

# Task1

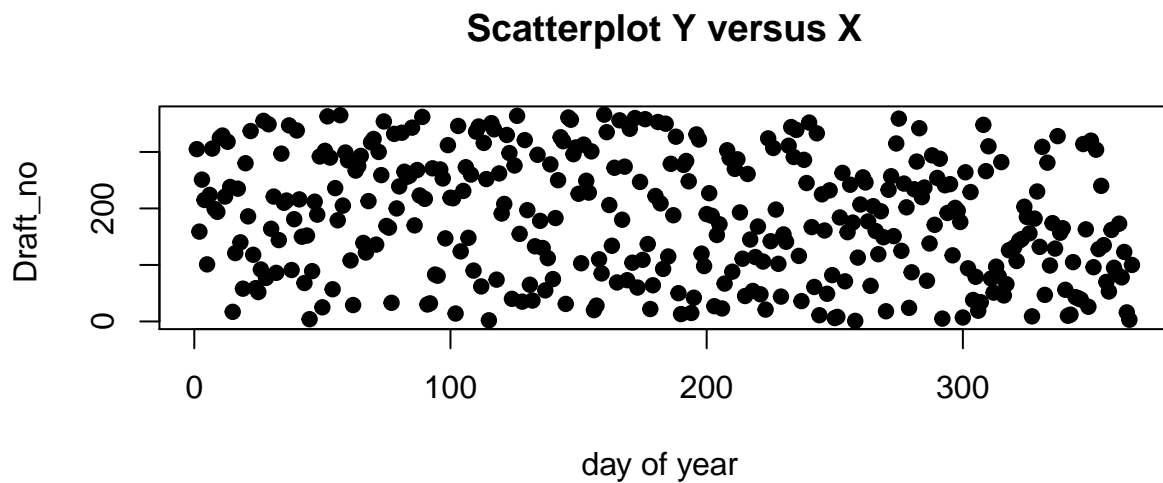
Martynas Lukosevicius, Alejo Perez Gomez, Shwetha Vandagadde Chandramouly

04/12/2020

## Question 1: Hypothesis testing

1.

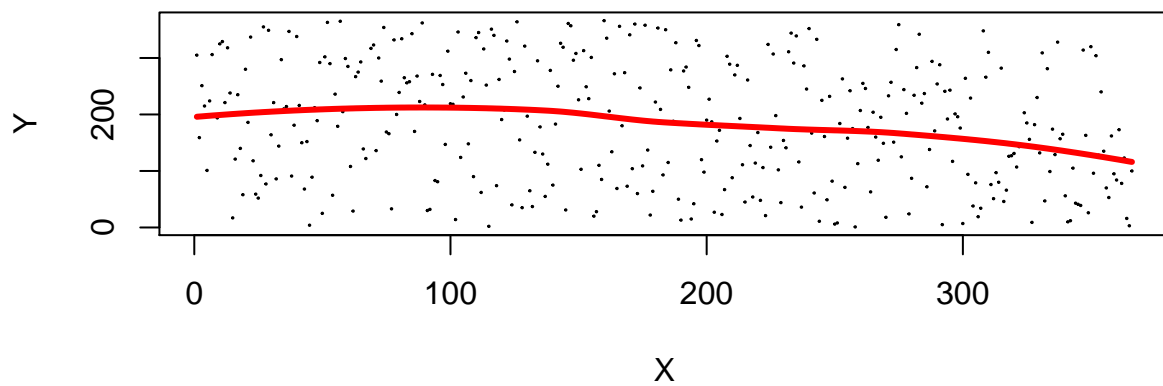
For this question we are required to make a scatter plot and conclude whether the lottery seems random.



By judging based on our plot, lottery looks random.

2.

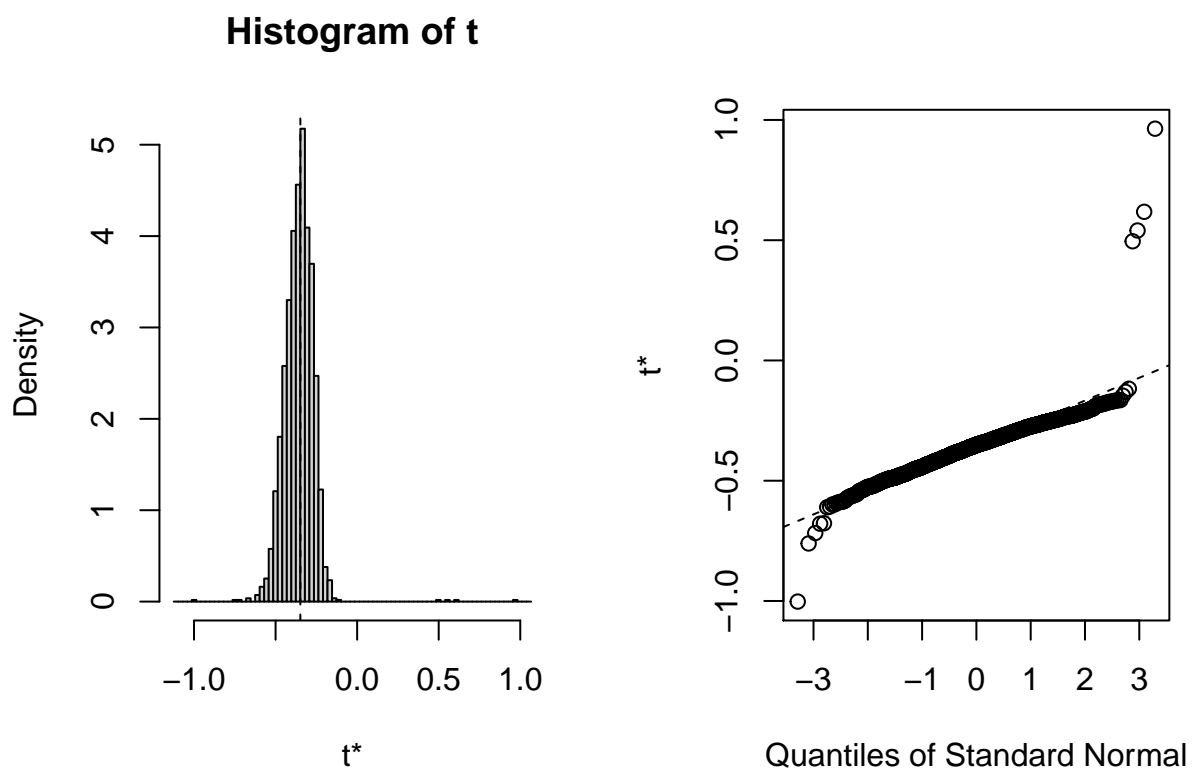
An estimate  $\hat{Y}$  will be computed using and afterwards plot  $\hat{Y}(X)$  adding it to the previous plot.



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

3.

For this section we will use the statistic given, from where we intuit it stands for a slope in  $\hat{Y}(X)$



For this hypothesis testing let our hypothesis be.

$H_0 : t = 0$  - lottery is random

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

We will consider two sided p-value: 0.0035. That is because we account for values that would reject the null hypothesis above and below  $t = 0$ .

As p-value results in less than 0.05 that lead us reject null hypothesis, meaning that lottery is not random.

#### 4.

Permutation test function will be used in this occasion to evaluate the next hypothesis analysis with  $B = 2000$ :

$H_0 : t = 0$  - lottery is random

$H_a : t \neq 0$  -lottery 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)  
}
```

The permutation test when  $B = 2000$  results in a p-value = 0.146.

#### 5.

A crude estimate of the power of the test constructed in Step 4 will be made.

The table bellow shows the p-values for alpha 0.1:10 by 0.1 for which p is not equal to 0.

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

The computed 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

In this section we are required to use bootstrapping and jackknife techniques to estimate some unknown parameters at population level based on the sampling knowledge comprised in confidence intervals.

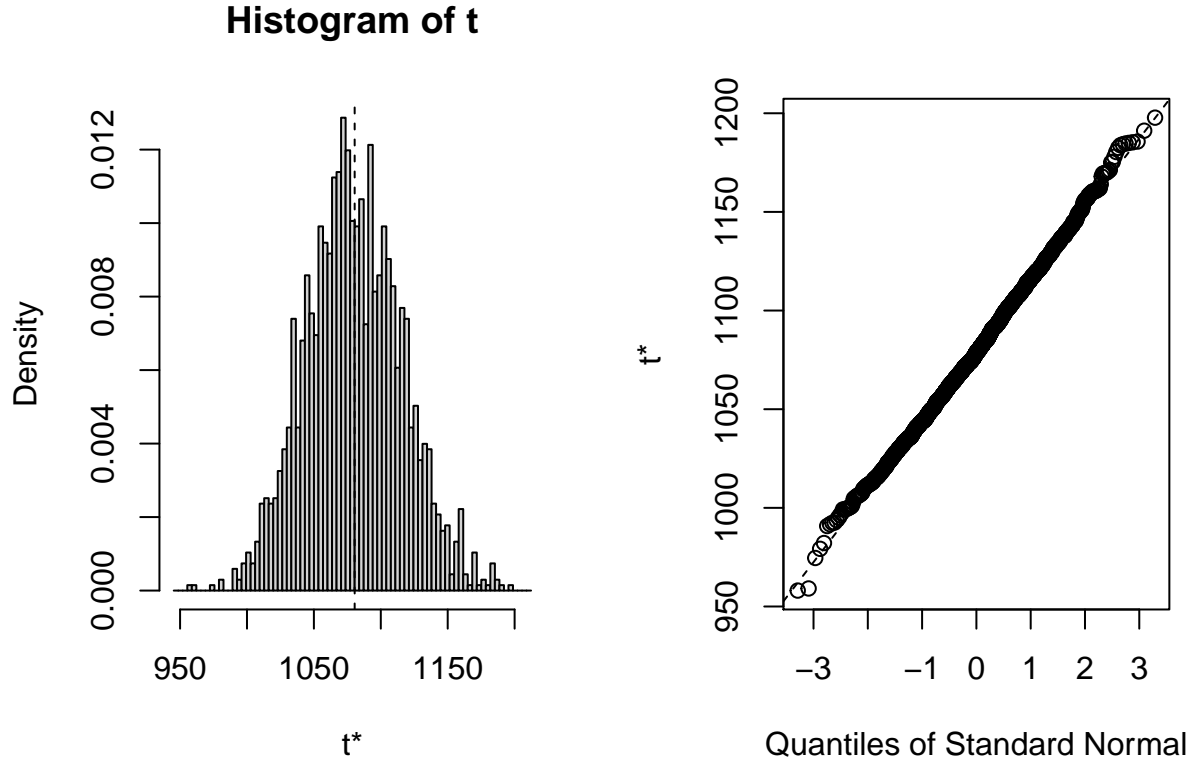
1.

Histogram of the Data and distribution-based approach.



It resembles a Gamma distribution with shape = 3, scale = 2.

2.



After applying the aforementioned techniques we encountered this parameter estimations.

To calculate the Bias-Correction we applied the ensuing formula. Note  $B$  will be our number of sub-samplings,  $T$  stands for our Data statistic and  $T_i^*$  our statistic for sub-samplings.

$$T_1 = 2T(D) - \frac{1}{B} \sum_{i=1}^B T_i^*$$

In order to calculate the variance, the following formula will be used:

$$Var[\hat{T}(\hat{u})] = \frac{1}{B-1} \sum_{i=1}^B (T(D_i)^* - \bar{T}(D^*))^2$$

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.

For this section the same thing as in the previous point will be calculated by using jackknife instead. This estimation will be ruled by this mathematical expression:

$$Var[\hat{T}(\hat{\mathfrak{u}})] = \frac{1}{n(n-1)} \sum_{i=1}^n ((T_i^*) - J(T)^2)$$

Where  $T_i^* = nT(D) - (n-1)T(D_i^*)$  and  $J(T) = \frac{1}{n} \sum_{i=1}^n T_i^*$

Variance using jackknife: 1320.9110441, the difference obtained between jackknife and bootstrap is: 40.343558. As can we see the jackknife method tends to overestimate variance.

### 4.

In the fourth point we will compare the confidence intervals obtained with respect to their length and the location of the estimated mean in such intervals.

The 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

The mean location shows the portion of interval length from the beginning of the interval until the mean.