#Question 1

> dbinom(12,30, p = 1/3)

[1] 0.1101246

> seqs <- 0:30

> plot(dbinom(seqs,30, p = 1/3))

![A close up of a piece of paper

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> 30 \* 1/3

[1] 10

> 10 \*(1-1/3)

[1] 6.666667

> #Question 2 Chika Igba and Dr. Foder helped with this.

> seqs2 <- c(0:100)

> #2A

> plot(dbinom(seqs2, 100,p = .4))

![A picture containing screenshot

Description automatically generated]()

> #2B

> binom.test(53,100,p = .4, alternative = "two.sided")

Exact binomial test

data: 53 and 100

number of successes = 53, number of

trials = 100, p-value = 0.01036

alternative hypothesis: true probability of success is not equal to 0.4

95 percent confidence interval:

0.4275815 0.6305948

sample estimates:

probability of success

0.53

> #2C

> binom.test(53,100,p = .4, alternative = "greater")

Exact binomial test

data: 53 and 100

number of successes = 53, number of

trials = 100, p-value = 0.005761

alternative hypothesis: true probability of success is greater than 0.4

95 percent confidence interval:

0.4430853 1.0000000

sample estimates:

probability of success

0.53

> sum(dbinom(53:100,100,.4))

[1] 0.005760648

> #Question 3

> #3A

> myVals <- rbinom(1000,10000,1/2)

> #3B

> mean(myVals)

[1] 5002.067

> var(myVals)

[1] 2342.347

> 10000 \* 1/2

[1] 5000

> 5000 \* (1-1/2)

[1] 2500

> #3C Anu Ginni helped me with this

> pvals <- c()

> for (i in 1:length(myVals))

+ {

+ pvals[i] <- binom.test(myVals[i],10000, p = 1/2)$p.value

+ }

> hist(pvals, breaks = 50)

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#So I expected for p values .49 and .51 to be similar but I did not expect for them to be so different from ½. I thought that they would be more similar, but I got a different number. I think they were different because of the p-value. The p-value at .5 allows us to accept the null hypothesis, however, when you change the p-value you reject the null hypothesis.

pvals2 <-c()

for (i in 1:length(myVals))

{

pvals2[i] <- binom.test(myVals[i],10000, p = .49)$p.value

}

hist(pvals2, breaks = 50)

![A close up of a piece of paper

Description automatically generated]()

pvals3 <-c()

for (i in 1:length(myVals))

{

pvals3[i] <- binom.test(myVals[i],10000, p = .51)$p.value

}

hist(pvals3, breaks = 50)

![A screenshot of a cell phone

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