Computational Statistics

Lab 5

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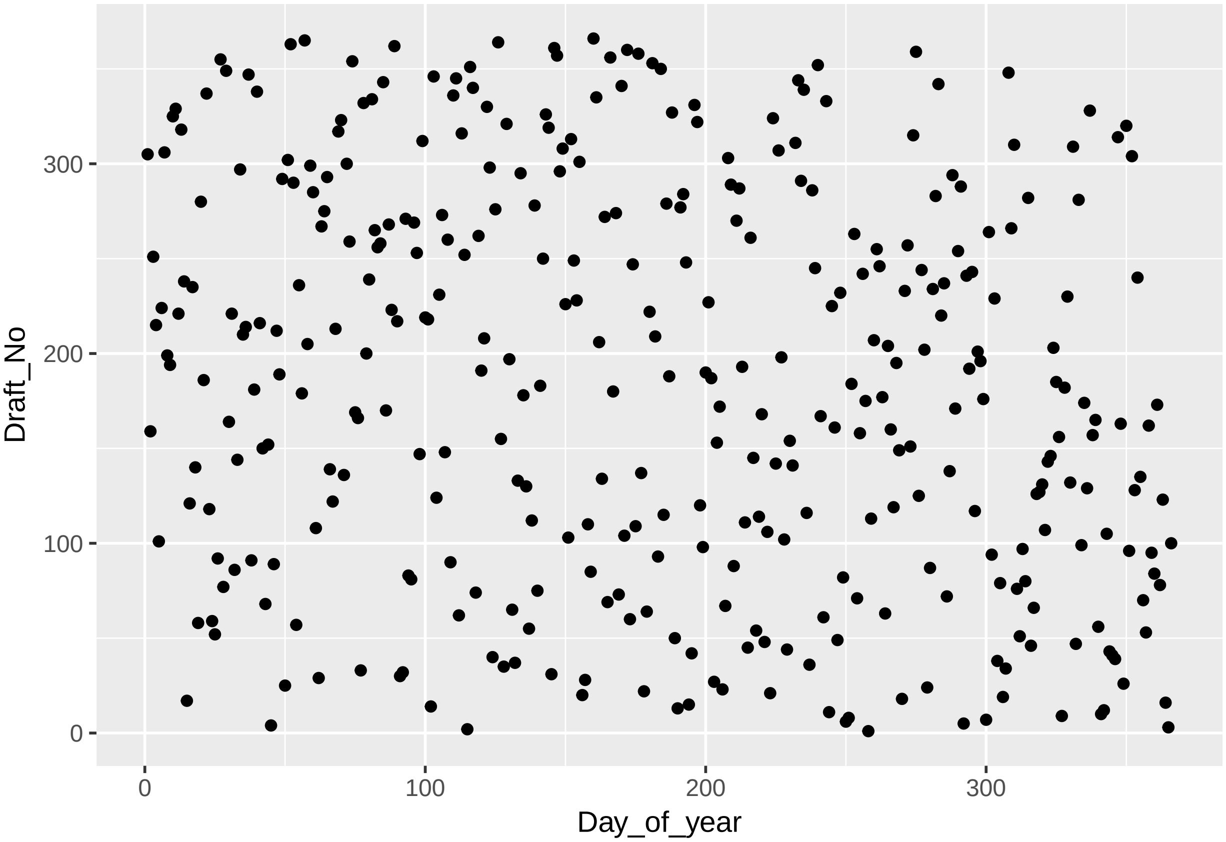
Question 1

1.1

```r
library(ggplot2)

lottery <- read.csv2("../data/lottery.csv")

q11 <- ggplot(lottery, aes(x = Day_of_year, y = Draft_No)) + geom_point()
plot(q11)
```



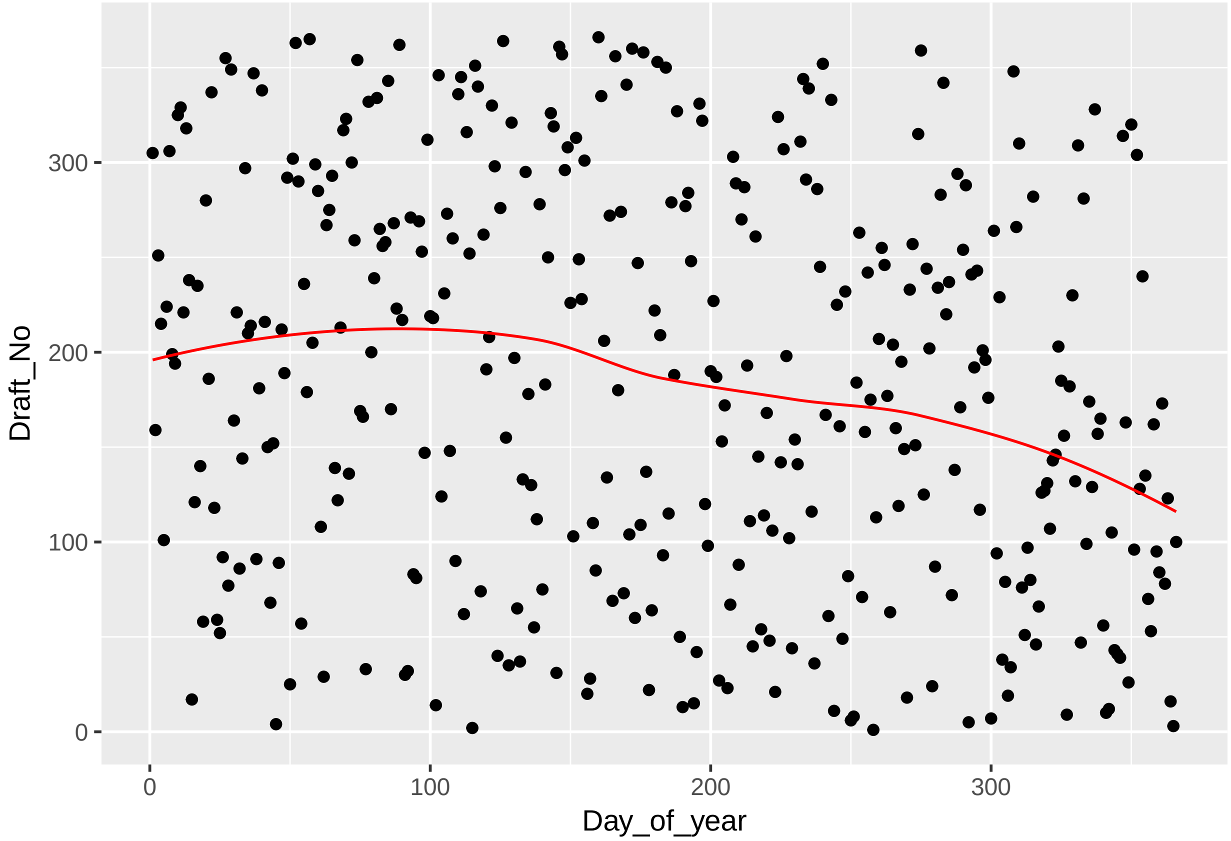
```r
data <- data.frame(x=lottery$Day_of_year, y=lottery$Draft_No)
```

The data looks random although there might be some sort of skewness in the right side of the graph were there are a lacking some observations and therefore having a lower probability of getting selected.

1.2

```
loessfit <- loess(y ~ x, data=data)
data$pred <- predict(loessfit, data$x)

q12 <- q11 + geom_path(data = data, aes(x=x, y=pred), col = "red")
plot(q12)
```



The fit (line) doesn't seem straight and seems to have a decreasing trend which would support previous statements of people born on a days later on in a year has a lower probability of beeing selected.

1.3

```
teststat <- function(model) {
    function(data) {
        xa <- data$x[which.min(data$y)]
        xb <- data$x[which.max(data$y)]

        fit <- model(y ~ x, data)

        ya <- predict(fit, xa)
        yb <- predict(fit, xb)

        (yb - ya) / (xb - xa)
    }
}

teststat_boot <- function(data, idx, stat) {
    data <- data[idx,]
    stat(data)
}
```

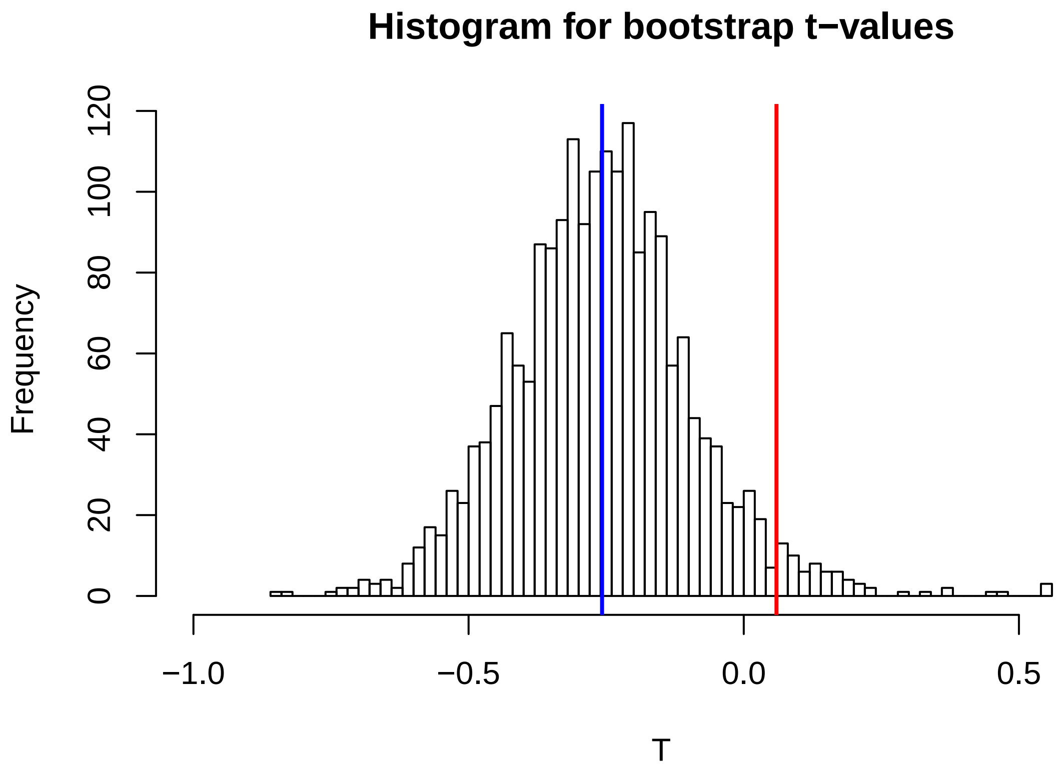
```
library(boot)

B <- 2000

set.seed(123456)
npboot <- boot(data=data, statistic=teststat_boot, R=B, stat=teststat(model=loess))
pvalue <- sum(npboot$t > 0) / B
pvalue
```

```
## [1] 0.059
```

```
hist(npboot$t, xlim = c(-1,0.7), breaks = 50,
     main = "Histogram for bootstrap t-values", xlab ="T")
abline(v=pvalue, col = "red", lwd = 2)
abline(v=mean(npboot$t), col="blue", lwd=2)
```



The p-value was calculated to 0.06 and we can't reject the nullhypothesis at a 0.05 alpha-level. We conclude Ho and that the lottery is random.

1.4

```r
teststat_permutation<- function(data, B, stat) {
    n <- nrow(data)
    statistics <- rep(0, B)
    newdata <- data.frame(x=data$x, y=sample(data$y, n))

    for (b in 1:B) {
        statistics[b] <- stat(newdata)
        newdata$y <- sample(data$y, n)
    }

    sum(abs(statistics) >= abs(stat(data))) / B
}

set.seed(123456)
pvalue2 <- teststat_permutation(data, B, teststat(loess))
pvalue2
```

```
## [1] 0.092
```

We conclude Ho in this test as well, the lottery is random.

1.5

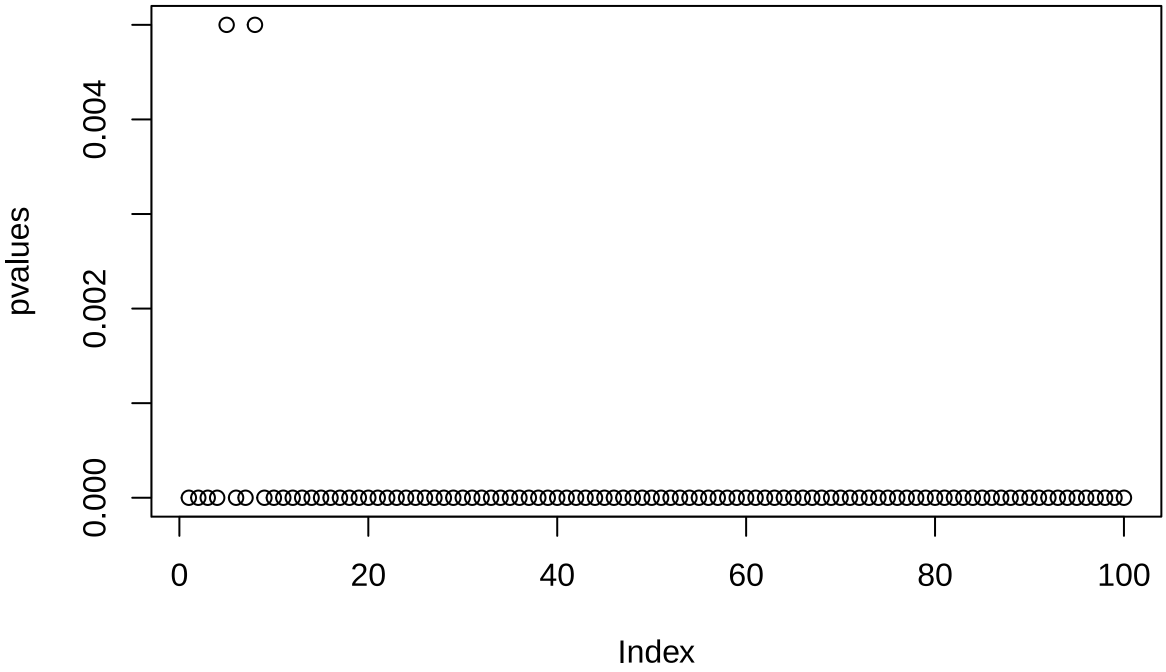
```r
genranddata <- function(x, alpha) {
    data.frame(x=x, y=pmax(0, pmin(alpha * x + rnorm(length(x), mean=183, sd=10), 366)))
}

alphas <- seq(0.1, 10, by=0.1)
pvalues <- rep(0, length(alphas))

set.seed(123456)

for (i in 1:length(alphas)) {
    newdata <- genranddata(data$x, alphas[i])
    pvalues[i] <- teststat_permutation(newdata, 200, teststat(loess))
}

plot(pvalues)
```



```r
print(sum(pvalues <= 0.05))
```

```
## [1] 100
```

Since we reject Ho in every test the power will be 1 becaus we can't have any Type-2 errors when we reject everything. This isn't strange since the test-data is obviously non-random and gives us an indication that the test-statistic is a good one.

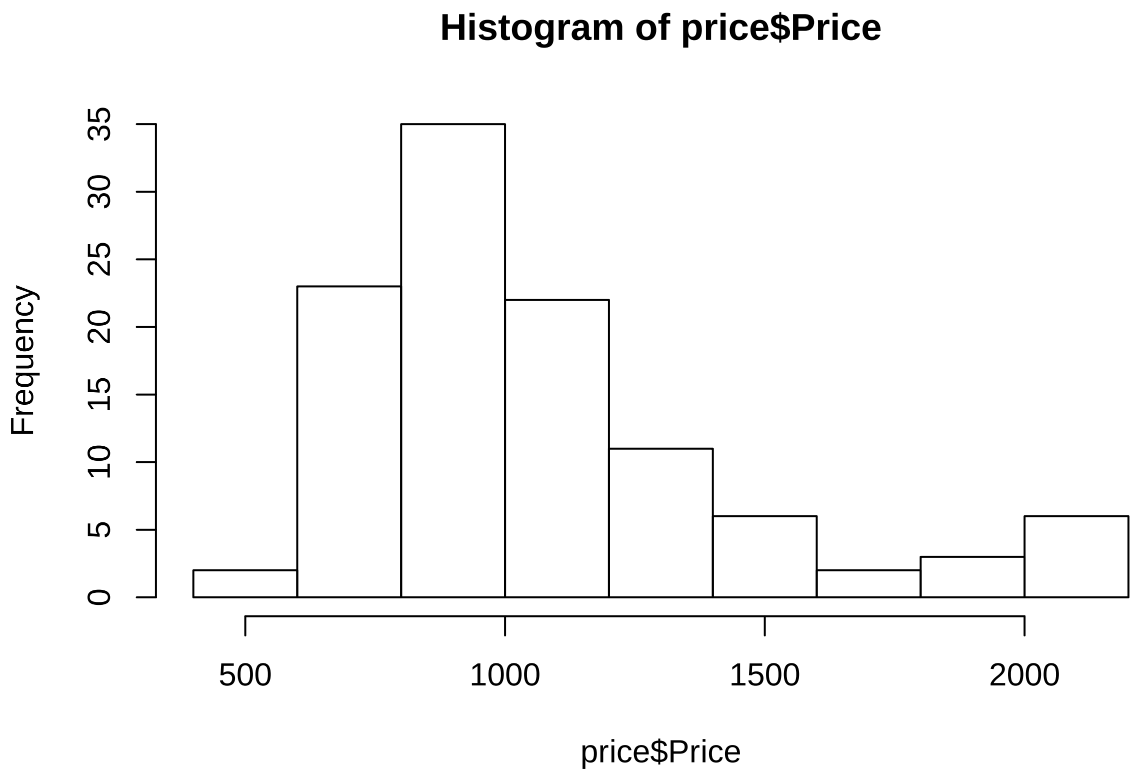
Question 2

2.1

```
price <- read.csv("../data/prices1.csv", sep=";")
mean(price$Price)
```

```
## [1] 1080
```

```
hist(price$Price)
```



Looks like a Gamma distribution.

2.2

```
bootmean <- function(data,ind){
  data <- data[ind]
  mean(data)
}

B <- 2000

estmean <- boot(data = price$Price,bootmean, R = B)

2 * estmean$t0 - mean(estmean$t)
```

```
## [1] 1081
```

```r
mean(estmean$t- estmean$t0)
```

```
## [1] -0.36
```

```r
sum((estmean$t - mean(estmean$t))^2) / (B - 1)
```

```
## [1] 1264
```

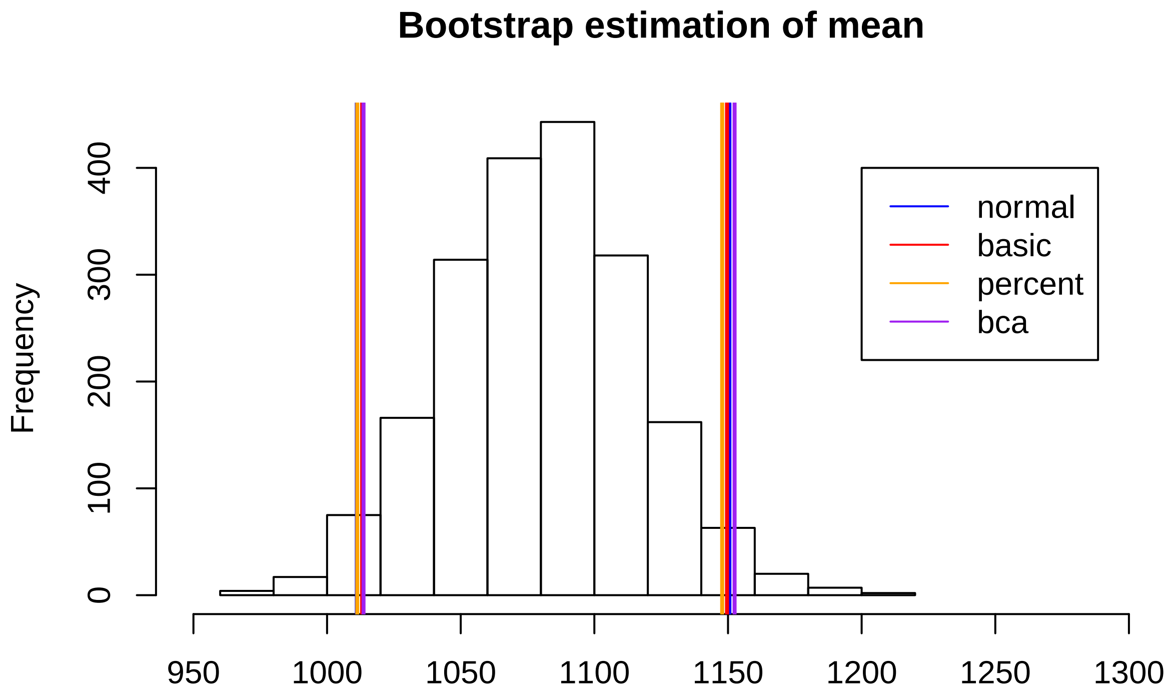
```r
cibo <- boot.ci(estmean)
```

```
## Warning in boot.ci(estmean): bootstrap variances needed for studentized
## intervals
```

```r
print(cibo)
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 2000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = estmean)
##
## Intervals :
## Level      Normal              Basic
## 95%   (1011, 1151 )   (1013, 1150 )
##
## Level     Percentile            BCa
## 95%   (1011, 1148 )   (1014, 1152 )
## Calculations and Intervals on Original Scale
```

```r
hist(estmean$t, xlim = c(950,1300), main = "Bootstrap estimation of mean", xlab = "")
abline(v=cibo$normal[2:3], col = "blue", lwd = 2)
abline(v=cibo$basic[4:5], col = "red", lwd = 2)
abline(v=cibo$percent[4:5], col = "orange", lwd = 2)
abline(v=cibo$bca[4:5], col = "purple", lwd = 2)
legend(y=400, x=1200, c("normal","basic","percent","bca"), lty = c(1,1),
       col=c("blue", "red", "orange", "purple"))
```



2.3

```
jackknife <- function(data,B,tstat){
  stopifnot(B >= 0 && B <= length(data))
  est <- rep(1, times = B)
  for(i in 1:B){

    est[i] <- tstat(data[-i])

  }
  return(est)
}

jackest <- jackknife(price$Price, B = length(price$Price), tstat = mean)

mean(jackest)
```

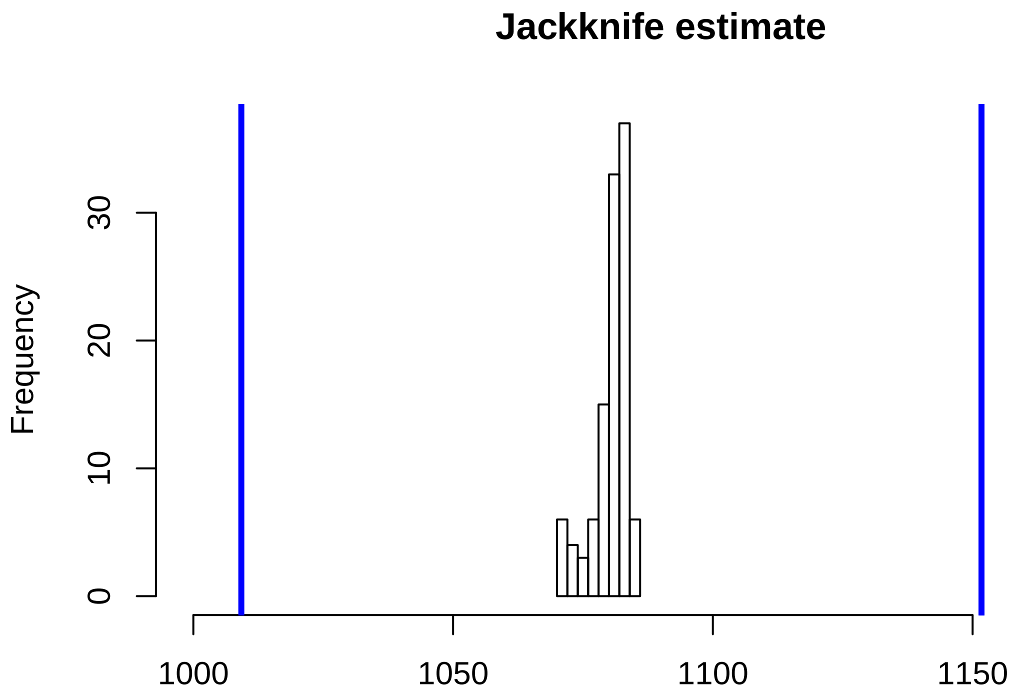
```
## [1] 1080
```

```
n <- length(price$Price)

tstar <- n*mean(price$Price)-(n-1)*jackest
JT <- mean(tstar)
jackvar <- (1 / (n * (n - 1))) * sum((tstar - JT)^2)
```

```
lowerci <- JT - 1.96 * sqrt(jackvar)
upperci <- JT + 1.96 * sqrt(jackvar)

hist(jackest,breaks = 10, xlim = c(1000,1180), xlab = "" ,main = "Jackknife estimate")
abline(v=lowerci, col ="blue", lwd = 3)
abline(v=upperci, col ="blue", lwd = 3)
```



2.4

```
library(knitr)
options(digits=2)

cimatrix <- rbind(
  c("Normal", cibo$normal[2], mean(estmean$t), cibo$normal[3]),
  c("Percent", cibo$percent[4], mean(estmean$t), cibo$percent[5]),
  c("Basic", cibo$basic[4], mean(estmean$t), cibo$basic[5]),
  c("Bca", cibo$bca[4], mean(estmean$t), cibo$bca[5]),
  c("Jackknife", lowerci, mean(jackest), upperci)
)
colnames(cimatrix) <- c("Name", "Lower", "Mean", "Upper")

cimatrix[, 2:4] <- round(as.numeric(cimatrix[, 2:4]))

kable(cimatrix)
```

Name	Lower	Mean	Upper
Normal	1011	1080	1151
Percent	1011	1080	1148
Basic	1013	1080	1150
Bca	1014	1080	1152
Jackknife	1009	1080	1152

The normal, percent and the basic along with the Jackknife confidence intervals are moving in a similar range with only small differences inbetween them. The only one sticking out is the bca CI with overall higher estimations than the rest.