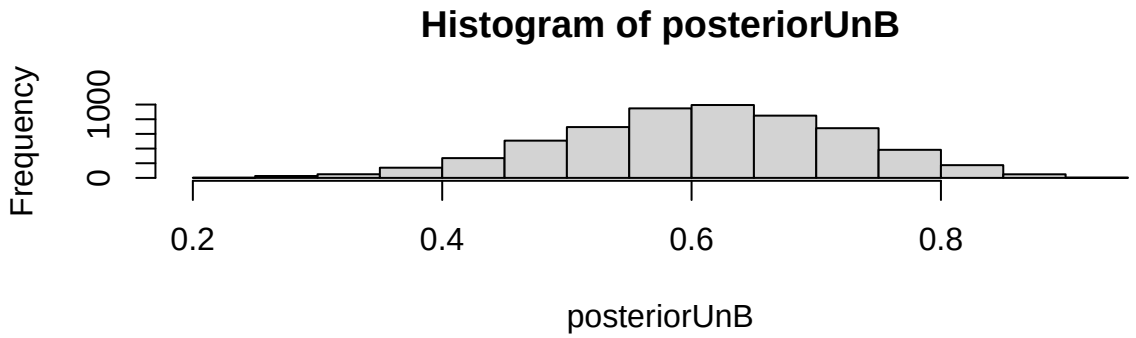



```r
# Define the generative model of uninformative prior:
generativemodelUnA <- function(theta) {
  rbinom(1, 16, theta)
}
generativemodelUnB <- function(theta) {
  rbinom(1, 16, theta)
}


# Simulate and store data from uninformative prior:
simdataUnA <- rep(NA, n)
for(i in 1:n) {
  simdataUnA[i] <- generativemodelUnA(priorUnA[i])
}
simdataUnB <- rep(NA, n)
for(i in 1:n) {
  simdataUnB[i] <- generativemodelUnA(priorUnB[i])
}

# Filter out all draws that do not match the data of the uniform prior:
posteriorUnA <- priorUnA[simdataUnA == 6]
hist(posteriorUnA)
length(posteriorUnA)
```

```
## [1] 5978
```

```
posteriorUnB <- priorUnB[simdataUnB == 10]
hist(posteriorUnB)
```





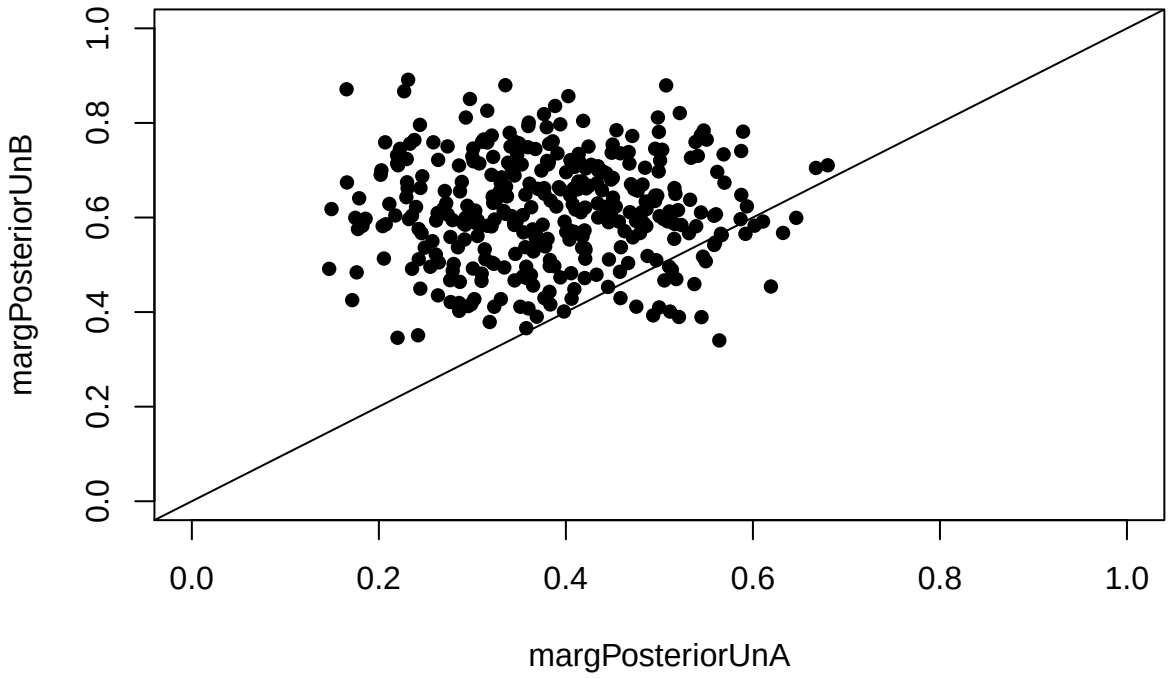

```
length(posteriorUnB)
```

```
## [1] 5768
```

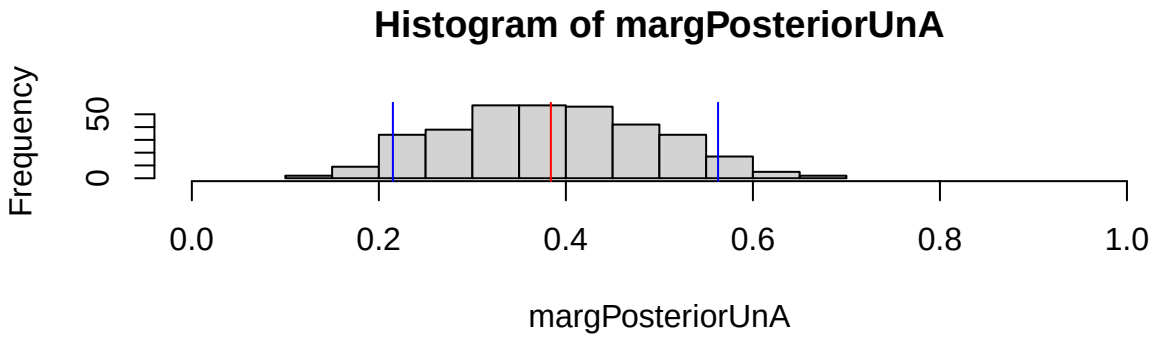
```
# Condition on observed data
ind = ( (simdataUnA==6) & (simdataUnB==10) )
ind[1:20]
```

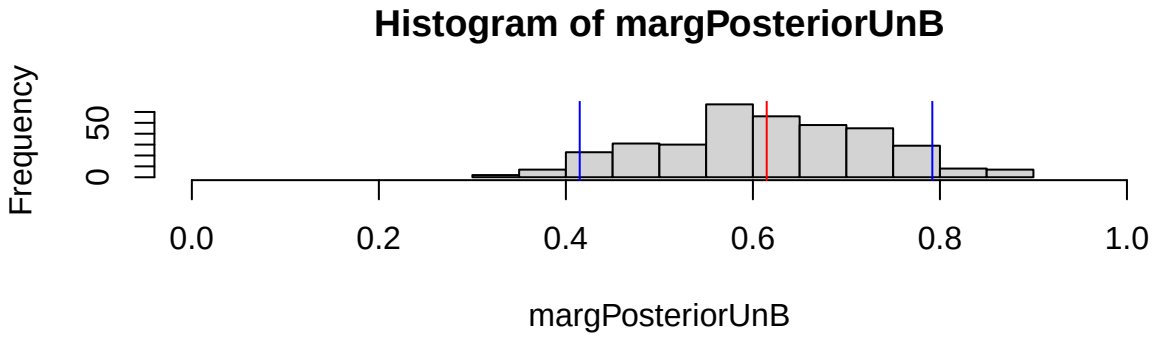
```
##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
margPosteriorUnA <- priorUnA[ind]
margPosteriorUnB <- priorUnB[ind]

# evaluate results
par(mfrow=c(1,1))
plot(margPosteriorUnA, margPosteriorUnB, cex=1, pch=16, xlim=c(0,1), ylim=c(0,1))
abline(0,1)
```




```
par(mfcol=c(2,1))
hist(margPosteriorUnA,xlim=0:1)
abline(v=mean(margPosteriorUnA),col="red")
abline(v=quantile(margPosteriorUnA,c(0.05,0.95)),col="blue")
hist(margPosteriorUnB,xlim=0:1)
abline(v=mean(margPosteriorUnB),col="red")
abline(v=quantile(margPosteriorUnB,c(0.05,0.95)),col="blue")
```






```
par(mfcol=c(1,1))
```

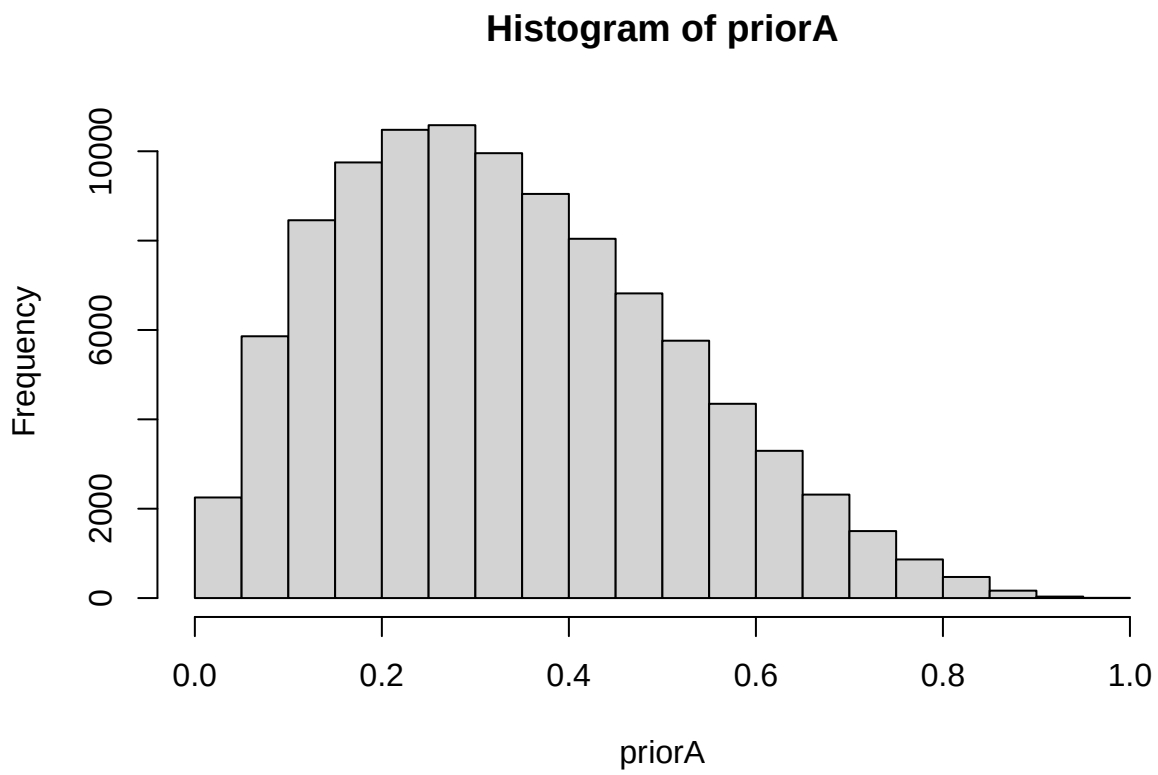
This would be the approach per prior. But in the solution was a way easier approach to do so. This one is used beneath.

Question 1, Task 1

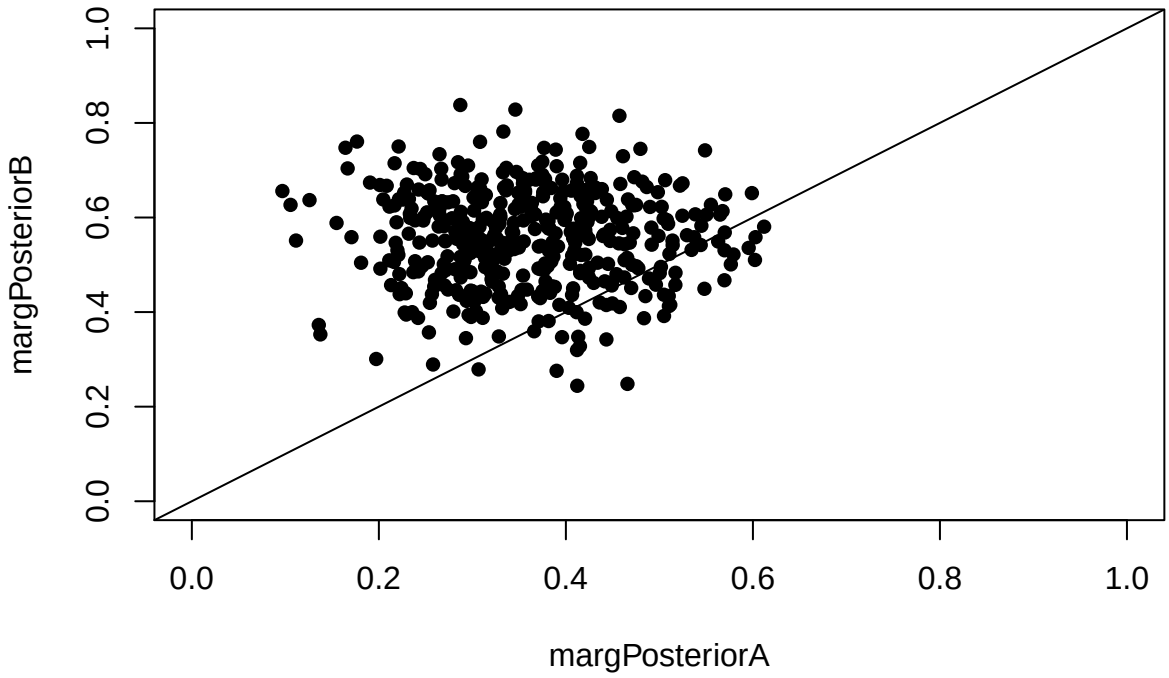
> Why are there these warning in the model data simulation process in this kind of approach? I adjusted n for the binomial sampling in rbinom to the singnups. Which is apparently wrong.

```
# number of samples
nSamples = 100000

# Data
asked    = 16 # number of asked/invited people
SingnupA =  6 # number of signups with method A
SingnupB = 10 # number of signups with method B

# Simulate prior
# Case 1
```

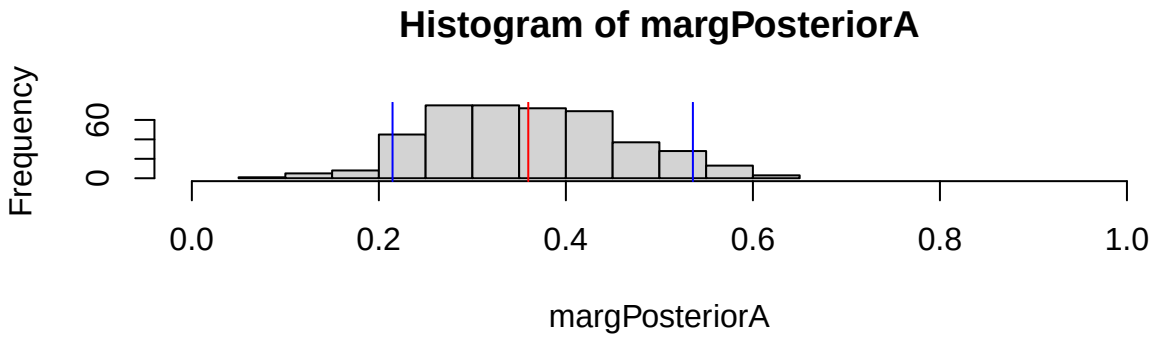
```
priorA = runif(nSamples,0,1)
priorB = runif(nSamples,0,1)
# Case 2
priorA = rbeta(nSamples,2,4)
priorB = rbeta(nSamples,2,4)
# Case 3
# priorA = rbeta(nSamples,3,25)
# priorB = rbeta(nSamples,3,25)
hist(priorA)
```

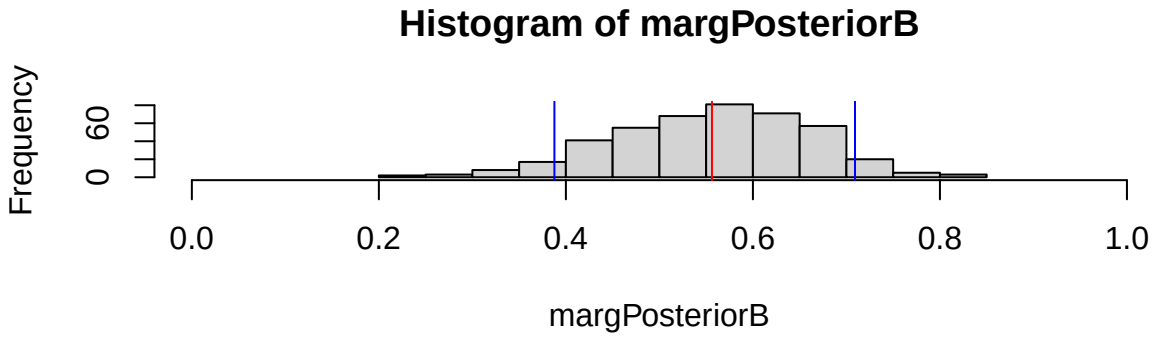



```
# Simulate generative model (likelihood)
simSingnupA = rbinom(nSamples,asked,priorA)
simSingnupB = rbinom(nSamples,asked,priorB)

# Condition on observed data
ind = ( (simSingnupA==SingnupA) & (simSingnupB==SingnupB) )

margPosteriorA = priorA[ind]
margPosteriorB = priorB[ind]

# evaluate results
par(mfrow=c(1,1))
plot(margPosteriorA,margPosteriorB,cex=1,pch=16,xlim=c(0,1),ylim=c(0,1))
abline(0,1)
```




```
par(mfcol=c(2,1))
hist(margPosteriorA, xlim=0:1)
abline(v=mean(margPosteriorA),col="red")
abline(v=quantile(margPosteriorA,c(0.05,0.95)),col="blue")
hist(margPosteriorB, xlim=0:1)
abline(v=mean(margPosteriorB),col="red")
abline(v=quantile(margPosteriorB,c(0.05,0.95)),col="blue")
```






```
par(mfcol=c(1,1))
print(mean(margPosteriorA)); mean(margPosteriorB)
```

```
## [1] 0.3597709
```

```
## [1] 0.5562105
```

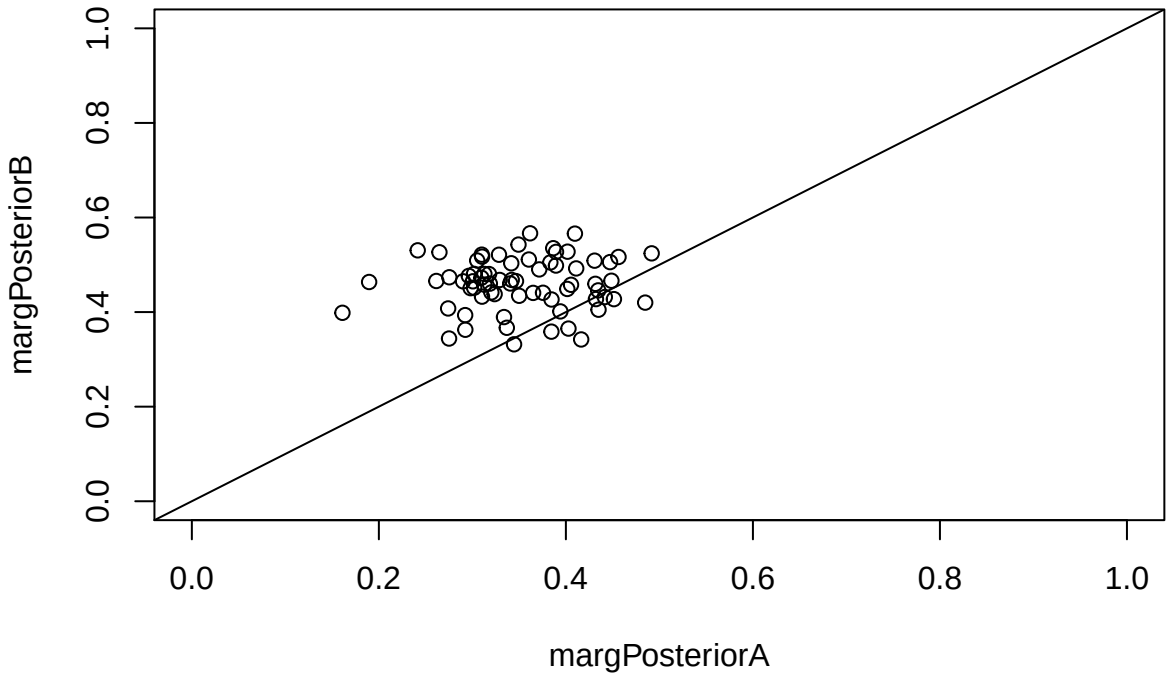
Question 2, Task 1

If i use a prior of beta(3, 25) i do not get any marginal posteriors. Why is that?

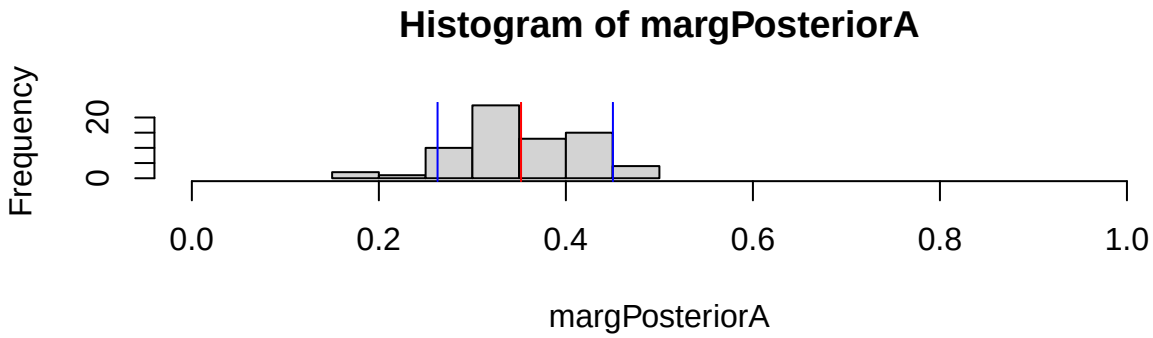
Task 2

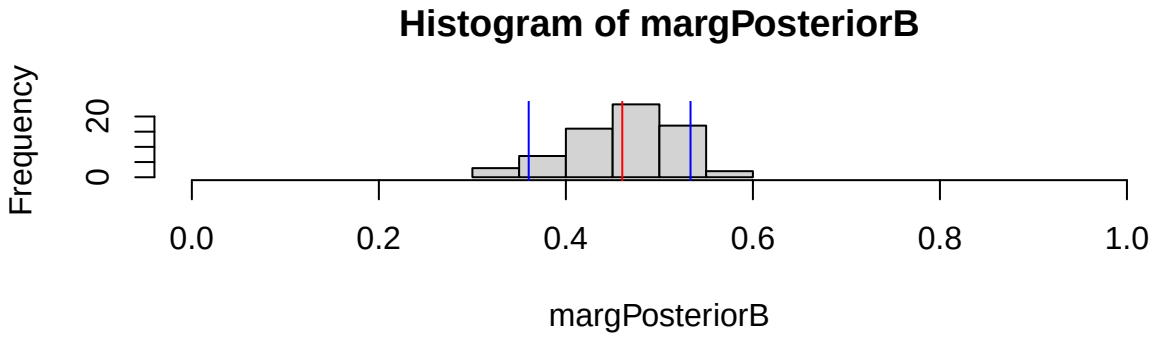
Evaluate the influence of prior assumptions and increasing data on the results of a Bayesian analysis. Consider Swedish Fish Inc. would have asked 32 (instead of 16) people, with the following results: - Method A: 12 out of 32 signed up and - method B: 20 out of 32 signed up. Again, use a uniform prior, a Beta(2, 4) prior and a Beta(3, 25) prior and compare the resulting marginal posterior distributions. Compare your results with the results from task 1.

```r
# number of samples
n <- 100000

# Signups
asked <- 32
signupA <- 12
signupB <- 20

# Simulate just the prior you wish to investigate:
## uniform prior
priorA <- runif(n, 0, 1)
priorB <- runif(n, 0, 1)

## beta(2,4) prior
priorA <- rbeta(n, 2, 4)
priorB <- rbeta(n, 2, 4)

## beta(3, 25) prior
priorA <- rbeta(n, 10, 20)
priorB <- rbeta(n, 10, 20)

# simulate generative model
simSignupA <- rbinom(n, asked, priorA)
simSignupB <- rbinom(n, asked, priorB)

# condition on observed data
ind <- ( (simSignupA == signupA) & (simSignupB == signupB) )

margPosteriorA <- priorA[ind]
margPosteriorB <- priorB[ind]

# inspect results
par(mfrow=c(1,1))
plot(margPosteriorA, margPosteriorB, xlim = c(0, 1), ylim = c(0, 1))
abline(0, 1)
```




```
par(mfrow=c(2, 1))
hist(margPosteriorA, xlim=0:1)
abline(v = mean(margPosteriorA), col = 'red')
abline(v = quantile(margPosteriorA, probs = c(0.05, 0.95)), col = 'blue')

hist(margPosteriorB, xlim = 0:1)
abline(v = mean(margPosteriorB), col = 'red')
abline(v = quantile(margPosteriorB, probs = c(0.05, 0.95)), col = 'blue')
```






```
print(paste('Mean marginal PosteriorA:', round(mean(margPosteriorA), 4)))
```

```
## [1] "Mean marginal PosteriorA: 0.352"
```

```
print(paste('Mean marginal PosteriorB:', round(mean(margPosteriorB), 4)))
```

```
## [1] "Mean marginal PosteriorB: 0.4603"
```

The differences compared to the first task are about 1%, so it is not that much of a difference.

Task 3

John has two children. Given that at least one is a boy, what's the probability he has two boys?

Hint: Draw a tree.

Ω = {BB, BG, GB, GG} -> All possibilities
A = {BB, BG, GB} -> P(A) that at least one is a boy = 3/4 = 0.75
B = {BB} -> P(B) of two boys = 1/4 = 0.25
B|A = {BB}|{BB, BG, GB} -> P(B|A) that he has two boys given at least one is a boy = 1/3 = 0.33

P(B, A) = P(A) * P(B|A) = 0.75 * 0.33 = 0.25

Question Task 3

- Why is the above solution not correct? Why is it just 1/3 and not 1/4?

Task 4

Automated email classification

Suppose an online shop wants to forward all unspecified emails to the technical support (helpdesk) or the sales department (sales).

In general **75%** of all unspecified emails have contents that belong to the sales department, the remaining emails have contents belonging to the helpdesk. You noticed, that most emails containing the string cost in the body of the email, should be forwarded to the sales department.To quanfify this, you carry out an experiment:

- 100 unspecified emails have been evaluated, that had contents belonging to the helpdesk.

10 of them contained the string cost: P(cost | heldpesk) = 0.1.

- 100 unspecified emails heve been evaluated, that had contents belonging to the sales department. 80 of them contained the string cost: P(cost | sales) = 0.8.

Calculate the probability of the naive Bayes classifier: P(sales | cost).

P(sales | costs)
$= \frac{P(costs|sales)*P(sales)}{P(costs)}$

$= \frac{P(costs|sales)*P(sales)}{P(costs|sales)*P(sales)+P(costs|helpdesk)*P(helpdesk)}$

$= \frac{0.8*0.75}{0.8*0.75+0.1*0.25}$

$= 0.96$