STA 511 Homework #6

Suruchi Jaikumar Ahuja

December 8

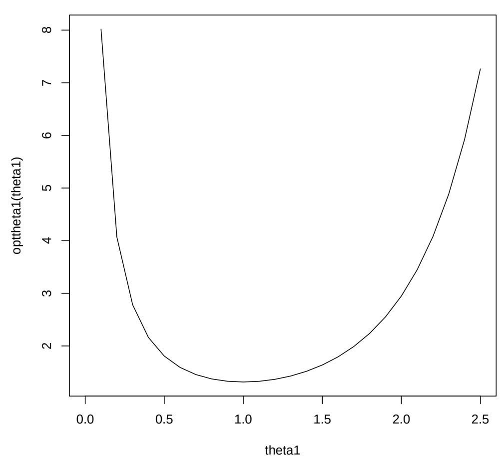
1. Question 1

   (a) Given g(x) $= \dfrac{\theta}{2}e^{-\theta|x|}$ for $\theta > 0$;

   f(x) is the standard normal pdf and is given by f(x) $= \dfrac{1}{\sqrt{2\pi}}e^{\frac{-x^2}{2}}$

   For optimal θ refer to Figure 1.[1]

Figure 1: Optimal θ value



$$c = sup\frac{f(x)}{g(x)}$$

[1]Refer Appendix 1a for the R code for optimal rejection constant.

$$= sup\frac{\frac{1}{\sqrt{2\pi}}e^{\frac{-x^2}{2}}}{\frac{\theta}{2}e^{-\theta|x|}}$$

$$= \frac{1}{\sqrt{2\pi}}\frac{2}{\theta}e^{-\frac{x^2}{2}+\theta|x|}$$

So,

$$c \rightarrow \begin{cases} \frac{1}{\sqrt{2\pi}}\frac{2}{\theta}e^{-\frac{x^2}{2}+\theta(x)} if x \geq 0 \\ \frac{1}{\sqrt{2\pi}}\frac{2}{\theta}e^{-\frac{x^2}{2}-\theta(x)} if x < 0 \end{cases}$$

Now setting the dervatives to zero,
$\frac{d}{dx}\frac{1}{\sqrt{2\pi}}\frac{2}{\theta}e^{-\frac{x^2}{2}+\theta(x)} =^{set} 0$ if $x \geq 0$
$\frac{d}{dx}\frac{1}{\sqrt{2\pi}}\frac{2}{\theta}e^{-\frac{x^2}{2}-\theta(x)} =^{set} 0$ if $x < 0$
$\rightarrow \sqrt{\frac{2}{\pi\theta^2}}e^{-\frac{x^2}{2}+\theta x}(-x+\theta) = 0$ if $x \geq 0$
$\rightarrow \sqrt{\frac{2}{\pi\theta^2}}e^{-\frac{x^2}{2}+\theta x}(-x-\theta) = 0$ if $x < 0$

Now, the critical points are chosen as

$$x = \theta for x \geq \theta$$

$$x = -\theta for x < \theta$$

$c_\theta = \sqrt{\frac{2}{\pi\theta^2}}e^{-\frac{\theta^2}{2}+\theta^2} \rightarrow \sqrt{\frac{2}{\pi\theta^2}}e^{\frac{\theta^2}{2}}$ for $x \geq 0$
And,
$c_\theta = \sqrt{\frac{2}{\pi\theta^2}}e^{-\frac{(-\theta^2)}{2}-\theta(-\theta)} \rightarrow \sqrt{\frac{2}{\pi\theta^2}}e^{\frac{\theta^2}{2}}$ for $x < 0$

Hence ,

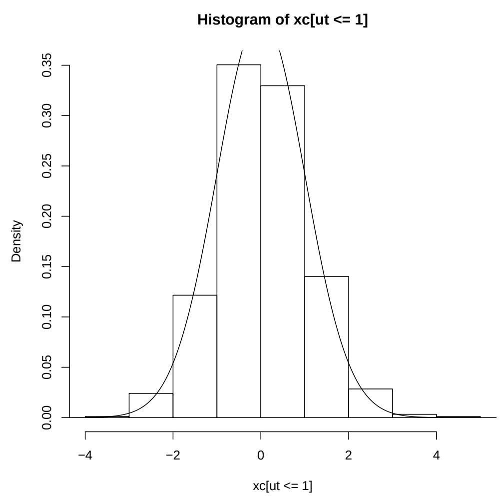
$$c_\theta = \sqrt{\frac{2}{\pi\theta^2}} e^{\frac{\theta^2}{2}}$$

for

$$-\infty < 0 < +\infty, \theta > 0$$

(b) Using Generalized Rejection Algorithm to obtain 1000 observations from N(0,1)
It is an almost normal distribution but not completely normal. (Refer to Figure 2).[1]

Figure 2: Histogram of observations from generalized rejection method.



(c) The Chi Square Test was performed to test the goodness of fit to determine the 1000 samples generated.[2] The X- squared - 1000
df value - 999
p-value - 0.4851
Here the Null Hypothesis is not rejected.

[1]Refer Appendix 1b for the R code
[2]Refer Appendix 1c for the R code for goodness of fit

2. Question-2

   (a) The method of moments estimator for α is found by equating the first sample moment and E(X)
   Thus,

$$E[X] = \frac{\alpha}{\beta} = \frac{\sum x_i}{n}$$

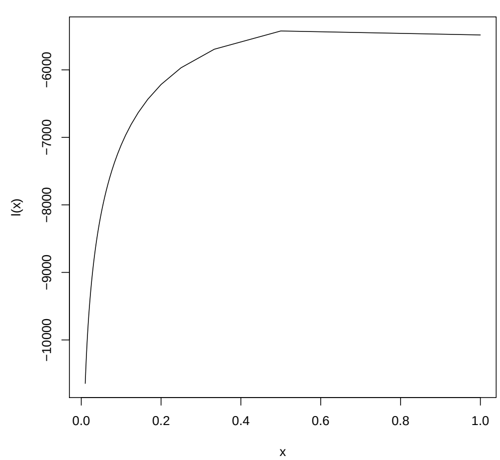
.

$$\Leftrightarrow \hat{\alpha}_{MOM} = \beta \frac{\sum x_i}{n}$$

   Given $\beta = 3.2$, the method of moments estimate for α was calculated to be 0.6859317. [1]

   (b) The Maximum likelihood estimate for α was calculated to be 0.687098.The approximate 95% confidence interval for α, which was calculated using Bootstrapping and normal interval, is (0.6577010, 0.7164952).
   Refer to Figure 3 [2]

Figure 3: Plot of MLE of α



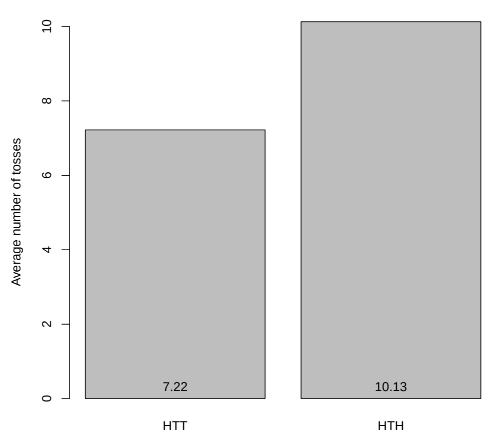
[1]Refer Appendix 2a for the R code used to compute the method of moment estimate.
[2]Refer Appendix 2b for the R code used to compute the MLE .

(c) The probability that a randomly selected policy has more than 2 claims in the year is $\pi = 0.00306643$.
The approximate 95% confidence interval for π, which was calculated using the Bootstrap Technique, is (0.01912874, 0.03139446).[1]

3. Question 4

   (a) Theoretically, the probability of occurrence of HTT and HTH patterns occur are equal to $(\frac{1}{2})^3$.
   Thus, the expected number of occurrences in **n** tosses=$n * (\frac{1}{2})^3$
   When we use simulation, the average number of tosses to obtain Pattern 1(HTH) is 7.22 and the average number of tosses to obtain Pattern 2 (HTT) is 10.13.
   (Refer to Figure 4)
   The results are surprising as they indicate higher average tosses for HTT than HTH because theoretically they must be equal.[2]

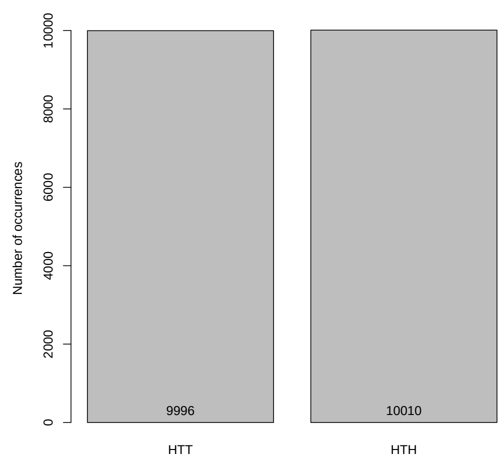
Figure 4: Average Number of tosses for pattern 1 and pattern 2



[1]Refer Appendix 2c for the R code used to compute the estimator and the Confidence intervals.
[2]Refer Appendix 3a for the R code used to calculate the average number of tosses.

(b) The number of occurrences of the HTH and HTT patterns in 100,000 trials are 9996 and 10010 respectively. (Refer to Figure 5). [1]

Figure 5: Number of occurences of Pattern1 and Pattern2



4. Question 5

   $X_1, X_2......X_n\ (a, 5)$

   (a)

$$f(x) \rightarrow \begin{cases} \frac{1}{b-a}\ if\ a < x < b \\ \\ 0\ otherwise \end{cases}$$

$$= f(x) \rightarrow \begin{cases} \frac{1}{5-a}\ if\ a < x < b \\ \\ 0\ otherwise \end{cases}$$

[1]Refer Appendix 3b for the R code used to calculate the average number of tosses.

$$\mu = E[X]$$

$$= \int_a^5 x.f(x)$$

$$= \int_a^5 x.\frac{1}{5-a}dx$$

$$= \frac{5+a}{2} = \bar{X}$$

Hence,

$$\hat{a}_{MOM} = 2\bar{X} - 5$$

(b) Maximim Likelihood Estimator of a

$$f(x) \rightarrow \begin{cases} \frac{1}{b-a} \ if \ a < x < 5 \\ \\ 0 \ otherwise \end{cases}$$

$$L(x|a) = \begin{cases} \prod_{i=1}^{n} \frac{1}{5-a} \ if \ a < x < 5 \\ \\ 0 \ otherwise \end{cases}$$

$$L(x|a) \rightarrow \begin{cases} \frac{1}{5-a}^{n} \; if \; a < x < 5 \\ \\ 0 \; otherwise \end{cases}$$

To maximize the L(x—a) , the value of (5-a) must be small and that is done using the min function.

$$a \leq min(X_1, X_2......X_n)$$

$$\hat{a}_{MLE} = min(X_1, X_2......X_n)$$

Hence,

$$\hat{a}_{MLE} = X_{(1)}$$

(c) Maximum Likelihood Estimator of τ

$$\tau = E[X] = \int_a^5 x.f(x)dx$$

Where,

$$f(X) = frac15 - a$$

So,

$$= \int_a^5 X.\frac{1}{5-a}$$

$$\frac{1}{2}(\frac{5^2 - a^2}{5-a})$$

$$\tau = \frac{5+a}{2} \rightarrow \frac{5+X_1}{2}$$

(d) Here $\hat{\tau}$ is the MLE of τ,
and $\bar{\tau}$ is the methods of moment estimator of τ = E[X]
a=1, and n= 10[1]

The coverage probability for a 95% confidence interval forτ was computed as:
Normal CI :(2.76,3.43)
Pivotal CI :(2.35,3.11)
Percentile CI :(3.10, 3.91)

The coverage probability for a 95% confidence interval forτ using $\bar{\tau}$:
Normal CI :(1.88,3.39)
Pivotal CI :(1.90,3.36)
Percentile CI :(1.89, 3.39)

[1]Refer Appendix 5d for the R code used to calculate the confidence intervals.

Appendix-1a

```
 x<-seq(-10,10,length=100)
 opttheta <- function(x,theta){
    (sqrt(2/(pi*theta^2))*exp(-(x)^2+theta*abs(x)))
  }
 theta=1
 theta1=seq(0,2.5,0.1)
 opttheta1 <- function(theta1){
  (sqrt(2/(pi*theta1^2))*exp((theta1^2)/2))
  }

X11()
plot(theta1,opttheta1(theta1),type="l")
```

Appendix-1b

```
func1 <- function(x,theta=1){
  x <- ((theta/2)*exp(-theta*abs(x)))/((1/(2*pi)^0.5)*exp((-x^2)/2))
  return(x)
  }

a <- (sqrt(2)/pi)*exp(.5)
xc <- rlaplace(1000,0,1)
uc <- runif(1000,0,1)
tc <-  a*sapply(xc, func1)
ut <- uc*tc

X11()
hist(xc[ut <=1], prob=T)
p<-ut <=1
p1<-rnorm(x)

X11()
hist(xc[ut <=1], prob=T)
p<-ut <=1
p1<-rnorm(x)

x=seq(-10,10,length=1000)
lines(x,dnorm(x))
sum(ut<=1)/1000
```

Appendix-1c

```
p<-ut <=1
p1<-rnorm(x)
chisq.test(p,rnorm(x))
```

Appendix-2a

```
library(base)
 #Initializing given data
  data = c(rep(0,7840),rep(1,1317),rep(2,239),rep(3,42),rep(4,14),rep(5,4),rep(6,4),7)
 beta=3.2;

m=mean(data);
alpha.mom=m*beta;
alpha.mom
```

Appendix-2b

```
data = c(rep(0,7840),rep(1,1317),rep(2,239),rep(3,42),rep(4,14),rep(5,4),rep(6,4),7)
beta=3.2;

logfn1 <- function (alpha){
  ba <- beta ^alpha
  dr <- (beta+1)^(alpha+data)
  return(-sum(log((ba)*gamma(alpha+data)/(factorial(data)*gamma(alpha)*dr))))
}
a <-c()
y <- c()
for(i in 1:100){
  a[i] <- 1/i
  y[i] <- logfn1(a[i])
}
z=-y
x11()
plot(a,z, xlab="x", ylab="l(x)",'l');
#finding the maximum of the function
mle_alpha <- nlminb(0.5,logfn1)$par
mle_alpha

fn <- function(alpha,data){
  ba <- beta ^alpha
  dr <- (beta+1)^(alpha+data)
  return(-sum(log(ba*gamma(alpha+data)/(factorial(data)*gamma(alpha)*dr))))
}

#finding confidence intervals
```

```
n=length(data);
B=100
mle_alpha_boot=c()
for(i in 1:B){
  boot_obs=sample(1:n,n,replace=T)
  y_boot = data[boot_obs]
  for (j in 1:10)
  {
    a[j]=1/j
    y[j]=fn(a[j],y_boot)
  }
  mle_alpha_boot[i]=nlminb(0.5,fn,data=y_boot)[[1]];
}
se = sqrt(var(mle_alpha_boot))
#Calculating the Normal confidence interval
Normal = c(mle_alpha_boot-2*se, mle_alpha_boot+2*se)
```

Appendix-2c

```
n=length(data);
#calculating the observed probability of more than 2 claims
          prob <- data[data[]==2]
          prob <- length(prob)/n;
#finding confidence intervals using Bootstrap technique

prob.boot=c();
pb=c();
for(i in 1:100){
  x <- sample(1:n,n,replace=T)
  x.bootstrap <- data[x]
  pb <- x.bootstrap[x.bootstrap[]>2]
  prob.boot[i] <- length(prob.boot)/n;
}
serror = sqrt(var(prob.boot))

#Calculating the Normal confidence interval
Normal = c(prob-2*serror, prob+2*serror)
```

Appendix-3a

```
#Creating two column vectors of size 100 with all values 3.
    X1=c(rep(3,100))
    X2=c(rep(3,100))
```

```
for(i in 1:100)
{
  #let X1[i] be the variable to count the number of trials to get  HTT at the ith trial
  y=round(runif(X1[i],0,1))
  while((y[X1[i]-2]!=1)||(y[X1[i]-1]!=0)||(y[X1[i]]!=0)) # checking for pattern 1
     {
        X1[i] <- X1[i]+1;
        y[X1[k]]<- round(runif(1,0,1))
     }

  #let X2[k] be the variable to count the number of trials to get  HTH at the kth trial
  y=round(runif(X2[i],0,1))
  while((y[X2[i]-2]!=1)||(y[X2[i]-1]!=0)||(y[X2[i]]!=1)) # checking for pattern 2
  {
        X2[i] <- X2[i]+1;
    y[X2[i]] <- round(runif(1,0,1))
  }
}
#Gives mean number of tosses required to observe each pattern
pattern1 <- mean(X1)
pattern2 <- mean(X2)

figure <- barplot(c(pattern1,pattern2), names.arg=c("HTT","HTH"),ylab="Average number of tosses")
text(figure,0,c(pattern1,pattern2),cex=1,pos=3)
```

Appendix-3b

```
x=round(runif(100000,0,1));
a=0;
b=0;
#Checking for Patterns HTT and HTH
for(i in 3:100000)
{
  if((x[i-2]==1)&(x[i-1]==0)&(x[i]==0))
    a=a+1
  if((x[i-2]==1)&(x[i-1]==0)&(x[i]==1))
    b=b+1
}
figure=barplot(c(a,b), names.arg=c("HTT","HTH"),ylab="Number of occurrences")
text(figure1,0,c(a,b),cex=1,pos=3)
```

Appendix-5d

```
library("base")
x<-runif(10,1,5)
```

```
i=1
for(i in 1:100)
{
  boot <- sample(seq(1:10),10,replace=T)
  x.boot <- x[boot]
  mle.a <- min(x.boot[])
  mle.tau <- (5 + mle.a)/2
  tau <-(5+1)/2
  mom.tau <- (5+2(min(boot.obs)-5))/2
}
Normal = c(tau-2*se, tau+2*se)
pivotal = c(2*tau-quantile(x.boot,.975),2*tau-quantile(x.boot,.025))
percentile = c(quantile(x.boot,.025),quantile(x.boot,.975))
Normal1 = c(mom.tau-2*se, mom.tau+2*se)
pivotal1 = c(2*mom.tau-quantile(x.boot,.975),2*mom.tau-quantile(x.boot,.025))
percentile1 = c(quantile(x.boot,.025),quantile(x.boot,.975))
```