Task1

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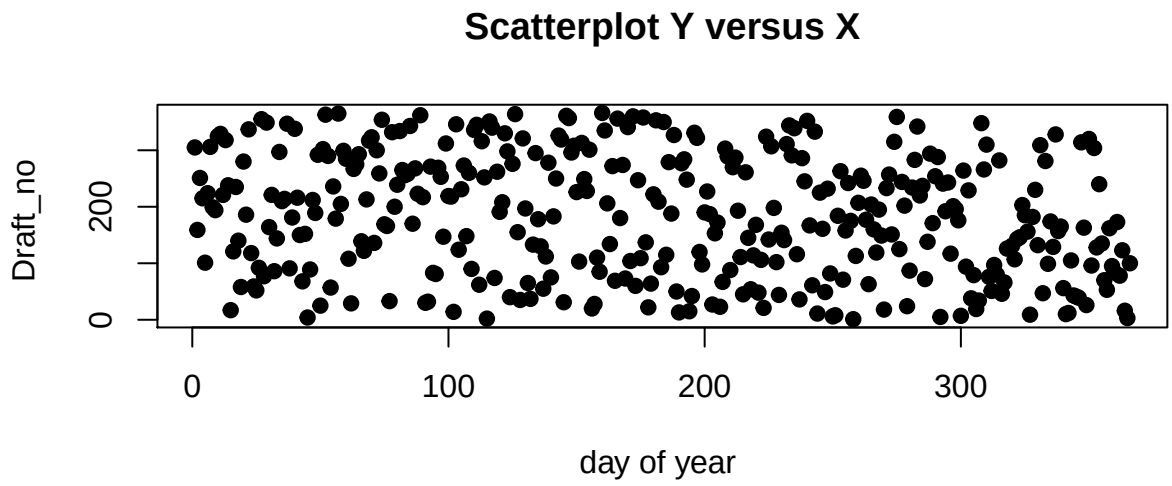
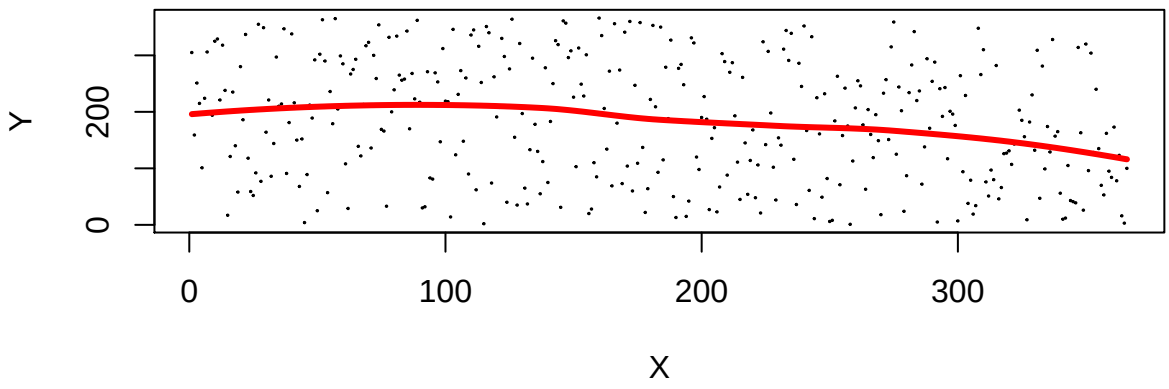
Question 1: Hypothesis testing

1.



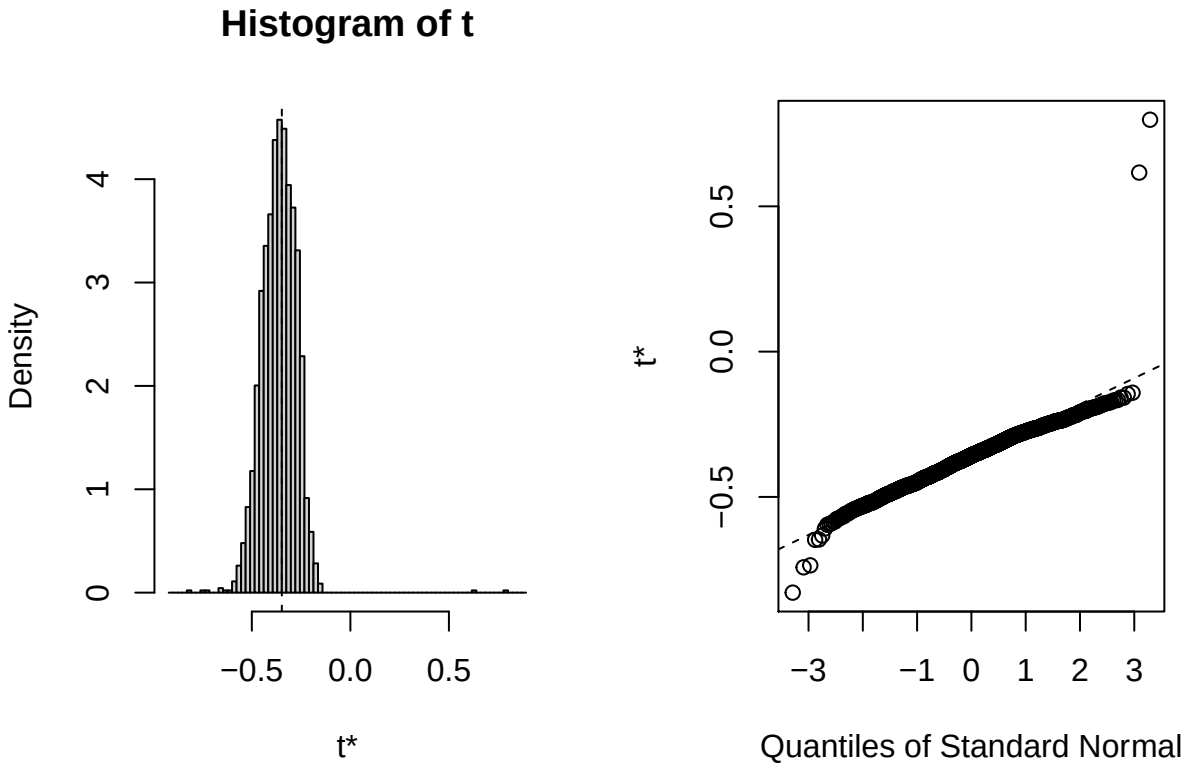
From the plot lottery looks random

2.



From estimates we can see that there is some pattern in the data, however its hardly visible.

3.



$H_0 : t = 0$ - lotery is random

$H_a : t \neq 0$ -lotery is not random

two sided p-value: 0.0025

p- value is less than 0.05 so we reject null hypothesis, meaning that lotery is not random

4.

permutation test function:

$H_0 : t = 0$ - lotery is random

$H_a : t \neq 0$ -lotery is not random

```
permutation_test <- function(data, B){

  origin_loes <- loess(Draft_No ~ Day_of_year, data)
  t_origin <- statis(data, origin_loes)

  stat= numeric(B)
  n = dim(data)[1]
  for(b in 1:B){
    perm_data <- data.frame(data)
    perm_data$Day_of_year = sample(data$Day_of_year, n)
    loes_h1 <- loess(Draft_No ~ Day_of_year, perm_data)
    stat[b] <- statis(perm_data,loes_h1)
  }
  # statistic from original dat

  p_value <- sum(abs(stat) >= abs(t_origin))/B
  return(p_value)
}
```

permutation test when B = 2000: p-value = 0.1445

5.

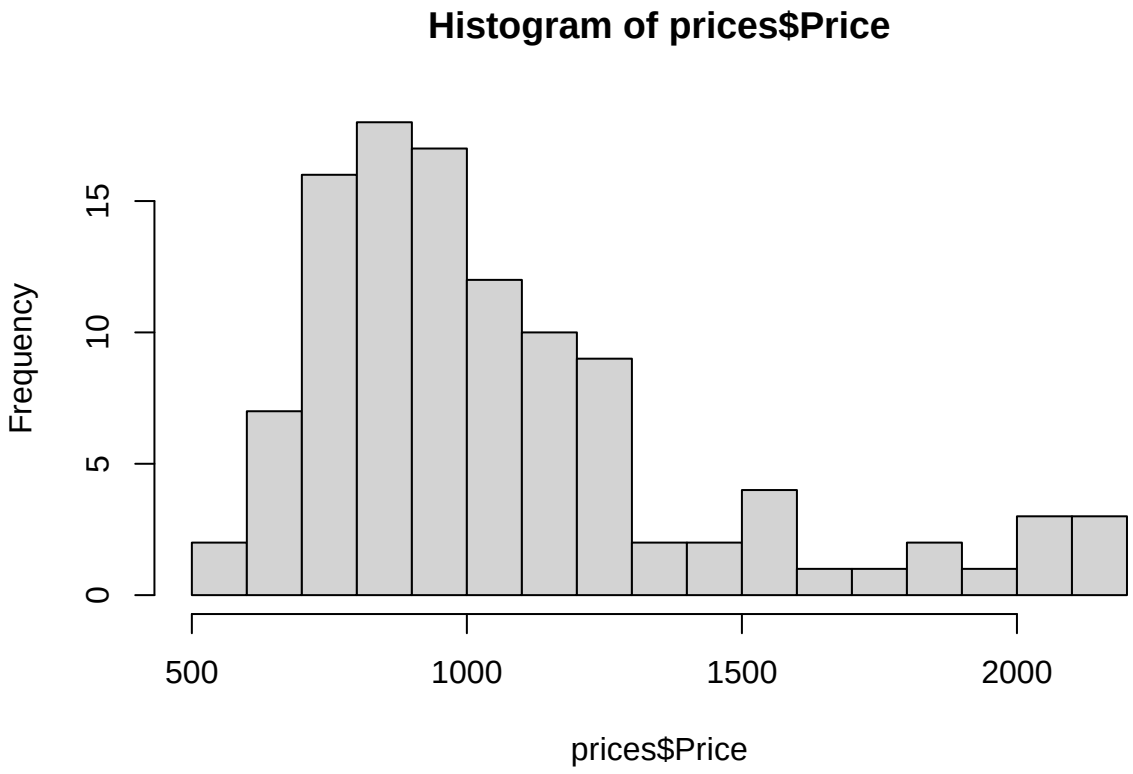
table bellows shows p values for alpha 0.1:10 by 0.1 for which p is not equal to 0

```
## [1] "all p values are 0"
```

power of the test is: 1-type 2 error. type 2 error is a probability of failing to reject H_0 when H_a is true. We know that our generated data samples are not random. The amount of rejected $H_0 : 0$. As a result type 2 error is: 0, and power of the test is: 1.

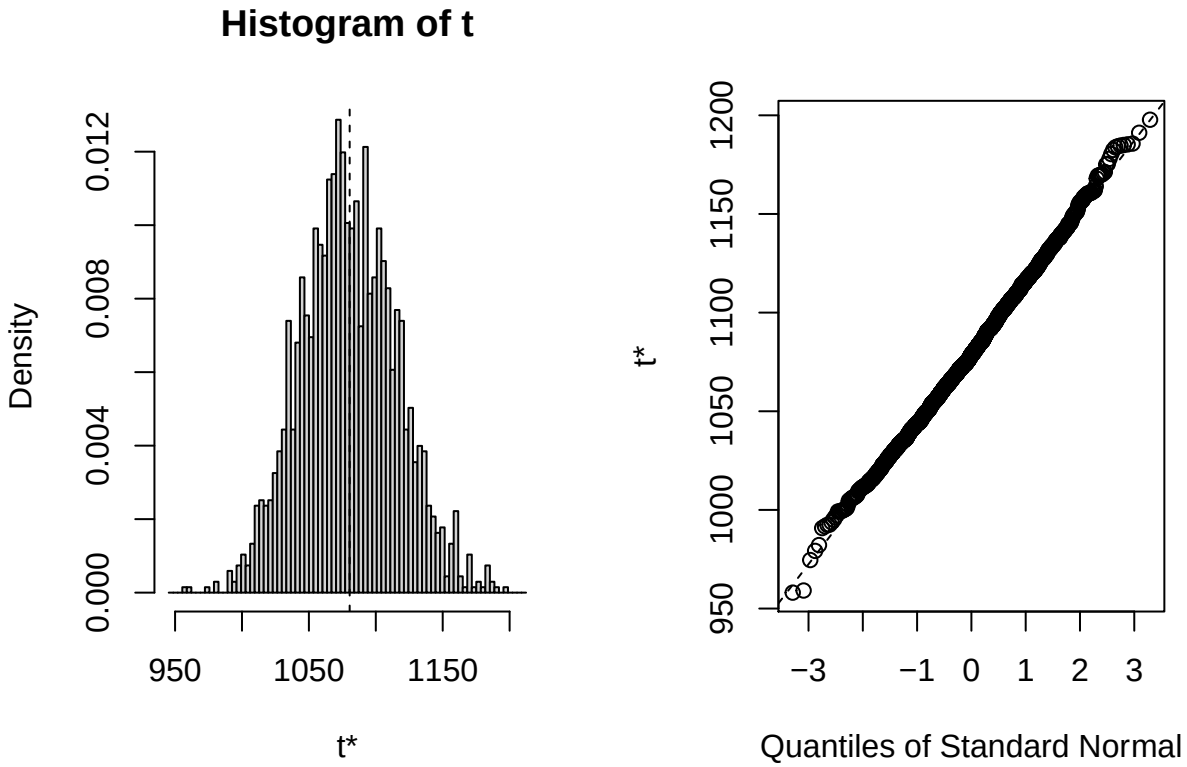
Question 2: Bootstrap, jackknife and confidence intervals

1.



Reminds Gamma with shape = 3, scale = 2.

2.



Bootstrap bias-correction: 1081.1160955. Variance - 1280.567486.

95% confidence intervals:

	low	high
percentile	1012.310	1152.771
BCa	1017.472	1160.455
first-order normal	1010.979	1151.253

3.

variance using jackknife: 1320.9110441 , difference between jacknife and bootstrap: 40.343558.

4.

Table below compares confidence intervals:

	low	high	length	location of mean
percentile	1012.310	1152.771	140.4607	0.4852763
BCa	1017.472	1160.455	142.9831	0.4406176
first-order normal	1010.979	1151.253	140.2747	0.4954135

location of mean shows portion of interval length from the beginning of the interval to the mean