## STA511 Homework #2

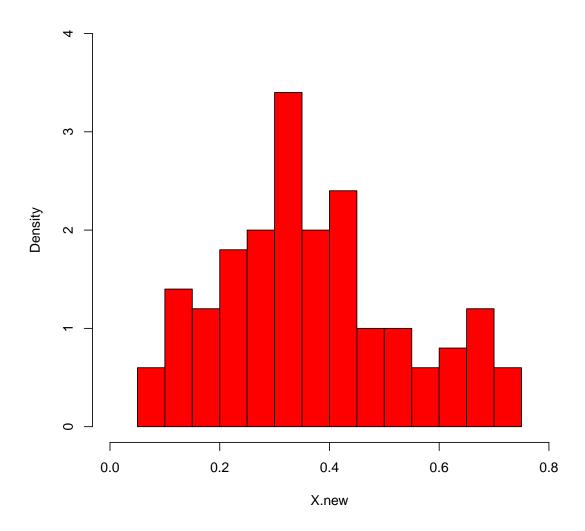
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- 1. No work required for question 1
- 2. Newton Raphson algorithm was implemented from a beta distribution for 100 observations. The stopping rule was  $|x_i x_{i-1}|$ . Using set.seed(333), the average number of iterations was 3.5, and the accepted observations can be seen in Figure 1.

Figure 1: Histogram of Accepted Observations From Beta Distribution using Newton-Raphson method.

## **Newton-Raphson Method Accepted Observations**



The R code for Question 2 can be seen below:

rm(list=ls())
set.seed(333)

```
nsims <- 100
iterations <- c()
X.new \leftarrow c()
random.dist <- runif(1000)</pre>
for(i in 1:nsims){
        U <- random.dist[i]</pre>
        alpha <- 3
        beta <- 5
        x.old <- 0.5
        N <- 10 #random number that is bigger than 1 so 'j' in the while loop keepings resetting
         i <- 1
        while(j \le N){
                 x.new <- x.old - ((pbeta(x.old, alpha, beta) - U)/dbeta(x.old, alpha, beta))</pre>
                 j < -j + 1
                 if(abs(x.new - x.old) < 0.05) {
                          break
                 x.old <- x.new
        X.new[i] <- x.new</pre>
        print(X.new)
        iterations[i] <- j</pre>
}
mean(iterations)
pdf("hw2-q2.pdf")
hist(X.new, xlim=c(0,0.8), ylim=c(0,4), probability=TRUE, breaks=20, col="red",
     main="Newton-Raphson Method Accepted Observations")
dev.off()
```

- 3. The Chi-square  $(\chi^2)$  and Kolmogorov-Smirnov (KS) tests were compared for type I error (part a) and power (part b).
  - (a) Random uniform numbers between 0 and 1 were generated using the runif command in R, with sample sizes of n = 10, 25, 50, 100. This was simulated 500 times and the p-values < 0.05 were reported in Table 1. The results can be interpreted such that as sample size increases towards n=50, the type I error increases for the  $\chi^2$  increases to about 5%. As the sample size increases past n=50, the type I error begins to decrease. The KS type I errors that fell under the p-value < 0.05 criteria, were always around 0.05 no matter how large the sample size increased. This indicates that the KS value may be more appropriate for small and larger sample sizes.

Table 1: Type I Error was compared between Chi-squared and Kolmogorov-Smirnoff Tests. The values shown are the frequency of acceped type I error p-values (p < 0.05) relative to total number of simulations

	Chi-square Test	Kolmogorov-Smirnoff Test
n = 10	0.024	0.050
n = 25	0.034	0.048
n = 50	0.046	0.046
n = 100	0.030	0.054

The code for question 3a:

(b) The power was compared between  $\chi^2$  and KS tests. The power increased as sample size increased for  $\chi^2$ . As shown in Table 2, the power was again towards its maximum for any sample size, similar to the type I error result. This indicates that the KS test has more power when computing random beta distributions. This may be because rbeta is NOT a good random number generator.

Table 2: Chi-square and KS test compared for Power. The accepted values presented are frequencies relative to total number of simulations.

	Chi-square Test	Kolmogorov-Smirnoff Test
n = 10	0.01	1.00
n = 25	0.14	1.00
n = 50	0.57	1.00
n = 100	0.98	1.00

```
sample.size <- c(10, 25, 50, 100)
shape1 <- 3
shape2 <- 5
nsims <- 500

mat <- matrix(c(1:2*length(sample.size)),ncol=2, nrow=length(sample.size))
for (i in 1:length(sample.size)){
    ks.results <- list()
    chisq.results <- list()
    for (j in 1:nsims){
        #rbeta with shape1=3, shape2=5
        r <- rbeta(sample.size[i], shape1, shape2)
        #pbeta because you need to compare cdf
        ks.results[j] <- ks.test(r, "pbeta", 0, 1)$p.value</pre>
```

r.counts <- hist(r, breaks=10, plot=FALSE)\$counts
chisq.results[j] <- chisq.test(r.counts)\$p.value</pre>

#using 10 bins for making counts

chi.final <- list(sum(chisq.results <= 0.05))
ks.final <- list(sum(ks.results <= 0.05))</pre>

rownames(mat) <- paste("n", sample.size, sep=" = ")</pre>

mat[i,1:2] <- do.call("cbind",c(chi.final,ks.final))</pre>

colnames(mat) <- c("Chi-square Test", "Kolmogorov-Smirnoff Test")</pre>

The code for question 3b is:

rm(list=ls())
set.seed(333)

}

}

4. Simulation conducted to compare Type I error for Chi-squared test for a random number generator 0 to 1. The sample sizes used are n = 10, 25, 50, 100, 500. The bins used were bins = 10, 25, 50, 100, 500. The results of these simulations are reported in Table 3. At a low sample sizes (n=10), as the number of bins increased, the more p-values that fall under the specified criteria (p < 0.05) increase in frequency. However, as sample size increases, the trend appears to be less clear, showing a more uniform distribution of accepted p-values. Next time in order to help me interpret these results better I will plot the results in histograms as well for visualization, but unfortunately due to time constraints, I was unable to do this.

Table 3: Simulation conducted to compare Type I error for Chi-squared test for a random number generator 0 to 1. The accepted values presented are frequencies relative to total number of simulations.

	n = 10	n = 25	n = 50	n = 100	n = 500
bin = 10	0.024	0.026	0.040	0.038	0.052
bin = 25	0.034	0.040	0.034	0.054	0.066
bin = 50	0.046	0.036	0.042	0.040	0.074
bin = 100	0.052	0.032	0.026	0.064	0.048
bin = 500	0.084	0.058	0.048	0.060	0.056

Here is the code for question 4:

```
rm(list=ls())
set.seed(333)
sample.size <-c(10,25,50,100,500)
bins <-c(10,25,50,100,500)
mat <- matrix(c(length(sample.size)*length(bins)),ncol=length(sample.size), nrow=length(bins))</pre>
nsims <- 500
for (i in 1:length(sample.size)){
         for (p in 1:length(bins)){
                 chisq.results <- NULL</pre>
                 for (j in 1:nsims){
                          r <- round(runif(sample.size[i]),3)</pre>
                          r.counts <- hist(r, breaks=bins[p], plot=FALSE)$counts</pre>
                          chisq.results[j] <- chisq.test(r.counts)$p.value</pre>
                 }
                 chi.final <- sum(chisq.results <= 0.05)</pre>
                 mat[p,i] <- chi.final</pre>
         }
rownames(mat) <- paste("bin", bins, sep = " = ")</pre>
colnames(mat) <- paste("n", sample.size, sep = " = ")</pre>
print(mat)
```