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

```
rmpop <- pop

set.seed(123456)
while(nrow(rmpop) > 20){

  rmpop <- rmpop[-cityUnif(rmpop),]

}
```

1.4

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

```
##  [1] "Vingåker : 8911"        "Ydre : 3672"
##  [3] "Aneby : 6446"           "Borgholm : 10806"
##  [5] "Dals-Ed : 4729"         "Grästorp : 5857"
##  [7] "Gullspång : 5335"       "Hjo : 8859"
##  [9] "Strömstad : 11690"      "Hällefors : 7333"
## [11] "Ljusnarsberg : 5055"    "Skinnskatteberg : 4567"
## [13] "Rättvik : 10797"        "Bräcke : 6865"
## [15] "Dorotea : 2900"         "Vilhelmina : 7156"
```

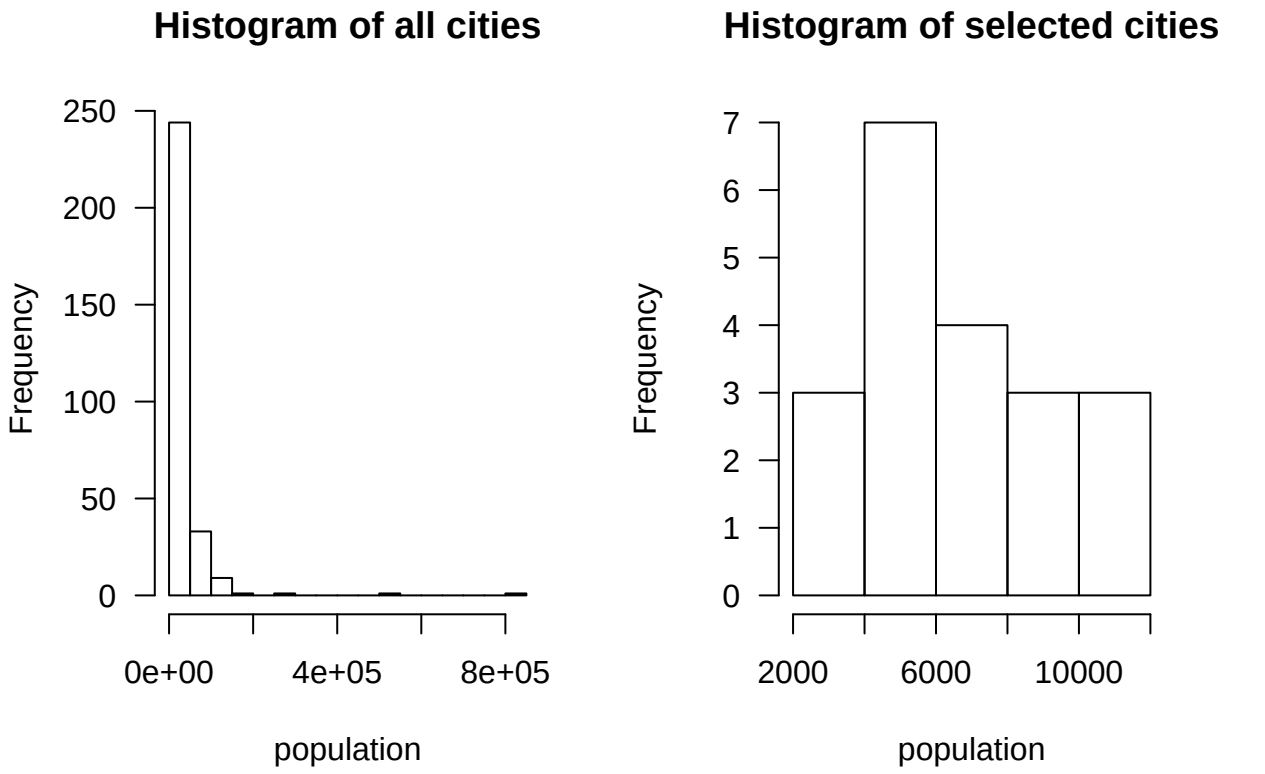
```
## [17] "Arjeplog : 3143"        "Jokkmokk : 5210"
## [19] "Älvsbyn : 8387"         "Övertorneå : 4920"
```

As seen in the output above, we in general select cities with small populations.

1.5

```
par(mfrow = c(1,2))

hist(pop$Population, main = "Histogram of all cities", xlab = "population", las = 1, breaks = 20)
hist(rmpop$Population, main = "Histogram of selected cities", xlab = "population", las = 1)
```




```
par(mfrow = c(1,1))
```

It selects cities with low population, it seems resonable given the large number of cities with small populations.

Question 2

2.1

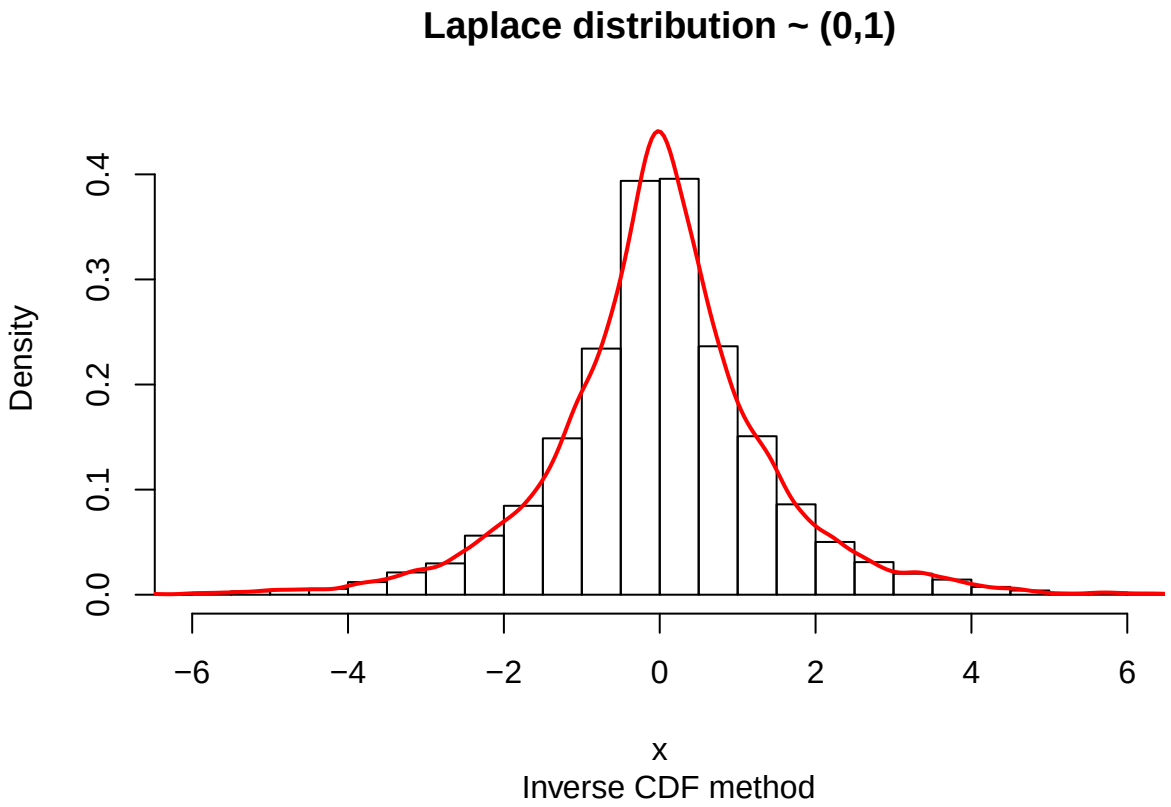
```
invLap <- function(){
rng <- runif(1)

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(0,0.45) , xlim = c(-6,6) , xlab = "x", main = "Laplace distributio
lines( density(plotdata), col = "red", lwd = 2)
```



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

2.2

```
ar <- function(c) {

  rej <- 0

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

     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 <- DE(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.

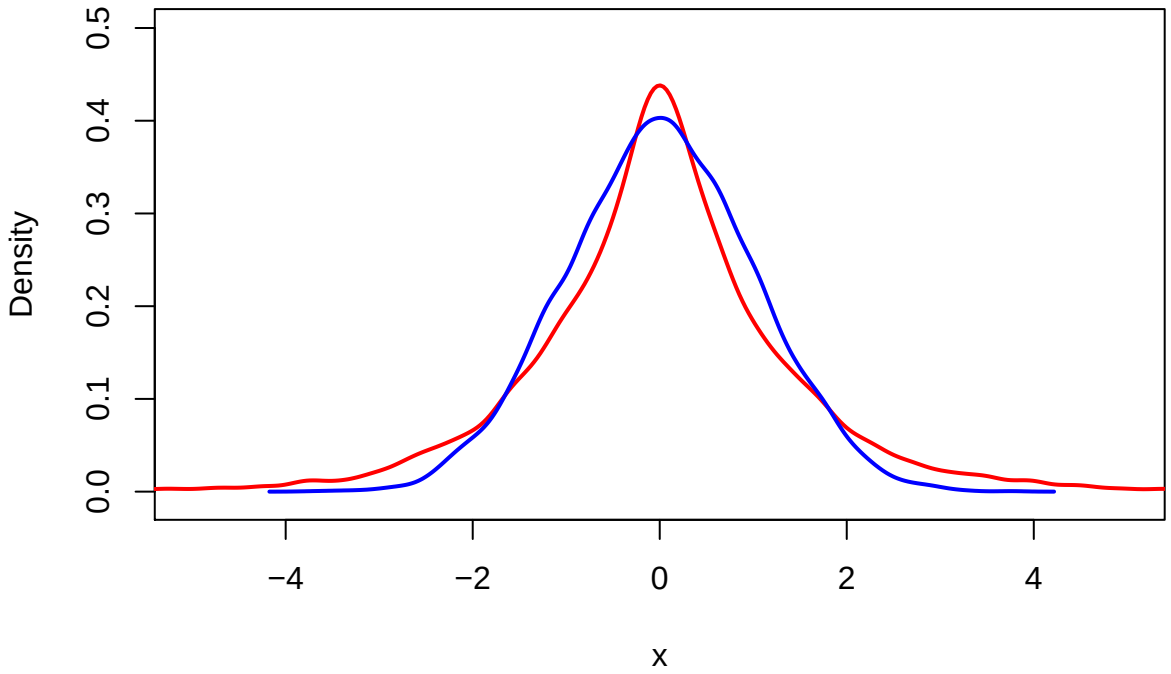
Choosing the appropriate c

```
plot(x = 0, y = 0, col ="white", xlim = c(-5,5), ylim = c(-0.01,0.5), xlab = "x",
     ylab = "Density" )

lap <- sapply(1:10000,FUN = function(x) invLap() )
lines( density(lap), col = "red", lwd = 2)

nor <- rnorm(10000,0,1)

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 normaldistribution.

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 soloution

$c = 1.315$

Simulation and comparison

```
ARsim <- data.frame(rn = 1, rej = 1)
for(i in 1:2000){

  ARsim[i,] <- ar(c = 1.315)

}
mean(ARsim$rej)
```

```
## [1] 0.32
```

```
mean(ARsim$rej /(ARsim$rej + 1))
```

```
## [1] 0.1298194
```

```
sum(ARsim$rej)/(sum(ARsim$rej)+2000)
```

```
## [1] 0.2424242
```

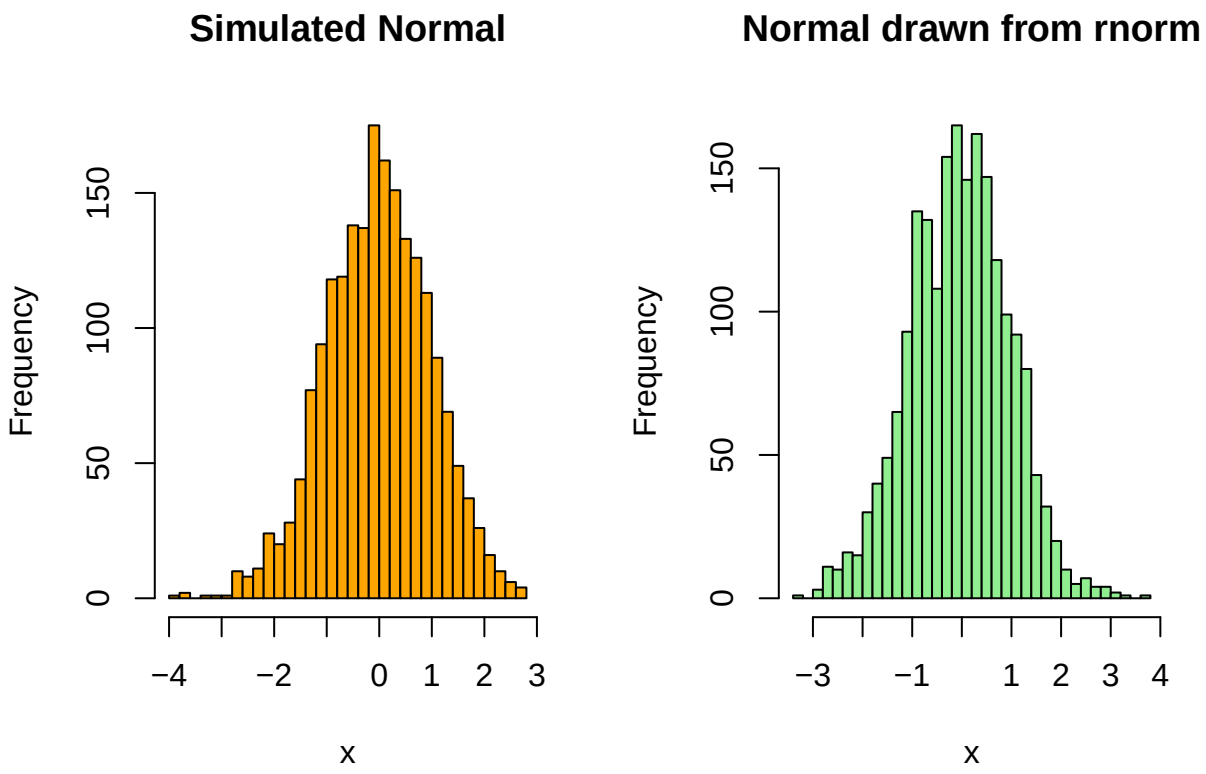
```
max(ARsim$rej)
```

```
## [1] 8
```

```
par(mfrow = c(1,2))

hist(ARsim$rn, main = "Simulated Normal", xlab = "x",
     col = "orange",  breaks = 30)

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




```
par(mfrow = c(1,1))
```

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 average rejection rate is $\frac{n(M-1)}{nM}$ since the expected number of itterations before a accepted value is M so intutively the number of rejections is $M-1$. n here is only the number of values that we use, but these cancle eachother out so they are not neccesary but we left them here for clarity.