

Homework 6 Solutions

```
set.seed(0)
```

Problem 1: Inverse Transform Method

Consider the *Cauchy random variable* X with probability density function

$$f_X(x) = \frac{1}{\pi} \frac{1}{(1+x^2)}, \quad -\infty < x < \infty.$$

- (1) [5 points] Let U be a uniform random variable over $[0,1]$. Find a transformation of U that allows you to simulate X from U .

Solution:

First note that

$$\int_{-\infty}^x \frac{1}{\pi} \frac{1}{(1+t^2)} dt = \cdots = \frac{1}{\pi} \arctan(x) + \frac{1}{2}.$$

Then

$$\frac{1}{\pi} \arctan(X) + \frac{1}{2} = U \longrightarrow X = \tan(\pi(U - 1/2))$$

- (2) [5 points] Write a **R** function called **cauchy.sim** that generates n simulated Cauchy random variables. The function should have the single input **n** and should use the inverse-transformation from Part 1. Test your function using 10 draws.

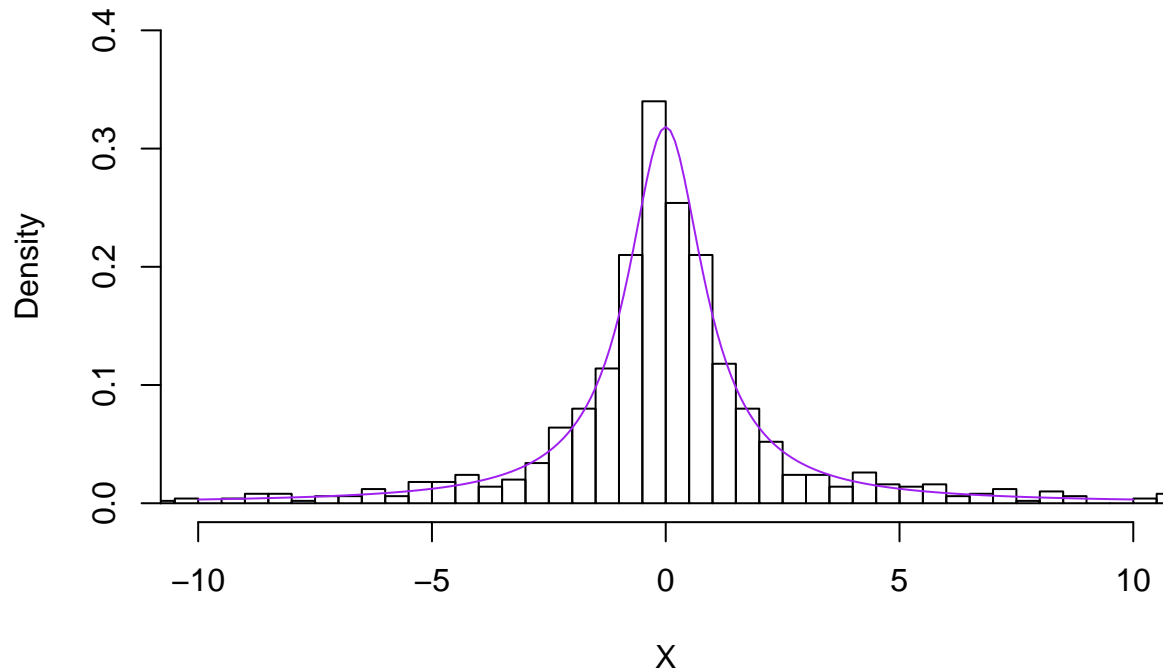
```
cauchy.sim <-function(n) {  
  
  U <- runif(n)  
  return(tan(pi*(U-1/2)))  
  
}  
cauchy.sim(10)
```

```
## [1]  2.9723830 -0.9070131 -0.4248394  0.2329576  3.3710605 -1.3611982  
## [7]  3.0255173  5.6954298  0.5530230  0.4294381
```

- (3) [5 points] Using your function **cauchy.sim**, simulate 1000 random draws from a Cauchy distribution. Store the 1000 draws in the vector **cauchy.draws**. Construct a histogram of the simulated Cauchy random variable with $f_X(x)$ overlaid on the graph. **Note:** when plotting the density curve over the histogram, include the argument **prob = T**.

```
cauchy.draws <- cauchy.sim(1000)  
hist(cauchy.draws,prob = T,main="Cauchy Draws",xlab="X",breaks=10000,xlim=c(-10,10),ylim=c(0,.4))  
x <- seq(-10,10,by=.1)  
lines(x,1/(pi*(1+x^2)),col="purple")
```

Cauchy Draws



Problem 2: Reject-Accept Method

Let random variable X denote the temperature at which a certain chemical reaction takes place. Suppose that X has probability density function

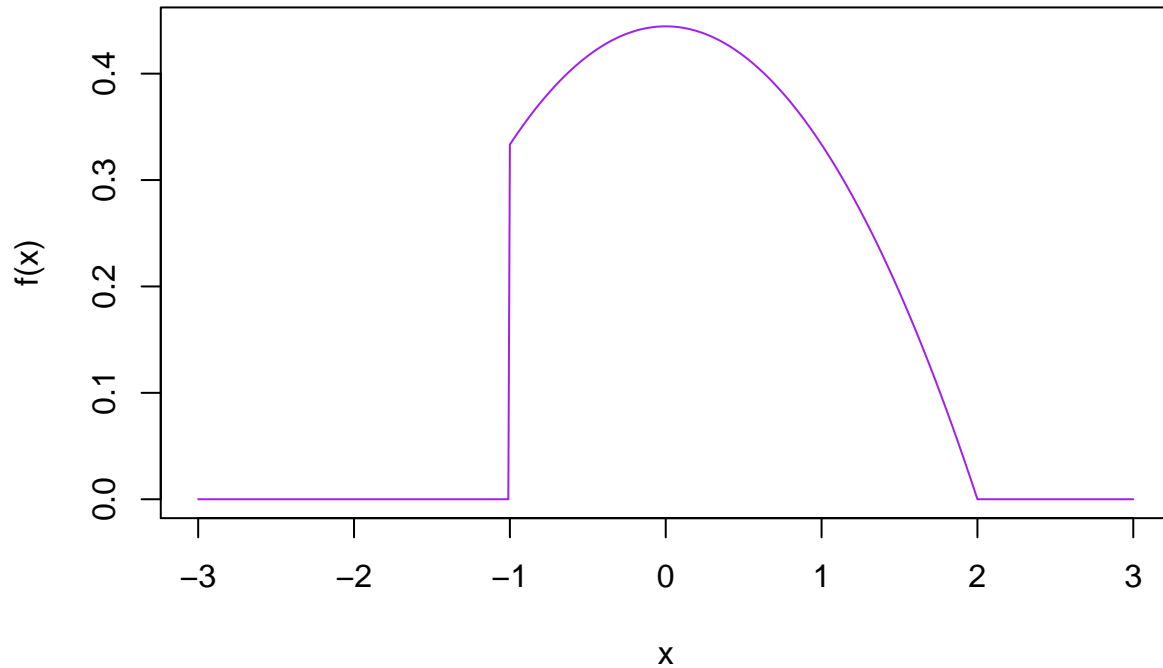
$$f(x) = \begin{cases} \frac{1}{9}(4 - x^2) & -1 \leq x \leq 2 \\ 0 & \text{otherwise} \end{cases}$$

Perform the following tasks:

- (4) [5 points] Write a function `f` that takes as input a vector `x` and returns a vector of `f(x)` values. Plot the function between -3 and 3 . Make sure your plot is labeled appropriately.

```
f <- function(x) {
  ifelse((x < -1 | x > 2), 0, (1/9)*(4 - x^2))
}
x <- seq(-3, 3, by = .01)
plot(x,f(x),main="Target Distribution",ylab="f(x)",type="l",col="purple")
```

Target Distribution



- (5) [5 points] Determine the maximum of $f(x)$ and find an envelope function $e(x)$ by using a uniform density for $g(x)$ and setting $\alpha = 1/\max_x\{f(x)\}$ as in class. Write a function `e` which takes as input a vector `x` and returns a vector of `e(x)` values.

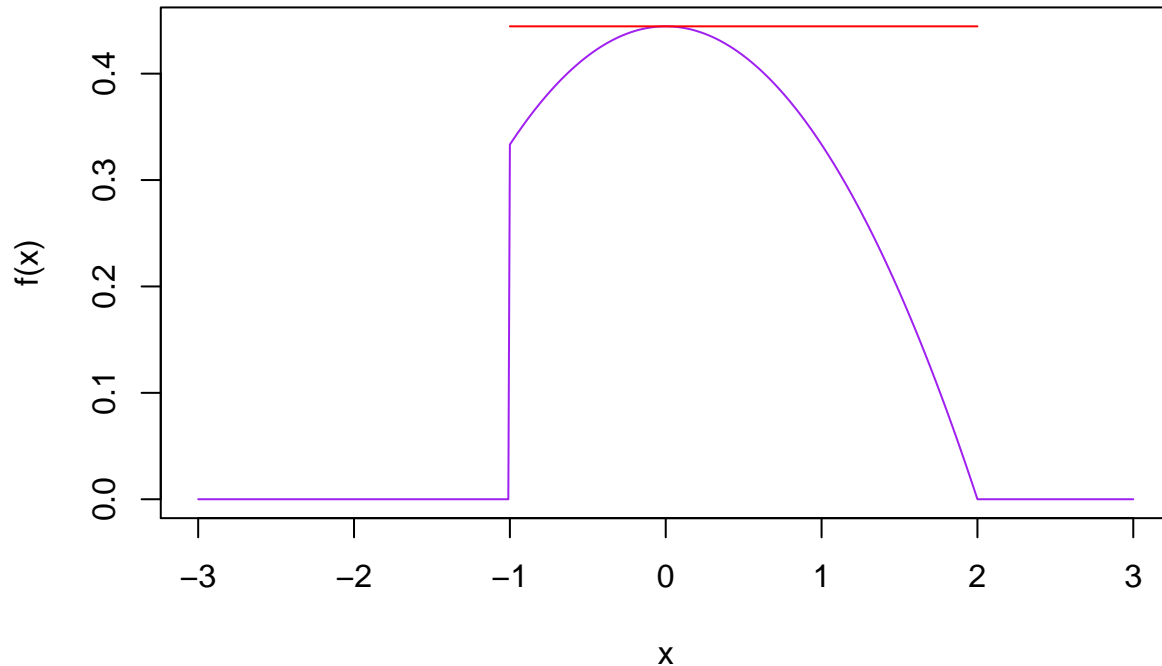
Note that

$$f'(x) = \begin{cases} -\frac{2x}{9} & -1 \leq x \leq 2 \\ 0 & \text{otherwise} \end{cases}$$

Setting the above equal to 0 we find that the maximum occurs at $x = 0$ and $f(0) = 4/9$.

```
f.max <- 4/9
e <- function(x) {
  ifelse((x < -1 | x > 2), Inf, f.max)
}
plot(x,f(x),main="Target Distribution",ylab="f(x)",type="l",col="purple")
lines(x,e(x),col="red")
```

Target Distribution



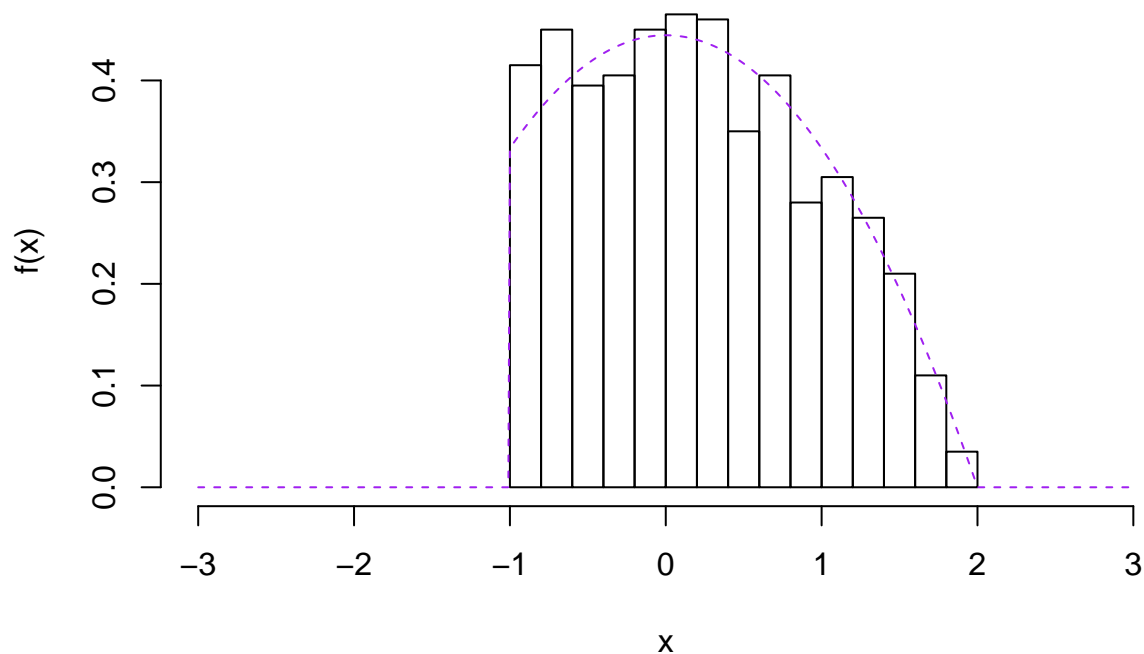
- (6) [5 points] Using the *Accept-Reject Algorithm*, write a program that simulates 1000 draws from the probability density function $f(x)$ from Equation ??.

```
n.samps <- 1000 # Samples desired
n <- 0 # counter for number samples accepted
samps <- numeric(n.samps) # initialize the vector of output
while (n < n.samps) {
  y <- runif(1, min = -1, max = 2) # random draw from g
  u <- runif(1)
  if (u < f(y)/e(y)) {
    n <- n + 1
    samps[n] <- y
  }
}
```

- (7) [5 points] Plot a histogram of your simulated data with the density function f overlaid in the graph. Label your plot appropriately.

```
hist(samps, prob = T, ylab = "f(x)", breaks=20, xlab = "x", main = "Histogram of Reject-Accept Method Dr
lines(x, f(x), lty = 2,col="purple")
```

Histogram of Reject–Accept Method Draws



Problem 3: Reject-Accept Method Continued

Consider the standard normal distribution X with probability density function

$$f(x) = \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{1}{2}x^2\right), \quad -\infty < x < \infty.$$

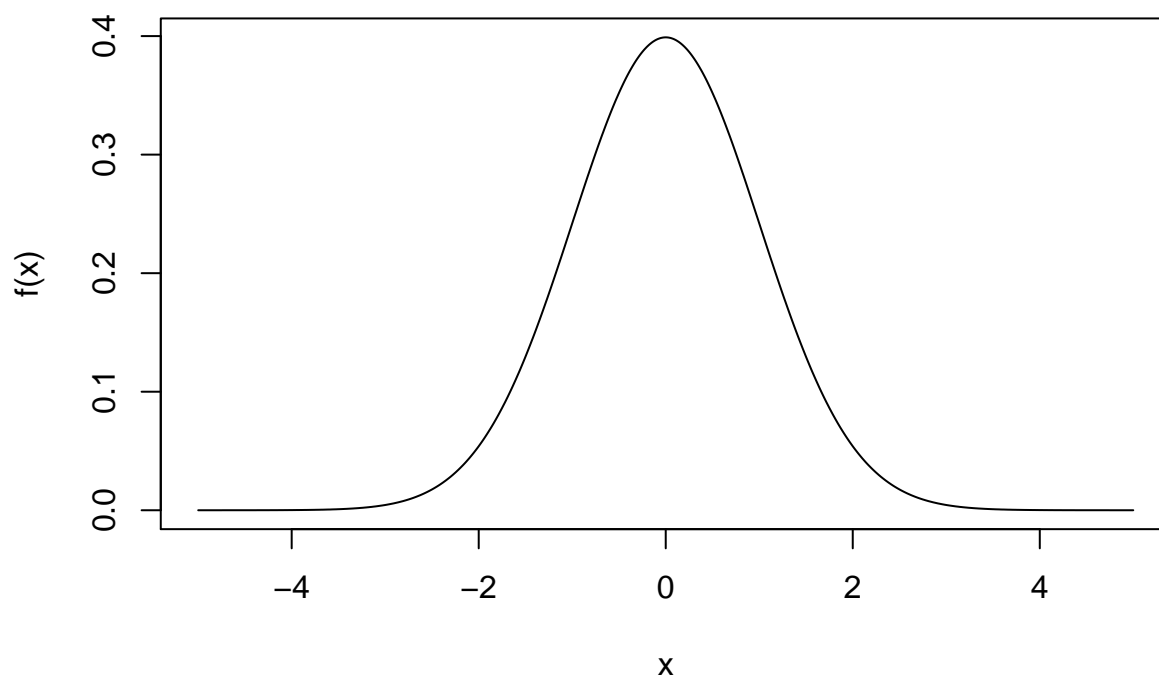
In this exercise, we will write a function named **normal.sim** that simulates a standard normal random variable using the **Accept-Reject Algorithm**.

Perform the following tasks:

- (8) [5 points] Write a function **f** that takes as input a vector **x** and returns a vector of **f(x)** values. Plot the function between -5 and 5 . Make sure your plot is labeled appropriately.

```
f <- function(x) {  
  return(1/sqrt(2*pi)*exp(-x^2/2))  
}  
x <- seq(-5,5,by=.01)  
plot(x,f(x),main="Standard Normal Density",ylab="f(x)",type="l")
```

Standard Normal Density



- (9) [5 points] Let the known density g be the Cauchy density defined by pdf

$$g(x) = \frac{1}{\pi} \frac{1}{(1+x^2)}, \quad -\infty < x < \infty.$$

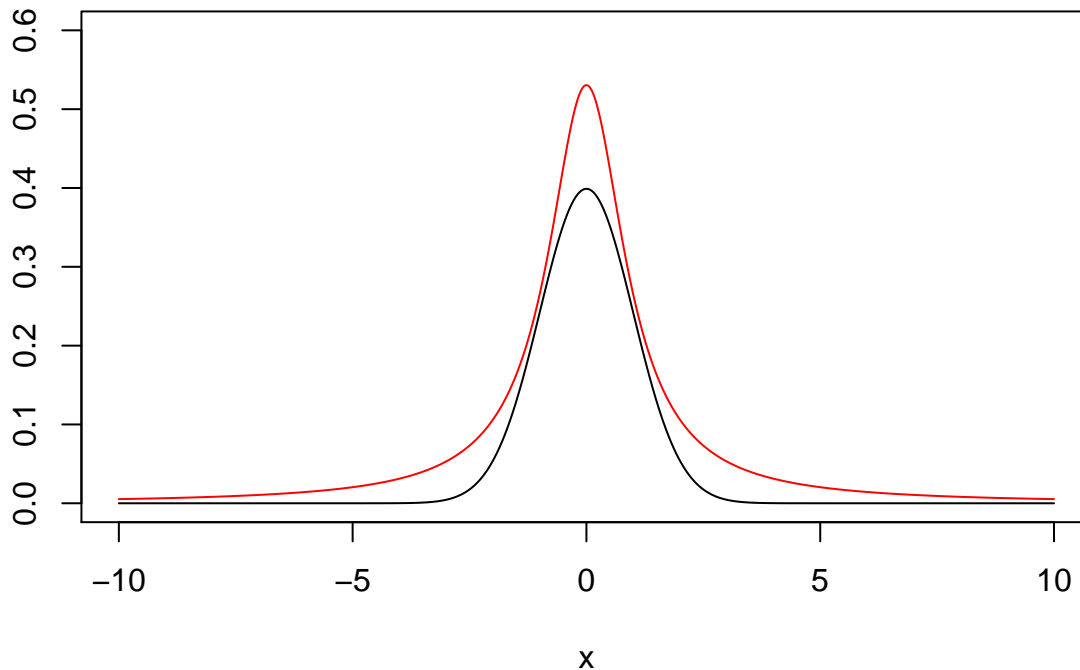
Write a function **e** that takes as input a vector **x** and constant **alpha** ($0 < \alpha < 1$) and returns a vector of **e(x)** values. The envelope function should be defined as $e(x) = g(x)/\alpha$.

```
e <- function(x,alpha=1) {  
  return(1/(alpha*pi*(1+x^2)))  
}
```

- (10) [5 points] Determine a “good” value of α . To show your solution, plot both $f(x)$ and $e(x)$ on the interval $[-10, 10]$.

```
x <- seq(-10,10,by=.01)  
plot(x,f(x),main="Cauchy Envelope Over 5 Standard Normal",ylab="",type="l",ylim=c(0,.60))  
lines(x,e(x,alpha=.60),main="Standard Normal Density",ylab="f(x)",col="red")
```

Cauchy Envelope Over 5 Standard Normal



```
all(f(x)<e(x,alpha=.65))
```

```
## [1] TRUE
```

A “good” value of α is somewhere near .6.

- (11) [5 points] Write a function named **normal.sim** that simulates **n** standard normal random variables using the **Accept-Reject Algorithm**. The function should also use the **Inverse-Transformation** from Part 1. Test your function using **n=10** draws.

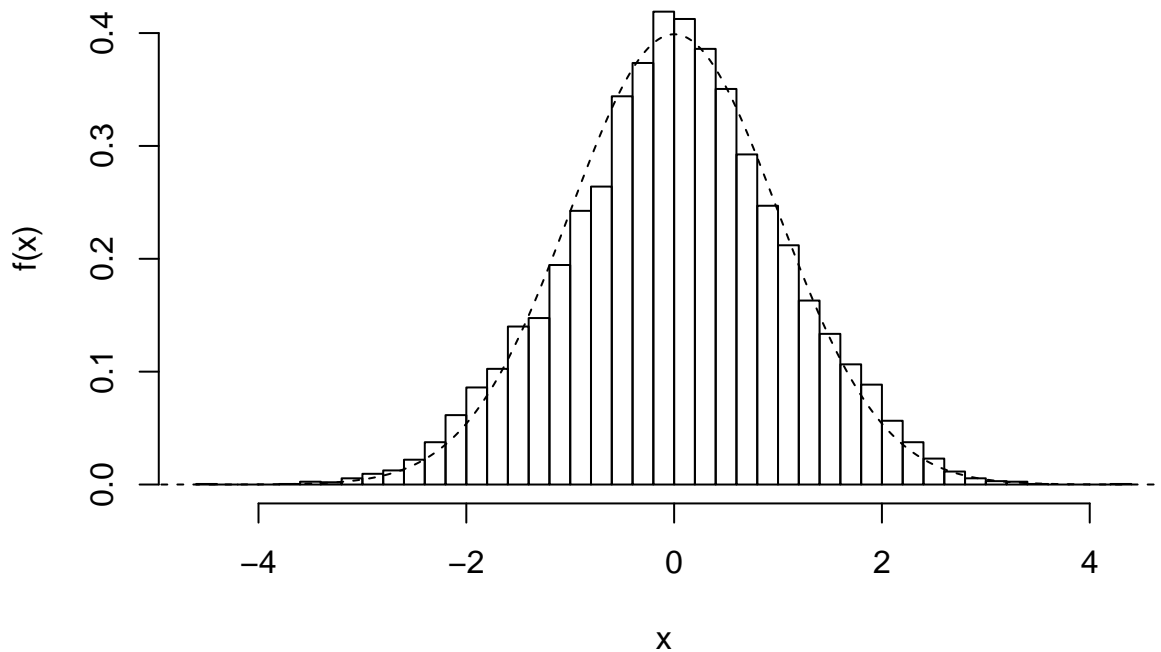
```
normal.sim <- function(n.samps) {
  n      <- 0      # counter for number samples accepted
  samps  <- numeric(n.samps) # initialize the vector of output
  while (n < n.samps) {
    y <- cauchy.sim(1) # random draw from g
    u <- runif(1)
    if (u < f(y)/e(y)) {
      n      <- n + 1
      samps[n] <- y
    }
  }
  return(samps)
}
normal.sim(10)
```

```
## [1] -0.49721504  1.58341903 -0.27305100  0.02052886 -2.38300486
## [6]  2.08639932  0.42237551 -0.96118393 -1.22534003 -1.68994926
```

- (12) [5 points] Using your function **normal.sim**, simulate 10,000 random draws from a standard normal distribution. Store the 10,000 draws in the vector **normal.draws**. Construct a histogram of the simulated standard normal random variable with $f(x)$ overlaid on the graph. **Note:** when plotting the density curve over the histogram, include the argument **prob = T**.

```
normal.draws <- normal.sim(10000)
hist(normal.draws, prob = T, ylab = "f(x)", breaks=50, xlab = "x", main = "Histogram of Reject-Accept Me
lines(x, f(x), lty = 2)
```

Histogram of Reject–Accept Method Draws



Part 3: Simulation with Built-in R Functions

Consider the following “random walk” procedure:

- Start with $x = 5$
- Draw a random number r uniformly between -2 and 1 .
- Replace x with $x + r$
- Stop if $x \leq 0$
- Else repeat

Perform the following tasks:

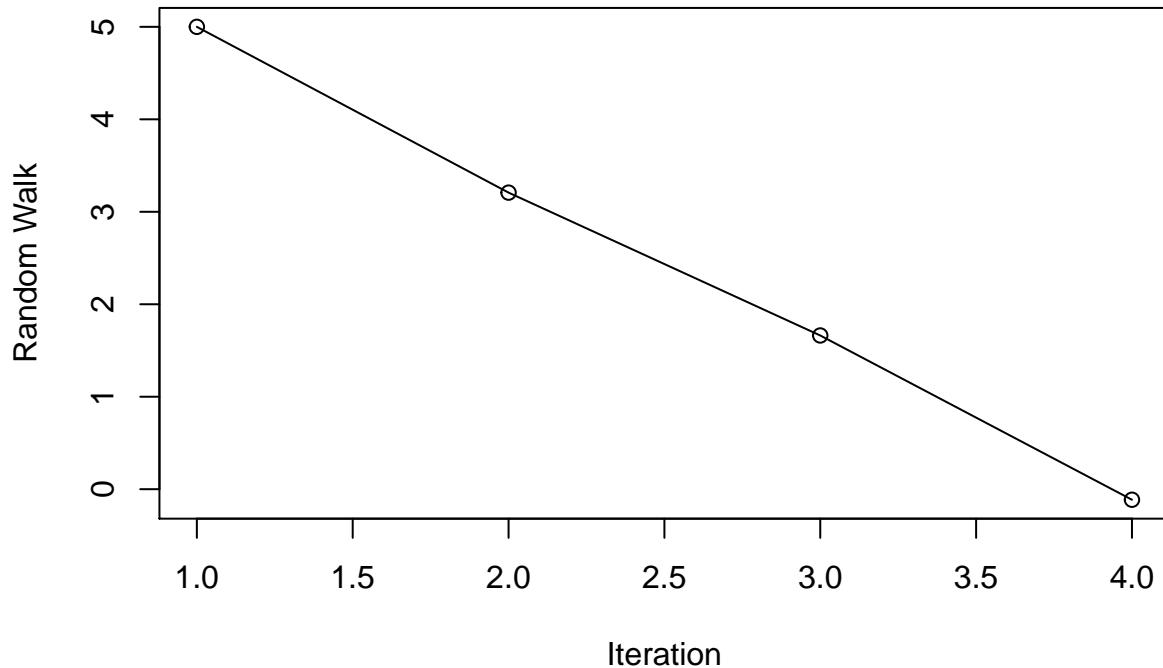
- (13) [5 points] Write a `while()` loop to implement this procedure. Importantly, save all the positive values of x that were visited in this procedure in a vector called `x.vals`, and display its entries.

```
x.vals <- 5
i <- 1
while(x.vals[i] > 0) {
  r <- runif(1, min = -2, max = 1)
  x.vals <- c(x.vals, x.vals[i] + r)
  i <- i+1
}
x.vals

## [1] 5.0000000 3.2071865 1.6623219 -0.1140127
```


- (14) [5 points] Produce a plot of the random walk values `x.vals` from above versus the iteration number. Make sure the plot has an appropriately labeled x-axis and y-axis. Also use `type="o"` so that we can see both points and lines.

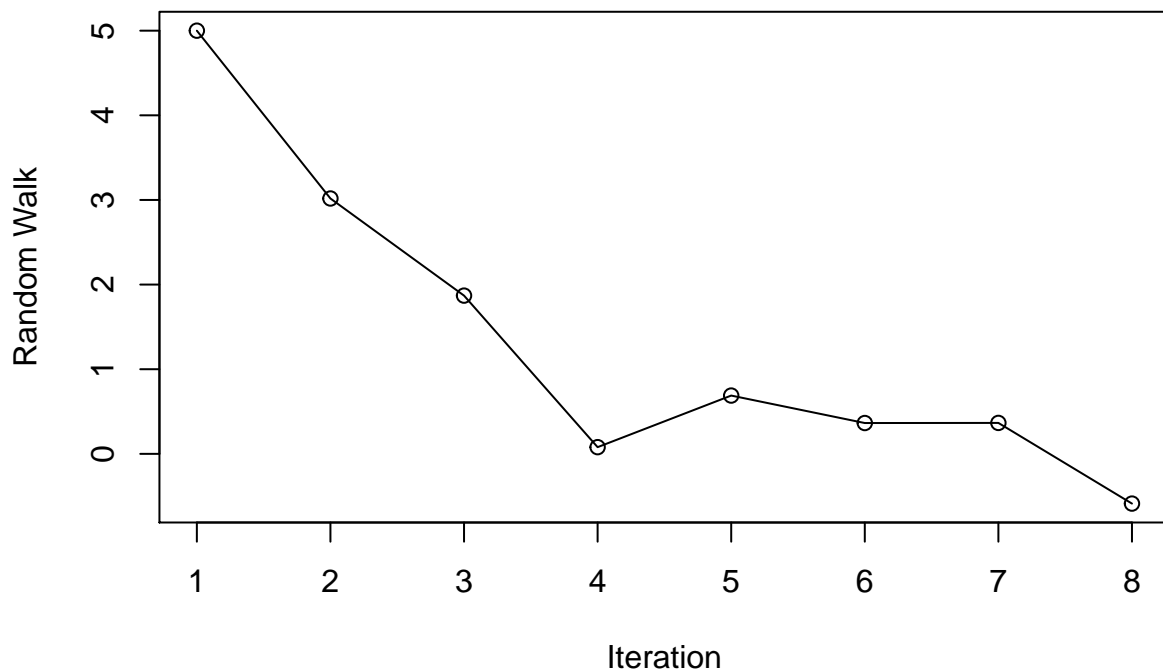
```
plot(1:length(x.vals), x.vals, type = "o", xlab = "Iteration", ylab = "Random Walk")
```



- (15) [5 points] Write a function `random.walk()` to perform the random walk procedure that you implemented in question (9). Its inputs should be: `x.start`, a numeric value at which we will start the random walk, which takes a default value of 5; and `plot.walk`, a boolean value, indicating whether or not we want to produce a plot of the random walk values `x.vals` versus the iteration number as a side effect, which takes a default value of `TRUE`. The output of your function should be a list with elements: `x.vals`, a vector of the random walk values as computed above; and `num.steps`, the number of steps taken by the random walk before terminating. Run your function twice with the default inputs, and then twice with `x.start` equal to 10 and `plot.walk = FALSE`.

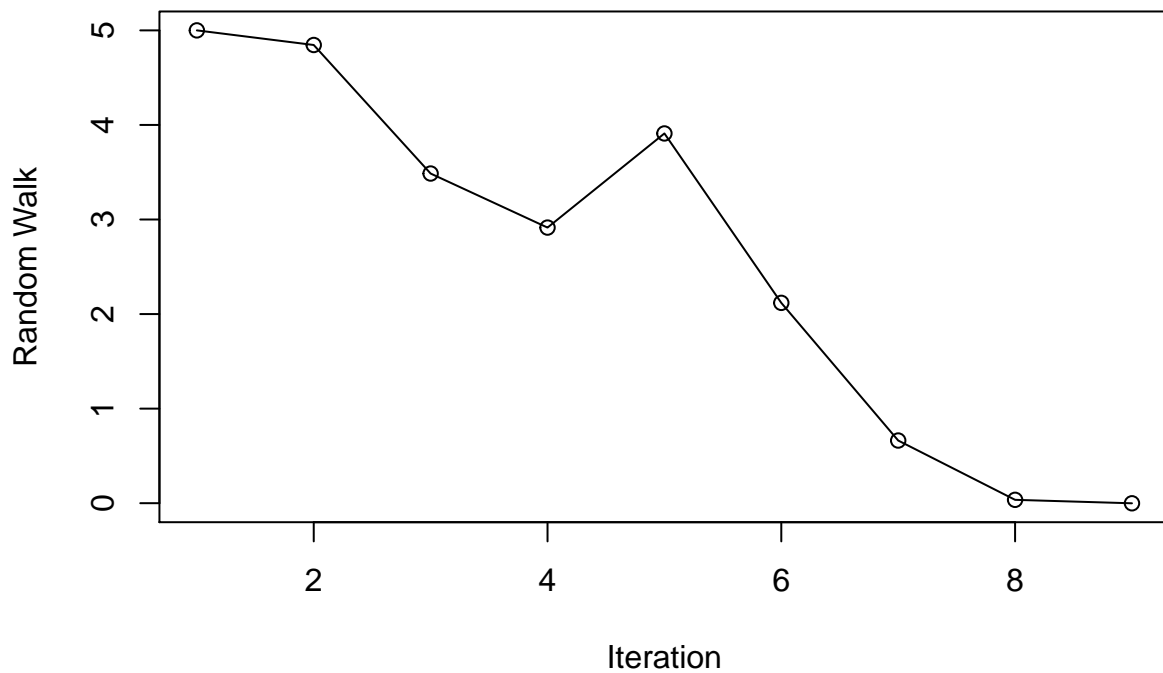
```
random.walk <- function(x.start = 5, plot.walk = TRUE) {
  x.vals <- 5
  i <- 1
  while(all(x.vals[i] > 0)) {
    r <- runif(1, min = -2, max = 1)
    x.vals <- c(x.vals, x.vals[i] + r)
    i <- i+1
  }
  if (plot.walk) {plot(1:length(x.vals), x.vals, type = "o", xlab = "Iteration", ylab = "Random Walk")}
  return(list(x.vals = x.vals, num.steps = i))
}

random.walk()
```



```
## $x.vals
## [1] 5.00000000 3.01735277 1.86972172 0.07893182 0.68878691 0.36417869
## [7] 0.36533533 -0.58770197
##
## $num.steps
## [1] 8
```

```
random.walk()
```



```
## $x.vals
## [1] 5.00000000 4.84542755 3.48611170 2.91467132 3.91003038
## [6] 2.11831721 0.66259682 0.03557377 -0.00109329
```

```
##
## $num.steps
## [1] 9

random.walk(x.start = 10, plot.walk = FALSE)

## $x.vals
## [1] 5.0000000 5.7114786 5.0586144 3.7207443 3.6068736 2.1901089
## [7] 1.9857527 0.6998041 0.9923582 -0.8100799
##
## $num.steps
## [1] 10

random.walk(x.start = 10, plot.walk = FALSE)
```

```
## $x.vals
## [1] 5.0000000 5.0974495 3.5438568 3.0221654 3.6899293 2.6229215
## [7] 3.4740686 2.8401605 1.4167094 0.5729083 -1.2392308
##
## $num.steps
## [1] 11
```

- (16) [5 points] We'd like to answer the following question using simulation: if we start our random walk process, as defined above, at $x = 5$, what is the expected number of iterations we need until it terminates? To estimate the solution produce 10,000 such random walks and calculate the average number of iterations in the 10,000 random walks you produce. You'll want to turn the plot off here.

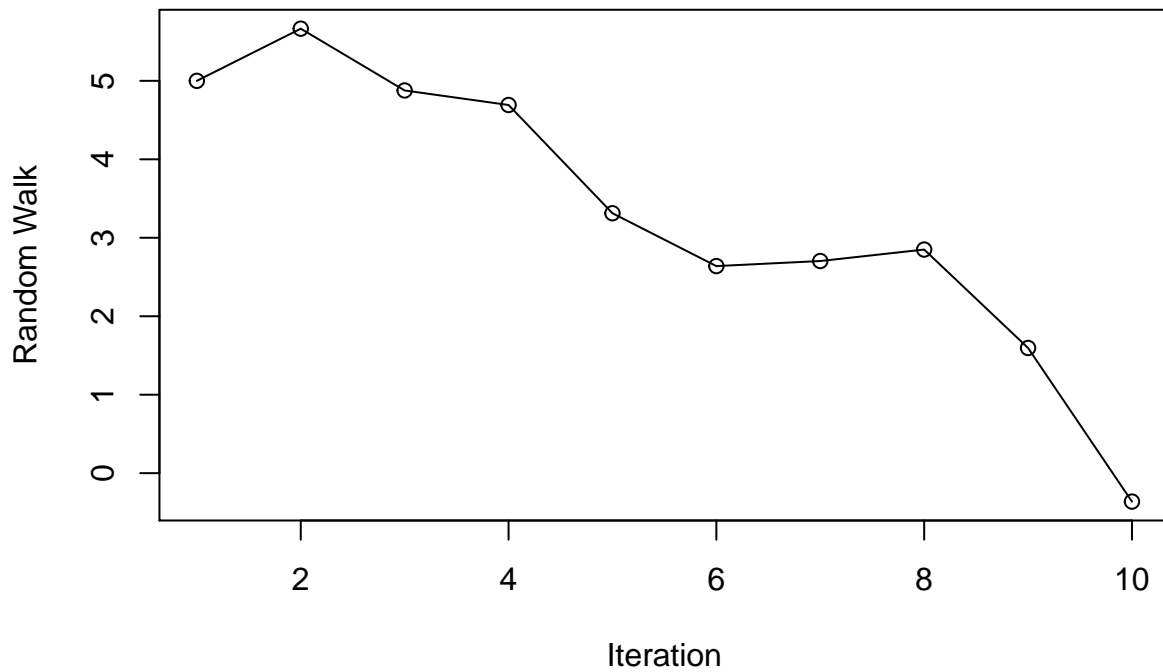
```
n      <- 10000
iters <- rep(NA, n)
for (i in 1:n) {
  iters[i] <- random.walk(plot.walk = FALSE)$num.steps
}
mean(iters)
```

```
## [1] 12.2637
```

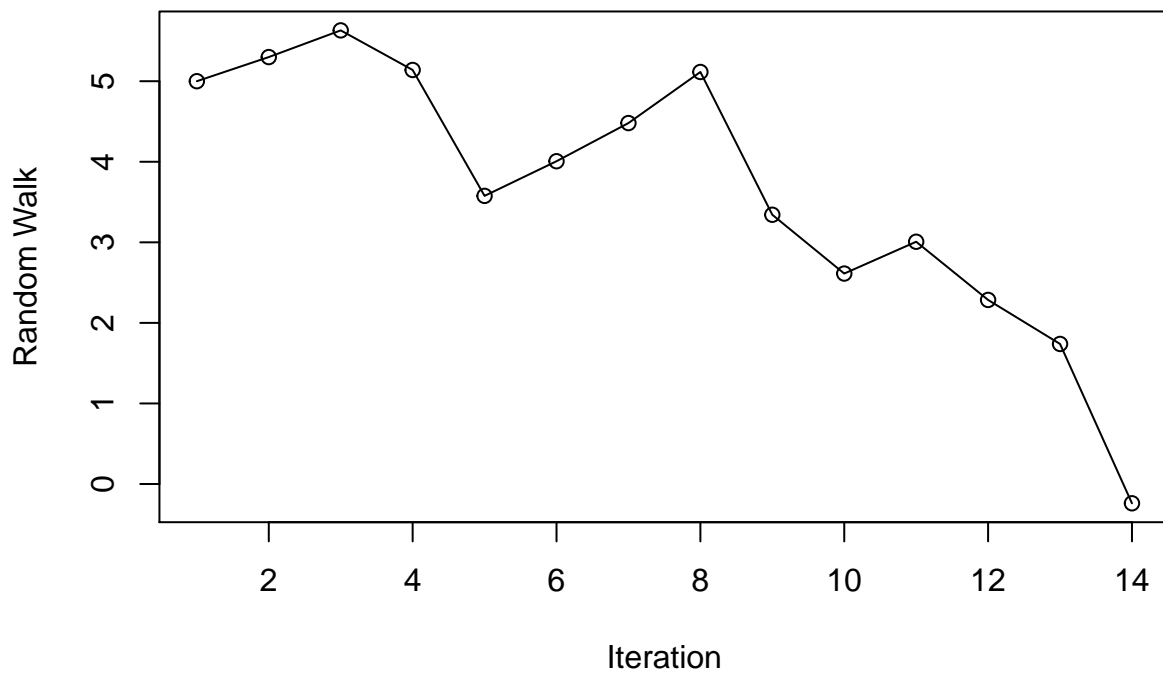
- (17) [5 points] Modify your function `random.walk()` defined previously so that it takes an additional argument `seed`: this is an integer that should be used to set the seed of the random number generator, before the random walk begins, with `set.seed()`. But, if `seed` is `NULL`, the default, then no seed should be set. Run your modified function `random.walk()` function several times with the default inputs, then run it several times with the input seed equal to (say) 33.

```
random.walk <- function(x.start = 5, plot.walk = TRUE, seed = NULL) {
  if (!is.null(seed)) {set.seed(seed)}
  x.vals <- 5
  i <- 1
  while(all(x.vals[i] > 0)) {
    r <- runif(1, min = -2, max = 1)
    x.vals <- c(x.vals, x.vals[i] + r)
    i <- i+1
  }
  if (plot.walk) {plot(1:length(x.vals), x.vals, type = "o", xlab = "Iteration", ylab = "Random Walk")}
  return(list(x.vals = x.vals, num.steps = i))
}

random.walk()
```



```
## $x.vals
## [1] 5.0000000 5.6647497 4.8775822 4.6920773 3.3125890 2.6390292
## [7] 2.7038196 2.8499278 1.5953446 -0.3620453
##
## $num.steps
## [1] 10
random.walk()
```



```
## $x.vals
## [1] 5.0000000 5.2995138 5.6306227 5.1392818 3.5765091 4.0065142
## [7] 4.4803391 5.1143302 3.3420495 2.6121840 3.0073434 2.2848666
```

```
## [13] 1.7385892 -0.2391146
##
## $num.steps
## [1] 14

random.walk(seed = 33, plot.walk = FALSE)

## $x.vals
## [1] 5.0000000 4.3378214 3.5217724 2.9729590 3.7295869 4.2612312
## [7] 3.8132800 3.1246550 2.1542497 0.2008006 -1.4452259
##
## $num.steps
## [1] 11

random.walk(seed = 33, plot.walk = FALSE)

## $x.vals
## [1] 5.0000000 4.3378214 3.5217724 2.9729590 3.7295869 4.2612312
## [7] 3.8132800 3.1246550 2.1542497 0.2008006 -1.4452259
##
## $num.steps
## [1] 11
```

Part 4: Monte Carlo Integration

The goal of this exercise is to estimate the mathematical constant π using **Monte Carlo Integration**. Consider the function

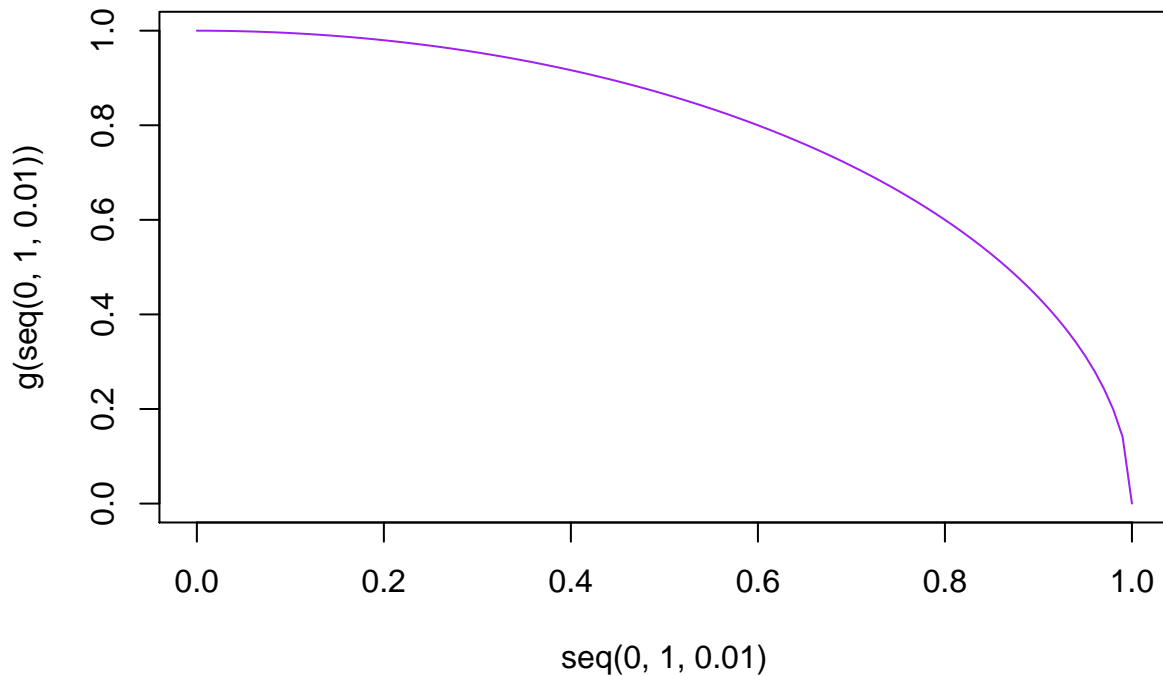
$$g(x) = \begin{cases} \sqrt{1-x^2} & 0 \leq x \leq 1 \\ 0 & \text{otherwise} \end{cases} \quad (1)$$

The above function traces out a quartile circle over the interval $[0, 1]$.

Perform the following tasks:

18) [5 points] Run the following code:

```
g <- function(x) {
  return(sqrt(1-x^2))
}
plot(seq(0,1,.01),g(seq(0,1,.01)),type="l",col="purple")
```



The

above code should produce the plot of a quarter circle.

- 19) [5 points] Identify the true area under the curve $g(x)$ by using simple geometric formulas.

$$\frac{\pi r^2}{4} = \frac{\pi * 1^2}{4} = \frac{\pi}{4}$$

- 20) [5 points] Using **Monte Carlo Integration**, approximate the mathematical constant π within a 1/1000 of the true value. When performing this simulation, make sure to choose a probability density function that has support over the unit interval, i.e. `uniform(0,1)` or `beta(α , β)`.

```
# Choose n=1000^2
X <- runif(1000^2)
pi.est <- mean(4*sqrt(1-X^2))
pi.est
```

```
## [1] 3.142523
```

```
abs(pi-pi.est)
```

```
## [1] 0.0009306794
```

Please submit the knitted .pdf file!