Computer Lab 5

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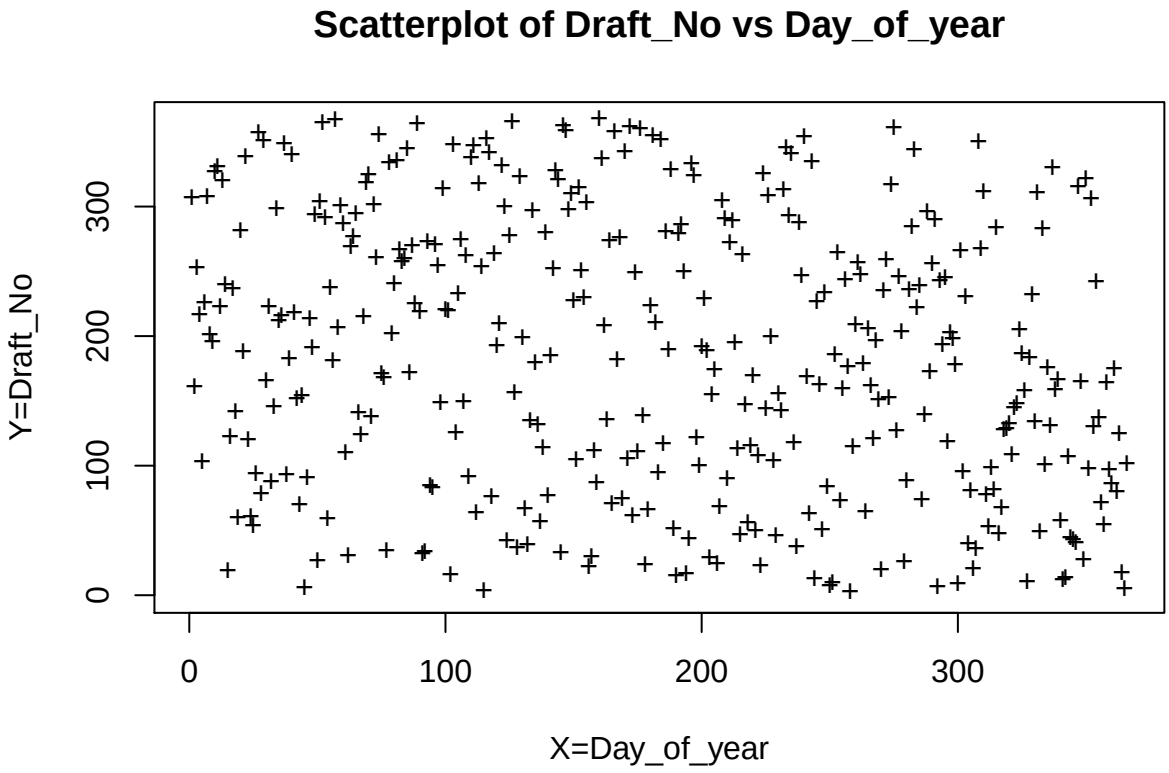
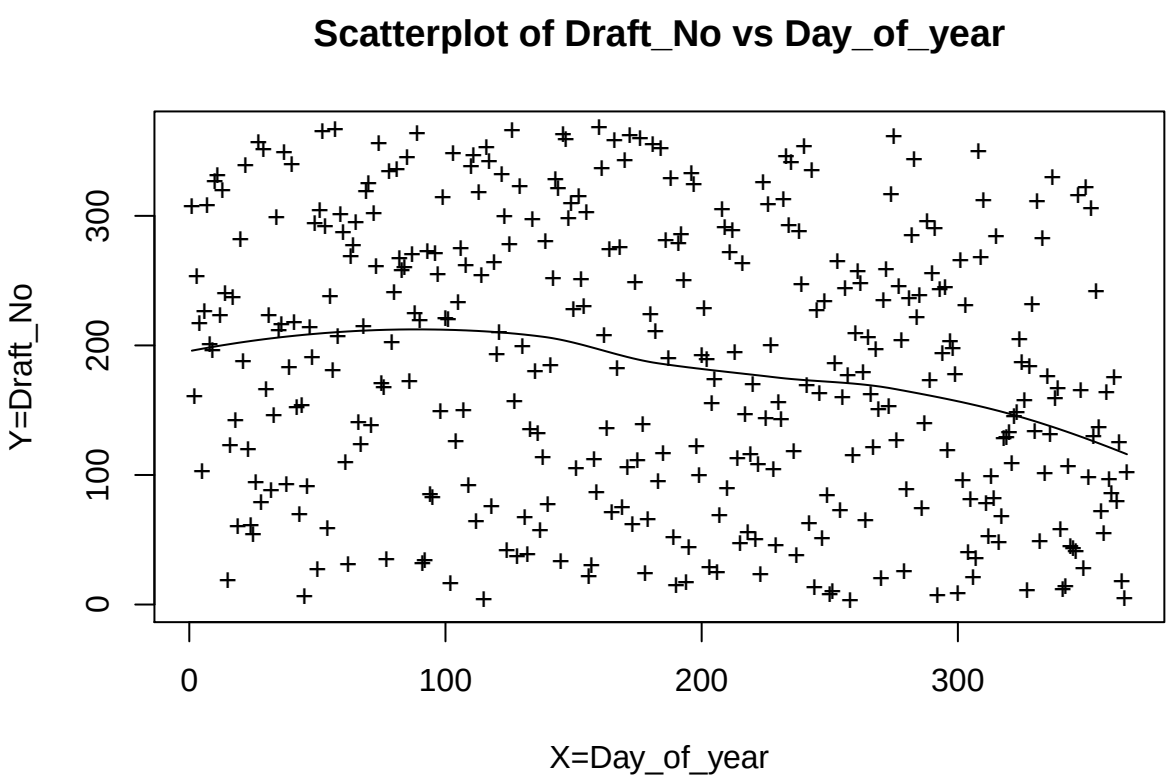
Assignment 1

We have the draft lottery data where each of the 366 possible birthdates correspond to a draft number. The scatterplot of draft number vs day of year is plotted.



We see that there is no obvious dependency between the variables in the data. In order to test this we fit a `loess` local polynomial regression model to the data.



With default settings the `loess` fit does not indicate any trend in the data. The draft numbers still look to be randomly allocated. In order to acertain that the lottery is random, we will perform a hypothesis test by non-parametric bootstrap estimation of the distribution of the test statistic

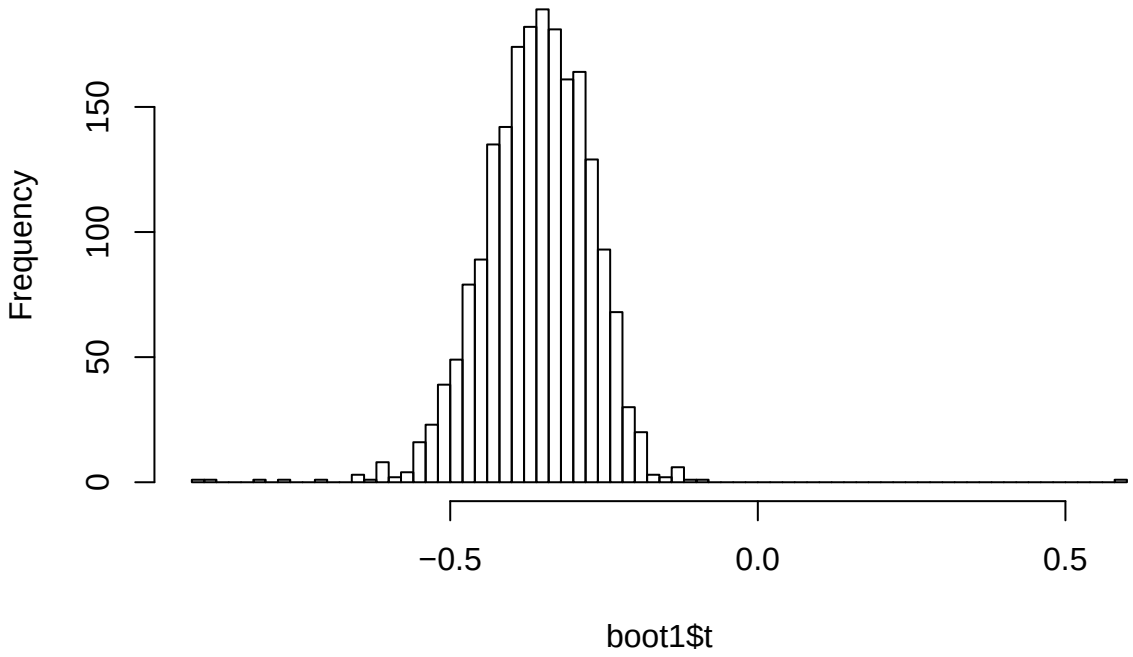
$$T = \frac{Y(\hat{X}_b) - Y(\hat{X}_a)}{X_b - X_a} \quad where$$

$$X_b = argmax_X \hat{Y}, X_a = argmin_X \hat{Y}$$

$\hat{Y}$ is the value of the `loess` model created from the data. If the lottery is not random, then the value of T should in all probability be positive. We create 2000 Bootstrap replicates or T and see how often it is larger than zero.

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = data, statistic = bigT, R = 2000)
##
##
## Bootstrap Statistics :
##       original     bias    std. error
## t1* -0.3479163 -0.0106269  0.08796774
```

```
## [1] "P-value of T greater than zero outcome:  5e-04"
```



As we see, the p-value is very low, low enough to say that the lottery appears to be random according to this test. We also see that most of the bootstrap T-statistic values are below zero, not above zero.

Let us do further hypothesis testing by using a permutation test, where we permute the day of year variable, then calculate test statistic T. We replicate this procedure 2000 times and then take the p-value to be the proportion of T:s greater than the empirical value of the test statistic, in this case the empirical value is $T_0 = -0.3479$.

```
## [1] "p-value from permutation testing:  0.924"
```

We discover that the p-value is far too high to reject the null hypothesis. The fact that the p-value is higher than one half could possibly be explained by the fact that the empirical observation of T is a negative number.

Let us try to crudely estimate the power of this permutation test by creating non-random (alternative hypothesis) ''draft number" data $Y(x)$ using the day of year data column x of the form

$$Y(x) = \max(0, \min(\alpha x + \beta, 366)) \quad where$$

$$\alpha = 0.1 \quad and \quad \beta \sim N(183, 100)$$

Since this data is non-random, the permutation test function as written by me should return very low p-value.

```
## [1] "p-value from permutation testing non-random Draft_No, alpha = 0.1:  0"
```

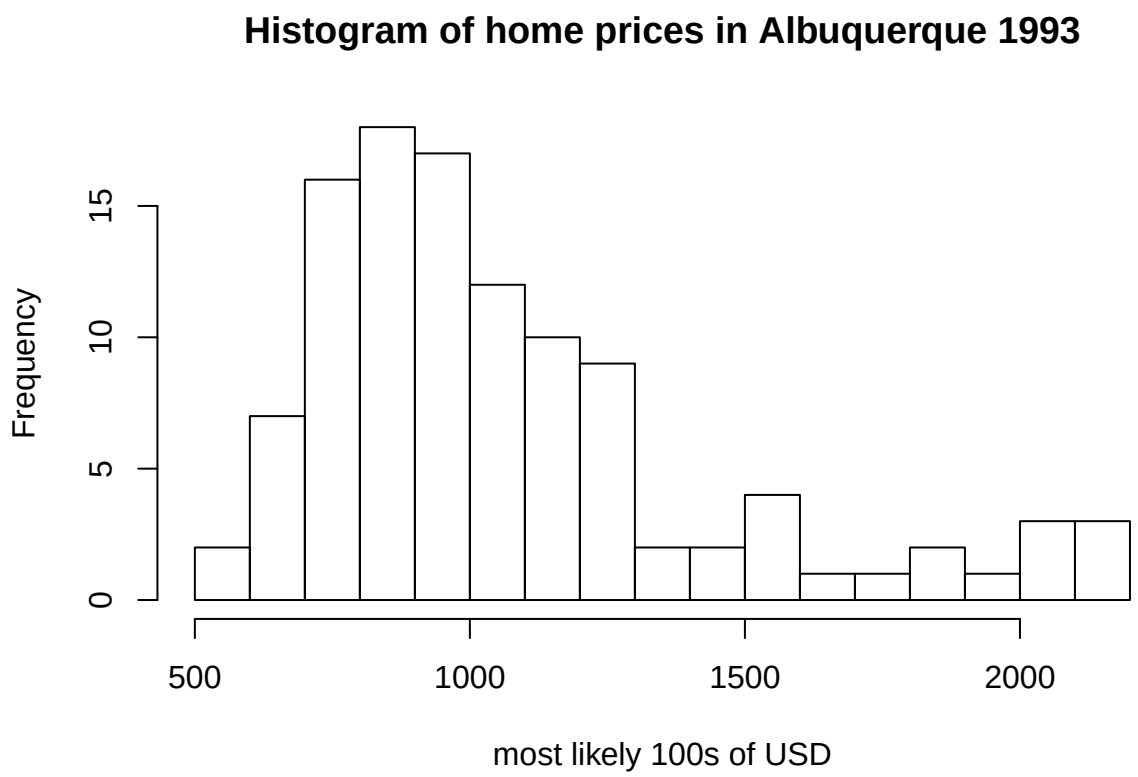
It does look as if that would be the case. We continue this line of exploration by setting α to $0.1, 0.2, \ldots, 10$ and see when the permutation test will reject the null hypothesis (data is random) at 5% significance level. We then take the proportion of (absolutely correct) rejections to be the crude estimate of the power of the test.

```
## [1] "Crude estimate of Power of the test statistic T:  1"
```

The power estimated would indicate that this is a good test for non-randomness. However, I would like to point out that above $\alpha = 0.5$ increasingly the Draft numbers take on the maximum value of 366 and that might affect the result.

Assignment 2

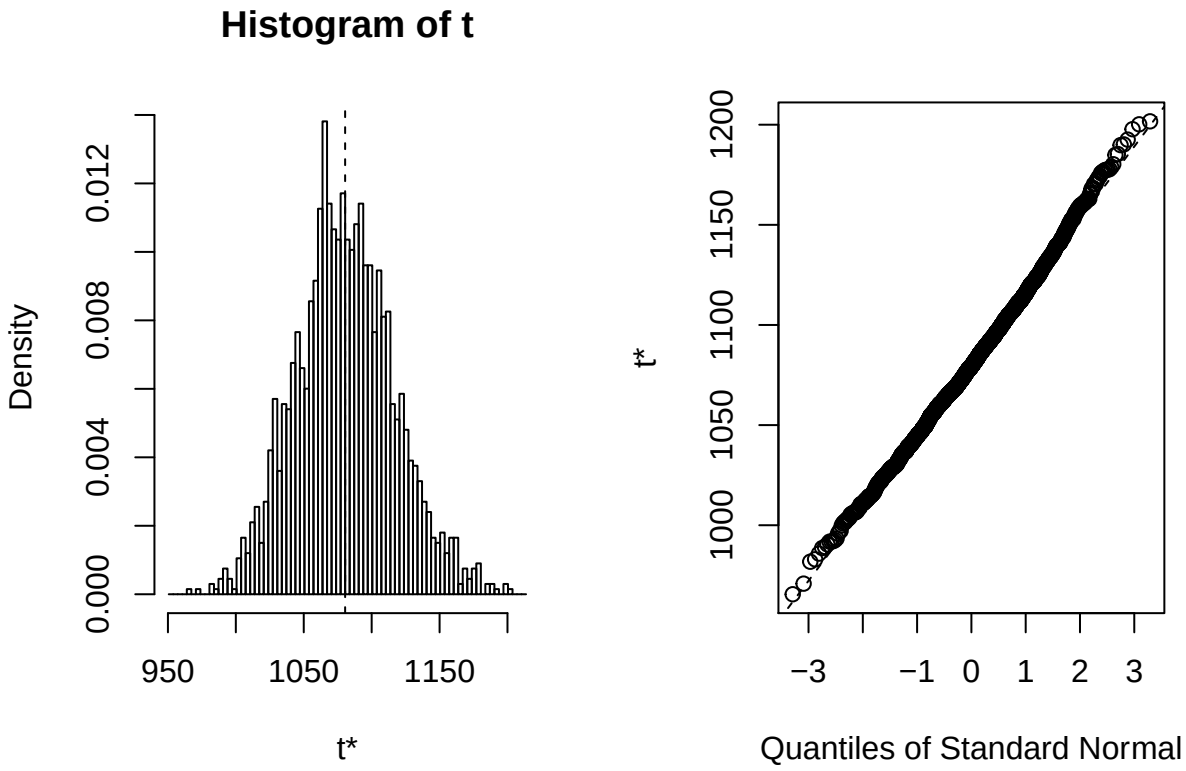
We have the home prices in Albuquerque 1993 and we plot a histogram and find the mean home price.




```
## [1] "mean price of home in Albuquerque 1993:  1080.473 hundred USD"
```

I can not say for sure, but I believe the price unit is hundreds of USD. The distribution of home prices look a little like a chi-squared distribution.

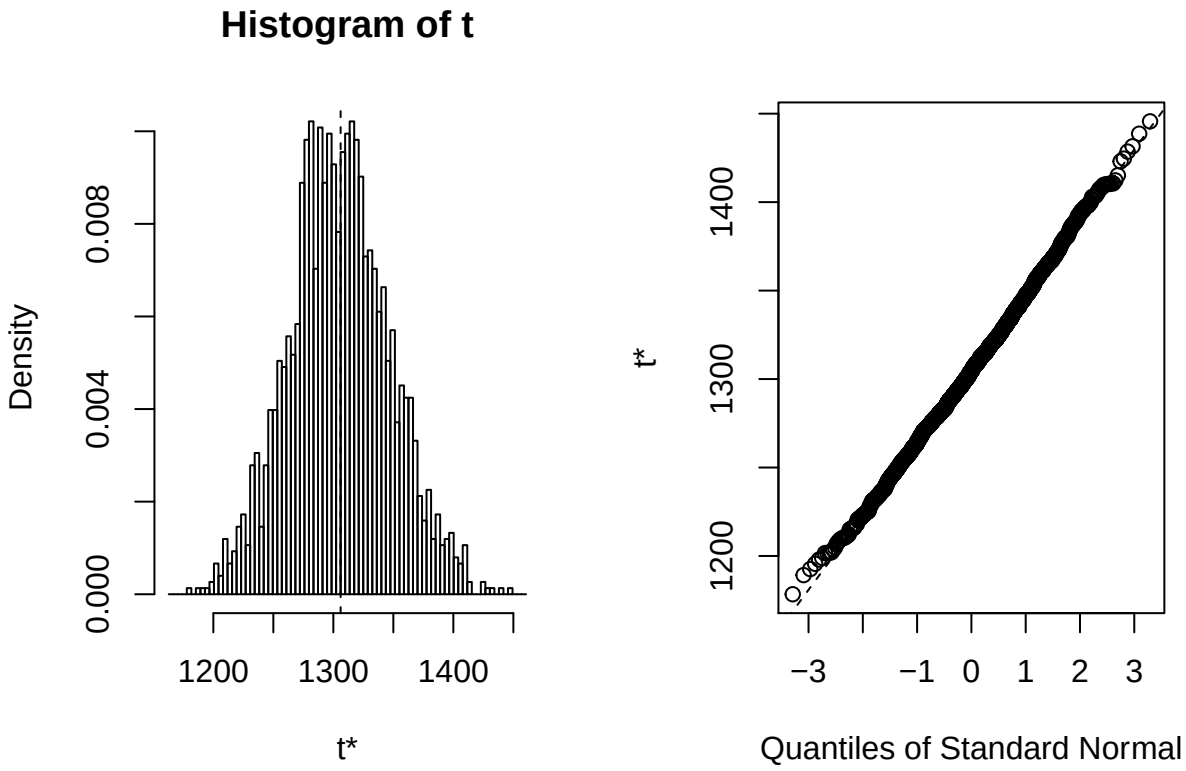
We are going to estimate the distribution of the mean home price using bootstrap. We run bootstrap once to generate 2000 mean home prices, we estimate the bias-correction for the bootstrap mean house price and then we are going to use those bootstrap mean home prices to find the estimate of the variance of bootstrap mean house prices, using 2000 bootstrap replicates.




```
## [1] "Bootstrap mean house price bias-correction estimate -0.21  hundred USD"
```

```
## [1] "Bias-corrected bootstrap estimate of mean house price:  1080.262  hundred USD"
```

We can see that the bootstrap mean house prices are almost perfectly normally distributed and the bias in mean house price is very small.




```
## [1] "Bootstrap estimate of variance of mean house price:  1305.305  hundred USD squared"
```

We can compare the estimate of the variance of mean house price to an estimate of the variance of mean house price obtained using the jackknife method.

```
## [1] "Estimate of variance of mean home price by jackknife:  1320.911  hundred USD squared"
```

We find that the variance estimate generated by the jackknife method is slightly higher than the bootstrap variance estimate.

Now we create 95% bootstrap confidence intervals for the mean house price using the normal approximation method, the percentile method and the BCa method and compile the data in a table.

```
##                         method    lower    upper   length midpoint
## 1        Normal Approximation 1009.431 1151.094 141.6636 1080.262
## 2 bootstrap percentile method 1011.916 1157.789 145.8723 1084.852
## 3                  BCa method 1015.600 1161.730 146.1294 1088.665
```

We find that as one goes down the table the confidence interval shifts slightly higher. Interestingly, the normal approximation midpoint is the same value as the bias-corrected bootstrap estimate of the mean house price.(Possibly this is because the bootstrap home mean prices are almost normally distributed)

Appendix

R code

```
library(bootstrap)
library(boot)
library(XLConnect)
wb = loadWorkbook("lottery.xls")
wb2 = loadWorkbook("prices1.xls")
data = readWorksheet(wb,sheet = "Sheet1" ,header = TRUE)
#data is changed around alot in data$Draft_No. reset often.
data2 = readWorksheet(wb2,sheet = "Sheet1" ,header = TRUE)

plot(data$Day_of_year,data$Draft_No,xlab="X=Day_of_year",ylab="Y=Draft_No",pch="+",
     main="Scatterplot of Draft_No vs Day_of_year")
#It looks random
polyfit <- loess(Draft_No ~ Day_of_year,data=data)
plot(data$Day_of_year,data$Draft_No,xlab="X=Day_of_year",ylab="Y=Draft_No",pch="+",
     main="Scatterplot of Draft_No vs Day_of_year")
lines(polyfit$fitted)
bigT <- function(dat,index){
  dat2 <- dat[index,]
  poly <- loess(Draft_No ~ Day_of_year, data = dat2)
  smallest <- which.min(poly$fitted)
  largest <- which.max(poly$fitted)
  TEE <- (poly$fitted[largest] - poly$fitted[smallest]) /
    (dat2$Day_of_year[largest] - dat2$Day_of_year[smallest])
  return(TEE)
}
set.seed(-3447)
boot1 <- boot(data,bigT,R=2000)
boot1
signif1 <- mean(boot1$t > 0)
paste("P-value of T greater than zero outcome: ",signif1) # P-level
hist(boot1$t,breaks = 100)

originalT <- boot1$t0
permfun <- function(data,B){
  n <- dim(data)[1]
  permvec <-rep(0,B)
  for(i in 1:B){
    rando <- sample(1:n,n)
    dat2 <- data.frame(day = rando, draft = data$Draft_No)
    poly <- loess(draft ~ day, data = dat2)
    smallest <- which.min(poly$fitted)
    largest <- which.max(poly$fitted)
    TEE <- (poly$fitted[largest] - poly$fitted[smallest]) /
      (dat2$day[largest] - dat2$day[smallest])
    permvec[i] <- TEE
  }
  poly <- loess(Draft_No ~ Day_of_year, data = data)
  smallest <- which.min(poly$fitted)
  largest <- which.max(poly$fitted)
```

```
  originalstatistic <- (poly$fitted[largest] - poly$fitted[smallest]) /
    (data$Day_of_year[largest] - data$Day_of_year[smallest])
  prop <- mean(permvec > originalstatistic)
  return(prop)
}
set.seed(-3447)
pval2 <- permfun(data,B= 2000)
paste("p-value from permutation testing: ",pval2)
alpha <- 0.1

nonrandgen <- function(data,alpha){
  nonrandY <- numeric(366)
  for(i in 1:366){
  beta <- rnorm(1,183,10)
  nonrandY[i] <- max(0,min(alpha * data$Day_of_year[i] + beta, 366))
  }
  return(nonrandY)
}
#look, above alpha = 0.5 we get the ceiling alot.
# what is the point?
#nvm, forgot about the permutation of days

nonrandY <- nonrandgen(data,alpha)
data$Draft_No <- nonrandY
pval3 <- permfun(data,B = 200)
paste("p-value from permutation testing non-random Draft_No, alpha = 0.1: ",pval3)
alpha <- seq(from = 0.1, to = 10 , by = 0.1)

pvals <- rep(0,length(alpha))
for(j in 1:length(alpha)){
  nonrandY <- nonrandgen(data,alpha[j])
  data$Draft_No <- nonrandY
  pvalcurr <- permfun(data, B = 200)
  pvals[j] <- pvalcurr
}
paste("Crude estimate of Power of the test statistic T: ", round(mean(pvals < 0.05),2))
hist(data2$Price,breaks = 20,main="Histogram of home prices in Albuquerque 1993",
     xlab="most likely 100s of USD")
paste("mean price of home in Albuquerque 1993: ",round(mean(data2$Price),3),"hundred USD")
m <- length(data2$Price)

meanstat <- function(data,ind){
  datar <- data[ind,]
  res <- mean(datar$Price)
  return(res)
}
set.seed(-3447)
boot2 <- boot(data2,meanstat, R = 2000)
#hist(boot2$t,main="Histogram of bootstrap mean house prices",xlab = "mean house price")
plot(boot2)

#bias correction
```

```r
biascorrectedest <- 2 * mean(data2$Price) - mean(boot2$t)
paste("Bootstrap mean house price bias-correction estimate",
      round(mean(data2$Price) - mean(boot2$t),3)," hundred USD")
paste("Bias-corrected bootstrap estimate of mean house price: ",
      round(biascorrectedest,3)," hundred USD")
varstat <- function(data,ind){
  datar <- data[ind,]
  res <- var(datar)
  return(res)
}
set.seed(-3447)
boot3 <- boot(boot2$t,varstat, R = 2000)
plot(boot3)
paste("Bootstrap estimate of variance of mean house price: ",
      round(mean(boot3$t),3)," hundred USD squared")
varbyjack <- jackknife(data2$Price,mean)
Tstarjs <- m * rep(mean(data2$Price),m) - (m-1) * varbyjack$jack.values
jackknifedT <- mean(Tstarjs) # this is the same as mean of house price...
jackvarofmeans <- sum((Tstarjs-jackknifedT)^2) / (m*(m-1)) # is the same as varbyjack$jack.se^2
paste("Estimate of variance of mean home price by jackknife: ",
      round((varbyjack$jack.se)^2,3)," hundred USD squared")
set.seed(-3447)
confintsboot <- boot.ci(boot2, type=c("norm","perc", "bca"))
normci <- confintsboot$normal
percci <- confintsboot$percent
bcaci <- confintsboot$bca
confintinfos <- data.frame(method = c("Normal Approximation",
                                      "bootstrap percentile method","BCa method"),
           lower = c(normci[2],percci[4],bcaci[4]),upper = c(normci[3],percci[5],bcaci[5]),
           length = c(normci[3] - normci[2],percci[5] - percci[4],bcaci[5]-bcaci[4]),
           midpoint = 1/2 * c(normci[3] + normci[2],percci[5] + percci[4],bcaci[5] + bcaci[4]))
confintinfos #as you go down the list the interval creeps higher,
#also normal approx midpoint is same as bias corrected bootstrap est.
## NA
```