# STAT 5443: Homework 2

Daniel Kiser

February 21, 2018

## Problem 1

• To use the inverse CDF transform method, we first find the cdf of p(x) by taking the integral of sin(x):

$$F(t) = \int_0^t \sin(x) = 1 - \cos(t)$$

Then we find the inverse of F(x):

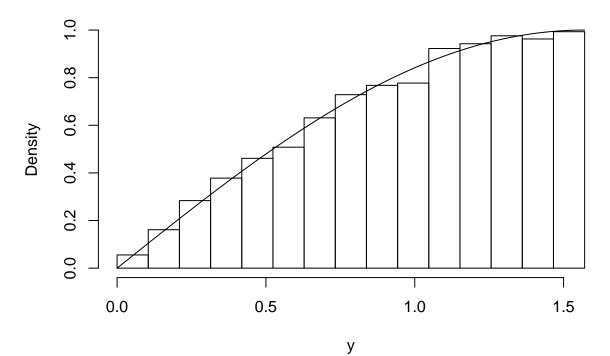
$$u = 1 - cos(x) >> u - 1 = -cos(x) >> 1 - u = cos(x) >> x = cos^{-1}(1 - u)$$

which is equivalent to:

$$x = \cos^{-1}(u)$$

```
sinrand <- function(n) {
    u <- runif(n)
    x <- acos(u)
    return(x)
}
y <- sinrand(10000)
hist(y, freq = F, breaks = seq(0, pi/2, pi/30))
curve(sin(x), from = 0, to = pi/2, add = T)</pre>
```

## Histogram of y



• If we use a uniform density on the interval  $(0, \pi/2)$  as our proposal density, then we implement our rejection sampling method as follows:

```
g_density <- function(x) {</pre>
    u \leftarrow dunif(x, min = 0, max = pi/2)
    return(u)
}
g_rv <- function() {</pre>
    u \leftarrow runif(1, min = 0, max = pi/2)
    return(u)
}
mysin <- function(x) {</pre>
    y \leftarrow sin(x)
    return(y)
}
accept_reject <- function(n, known_g_density, known_g_value,</pre>
    p, M) {
    y <- numeric(n)
    for (i in 1:n) {
         x <- known_g_value()</pre>
         u <- runif(1, min = 0, max = M * known_g_density(x))</pre>
         while (u > p(x)) {
              u <- runif(1, min = 0, max = M * known_g_density(x))</pre>
              x <- known_g_value()
         y[i] \leftarrow x
    }
    return(y)
}
```

To find our value for M, we first find the maximum value of our proposal density, which we designate as g(x):

```
max <- dunif(0, min = 0, max = pi/2)
max</pre>
```

#### ## [1] 0.6366198

Since  $\sin(x)$  is largest at  $\sin(\pi/2) = 1$ , and since g(x) = 0.6366198 for all values of x, we calculate M as:

$$M = \frac{1}{g(x)}$$

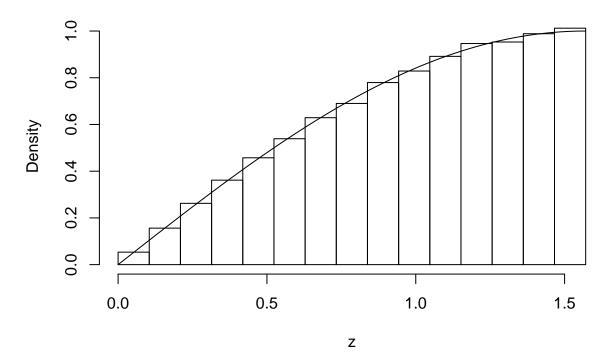
```
M <- 1/max
```

#### ## [1] 1.570796

We draw 100000 samples from out simulated distribution and compare the resulting histogram to the true density:

```
z <- accept_reject(1e+05, g_density, g_rv, sin, M)
hist(z, freq = F, breaks = seq(0, pi/2, pi/30))
curve(sin(x), from = 0, to = pi/2, add = T)</pre>
```

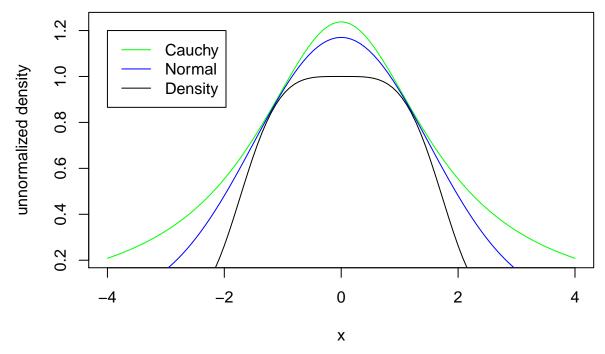
## Histogram of z



## Problem 2

First, we find a good proposal density from which to draw samples. We consider the Cauchy and Normal distributions:

```
unscaled_pdf <- function(x) {
    exp((-x^4)/12)
}
norm_scaled_density <- function(x) {
    dnorm(x, sd = 1.5) * 4.4
}
cauchy_scaled <- function(x) {
    dcauchy(x, scale = 1.8) * 7
}
curve(cauchy_scaled, from = -4, to = 4, col = "green", ylab = "unnormalized density")
legend(x = -4, y = 1.2, lty = c(1, 1, 1), col = c("green", "blue",
    "black"), legend = c("Cauchy", "Normal", "Density"))
curve(norm_scaled_density, from = -4, to = 4, col = "blue", add = T)
curve(unscaled_pdf, from = -4, to = 4, add = T)</pre>
```



A normal distribution with a standard deviation of 1.5 and scaled by 4.4 appears to fit much more closely than the cauchy distribution with a scale of 1.8 and scaled by 7. We can verify this since the probability of a sampled value being accepted is 1/M. Thus, the probability of a sampled value being accepted using the normal distribution is 1/4.4 = 0.2272727 while the probability of a sampled value being accepted using the cauchy distribution is 1/7 = 0.1428571. Clearly, the normal distribution is the more efficient proposal density. Our accept-reject algorithm for an unnormalized density is as follows:

```
unnorm_accept_reject <- function(n, rproposed, dproposed, pdf,
    M) {
    x <- numeric(n)
    i = 1
    while (i <= n) {
        theta <- rproposed()
        u <- runif(1) * M * dproposed(theta)
        if (u <= pdf(theta)) {
            x[i] <- theta
            i <- i + 1
        }
    }
    return(x)
}</pre>
```

We also write a function to generate values from a normal distribution with a standard deviation of 1.5, and we set M = 4.4:

```
# function to generate normal value with sd = 1.5
norm_scaled_value <- function() {
    rnorm(1, sd = 1.5)
}

M <- 4.4

# generate samples
z <- unnorm_accept_reject(10000, norm_scaled_value, norm_scaled_density,</pre>
```

```
unscaled_pdf, M)
```

To verify that our algorithm works, we use the integrate() function in R to normalize our target density and compare our target density with our generated sample:

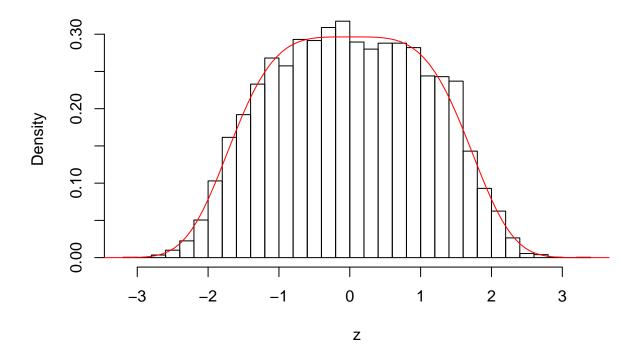
```
# plot histogram
hist(z, freq = F, breaks = 40)

# integrate and normalize target density and compare
# normalized density with generated sample
integrate(unscaled_pdf, lower = -Inf, upper = Inf)

## 3.37401 with absolute error < 0.00033

pdf <- function(x) {
    exp((-x^4)/12)/3.37401
}
curve(pdf, from = -4, to = 4, add = T, col = "red")</pre>
```

## Histogram of z



### Problem 3

1) The method we use to sample from Y is Sampling Importance Sampling (SIR). First, we generate a sample from a known distribution, in this case the exponential distribution, since the exponential distribution has the same support as the target distribution:

```
set.seed(1234)
x <- rexp(10000)
# density function of Y</pre>
```

```
edelman <- function(y) {
    fy <- (1 + sqrt(y))/(2 * sqrt(y)) * exp(-(y/2 + sqrt(y)))
    return(fy)
}</pre>
```

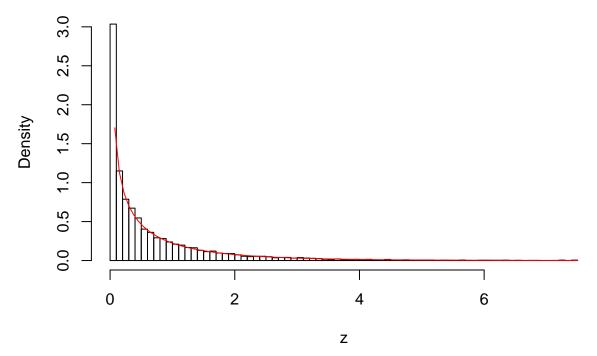
Next, we write a function to compute the importance weight for each value of x generated from the exponential distribution:

```
w <- function(y) {
    wi <- edelman(y)/dexp(y)
    wn <- sum(wi)
    wi <- wi/wn
    return(wi)
}
weights <- w(x)</pre>
```

We use those weights to sample from the values of the exponential distribution, with each weight being the probability that a particular value will be chosen:

```
z <- sample(x, 1e+05, replace = T, prob = weights)
# verify that sampling is correct by comparing histogram with
# true density
hist(z, freq = F, breaks = 100)
curve(edelman, add = T, col = "red")</pre>
```

### Histogram of z



2) To test our method, we estimate E(log(Y)) by simple Monte Carlo. We repeatedly sample the weighted values drawn from the exponential distribution, take the log, and find the mean. This creates an estimated distribution for E(log(Y)), which we use to find the estimated mean and confidence intervals.

```
E <- numeric(1000)
for (i in 1:1000) {
    z <- sample(x, 10000, replace = T, prob = weights)
    h <- log(z)
    E[i] <- mean(h)
}
mean(E)

## [1] -1.684035

CI <- c(quantile(E, 0.005), quantile(E, 0.995))
CI

## 0.5% 99.5%
## -1.741937 -1.630399</pre>
```

Thus, we find that our estimation of E(log(Y)) matches that of Edelman(1988), which was -1.68788.