

MA677_HW3

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```
mu = read.table("maybe_uniform.txt")
```

```
## Warning in read.table("maybe_uniform.txt"): incomplete final line found by  
## readTableHeader on 'maybe_uniform.txt'
```

```
mu<-c(mu[1,],mu[2,],mu[3,],mu[4,],mu[5,])
```

```
mu<-as.numeric(mu)
```

```
ks.test(mu, "punif")
```

```
##
```

```
## One-sample Kolmogorov-Smirnov test
```

```
##
```

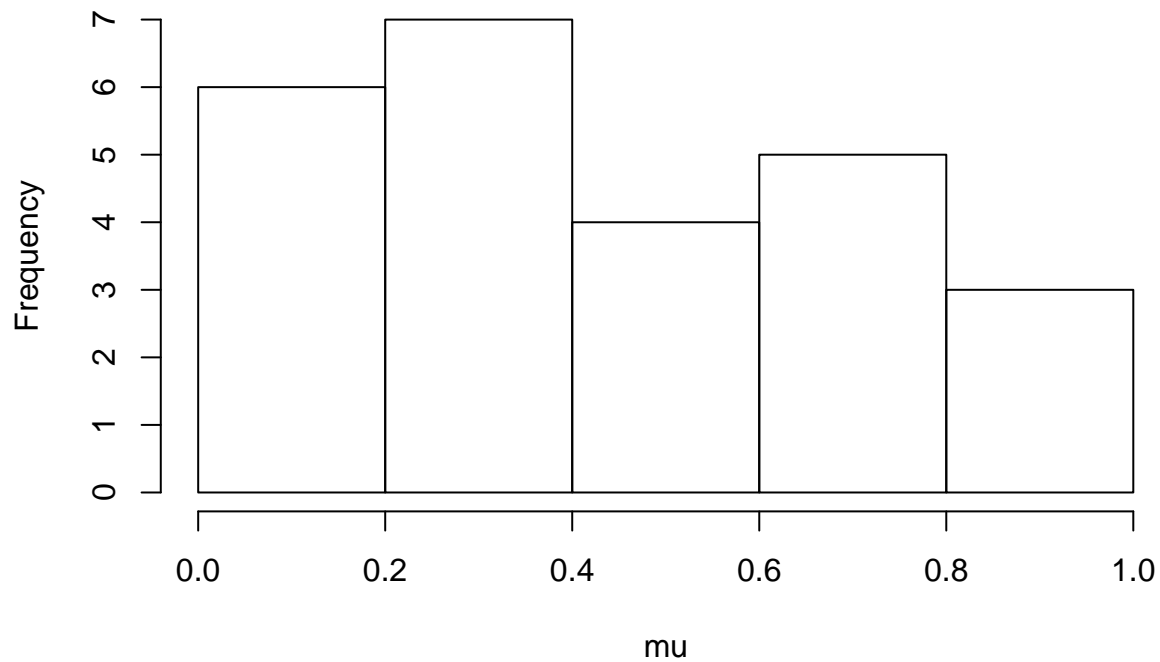
```
## data: mu
```

```
## D = 0.18, p-value = 0.3501
```

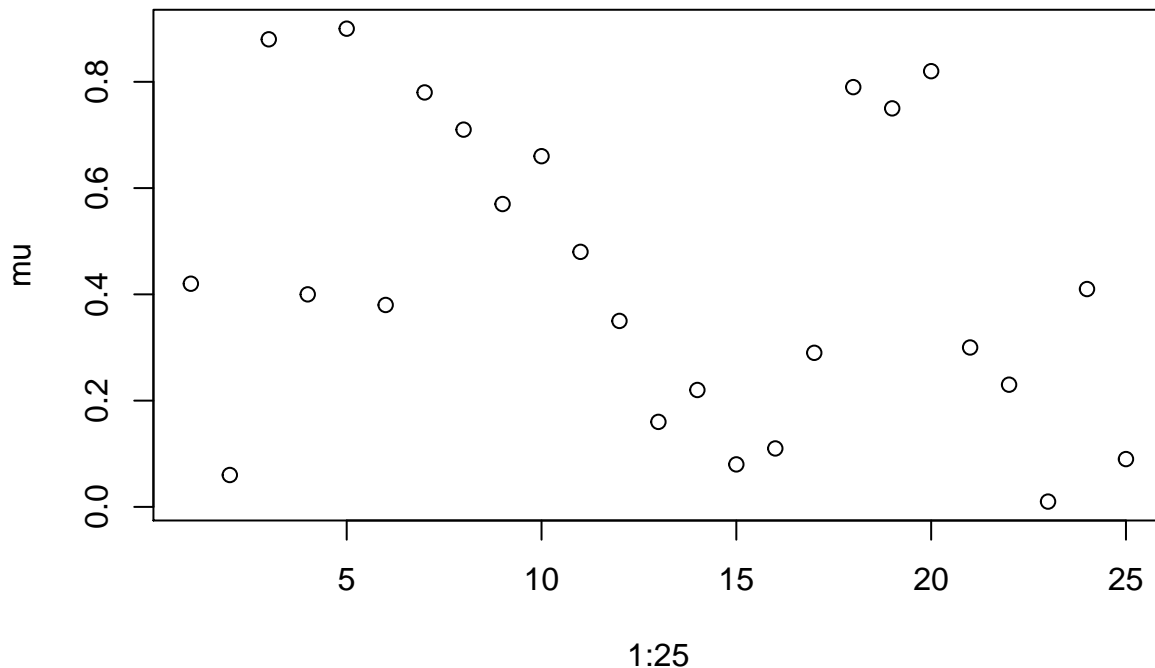
```
## alternative hypothesis: two-sided
```

```
hist(mu)
```

Histogram of mu



```
plot(1:25,mu)
```



Given the p value of KS test being 0.35, we fail to reject the null hypothesis that the data from maybe_uniform.txt is uniformly distributed.

```
x<-seq(-10, 10, by=0.001)
fx <- ifelse(x > 0 & x <=0.5, 2/3,
  ifelse(x > 0.5 & x < 1, 1/2, 0))
ks.test(fx,mu)
```

```
## Warning in ks.test(fx, mu): p-value will be approximate in the presence of
## ties
```

```
##
## Two-sample Kolmogorov-Smirnov test
##
## data: fx and mu
## D = 0.95005, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

From the KS test, we could see that the data does not have matched distribution with the piecewise model, with very small p value and much higher D value than the previous one. Thus, the model is not better than uniform distribution.

```
ks.test(mu, "pgamma", rate = 2, shape = 1)
```

```
##
## One-sample Kolmogorov-Smirnov test
##
## data: mu
## D = 0.1653, p-value = 0.4535
## alternative hypothesis: two-sided
```

The KS test of gamma distribution with rate = 2 and shape = 1 gives even smaller D value than uniform distribution, showing the gamma distribution is a bit better.

Problem 2

```
mn = read.table("maybe_normal.txt")
mn<-c(mn[1,],mn[2,],mn[3,],mn[4,],mn[5,])
mn<-as.numeric(mn)
```

```
n25 <- rnorm(25, 26, 4)
ks.test(mn, n25)
```

```
##
## Two-sample Kolmogorov-Smirnov test
##
## data: mn and n25
## D = 0.28, p-value = 0.285
## alternative hypothesis: two-sided
```

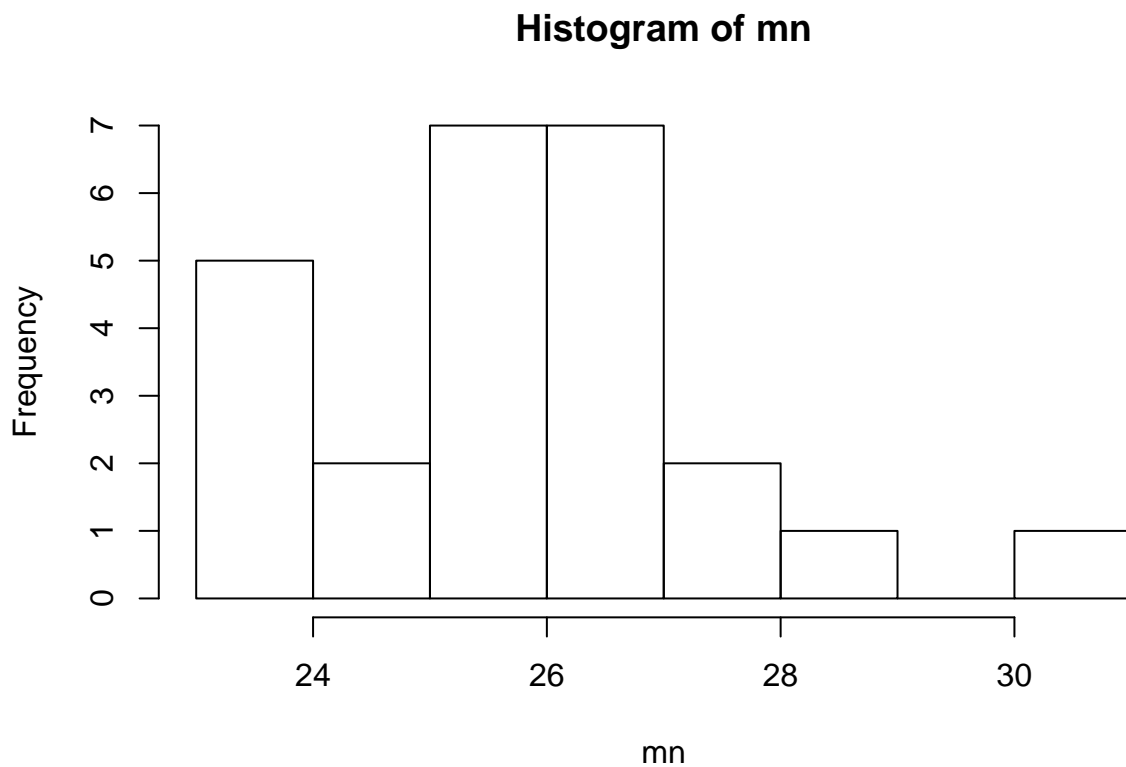
```
mean(mn)
```

```
## [1] 25.82532
```

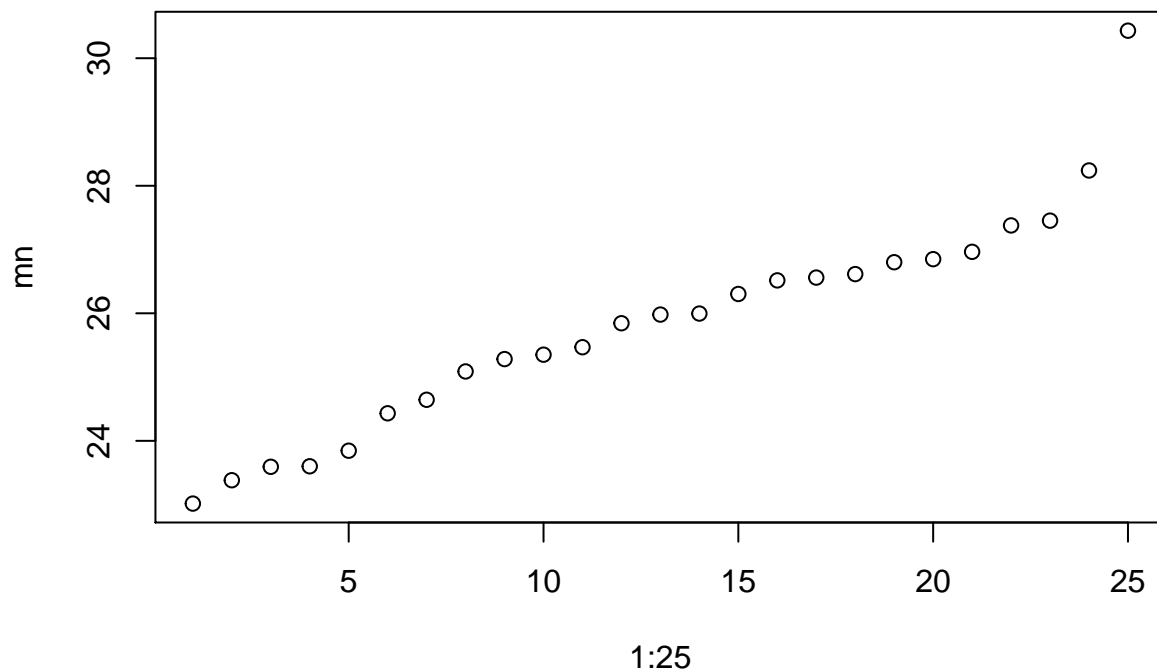
```
var(mn)
```

```
## [1] 2.898906
```

```
hist(mn)
```



```
qqplot(1:25,mn)
```



Given the p value of KS test being 0.285, we fail to reject the null hypothesis that the data from maybe_normal.txt is normally distributed.

Problem 3

```
X = read.table("maybe_same_1.txt")
```

```
## Warning in read.table("maybe_same_1.txt"): incomplete final line found by
## readTableHeader on 'maybe_same_1.txt'
```

```
X<-c(X[1,],X[2,],X[3,],X[4,],X[5,])
```

```
X<-as.numeric(X)
```

```
Y = read.table("maybe_same_2.txt")
```

```
## Warning in read.table("maybe_same_2.txt"): incomplete final line found by
## readTableHeader on 'maybe_same_2.txt'
```

```
Y<-c(Y[1,],Y[2,],Y[3,],Y[4,],Y[5,])
```

```
Y<-as.numeric(Y)
```

```
X2<-X+2
```

```
ks.test(X, Y)
```

```
## Warning in ks.test(X, Y): cannot compute exact p-value with ties
```

```
##
```

```
## Two-sample Kolmogorov-Smirnov test
```

```
##
```

```
## data: X and Y
```

```
## D = 0.25, p-value = 0.491
```

```
## alternative hypothesis: two-sided
```

```
ks.test(X+2, Y)
```

```
## Warning in ks.test(X + 2, Y): cannot compute exact p-value with ties
```

```
##
```

```
## Two-sample Kolmogorov-Smirnov test
```

```
##
```

```
## data: X + 2 and Y
```

```
## D = 0.65, p-value = 0.0001673
```

```
## alternative hypothesis: two-sided
```

Given the p value of KS test between X and Y being 0.491, we fail to reject the null hypothesis that X and Y are from the same distribution.

The p value of KS test between X+2 and Y is 0.0001673, it is likely we could reject the null hypothesis that X+2 and Y are from the same distribution.

Problem 4

```
NS <- readRDS("norm_sample.Rdata")
```

```
NS <- as.data.frame(NS)
```

```
colnames(NS) <- "x"
```

```
NS_d <- ecdf(NS$x)
```

```
NS$ecdf <- NS_d(NS$x)
```

```
NS$nm <- pnorm(NS$x)
```

```
NS$D <- NS$ecdf - NS$nm
```

```
max(abs(NS$D))
```

```
## [1] 0.1372427
```

```
ks.test(NS$x, "pnorm", 0, 1)
```

```
##
```

```
## One-sample Kolmogorov-Smirnov test
```

```
##
```

```
## data: NS$x
```

```
## D = 0.17724, p-value = 0.3683
```

```
## alternative hypothesis: two-sided
```

The calculated D value is 0.137, the KS test D value is 0.177. From the test, we fail to reject the null hypothesis that the normal sample data is normally distributed.

Problem 5

fujiquakes

```
FJ <- read.table("fujiquakes.dat", header = T)
```

```
FJ_d <- ecdf(FJ$mag)
```

```
# 95% CI for F(4.9) - F(4.3)
```

```
CI<-sum((FJ$mag<=4.9) & (FJ$mag>4.3))
```

```
binconf(CI,length(FJ$mag),method="wilson",0.05)
```

```
## PointEst      Lower      Upper
```

```
##      0.526 0.4950118 0.5567892
```

faithful

```
FF <- read.table("faithful.dat", header = T, skip = 25)
f_d <- ecdf(FF$waiting)
# 90% confidence interval for mean
m <- mean(FF$waiting)
se <- sd(FF$waiting)/sqrt(length(FF$waiting))
print(paste0("90% CI for mean waiting time is [",
             round(m-1.64*se,2),", ", round(m+1.64*se,2),"]"))
```

```
## [1] "90% CI for mean waiting time is [69.55, 72.25]"
```

```
# median waiting time
summary(f_d)
```

```
## Empirical CDF:      51 unique values with summary
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   43.00  56.50   70.00   69.67  82.50   96.00
```