Computational Statistics

Lab 3

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Question 1

1.1

```
pop <- read.csv2("../data/population.csv", encoding = "latin1")
```

1.2

```
cityUnif <- function(data){
    data$prob <- data$Population / sum(data$Population)
    data$cumprob <- cumsum(data$prob)
    return(which.min(data$cumprob < runif(1)))
}
```

1.3

```
n <- 20
rmpop <- pop
selpop <- data.frame()

set.seed(123456)

for (i in 1:n) {
    popidx <- cityUnif(rmpop)
    selpop <- rbind(selpop, rmpop[popidx,])
    rmpop <- rmpop[-popidx,]
}
```

1.4

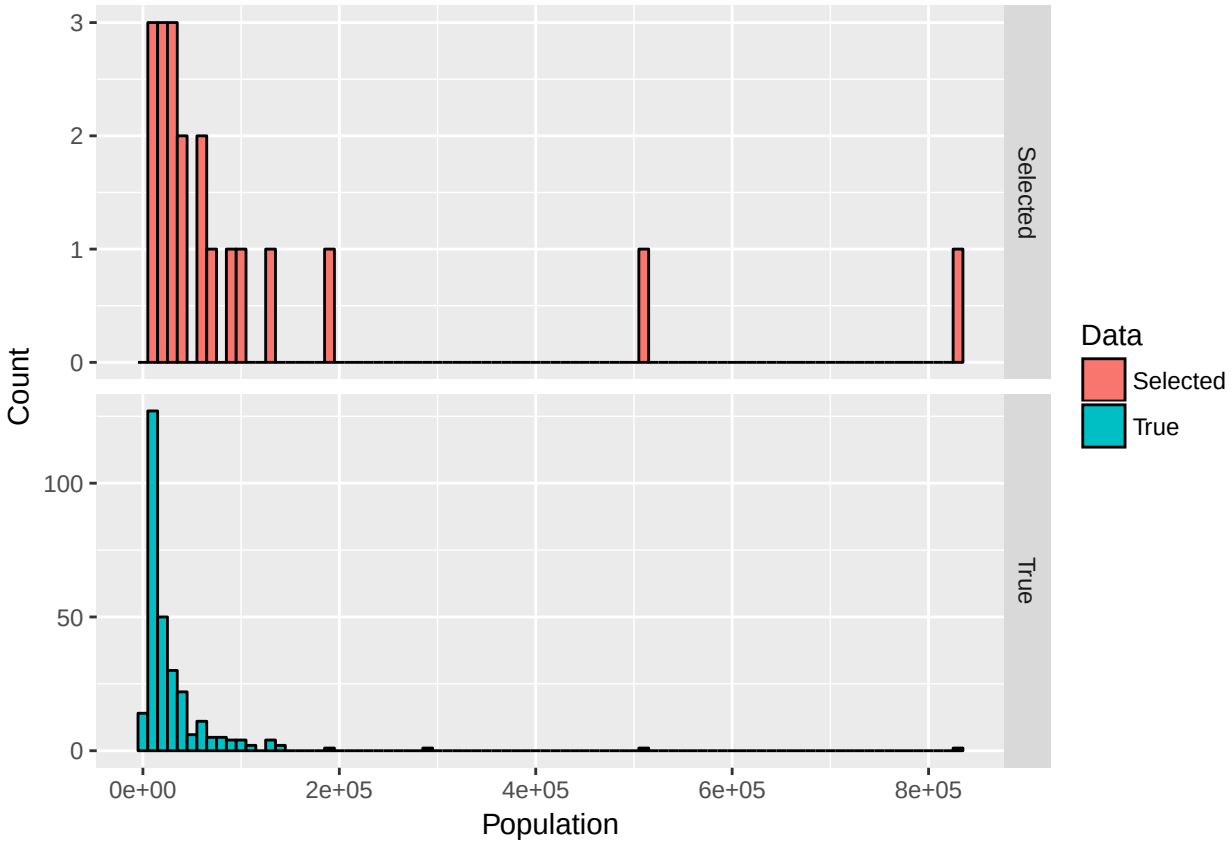
```
print(paste(as.character(selpop$Municipality), ":", selpop$Population))
```

```
##  [1] "Karlskoga : 29742"    "Ulricehamn : 22753"   "Kalmar : 62388"
##  [4] "Jönköping : 126331"   "Ljungby : 27410"      "Täby : 63014"
##  [7] "Trelleborg : 41891"   "Stockholm : 829417"   "Luleå : 73950"
## [10] "Uppsala : 194751"     "Fagersta : 12249"     "Göteborg : 507330"
## [13] "Sundsvall : 95533"    "Gävle : 94352"        "Piteå : 40860"
## [16] "Ovanåker : 11530"     "Smedjebacken : 10758" "Katrineholm : 32303"
## [19] "Nybro : 19576"        "Hallsberg : 15235"
```

As seen in the output above, we in general select cities with large populations. This is logical since the selection of cities is based on the population thus making it more likely to pick larger cities.

1.5

```
library(ggplot2)

true_pop <- data.frame(pop=pop$Population)
picked_pop <- data.frame(pop=selpop$Population)

true_pop$data <- "True"
picked_pop$data <- "Selected"

plot_data <- rbind(true_pop, picked_pop)

ggplot(plot_data, aes(pop, fill=data)) +
    geom_histogram(color="black", binwidth=10000) +
    facet_grid(data ~ ., scales="free_y") +
    xlab("Population") + ylab("Count") +
    labs(fill="Data")
```



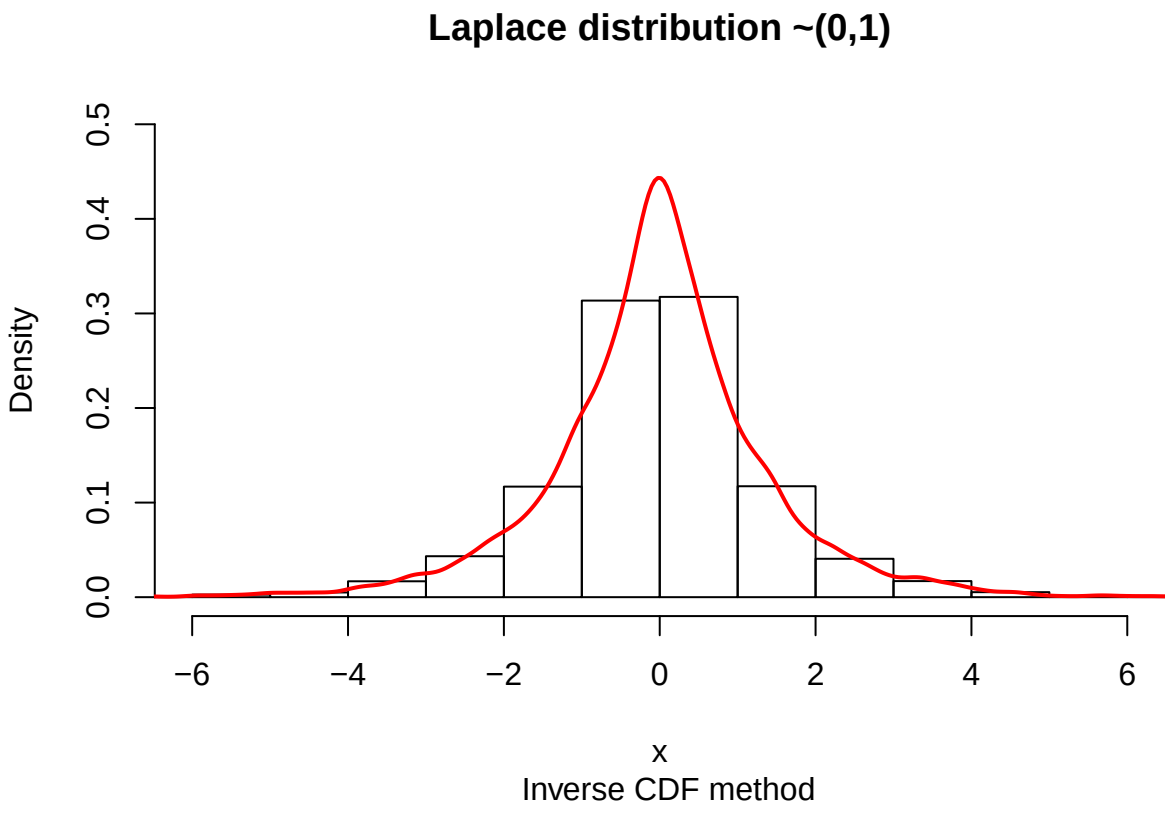
In the histograms above the width of a staple is 10000 and we can see that in the data set most cities are $\leq$ 50000 in population and the cities we selected are all over the place in terms of size. We can see that there are only a few cities that are very large and most of those are selected as we would expect and a approximately half of the selected are mid-sized cities due to the frequency of those.

Question 2

2.1

```
invLap <- function(){
    rng <- runif(1)

    if(rng > 0.5) {
        return(-log(2 - 2 * rng) )
    } else {
        return(log(2 * rng))
    }
}
```

```
plotdata <- sapply(1:10000,FUN = function(x) invLap())

hist(plotdata, prob = TRUE, ylim = c(0,0.5), xlim = c(-6,6),
     xlab = "x", main = "Laplace distribution ~(0,1)",
     sub = "  Inverse CDF method", breaks = 20)
lines(density(plotdata), col = "red", lwd = 2)
```



Yes, the histogram and the density-curve we included seems reasonable compared to the normal shape of a Laplace distribution.

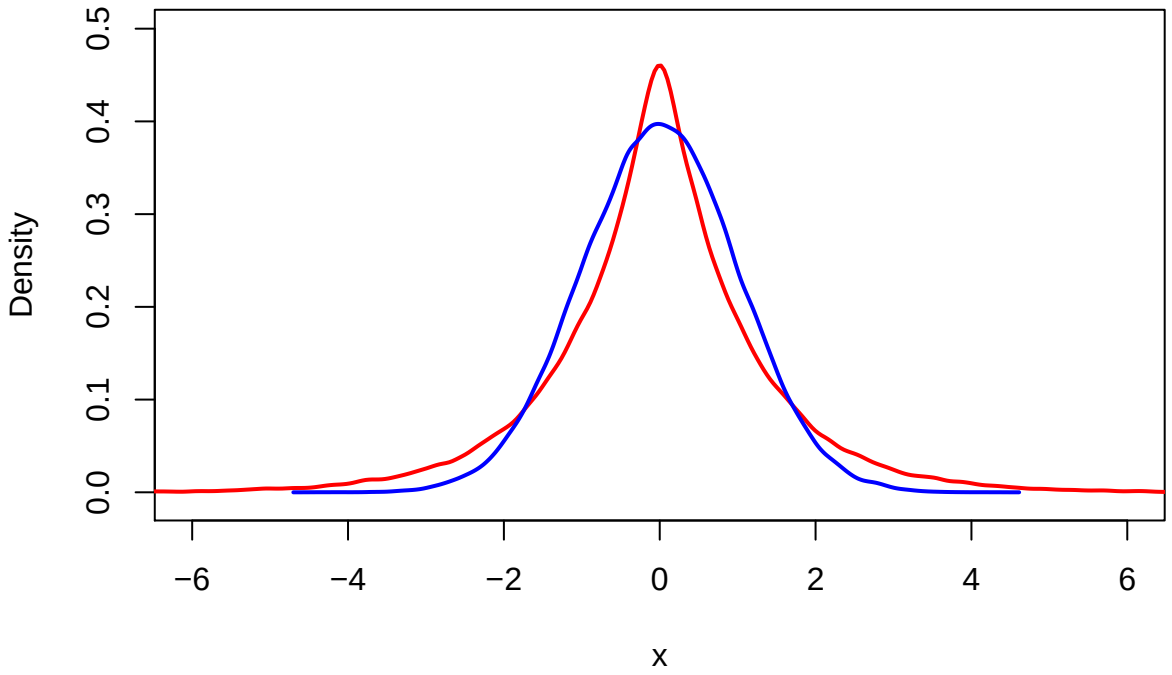
2.2

```
DE01 <- function(x) {
    (1 / 2) * exp(-abs(x))
}

ar <- function(c) {
  rej <- 0

  generated <- FALSE
  x <- c()

  while(!generated){
      y <- invLap() # Y ~ f_y
      u <- runif(1) # U(0,1)

      fx <- dnorm(y, mean = 0, sd = 1) # fx(y)
      fy <- DE01(y) #f_y

      if(u < fx / (c * fy)){
          return(c(y, rej))  #alt. set x <- y and generated = TRUE, to end the loop
      }

      rej <- rej + 1
  }
}
```

Here is our function.

Choosing the appropriate c

```
set.seed(123456)
n <- 100000
lap <- sapply(1:n,FUN = function(x) invLap())
nor <- rnorm(n, 0, 1)

plot(x = 0, y = 0, col ="white", xlim = c(-6,6),
     ylim = c(-0.01, 0.5), xlab = "x",
     ylab = "Density" )
lines(density(lap), col = "red", lwd = 2)
lines(density(nor), col = "blue", lwd = 2)
```



Our approach for approximating c was to try to make a laplace-curve that would as much as possible cover the whole density-curve for the normal distribution.

For x $>$ 0 since it is symmetric

$cf_y(x) - f_x(x) = 0$

$c/2e^{-x} - 1/(\sqrt{2\pi})e^{-x^2/2} = 0$

$log(c/2) - x - log(1/(\sqrt{2\pi})) + x^2/2 = 0$

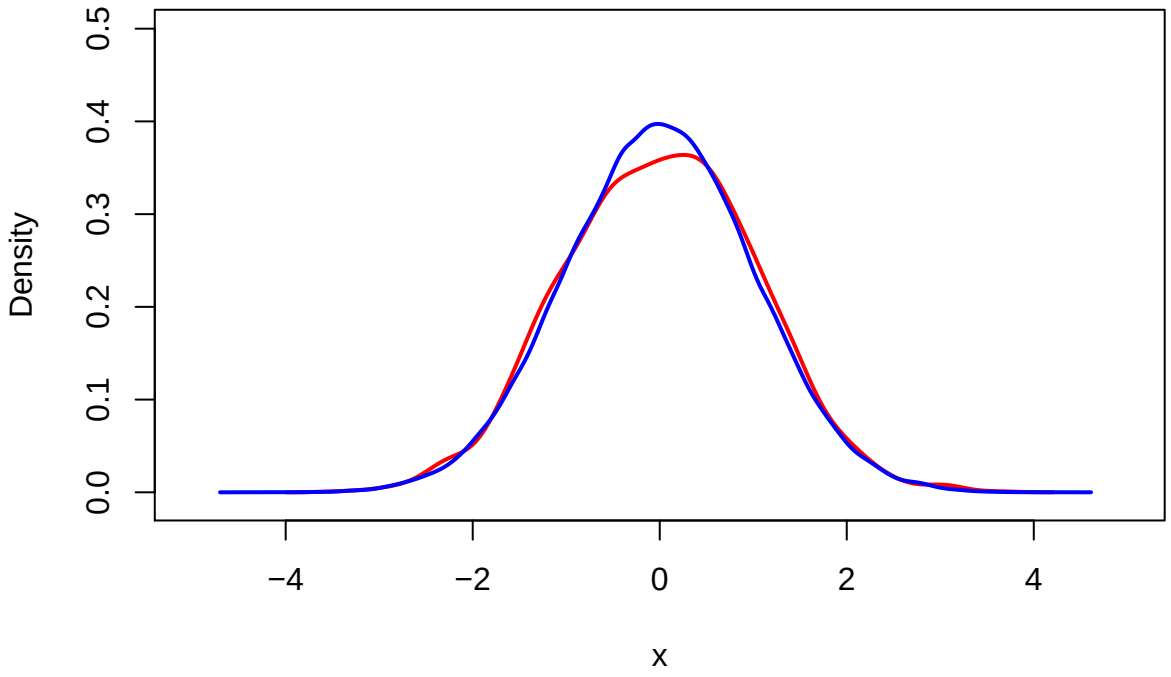
after some equation-solving we come to the solution

$c = 1.315$

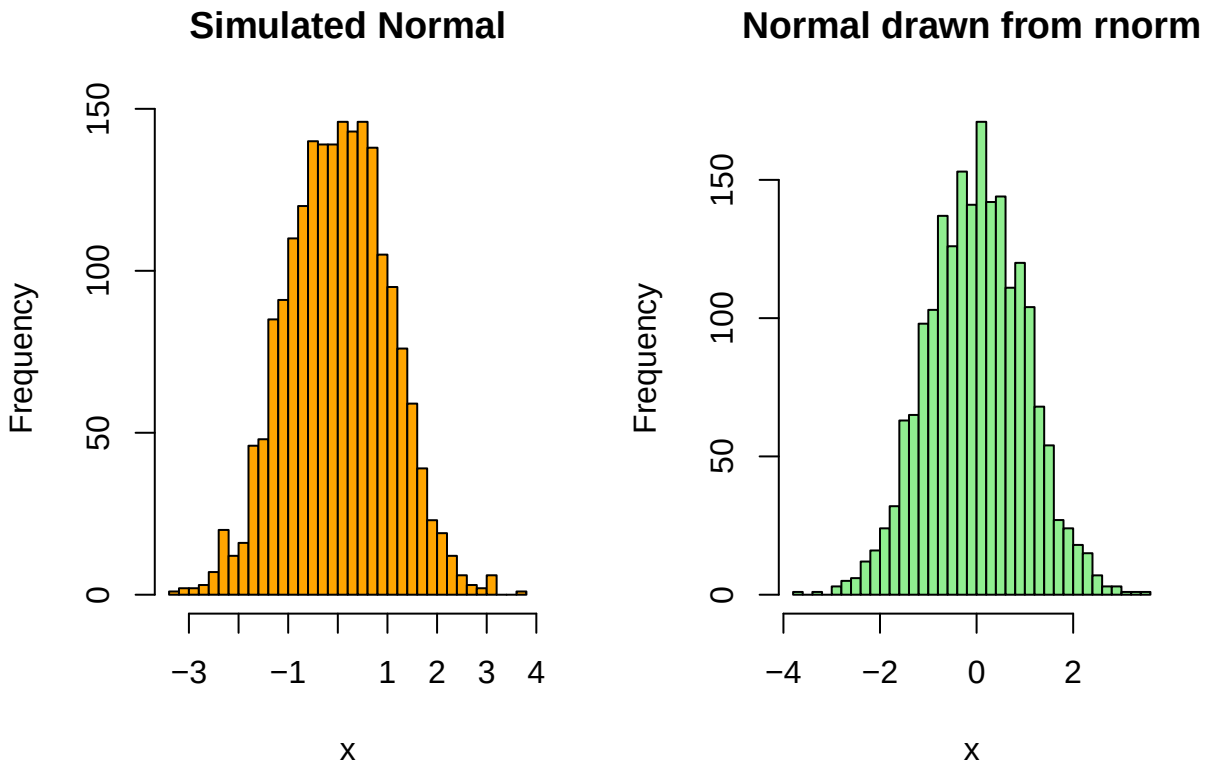
Simulation and comparison

```
ARsim <- data.frame(rn = 1, rej = 1)
c <- 1.32

for(i in 1:2000){
    ARsim[i,] <- ar(c=c)
}
```

```
plot(x = 0, y = 0, col ="white", xlim = c(-5,5),
     ylim = c(-0.01,0.5), xlab = "x", ylab = "Density" )
lines(density(ARsim$rn), col="red", lwd=2)
lines(density(nor), col="blue", lwd=2)
```




```
par(mfrow = c(1,2))
hist(ARsim$rn, main = "Simulated Normal", xlab = "x",
     col = "orange",  breaks = 30)

set.seed(123456)
hist(rnorm(2000,0,1), main = "Normal drawn from rnorm", xlab = "x",
     col = "lightgreen", breaks = 30 )
```



The simulated one is a bit more rough around the edges and more narrow in the center in comparison to the

histogram drawn from the rnorm.

The expected rejection rate is $\frac{n(M-1)}{nM}$ since the expected number of iterations before a accepted value is M so intuitively the number of rejections is $M-1$. n here is only the number of values that we use, but these cancel each other out so they are not necessary but we left them here for clarity. The theoretical rejection rate would be 0.242 and what we empirically found was 0.262 which is reasonably close.